

## ADDENDUM to the ICOM8 Program

### I. ADDITIONS TO THE PROGRAM

**A. Poster Session 1b:** Role of mycorrhizal networks for individuals, communities and ecosystems; **Monday, August 3, 1:00-1:50 PM**

#### PS 1-71

**Mycorrhizal status of northern highbush blueberry (*Vaccinium corymbosum* L.) on the Ljubljana Marshes nature reserve area**

ŠIBANC, N.<sup>1,2</sup>, Palčič, T.<sup>1</sup>, and I. Maček<sup>1,2</sup>

<sup>1</sup>University of Ljubljana, Biotechnical Faculty, Department of Agronomy, Slovenia;

<sup>2</sup>University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies, Slovenia, natasa.sibanc@bf.uni-lj.si

**Abstract:** Northern highbush blueberry (*Vaccinium corymbosum* L.) plantations are rapidly spreading on the Ljubljana Marshes nature reserve area. Conditions are suitable for blueberry productivity, including acidic peat soil, high groundwater level and suitable climate. Despite the fact that this is a protected area there is no data on the diversity and seasonal dynamics of communities of ericoid mycorrhizal fungi in plantations of blueberries on the Ljubljana Marshes or the potential input of the non-indigenous fungi into this system with the newly imported seedlings. Furthermore, there is no data on how different agri-techniques, such as fungicide treatment, affect ericoid mycorrhizas on blueberry. We sampled blueberry roots of the newly imported seedlings, and in two plantations aged 18 and 30 years in October 2013, and in April and June 2014 to study the seasonal dynamics of ericoid mycorrhizal fungal communities in this area. Roots were inspected for mycorrhizal colonization and DNA was extracted from homogenized dried roots, followed by PCR using ITS1F and ITS4R primers and preparation of ITS rRNA clone libraries. We predict that increasing age of blueberry plantations results in an increase in species richness of ericoid mycorrhizal fungi. Our data have already shown that the new seedlings, imported from a producer in Italy, are not mycorrhizal and are therefore not a source of potentially new fungal taxa. This work will contribute to describing diversity of ericoid mycorrhizal fungi and the seasonal dynamics of their communities for the first time in the Ljubljana Marshes reserve area and also in Slovenia.

**B. Poster Session 2b:** Strategies to preserve and restore mycorrhizas for sustainable forestry; **Tuesday, August 4, 1:00-1:50 PM**

#### PS 2-32B

**Does nursery management practice influence root associated fungal community? A case study of Scots pine (*Pinus sylvestris* L.) seedlings**

Rudawska, M.<sup>1</sup>, M. Pietras<sup>1</sup>, T. LESKI<sup>1</sup>, L. Tedersoo<sup>2</sup>, M. Bahram<sup>2</sup> and H. Kwaśna<sup>3</sup>

<sup>1</sup>Institute of Dendrology of the Polish Academy of Sciences, 5 Parkowa Str., 62-035 Kórnik, Poland, mariarud@man.poznan.pl; <sup>2</sup>Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia;

<sup>3</sup>Department of Forest Pathology, Poznań University of Life Sciences, Poznań, Poland

**Abstract:** Nursery managers have long recognized the importance of well-developed mycorrhizas for healthy seedling growth in the nursery and desired performance after outplanting. However, it is still unclear if intensive and long lasting nursery practices (fertilization, irrigation, and mechanical and chemical weed and pest control) influence the diversity of root-associated fungal communities. The objective, therefore, was to evaluate the composition of fungal communities inhabiting Scots pine seedling roots and surrounding bulk soil in bare-root forest nurseries in Poland that have been under cultivation for 20, 40, and 60 years. Naturally regenerated pine seedlings originating from clear-cuts of nearby forests were used as a reference. We used next-generation sequencing (454 pyrosequencing) to determine whether the composition of fungal communities (saprotrophic, pathogenic, mycorrhizal) differed among three forest bare-root nurseries. A special emphasis in our studies has been on ectomycorrhizal (ECM) fungi. In total,

917 operational taxonomic units (OTUs) of fungi have been obtained from root and soil samples. The number of OTUs from the nursery samples (580) were very similar to that obtained from clear-cuts (585). Among those, 46 and 52 ECM fungal OTUs were found exclusively from nursery or clear-cut samples, respectively, and 45 were common to both sample types. Unexpectedly, the number of overall fungal (293-320) and ECM OTUs (44-47) were very similar among nurseries of different ages. The most abundant OTUs detected in forest nurseries belonged to the *Russula-Lactarius*, *Amanita*, *Inocybe*, *Tomentella-Thelephora*, *Meliniomyces*, *Wilcoxina*, and *Terfezia-Peziza* lineages. *Suillus-Rhizopogon* OTUs were found exclusively in nurseries and *Elaphomyces* OTUs were found in clear-cuts. In conclusion, this study highlights, for the first time through 454 pyrosequencing, the richness and diversity of the fungal communities in forest nurseries and demonstrate that even long lasting silvicultural practices in the nursery do not lead to the impoverishment of the ECM community.

## **C. Poster Session 4a: Mycorrhizas and Global Change; Friday, August 7, 1:00-1:50 PM**

### **PS 4-32B**

#### **Variation in arbuscular mycorrhizal fungal communities in alpine steppe along a precipitation gradient on the Tibetan Plateau**

**ZHANG, J.**<sup>1</sup>, B. Ji<sup>2</sup> and X. Cui<sup>1</sup>

<sup>1</sup>College of Life Sciences, University of Chinese Academy of Sciences, Beijing 100049, China

<sup>2</sup>College of Forestry, Beijing Forestry University, Beijing 100083, China

**Abstract:** As the Earth's third pole, the Tibetan Plateau represents one of the largest and most unique habitats for various forms of organisms including arbuscular mycorrhizal fungi (AMF). By forming symbiotic relationships with most plants, AMF are potentially important for the establishment and stability of grassland communities on the Plateau. However, little is known about the community composition of AMF or how AMF respond to environmental factors in this harsh environment. This study tested if water availability influenced the spatial distribution of AMF communities at a regional scale as precipitation varies substantially along the alpine steppe on the Tibetan Plateau. Samples were taken from five sites along a 1000-km transect of alpine steppe in which precipitation increased from 100 mm to 400 mm eastwardly, and the altitude varied from 4400 to 4800 m a.s.l. Roots and rhizosphere soils were collected under three dominant species, *Stipa purpurea*, *Potentilla bifurca* and *Leontopodium nanum*. AMF richness and community composition were assessed by PCR amplification of 18S rRNA genes, cloning, sequencing and phylogenetic analyses. A total of 34 AMF phylotypes were identified from rhizosphere soils based on 2294 clones. They belonged to eight genera in six families, including *Glomus*, *Diversispora*, *Claroideoglomus*, *Paraglomus*, *Rhizophagus*, *Funneliformis*, *Archaeospora*, and *Ambispora*. The dominant genera were *Glomus* and *Diversispora*, representing approximately 34% and 33% of the total clones respectively. *Claroideoglomus* accounted for 22% of the clones. AMF community composition varied significantly among sites, and AMF diversity decreased with the reduction of precipitation. AMF phylotype richness was higher in rhizosphere soils than in roots for all three plant species, whereas AMF community composition did not vary among host plant species. Our preliminary results suggested that at a regional scale water availability could drive the changes of AMF communities in alpine steppe on the Tibetan Plateau.

## **II. CHANGES IN DAY OF PRESENTATION**

A. **PS 2-32C** Cuong, B.V. and **P. FRANKEN** - *Acclimatization of arbuscular mycorrhizal fungi to heavy metal stress*, **Tuesday, August 4, 2015, 1:00-1:50** (Formerly PS 3-31, Thursday, August 6, 2015)

B. **PS 4-85 SRIVASTAVA, S.**, D. Cahill and A. Adholeya - *Mycorrhiza as an elicitor for rosmarinic acid in a co-culture system with hairy roots of Ocimum basilicum*, **Friday, August 7, 2015** (Formerly PS 2-56, Tuesday, August 4, 2015)

## **III. CANCELLED PRESENTATIONS**

A. **Monday, August 3, 2015**

**PS 1-49 LI, A.R.**, K.Y. Guan, X.L. Sui, X.Y. Huang, Y. Chen, R. Stonor, S.E. Smith and F.A. Smith - *AM fungi in roots of hemiparasitic Pedicularis: friends or foes?*

**B. Tuesday, August 4, 2015**

**PS 2-20 CHAUBEY, O.P.**, Priyanka Bohre, Jamaluddin and G. Krishnamurthy - *Restore mycorrhiza for sustainable forestry*

**C. Thursday, August 6, 2015**

**PS 3-22 BAHER, N.** - *Protective effect of AM fungi on nitrogen fixation and proline molecule as a stress signaling in chickpea nodules under saline condition*

**PS 3-34 JACH-SMITH, L.C.** and R.D. Jackson - *N fertilizer effects on arbuscular-mycorrhizae fungi abundance and function in a perennial grass cropping system*

**D. Friday, August 7, 2015**

**PS 4-81 SAMBODO, C.**, F.E. Astanti and Sukarsono - *Ectomycorrhizal garden as fruiting body provider*

## ICOM 8 Paper and Poster Abstracts

Abstracts are organized alphabetically by presenting author.

### LT 3-6 Response of arbuscular mycorrhizal fungi to defoliation of ryegrass (*Lolium rigidum*) as a function of soil depth

Fan, J.W.<sup>1,2</sup>, Z.M. Solaiman<sup>2</sup>, B.S. Mickan<sup>2</sup>, Y.L. Du<sup>1</sup>, F.M. Li<sup>1</sup> and L.K. ABBOTT<sup>2</sup>

<sup>1</sup>Institute of Arid Agroecology, Lanzhou University, Lanzhou, China; <sup>2</sup>School of Earth and Environment, The University of Western Australia, Crawley, 6009, Australia, Lynette.Abbott@uwa.edu.au.

**Abstract:** Grazing can alter abundance and diversity of arbuscular mycorrhizal (AM) fungi. We investigated how defoliation influenced mycorrhiza formation in relation to soil depth. Mycorrhizas were assessed in simulated pasture swards of ryegrass (*Lolium rigidum* cv. Wimmera) grown for six months in a glasshouse. Defoliation was imposed at two frequencies throughout the growing period and control plants were not defoliated. The sward was grown in soil from an annual pasture in southwestern Australia with a naturally occurring community of AM fungi. Mycorrhizas were assessed in three layers of the soil profile (0-5, 5-10, 10-15 cm). The three defoliation treatments were compared for their effects on several root traits (root length, root mass, specific root length), nutrient uptake, concentration of soluble carbon and soil microbial biomass in rhizosphere and bulk soil, and mycorrhiza formation (% root length colonized, root length colonized, relative abundance of dominant AM fungal morphotypes). The proportion of roots colonized by AM fungi increased with increasing defoliation frequency, regardless of soil depth. In contrast, the length of root colonized by AM fungi decreased with defoliation, most markedly below 5 cm. Within sections of root colonized by one of the two dominant morphotypes of AM fungi, the occurrence of vesicles decreased with increasing defoliation frequency at each soil depth. The pattern of vesicle abundance in roots colonized by this morphotype corresponded with the concentration of soluble carbon and microbial biomass carbon in the rhizosphere and bulk soil. Overall, more vesicles were present when soluble carbon was higher, indicating that vesicle formation by this fungus was limited by the availability of soluble carbon. Effects of defoliation on both the proportion of roots colonized by AM fungi and the length of roots colonized could have implications for mycorrhiza function as well as for mycorrhiza formation from season to season.

### PS 4-1 Impact of soil stockpiling on distribution and diversity of arbuscular mycorrhizal fungi

ADELEKE, R.A.<sup>1,2</sup> and C. Nwangburuka<sup>1,3</sup>

<sup>1</sup>Microbiology and Environmental Biotechnology Research Group, ARC-Institute for Soil, Climate and Water, Pretoria, South Africa, adeleker@arc.agric.za; <sup>2</sup>Environmental Sciences and Management (Subject Group: Microbiology), North-West University, Potchefstroom Campus, Potchefstroom, South Africa; <sup>3</sup>Department of Agronomy, Babcock University Ogun state, Nigeria.

**Abstract:** Arbuscular mycorrhizal (AM) fungi are an integral part of a functional terrestrial ecosystem because of their influence on nutrient cycling and plant responses to stress. We assessed the AM fungal distribution in a selection of stockpiled soils excavated during opencast mining activities in the Mpumalanga province of South Africa. There is ample evidence that top soil stripping during stockpiling activities alters most soil physical properties leading to a decline in soil biological status and organic matter in reclaimed systems. To accommodate natural soil variation across the coal mining areas of the Highveld, a number of stockpile study sites (three) were established at various coal mines. Research sites included Kleinkopje (Mine A), Dorstfontein (Mine B) and Klipspruit (Mine C). For each of these sites, control sites (agricultural farmland) were identified for sample collection and analyses. At each site, sampling of stockpiled topsoil and subsoil was carried out. Stockpiled soils across the mine fields were then characterised for their AM diversity. To capture the diversity of AM fungi present in maize fields, we established trap cultures for each individual field sampling point as well as their controls, using maize plants to bait AM fungi and support their sporulation under shared conditions of a climate controlled greenhouse. We were able to investigate stockpiled-influenced diversity patterns. We found irregularities in the AM fungal taxon abundances. There was no consistency in abundance and distribution across the various topsoil and subsoil. Our results therefore suggest that species distribution and diversity were significantly affected by soil stockpiling.

ADHOLEYA, A.<sup>1</sup>

<sup>1</sup>The Energy and Resources Institute, D S Block, Lodi Road, New Delhi, India, Adholeya1@gmail.com.

**Abstract:** Seed treatment with pesticides and biological agents is used widely to improve seed vigor and promote consistent germination. The use of AMF for seed treatment has been much less well explored. This is primarily attributed to the complexity of the interactions of AMF with other biologicals and chemicals applied to the seed coat. The impact of seed treatments with fungicides and insecticides on AMF was evaluated in a series of experiments. Chemical treatments of seeds reduced the ability of AMF to colonize emerging roots. Various formulations and application methods revealed that seed priming and encapsulation can promote AMF colonization and increase nutrient acquisition by selected crops.

**Field response of *Cucumis sativus* to a combination of arbuscular mycorrhizal fungi, vermicompost, and different fertilization doses**

PS 3-20 AGUILAR, D.T.<sup>1</sup>, L.L. Capistrán<sup>1</sup>, J. Banuelos<sup>1</sup> and D.S. Hernández<sup>1</sup>

<sup>1</sup>Universidad Veracruzana, Lomas del Estadio S/N, Zona Universitaria, CP 91000, Xalapa, Veracruz, México, doratrejo@gmail.com.

**Abstract:** Crop production usually employs inorganic fertilizers at ever increasing costs. It has been estimated that for cucumber production utilizing 500 kg/ha of fertilizer, this input represents 25% of the total production costs. Moreover, application of inorganic fertilizers in monocultures for more than 10 years has resulted in soil acidification and reduction in soil fertility. Arbuscular mycorrhizal fungi (AMF) are a potential biological alternative to reduce this impact. Therefore, a field study was conducted to compare cucumber response to two fertilizer rates, with and without vermicompost, and with and without AMF inoculation. The experiment was a factorial design with randomized blocks, eight treatments, and four replicates (factor 1 - AMF, factor 2 - vermicompost, factor 3 - 2 rates of fertilizer). The evaluated parameters were: AMF root colonization, plant height, number of flowers, number of fruits, yield in two harvests, shelf life, firmness, cucumber length, diameter, circularity, width, size, area, and perimeter. We found significant differences due to the AMF treatment for most of the fruit parameters assessed. The additive effect of the AMF and 50% of the fertilizer, promoted a higher number of flowers. There were no differences in yield in the AMF-50% fertilizer and vermicompost compared to the controls. We observed that the addition of AMF could reduce the application of inorganic fertilizer.

**PS 2-34 No response of maize mycorrhizas to herbivory by *Spodoptera frugiperda***

AGUILAR-AGUILAR, R.<sup>1,2</sup>, Y. Carreon Abud<sup>2</sup>, E. del Val de Gortari<sup>1</sup> and J. Larsen<sup>1</sup>

<sup>1</sup>Research Institute of Ecosystems and Sustainability, National Autonomous University of Mexico, Morelia 58190 Mexico, aguilaricardo@hotmail.com; <sup>2</sup>Faculty of Biology, University of Michoacan San Nicolas de Hidalgo, Morelia 58030, Mexico.

**Abstract:** Response of maize mycorrhizas to fertilization, plant genotype, and insect herbivory by the fall armyworm (*Spodoptera frugiperda*) was examined in a growth chamber pot experiment with a randomized factorial design. The main factors studied included 1) maize genotype (landrace and hybrid), 2) fertilization (mineral and vermicompost), and 3) *S. frugiperda* (with and without). Each of the eight treatments had six replicates for a total of 72 experimental units. Plants were grown in an agricultural soil from a maize field mixed with sand (1:1, w/w). Fertilizer, in terms of minerals (full) and vermicompost (10%, v/v), was added to the soil prior to sowing. Four weeks after sowing, five *S. frugiperda* larvae (stage L3) were applied to the plants. All plants were then covered with a white transparent cloth to maintain the larvae in their respective treatments. Insects were left feeding for ten days, and then plants were harvested. Variables measured included shoot and root dry mass, arbuscular mycorrhizal fungi (AMF) root colonization, *Pythium* root infection, and biomass and length of *S. frugiperda* larvae. Insect herbivory caused total foliage damage independent of maize genotype and fertilization. The highest biomass of *S. frugiperda* larvae was found in association with fertilized plants.

Herbivory had no effect on AMF root colonization, but increased root infection by the oomycete pathogen *Pythium* sp. in roots of landrace maize occurred in combination with vermicompost. In conclusion, our results indicate that maize mycorrhizas may maintain their photosynthate sink strength despite the complete foliar damage caused by insect herbivory.

**PS 4-57 Morphotaxonomic, fatty acid methyl esterase profiling and rDNA sequence based characterization of arbuscular mycorrhiza fungi obtained from arid and semi-arid regions of India**

**AHUJA, P.<sup>1</sup>**, K. Sunar<sup>1</sup>, B. Sashidhar<sup>1</sup>, M. Ghorui<sup>1</sup> and A. Adholeya<sup>1</sup>

<sup>1</sup>Centre for Mycorrhiza Research, Biotechnology and Management of Bioresources Division, The Energy and Resources Institute (TERI), New Delhi, India, priya.ahuja@teri.res.in.

**Abstract:** The occurrence and diversity of arbuscular mycorrhiza fungi (AMF) associated with plants growing in west and northwest regions of India was investigated. A total of 171 trap cultures were raised from eighteen regions of (West) Gujarat and 23 trap cultures from three regions of (North-West) Rajasthan. Trap cultures were screened for abundance of AMF spores and monosporals were raised with *Sorghum bicolor* as the host plant. A total of 447 monosporal cultures were obtained from all these regions. A multiple approach for species identification comprised of light and scanning electron microscopy based morphotaxonomic analysis, Fatty Acid Methyl Ester (FAME) profile based biochemical profiling and nuclear encoded ITS-LSU based molecular identification was carried out. Morphological studies of AMF showed globose, subglobose, ovoid, oblong, and irregular shapes of the spores. The colour of the spores ranged from hyaline, orange, pale yellow to yellow brown with spore size ranging from 60-260 µm. Morphological characters were found to be unique within certain genera and families. FAME profiles showed that all the AMF spores contain marker fatty acid C 16:1 (C-9) as well as other 27-30 different fatty acids among which seven of them were common to most of the genera. The n-rDNA sequences containing the ITS-LSU sequences were used to confirm the identity of the AMF isolates through BLAST analysis and phylogenetic studies. Characterization of these cultures enumerated a variety of species like *Glomus etunicatum*, *Funneliformis mossae*, *Rhizophagus irregularis*, *Funneliformis coronatum*, *Acaulospora* sp., and *Paraglomus* sp. Among all the AMF isolates *Glomus etunicatum* and *Funneliformis* sp. were the dominant species. Diversity of AMF in our study suggests that this could be an opening point for the development of well performing and adapted inocula suitable for crop improvement in arid and semiarid regions.

**PS 4-58 Application of arbuscular mycorrhizal fungi for cultivation of aromatic plant *Cymbopogon flexuosus* in alkaline soils of Uttar Pradesh, India**

**AKHTAR, O.<sup>1</sup>**, H.K. Kehri<sup>1</sup> and V. Khare<sup>1</sup>

<sup>1</sup>Department of Botany, University of Allahabad, Allahabad, U.P., 211002, India, ovoidakhtar@gmail.com.

**Abstract:** Essential oils are in constant demand all over the world and constitute an important sector of trading in the international market. In most of the developing countries, including India, the commercial cultivation of aromatic plants is now focused on marginal lands, which are lying fallow at present. One of the important categories of such soil is alkaline soil that occupies an extensive area in the Indo-Gangetic plains of northern India. However, poor physical property, high pH, high ESP, and accumulation of CO<sub>3</sub><sup>2-</sup> and HCO<sub>3</sub><sup>-</sup> ions of the soil render it inhospitable for normal crop production. Application of arbuscular mycorrhizal (AM) fungi seems to be a promising option. In view of the above-stated facts, the present study has been planned to explore the potential for indigenous AM fungi to improve the establishment, survival, and performance of the aromatic plant *Cymbopogon flexuosus* in alkaline soil. A pot experiment has been conducted with four different treatment series using a complete randomized design under greenhouse conditions. Data on growth, and microbiological and physiological parameters were recorded. Alkalinity adversely affected root/shoot biomass and essential oil production in *C. flexuosus*. Addition of AM fungi nullified the adverse effects of alkalinity to a greater extent, and improved the overall performance by providing nutritional, as well as non-nutritional benefits, like increased photosynthetic pigments and protein content, reduction in proline concentration, low permeability of the root plasma membrane, and increased antioxidant defense system by increasing catalase and ascorbate activity. Detailed results will be presented during conference proceedings.

## CS 4-1 An overview about the study of arbuscular mycorrhizal fungi under petroleum hydrocarbon-contaminated systems in Mexico

**ALARCÓN, A.**<sup>1</sup>, R. Ferrera-Cerrato<sup>1</sup>, A. Franco-Ramírez<sup>1</sup>, A. Hernández-Ortega<sup>1,2</sup>, M.E. Díaz-Martínez<sup>1</sup>, L.V. Hernández-Cuevas<sup>3</sup>, P.A. Quintanar-Isaias<sup>4</sup> and F.T. Davies Jr.<sup>5</sup>

<sup>1</sup>Departamento de Microbiología, Postgrado de Edafología, Colegio de Postgraduados, aalarconcp@gmail.com;

<sup>2</sup>Facultad de Ciencias Biológicas y Agropecuarias, Universidad de Colima; <sup>3</sup>Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, <sup>4</sup>Universidad Autónoma Metropolitana-Iztapalapa; <sup>5</sup>Department of Horticulture, Texas A&M University, USA.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are significant biological components in the rhizosphere, and can improve growth, nutrition, and adaptation of plants under stressful environmental conditions. Mexico is an important country for exploiting and producing oil byproducts and, as a consequence, these industrial activities represent a potential risk for soil contamination affecting plant growth and microbial diversity. Thus, studies focused on the ecology of AMF in soils chronically contaminated with petroleum hydrocarbons have demonstrated the presence of these fungi in the rhizosphere of grass species and citrus trees. Furthermore, the application of polycyclic aromatic hydrocarbons (PAHs), such as phenanthrene or benzo[a]pyrene, significantly diminished spore germination under *in vitro* conditions. Using mesocosms containing agricultural soil contaminated with several concentrations of crude oil during a 2-year study, it was determined that the AMF population (determined by the presence of spores) showed variation in the abundance and presence of AMF species. In addition, the benefits of AMF to plants used for phytoremediation of petroleum-contaminated soils demonstrated that these fungi enhanced some physiological responses such as photosynthesis and water use efficiency (e.g., *Lolium perenne*) and improved growth and nutritional status (e.g., *Melilotus albus*). Likewise, the inoculation of *Medicago sativa* with AMF resulted in attenuation of oxidative stress due to diesel contamination and improved root hydraulic conductance. Finally, the benefits of AMF during a phytoremediation process are also related to improved dissipation of diesel, crude oil, or PHA's (~20%) when inoculated alone or in combination with hydrocarbonoclastic bacteria or filamentous fungi such as *Cunninghamella elegans* or *Trichoderma* species.

## PS 1-1 Communities of arbuscular mycorrhizal fungi in five ecosystems at the Tlaloc Volcano, Mexico

Franco-Ramírez, A.<sup>1</sup>, L.V. Hernández-Cuevas<sup>2</sup>, **A. ALARCÓN**<sup>1</sup>, J.J. Almaraz<sup>1</sup>, J. Pérez-Moreno<sup>1</sup>, R. Ferrera-Cerrato<sup>1</sup>, F.J. Alvarez-Sanchez<sup>3</sup>, A.T. Chávez-Bárcenas<sup>4</sup> and S.L. Stürmer<sup>5</sup>

<sup>1</sup>Postgrado de Edafología, Colegio de Postgraduados, aalarconcp@gmail.com; <sup>2</sup>Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala; <sup>3</sup>Facultad de Ciencias, Universidad Nacional Autónoma de México;

<sup>4</sup>Facultad de Agrobiología "Presidente Juárez", Universidad Michoacana de San Nicolás de Hidalgo; <sup>5</sup>Departamento de Ciencias Naturais, Universidad Regional de Blumenau, Brazil.

**Abstract:** Ecological studies concerning the evaluation of richness and diversity of arbuscular mycorrhizal fungi (AMF) of temperate forests of Mexico are scant. This study evaluated the presence of AMF morphospecies of rhizosphere samples from five ecosystems from the Tlaloc Volcano (Estado de Mexico): agricultural sites (2626-2986 m a.s.l.), *Cupressus* forest (2771-2991 m a.s.l.), *Quercus* forest (2726-2991 m a.s.l.), *Abies* forest (3093-3489 m a.s.l.), and *Pinus* forest (3675-3935 m a.s.l.). AMF spores were extracted and identified from field samples, and from trap cultures after one and two years of propagation under greenhouse conditions, and identified through morphological analysis of spore walls. Species richness and diversity indices were calculated after species identification and spore counting, and presence-absence data were used for similarity analysis among vegetation types. Agricultural sites had the highest AMF richness (8 species from field samples), *Quercus* and *Pinus* forests showed the lowest values of AMF richness (5 and 4 species, respectively). Agricultural sites had the highest values of Shannon index (1.947) being statistically different from all other areas (1.7 for *Cupressus* forest to 1.3 for *Pinus* forest values) (Bootstrap analysis, p=5%). AMF species composition in field samples of *Cupressus* and *Quercus* forests were the most similar each other (0.54 Sorensen index value). Trap cultures increased the AMF richness in all vegetation types, being most favorable for *Cupressus*, agricultural sites, and *Abies*, which increased from 6 to 14 species, from 8 to 13 species, and from 4 to 9 species, respectively after two years; *Quercus* and *Pinus* had the lowest richness, from 5 to 6 species, and from 4 to 5 species each. Richness increased after AMF propagation. AMF communities from each type of vegetation of Tlaloc Volcano have particular properties and assemblages of AMF species, even after analysis.



**AL-BARAKAH, F.N.<sup>1</sup>** and M.A.U. Mridha<sup>1</sup>

Soil Science Department, College of Food and Agricultural Sciences, King Saud University, P. O. Box. 2460 Riyadh 11451, Saudi Arabia, barakah@ksu.edu.sa.

**Abstract:** *Sesbania bispinosa* (Jacq.) W.F. Wight, a tropical legume plant was grown under greenhouse conditions in calcareous soils collected from different locations with different types of vegetation to study the infectivity of arbuscular mycorrhizal fungi (AMF). Soil samples were collected from seven locations (Al-Khabia, Al-Khararah, Al-Ghat, Dirab, Huraymila, Thumamah, and Umm Al Khappas) for the present study. The seeds of *Sesbania* were sown in soils kept in replicated plastic pots containing 1 kg of soil. The roots and soil samples were collected after 30, 45 and 60 days of growth to record the infectivity of arbuscular mycorrhizal fungi (AMF). The total colonization with mycelium, as well vesicular and arbuscular colonization varied among locations. AMF infectivity began after 30 days of growth and increased up to 60 days of growth in all the soils. Increases in vesicles and arbuscules were recorded with increased age of the plants also. The highest percentage of vesicles was observed after 60 days of growth and it was varied among the soils from different locations. The same trend was followed in case of arbuscular colonization. The structural colonization was recorded to highlight the importance of colonization and it was also varied with location and age of the plants. The diversity of AMF spore populations was recorded and mostly different types of *Glomus* spp. were found from the soils. It was concluded from the present study that *Sesbania* plants may be introduced in calcareous soils of Saudi Arabia as mycotrophic green manure plants for sustainable agriculture in Saudi Arabia.

**PS 1-2 Changes in ectomycorrhizal fungal community composition and diversity along a two-million year coastal dune chronosequence in a biodiversity hotspot**

**ALBORNOZ, F.E.<sup>1</sup>**, F.P. Teste<sup>1,2</sup>, H. Lambers<sup>1</sup>, M. Bunce<sup>4</sup>, D.C. Murray<sup>4</sup>, N.E. White<sup>4</sup> and E. Laliberté<sup>1,3</sup>

<sup>1</sup>School of Plant Biology, The University of Western Australia, 35 Stirling Highway, Crawley (Perth), WA 6009, Australia, felipe.albornozramirez@research.uwa.edu.au; <sup>2</sup>Grupo de Estudios Ambientales, IMASL-CONICET & Universidad Nacional de San Luis, Avenida Ejercito de los Andes 950, San Luis 5700, Argentina; <sup>3</sup>Institut de Recherche en Biologie Végétale, 4101 Sherbrooke Est, Montréal, QC H1X 2B2, Canada; <sup>4</sup>Trace and Environmental DNA (TrEnD) Laboratory, Department of Environment and Agriculture, Curtin University, Perth, Western Australia 6102, Australia.

**Abstract:** Ectomycorrhizal (ECM) fungi enhance plant nitrogen (N) and phosphorus (P) acquisition. During long-term soil and ecosystem development, plant growth shifts from being N-limited to P-limited. However, how community composition and diversity of ECM fungi change during ecosystem development remains unknown. We studied ECM communities and diversity along a two million year Australian dune chronosequence, which shows a clear shift from N- to P-limitation of plant growth with increasing soil age. We hypothesised that ECM community composition strongly varies along the chronosequence, reflecting soil properties, and that diversity increases during pedogenesis. We grew two ECM plant species in soils collected from five distinct chronosequence stages, and quantified ECM operational taxonomy units (OTU) and diversity on roots using next-generation sequencing. To distinguish changes in ECM community composition due to soil properties vs ECM inoculum, we used three soil treatments: i) unaltered soil from each stage (“as is”), ii) triple-pasteurised, mixed soil from all five stages, with addition of live soil inoculum from each particular stage (“specific inoculum”), and iii) triple-pasteurised soil from particular stages, with addition of mixed live inoculum from all five stages (“average inoculum”). We obtained 175 unique ECM OTUs. ECM differed considerably among chronosequence stages in the “as is” treatment, and these differences were associated with shifts in soil pH and nutrients. Furthermore, OTU richness declined with soil age in the “as is” treatment. In contrast, there were no differences in ECM community composition or richness in the other two soil treatments. We suggest that strong changes in ECM community composition and diversity along this chronosequence do not simply reflect differences in soil abiotic properties or ECM inoculum, but reflect complex long-term interactions between these factors. Finally, we surmise that the decline in OTU richness is due to few ECM species being effective at acquiring P from severely P-impooverished soils.



### LT 3-7 Effects of coffee farm management practices on arbuscular mycorrhizal fungal communities

**ALDRICH-WOLFE, L.<sup>1</sup>**, R.J. Asheim<sup>1</sup>, K.L. Black<sup>1</sup>, E.D.L. Hartmann<sup>1</sup>, P.G. Johnson<sup>1</sup>, R.D. McGlynn<sup>1</sup>, S.J. Redmond<sup>1</sup>, L.C. Schmaltz<sup>1</sup> and W.G. Shivega<sup>1</sup>

<sup>1</sup>Biology Department, Concordia College, Moorhead, Minnesota 56562 USA, laldrich@cord.edu.

**Abstract:** The majority of crops are cultivated on farms that fall along a continuum from conventional to organic management, and coffee is no exception. How do differences in management affect mycorrhizal associations? What are the long-term consequences for soil fertility? We sought to address the first question by comparing management practices and their effects on soil parameters, including coffee root colonization and species richness of arbuscular mycorrhizal (AM) fungi, for 25 coffee fields in two regions of Costa Rica. Four factors consistently differed between conventionally-managed and organic fields: shade, shade tree diversity, leaf litter, and available nitrate in the soil. Organic fields had more than twice as many shade tree species, twice as much shade, nearly twice as much leaf litter, and one-third as much soil nitrate as conventional fields. Root colonization by AM fungi declined with elevation. Consequently, root colonization was higher in coffee from organic fields than in coffee from conventional fields, but only in the lower elevation coffee-growing region. Root colonization was positively correlated with aspects of tree cover (shade, leaf litter, tree richness) and negatively correlated with soil nitrate availability. Species richness of spores of AM fungi did not differ between organic and conventional farms. However, our study of coffee root fungi in these fields using high-throughput sequencing of the internal transcribed spacer (ITS) region of ribosomal DNA found negative correlations of richness with soil nitrate and phosphorus availability, and positive correlations of richness with aspects of tree cover. Our results suggest, to the extent that root colonization by AM fungi is important for coffee production and richness of AM fungi is important for long-term soil fertility, that coffee farms managed for tree species diversity, soil cover, and minimal additions of nitrate, will maintain higher root colonization by and a greater diversity of AM fungi.

### SY 4-1 Impacts of nitrogen deposition and invasive species on arbuscular mycorrhizae and their functioning

**ALLEN, E.B.<sup>1</sup>**

<sup>1</sup>Department of Botany and Plant Sciences and Center for Conservation Biology, University of California Riverside, Riverside, CA 92521 USA, edith.allen@ucr.edu.

**Abstract:** Anthropogenic nitrogen (N) deposition and invasive species have major impacts on global biodiversity, along with land use change and climate change. Invasive species are causing vegetation-type conversion across the globe, sometimes driven by N deposition. They also have major impacts on mycorrhizal diversity and functioning, as observed in California coastal sage scrub, a Mediterranean-type shrubland. N deposition that originates from fossil fuel emissions and agriculture creates gradients downwind of sources of emission from high to low deposition. One gradient ranging from 20 to 8 kg N ha<sup>-1</sup>yr<sup>-1</sup> resulted in a soil gradient with 90 to 10 µg/g extractable N, and was assessed for arbuscular mycorrhizal fungi (AMF). The richness of AMF morphospecies increased along this gradient from 12 to 19 species, with a lower proportion of large-spored species in high-N soils. Both spore density and shrub root colonization increased along the N gradient. Invasive annual grass productivity also increased under elevated N, providing fuel for more frequent fires. A greenhouse experiment was done to assess the impacts of AMF inoculum from high and low N soils on the native shrub *Artemisia californica* and the exotic grass *Bromus rubens*. Invasive grasses are preferential hosts for the fine AMF *Glomus tenue* which is indifferent to elevated N in promoting host response, while native species host multiple species of coarse AMF that are poor mutualists under elevated N. *Artemisia* had a negative growth response to inoculum from high-N soils, while *Bromus* had a positive response, in part explaining the poor post-fire recruitment of *Artemisia* in high-N soils. Shifts in species composition and functioning of AMF may drive vegetation-type conversion from native shrubland to exotic grassland.

## LT 1-12 The response of fungal communities to nitrogen and phosphorus fertilization in a spruce forest

ALMEIDA, J.P.<sup>1</sup>, N. Rosenstock<sup>1</sup> and H. Wallander<sup>1</sup>

<sup>1</sup>Microbial Ecology Group, Department of Biology, Lund University, Ecology Building Sölvegatan 37 Lund-Sweden, jpalmeidava@gmail.com.

**Abstract:** Nitrogen (N) and phosphorus (P) are the two most important macronutrients in plant nutrition and ectomycorrhizal fungi are able to mineralize and transfer these nutrients to plants in exchange of photosynthetic carbon. The flux of N and P into the plants may vary depending on the mycorrhizal fungal community composition because ectomycorrhizal species differ in their abilities to mineralize and transfer N and P. A community composition analysis was performed in an experimental Norway spruce forests in southern Sweden using next generation sequencing. Fungal ingrowth mesh bags were placed in N and N plus P fertilization plots to evaluate fungal community composition changes in different fertilization regimes. Additionally, to test the influence of a P source, some mesh bags were amended with apatite (1%) and were compared with mesh bags filled with quartz. The statistical analysis showed that ectomycorrhizal communities in apatite mesh bags were significantly different from the communities in quartz mesh bags in the control and in the N treatment, but not in the N plus P treatment. Phosphorus fertilization in this treatment probably alleviated the P limitation, which impaired the response to the apatite addition. The ectomycorrhizal species *Boletus badius* was more abundant in the N treatment than in the control or the N plus P treatment. Additionally, *B. badius* was more abundant in mesh bags with apatite than in mesh bags with quartz in all fertilization treatments. Its increase in abundance in apatite mesh bags suggests that it may be more efficient in utilizing P from the apatite compared to other ectomycorrhizal fungal species. Ectomycorrhizal diversity did not show any clear pattern among the fertilization treatments, or between apatite and quartz mesh bags. Gene expression studies of P uptake will be conducted under controlled laboratory conditions with this species. Moreover, oxalic acid accumulation in mesh bags from the experimental plots will be used as a proxy for apatite weathering.

## PS 4-2 Role of arbuscular mycorrhizal fungi in mitigating abiotic salt stress in white lupine (*Lupinus termis* Forsik) via the modulation of antioxidant defense systems

Hashem, A.<sup>1</sup>, A.A. ALQARAWI<sup>2</sup>, E.F. Abd-Allah<sup>2</sup>, D. Egamberdieva<sup>3</sup> and M.S. Alwhibi<sup>1</sup>

<sup>1</sup>Department of Botany and Microbiology, Faculty of Science, King Saud University, Riyadh 11451, Saudi Arabia, alqarawi@ksu.edu.sa; <sup>2</sup>Department of Plant Production, Faculty of Food and Agricultural Sciences, King Saud University, Riyadh, Saudi Arabia; <sup>3</sup>Institute for Landscape Biogeochemistry, Leibniz Centre for Agricultural Landscape Research (ZALF), 15374 Müncheberg, Germany.

**Abstract:** Antioxidants protect plant organelles from oxidative damage caused by abiotic salt stress. In this study, we investigated the role of selected arbuscular mycorrhizal fungi (AMF) on the induction of acquired systemic resistance in white lupine (*Lupinus termis* Forsik) against the adverse impact of salinity (200 mM NaCl) via production of reactive oxygen species (ROS) and enzymatic as well as non-enzymatic antioxidants. The results indicated that salt stress increased the levels of malondialdehyde (MDA) and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>), however the usage of AMF resulted in decreased levels of both MDA and H<sub>2</sub>O<sub>2</sub>. Salinity caused substantial increases in both the enzymatic (glutathione reductase, catalase, superoxide dismutase, ascorbate peroxidase) and non-enzymatic antioxidants (monodehydroascorbatereductase, glutathione S-Transferase, dehydroascorbatereductase, glutathione, oxidized glutathione) of *L. termis*. The soil application of AMF had a positive impact on the oxidative system in salt stressed plants. In the absence of salt stress, AMF activated acquired systemic resistance, shifting the plant physiology towards anabolism. In conclusion, AMF could protect white lupine plants against the abiotic damage of salt and allow them to withstand its deleterious impact.

### PS 1-3 The origins of regional species pools among North American ectomycorrhizal fungi: mapping predictions based on alternative hypotheses

ALTWASSER, B.A.<sup>1</sup>, B.J. Pickles<sup>2</sup>, M.M. Hart<sup>1</sup> and J. Pither<sup>1</sup>

<sup>1</sup>Irving K. Barber School of Arts and Sciences, Department of Biology, University of British Columbia, Okanagan campus, 3187 University Way, Kelowna, BC V1V 1V7 Canada, brittany\_altwasser@hotmail.com; <sup>2</sup>Department of Forest Sciences, University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4 Canada.

**Abstract:** Research examining diversity patterns among ectomycorrhizal fungi (EMF) has begun to broaden its scope, from a long-standing focus on patterns within individual forest stands and landscapes, to a growing interest in variation across biogeographic extents. However, the emerging patterns are difficult to interpret, as we presently have a limited understanding of how richness and composition of regional species pools (RSPs) vary geographically, and more fundamentally, of how the RSPs of EMF originate. Here, we propose and explore alternative hypotheses about the origins of RSPs within North America, with the ultimate objective being to optimize future sampling efforts aimed at obtaining a more thorough and accurate accounting of how EMF diversity varies throughout the continent. We first provide an overview of the various local- to biogeographic-scale factors that have been hypothesized to influence EMF diversity. We then present maps that combine these factors in ways that reflect alternative hypotheses about the relative importance of processes acting on local versus regional spatial scales, and on short versus long temporal scales. Our maps therefore represent hypothesis-specific predictions about how RSP diversity should vary geographically within North America. Although qualitative, our analyses reveal potential “hotspots” of RSP diversity that reflect the geographical convergence of multiple processes (e.g., contemporary soil conditions, historical habitat) that are thought to enhance EMF diversity. We then compare our qualitative predictions to empirical observations, and assess how past sampling efforts intersect the prediction space of our alternative hypotheses. We conclude with a map depicting priority areas for future sampling within North America.

### LT 1-4 Diversity of ectomycorrhizal fungi from a Mexican tropical dry forest

ALVAREZ-MANJARREZ, J.<sup>1</sup> and R. Garibay-Orijel<sup>1</sup>

<sup>1</sup>Laboratorio de Sistemática y Ecología de Micorrizas, Instituto de Biología, UNAM, Tercer Circuito s/n, Ciudad Universitaria, C.P. 04510 México, D.F., México, julieta.micorriza@gmail.com.

**Abstract:** Most works about ectomycorrhizae are focused in temperate and boreal forests. The explorations in the tropics have been increasing in tropical rain forest, leaving behind the tropical dry forest (TDF) ecosystem, that cover 1048700 km<sup>2</sup> in the Neotropics. This study was made at the Chamela Biological Station (19° 30' N, 105° 03' W) in Jalisco, Mexico, where the principal ecosystem is the TDF. Our aim was to describe the diversity of ectomycorrhizal mushrooms either way by their sporocarps or ectomycorrhizae (ECM). All the sporocarps were sampled and below them we collected soil-cores. In total we sampled 29 ectomycorrhizal fungi sporocarps (*Tomentella*, *Tremelloscypha*, and *Thelephora*). The soil was sieved, and roots were revised with a stereomicroscope. All root tips with ECM appearance were characterized by morphotypes and their DNA was extracted. To recognize the mycobionts we amplified the ITS from ECM and sporocarps. The sequences were assembled to 97% similarity to form MOTUs, giving a total of 10 MOTUs and 9 unique sequences. The most abundant ECM was *Tremelloscypha* sp., *Thelephora versatilis*, and *Clavulina* sp. 1. The rarefaction analysis showed that we have not saturated the species accumulation curve yet. For the recognition of the phytobiont, we amplified the *rbcL* region from cpDNA. The molecular marker only resolved to family level and determined that Achatocarpaceae, Araliaceae, Fabaceae subfamilies Caesalpinioideae and Papilionoideae, Moraceae, Nyctaginaceae, Polygonaceae, and Sapotaceae presented ectomycorrhizal associations. Although Fabaceae is the most diverse family in the study site, this was not the main ectomycorrhizal host family. Preliminarily, our data suggest that in this ecosystem the ECM fungi have a strong host preference and specificity. Given that ECM hosts are scattered in the area, the ectomycorrhizal fungi distribute in small islands according to its host abundance and distribution.

**PS 2-16 Is the extraradical mycelium of arbuscular mycorrhizae related to biomass and osmotic potential changes in two species in a pasture derived from a tropical rain forest?**

**ÁLVAREZ-SÁNCHEZ, J.<sup>1</sup>**, A. Serrano-Ysunza<sup>1</sup>, I. Sánchez-Gallen<sup>1</sup> and N. Chavarría<sup>1</sup>

<sup>1</sup>Departamento de Ecología y Recursos Naturales, Facultad de Ciencias, Universidad Nacional Autónoma de México, javier.alvarez@ciencias.unam.mx.

**Abstract:** Tropical rain forest deforestation is a large-scale disturbance that has an impact on environmental conditions at different scales. Studies in the Los Tuxtlas forest (Veracruz, Mexico) confirm that temperature, humidity, and pH change across the border between cattle pastures and conserved forest, but it is not known how these changes modify arbuscular mycorrhizal fungi (AMF) functioning. Our main goal was to assess the response of tropical forest seedlings and their associated mycorrhizal fungi under water stress conditions, and to analyze the effects of the plant-fungi relationship of the fungal counterpart. Two tree species were selected, *Poulsenia armata* (shade tolerant) and *Trema micrantha* (light demanding), and grown in a cattle pasture for nine months. Prior to transplant, we applied one of two treatments, with or without (control) AMF inoculation. The previously inoculated plants of both species had the highest mean extraradical mycelium production, intraradical colonization, and osmotic potential ( $p < 0.05$ ). By the end of winter the hydric status of both plant species reached its lowest value, close to wilting point. The treatment  $\times$  collection time interaction was a significant factor ( $p < 0.05$ ) for relative growth rate and intraradical colonization of *P. armata*; the highest percent colonization values coincided to the lowest growth rates for this species. AMF inoculation assured tropical rain forest seedling performance under drastic environmental conditions before reaching a water stress threshold. After reaching the threshold, both plant and fungi had low functioning. This should be taken into account in order to improve the results of rain forest restoration strategies.

**PS 4-1 New Neotropical genera of ectomycorrhizal sequestrate *Boletaceae***

**AMSES, K.R.<sup>1</sup>**, T.F. Elliott<sup>2</sup>, M.E. Smith<sup>3</sup> and T.W. Henkel<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Humboldt State University, Arcata, California 95521 USA, kra20@humboldt.edu;

<sup>2</sup>Department of Biology, Warren Wilson College, Swannanoa, North Carolina 28167 USA; <sup>3</sup>Department of Plant Pathology, University of Florida, Gainesville, Florida 32611 USA.

**Abstract:** Ectomycorrhizal (ECM) fungi, and in particular sequestrate truffle-like forms, are poorly known from the Neotropics. In an effort to close this knowledge gap three new genera of hypogeous ECM “false truffles” will be presented from the tropical rainforests of Guyana. Collected in forests dominated by ECM trees in the leguminous genera *Dicymbe* and *Aldina*, and the endemic dipterocarp genus *Pakaraimaea*, these fungi are part of an assemblage of nearly 300 species of ECM fungi documented from these ectotrophic forests over eighteen years of sampling. A multi-locus molecular phylogenetic analysis indicates placement of these fungi within the *Boletaceae* (*Boletales*, *Agaricomycetes*, *Basidiomycota*) and informs their relationships with previously described epigeous and hypogeous boletes. Morphological features corroborate erection of the new genera. The mycorrhizal status of these fungi and their potential contributions to host tree dominance will be discussed.

**PS 4-3 Impacts of climate change factors on eucalypt ectomycorrhizal fungi**

**ANDERSON, I.C.<sup>1</sup>**, J.M. Plett<sup>1</sup>, B. Drigo<sup>1</sup>, K. Keniry<sup>1</sup>, F. Martin<sup>2</sup> and A. Kohler<sup>2</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, University of Western Sydney, Richmond NSW 2753, Australia, i.anderson@uws.edu.au; <sup>2</sup>INRA, UMR 1136 INRA-University of Lorraine, Interactions Arbres/Microorganismes, Laboratory of Excellence ARBRE, INRA-Nancy, 54280 Champenoux, France.

**Abstract:** We used a combination of controlled environment glasshouse and microcosm experiments to investigate the effects of elevated atmospheric CO<sub>2</sub>, temperature and drought on Australian forest soil fungi, including those that form ectomycorrhizal associations with eucalypts. *Eucalyptus saligna* and *E. sideroxylon* seedlings were grown in field soil and maintained for 5 months under sub-ambient (280 ppm), ambient (380 ppm) and elevated (640 ppm) atmospheric

CO<sub>2</sub> conditions at both 26°C and 30°C. Multivariate analyses of molecular data showed a significant ( $P < 0.035$ ) separation between fungal communities associated with the two different tree species and a clear separation between the communities from the 280, 400 and 640 ppm CO<sub>2</sub> treatments at 34°C. This response appeared to be plant-dependent at 280 and 400 ppm CO<sub>2</sub>, however, all 640 ppm CO<sub>2</sub> samples clustered together regardless of tree species. Interestingly, several of the key fungal species identified to respond strongly to the climate change factors were ectomycorrhizal fungi, including *Pisolithus* sp. We performed a subsequent microcosm experiment and used transcriptomics to investigate the response of *E. grandis* (for which a genome sequence is available) to colonization by different *Pisolithus* isolates under ambient (400 ppm) and elevated (650 ppm) CO<sub>2</sub>. Our data showed that *E. grandis* varies in its susceptibility to colonization by different *Pisolithus* isolates in a manner that is not predictable by geographic origin or the ITS-based phylogeny of the fungal partner. Further, elevated levels of CO<sub>2</sub> alter the receptivity of *E. grandis* to *Pisolithus*, which is correlated to a dramatic shift in the transcriptomic profile of the root. These data provide a starting point for understanding how future environmental change may alter the signalling between plants and their ectomycorrhizal partners and is a step towards determining the mechanism behind observed shifts in eucalypt-associated fungal communities exposed to elevated atmospheric CO<sub>2</sub>.

**PS 3-58 Inter- versus intraspecific variability in the arbuscular mycorrhizal (AM) symbiosis: can adaptation of AM fungi to their host contribute to reduce variability in plant growth response?**

**ANTUNES, P.M.**<sup>1</sup>, A.M. Koch<sup>2</sup>, H. Maherali<sup>3</sup>, J.N. Klironomos<sup>2</sup>, O. Pietrangelo<sup>1</sup>, J. Boudreau<sup>1</sup> and L. Sanderson<sup>1</sup>

<sup>1</sup>Department of Biology, Algoma University, Sault Ste. Marie, Ontario, P6B 2G4, Canada, antunes@algomau.ca;

<sup>2</sup>Department of Biology, University of British Columbia, Okanagan campus, Kelowna, British Columbia, V1V 1V7, Canada;

<sup>3</sup>Department of Integrative Biology, University of Guelph, Guelph, Ontario, N1G 2W1, Canada.

**Abstract:** Plant responses to arbuscular mycorrhizal (AM) fungi are highly variable. Here we examined, 1) whether AM fungal morphology and growth influence plant response and 2) whether adaptation to host can contribute to reduce plant growth variability in response to different AM fungal isolates. To address the first question, we grew 56 isolates comprising 17 genera and 6 Glomeromycota families in a common garden experiment with three plant host species. We found that, when averaged across species, a majority of the variation (>85%) in AM fungal morphological and growth traits was associated with divergences above the species level. In contrast, a majority of the variation in AM fungal effects on the average biomass of plant host species was associated with divergences among isolates within species (~70%). Despite this asymmetry in fungal morphology/growth and host biomass response, most AM fungi were mutualistic and plant biomass and AM fungal reproduction, assessed as spore volume, were positively correlated across the Glomeromycota. Our findings show that fungal morphology and growth traits are not necessarily good predictors of their effects on host biomass, but positive plant-fungal feedbacks can still contribute to maintaining this symbiosis as a mutualism. To address the second question, we first trained two AM fungal isolates for six months with each of two hosts. Each isolate inoculum started from a single spore. We allowed the establishment of a common mycorrhizal network between hosts while preventing root mixing using a double compartment system. Second, we conducted an experiment to test whether each isolate favoured the growth of its “trainer” host compared to the other host under two contrasting phosphorus regimes. Results will be presented at the conference. If adaptation of AM fungi to host symbiont is supported by our data, studies not taking this into account may be incorrectly estimating symbiotic effects.

**PS 3-21 Growth response of ají dulce (*Capsicum chinense*) to commercial *Glomus intraradices***

**APONTE-LÓPEZ, C.M.**<sup>1</sup>, M.J. Cafaro<sup>1</sup> and L. Wessel-Beaver<sup>2</sup>

<sup>1</sup>Biology Department, University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico 00680, carla.aponte@upr.edu;

<sup>2</sup>Crops and Agroenvironmental Sciences, University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico 00680.

**Abstract:** *Capsicum chinense* is widely cultivated in the Caribbean region. Most types are pungent, such as ‘Scotch Bonnet’ and ‘Habanero’. In Puerto Rico non-pungent types are preferred and referred to as “ají dulce” or sweet chili pepper. Sweet chili pepper is one of the main crops cultivated on the island and is consumed as part of the local cuisine. It is also known for being a good source of vitamins A, C, and E and for its antioxidant properties. Currently, in commercial agricul-



ture, the use of chemical fertilizers dominates the local market, while biological ones are overlooked. Symbiotic relationships between mycorrhizal fungi and the roots of vascular plants can serve as biological crop enhancers. The purpose of this research is to determine, characterize, and identify the mycorrhizae associated with locally grown *C. chinense* in the western area of Puerto Rico. We collected ají dulce roots and surrounding soil from plants growing in experimental plots at UPRM. Roots were cleared in KOH 10% at 60°C for one hour and then placed in 2% HCl for 20 minutes, stained using Trypan blue 0.4% for 72 hours, and preserved in glycerol. After processing samples and staining, fungi were morphologically identified using taxonomic keys. Among the genera identified so far, we found *Glomus* and *Acaulospora*. We also grew ají dulce under two treatments using commercial Promix® BX for general purpose and Promix® mycorrhizae (*G. intraradices*). Significant differences were obtained when compared using ANOVA, obtaining a p-value <0.0001 between Promix® mycorrhizae and Promix® BX treatments where the first one resulted in greater stem length, fruit, and leaf number.

#### PS 1-40 Mycorrhizal fungal communities in a coastal oak (*Quercus dentata*) forest

ARAI, H.<sup>1</sup>, K. Obase<sup>2</sup>, Y. Tamai<sup>1</sup>, T. Yajima<sup>1</sup> and T. Miyamoto<sup>1</sup>

<sup>1</sup>Laboratory of forest resource biology graduate school of agriculture Hokkaido university N-9, W-9, kita-ku, Sapporo, Hokkaido, 060-8589, Japan, harai@for.agr.hokudai.ac.jp; <sup>2</sup>Department of Plant Pathology, University of Florida, 2523 Fifi Hall, Gainesville, FL 32611-0680, USA.

**Abstract:** *Quercus dentata* (Fagaceae) is tolerant of salinity and drought, and is one of the dominant tree species of the coastal forests in Hokkaido, northern Japan. Coastal areas are exposed to high salinity and drought stress and plant growth is restricted under such harsh conditions. In the present study, we conducted a greenhouse experiment using indigenous sandy soils and seeds to clarify the mycorrhizal fungal communities in a coastal forest containing *Q. dentata*. Almost all the seeds rooted within two months of planting, but in the sterilized soil the root system tended to be undeveloped and almost all the root tips were covered with root hair. Within three months, the colonization rate of arbuscular mycorrhizal or ectomycorrhizal fungi was only 30% for root tips from non-sterilized soil, and others were non-mycorrhizal. The colonization of dark septate endophytes (DSE) or arbuscular mycorrhizal fungi were not observed in the root tips with root hair. The root tips without root hair and mantle were frequently colonized by DSE, but the colonization of arbuscular mycorrhizal fungi was rarely observed. The ectomycorrhizal fungus *Cenococcum geophilum* was common, and *Tomentella* sp. and *Helotiales* sp. were also observed. In the four-month-old seedlings planted in sterilized soil, the root systems tended to be undeveloped, same as the three-month-old seedlings. In the non-sterilized soil, the root tips with root hair were rarely observed and 73% of root tips were ectomycorrhizal. The relative frequency of *C. geophilum* decreased, and the other species, such as *Tuber* sp. and *Hymenogaster* sp., were common; *Hebeloma* sp. and *Scleroderma* sp. were also observed.

#### PS 4-60 Mycoheterotrophy in Chilean endemic orchids: exploring their mycorrhizal status

ARRIAGADA, C.<sup>1</sup>, H. Herrera<sup>1</sup>, R.Valadares<sup>2</sup> and D. Contreras<sup>3</sup>

<sup>1</sup>Laboratorio de Biorremediación Facultad de Ciencias Agropecuarias y Forestales, Departamento de Ciencias Forestales, Universidad de La Frontera, Temuco Chile, cesar.arriagada@ufrontera.cl; <sup>2</sup>Instituto Tecnológico Vale, Rua Boaventura da Silva 955.Cep 66050-090, Belém-PA, Brasil; <sup>3</sup>Facultad de Ciencias Básicas, Universidad Católica del Maule, Avda, San Miguel 3605, Casilla 617, Talca, Chile.

**Abstract:** Orchid mycorrhizal fungi are a particular trophic interaction. This symbiotic relationship is characterized for the possibility that mutualism may transition to commensalism or parasitism, or vice versa, through different stages of development. Under natural conditions, all orchids must be associated to a certain fungus to germinate their tiny seeds. This symbiosis is maintained throughout life in mycoheterotrophic orchids, although the denominated green orchids do not need a mycorrhizal fungus during autotrophic stages, but these symbionts are essential to sustain the normal growth during the seedling or mycoheterotrophic stage. The degree of specificity between fungus and orchid is a significant factor determining chances of successful seedling establishment. On the contrary for species exhibiting diverse associations this factor may not be limiting. Little is known about Chilean Orchidaceae plants and their mycorrhizas, a key issue to design protection actions to save endangered species. To know potential mycorrhizal partners an analysis of root fungal endophytes of seven Chilean orchid species (*Chloraea chrysantha*, *C. gaviu*, *C. blettioides*, *C. crispa*, *C. lamellata*, *C. gran-*



*diflora*, and *Bippinula fimbriata*) was carried out in the Maule region of Chile. The main characteristic of the mycorrhizal form genus Rhizoctonia-like fungi was assessed through confocal microscopy and identified through PCR-ITS sequencing. Eighteen fungal groups were isolated, belonging to the groups Rhizoctonia-like fungi (*Tulasnella calospora*, *Ceratobasidium* sp., and *Rhizoctonia solani*), endophytes (*Phomopsis columnaris*, *Catelunostroma* sp.) and dark septate endophytes (*Leptodontidium orchidicola* and *Cadophora* sp.). Internal transcribed spacer (ITS) sequencing showed a high diversity of fungi colonizing the roots. We showed that orchids from Andes mountain range presented a higher colonization rate by dark septate endophytes. The high amount of Rhizoctonia-like fungi obtained from Coastal mountain range, suggest that orchids need this kind of fungi to complement energetic demands through mycoheterotrophy.

#### PS 2-17 Effect of forest litter amendment on survival and ECM community structure of Scots pine (*Pinus sylvestris* L.) seedlings outplanted on four different sites

AUČINA, A.<sup>1</sup>, M. Rudawska<sup>2</sup>, T. Leski<sup>2</sup>, A. Skridaila<sup>1</sup>, M. Pietras<sup>2</sup> and D. Ryliškis<sup>1</sup>

<sup>1</sup>Botanical Garden of Vilnius University, 43 Kairėnų Str., LT-10239 Vilnius, Lithuania, algis.aucina@gf.vu.lt; <sup>2</sup>Institute of Dendrology, Polish Academy of Sciences, 5 Parkowa Str., 62-035 Kórnik, Poland.

**Abstract:** Scots pine (*Pinus sylvestris* L.) is found in Europe and is one of the most important timber conifer species, with high commercial and ecological value. In Lithuania, Scots pine represents approximately 37% of the forest area and the entire seedling stock is produced in bare-root forest nurseries. In nursery management practices, forest litter is sometimes used as a rich source of soil organic matter and nutrients that significantly improve the characteristics of the soil and positively affect seedling growth and their ectomycorrhizal (ECM) communities. The aim of the present investigation was to determine the effect of pine litter pre-treatment during the two year nursery phase on growth and ECM community structure of Scots pine seedlings after outplanting into a forest clear-cut (S1), a site contaminated by chemical emissions (S2), abandoned agricultural land (S3), and coastal sand dunes (S4) in Lithuania. Seedlings not treated by forest litter and grown in nursery mineral soil have been used as a reference. Three years after field outplanting at site S1 and S4, untreated seedlings showed significantly higher mortality than seedlings that were pre-treated with pine forest litter during the nursery phase. The roots of both untreated and treated seedlings were naturally colonized by ECM fungi occurring in the nursery and by indigenous ECM fungi characteristic of each study site (14-22 ECM fungal species depending on the site). Ectomycorrhizal communities of Scots pine from sites S1-S3 were dominated by *Wilcoxina mikolae* and *Thelephora terrestris*, while seedlings from site S4 were dominated by *Cenococcum geophilum*. However, ANOSIM analysis revealed that only on site S2 and S3 did litter pre-treatment significantly influenced ECM fungal communities. We conclude that use of forest litter in nursery practice improves adaptability of seedlings to unfavourable environmental conditions after outplanting and may be a recommended for the production of higher quality nursery stock with improved field performance.

#### PS 1-5 Patterns and drivers of spatial diversity of arbuscular mycorrhizal fungal communities from a temperate forest in the Nearctic-Neotropical transition

ÁVILA-VAL, T.C.<sup>1</sup>, M.E. Gavito<sup>1</sup>, H. Arita<sup>1</sup>, T.G. Cornejo-Tenorio<sup>1</sup> and G. Ibarra-Manrique<sup>1</sup>

<sup>1</sup>Instituto de Investigaciones en Ecosistemas y Sustentabilidad Universidad Nacional Autónoma de México-campus Morelia 58190, Morelia, Michoacán, Mexico, tereavilaval@yahoo.com.mx.

**Abstract:** The Mexican volcanic belt, besides being a transitional biogeographic region, is considered environmentally very heterogeneous. This region has been shown to host high species richness and beta diversity of plants and mammals. Spatial diversity patterns of AM fungi in this region are unknown. The objective of this work was to assess the patterns and controlling factors of spatial diversity of AMF communities in a 170 ha unmanaged temperate forest in Uruapan, Michoacán, Mexico. We hypothesized that AMF diversity would be determined mainly by the plant diversity present at each point and, to a lower extent, by local environmental factors. We established four 8 x 8 m grids in a nested design that allowed us to evaluate all scales with the same representativeness: area  $A_0=256 \text{ m}^2$ ,  $A_1=64 \text{ m}^2$ ,  $A_2=16 \text{ m}^2$ ,  $A_3=4 \text{ m}^2$ ,  $A_4=1 \text{ m}^2$ , since we sampled half of the squares within each scale after the smallest scale. We measured plant cover and species richness, AMF morphospecies richness, canopy closure, and soil variables (compaction, texture, organic matter, pH, available N, and P), for each of the 64 squares of 1 m<sup>2</sup> sampled. We found 57 plant species, mainly within the

Asteraceae, Fabaceae, and Poaceae. Plant species richness varied from 4 to 15 per m<sup>2</sup>. We found 32 AMF species with a predominance of the Diversisporales, and the families Acaulosporaceae, Gigasporaceae, and Glomeraceae. AMF species richness varied from 1 to 13 per m<sup>2</sup>. Despite being measured at small scales, both beta diversity and species turnover were high, and followed similar patterns as those shown for other organisms in this region at much higher scales (1, 10, 100 km<sup>2</sup>). Soil pH was among the most important controlling environmental factors.

**PS 4-61 Assessment of community structure of arbuscular mycorrhizal fungi associated with rice varieties in five states of Nigeria**

**BABALOLA, O.A.**<sup>1</sup>, A.A. Olubode<sup>1</sup>, M.O. Atayese<sup>2</sup>, M.O. Dare<sup>1,3</sup> and C.O. Adejuyigbe<sup>1</sup>

<sup>1</sup>Department of Soil Science and Land Management, Federal University of Agriculture, Abeokuta, Nigeria, bimbola05@yahoo.com; <sup>2</sup>Department of Plant Science and Crop Production, Federal University of Agriculture, Abeokuta, Nigeria; <sup>3</sup>Department of Biological Sciences, Faculty of Agriculture, Science and Technology, North-West University, Mafikeng Campus, Mmabatho, South Africa.

**Abstract:** The symbiotic association between arbuscular mycorrhizal fungi (AMF) and the roots of plants is widespread in natural environments and it is highly beneficial to plants, increasing their nutrient uptake and tolerance to disease and drought. This symbiotic association was surveyed in rice grown on farmers' fields in five Nigerian states (Osun, Oyo, Ogun, Ekiti, and Niger). The AMF spores were isolated and identified using information from the Network for Vesicular Arbuscular Mycorrhiza (INVAM), and percent root colonization was evaluated by spreading stained roots evenly in grid plates, and observing scanned vertical and horizontal lines under dissecting microscope. The thirteen rice varieties observed on farmers' fields had varying degrees of association with AMF. Rhizosphere soils of *Ofada*, NERICA 1 and ITA 150 had significant spore counts of 227, 177 and 144 per 20 g soil respectively while roots of *Ofada*, UORG, NERICA 8, NERICA 1 and UN111 had significant colonizations of 70.4 %, 67.9 %, 65.3 %, 52.1 % and 49.8 % respectively. Four genera, (*Gigaspora*, *Glomus*, *Scutellospora*, and *Acaulospora*) and thirteen species were encountered in the five states. Spores of *Glomus mossaeae*, *G intraradices*, and *Gigaspora* sp. were isolated from all the five states. Relative abundance of spores varied among the states and also among the species, spores of *Glomus* species were high in all the five states while spores of *Acaulospora*, *Gigaspora*, and *Scutellospora* species were significant only in Ogun state. Thus total spore abundance, species evenness and H' index were significantly higher in Ogun state than other states, H' index was highest in Ogun state (2.2), followed by in Osun state (1.9) and lowest in Oyo state (0.7). It was concluded that the diversity and population of AMF was enhanced on rice grown in Ogun state as a result of higher number of varieties planted in that state.

**PS 4-35 Identification of orchid mycorrhizal fungi in roots of the endangered orchid *Cypripedium macranthum* in Korea**

**BAE, Y.R.**<sup>1</sup>, H.K. Han<sup>1</sup> and A.H. Eom<sup>1</sup>

<sup>1</sup>Department of Biology Education, Korea National University of Education, Cheongju, Chungbuk 363791, Korea, soonsooyura@gmail.com.

**Abstract:** Orchids of the genus *Cypripedium* are mostly distributed in temperate regions in the Northern hemisphere including Korea. *Cypripedium macranthum* is endangered in Korea because of habitat disruption and overexploitation for horticultural purposes. Similar to other orchids, this species depends on orchid mycorrhizal fungi (OMF) for germination and early growth of the plants. This symbiotic relationship between orchids and OMF is important for distribution and restoration of the orchids. In this study, we compared OMF communities colonizing the roots of *C. macranthum* collected from different sites in Korea. Pelotons were observed in the cortical cells of roots, indicating mycorrhizal colonization. A total of 24 OMF strains were isolated from surface-sterilized roots of *C. macranthum* and identified using morphological characteristics of the fungal hyphae and growth in culture. Genomic DNA was extracted from the isolated fungal strains and the internal transcribed spacer (ITS) region was amplified using the ITS1-OF and ITS4-OF primer pair. Phylogenetic analysis using sequence obtained from 24 strains showed that strains isolated from 8 orchids in 2 different sites were identified as a single species of OMF belonging to the family Tulasnellaceae. The results suggest that *C. macranthum* from Korean sites sampled in this study has a specific symbiotic relationship with an OMF species.

## PS 3-22 Protective effect of AM fungi on nitrogen fixation and proline molecule as a stress signaling in chickpea nodules under saline condition

BAHER, N.<sup>1</sup>

<sup>1</sup>Assistant Professor, Department of Agronomy and Breeding, Payam Noor University, Tehran, Iran, nvdbaher@gmail.com.

**Abstract:** Proline, an amino acid, which is elevated in response to diverse types of abiotic stresses has several roles such as turgor generation, storage of carbon and nitrogen, stabilization of the structure of proteins by acting as a molecular chaperone, balance of redox status, stress signaling. Arbuscular mycorrhizal (AM) fungi are ubiquitous symbionts known to exist in saline environments, where they can alleviate the negative effects induced by soil salinity. In legume nodules, proline serves as both an energy source and a possible nitrogen carrier to the bacteroid. The association of chickpea roots with the AM fungus, *Glomus mosseae*, was examined to determine the role of AMF in overcoming the toxic effects of salinity on nodulation and N<sub>2</sub> fixation. The contribution of variation in AM fungi to proline turnover was also assessed. Two genotypes [PBG 5 (salt-tolerant) and CSG 9505 (salt-sensitive)] were subjected to saline treatments with and without mycorrhizal inoculation. Investigations revealed that salinity inhibited nodulation and nitrogen fixation with a higher decline in sensitive genotype (CSG 9505). Salinity triggered an inhibition of proline dehydrogenase (ProDH) activity and an increase in proline content. AM colonization was reduced with increasing salinity levels but mycorrhizal dependency (MC) increased. AM plants not only showed improved nodule number, nodule dry mass and nodular activity (leghemoglobin, acetylene-reduction activity [ARA], nitrogen content) but they also had higher proline content, which was correlated with high pyrroline-5-carboxylate synthetase (P-5-CS) and glutamate dehydrogenase (GDH) activities, concomitant with reduced ProDH. PBG 5 showed higher responsiveness to AM inoculations than CSG 9505. This result suggests that accumulation of proline could be an important strategy for sustainability of AM plants under saline agriculture and that high proline turnover in *G. mosseae* colonized roots results in a more stable symbiosis under salinity.

## CS 2-1 Insight into underlying mechanisms shaping local-scale distribution of ectomycorrhizal fungi by using network analysis

BAHRAM, M.<sup>1,2</sup>, H. Harend<sup>1</sup> and L. Tedersoo<sup>3</sup>

<sup>1</sup>Institute of Ecology and Earth Sciences, University of Tartu, 50411 Tartu, Estonia, bahram@ut.ee; <sup>2</sup>Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University, SE 75236 Uppsala, Sweden; <sup>3</sup>Natural History Museum, University of Tartu, 50411 Tartu, Estonia.

**Abstract:** Network analysis can help elucidate complex networks of interactions in diverse fungal communities. Here we used a network approach to address bipartite (plant-fungi) and co-occurrence networks (fungi-fungi) in ectomycorrhizal (EM) fungi, which could provide useful information about the underlying mechanisms of their community assembly. First, we examined interaction networks between EM plants and fungi by analyzing the main network properties - nestedness and modularity. We found some level of modularity in certain EM fungal communities, which can be ascribed to partner selectivity and, thus, context dependent. Our data also showed that EM networks exhibit non-nested patterns, which is in contrast to other mutualistic interactions. The low level of nestedness may indicate no plant preference for generalist EM fungi over specialists. This can stem from a strong selection pressure of host in choosing its mycobionts as suggested from the substantial host phylogeny effect on EM fungal richness and community. We also analyzed co-occurrence network structure of EM fungi in eight forests representing different biomes of the world. We used Illumina MiSeq sequencing analysis of ITS region for molecular identification. Our prediction is that network topology is strongly affected by ecosystem properties. We established our plots in monodominant and homogenous areas to reduce the effect of environmental heterogeneity, and collected ~60 soil samples per site (467 samples in total). Topology of these networks in relation to biotic and abiotic factors and co-occurrence patterns of different taxonomic groups will be discussed.

BAINARD, L.<sup>1</sup>, C. Hamel<sup>1</sup>, B. Cade-Menun<sup>1</sup>, P.L. Chagnon<sup>2</sup>, K. LaForge<sup>1</sup> and Y. Gan<sup>1</sup>

<sup>1</sup>Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada, lbainard@gmail.com; <sup>2</sup>University of Alberta, Edmonton, AB, Canada.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) play an important role in the functioning and sustainability of agroecosystems, but they are also susceptible to changes in land use. The goal of this study was to understand the impact of land use on AMF communities and the factors that drive their assembly in the semiarid prairie landscape. Soil samples were collected in early spring and summer from the four major land use types in this region: (1) annually cropped fields, (2) seeded pastures (crested wheatgrass), (3) native prairie rangeland, and (4) roadsides. We used 454 GS FLX+ pyrosequencing to characterize the diversity and composition of AMF communities in soil and spore samples. There were significant differences in litter and vegetation cover, and physical and chemical properties of the soil among the land use types. The impact of land use on soil properties was primarily observed in the top layer (0-15 cm) of soil. We found that annual cropping altered the composition and reduced the richness and diversity of AMF communities in soil samples in the spring and summer. The strongest impact of land use was in the topsoil layer, but an effect was also evident in the lower soil depths (15-60 cm). Comparison of soil and spore samples revealed different AMF community profiles and effects of land use. *Glomus* was the dominant taxa in soil samples (49%) but was rare in spore samples (6.5%), which were primarily composed of *Claroideoglomus* (35%) and *Diversispora* (41%) taxa. Land use had no effect on richness and diversity of AMF spore communities, but annually cropped fields harboured a distinct community compared to other land use types. Soil properties (i.e., clay content, pH, organic C, phosphate, Fe, and Mg) and vegetation cover were identified as the primary factors driving the assembly of AMF communities. Structural equation modeling revealed that land use primarily impacts AMF communities indirectly through the modification of soil properties and vegetation cover.

### LT 3-3 Tree harvest induces dramatic changes in the functioning of forest soils and largely affects both ectomycorrhizal and saprotrophic fungi

BALDRIAN, P.<sup>1</sup>, M. Charvátová<sup>1</sup>, T. Poláčeková<sup>1</sup> and M. Tomšovský<sup>2</sup>

<sup>1</sup>Laboratory of Environmental Microbiology, Institute of Microbiology of the ASCR, Prague, 14220 Czech Republic, baldrian@biomed.cas.cz; <sup>2</sup>Department of Forest Protection and Wildlife Management, Mendel University in Brno, Brno, 61300 Czech Republic.

**Abstract:** Forest trees act as major suppliers of C to forest soils through their production of litter and C rhizodeposition. Ectomycorrhizal (ECM) fungi produce their mycelia on expense of the rhizodeposited C, and thus, are dependent on their host. Here we tracked fungal community composition in fine roots, rhizosphere soil (soil adhering to roots), and bulk soil of a spruce (*Picea abies*) forest over one year following tree harvest, with a focus on ECM fungi. Under living trees, the rhizosphere contained significantly more fungal biomass than the bulk soil, and slightly less than roots. After tree harvest, fungal biomass in bulk soil remained unchanged, but it decreased 4-fold in the rhizosphere, while it increased up to 5-fold in decomposing roots. This was associated with an increase in the activity of decomposition-related enzymes in roots, and a decrease in rhizosphere. Fungal community composition changed over time. In the soil and rhizosphere, the share of sequence reads of ECM fungi decreased from 50% under living trees to 35% after two months post-harvest, and down to 12% after one year. In the roots of living trees, ECM fungi represented 56% of all sequences and largely persisted until two months, but their abundance dropped to 5% after five months, and <2% after one year, to be replaced by wood-decomposing taxa. Recently, the saprotrophic abilities of ECM fungi are under debate, and indirect evidence increases about the possible ability of certain taxa to decompose biopolymers. It is apparent that ECM fungi were able to persist on roots for some time after tree harvest, and might have potentially contributed to decomposition of easily available compounds, while later they were unable to thrive on the remaining recalcitrant root biomass. Interestingly, abundance of some ECM fungi (e.g., *Amanita* and *Hygrophorus*) decreased rapidly after tree harvest, while others (*Russula*) maintained a high abundance for a long time.



**PS 4-62 Management of mycorrhizal fungal propagules by using pioneer plant species in disturbed sclerophyllous forest in Madagascar**

**BAOHANTA, R.**<sup>1</sup>, H. Randriambanona<sup>1</sup>, M.D. Andrianandrasana<sup>2</sup>, H.T. Andrianarimanana<sup>2</sup>, E. Rajaonarimamy<sup>2</sup>, A.T. Razakatiana<sup>2</sup>, R. Duponnois<sup>3</sup> and H. Ramanankierana<sup>1</sup>

<sup>1</sup>Laboratoire de Microbiologie de l'Environnement, Centre National de Recherches sur l'Environnement, BP 1739, Antananarivo, Madagascar, ninish.rondro@yahoo.fr; <sup>2</sup>Laboratoire de Biotechnologie-Microbiologie, Département de Biochimie Fondamentale et Appliquée, Faculté des Sciences Université d'Antananarivo Madagascar; <sup>3</sup>IRD, Laboratoire des Symbioses Tropicales et Méditerranéennes (LSTM), UMR 113 CIRAD/INRA/IRD/SUPAGRO/UM2, Campus International de Baillarguet, TA A-82/j, Montpellier, France.

**Abstract:** Studies have been conducted in a highly disturbed sclerophyllous forest in Arivonimamo, Madagascar. We hypothesized that some pioneer plant species could improve mycorrhizal soil infectivity by stimulating mycorrhizal propagules in soil. Therefore, after floristic inventories, the mycorrhizal status of each shrub identified as pioneer species was described. Soil mycorrhizal infectivity was also evaluated by spore numeration, evaluating the most probable number (MPN) of mycorrhizal propagules, which are able to infect a host plant, and by hyphal length measurement. The most dominant mycotrophic pioneer plant species with high MSI and the native tree, *Uapaca bojeri*, were then cultivated in bare soil and in soil previously colonized by the alien species, *Pinus patula*. Root colonization by mycorrhizal fungi and the structure of the mycorrhizal association with the pioneer plant species were assessed after five months using plants grown in greenhouse conditions. We recorded 10 pioneer shrubs species associated with mycorrhizal fungi (arbuscular mycorrhizae (AM), ectomycorrhizae, or both) within the sclerophyllous forest. Compared to bare soil, AM spore density and hyphal length were significantly higher in soil collected under these species, especially in soil collected under the shrub, *Leptolaena bojeriana*. It was also observed that the MPN of mycorrhizal propagules was significantly higher in soil collected under this pioneer plant species. Greenhouse experiments showed that *L. bojeriana* exhibited a higher mycorrhizal rate and a higher diversity of associated mycorrhizal fungi when cultivated in bare soil and in exotic species soil compared to the native tree, *U. bojeri*. These results suggest that the shrub, *L. bojeriana*, can stimulate fungal propagules and other soil microorganisms, which can infect or positively influence the development of other plant species.

**PS 3-11 Belowground carbon allocation to ectomycorrhizal fungi associated with *Fagus grandifolia* in response to N, P, and Ca additions in northern hardwood forests**

**BARNER, J.C.**<sup>1</sup>, T.R. Horton<sup>2</sup> and R.D. Yanai<sup>1</sup>

<sup>1</sup>Department of Forest and Natural Resources Management, State University of New York College of Environmental Science and Forestry, Syracuse, NY 13210, USA, jcbarnersyr.edu; <sup>2</sup>Department of Environmental and Forest Biology, Statue University of New York College of Environmental Science and Forestry, Syracuse, NY 13210, USA.

**Abstract:** Carbon allocation from plant hosts to mycorrhizal fungi directly influences how symbiotic host trees acquire nutrients, and impacts the stability of labile C pools in the soil. Temperate ecosystems that exhibit nutrient limitation often host dominant tree species that associate mutualistically with ectomycorrhizal (ECM) fungal partners. These fungi exact a large C cost on the tree in exchange for increased access to a greater variety and spatial availability of essential nutrients. Increased exploitation of the soil volume by fungal mycelium can lead to heightened resistance of plant hosts to stressors and contribute to carbon sequestration belowground. Reductions in fungal species diversity and the loss of medium to long distance exploration types has been shown in response to inorganic N additions, but the impact of other growth limiting macronutrients, such as P and Ca, on ECM fungal communities is less well known. As part of a multi-year forest fertilization experiment in the White Mountains of New Hampshire, we sought to determine C allocation from plant hosts to ECM fungi in response to nutrient additions. One and three year old *Fagus grandifolia* seedlings ( $n = 70$ ) were collected from five 1,600 m<sup>2</sup> fertilization treatment plots ( $r = 3$ ) in August 2014 to examine the response of fungal C allocation to four years of fertilization with N (30 kg N/ha/yr as NH<sub>4</sub>NO<sub>3</sub>), P (10 kg P/ha/yr as NaH<sub>2</sub>PO<sub>4</sub>), N + P (30 kg N/ha/yr + 10 kg P/ha/yr), and Ca (1,000 kg Ca/ha as CaSiO<sub>3</sub>), versus a control treatment. Early morphotyping results suggest that medium to long distance exploration types are less abundant in N and N + P plots than others. Molecular approaches are now being applied to identify the fungi. These results will be used to discuss changes in fungal richness and diversity under different nutrient treatments and the impacts on belowground C pools.

**PS 2-18 The presence of chestnut blight (*Cryphonectria parasitica*) decreases ectomycorrhizal inoculum potential and seedling recruitment survival in restoration plantings**

**BAUMAN, J.M.**<sup>1</sup> and A. Santas<sup>2</sup>

<sup>1</sup>Western Washington University, 1000 Olympic College Way NW, Poulsbo, Washington, 98370, Jenise.Bauman@wwu.edu; <sup>2</sup>Muskingum University, 163 Stormont Street, New Concord, OH 43762.

**Abstract:** Anthropogenic disturbances, such as mining for coal, have caused significant disturbance to the Appalachian forests of eastern North America. Ectomycorrhizal (ECM) fungi are an intricate part of the belowground ecology and act as important drivers contributing to forest tree establishment in disturbed soils. Proper site preparation, such as deep soil ripping, increases the association between American chestnut seedlings and ECM fungi on a coal mined site in Ohio, U.S.A. The natural infection of the chestnut blight fungus (*Cryphonectria parasitica*) was documented causing stem cankers and significant seedling dieback. Previous studies have documented that photosynthetic tissue loss is correlated to diminished ECM, suggesting carbon as a mechanism driving ECM colonization. Therefore, we hypothesized a similar pattern; the presence of disease would decrease ECM colonization on roots, thereby compromising the inoculum potential in the field. To test this, 75 six-year-old established chestnut trees were selected as parent trees and represented the following: 1) healthy chestnut tree free of chestnut blight, 2) chestnut seedlings with 50% dieback and the presence of chestnut blight, and 3) seedlings recorded as dead in the field after 5 growing seasons. One chestnut seed was planted 24 cm from the base of each parent tree. ECM colonization was quantified by root tip counts and genera determined by fungal DNA sequencing of the internal transcribed (ITS) region. Our results demonstrated that the healthier the tree host, the greater the survival of the germinating chestnut seedlings ( $P = 0.01$ ) and the increase in ECM root tips ( $P = 0.002$ ). In addition, chestnut seedlings that germinated from seeds planted in close proximity to healthy trees were significantly larger than those planted close to diseased trees ( $P = 0.04$ ). This indicates that healthy trees can facilitate the establishment of new seedlings; however, disease decreases inoculum potential of parent trees in chestnut restoration.

**LT 2-1 The *Hebeloma cylindrosporum* phosphate transporter HcPT2 was involved in phosphate efflux at the fungus-plant interface**

**BECQUER, A.**<sup>1</sup>, K. Garcia<sup>2</sup>, L. Amenc<sup>1</sup>, S. Ruset<sup>1</sup>, Y. Baeza<sup>1</sup>, S. Zimmermann<sup>3</sup> and C. Plassard<sup>1</sup>

<sup>1</sup>INRA, UMR 1222 Eco&Sols, 2 Place Viala, 34060 Montpellier Cedex 2, France, adeline.becquer@supagro.inra.fr;

<sup>2</sup>University of Wisconsin, Department of Agronomy, 219 Moore Hall, 1575 Linden Drive, Madison, WI, USA; <sup>3</sup>Biochimie et Physiologie Moléculaire des Plantes, UMR 5004, CNRS/INRA/Supagro/UM2, Campus INRA/Supagro, 2 Place Viala, 34060 Montpellier Cedex 2, France.

**Abstract:** Ectomycorrhizal (ECM) symbiosis is defined as a mutual association between fungal symbionts and roots of woody plants. This symbiosis is strongly represented in temperate and boreal forests and is considered to be the most widespread means of increasing P acquisition by trees. Despite the importance of the ECM association, current knowledge about molecular mechanisms involved in membrane transport between the two partners is still limited. Therefore, the identification of the mechanisms essential for the symbiosis is a major issue. To better understand these mechanisms, we used a model association between the ECM basidiomycete *Hebeloma cylindrosporum* and the maritime pine *Pinus pinaster*. The fungal genome contains three transporters of Pi (*HcPT1.1*, *HcPT1.2*, and *HcPT2*), which have been already characterized as H<sup>+</sup> Pi carriers. We hypothesized that one of these carriers could be responsible for both influx and efflux of Pi from the soil to the fungus and from the fungus to the plant. Our results suggest that HcPT2 would be the best candidate to fill both roles. An *in vitro* ectomycorrhizal system was used to investigate phosphate flux from *H. cylindrosporum* toward a liquid compartment containing pine roots. Interestingly, the expression pattern of *HcPT2* was correlated to fungal phosphate efflux. Moreover, immuno-localization experiments showed that the protein is located (i) in the extraradical hyphae and the fungal sheath, compatible with Pi uptake, and (ii) within the Hartig net, which is the place of exchange between fungal and host cells. In order to study more specifically the role of HcPT2 at the fungus-plant interface, overexpressing and knock-down transgenic *H. cylindrosporum* strains were produced. Fungal strains with up regulated expression of *HcPT2* increased phosphate efflux within the interaction medium, supporting a role of HcPT2 in phosphate transfer to the plant. In addition, the modification of *HcPT2* expression strongly affects Pi nutrition of *P. pinaster*.



## PS 4-4 A decade of increased temperature affects soil fungal communities

**BELUS, M.T.**<sup>1</sup>, B.A. Hungate<sup>2</sup>, G.W. Koch<sup>2</sup> and R.L. Mau<sup>2</sup>

<sup>1</sup>Northern Arizona University, Department of Biological Sciences, Flagstaff, AZ, 86011, mtb82@nau.edu; <sup>2</sup>Northern Arizona University, Center for Ecosystem Science and Society, Flagstaff, AZ, 86011.

**Abstract:** In the American Southwest, climate change is expected to intensify drought and elevate temperature. An understanding of ecosystem responses to long-term temperature augmentation is imperative for climate change research. Specifically, soil fungal responses to warming are poorly characterized in recent literature and knowledge of fungal community responses to warming is necessary to complement current climate change research. We used an elevation gradient in Flagstaff, Arizona that spans the mixed conifer, ponderosa pine, pinyon-juniper woodland, and high desert grassland ecosystems. We transplanted intact grassland communities to lower elevation ecosystems to simulate future climate predictions for the Southwest. Soil was contained in sunken PVC cylinders for each control and transplant site. Precipitation interceptors were used to compensate for lower precipitation in the warming treatment. Soil samples were collected ten years after transplantation. Community composition was determined using the ITS1 region of ribosomal DNA. Statistical analyses of fungal communities from ambient and warmed treatments indicate a significant influence of warming on fungal community composition. Communities exposed to long-term warming no longer resemble their parent communities at ambient temperatures. Indicator species analysis shows different occurrences of putative dark septate endophytes (DSE) between control and transplanted soil. Different indicator species from the orders of *Pleosporales*, *Helotiales*, *Hypocreales*, *Eurotiales*, and *Xylariales* were found in the mixed conifer, pinyon-juniper, and high desert grassland soils. A unique occurrence of indicator species from each of these groups was found in soil at ambient temperatures or elevated temperatures. Conversely, some DSE taxa were unaffected by the warming treatment. Complementary research on the plant community response in this experiment indicated that warming altered plant community composition, richness, and evenness. The changes in the DSE community are congruent with the changes observed in plant communities. A shift in plant and fungal communities due to long-term warming has important implications for plant symbioses.

## CS 8-1 Sustainable nutrient cycling through soil biota

**BENDER, S.F.**<sup>1</sup> and M.G.A. van der Heijden<sup>1,2</sup>

<sup>1</sup>Plant Soil Interactions, Institute for Sustainability Sciences, Agroscope, Reckenholzstrasse 191, CH-8046 Zurich, Switzerland, franz.bender@agroscope.admin.ch; <sup>2</sup>Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, CH-8057, Switzerland.

**Abstract:** Efficient resource use is a key factor for sustainable agricultural production and a necessity for meeting future global food demands. However, the factors that affect nutrient use efficiency in agro-ecosystems are only partly understood. Arbuscular mycorrhizal fungi (AMF) are well known to contribute to plant nutrition, and there is recent evidence that AMF can reduce nutrient loss from soil. In natural soils, AMF are interacting with a variety of other soil biota. Little is known about the potential of these organisms and their interactions to enhance nutrient use efficiency and sustainability in agriculture. We investigated the influence of soil biota on nutrient cycling and plant performance in outdoor, open-top lysimeters comprising a volume of 230 L. The lysimeters were filled with sterilized soil in two horizons and inoculated with a reduced soil-life inoculum (microbially dominated) and an enriched soil-life inoculum containing soil organisms <2 mm and AMF. An agricultural crop rotation was planted, and nutrient leaching losses after rain, plant biomass and nutrient contents were assessed over a period of almost two years. The presence of enriched soil-life inoculum greatly enhanced plant growth and nutrition and strongly reduced nitrogen leaching losses as well as emissions of the greenhouse gas N<sub>2</sub>O. Moreover, we tested the success of AMF inoculation on plant productivity and nutrient leaching in different agricultural soils and under differing farming practices. Effects of arable management, AMF inoculation, and their interactions on the plant-soil systems were investigated. While management practices influenced nutrient leaching losses and N<sub>2</sub>O emissions, AMF inoculation had variable impact. Inoculation of field soil with AMF enhanced plant yield in some soils but not in others. Our results indicate that soil biota have a huge potential to enhance agricultural sustainability, but the success of field inoculations with AMF may depend on environmental conditions.

## CS 5-1 Can we make general statements about the effects of AM fungi on plant-insect interactions?

**BENNETT, A.E.**<sup>1</sup>

<sup>1</sup>Ecological Sciences, James Hutton Institute, Errol Road, Invergowrie, Dundee DD2 5DA UK, Alison.Bennett@hutton.ac.uk.

**Abstract:** As ecologists, we seek to understand the world around us through a set of general rules; as mycorrhizal mycologists, we seek to understand how mycorrhizal fungi alter those general rules and structure communities. The realization that arbuscular mycorrhizal (AM) fungi could alter host chemistry through priming of plant hormonal response systems has produced a wide array of literature looking at the influence of AM fungi on herbivores, predators of herbivores, and pollinators. As this body of literature grows, we search for a consistent pattern of AM fungal influence. In this talk I will address the generality of AM fungal effects on plant-insect interactions by focusing on research manipulating diversity at multiple levels within these interactions. I will focus on the influence of AM fungi on *Solanum*-aphid-parasitoid interactions as well as other AM fungi-plant-insect systems studied by my group. In particular, I will assess variation in AM fungal-plant-insect interactions due to host plant species or genotype and herbivore species and genotype. I will then discuss whether variation introduced by these factors is greater than the variation introduced by AM fungi. Finally, I will suggest when and where variation in response to AM fungi within a group (e.g., host plant) might increase the influence of AM fungi on plant-insect interactions.

## PS 2-35 Characterizing soils and fungal communities of Douglas-fir (*Pseudotsuga menziesii*) stands that naturally produce Oregon white truffles (*Tuber oregonense* and *T. gibbosum*)

**BENUCCI, G.M.N.**<sup>1</sup>, C. Lefevre<sup>2</sup> and G. Bonito<sup>1</sup>

<sup>1</sup>Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, Michigan 48824 USA, benucci@msu.edu; <sup>2</sup>New World Trufferies, Inc., P.O. Box 5802 Eugene, Oregon 97405 USA.

**Abstract:** Many truffle species are endemic to North America. Some of these species have commercial value such as *Tuber oregonense* and *T. gibbosum*, the Oregon white truffles. These species form ectomycorrhizas with Douglas-fir (*Pseudotsuga menziesii*) and naturalize and sometimes fruit abundantly in early successional forest regrowth. The goal of this study was to characterize soils and fungal communities associated with truffle-producing Douglas-fir sites in Oregon. Improved understanding of belowground root associations of Douglas-fir in natural truffle-producing sites has both ecological and economic relevance. We sampled roots from five trees at four different Douglas-fir truffle-producing sites (n=20). Roots were washed with Tween 20 and water, dried with silica gel, and crumbled to break the fine roots from higher order roots. DNA was extracted from roots with CTAB. We amplified the internal transcribed spacer (ITS) region of the nuclear ribosomal DNA (nrDNA) and sequenced amplicons with 454 pyrosequencing to characterize the fungal communities. After trimming and quality checking, we were left with 15,713 reads that assembled in 151 fungal OTUs. Pezizomycetes (*Tuber* and Pyronemataceae) were most abundant followed by the Helotiales. Agaricomycetes were also in high abundance represented most by Thelephoraceae, Russulaceae, and Inocybaceae. A total of six *Tuber* species were detected. *Tuber gibbosum* was the most abundant OTU in the entire dataset. *Tuber oregonense* and *T. whetstonense* were also abundant but were distributed differently among sites. This study represents the first characterization of the fungal communities in Douglas-fir stands producing Oregon white truffles. We found that *T. gibbosum* and *T. oregonense* can be dominant as ectomycorrhizal symbionts of Douglas-fir making them important to forest health, food webs, and as a non-timber forest resource which is especially important to rural economies. More in-depth studies on truffle ecology are fundamental to future re-forestation programs in the Pacific Northwest.

## PS 2-1 Can arbuscular mycorrhizal fungi contribute to herbivore resistance in rice?

BERNAOLA, L.<sup>1</sup> and M.J. Stout<sup>1</sup>

<sup>1</sup>Department of Entomology, Louisiana State University Agricultural Center (LSU AgCenter), Baton Rouge, Louisiana 70803 USA, lbernaola@agcenter.lsu.edu.

**Abstract:** Rice, *Oryza sativa*, in Louisiana faces hardships from both above-ground and below-ground stressors, and rice plants defend themselves against harmful insects and pathogens in many ways. Interactions between plants and herbivores and between plants and arbuscular mycorrhizal fungi (AMF) are ubiquitous in terrestrial ecosystems and may be interconnected by complex regulatory networks via a shared host plant. Arbuscular mycorrhizal fungi are symbiotic associations in many plant roots thought to play a central role in plant nutrition, growth, and fitness. Previous studies suggest that AMF colonization makes rice more susceptible to insect and pathogen attack. We hypothesize that the interaction of AMF with rice roots activates responses that change the resistance of rice to pests. Our aims are to investigate if AMF colonization increases nutrient uptake by rice, thereby making rice plants more susceptible to rice water weevil (RWW) and fall armyworm (FAW), to investigate the effects of AMF colonization on performance of herbivores, and to investigate if AMF symbiosis affects plant signaling pathways related to plant defense by comparing the transcriptional changes triggered in rice leaves with AMF. Field and greenhouse studies showed that performance of the insects (RWW and FAW) were higher on rice plants treated with AMF, and nutritional analyses of root and shoot tissues indicated no significant difference in the concentration of nutrients in plants colonized by mycorrhizal fungi, suggesting that the observed difference in plant resistance were due to changes in defense-related pathways. In addition, we showed that root colonization by AMF is accompanied by the expression of genes that play a regulatory role in host defense responses. These results suggest that AMF colonization influences processes in the rice root system making it more susceptible to insect attack. Understating interactions among above- and below-ground organisms may help in developing novel methods for managing pests of rice.

## PS 4-63 Arbuscular mycorrhiza mediates silicon uptake and improves nutrient status, restores ionic balance as well as resultant yield in *Cicer arietinum* L. genotypes subjected to long term salinity

BHANDARI, P.<sup>1</sup> and N. Garg<sup>1</sup>

<sup>1</sup>Department of Botany, Panjab University, Chandigarh-160014, INDIA, purnima3320@gmail.com.

**Abstract:** Silicon (Si) uptake varies among plant species and has been found to be low in legumes (<0.5%). Both Si amendment to the soil and arbuscular mycorrhizal (AM) symbiosis stimulate plant tolerance to salt stress. However, reports on the comparative role of exogenous application of Si and AM inoculations, as well as their interactive effects through combined treatments, in improving plant resilience to salt stress are lacking. Few reports indicate that AM fungi increase Si uptake. Therefore, pot trials were undertaken to ascertain the influence of AM fungal specie - *Funneliformis mosseae* and/or Si supplementation (at 4mM) on Na<sup>+</sup> uptake and translocation, nutrient acquisition (N, P, K<sup>+</sup>, Ca<sup>2+</sup>) and resultant yield in salt tolerant (HC 3) and sensitive (CSG 9505) *Cicer arietinum* L. (chickpea) genotypes under salinity stress (0-100mM). Results indicated that both, Si and mycorrhiza improved plant biomass by reducing Na<sup>+</sup> uptake and enhanced yield through improved nutrient status under salt stress. Si-mediated benefits were elicited through significantly reduced Na<sup>+</sup> uptake, coupled with enhanced K<sup>+</sup>, Ca<sup>2+</sup> contents thereby restoring the K<sup>+</sup>/Na<sup>+</sup>, Ca<sup>2+</sup>/Na<sup>+</sup> ratios and growth under stressed environments. On the other hand, strategy adopted by *F. mosseae* inoculated plants was directed towards enhanced N, P acquisition, resulting in improved plant growth and seed yield. HC 3 was more responsive to mycorrhization and led to higher Si uptake than CSG 9505. Interestingly, under combined treatments, the benefits achieved were significantly higher than the individual Si or AM applications, suggesting that mycorrhiza mediated Si absorption from the soil contributed to enhance salt tolerance and seed yield in chickpea plants. Results from the present study strongly highlight that the usage of combined Si-mycorrhization is an effective strategy for increasing chickpea productivity in salt contaminated areas.

**PS 1-35 Morphology and a LSU phylogeny reveal *Archaeospora trappei* and *Ar. schenckii* are synonymous and mode of spore formation resolves only stable population-level variation**

**BILLS, R.B.**<sup>1</sup> and J.B. Morton<sup>1</sup>

<sup>1</sup>Division of Plant and Soil Sciences, West Virginia University, Morgantown, West Virginia, 26506 USA, rbills@mix.wvu.edu.

**Abstract:** *Archaeospora*, the only genus in the deeply rooted family *Archaeosporaceae*, contains two species, *Ar. trappei* and *Ar. Schenckii*, that form spores from the hypha of a precursor sporiferous saccule, either laterally (acaulosporoid) or internally (entrophosporoid). Despite divergent modes of spore formation, the morphology of spores is identical. A phylogeny of a 720 bp region of the 28S ribosomal RNA (LSU) gene from one *Ar. schenckii* strain and ten *Ar. trappei* strains provided evidence that the mode of spore formation was a stable polymorphism within one monophyletic clade. Some sequences of *Ar. trappei* segregated into a highly supported subclade, but others grouped closely with *Ar. schenckii*. Sub-clade structure within a species using the LSU gene is not unusual as sequence polymorphisms are also found in *Paraglomerus occultum*, *Ambispora gerdemannii*, and other clades. This dimorphic phenotype is also not unique. The entrophosporoid mode of spore formation is rare, but it is widely convergent in different families of *Glomeromycota*. For example, few species in *Acaulosporaceae* are entrophosporoid relative to the total number of taxa. Geographically, few strains of *Ar. schenckii* are known compared to globally distributed strains of *Ar. trappei*. Collectively, these patterns indicate *Ar. trappei* and *Ar. schenckii* are not sufficiently distinct genetically and morphologically to warrant species separation. Therefore, they are synonymized as *Ar. trappei*. This, and other studies, indicate fixation of morphological and sequence variants may not always be indicative of speciation events. While the entrophosporoid phenotype discriminates at the species level in other lineages such as *A. colombiana* and *A. mellea*, it is only a population-level variant in *Ar. trappei*. Mode of spore formation, therefore, is a character with different levels of taxonomic resolution.

**PS 2-19 Rehabilitation of degraded drylands through exclosures enhances the density and root colonization of arbuscular mycorrhizal fungi in the highlands of Tigray, Northern Ethiopia**

**BIRHANE, E.**<sup>1</sup>, K.M.G. Medhn<sup>1</sup>, T. Taddesse<sup>1</sup> and K.H. Gebriel<sup>1</sup>

<sup>1</sup>Mekelle University, Department of Land Resources Management and Environmental Protection P.O. Box 231, Mekelle, Ethiopia, emiru.birhane@gmail.com.

**Abstract:** Exclusion of degraded lands from anthropogenic interference was among the methods used for the rehabilitation of degraded lands in tropical semiarid areas. Exclosures can foster secondary forest succession by improving soil conditions, attracting seed-dispersal agents, and modifying microclimate for understory growth. We compared woody plant diversity, arbuscular mycorrhizal fungi (AMF), and soil chemical properties in an exclosure treatment and in grazed land. Vegetation data were collected using 100 m<sup>2</sup> plots. Soil and root samples were collected from four sides of each plant in each plot to make one composite sample per plant. Therefore, 1,763 plants provided 1,763 composite soil and root samples for spore extraction and root colonization identification. Soil for physicochemical properties were collected from the 4 corners and center of 5 × 5 m plots, which were inside the 10 × 10 m plot. A total of 61 woody plant species belonging to 41 families were recorded. Diversity and species richness were higher in the exclosure. Exclosures greater than 30 years old had the highest diversity and richness followed by the foot slopes, grazed land, the youngest exclosure, and the upper elevation site. Spore density and root colonization were higher in the exclosures compared to the grazed land and increased with the age of exclosures. The foot slope had greater spore density and root colonization than middle and upper slope. Soil chemical properties were highest in the oldest exclosures and foot slopes followed by the grazed land, youngest exclosure, and the upper elevation site. AMF was significantly positively correlated with soil chemical properties. Using exclosures is an instrumental strategy to improve and restore the AMF spore density, root colonization, and woody species diversity.

#### LT 4-13 **Photosynthesis in mycorrhiza symbiosis: distinguishing between the impact of nutritional, hormonal, and stomatal responses on host photosynthesis**

**BITTERLICH, M.**<sup>1,2</sup>, J. Gräfe<sup>1</sup> and P. Franken<sup>1,2</sup>

<sup>1</sup>Leibniz Institute of Vegetable and Ornamental Crops Großbeeren/Erfurt e.V., Großbeeren 14979, Germany, bitterlich@igzev.de; <sup>2</sup>Humboldt University Berlin, Department of Plant Physiology, Philippstr. 13, Berlin 10115, Germany.

**Abstract:** The influence of mycorrhiza colonization on host gas exchange was examined over decades on a broad range of plant-fungus combinations resulting in an array of findings and conclusions. Changes in source leaf carbon exchange rates were mainly attributed to mycorrhizal stimulation of stomatal conductance, C sink metabolism, nutrient accumulation, morphological changes, or alteration of plant hormonal traits. There is still a lack of understanding how this complex relationship reacts to different conditions making it difficult to predict whether the fungus acts as a mutualist, commensalist, or parasite. With a drying cycle experiment using randomized blocks and the study organisms tomato and *Funneliformis mosseae*, we were able to show that a continuum exists within one plant-fungus combination. Results ranged from higher assimilation rates to maintaining similar assimilation rates with lower stomatal conductance over wide opened stomata to elevated nutrient content (N, P) without increased assimilation rates. We used state of the art modeling of photosynthesis to evaluate effects of mycorrhization on stomatal limitation of photosynthesis, mesophyll conductance to CO<sub>2</sub>, carboxylation efficiency, chloroplast CO<sub>2</sub> concentration, and electron transport through the thylakoid membrane in response to declining water availability. We carefully characterized the plant and soil water status, reshaping of the plant and root architecture induced by mycorrhiza, and leaf hormonal and optical traits. We are able to distinguish between morphological, nutrient, and water effects on photosynthesis and can explain higher and lower water use efficiencies upon mycorrhization. In most cases, reduction of photoassimilation by drought is caused more by a limitation of mesophyll processes than by stomata closure. Under severe drought, however, the opposite can be the case. By examination and application of the growth conditions favorable for the fungus, we show that mycorrhiza leads to higher *in vivo* photosynthesis and production of photoassimilates. We also discuss whether a stimulated sink metabolism can drive photosynthesis.

#### LT 1-1 **The diversity of ericaceous root fungi in South Africa: A comparative approach**

**BIZABANI, C.**<sup>1</sup> and J.F. Dames<sup>1</sup>

<sup>1</sup>Department of Biochemistry and Microbiology, Mycorrhizal Research Laboratory, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa, C.Bizabani@ru.ac.za.

**Abstract:** Identification of mycorrhizal and root associated fungi plays a vital role in understanding their ecological niches with regard to plant growth. Culture-based techniques and Sanger sequencing have contributed immensely to the identification of ericoid fungi. This technique relies on pure cultures and has a bias towards the recovery of fast growing, sporulating ascomycetes. The introduction of direct sequencing techniques such as 454 pyrosequencing has resulted in detection of a greater diversity of root associated fungi in other plant genera. This study investigated the diversity of root fungi associated *Erica* plants growing in the fynbos of South Africa using culture-based based Sanger sequencing and 454 pyrosequencing. Hair roots were sampled from six *Erica* species. Fungi were isolated in various culture media from a sub-sample of the respective hair roots. Sanger sequencing and Basic Local Alignment Search Tool was used for molecular identification. For direct sequencing, DNA was extracted from the remaining hair root sub-samples and amplified using tagged multiplex primers that targeted the ITS2 region, prior to 454 pyrosequencing. Data was analysed using fungal pipeline on Mothur software and R software for statistical analysis. Both techniques revealed fungi belonging to the order Helotiales were dominant. These included common Ericaceae root associated fungi such as *Oidiodendron*, *Meliniomyces*, *Phialocephala*, *Cadophora*, *Leohumicola*, and unclassified species. *Rhizoscyphus erica* was notably absent. The abundance of Basidiomycetes increased to 27% in pyrosequencing from 3% recovered in culture. This includes Sebaciniales that were absent in culture. Glomeromycetes were detected only using pyrosequencing from 3 *Erica* species. Pyrosequencing revealed a greater fungal diversity in *Erica* roots than culture-based techniques. However, taxonomic classification to genus and species level was poor compared to culture based technique. Therefore, concurrent use of both techniques in determining root fungal diversity gives a better outcome than either technique used alone.



## LT 2-4 *Hadrolaelia jongheana*, endangered orchid: symbiotic propagation study case

**BOCAYUVA, M.F.<sup>1</sup>**, C.A. Vieira<sup>1</sup>, A.C.F. Cruz<sup>1</sup>, E.F. Freitas<sup>1</sup>, T.G.R. Veloso<sup>1</sup> and M.C.M. Kasuya<sup>1</sup>

<sup>1</sup>Departamento de Microbiologia, Universidade Federal de Viçosa, Av. P. H. Rolfs, Campus UFV, Viçosa, Minas Gerais, 36570-000, Brazil, melissabocayuva@hotmail.com.

**Abstract:** The use of mycorrhizal orchids *in vitro* is a common practice used to produce healthy plants for conservation. The incentive for this symbiosis is performed during seed germination, but studies that determine the mycorrhizal capacity associated with orchid development are not enough. *Hadrolaelia jongheana* were germinated *in vitro* in association with *Tulasnella* sp. M65 on oatmeal agar (OMA). After protocorm formation, they were placed in two different media, OMA and OMA + nutrients + activated coal (OMA + M). After seven months the following variables were evaluated: plant height, number of leaves, longest leaf length, number of roots, root diameter, and mycorrhizal colonization (by sampling three root regions, apical, median, and basal). Acclimatized plant survival was 100%. OMA + M was the best culture media for plant height and root number and diameter. Higher mycorrhizal occurrence was also found associated with the OMA + M treatment, and mycorrhizal colonization was higher in the median and basal root regions. We conclude that the amount of nutrients added to the culture media for orchid development is essential to form plants of higher quality, ensuring constant material for endangered species conservation, and do not affect mycorrhizal colonization.

## PS 3-59 What stabilizes the ectomycorrhizal mutualism? An experimental test of partner choice by *Pinus muricata* in association with *Suillus brevipes*

**BOGAR, L.M.<sup>1</sup>** and K.G. Peay<sup>1</sup>

<sup>1</sup>Department of Biology, Stanford University, Stanford, CA 94305 USA, lbogar@stanford.edu.

**Abstract:** Ectomycorrhizal relationships can be thought of as trading agreements between plants and fungi. In most cases, the market helps both partners acquire the goods and services they need. It remains unclear, however, what keeps this market stable. One mechanism that could stabilize these interactions is preferential allocation of resources to the best available plant or fungal partner. It is known that arbuscular mycorrhizal plants and fungi are capable of this kind of regulation, but the issue has not been explored in ectomycorrhizas. To test this hypothesis, we manipulated partner quality in a split-root experiment using *Pinus muricata* (bishop pine) seedlings and *Suillus brevipes* (slippery Jack) fungi. We manipulated partner quality by planting separate chambers with hyphal ingrowth bags containing either sand (low quality) or a mixture of sand and casein (high quality). After ten weeks, pines will be labeled with <sup>13</sup>CO<sub>2</sub>, and carbon allocation to each root compartment will be measured using isotope mass spectrometry. Although both root compartments have the same fungal genotype, the fungus with access to protein is expected to provide more nitrogen to the plant than the fungus with access to only a sand bag. If plants are able to allocate resources based on partner quality, we expect that plants will allocate more carbon to the fungi that have access to protein-filled bags than to the fungi that have access to the sand bags and that this difference will be even more pronounced when the plant has a choice between one of each type. This result would demonstrate that the regulated exchange of photosynthetic carbon for soil-derived nitrogen in ectomycorrhizal associations does not require the plant to distinguish between fungal genotypes and that the trade can be controlled at fine spatial scales, suggesting that ectomycorrhizal and arbuscular mycorrhizal associations may operate in similar ways.

## KN 4 Arbuscular mycorrhizas: at the root of plant productivity

Giovannetti, M.<sup>1</sup>, M. Chialva<sup>1</sup>, V. Volpe<sup>1</sup>, M. Novero<sup>1</sup>, A. Salvioli<sup>1</sup>, X. Xie<sup>1</sup>, D. Patono<sup>1</sup> and **P. BONFANTE<sup>1</sup>**

<sup>1</sup>Department of Life Sciences and Systems Biology, University of Torino, Italy, paola.bonfante@unito.it.

**Abstract:** Arbuscular mycorrhizas (AM) are widespread symbioses that allow plants to receive minerals from the symbiotic fungus, which in turn get back carbon completing its life cycle. In poor nutrient conditions, AM fungi improve plant phosphate, nitrogen, and sulphur acquisition. The aims of this presentation are to provide an overview on the mechanisms that allow plants to uptake minerals and to reveal how mycorrhizal fungi may have a systemic impact on crops. Using a combination of genetics and molecular approaches, we demonstrate how the phosphate transporter of



*Lotus japonicus* (*LjPT4*) is active in root arbusculated cells as well as in root tips, where it creates a link among AM status, root branching, and environmental phosphate concentration. On the other hand, the sulphur transporter (*LjSultr1:2*) is expressed in arbusculated cells and in non-mycorrhizal roots, pointing at its role both in direct and fungal-mediated uptake. The results demonstrate how the symbiotic pathway for nutrient acquisition changes depending on the considered element. To understand the systemic effect of the symbiosis on tomato fruits, we used RNA-Seq to perform global transcriptome profiling on tomato fruits. We found that the fruits of mycorrhizal plants show gene transcripts, which are characteristic of a climacteric fleshy fruit, and are AM-independent, as well as transcripts characteristic of the mycorrhizal status. In addition, the investigation of tomato mutants, which are involved in ripening process, reveal an unexpected cross-talk between AM and fruit ripening. In conclusion, by improving the nutritional status and by affecting the source-sink relationships of the whole plant, mycorrhization has a strong impact on nutrition, health, and productivity of plants.

### PS 3-23 Digging deeper: occurrence of arbuscular mycorrhizal fungi at different soil depths in *Eucalyptus grandis* and *Acacia mangium* plantations

de Araujo Pereira, A.P.<sup>1</sup>, M.C. Santana<sup>1</sup>, J.A. BONFIM<sup>1</sup>, D.L.C. Mescolotti<sup>1</sup> and E.J.B.N. Cardoso<sup>1</sup>

<sup>1</sup>Department of Soil Science, Soil Microbiology Laboratory, College of Agriculture “Luiz de Queiroz” - University of São Paulo (ESALQ / USP). Avenida Pádua Dias, 11, CEP 13418-900. Piracicaba, SP, Brazil, ejbncard@usp.br.

**Abstract:** Recently, studies have shown positive responses in intercropped *Eucalyptus* and *Acacia mangium* plantations. The aim of this study was to evaluate the influence of pure and mixed systems (*E. grandis* and *A. mangium*) on the occurrence and diversity of arbuscular mycorrhizal fungi (AMF) in a gradient of soil depth. In this context, deep trenches were opened in pure stands of *Acacia* (100A), *Eucalyptus* (100E), and mixed systems (A+E). In mixed forest plantations, soil and roots were sampled at the base of *Acacia* (A+E) and the base of *Eucalyptus* (E+A). Soil samples at ten increasing depths from zero down to 800cm were obtained, with four replicates each. Regarding the presence of AMF, we found low root colonization rates and low abundance of AMF spores in all treatments, although 100E presented higher colonization rates than the others. Altogether, 16 AMF species were found, most of them belonging to the genus *Acaulospora*. Even though they were found in low numbers, AMF spores and root colonization were present even at the greatest depth. Processes involving the occurrence and diversity of AMF is a crucial point in understanding the development of forest plantations, mainly by involving the biogeochemical cycles, when seeking for new promising approaches and sustainability parameters.

### PS 1-6 Root and rhizosphere soil diversity of arbuscular mycorrhizal fungi in a Brazilian Atlantic forest toposequence

BONFIM, J.A.<sup>1</sup>, F. Oehl<sup>2</sup> and E.J.B.N. Cardoso<sup>1</sup>

<sup>1</sup>University of São Paulo, ESALQ, Pádua Dias Ave, no. 11, CEP 13418-900, Piracicaba, SP, Brazil, bonfimjoice@gmail.com;

<sup>2</sup>Agroscope, Federal Research Institute for Sustainability Sciences, Plant-Soil Interactions, Reckenholzstrasse 191, CH-8046 Zürich, Switzerland.

**Abstract:** The Atlantic forest in Brazil, a biodiversity hotspot, is considered a priority biome for diversity research because is one of the most threatened tropical forests in the world. We studied the diversity of arbuscular mycorrhizal fungi (AMF) in the Atlantic rain forest in Serra do Mar Park (SE Brazil), in roots of seven host plants and their rhizosphere soils in relationship with their soil environment, altitude and seasonality. The studied plots are located along an elevation gradient located at 80, 600 and 1000m a.s.l. Soil samples were collected (0-20cm) in four seasons from SE Brazilian, winter 2012 to autumn 2013. AMF spores were morphologically classified, and chemical, physical and microbiological soil characteristics were determined. AMF diversity in roots was evaluated using the NS31/AM1 primer pair, cloning and sequencing. Multivariate canonical discriminant analysis (CDA) and redundancy analysis (RDA) were applied to the data. In the rhizosphere soil 58 AMF species were identified. The genera *Acaulospora* and *Glomus* were predominant. However, in the roots, only 14 AMF sequencing groups were found and all had high similarity to the genus *Glomus*. The AMF community structure varied between areas and seasons and some species are more important than other areas for the separation of the sites. The soil characteristics showed a strong relationship with the occurrence of certain species. The highest AMF species diversity, based on Shannon's diversity index, was found for the highest altitude under study. Seasonality seemed not to affect the diversity. Our results show a high AMF diversity, higher than commonly found in

the Atlantic Forest. Another interesting finding is that the AMF community detected in roots or in the rhizosphere are completely different from each other and that differences in the community structure are related to variations in altitude even in geographically close lying sites.

#### PS 1-7 Drivers of arbuscular mycorrhizal fungi (Glomeromycota) communities along a European transect

**BOUFFAUD, M.L.**<sup>1,2</sup>, D. van Tuinen<sup>1</sup>, D. Wipf<sup>3</sup> and D. Redecker<sup>3</sup>

<sup>1</sup>INRA, UMR 1347 Agroécologie, 17 Rue Sully, BP 86510, 21065 Dijon Cedex, France, marie-lara.bouffaud@ufz.de;

<sup>2</sup>Present address: Department of Soil Ecology, UFZ-Helmholtz Centre for Environmental Research, D-06120 Halle (Saale), Germany, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, D-04103 Leipzig, Germany;

<sup>3</sup>Université de Bourgogne, UMR 1347 Agroécologie, 17 Rue Sully, BP 86510, 21065 Dijon Cedex, France.

**Abstract:** Arbuscular mycorrhiza is an extremely widespread symbiosis between plants and fungi from the Glomeromycota phylum. In their interaction with at least 65% of land plants including many crops, arbuscular mycorrhizal fungi (AMF) are involved in many important ecosystem functions and processes, including nutrient cycling and plant productivity. However, most studies addressing glomeromycotan community structure have been conducted at relatively small scale, with only a few ones analyzing AMF diversity at the regional scale or above, therefore the understanding of the geographic distribution of these fungi remains limited. Some AMF taxa seem to be surprisingly widespread and many cannot as yet be directly linked to a certain set of environmental conditions. Our study used the soil sampling scheme of the European project ECOFINDERS. In this project, the biodiversity of a large range of different groups of soil microorganisms was analyzed to assess soil functioning and to define indicators of soil health across Europe. The objective of our study was (i) to characterize the diversity of glomeromycotan fungi on the European scale, (ii) to define environmental factors influencing it, and (iii) to determine if a geographic structure exists for AMF. We therefore used pyrosequencing of the rDNA Internal Transcribed Spacer region to study glomeromycotan community structure in a transect of 54 samples. Environmental factors explained a large part of AMF community structure. We identified indicator species for these parameters, as well as generalists occurring across a wide range of samples, and assessed the influence of geography on community structure.

#### CS 1-4 Using proteomes of three *Rhizophagus* species in *Glomeromycota* to infer phylogenetic relationships

**BOYCE, G.R.**<sup>1</sup> and J.B. Morton<sup>1</sup>

<sup>1</sup>Division of Plant and Soil Sciences, West Virginia University, Morgantown, West Virginia, 26506 USA, gboyce@mix.wvu.edu.

**Abstract:** *Rhizophagus intraradices* and *R. irregularis* are closely related sister species based on rDNA sequence data, but they differ little in morphology and life history traits. Given that relationships among species in *Glomeromycota* is currently based on a single gene phylogeny, this study sought to determine the degree of divergence between both of these species and another related fungus, *R. clarus*, based on a broad sampling of expressed gene products. For each fungus, approximately 1,000 spores of a representative strain were enzymatically digested. Peptides were mapped using a thermo Q Exactive high accuracy mass spectrometer. Data were analyzed using Scaffold proteomic software. Masses of more than 70,000 unique peptides were profiled which then were matched to 7,279 proteins identified with >95% confidence. This sampling comprised 24% of the Uniprot theoretical proteome of *R. irregularis*. Of these proteins, 1,771 were known and the remainder was uncharacterized. Some of the latter appeared to be conserved across all three species, and they are being annotated. Among the characterized proteins, 39% were unique to *R. clarus*, whereas only 7% and 9% were unique to *R. intraradices* and *R. irregularis*, respectively. The degree of similarity in the profiles of the latter two species was an order of magnitude higher than similarity between them and *R. clarus*. These expressed protein profiles indicate phylogenetic distance between *R. intraradices* and *R. irregularis* is not as great as that depicted by the rDNA phylogeny. This spectrometric evidence, together with comparable patterns of rDNA evolution in other monophyletic taxa, suggests that rRNA genes may be retaining stable divergent polymorphisms that overestimate speciation events. Further elucidation of the proteomes of closely, as well as distantly, related lineages has the potential to clarify phylogenetic relationships, identify new genes for sequence analysis, and better understand functional relationships.

## PS 3-24 The use of AMF to improve soft fruit production in commercial substrate growing systems

BOYER, L.R.<sup>1</sup>, N. Gulbis<sup>2</sup>, K. Hajdu<sup>2</sup> and X. Xu<sup>1</sup>

<sup>1</sup>East Malling Research, East Malling West Malling, Kent, UK, ME19 6BD, louisa.robinson-boyer@emr.ac.uk; <sup>2</sup>Palntworks Ltd, Unit 930 Cornforth Drive, Kent Science Park, Sittingbourne, Kent, UK, ME9 8PX.

**Abstract:** Strawberry is an important crop within the UK and in 2011 accounted for 62% of all soft fruit production. For the past 40 years, soil borne diseases affecting strawberry production, primarily *Verticillium* wilt, has been controlled using chemical fumigation. Methyl bromide has already been banned for use in the EU and others are facing an uncertain future with legislation changes surrounding the use of pesticides. Although alternatives to these chemicals are being investigated, currently no effective control is available. To mitigate this threat and to extend the soft fruit season, nearly half of the UK strawberry production is in substrate (predominantly coir) under protection. Arbuscular mycorrhizal fungi (AMF) has been shown to provide beneficial effects to strawberry growth and yield at East Malling Research in the UK. The maintenance of a microbial population may be increasingly fundamental to the sustainable food security. Substrates such as coir are usually depleted of microbes including AMF and as such the introduction of beneficial microbes are more likely to generate benefits in commercial cropping systems. We report the benefit of inoculating strawberry in coir substrates under commercial fertigation treatments using different water regimes and nitrogen addition. Plant growth effects and fruit yields were analysed. The results show a consistent increase in the fresh weight of strawberry plants and increase in the yield of class I fruit. Both the number of fruit produced and the average weight of fruit were increased with AMF inoculation. However, microscopic root length colonisation was low in plants grown in coir compared to different substrates (e.g., soil and Terragreen). The structure of AMF colonising strawberry and maize roots grown in coir shows some physical differences from usual AMF structure in other substrates.

## CS 6-1 The global importance of mycorrhizas: scaling up from roots to continents

BRUNDRETT, M.<sup>1</sup>

<sup>1</sup>Department of Parks and Wildlife, Swan Region, Locked Bag 104, Bentley Delivery Centre, West Australia, 6983, Australia, mark.brundrett@dpaw.wa.gov.au.

**Abstract:** Effective definitions of mycorrhizas are required to provide consistent diagnosis of associations and minimise errors in mycorrhizal species lists. Another major cause of uncertainty involves the presence of mycorrhizal fungi in non-host plants, as these fungi are also potent endophytes. Plants that are fully nonmycorrhizal (NM) and those with inconsistent or facultative associations have similar ecological roles, frequently occur in extreme habitats where inoculum is limited and are often confusing. Issues concerning the identification of mycorrhizal fungi will also be briefly considered. A database that includes information on 10,000 plant species allowed data to be extrapolated to 99% of flowering plants with a high degree of consistency in most families. Case studies using root observations and floristic data will show the relative diversity or dominance of plants with different nutritional strategies at spatial scales from local areas to continents. These include ancient, highly infertile soils in the West Australian Wheatbelt, tropical Australia (Kakadu Park), Canadian deciduous forests, and eucalyptus forests. A transect across Australia will be used to illustrate symbiotic trends from temperate to tropical and arid to wet habitats in a wide diversity of soils. Australian diversity maps will illustrate the relative importance of ectomycorrhizal plants, NM plants, such as parasites and carnivores, and nitrogen fixing plants. In conclusion, mycorrhizas are important in almost every habitat and situation except for some of the harshest landscapes on Earth. However, we still need to improve the accuracy of surveys to identify mycorrhizas. In many cases, investigations of roots are not even required because we may get more accurate results by extrapolating from floristic data using knowledge of mycorrhizal plant families. However, there are exceptions to this generalisation and these include the two largest Australian plant families, Fabaceae and Myrtaceae, where root strategies are very complex and seem to evolve more rapidly than in any other family.

**BRUNS, T.**<sup>1</sup>

<sup>1</sup>Department of Plant and Microbial Biology, University of California, Berkeley, pogon@berkeley.edu.

**Abstract:** Fire is a natural part of most western forest ecosystems, and while plant strategies for surviving or recolonizing after fire are well known, much less is known about how fungi deal with this common disturbance. This talk will review some of the details that are known about how fungi behave and recolonized following severe, stand-replacing fires. Examples will be drawn primarily from studies of the Mt Vision Fire in Pt Reyes National Seashore and the more recent Rim Fire in Stanislaus National Forest and Yosemite National Park. These examples will also trace the development of “molecular ecology” from the crude RFLP days to the current high-throughput sequence.

**PS 3-60 The composition of arbuscular mycorrhizal communities is determined by the nutrient demand of the host plant and the availability of nutrients for the fungal symbionts**

**BÜCKING, H.**<sup>1</sup>, J.A. Mensah<sup>1</sup>, C.R. Fellbaum<sup>1</sup>, E.T. Kiers<sup>2</sup> and P.E. Pfeffer<sup>3</sup>

<sup>1</sup>Biology and Microbiology Department, South Dakota State University, Brookings, South Dakota 570017 USA, heike.bucking@sdstate.edu; <sup>2</sup>Institute of Ecological Science, Vrije Universiteit, HV Amsterdam 1081 Netherlands; <sup>3</sup>USDA, Agricultural Research Service, Eastern Regional Research Center, Wyndmoor Pennsylvania 19038-8598 USA.

**Abstract:** Arbuscular mycorrhizal (AM) interactions involve many-to-many interactions; each host plant is simultaneously colonized with multiple fungal species, and each AM fungus colonizes multiple host plants and forms common mycorrhizal networks (CMN). Despite the fact that the nutrient benefit for an individual host is determined by the composition of these AM fungal communities, we currently have no information how the composition of these communities is controlled. We studied this question in newly developed multi-chamber systems with two outer donor plants and one target plant. The donor plants were colonized with two different AM fungal species that differed in their mutualistic benefit. We tested how nutrient transport within CMN is affected by the nutrient demand of the target plant, and we studied how the nutrient demand and the availability of nutrients for individual mycorrhizal fungi affects the fungal community composition. We found that the transfer of nitrogen from the donor plant compartment to the target plant depended on the fungal species and on the nutrient demand of the target plant. Both fungi transferred more nitrogen to the target plant when the plant was under nitrogen stress. The q-PCR analysis of the AM fungal community composition revealed that the community composition depended on both the nutrient demand of the target plant and the access of nutrients for individual fungal species. Low beneficial fungal strains had a competitive advantage in establishing interactions with the target plant when they had access to a nutrient that the host plant was in need of. These results provide the first evidence that the host plays a critical role in the AM fungal community composition. The results are discussed in the context of our previously shown data that suggest nutrient and carbon exchange in the AM symbiosis is controlled by biological market dynamics.

**PS 2-36 Positive response of AM fungi to soil organic N correlates with abundance of ammonia oxidizers**

**BUKOVSKÁ, P.**<sup>1</sup>, M. Gryndler<sup>1</sup>, H. Gryndlerová<sup>1</sup>, D. Püschel<sup>1</sup> and J. Jansa<sup>1</sup>

<sup>1</sup>Institute of Microbiology, Czech Academy of Sciences, Vídeňská 1083, 14220 Prague 4, Czech Republic, bukovska@biomed.cas.cz.

**Abstract:** A large fraction of mineral nutrients in natural soil environments is recycled from complex and heterogeneously distributed organic sources and explored by both roots and/or their associated mycorrhizal fungi. Responses of arbuscular mycorrhizal (AM) hyphal networks to soil organic patches are, however, still little understood and so is the involvement of other microbes in this interaction. Therefore, we conducted a multiple choice experiment addressing AM hyphal responses by *Rhizophagus irregularis* and *Claroideoglomus claroideum* to different qualities of soil patches within the root-free zone. Furthermore, we profiled the prokaryotic and fungal communities in the patches by 454-sequencing to identify microorganisms that may explain the patterns of recorded AM hyphal growth. The colonization of the patches by AM fungi was assessed microscopically and by quantitative real-time PCR (qPCR) with



AM taxon-specific markers. Both of these approaches showed that AM hyphae responded positively to nitrogen (N)-containing organic amendments (i.e., chitin, DNA, albumin, and clover biomass) while no responses were recorded for cellulose, phytate, or inorganic phosphate as compared to the non-amended soil patch. Bioinformatics analysis including all the different types of patches from the *Rhizophagus*-inoculated pots provided deep insight into the structure of microbial communities. Abundance of several prokaryotes including *Nitrosospora* sp. (an ammonium oxidizer) showed a tight and positive correlation with AM hyphal proliferation within the soil patches. Abundance of some other prokaryotes correlated negatively, whereas almost no correlations were observed between AM hyphal proliferation and abundance of saprotrophic fungi. These results may indicate a causal (functional) relationship between some bacteria and AM fungi involved in N (re-) cycling and possibly implicates them in the N transfer from the organic N source in the soil via AM hyphae to the plants. Further studies scrutinizing the exact mechanisms of this inter-kingdom association are required.

#### PS 1-41 **Mycorrhizae, dual host plants, and mycorrhizal networks in the revegetation of the Elwha Basin, Washington, USA**

Clausen, K.A.<sup>1</sup>, A.M. Cortese<sup>1</sup>, K. Taylor<sup>1</sup> and **R.A. BUNN**<sup>1</sup>

<sup>1</sup>Department of Environmental Sciences, Huxley College, Western Washington University, ES Bldg. 522, 516 High St., Bellingham, WA 98225-9181, USA, Rebecca.bunn@wwu.edu.

**Abstract:** The removal of two dams from the Elwha River, Washington, USA left behind 800 acres of dewatered reservoir sediments, a poorly understood growing environment for revegetating plant communities. In a series of field surveys and greenhouse experiments, we examined the potential importance of mycorrhizal fungi for plants recolonizing these sediments. We (1) examined the abiotic characteristics of Elwha fine sediments to quantify potential limiting factors for plant growth, (2) quantified the availability of the important plant symbionts, arbuscular mycorrhizal and ectomycorrhizal fungi, (3) evaluated the success of commercial and whole soil mycorrhizal inoculum amendments on arbuscular mycorrhizal and ectomycorrhizal formation and function in Scouler's willow (*Salix scouleriana*), and (4) assessed the importance of dual host plants for arbuscular mycorrhizal and ectomycorrhizal hosts that share the same mycorrhizal network. Based on our study, the exposed reservoir sediment seems to be a harsh growing environment for colonizing plants due to its acidity, low % organic matter, homogeneity, and low levels of viable fungal propagules. Despite those findings, neither willow plants nor their mycorrhizal symbionts were inhibited by reservoir silt in the greenhouse. Mycorrhization of willow plants was increased with the addition of whole soil inoculum; however, willow plants formed mycorrhizae even without amendments. Amendments may result in more functional mycorrhizae as willows had more favorable N:P ratio which may have an influence on the long-term fitness of plants. In our last greenhouse study, we grew an AM host, yarrow (*Achillea millefolium*), and an ectomycorrhizal host, Douglas fir (*Psuedotsuga menziesii*), with and without the dual host plant Scouler's willow in mesocosms that allowed or prevented connection of mycorrhizal networks. We found extraradical hyphal densities were reduced in mesocosms where networks were not allowed to form. Host plants seemed unaffected, however, as we found no differences in plant biomass or levels of colonization.

#### PS 4-5 **Do native and invasive plants differ in their interactions with arbuscular mycorrhizal fungi? A meta-analysis**

**BUNN, R.A.**<sup>1</sup>, P.W. Ramsey<sup>2</sup> and Y. Lekberg<sup>2,3</sup>

<sup>1</sup>Department of Environmental Sciences, Huxley College, Western Washington University, ES Bldg. 522, 516 High St., Bellingham, WA 98225-9181, USA, Rebecca.bunn@wwu.edu; <sup>2</sup>MPG Ranch, 1001 S Higgins Ave, Suite A3, Missoula, MT 59801 USA; <sup>3</sup>Department of Ecosystem and Conservation Sciences, University of Montana, Missoula, MT 59802 USA.

**Abstract:** Increased global connectivity of humans has accelerated the rate at which exotic plants are introduced to novel environments. Arbuscular mycorrhizal (AM) fungi have the potential to influence invasion trajectories of exotic plants and two divergent hypotheses have emerged: the degraded and enhanced mutualism hypotheses. Both are based on the invasive plant interacting differently with AM fungi relative to the native community. In the degraded mutualism hypothesis the invader is posited to have a low (or no) AM dependency and to inhibit AM fungi, thereby reducing the competitiveness of more mycotrophic natives. In the enhanced mutualism hypothesis the invasive plant is posited to have high AM dependency and to receive a greater benefit from mutualists than native plants, conferring a competitive advantage to the invader. We used a meta-analysis approach on 67 publications, involving 70 native and 55 invasive

species to assess differences between native and invasive plants in AM colonization, AM dependency and host quality. We found no evidence that average colonization, growth responses and host quality differ between native and invasive plants, although growth responses (positive and negative) to AM fungi appear dampened among invasive plants. Instead of plant status (invasive vs. native), functional group (forb vs. grass) was an important explanatory variable. In general, forbs were more colonized than grasses and tended to respond positively to AM fungi, whereas growth responses in grasses were neutral or negative. In conclusion, neither the degraded nor the enhanced hypotheses were supported. Instead, our results indicate that AM fungi are most likely to influence invasion trajectories when native and invasive plants belong to different functional groups.

#### LT 2-10 Mycorrhiza-induced pathogen resistance in wheat, more than the sum of its parts?

**CAMERON, D.D.<sup>1</sup>**, R. Summers<sup>2</sup>, E. Parker<sup>1</sup>, H.B. Hughes<sup>1</sup>, K.J. Field<sup>3</sup>, S. Tille<sup>1</sup>, M.M. Burrell<sup>1</sup>, J. Ton<sup>1</sup>, J.R. Leake<sup>1</sup> and A.P. de Luque<sup>1,4</sup>

<sup>1</sup>Department of Animal and Plant Sciences, University of Sheffield, S10 2TN, UK, d.cameron@sheffield.ac.uk; <sup>2</sup>RAGT Seeds, Ickleton, Cambridge; <sup>3</sup>School of Biology, Faculty of Biological Sciences, University of Leeds, LS2 9JT, UK; <sup>4</sup>IFAPA, Centro Alameda del Obispo, Área de Mejora y Biotecnología, Avda. Menéndez Pidal s/n, Apdo. 3092, 14080 Córdoba, Spain.

**Abstract:** Plants can develop an enhanced defensive capacity against pathogens in response to colonisation by arbuscular mycorrhizal fungi (AMF). This 'mycorrhiza-induced resistance' (MIR) provides systemic protection against a wide range of attackers and shares characteristics with systemic acquired resistance (SAR) after pathogen infection and induced systemic resistance (ISR) following root colonisation by non-pathogenic rhizobacteria. It is commonly assumed that fungal stimulation of the plant immune system is solely responsible for MIR. Here, we present a novel 4-phase model of MIR that integrates different aspects of the induced resistance phenomenon in wheat: Phase I - root exudation of mycorrhiza-recruiting chemicals, Phase II - the plant immune system responding to infection by AMF, Phase III - immune suppression by AMF and recruitment of mycorrhizosphere bacteria, Phase IV - establishment of the mycorrhizosphere and induction of systemic resistance by mycorrhizosphere bacteria. Using a combination of biochemical (metabolomic) profiling integrated with phenotypic characterization, we validate this model, and in so doing, demonstrate that MIR is a cumulative effect of direct plant responses to mycorrhizal infection and indirect immune responses to ISR-eliciting rhizobacteria in the mycorrhizosphere. Moreover, we demonstrate that MIR can provide robust protection from agriculturally significant pathogens in wheat.

#### PS 4-64 Community composition and structure of arbuscular mycorrhizal fungi in the rhizosphere of poblano pepper

**CARBALLAR-HERNÁNDEZ, S.<sup>1</sup>**, L.V. Hernández-Cuevas<sup>2</sup>, A. Alarcón<sup>1</sup>, R. Ferrera-Cerrato<sup>1</sup>, N.M. Montaña-Arias<sup>3</sup>, J. Larsen<sup>4</sup> and A.M. Montiel-González<sup>2</sup>

<sup>1</sup>Postgrado de Edafología, Colegio de Postgraduados, carballar18@gmail.com; <sup>2</sup>Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala; <sup>3</sup>Departamento de Biología, División de Ciencias Biológicas y de la Salud, Universidad Autónoma Metropolitana-Iztapalapa; <sup>4</sup>Laboratorio de Agroecología, Centro de Investigaciones en Ecosistemas-Morelia, Universidad Nacional Autónoma de México.

**Abstract:** Poblano pepper is a variety of *Capsicum annuum* L., with high gastronomic and cultural value, which associates with arbuscular mycorrhizal fungi (AMF). Nevertheless, little is known about the AMF communities of poblano pepper at field conditions. This study determined the composition and structure of AMF communities of poblano pepper at San Pedro Cholula, Puebla (Mexico), by collecting rhizosphere soil samples from six sites with different agronomical inputs. For each site, the number of spores, relative abundance, and frequency of AMF species were estimated. Identification of AMF species was based on morphological features of the spore walls. The Pielou's evenness index, the Simpson's dominance index, and the Shannon-Wiener's diversity index were used for describing the structure of AMF communities. The  $\beta$ -diversity was estimated through the presence-absence of AMF species among sites by using the Sorensen coefficient. The analysis of variance showed significant differences ( $P < 0.01$ ) in the number of spores among the six sites. A total of 33 AMF morphospecies were identified, belonging to 12 genera and seven families, but ten species were shared in all sampling sites. *Funneliformis geosporum*, *Claroideoglossum claroideum*, and *C. luteum* were



the more abundant and frequent species. By comparing richness and diversity of AMF with a t-student test modified by Hutchinson, we observed significant differences ( $P < 0.01$ ) among sites. The most diverse and even AMF community (2.52 and 0.89, respectively) was found in those sites with moderate agronomic management, the lowest values were obtained in that site with high agronomic inputs (1.90 and 0.67, respectively). In contrast, the highest dominance was recorded in those sites with high inputs. The similarity of the AMF species composition among sites was high (85%), indicating that  $\beta$ -diversity is low.

#### PS 1-42 **Functional traits of arbuscular mycorrhizal fungal communities along succession in a tropical dry forest ecosystem**

**CARRILLO-SAUCEDO, S.M.**<sup>1</sup> and M.E. Gavito<sup>1</sup>

<sup>1</sup>Instituto de Investigaciones en Ecosistemas y Sustentabilidad. Universidad Nacional Autónoma de México-campus Morelia, 58090, Morelia, Michoacán, México, mcarrillo@cieco.unam.mx.

**Abstract:** Functional traits in natural communities of arbuscular mycorrhizal (AM) fungi are poorly understood. Tropical dry forests are currently highly dynamic ecosystems due to continuous transformation and land cover change. The high environmental heterogeneity resulting from land conversion likely selects the AM fungal species present in each community as a function of the traits that are more relevant to each new environment. To test this hypothesis we 1) described the composition of AM fungal communities in field sites of different successional stages, 2) measured some of their extraradical mycelium traits (hyphal length and hyphal allocation to diameter categories), and 3) explored the relation between community composition, mycelium traits, and environmental heterogeneity. We set up an experiment to measure community mycelium traits in pots using the same disinfected soil. Native AM fungal communities from active pastures, successional fields of different ages, and old-growth forests were used to inoculate a native, generalist host. Mycelium traits were measured after four months by microscopy and image analysis. We found that AM fungal communities from this ecosystem shared on average 60% of their species. Morphotypes were predominantly thick-walled, ornamented, and sporocarpic Glomerales. A cluster analysis divided the communities mainly into an early and late succession group, but there were also sites of discordant age within each group and out-groups. We found that the early succession communities, which are exposed to the driest and warmest environments, produced the thickest mycelium. Mid-succession communities, which are exposed to the coolest and more humid environments under low and thick canopy closure, presented the longest and finest mycelium. Late succession communities, which are exposed to intermediate levels of humidity and temperature, and found in a more structured canopy, showed intermediate values of most mycelium traits. Differences were, however, of small magnitude. We are currently investigating the plasticity of these traits under water stress, a factor that likely contributes to the shaping of AM fungal communities.

#### PS 4-65 **Assessing the progress of colonisation by arbuscular mycorrhiza of four plant species under different temperature regimes**

**CARVALHO, M.**<sup>1</sup>, I. Brito<sup>1</sup>, L. Alho<sup>1</sup> and M.J. Goss<sup>2</sup>

<sup>1</sup>University of Évora, ICAAM, Apartado 94, 7002 - 540 Évora, Portugal, mjc@uevora.pt; <sup>2</sup>University of Guelph, Kemptville Campus, Kemptville K0G 1J0, Ontario, Canada.

**Abstract:** To capitalize on the benefits offered by arbuscular mycorrhizal fungi (AMF) in agricultural systems the effect of low soil temperature has to be taken into consideration over large areas of the planet. However, the effect of suboptimal root zone temperatures on AMF colonisation is poorly understood. It has been suggested that responses depend on the host plant species. We hypothesized that this interdependence is a function of the parameter used to assess the presence of AMF in the roots. In a pot experiment with non-sterilized soil, we investigated the influence of three soil temperatures (10, 15 and 20 °C) on the progress of root colonisation of four host plant species (*Ornithopus compressus*, *Lolium rigidum*, *Triticum aestivum*, and *Zea mays*) by indigenous AMF. Plant root density, arbuscular colonisation rate (AC) and colonised root density (CRD) were assessed 14, 28 and 42 days after sowing. Based on CRD, the effect of temperature on the progress of root colonisation by AMF was independent of the host plant species. The apparent influence of the host plant species was only due to the species-specific effect of soil temperature on root growth and therefore on AC. The host plant species only determined the minimum temperature for the AM colonisation initiation,

possibly due to species-specific response of root growth and exudation to cool temperatures. Differences between plant species in the degree of mycotrophy might result from different root growth rates, which influence AC. Consequently, CRD should also be used to compare the level of AMF colonisation between different plant species.

## CS 8-2 The role of arbuscular mycorrhizas in agriculture: insights from a mycorrhiza defective tomato mutant

CAVAGNARO, T.R.<sup>1</sup>, S.J. Watts-Williams<sup>2</sup>, T.M. Bowles<sup>3</sup> and L.E. Jackson<sup>3</sup>

<sup>1</sup>School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, PMB 1 Glen Osmond, SA, 5064, Australia, timothy.cavagnaro@adelaide.edu.au; <sup>2</sup>Boyce Thompson Institute for Plant Research, Tower Rd, Ithaca, NY, USA;

<sup>3</sup>Department of Land, Air and Water Resources, The University of California Davis, 1 Shields Ave, Davis, CA 95616, USA.

**Abstract:** Arbuscular mycorrhizas (AM) play an important and increasingly well-recognized role in agroecosystems. However, the near ubiquity of arbuscular mycorrhizal fungi in soils can make studying their functioning in the field challenging. One way of meeting this challenge is to grow mycorrhiza defective mutants and their mycorrhizal wild-type progenitors in field soils. We have used this approach in a wide range of agricultural soils from both Australia and California to gain insights into the formation and functioning of AM. These approaches include field surveys and experiments, highly mechanistic glasshouse-based studies, the use of isotopic tracers, and gene expression studies. We will provide an overview of much of this work, with an emphasis on 1) formation of AM under different field conditions and its relationship to soil management and fertility, 2) effects of forming AM on plant growth, both for biomass allocation and agronomic yields, and 3) consequences of forming AM on plant nutrient uptake, soil nutrient cycling, and nutrient loss. The emphasis will be to synthesize these findings to understand AM functioning in intensively-managed agricultural systems, and how various management practices may bolster AM communities to improve functioning. Finally, we will consider some of the limitations and advantages of using mutant-based approaches to studying AM in field soils, with a view to stimulating and guiding future work in this area.

## PS 1-8 Arbuscular mycorrhizal fungi from New Caledonia: first identification from roots of *Phyllanthus* and *Psychotria* in ultramafic and volcano-sedimentary soils

CAVALOC, Y.<sup>1</sup>, S. Gensous<sup>1</sup> and H. Amir<sup>1</sup>

<sup>1</sup>LIVE EA 4243, University of New-Caledonia, BPR4, 98851 Noumea Cedex, New-Caledonia, yvon.cavaloc@univ-nc.nc.

**Abstract:** New Caledonia, a tropical archipelago in the South Pacific, is known as one of the unique biodiversity hot spot displaying an exceptionally high concentration of endemic and endangered plant species. Over 3,200 species represent the actual flora of which 74% are endemic to the archipelago. The high percentage of vascular plant endemism is mainly due to plant communities developed on ultramafic serpentine rocks covering one third of the main island. Consequently New Caledonia has also been listed among the world's main hotspots for metallophytes with 2,145 serpentine plant species, among which 82% are endemic. Numerous studies have reported the influence of mycorrhizal fungi on plant tolerance to toxic elements in soils contaminated with heavy metals. However, despite the importance that might have those fungi on plant growth on metals, nothing is known about their diversity in New Caledonia. Based on the molecular analysis of 18S rDNA, we have analyzed the diversity of arbuscular mycorrhizal fungi (AMF) present in ultramafic or volcano-sedimentary soils. This analysis has been performed on roots of two plant genera: *Phyllanthus* and *Psychotria*. These two genera are highly represented in both soils and exhibit species that have developed alternative strategies toward nickel, which is very abundant in New Caledonia. *Psychotria gabriellae* and *Phyllanthus favieri* are indeed nickel hyperaccumulators. The obtained sequences were grouped within operational taxonomic units (OTUs) for taxonomic identification. In this study, we show that soil composition influences the AMF assembly. We also show that hyperaccumulating plant species harbour specific AMF communities. Furthermore, we identify novel SSU sequences that could correspond to yet unidentified fungi raising the possibility of discovering new AMF taxa in this poorly studied geographical area.

#### LT 4-5 Mass-produced genetically modified *Rhizophagus irregularis* alter cassava production in field

CEBALLOS, I.C.<sup>1</sup>, A. Rodriguez<sup>1</sup> and I.R. Sanders<sup>2</sup>

<sup>1</sup>Department of Biology, Universidad Nacional de Colombia, Avenida Carrera 30 # 45, Bogotá, Colombia, icceballos@unal.edu.co; <sup>2</sup>Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland.

**Abstract:** We have previously shown that *in vitro* mass-produced *Rhizophagus irregularis* significantly increases the production of cassava in the field. Manipulating the genetics of *R. irregularis* by crossing and segregation of different cultured fungal lines could be used to further increase cassava production. The objective of this work was to study if genetically manipulated arbuscular mycorrhizal fungal (AMF) lines lead to differences in cassava growth in the field and in the presence of a native AMF community. We inoculated cassava varieties (var. MCOL2737 and var. COL4574) with 15 *in vitro* mass-produced lines of *R. irregularis* and evaluated the growth and root production. This experiment was established in the eastern plains region of Colombia (Yopal) in two successive years. The root weight varied according to the AMF line (from a positive to a negative effect), and the responses induced by each line were also different between cassava varieties. Fungal lines also had an effect on total AMF colonization, but there was no correlation between production and colonization. There was no significant difference in the effects of the lines in the two years, showing that the results were reproducible. We also established the experiment in Santana, where the climate and soil are different. In Santana, there was no significant effect of AMF lines. We conclude that genetic manipulation of AMF had an effect on cassava growth and root production in Yopal. Furthermore, the AMF lines effect on growth, production, and colonization depended on the cassava variety and the environment. We demonstrated that manipulating within-species genetic variation in AMF could be used to design AMF that have a desired effect on a given crop in a particular environment.

#### SY 3-2 The structure of mycorrhizal interactions: the need for a mechanism-oriented approach to interpret community-level patterns

CHAGNON, P.L.<sup>1,2</sup>, R.L. Bradley<sup>1</sup> and J.N. Klironomos<sup>3</sup>

<sup>1</sup>Université de Sherbrooke, Sherbrooke, QC, Canada, J1K 2R1, pchagnon@ualberta.ca; <sup>2</sup>University of Alberta, Edmonton, AB, Canada, T6G 2R3; <sup>3</sup>University of British Columbia, Kelowna, BC, Canada, V1V 1V7.

**Abstract:** It is well known that mycorrhizal networks provide many valuable ecosystem services such as nutrient retention, increased primary productivity, and nutrient cycling in terrestrial ecosystems. However, much less is known about the resistance and resilience of these systems when facing disturbances. Recent studies have shown that mycorrhizal networks tend to be built around a few highly generalist species, and are characterized by an absence of reciprocal specialization (i.e., nestedness of interactions). Such structure has been argued to favor community stability and resilience by theoretical studies. However, a key aspect of real ecological networks missing from those theoretical studies was the notion of flexibility in interactions. Here, we characterized mycorrhizal interactions for 18 local networks, and we show that although local networks tended to display a deterministic structure, much variability could be seen among networks, even at small spatial scales. This questions the relevance of seeing ecological network structure as a feature arising from a selection towards higher community stability (as suggested by theoretical studies). From our results, it rather seems that one key mechanism stabilizing mycorrhizal networks could be flexibility in interaction patterns. Approaches to better understand the mechanistic drivers of mycorrhizal network structure are discussed.

#### PS 2-2 Excessive Cd induced protein adhered with cell wall of *Laccaria bicolor*

CHAI, L.<sup>1</sup> and Y. Huang<sup>1</sup>

<sup>1</sup>College of Environmental Sciences and Engineering, Peking University, Beijing, China, dclinet5727@gmail.com.

**Abstract:** It is well known that ectomycorrhizal fungi exhibit high tolerance to excessive amounts of heavy metals in the environment. Fungal slime exudate from ectomycorrhizal mycelium is believed to be an important component in the chelation of excessive heavy metals, especially those closely adhered to the cell wall, and plays an important role in the extracellular chelation process under heavy metal stress. To understand this process, it is necessary to efficiently

separate slime from the cell. Therefore, six different separation processes, including three chemical and three physical methods, were employed to separate the mycelia exudate slime of the ectomycorrhizal fungi *Laccaria bicolor* from its cell wall. Compared to chemical methods, physical methods show higher separation efficiency with a relatively high amount of protein harvested from the extraction, and ultra-sonication at 150w for 1 minute had the highest efficiency. With the separation process, more proteins were extracted from *L. bicolor* mycelium under Cd stress at 1ug/ml than from those in the control, indicating that expression levels of certain proteins were elevated by Cd stress. The SDS-PAGE profile of these proteins indicates three new bands located between 43kDa to 31kDa, which might hint at a Cd stress induced change of protein components in mycelia exudate slime. The identification and metal-binding behavior of these proteins need further study to understand the tolerance mechanisms of ectomycorrhizal fungi under heavy metal stress.

### PS 3-25 The effects of land use change in tropical peat on vesicular arbuscular mycorrhiza of sago palm (*Metroxylon sagu* Rottboll)

CHAN, M.K.Y.<sup>1</sup>

<sup>1</sup>Faculty of Plantation and Agrotechnology, Universiti Teknologi MARA, Malaysia, drmchan@sarawak.uitm.edu.my.

**Abstract:** Sago palm, a source of commercial starch, is an extremely hardy plant, thriving in swampy, acidic peat soils where few other crops survive. They continually produce suckers maturing at 10 to 15 years virtually producing palms in perpetuity with no necessity for replanting. Sarawak, Malaysia embarked into the world first large-scale commercial plantation of sago palm in drained peat. An arbuscular mycorrhizal (AM) fungus belonging to the Glomales of the Zygomycetes was isolated from wild sago palm roots. A study was therefore conducted to investigate whether the change of peat soil environment affected the relationship between the AM fungus and sago palm. Soil and root samples were collected using systematic random sampling across the field using a diagonal straight line transect at three metre interval from sago palm planted in drained peat and wild sago palm in waterlogged peat. The pH of the drained peat and waterlogged peat was 3.4 and 3.8, respectively. Using the wet sieving and decanting technique, 511 AM spores/100 g of drained peat and 194 AM spores/100 g of peat were obtained. The infectivity percentage of the roots, using gridline intersect method was 88%, ranging from 40 to 100% in the roots from drained peat as compared to the 100% in peat. There was no difference in infectivity of the AM fungus inoculum from drained peat and waterlogged peat on the alternate host *Allium* sp., both responses were 35%. There was a positive correlation between spore abundance and soil phosphate as the drained peat has higher phosphate content from fertilizer application. This study demonstrated that drainage has not affected the relationship between the AM fungi and sago palm, but the application of phosphate has reduced the infectivity.

### PS 2-3 Evolution and diversity of sexually-related genes in a supposed asexual arbuscular mycorrhizal fungus

CHARRON, P.<sup>1</sup>, T. Marton<sup>1</sup> and N. Corradi<sup>1</sup>

<sup>1</sup>Center for Advanced Research in Environmental Genomics, University of Ottawa, Ottawa, Ontario K1N 6N5 Canada, philippechar@hotmail.com.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are ancient organisms that form symbioses with more than 80% of land plants. Fossil evidence of this partnership dates back 500 million years ago, when land was first colonized by plants. The mutualistic relationship between host roots and the fungus consists of an exchange of carbohydrates for water and minerals (phosphorus and nitrogen), compounds that are essential to the proliferation of both organisms. Despite their extraordinary longevity, a lack of evidence supporting sexual reproduction has led to assumption that AMF are purely clonal organisms. However, recent genome analyses are starting to challenge this notion. Specifically, AMF genomes encode for a large number of homologues of proteins that are linked to sexual processes in other eukaryotes, including several typically involved in partner recognition, such as mating-type high mobility group (MAT-HMG) proteins found in mating-type loci. The present study expands the current knowledge of sex-related genes in AMF by exploring new genome data obtained from several isolates of the AMF model *Rhizophagus irregularis*. These new investigations reveal that a single isolate can potentially code 227 MAT-HMGs, or 54% more than previously reported. Furthermore, these genes differ considerably in both number and structure among isolates of *R. irregularis*, supporting the presence of substantial genome plasticity in this species. Some MAT-HMGs display unique genomic organizations that are reminiscent of operons, whereas others are similar to MAT-loci of the Zygomycota and Ascomycota phyla. In retrospect, this research uncovers an unprecedented amount of AMF genes that are homologues to sex-related genes of other fungi, and reveals for the first time their atypical genomic architecture.

CHARTIER FITZGERALD, V.<sup>1</sup>, G. Hawley<sup>2</sup> and J.F. Dames<sup>1</sup>

<sup>1</sup>Department of Microbiology and Biochemistry, Mycorrhizal Research Laboratory, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa, g08c1015@campus.ru.ac.za; <sup>2</sup>Coastal and Environmental Services, 16 Tyrell Rd, Berea, East London, 5241, South Africa.

**Abstract:** Within South Africa natural forests are rare, occurring over only 8% of the country's surface, thus the forestry industry is dependent on plantations of exotic pine and eucalyptus species. Plantations cover approximately 1.3 million hectares of land with approximately 52% of the plantations being *Pinus* species. The forestry industry is facing increasing pathogen pressure. *Fusarium circinatum* has become one of the greatest constraints on the pine industry, especially to *P. patula*. This fungus has been estimated to cost the forestry industry in excess of ZAR 12 million per annum. It is often not identified in nursery seedlings until after commercial planting resulting in extremely high levels of mortality. Nursery seedlings in South Africa are not inoculated with ectomycorrhizal (ECM) fungi or other beneficial microbes. The application of an ECM fungal inoculum during the seedling production could potentially increase seedling growth and development and increase survival in the field, specifically reducing the effects of *F. circinatum*. A preliminary investigation into the presence and percentage ECM colonisation of *P. patula* seedlings from 10 different South African nurseries was conducted. The average natural percentage colonisation of these nurseries was low, ranging from 2 - 21%. Approximately 10 different morphotypes were noted to occur on the seedlings as a result of natural inoculations. Morphotypes ranged from simple to tubercle ramification with smooth to cottony mantle surfaces. Full morphological characterisation and molecular identifications using the ITS gene will be presented. Further studies will include inoculation with selected ECM fungal isolates as well as mycorrhizal helper bacteria to assess biocontrol potential against *F. circinatum*.

PS 2-20 Restore mycorrhiza for sustainable forestry

CHAUBEY, O.P.<sup>1</sup>, P. Bohre<sup>1</sup>, Jamaluddin<sup>2</sup> and G. Krishnamurthy<sup>1</sup>

<sup>1</sup>State Forest Research Institute, Jabalpur - 482008 (M.P.) India, chaubey.dr@gmail.com; <sup>2</sup>Rani Durgawati University, Jabalpur- 482001(M.P.) India.

**Abstract:** Arbuscular mycorrhizal fungi (AMF), the synonym of VAM fungi, are important soil microbes that form symbiotic associations with most terrestrial plants on Earth. These mycorrhizae can grow inside plant roots and serve them in a number of ways. The most important role of mycorrhizal fungal hyphae is to extend the surface area of roots. These fungi improve availability of nutrients in utilizable forms. Their ability to bind soil particles and their role in removing heavy metals from overburden soils and retaining them in their cell walls, proved to be excellent in reclamation efforts. Mycorrhizal diversity increases with plant species diversity as the potential number of associations increases. The use of AMF in ecological restoration has been shown to enable host plant establishment on degraded soils by improving soil quality and health (phytoremediation) through influencing physical and biological properties (including the restoration of native AMF), as well as affecting soil nitrogen and organic matter content. AMF species vary in frequency among plant species, and grasses tend to harbor more AMF. In our study, older plantations had large populations of arbuscular mycorrhizal spores of different species. In younger plantations, the AMF spores gradually decreased due to less available carbon and other nutrients. The role of AMF was to recover the nutrient status of coalmine spoil soil. AMF were recognized as the driving force behind nutrient transformations in soil and, thus, have a major role in sustainable forestry and ecosystem functioning. In this context, an ecosystem approach for rehabilitation of mine spoils and overburden areas should be adopted. Plantations of native species of high productivity and soil conserving species, based on high photosynthetic ability and soil conserving efficiency, should be preferred and encouraged.



### LT 3-12 MycoDB: a global database for mycorrhizal meta-analyses

**CHAUDHARY, V.B.**<sup>1</sup>, A. Antoninka<sup>2</sup>, J. Bever<sup>3</sup>, J. Cannon<sup>4</sup>, A. Craig<sup>2</sup>, J. Duchicella<sup>3</sup>, A. Frame<sup>8</sup>, C. Gehring<sup>2</sup>, M. Ha<sup>4</sup>, M. Hart<sup>13</sup>, J. Hopkins<sup>3</sup>, B. Ji<sup>3</sup>, N.C. Johnson<sup>2</sup>, W. Kaonongbua<sup>5</sup>, J. Karst<sup>14</sup>, R. Koide<sup>15</sup>, J. Lamit<sup>16</sup>, L. McCormack<sup>17</sup>, J. Meadow<sup>6</sup>, B. Milligan<sup>7</sup>, J. Moore<sup>18</sup>, T. Pendergast<sup>8</sup>, B. Piculell<sup>4</sup>, B. Ramsby<sup>4</sup>, M. Rúa<sup>4</sup>, S. Simard<sup>19</sup>, S. Shrestha<sup>12</sup>, J. Umbanhowe<sup>8</sup>, W. Viechtbauer<sup>9</sup>, L. Walters<sup>11</sup>, G. Wilson<sup>12</sup>, P. Zee<sup>10</sup> and J. Hoeksema<sup>4</sup>

<sup>1</sup>Loyola University Chicago, Chicago, IL, vchaudhary@luc.edu; <sup>2</sup>Northern Arizona University, Flagstaff, AZ; <sup>3</sup>Department of Biology, Indiana University, Bloomington, IN; <sup>4</sup>Department of Biology, University of Mississippi, University, MS; <sup>5</sup>King Mongkuts University of Technology Thonburi, Thailand; <sup>6</sup>Institute of Ecology and Evolution, University of Oregon, Eugene, OR; <sup>7</sup>Department of Biology, New Mexico State University; <sup>8</sup>University of North Carolina, Chapel Hill, Chapel Hill, NC; <sup>9</sup>Department of Psychiatry and Psychology, Maastricht University; <sup>10</sup>Department of Biology, Stanford University, Stanford, CA; <sup>11</sup>Enova International Inc., Chicago, IL; <sup>12</sup>Oklahoma State University, Stillwater, OK; <sup>13</sup>University of British Columbia Okanagan, Kelowna, BC; <sup>14</sup>University of Alberta, Edmonton, AB; <sup>15</sup>Brigham Young University, Provo, UT; <sup>16</sup>Michigan Technological University, Houghton, MI; <sup>17</sup>Penn State University, University Park, PA; <sup>18</sup>Colorado State University, Fort Collins, CO; <sup>19</sup>University of British Columbia, Vancouver, BC.

**Abstract:** Meta-analysis, the statistical combination of results of multiple studies, is an increasingly important tool to quantitatively address large-scale questions in ecology and evolution. As such, meta-analysis is a vital approach to integrating knowledge of mycorrhizal associations across continents and scales. We announce the public release of MycoDB, a database of 3,979 studies to aid in multi-factor meta-analyses to elucidate the ecological and evolutionary context in which mycorrhizal fungi are beneficial to plant productivity. Over a period of 10 years with nearly 80 collaborators, we compiled data on plant biomass response to addition of mycorrhizal fungi, including meta-analysis metrics (i.e., effect sizes, variance estimates, replication) and 14 additional explanatory variables that describe the biotic and abiotic context of each study. Published along with the experimental plant response data are phylogenetic trees for all plants and fungi included in the database. To our knowledge, MycoDB is the largest meta-analysis database of its kind. Thus far, the data have been used to demonstrate how soil biotic and abiotic complexity, local adaptation, and plant and fungal phylogenetic relationships can influence plant growth response to mycorrhizal fungal inoculation. The results of these studies are described in two subsequent presentations. We aim to share these data to 1) highlight significant gaps in mycorrhizal research with respect to scale, biomes, and continents, 2) promote synthesis in mycorrhizal research to evaluate the generality of mycorrhizal associations, and 3) encourage future meta-analyses to explore the ecological and evolutionary context of mycorrhizal functioning in ecosystems.

### PS 3-27 Innovative design to manage mycorrhizas in agroecological cropping systems

**CHAVE, M.**<sup>1</sup> and V. Angeon<sup>2,3</sup>

<sup>1</sup>INRA ASTRO UR 1321 Agrosystèmes Tropicaux F-97170 Petit-Bourg France, marie.chave@antilles.inra.fr; <sup>2</sup>Université des Antilles, CAEC, Petit Morne F-97232 Le Lamentin France; <sup>3</sup>INRA UR 143 Unité de Recherche en Zootechnie F-97170 Petit-Bourg France.

**Abstract:** Agroecology aims to design economically and environmentally efficient cropping systems, based on the exploitation of natural regulations. Arbuscular mycorrhizas are of growing interest for such an ecologization of agriculture, as they are likely to enhance crop health and productivity, reducing the use of chemicals. However, agroecology no longer offers one-stop solutions but calls for the implementation of participatory innovative design strategies. While managing mycorrhizas requires prior mastery of mycorrhizal-friendly practices, we analyzed the brakes and the levers identified by horticulture producers in Martinique (French West Indies). We implemented the KCP® (Knowledge Concepts Propositions) methodology, a new management science method for collective creative design, used in many industrial cases. Researchers, technical advisers and farmers were involved in a three step design strategy aimed at sharing knowledge on “How to enhance and benefit from mycorrhizas?”. We implemented: 1. a collaborative workshop for sharing Knowledge; 2. on farm surveys to assess Knowledge and mycorrhizas Concept appropriation 3. a final workshop to combine emerging Propositions. Our results show that two cohorts of farmers significantly differed. “Best learners” moved more easily from the knowledge-sharing phase (K) to the proposition of levers (P) than “In progress learners”. All the partners’ propositions were synthesized in a concept tree starting from an initial concept “CO: Mycorrhizas management” which

was progressively divided in sub-concepts. Most of the farmers' propositions rely on the sub-concept of mycorrhizal networks mobilization rather than on the introduction of propagules. Farmers suggested experimenting with native strains production through mycorrhizal crops cultivation in given pedoclimatic areas. They proposed to implement collective arrangements to define the convenient technology, as on farm production is labor-intensive and uncertain. The KCP® approach explored the whole potential of the "mycorrhizas management" concept, enabled relevant knowledge activation, acquisition and production, and resulted in a common research-action project.

### PS 3-61 Root mycorrhization and its influence on relative expression of sucrose metabolism genes in aboveground and belowground tissues

Salmeron-Santiago, I.A.<sup>1</sup>, J. Rivero-Bravo<sup>2</sup>, M.J. Pozo-Jiménez<sup>2</sup> and A.T. CHÁVEZ-BÁRCENAS<sup>1</sup>

<sup>1</sup>Laboratorio de Interacciones Planta-Ambiente, Facultad de Agrobiología "Presidente Juárez", Universidad Michoacana de San Nicolás de Hidalgo, Uruapan 60170 Mexico, tztzquichavez@gmail.com; <sup>2</sup>Departamento de Microbiología de Suelos y Sistemas Simbióticos, Estación Experimental del Zaidín, Granada E-18008 Spain.

**Abstract:** It has been suggested that sucrose metabolism is involved in supplying carbon to arbuscular mycorrhizae because synthesis and catabolism of sucrose support carbon flux among source and sink plant tissues. To explore the mechanisms that rule carbon allocation and distribution in plants during mycorrhizal symbiosis, the influence of the interaction established between the arbuscular mycorrhizal fungi (AMF) *Funneliformis mosseae* (BEG 12) and tomato plant roots over the gene expression of sucrose metabolism genes was analysed in aboveground and belowground tissues. Leaf and root tissues of plants maintained in a greenhouse for seven weeks after AMF inoculation were used to conduct gene expression analysis by real time RT-PCR. The genes selected to be analysed were: sucrose-phosphate synthase *spsA2* and *spsC*, which encode one of the key enzymes in sucrose synthesis and partitioning in plants, sucrose synthase genes *SUS1* and *SUS3*, and *Lin6* from an apoplastic invertase, which are involved in sucrose catabolism. Additionally, the content of soluble sugar fractions was quantified by colorimetric methods. It was found that the expression of *spsC* increases in leaf tissues of mycorrhizal plants compared with those that were non-mycorrhizal (NM); this effect was related to major accumulation of sucrose in leaf tissues. The expression of *SUS3* and *Lin6* also increases in leaves as a result of mycorrhization, which could be associated to both plant metabolism maintenance and sucrose transit augmentation through apoplast, respectively. It was also found that the expression of *SUS3* decreases in mycorrhizal plant roots compared to NM roots. These results suggest that arbuscular mycorrhizal symbiosis triggers sucrose synthesis in source tissues but causes a repression in the expression of genes involved in the synthesis of carbohydrate polymers in root tissues in order to preferentially canalize the sucrose catabolism products to sustain the symbiosis.

### LT 3-5 Mycelial production and standing fungal biomass are higher in temperate hardwood forests dominated by ectomycorrhizal trees than in forests dominated by arbuscular mycorrhizal trees

CHEEKE, T.E.<sup>1,2</sup>, R.P. Phillips<sup>1</sup>, A.L. Kuhn<sup>3</sup>, A. Rosling<sup>4</sup>, J.D. Bever<sup>1</sup> and P. Fransson<sup>2</sup>

<sup>1</sup>Department of Biology, Indiana University, Bloomington, IN 47405 USA, tcheeke@indiana.edu; <sup>2</sup>Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden; <sup>3</sup>State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210 USA; <sup>4</sup>Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden.

**Abstract:** Mycorrhizal mycelia are the dominant pathway through which nutrients are transported to trees and plant-derived carbon (C) enters forest soils. While much is known about the role mycorrhiza play in the transfer of C for nutrients, much less is known about these dynamics in stands dominated by tree species that associate with arbuscular mycorrhizal (AM) fungi versus those that associate with ectomycorrhizal (ECM) fungi. We quantified fungal mycelia production, fungal:bacterial ratios, and the activity of five extracellular enzymes across a gradient driven by tree species and their mycorrhizal associates in three temperate hardwood forests in central Indiana, USA. Ergosterol was used to measure fungal biomass; quantitative PCR was used to determine fungal:bacterial ratios; and enzyme activity was used to evaluate seasonal variation in C, N, and P acquiring enzymes in plots dominated by AM-associated trees, ECM-associated trees, and a mixture of AM-ECM trees. We found strong convergence in the degree to which the abundance of AM and ECM trees in a plot influenced fungal dynamics, as all three sites showed similar patterns across their respective mycorrhizal

gradients. Over a growing season, plots dominated by ECM trees had nearly three times more standing biomass of *Dikarya* than plots dominated by AM trees, and over 1.5 times more hyphal production. Fungal:bacterial ratios increased with increasing dominance of ECM-associated trees in all sites, and acid phosphatase activity was higher in ECM plots, while peroxidase activity was higher in AM plots. This study suggests that decomposition processes, soil C storage, and nutrient availability in temperate hardwood forests vary with the dominant tree species. Understanding the role of mycelial production and activity on soil nutrient availability is critical for predicting how forest ecosystems might respond to environmental perturbations such as climate change, where range shifts in dominant tree species are predicted to occur.

### CS 8-3 Ecological drivers for the biodiversity of AM fungi in the farming-pastoral ecotone of northern China

**CHEN, B.D.**<sup>1</sup>, D. Xiang<sup>1</sup>, E. Verbruggen<sup>2,3</sup>, Y.J. Hu<sup>1</sup>, Y.L. Chen<sup>1</sup> and M.C. Rillig<sup>2,3</sup>

<sup>1</sup>State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, 100085, P.R. China, bdchen@rcees.ac.cn; <sup>2</sup>Dahlem Center of Plant Sciences, Plant Ecology, Freie Universität Berlin-Institut für Biologie, Berlin, Germany; <sup>3</sup>Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB), Berlin, Germany.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are ubiquitous root symbionts that play key roles in supporting ecosystem sustainability. We adopted 454 pyrosequencing to examine the effects of different land use (grassland versus farmland) on AM fungal abundance, diversity, and community composition in a balanced sampling scheme across the farming-pastoral ecotone of northern China. We applied structural equation model (SEM), and multivariate analyses to disentangle direct and indirect effects mediated by measured biotic and abiotic factors of land use on AM fungi. Land use conversion from grassland to farmland significantly reduced AM fungal richness and extraradical hyphal length density, together with a clear change in AM fungal community composition. The abundance of four AMF genera, *Funnelformis*, *Claroideoglossum*, *Paraglossum*, and *Rhizophagus*, were significantly higher in farmland than in grassland, while the abundance of the genus *Glomus* was clearly reduced in farmland. SEM showed that effects of land use on AMF diversity and abundance were primarily mediated by soil available phosphorus and soil structural quality. Further analysis revealed that mycorrhizal fungi associated with high soil N: P ratios are more likely to be lost upon conversion from grasslands to arable agriculture. In contrast, land use remained a significant predictor of community composition when controlling for other environmental variables, indicating that factors such as soil disturbance and irrigation are likely to be important. Our study shows that land use has a partly predictable effect on AMF communities across this ecologically relevant area of China, and indicates which land-use practices are most detrimental to sustainability of this ecosystem.

### PS 1-9 Diversity of arbuscular mycorrhizal fungi in sugarcane fields of Southeastern China

**CHEN, T.S.**<sup>1</sup>, J.L. Zhang<sup>1</sup>, D.P. Li<sup>1</sup>, Q. Wang<sup>1</sup>, Y.Y. Long<sup>1</sup>, Y.Y. Huang<sup>2</sup> and S. Li<sup>3</sup>

<sup>1</sup>Micobiology Research Institute, Guangxi Academy of Agricultural Sciences, Nanning, Guangxi 530007 China, chen20409@hotmail.com; <sup>2</sup>Agricultural Resource and Environment Research Institute, Guangxi Academy of Agricultural Sciences, Nanning, Guangxi 530007 China; <sup>3</sup>Sugarcane Research institute, Guangxi Academy of Agricultural Sciences, Nanning Guangxi 530007 China.

**Abstract:** Over 20 years of continuous cropping of sugarcane in southern China, along with the over-application of chemical fertilizer, has not only contaminated the environment, but also deteriorated the soil, resulting in extremely low pH. Little has been known about the indigenous arbuscular mycorrhizal fungi (AMF) communities in sugarcane soils. We investigated the AMF communities in rhizosphere soils of sugarcane planting areas in Southeast Guangxi, China, and six spore species of AMF including two of *Glomus*, three of *Acaulospora* and one of *Scutellospora* were identified in the soil samples. Investigations show that *Acaulospora* and *Glomus* were predominant. The strain A. sp. 1 presents the maximum in both of two areas. Moreover, special species of A. sp. 2 and *S. gregaria* were found in Qinzhou and Beihai respectively. A field experiment was conducted to determine the influence of AMF inoculum on the indigenous AMF communities and sugarcane growth in latosol acid soil. The results showed that the communities of soil AMF were affected by AMF inoculum. Among four species of AMF in the original soil, A. sp. 1, A. sp. 2, G. sp. 4 and G. sp. 5, both G. sp. 5 and A. sp. 2 were affected by the AMF inoculum and chemical fertilizer application. AMF inoculum enhanced the absorption of available potassium by sugarcane, and increased the soil pH from 4.02 to 5.03 after crop harvest, while the treatment

with both AMF inoculum and chemical fertilizer decreased the soil pH to 4.33 compared with that of 4.49 in the control. Reducing half amount of chemical fertilizer did not negatively affect the cane yield. AMF inoculation stimulated the plant growth, improved the millable stalks, and increased the cane yield by 10 percent. We conclude that application of AMF inoculum is a strong potential for both economic and environmental benefits in the future.

#### PS 1-10 Biology of ectomycorrhizal *Scleroderma* fungi in Australasia

CHEN, Y.L.<sup>1,2</sup>, H.L. Tang<sup>1</sup> and X.L. He<sup>1</sup>

<sup>1</sup>College of Life Sciences, Hebei University, Baoding 071002, China, yinglongchen@hotmail.com; <sup>2</sup>School of Earth and Environment, The University of Western Australia, Crawley, WA 6009 Australia.

**Abstract:** Ectomycorrhizal fungi of the genus *Scleroderma* are often associated with plant roots in disturbed habitats around the world. However, the genus has a relatively low phylogenetic diversity under *Eucalyptus* plantations in Australasia based on morphological features of sporocarps and spores, and internal transcribed spacer (ITS) and large subunit (LSU) ribosomal DNA (rDNA) sequences. A total of 12 *Scleroderma* taxa were recognized from collections including three new species. *S. albidum*, *S. meridionale*, *S. septentrionale*, *S. verrucosum*, and two unnamed hypogenous taxa, collected from beneath *Eucalyptus* plantations in south-western Australian, were not recorded for China. Australian collections were separated from those gathered from south China with 99% bootstrap support for either ITS or the LSU. Phylogenetic analyses also showed that most Australian collections were distinct from the European and Malaysian taxa. Studies on the biology of *Scleroderma* showed fungal mycelia have unique characters, which differ with other mycorrhizal fungi. In pure culture, *Scleroderma* mycelia are smooth, pure white, and differentiated rhizomorphs often radiate through the growth medium. Mycorrhizas of *Scleroderma* are characterized by distinctly white, glabrous to sparingly tomentose, with mantle mycelium often giving rise to concolorous mycelia. At the genus level, *Scleroderma* has a wide host range including some Northern Hemisphere and Southern Hemisphere trees in unrelated families (e.g. Pinaceae and Myrtaceae), but host specificity exists in some species. Due to the availability of large quantities of spores from a few basidiomes and the ease of application for nursery inoculation needs, spore inoculum is preferable for application on an operational scale in many countries. Studies demonstrates that spore inoculum of *Scleroderma* is efficient for plantation species including *Eucalyptus*, *Pinus*, and *Acacia*. Optimisation of rooting medium is required to incorporate inoculation and seedling production. *Scleroderma* has shown great potential to inoculate seedlings of woody plants in assisting establishment of plantations and promoting host growth in the field. This study will enhance our understanding on the diversity, biology and host specificity of the *Scleroderma* fungi and the use of these mutualistic symbioses in plantation forestry.

#### PS 1-43 Deep-sequencing transcriptome of tomato to two soils containing their natural microbiota

CHIALVA, M.<sup>1</sup>, A. Salvioli<sup>1</sup>, P. Bagnaresi<sup>2</sup>, M. Novero<sup>1</sup>, S. Ghignone<sup>1,3</sup>, D. Spadaro<sup>4</sup> and P. Bonfante<sup>1</sup>

<sup>1</sup>Department of Life Sciences and System Biology, University of Torino, Viale P.A. Mattioli 25, I-10125 Turin, Italy, matteo.chialva@unito.it; <sup>2</sup>Genomics Research Centre CRA-GPG, via S. Protaso, 302 I – 29017 Fiorenzuola d'Arda, PC, Italy; <sup>3</sup>Istituto per la Protezione Sostenibile delle Piante (IPSP) – C.N.R., Viale P.A. Mattioli 25, I-10125 Turin, Italy; <sup>4</sup>Department of Agricultural, Forestry and Food Sciences (Di.S.A.F.A.), University of Torino, Largo Braccini 2, I-10095 Grugliasco, TO, Italy.

**Abstract:** Root-associated microbiota play a major role in shaping plant physiology under diverse environmental conditions. Such an impact may have systemic outcomes, also influencing traits of agronomic relevance. In particular, arbuscular mycorrhizae (AM) improve mineral nutrition and fortify plants against biotic and abiotic stresses. We took advantage of next-generation sequencing to study interactions between *Solanum lycopersicum* (tomato) and its root-associated microbiota. Two agricultural soils (RO and AL) containing diverse microbiota and with different biotic and abiotic features were considered. The RO and AL soils were conducive and suppressive, respectively, to the pathogen *Fusarium oxysporum* f. sp. *lycopersici* (FOL). A steamed, peat-moss soil was used as a control. Two tomato genotypes (FOL-resistant and susceptible) were grown in microcosms containing the three soils without pathogen inoculation. After three months, roots were sampled, AM colonization was assessed, and the transcriptome was analyzed by RNAseq. Morphological observations indicated that AM structures were present in the roots from RO soil, while their presence was severely reduced in AL soil. RNAseq analysis indicates that the two soils, with their microbiota, shape the root transcriptome differently than the steamed soil. Moreover, the soil type was shown to cause a more relevant impact on gene expression



than plant genotype, that is, AL soil activated metabolic pathways dealing with plant-defense irrespective of genetic background. However, comparing the profiles of the two genotypes, distinct sets of transcripts involved in plant-pathogen signaling emerged among the differentially expressed genes, suggesting that genotype is the second parameter that impacts the transcript profile interacting with the soil. Finally, a meta-transcriptome reconstruction confirmed the presence and activity of fungal communities strictly associated with the roots in both soils. Overall, our data sheds light on tomato responses to complex natural microbiota and suggest a strong interplay occurring between soil biotic and abiotic features, microbiota diversity, and genotype in tuning plant gene expression.

#### PS 1-11 Changes in ectomycorrhizal fungal communities due to forest thinning in Korea

CHOI, J.W.<sup>1</sup>, C.D. Koo<sup>2</sup> and A.H. Eom<sup>1</sup>

<sup>1</sup>Department of Biology Education, Korea National University of Education, Cheongju, Chungbuk 363791, Korea, [velo@live.co.kr](mailto:velo@live.co.kr); <sup>2</sup>Department of Forest Science, Chungbuk University, Cheongju, Chungbuk 361763, Korea.

**Abstract:** Ectomycorrhizal fungi (EMF) are important plant symbionts in forest ecosystems where the composition of the fungal community is known to be influenced by a variety of environmental factors. Thinning is the selective removal of trees, in order to maintain health of the forests. Subsequently, this practice alters the soil microorganisms as well as physical and chemical properties of the soil. In this study, we investigated the effect of forest thinning on communities of EMF in Korea. Root samples were randomly collected from both non-thinned and thinned forest sites in Korea dominated by *Pinus koraiensis*. Communities of EMF were assessed in terms of morphological characteristics and DNA sequence analysis of root tips. As a result, EMF genera: *Amanita*, *Lactarius*, *Leucopaxillus*, *Oidiodendron*, *Russula*, *Suillus*, *Thelephora*, and *Tomentella* were dominant at the study sites. We found that forest thinning significantly affected the composition and increased the species diversity of EMF communities. However, species evenness and colonization rates of EMF were not significantly different in both types of sites. Communities of EMF could also be affected by changes in carbon transfer from hosts and nutrient availability in the soil. These results suggest that forest thinning could be important to maintain EMF communities in Korean forests.

#### LT 3-8 Arbuscular mycorrhizal fungal diversity in Mediterranean drained peaty soils is affected by host plant and intensification of agricultural land-use

CICCOLINI, V.<sup>1</sup>, M. Öpik<sup>2</sup>, E. Bonari<sup>1</sup> and E. Pellegrino<sup>1</sup>

<sup>1</sup>Institute of Life Sciences, Sant'Anna School of Advanced Studies, 56127 Pisa, Italy, [v.ciccolini@sssup.it](mailto:v.ciccolini@sssup.it); <sup>2</sup>Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, 51005 Tartu, Estonia

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are ubiquitous plant root symbionts and have beneficial effects on soil quality, plant growth, and nutrition. All these benefits are declining with agricultural intensification, and little is known on how the AMF community composition varies in relation to this. Here, we investigated the effects of land use intensity and host plant identity on intraradical AMF communities of ten host plants. We performed a field experiment with four land-use types of different intensity: a cultivated peaty soil (CU), an energy crop plantation (BM), a managed grassland (GR), and an abandoned agricultural peaty soil (UNC). To evaluate the effect of the land use intensification on AMF communities, two common and co-occurring plant species were sampled (*Poa* sp. and *Calystegia sepium*) from all land use types. An additional eight plant species were sampled across land use types to test the plant host effect: *Arundo donax*, *Bromus tectorum*, *Helianthus annuus*, *Lolium perenne*, *Matricaria chamomilla*, *Miscanthus x giganteus*, *Phragmites australis*, and *Ranunculus acris*. AMF were identified by 454-sequencing of the SSU rRNA gene and assignment a virtual taxon (VT) identity. The community composition was evaluated both at a virtual taxa and a family based classification. Land use intensification had significant impact on AMF communities of *Poa* sp., but not of *C. sepium*. Indicator species (VT) for the cultivated systems (CU) were taxa in Glomeraceae, while taxa in Acaulosporaceae and Archaeosporaceae were indicators for the less intensively managed soils (BIOM) and Claroideoglomeraceae for the abandoned soil (UNC). Host plant identity also had a significant effect on AMF community composition. Differences were mainly driven by members of Archaeosporaceae, Claroideoglomeraceae, and Glomeraceae which were preferentially associated with *L. perenne*, *P. australis*, and *H. annuus*, *M. giganteus*, and *B. tectorum*, respectively. Our results emphasize that land use intensity has an important effect on AMF communities and suggest that these key microbes can be used as indicators of an appropriate soil management, taking into account the AMF-host plant preferences.



## PS 4-6 How soil carbon stocks depend on shifting mycorrhizal fungal guilds across forest-to-heath ecotones

CLEMMENSEN, K.E.<sup>1</sup>, R.D. Finlay<sup>1</sup> and B.D. Lindahl<sup>2</sup>

<sup>1</sup>Forest Mycology and Plant Pathology, Uppsala BioCenter, Swedish University of Agricultural Sciences, Box 7026, SE-75005 Uppsala, Sweden, karina.clemmensen@slu.se; <sup>2</sup>Soil and Environment, Swedish University of Agricultural Sciences Box 7014, SE-75005 Uppsala, Sweden.

**Abstract:** Ecotones between forests, dominated by ectomycorrhizal trees, and heathlands, dominated by ericoid mycorrhizal dwarf shrubs, are common in natural and cultural landscapes. Such ecotones are naturally found in transitions towards arctic and alpine zones, and ericaceous shrubs comprise an increasing share of primary production in aging forests. In cultural heathlands, tree regrowth has traditionally been restricted by grazing or biomass harvest. Recently, we showed that belowground carbon sequestration was lowest when ectomycorrhizal fungi dominated soil processes and increased when ericoid mycorrhizal fungi increased in dominance in old-growth boreal forests. This suggests that increasing forest cover or production with changes in climate or management practices could have drastic effects on soil carbon sequestration. To investigate the generality of these findings, we here present results from a subarctic-to-alpine ecotone from mountain birch forest to heath tundra. We found a strong positive coupling between tree abundance and ectomycorrhizal fungal growth (ingrowth bags), both of which were negatively coupled with carbon sequestration along the ecotone. By 454-sequencing we identified a shift in dominance from root-associated ascomycetes (mostly ericoid mycorrhizal) in the heath to cord-forming ectomycorrhizal fungi (mostly *Cortinarius* and *Leccinum* spp.) in the forest. High carbon/nitrogen-ratios and low inorganic nitrogen levels in the forest humus suggested a more efficient nitrogen mobilization, linked to the higher activities of these ectomycorrhizal fungi. Together, our data suggest that lower carbon sequestration rates in forests, despite higher litter inputs, are a consequence of more efficient ectomycorrhizal nutrient foraging from organic pools. When soil processes are dominated by stress-tolerant ericoid mycorrhizal plants and fungi, however, more carbon accumulates. We propose that a general trade-off between rapid growth and turnover vs. tolerance to exogenous stresses in mycorrhizal fungal communities is a main driver of soil carbon balance in ecto- and ericoid mycorrhizal dominated ecosystems.

## CS 5-2 Micromammal consumption of hypogeous fungi in eastern Canadian boreal forests

CLOUTIER, V.<sup>1,2</sup>, J.A. Fortin<sup>1,2</sup>, J. Ponchart<sup>1,2,3</sup>, J. Bérubé<sup>2,3</sup>, A. Desrochers<sup>1,2</sup> and Y. Piché<sup>1,2</sup>

<sup>1</sup>Université Laval, 2325 rue de l'Université, Québec (Qc) G1V 0A6, cloutierv@gmail.com; <sup>2</sup>Centre d'étude de la forêt, Case postale 8888, succ. Centre-ville Montréal (Qc) H3C 3P8; <sup>3</sup>Centre de foresterie des Laurentides, 1055 rue du PEPS, C.P. 10380, succ. Sainte-Foy Québec (Qc) G1V 4C7.

**Abstract:** The diversity and distribution of hypogeous fungal species can affect the capacity of forests to provide a viable habitat for micromammals, especially rodents. Because micromammals are the basic diet of many carnivores, changes in the diversity and distribution of hypogeous fungi could lead to major changes in ecosystem function. In Quebec, Canada, we know almost nothing about the diversity and distribution of hypogeous fungi and their role as food for mammalian dispersers. We used metagenomics to examine feces from wild micromammals for fungal material. We sampled four boreal forests of southern Quebec: Forêt Montmorency (Aug.-Oct. 2011), Parc national des Hautes-Gorges-de-la-Rivière-Malbaie (Aug.-Oct. 2011), Forêt Duparquet (Aug.-Dec. 2012), and Laurentides north of Montreal (Aug.-Dec. 2012). We found evidence of 27 species of hypogeous fungi including nine new records for the province of Quebec. Of 596 animal feces sampled about half contained spores from hypogeous fungi totalling nine micromammal species. This study is an important milestone for developing an understanding of hypogeous fungi of Quebec's boreal forests and their role as food for dispersers shaping ecosystem functions.

**COBB, A.B.**<sup>1</sup> and G.W.T. Wilson<sup>1</sup>

<sup>1</sup>Natural Resource Ecology and Management, Oklahoma State University, Stillwater, Oklahoma 74078 USA, abcobb@okstate.edu.

**Abstract:** Our greenhouse study investigated the effects of alternative farm inputs (compost and biochar) and arbuscular mycorrhizal (AM) fungal associations with grain sorghum on the productivity and nutritional quality of this important crop. These soil amendments can be reliably produced at various scales globally, with potentially lower cost than commercial fertilizers. We selected a mycorrhizal dependent sorghum cultivar and compared 10 different input treatments. One input blend contained 120 g worm compost and 30 g of biochar with ½ the recommended rate of urea/DAP fertilizer. Compared to a full rate of N and P fertilizer, this blend produced equal or greater plant biomass after 45 days of growth, with equal or greater tissue quality (protein, P, Fe, Zn), while supporting ~30% more AM fungi in the host plant's roots. This indicates these alternative inputs can boost belowground symbiosis and replace chemical fertilizers without reducing productivity. This project is the initial component of a larger research agenda. We are currently performing a second greenhouse trial investigating the response of additional sorghum varieties grown with these same soil inputs. Additionally, we have two field sites in Oklahoma and one in Nicaragua planted with a similar design. These studies were funded as part of a community economic development project by the Riata Center for Entrepreneurship and Opportunity International in Nicaragua.

PS 1-12 **Peering into the Mediterranean black box: *Lactifluus rugatus* ectomycorrhizas on *Cistus***

**COMANDINI, O.**<sup>1</sup>, L. Tedersoo<sup>2</sup>, M. Leonardi<sup>3</sup> and A.C. Rinaldi<sup>4</sup>

<sup>1</sup>Department of Life and Environmental Sciences, University of Cagliari, Monserrato (CA), Italy, ornella\_comandini@unica.it; <sup>2</sup>Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia; <sup>3</sup>Department of Environmental Sciences, University of L'Aquila, L'Aquila, Italy; <sup>4</sup>Department of Biomedical Sciences, University of Cagliari, Monserrato (CA), Italy.

**Abstract:** The basidiomycetous family *Russulaceae* has recently undergone a dramatic taxonomic revision. As for *Lactarius*, for example, analyses revealed two monophyletic clades, with the subgenera *Piperites*, *Russularia*, and *Plinthogalus* to constitute the larger genus *Lactarius sensu novo*, and the subgenera *Lactariopsis*, *Lactarius*, *Lactifluus*, *Russulopsis*, *Gerardii*, and the former *Lactarius* sect. *Edules* to constitute the newly erected genus *Lactifluus*. We describe the morpho-anatomical features of the ectomycorrhizas (ECMs) formed by *Lactifluus rugatus* (Kühner & Romagn.) Verbeken on *Cistus*, a genus containing about 20 species of woody shrubs typical of the Mediterranean maquis. The ECM identity was verified through molecular tools. Anatomically, the characteristic of *L. rugatus* mycorrhiza is the presence of abundant long (up to 40-45 µm) 'bottle-shape' cystidia on mantle surface. Indeed, the overwhelming majority of '*Lactarius*' mycorrhizas are acystidiate, while the mantle surfaces of *Russula* species from different sections (Plorantinae, Nigricantinae, Foetidinae) are more or less densely covered with cystidia. With *L. rugatus*, a total of three *Lactarius* + *Lactifluus* mycorrhizas have been described so far associated with *Cistus*, the others being *Lactarius cistophilus*, a member of sect. *Uvidi* subsect. *Uvidini*, and *Lactarius tesquorum*, member of sect. *Piperites*. The phylogenetic distance among these taxa is reflected by the diversity of the principal features of their ECMs, that do not share any common diagnostic structure. Only *L. rugatus* has numerous and peculiar cystidia that cover the mantle surface; *L. cistophilus* presents a pseudoparenchymatous outer mantle layer formed by epidermoid cells, while *L. tesquorum* has a plectenchymorous mantle formed by a loose net of hyphae. The three ECMs only share common host-dependent ECM features known for *Cistus*: small dimensions, small diameter of ECM tips and a quite thin mantle. To our knowledge, that of *L. rugatus* on *Cistus* is the first ECM description of a species belonging to *Lactifluus*, subgenus *Lactifluus*.

## PS 2-4 Characterizing zinc tolerance genes in *Suillus luteus*, an ectomycorrhizal fungus with properties promising for use in phytostabilization applications

CONINX, L.<sup>1</sup>, J. Ruytinx<sup>1</sup>, M.O. De Beeck<sup>2</sup>, J. Vangronsveld<sup>1</sup> and J. Colpaert<sup>1</sup>

<sup>1</sup>Centre for Environmental Sciences, Hasselt University, 3590 Diepenbeek, Belgium, coninxlaura@gmail.com; <sup>2</sup>Microbial Ecology Group, Department of Biology, Lund University, Ecology Building, SE-22 362 Lund, Sweden.

**Abstract:** Pyrometallurgical industry and mining activities have led to the contamination of vast areas with heavy metals. In these areas, biodiversity of plants and microorganisms is often greatly reduced. Surviving organisms are subjected to a high selection pressure for metal tolerance, often resulting in the evolution of metal tolerant ecotypes of plants, fungi, and bacteria. Zn contamination in the northern part of Limburg (Belgium), has led to the evolution of Zn tolerant ecotypes of *Suillus luteus* (L.) Roussel, an ectomycorrhizal basidiomycete that forms symbiotic associations with *Pinus sylvestris* L. These Zn tolerant ecotypes thrive in heavily contaminated soils and, in the meantime, protect their hosts from metal toxicity. This protective feature combined with the fact that *S. luteus* is a pioneer species common to sandy soils in temperate climate regions makes *S. luteus* a suitable candidate for use in phytostabilization applications. However, to fully exploit the potential of such applications, a better understanding of the Zn tolerance mechanism is crucial. Previous investigations have shown that the basis of the tolerance trait is a mechanism promoting Zn efflux. Yet, because Zn is an essential nutrient, many homeostatic pathways are expected to be involved in maintaining an optimal Zn concentration in all cell compartments. This makes it a challenging task to characterize the tolerance mechanism. Hence, we first focused on establishing which Zn homeostatic pathways are present in *S. luteus*. Here we report seven cation diffusion facilitator proteins and four Zrt- Irt-like proteins that have been identified in the *S. luteus* genome. Further characterization of these proteins and their response to increased zinc concentrations in zinc tolerant and sensitive isolates may lead to a better characterization of the zinc tolerance mechanism in *S. luteus*.

## PS 2-5 Poplar as a model for dissecting early mycorrhizal signaling in woody perennials

COPE, K.R.<sup>1</sup>, M. Venkateshwaran<sup>2</sup>, J. Maeda<sup>1</sup>, K. Garcia<sup>1</sup>, M. Caiping<sup>3</sup>, S.H. Strauss<sup>3</sup> and J.M. Ané<sup>1</sup>

<sup>1</sup>Department of Bacteriology, University of Wisconsin - Madison, Madison, Wisconsin 53706 USA, kcope@wisc.edu;

<sup>2</sup>School of Agriculture, University of Wisconsin - Platteville, Platteville, Wisconsin 53818 USA; Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon, 97331 USA.

**Abstract:** Two ecologically and economically important mycorrhizal symbioses are arbuscular mycorrhizae (AM) and ectomycorrhizae (ECM). Both types of symbiotic associations contribute to the sustainability and sustainability of natural ecosystems through nutrient cycling and carbon sequestration. Significant advances have been made over the past two decades in elucidating the molecular mechanisms controlling mutual recognition between AM fungi and their host plants. In contrast, our understanding of these mechanisms in ECM associations is still very limited. In AM associations, the fungus releases various signaling molecules that are recognized by the host plant, including lipochitooligosaccharides (LCOs) and chitooligosaccharides. We performed root hair deformation assays with common vetch to test the presence of LCOs in the exudates of several ECM fungi. It is known that non-sulfated LCOs trigger root hair deformation in common vetch; we found similar deformations in the presence of our ECM hyphal exudates. These results suggest that non-sulfated LCOs may be released by ECM fungi and could play a similar role in symbiotic signaling. However, we cannot exclude that different fungal molecules may have triggered the observed root hair deformations. In the model legume *Medicago truncatula*, LCOs activate a signal transduction pathway involving at least three key plant genes which are required for a functional symbiosis: *DMI1*, *DMI2*, and *DMI3*. Orthologous genes are present in poplar (*Populus trichocarpa*), which associates with both AM and ECM fungi. As such, we used RNA interference to generate poplar lines with reduced expression of these orthologous genes. Assessing the ability of AM and ECM fungi to colonize these transgenic lines will allow us to decode some of the regulatory components involved in the establishment of AM and ECM associations in woody perennials.

## PS 1-44 Encroachment by *Juniperus virginiana* alters biotic and abiotic soil characteristics of the tallgrass prairie

COPPICK, P.<sup>1</sup> and G. Wilson<sup>1</sup>

<sup>1</sup>Oklahoma State University, Natural Resource Ecology and Management, coppick@okstate.edu.

**Abstract:** The Great Plains grasslands of the US provide important ecosystem services. However, these grasslands are one of the most endangered ecosystems in the world, with as little as 1% of the historical range still intact. Historically, vast areas have been lost to row crop agriculture. Currently, one of the greatest threats to these grasslands, and grasslands worldwide, is the expansion of woody species. The invasion of native tree species, such as *Juniperus virginiana*, has multi-scale effects including loss of biodiversity, loss of habitat for wildlife species, and alterations in community- and landscape-level functions. Most previous studies have focused on aboveground assessments, yet above- and below-ground processes are clearly linked. In our study we assess belowground soil characteristics such as soil microbial community composition, including relative abundance of arbuscular mycorrhizal fungi, soil moisture, and aggregate stability of prairie sites converted to *J. virginiana* forests and adjacent non-invaded native prairie. To assess the influence of tree density, we included *J. virginiana* areas with moderate levels of tree density, as well as sites with closed forest. Our results show significant differences in microbial communities, with significant increases in arbuscular mycorrhizal fungi following tree establishment. In addition, soil moisture, organic carbon, and aggregate stability were greater in forested sites compared to the native prairie sites. Understanding how plant-soil-mycorrhizal associations are influenced by *J. virginiana* invasions may be a critical aspect of the ecology and management of this invading species, as well as the conservation and restoration of native ecosystems.

## PS 3-11 The Gadgil effect may explain monodominance in tropical montane forest

CORRALES, A.<sup>1</sup>, S.A. Mangan<sup>2</sup>, B.L. Turner<sup>3</sup>, K. Heineman<sup>4</sup> and J.W. Dalling<sup>1</sup>

<sup>1</sup>Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana-Champaign, IL 61801 USA, corrlsr@illinois.edu; <sup>2</sup>Department of Biology, Washington University in St. Louis, St. Louis, MO 63130-4899 USA; <sup>3</sup>Smithsonian Tropical Research Institute, Apartado Postal 0843-03092, Republic of Panama; <sup>4</sup>Program in Ecology, Evolution and Conservation Biology, University of Illinois at Urbana-Champaign, Urbana-Champaign, IL 61801 USA.

**Abstract:** Although moist tropical forests are renowned for high local tree species richness, numerous examples exist where a single tree species achieves monodominance, accounting for >60% of basal area in a forest stand. A common feature of many of these monodominant species is that they form associations with ectomycorrhizal (EM) fungi. Using *Oreomunnea mexicana* (Juglandaceae), a tree that forms monodominant stands in western Panama, we tested three hypotheses to explain how EM fungi allow a host tree species to achieve local monodominance: (1) by conferring resistance to soil-borne pathogens that are responsible for negative plant-soil feedback, (2) by enabling transfer of water, nutrients, or carbon from adults to juveniles through ectomycorrhizal networks, and (3) by reducing the availability of nitrogen to competing species. We tested for plant soil-feedback using a greenhouse experiment in which growth of seedlings of five species was measured after addition of conspecific or heterospecific soil inocula. We also tested for EM network effects in the field using nylon mesh to exclude hyphal connections. We found no evidence for positive plant-soil feedback or that ectomycorrhizal networks confer competitive advantage to *Oreomunnea* seedlings. However, we found ~3-fold more nitrate and ammonium concentrations outside than inside *Oreomunnea*-dominated patches. We hypothesize that reduced nitrogen availability is associated with the “Gadgil effect”, whereby reduced litter decomposition rates under EM dominated forest reduces the availability of mineral nitrogen to competing non-AM species allowing EM species dominance.

## PS 1-45 Mycorrhizal colonization of crops and weeds under competition

Massenssini, A.M<sup>1</sup>, M.R. Tótola<sup>1</sup> and M.D. COSTA<sup>1</sup>

<sup>1</sup>Departamento de Microbiologia, Universidade Federal de Viçosa, Viçosa, 36570-900, MG, Brazil, mauducos@gmail.com.

**Abstract:** Arbuscular mycorrhizal (AM) associations are of great ecological importance in natural and agricultural environments. Arbuscular mycorrhizal fungi (AMF) improve plant water and nutrient uptake in exchange for carbohydrates. The maintenance of the association is based on reciprocity, and the benefits for both partners regulate the extent of root length colonization. The majority of studies report fungal-plant relationships in single plant species systems, with scarce information about the interactions of crops and weeds with AMF. The objective of this study was to evaluate the effect of competition between two crops (*Zea mays* L. and *Glycine max* (L.) Merr.) and three weeds (*Ageratum conyzoides* L., *Ipomoea ramosissima* (Poir.) Choisy, and *Bidens pilosa* L.) on plant shoot biomass, plant P uptake, and mycorrhizal colonization by AMF. Plants were cultivated in a greenhouse experiment for 80 days with five monoculture treatments, one for each plant species, and ten competition treatments consisting of the cultivation of two plant species in the same pot. Decreases in plant shoot dry mass, plant P content, and mycorrhizal colonization of roots under competition were observed, although this was variable depending on the species combination analyzed. Under competition, both crops showed decreases in mycorrhizal colonization in the presence of the weeds tested, while the weed *A. conyzoides* showed increased mycorrhizal colonization. Among the species studied, *Z. mays*, *A. conyzoides*, and *B. pilosa* showed low dependency on AMF for growth and P uptake, while the opposite was observed for *G. max* and *I. ramosissima*. These observations show that competition between crops and weeds can change the AM association balance within agricultural plant communities.

## PS 2-37 Interactions between arbuscular mycorrhizal fungi, benzoxazinoids, and rhizosphere bacteria

COTTON, T.E.A.<sup>1</sup>, S.A. Rolfe<sup>1</sup>, D.D. Cameron<sup>1</sup>, G. Jander<sup>2</sup>, M. Erb<sup>3</sup> and J. Ton<sup>1</sup>

<sup>1</sup>University of Sheffield, Sheffield, UK, anne.cotton@sheffield.ac.uk; <sup>2</sup>Boyce Thompson Institute for Plant Research, Ithaca, NY, U.S.A.; <sup>3</sup>University of Bern, Bern, Switzerland.

**Abstract:** Arbuscular mycorrhizal (AM) fungi are known to alter belowground bacterial communities and enhance plant defensive capabilities against pathogens. However, little is known about the mechanisms by which this occurs. Recently it has been proposed that plant benzoxazinoids (BXs) in root exudates act as key regulators of these processes in cereals such as maize. BXs are tryptophan-derived secondary metabolites produced in many grass species that contribute to resistance against pests and diseases in the leaves. Belowground, they can act as recruitment signals for beneficial soil microbes such as *Pseudomonas putida*, which can prime inducible plant defences. Furthermore, previous studies have reported that AM fungi increase BX production in the roots. Together, this suggests that BXs act as important regulators of plant-mycorrhizal-bacterial interactions in the mycorrhizosphere. However, the complex relationships between AM fungi, host BX metabolism, and rhizobacteria have yet to be resolved. The European research consortium BENZEX will address this shortfall. Within this consortium, we will use maize plants with mutations in three BX biosynthesis genes (*Bx1*, *Bx2*, and *Bx6*) in conjunction with molecular methods, such as high throughput sequencing, to examine the global effects of BXs on AM fungi and associated rhizobacterial communities. Our results will enhance both our fundamental understanding of plant-mycorrhizal interactions and provide valuable insights into the potential application of AM fungi in sustainable crop production and protection.



## CS 4-2 Recovering lost ground: soil burn intensity impacts on nutrients and ectomycorrhizal communities of ponderosa pine seedlings

COWAN, A.D.<sup>1</sup>, J.E. Smith<sup>2</sup> and S.A. Fitzgerald<sup>3</sup>

<sup>1</sup>Department of Forest Ecosystems and Society, College of Forestry, Oregon State University, Corvallis, OR, ariel.cowan@oregonstate.edu; <sup>2</sup>USDA Forest Service, PNW Research Station, Corvallis, OR; <sup>3</sup>Department of Forest Engineering, Resources, and Management, College of Forestry, Oregon State University, Corvallis, OR.

**Abstract:** Fuel accumulation and climate shifts are predicted to increase the frequency of high-severity fires in ponderosa pine (*Pinus ponderosa*) forests of central Oregon. The combustion of fuels containing large downed wood can result in intense soil heating, alteration of soil properties, and mortality of microbes. Previous studies show ectomycorrhizal fungi (EMF) improve ponderosa seedling establishment after fire, but did not compare EMF communities at different levels of soil burn intensity in a field setting. For this study, soil burn intensity impacts on nutrients and EMF communities were compared at Pringle Falls Experimental Forest, La Pine, Oregon. Twelve replicate sites were used, each with three treatments applied: high intensity soil burn (HB), low intensity soil burn (LB), and unburned control (UB). HB treatments were created by the combustion of downed logs stacked together and LB treatments were applied by broadcast burning pre-existing ground fuels. Temperatures lethal to fungi were recorded at greater depths in HB soils. Ponderosa pine seedlings planted post-burn were harvested after four months for EMF root tip analysis. We found a) greater differences in soil nutrients in HB soils compared to LB and UB soils, b) no differences in richness and diversity, c) weak differences in relative abundance between UB and burn treatments, and d) differences in relative abundance correlated with carbon and organic matter contents. These results confirm the combustion of large downed wood can alter the soil environment beneath it. However, an EMF community similar to LB soils recolonized HB soils within one growing season. We theorize that quick recovery of EMF communities depends on the size of high burn patches, proximity of low and unburned soil, and survival of nearby hosts. The importance of mixed-severity fire in providing refuges for EMF communities may influence thinning and prescribed fire practices in ponderosa pine forest management.

## PS 2-21 A strategy to preserve native ectomycorrhizal fungi specific for threatened whitebark pine

CRIPPS, C.L.<sup>1</sup> and E. Lonergan<sup>2</sup>

<sup>1</sup>Plant Sciences and Plant Pathology Department, Montana State University, Bozeman, MT 59717, USA, ccripps@montana.edu; <sup>2</sup>Botanist, US Forest Service, Klamath National Forest, 1711 S. Main Street, Yreka, CA 96097.

**Abstract:** Whitebark pine (*Pinus albicaulis*) is a threatened five-needle pine limited to high elevations in western North America where it exists as magnificent forests or krummholz flagging on ridge tops. Populations are being decimated by white pine blister rust (*Cronartium ribicola*) and mountain pine beetles (*Dendroctonus ponderosae*); fire suppression and climate change contribute to the decline, over 90% in some areas. Forests at the top of watersheds slow runoff from snowmelt and pine nuts are an important food source for threatened grizzly bears. Whitebark pine hosts a limited number of ectomycorrhizal fungi (ECF) in the Greater Yellowstone Area. Fungi specific for this host play important ecological roles as food for mammals, as early colonizers of seedlings, and offer a competitive edge against spruce and fir encroachment. There is risk of losing these important fungi as their host declines. Large restoration efforts are underway and over 200,000 potentially rust-resistant seedlings have been planted in the western U.S., but survival rates are low. We are using spores of native ECF specific to five-needle pines to inoculate nursery seedlings before out-planting. In early trials, *Suillus* species outperformed those of *Rhizopogon* in efficient colonization of roots. *Suillus sibiricus* was the most effective and its spores were used to inoculate half of 1,000 seedlings planted in Waterton Lakes National Park in 21 plots under four site condition combinations (burned/not, beargrass/not); seedlings were also planted with/without a shelter object (stumps, logs, rocks). After 3 years, the highest seedling survival rates were for inoculated seedlings planted in burned areas with microsite, with a 15% increase attributed to inoculation. This strategy enhances putative rust resistance in the environment and serves to preserve host specific fungi critical to whitebark pine's survival; it is included in the USDA FS Range-wide Strategy for whitebark pine.

### CS 4-3 Conservation of ectomycorrhizal fungi in boreal forests – the significance of retention forestry and the value of national red lists

DAHLBERG, A.<sup>1</sup>

<sup>1</sup>Swedish University of Agricultural Sciences, Department of Forest Mycology and Plant Pathology P.O. Box 7026, 750 07 Uppsala, Sweden, anders.dahlberg@slu.se.

**Abstract:** Ectomycorrhizal fungi (EMF) depend on their symbiosis with their host trees. They are, therefore, sensitive to timber harvesting and disappear after clearcutting. Mycelia of EMF are perennial, potentially unlimited in time and space, and may become as old, or older, as trees. In an evolutionary perspective, mycelial legacies of EMF through forest generations have probably been an important fitness component. However, with modern forestry and clearcutting, effective spore dispersal may be selected for rather than mycelial longevity. A significant portion of the boreal EMF fungi are only, or predominantly, found in old growth conditions. The majority of the nationally red-listed EMF species are boreal forest species in Finland, Norway, and Sweden (~200 species), are mostly confined to old-growth conditions, and only rarely found in managed forests. In total, about 1,000 EMF species are reported from the boreal forests in the Nordic countries. These national red lists are important to identify conservation priorities and used to identify species actions programs. There is interest for retention forestry in the Nordic countries, and, although only carried out at small scales, has substantially increased during the last ten years. In a series of studies, the significance of retention trees in managed forests to facilitate the survival of EMF following cutting has been explored as a complement to protected areas. The significance of protecting forests to preserve EMF diversity, and considering retention practices in addition to having them assessed for the red list will be reviewed and discussed. Additionally, both potential biodiversity effects and functional effects will be discussed with different forest management practices.

### PS 2-22 The Global Fungal Red List Initiative aims to get ECM fungi globally red-listed in 2015

DAHLBERG, A.<sup>1</sup> and G.M. Mueller<sup>2</sup>

<sup>1</sup>Swedish University of Agricultural Sciences, Department of Forest Mycology and Plant Pathology P.O. Box 7026, 750 07 Uppsala, Sweden, anders.dahlberg@slu.se; <sup>2</sup>Chicago Botanic Garden, Glencoe, IL 60022, USA.

**Abstract:** Conservation of fungi is not yet commonly discussed, considered, or acted upon by the mycological community. Not coincidentally, fungi are rarely included in broader conservation discussions, policy decisions, or land management plans. However, species of fungi are not immune to the threats that put species of animals and plants at risk. Fungal species are threatened by habitat loss, loss of symbiotic hosts, pollution, over exploitation, and climate change, but the conservation status of the vast majority of fungal species has not been assessed. About 20,000 animal, fungal, and plant species are globally red-listed. The International Union for Conservation of Nature (IUCN) Red List of Threatened Species is the world's most comprehensive information source on the global conservation status of animal, fungi, and plant species. It aims to convey the urgency of conservation issues to the public and policy makers, as well as help the international community reduce species decline and extinction. However, only one macrofungus and four lichenized fungi are included in that list. The near lack of fungi on the global Red List greatly hinders the inclusion of fungi in conservation discussions, access to funding programs, policy decisions, and conservation action. The Fungal Global Red List Initiative is initiated and run by the five fungal specialist groups of the IUCN. The initiative aims to raise the awareness of fungal conservation among mycologists, the conservation community, policy makers, and the general public by globally red-listing at least 100 species by the end of 2015. The Red List assessment is accomplished through a public website (see <http://iucn.ekoo.se>) to facilitate acquisition and discussion of the data required for assessing conservation status. The assessment has taken place during a series of workshops during 2014-2015. Assessed ectomycorrhizal fungi suggested to the global Red List of IUCN will be presented.

## PS 2-38 Spekboom, AM fungi, and PGPR – is this a winning combination?

DAMES, J.F.<sup>1</sup> and A. Fulmaka<sup>1</sup>

<sup>1</sup>Department of Biochemistry and Microbiology, Mycorrhizal Research Laboratory, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa, J.dames@ru.ac.za.

**Abstract:** Spekboom (*Portulacaria afra*) is regarded as a suitable plant for restoring degraded semi-arid subtropical thicket in the Eastern Cape, South Africa as well as being a valuable asset for farmers in terms of browse value, soil retention, carbon sequestration, and carbon offset credits. An ambitious trial involving over 300 quarter hectare plots was planted with cuttings in 2008 as part of a restoration programme. Trial sites were assessed after five years and survival of cuttings was found to be only 26.3%. The aim of this study was to determine the interaction between arbuscular mycorrhizal (AM) fungi, rhizobacteria, and spekboom. Soil and root samples from selected trial sites were used to assess AM fungal spore abundance and colonization; isolation, characterization, and identification of rhizobacteria; and determining the interaction of the microbes on spekboom growth and tolerance to *Fusarium*. Arbuscular mycorrhizal spore abundance and percentage root colonisation did not differ between the three spekboom plots. Molecular analyses of the SSU region from the plots indicated that four families of AM fungi were present. These were identified as belonging to the families Ambisporaceae, Glomeraceae, Claroideoglomeraceae, and Paraglomeraceae. A suspected *Fusarium* pathogen was isolated and molecularly identified. Pathogenicity tests indicated reduced spekboom growth with poor root development. Of the 34 rhizobacterial isolates maintained in culture, six produced IAA, 27 produced siderophores, and 23 solubilised complexed inorganic phosphate. Rhizobacteria were molecularly identified as several *Bacillus* species with some *Enterobacter*, *Arthrobacter*, and *Microbacterium* species. Inoculation of spekboom cuttings with mycorrhizal fungi and selected rhizobacterial isolates significantly improved shoot height. Spekboom cuttings challenged with *Fusarium* and inoculated with mycorrhizal fungi and two rhizobacterial isolates significantly improved growth. The inoculation of cuttings in the nursery with mycorrhizal fungi and selected rhizobacteria is recommended prior to establishing spekboom in the field.

## LT 1-14 Independent mitochondrial and nuclear exchanges arising in *Rhizophagus irregularis* crossed isolates support the presence of a mitochondrial segregation mechanism

DAUBOIS, L.<sup>1</sup>, D. Beaudet<sup>1</sup>, M. Hijri<sup>1</sup> and I. De La Providencia<sup>1</sup>

<sup>1</sup>Institut de Recherche en Biologie Végétale, Université de Montréal and Jardin botanique de Montréal, 4101 Rue Sherbrooke Est, Montréal (Québec) H1X 2B2, Canada, laurence.daubois@umontreal.ca.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are obligate biotrophs that can exchange genetic information through hyphal fusions (i.e., anastomosis) with genetically compatible isolates belonging to the same species. The occurrence of transient mitochondrial length heteroplasmy through anastomosis between geographically distant *Rhizophagus irregularis* isolates was previously demonstrated in progeny spores resulting from crossing experiments. However, (1) the persistence of this phenomenon in monosporal culture lines from crossed parental isolates, (2) its correlation with nuclear exchanges, and (3) the potential mechanisms responsible for mitochondrial segregation are still unknown. Using the AMF model organism *R. irregularis*, we tested whether the presence of a heteroplasmic state in progeny spores was linked to the occurrence of nuclear exchanges, and whether the previously observed heteroplasmic state persisted in monosporal *in vitro* crossed-culture lines. We also investigated for the presence of a putative mitochondrial mechanism apparatus in Glomeromycota by searching orthologous proteins similar to those found in other fungal groups. Our findings suggest that mitochondrial segregation might take place either during spore formation or colony development, and that it might be independent of the nuclear segregation machinery. We present the basic building blocks for a better understanding of the mitochondrial inheritance process and segregation in these important symbiotic fungi, which promotes plant fitness and growth. It represents important applicable knowledge because it has been shown that different segregated lines of the same isolate can have variable effects on the host plant.

## PS 4-7 Nutrient enrichment effects on mycorrhizal fungi in southern Ecuador

DELAVAUX, C.<sup>1</sup>

<sup>1</sup>Yale University: School of Forestry and Environmental Studies, camille.delavaux@yale.edu.

**Abstract:** My research investigates the relationship between nutrient enrichment, specifically phosphorous and nitrogen, and arbuscular mycorrhizal fungal (AMF) inoculum potential in a tropical montane forest in southeastern Ecuador. There is yet to be a consensus on if nutrient enrichment is correlated with greater, reduced or no change in AMF in tropical systems. Previous work has failed to thoroughly address this broad, ecosystem scale question in the tropics. In this study, mean infection percentage testing is used to determine relative AMF abundance in 48 2x2 m plots of four different nutrient treatments: control, added N, added P, and added N and P. Findings from this research will fill gaps in the study of microbial ecology as well as tropical forest ecology, clarifying implications of future anthropogenic nutrient changes on AMF soil potential.

## PS 3-29 Intra-specific genetic variability in arbuscular mycorrhizal fungi had an effect on starch production in field but not on starch quality

DELGADILLO, C.A.<sup>1</sup>, I.C. Ceballos<sup>2</sup>, A. Rodriguez<sup>2</sup> and I.R. Sanders<sup>3</sup>

<sup>1</sup>Department of Engineering, Universidad Nacional de Colombia, Avenida Carrera 30 # 45, Bogotá, Colombia, cadelgadilloc@unal.edu.co; <sup>2</sup>Department of Biology, Universidad Nacional de Colombia, Avenida Carrera 30 # 45, Bogotá, Colombia; <sup>3</sup>Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland.

**Abstract:** Cassava (*Manihot esculenta* Crantz) is the most important crop for food security in Asia, Africa, and South America and feeds nearly one billion people in the world. Genetically different lines of *Rhizophagus irregularis* produced by *in vitro* crossing and segregation had a large effect on cassava root biomass production in the eastern plains region of Colombia. In this study, we also wanted to measure quantity and quality of starch extracted from cassava roots because product quality is also an important parameter for the evaluation of the human consumption of cassava. Quality is affected by several physiological and environmental factors, such nutrition and water. Because arbuscular mycorrhizal fungi (AMF) can reduce the negative impact of water stress on plants, they could potentially improve physico-chemical characteristics of starch extracted. In this field study, we measured the effect of different *R. irregularis* genotypes on the quantity and quality of starch extracted from cassava roots in two different varieties (var. MCOL2737 and var. COL4574). Quality variables assessed were starch production, starch pulp percentage, and starch titratable acidity. We found that inoculated AMF genotypes had a significant effect on the amount of extracted starch from cassava roots per plant, although the amount of extracted starch per gram was not affected. The amount of starch produced was correlated with cassava root weight. AMF genotypes did not produce statistical differences in pulp starch percentage or starch titratable acidity in field conditions. Future work should focus on, 1) evaluating the effect of other *R. irregularis* genotypes or AMF species, 2) analyzing how these fungi could affect cassava starch biosynthesis and its regulation, and 3) evaluating the AMF effect in other quality variables that are important for cassava human consumption.

## PS 3-30 Arbuscular mycorrhizal fungi inoculant types affect growth parameters of *Pisum sativum*

DESALEGN, G.<sup>1</sup>, R. Turetschek<sup>2</sup>, H.P. Kaul<sup>1</sup> and S. Wienkoop<sup>2</sup>

<sup>1</sup>University of Natural Resources and Life Sciences, Department of Crop Sciences, Division of Agronomy, Konrad-Lorenz Strasse 24, 3430 Tulln, Austria, getinet.desalegn@boku.ac.at; <sup>2</sup>University of Vienna, Department of Ecogenomics and Systems Biology, Althanstrasse 14, 1090, Vienna, Austria.

**Abstract:** The use of commercial arbuscular mycorrhizal fungi (AMF) inoculant is an emerging technology in field crop production to reduce the risk of yield-limiting phosphorus deficiency and costly over-fertilizing of agricultural lands. The aim of this investigation was to evaluate the effectiveness of AMF inoculant types on dry matter yield, plant height, leaf greenness, and green area of peas (*Pisum sativum* L.). Five experimental treatments including three types of AMF inoculants obtained with different carriers (humate, compost, and clay), one synthetic phosphorus (P) fertilizer

application, and control (non-mycorrhizal and non-phosphorus) were repeated four times in a pot culture. The results revealed significant ( $p < 0.05$ ) differences among treatments in green areas, plant height, leaf greenness, and dry matter production of peas. Notably, the clay-based inoculant showed the maximum green areas and leaf greenness, whereas the poorest results of these traits were observed in the control treatment. Overall, the AMF inoculants and the P fertilizer application equally and positively affected the growth traits of peas. Here we conclude that any one of the AMF inoculants could be used to improve pea productivity as well as to replace the costly synthetic P fertilizer in low phosphorus soils. Further research is still required to verify these results for large-scale application of AMF inoculants in agronomic practices under field conditions.

### CS 5-3 The fungal microbiome: a peek at plant-associated fungi and their endobacteria

DESIRÒ, A.<sup>1</sup>, P. Bonfante<sup>2</sup> and G. Bonito<sup>1</sup>

<sup>1</sup>Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, Michigan 48824, USA, adesiro@msu.edu; <sup>2</sup>Department of Life Sciences and Systems Biology, University of Turin, Turin 10125, Italy.

**Abstract:** Thousands of microbes are associated with plant roots in the root microbiome. Among them, mycorrhizal fungi represent one of the most important component of this belowground symbiosis. Mycorrhizal fungi are often associated with other microorganisms such as bacteria, which thrive on their outer surface or dwell inside their cytoplasm as endobacteria. An example of a fungus-bacteria interaction is provided by arbuscular mycorrhizal fungi (AMF) (phylum Glomeromycota), a basal group of obligate biotrophic fungi that colonize the roots of most land plants, improve plant growth, and provides pathogen protection and resistance to environmental stresses. These fungi represent a niche for hosting endocellular bacteria in their mycelium and spores, although the functional significance of this association is still not well understood. Two types of endobacteria are known in AMF, a rod-shaped Gram-negative  $\beta$ -proteobacterium called *Candidatus Glomeribacter gigasporarum* (CaGg) and a coccoid Mollicutes/*Mycoplasma*-related endobacterium (Mre). These two bacteria can thrive within a single cell or fungal spore, representing novel and poorly described microbiota. However, the presence of endobacteria is not exclusive of Glomeromycota. Another group of basal fungi closely related to AMF, the Mucoromycotina, has been reported to harbor endobacteria. A  $\beta$ -proteobacterium, phylogenetically closed to CaGg, has been reported in *Mortierella elongata*, a widespread fungal species that is commonly isolated from soils and plant rhizospheres. Mre have also been identified in *Endogone*, a group of mycorrhizal-like fungi associated with gymnosperms and bryophytes. The same Mollicutes endobacteria have been detected in *Sphaerocreas*, a lesser-known fungus with an enigmatic lifestyle that has been retrieved from bryophyte thalli. In conclusion, the widespread distribution of endobacteria along closely related lineages of plant-associated fungi raises new questions on their role in the evolution, diversification, and ecology of their fungal hosts and, consequently, in the history of plant-fungal-bacterial symbioses.

### CS 2-4 Mycorrhizal networks of *Cortinarius* spp. and *Betula nana* facilitate warming-induced regime shift of Arctic tundra

DESILPPE, J.R.<sup>1</sup>, M. Hartmann<sup>2</sup>, S.J. Grayston<sup>3</sup>, W.W. Mohn<sup>4</sup> and S.W. Simard<sup>3</sup>

<sup>1</sup>School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand, julie.deslippe@vuw.ac.nz;

<sup>2</sup>Forest Soils and Biogeochemistry, Swiss Federal Research Institute WSL, Zuercherstrasse 111, CH-8903 Birmensdorf, Switzerland and Molecular Ecology, Institute for Sustainability Sciences, Agroscope, Reckenholzstrasse 191, CH-8046 Zurich, Switzerland; <sup>3</sup>Department of Forest and Conservation Sciences, Faculty of Forestry, 2424 Main Mall, University of British Columbia, Vancouver, Canada V6T 1Z4; <sup>4</sup>Department of Microbiology and Immunology, Life Sciences Institute, University of British Columbia, Vancouver, Canada.

<sup>3</sup>Department of Forest and Conservation Sciences, Faculty of Forestry, 2424 Main Mall, University of British Columbia, Vancouver, Canada V6T 1Z4; <sup>4</sup>Department of Microbiology and Immunology, Life Sciences Institute, University of British Columbia, Vancouver, Canada.

**Abstract:** Climate warming is leading shrub expansion in Arctic tundra, but the role of ectomycorrhizal (ECM) fungi in this process is poorly understood. In a series of experiments focused on *Betula nana*, the dominant shrub increasing in Arctic Alaska, we assessed the effects warming on the composition of ECM community, and used <sup>13</sup>CO<sub>2</sub> labelling of plants to elucidate the potential for carbon (C) transfer through ECM networks involved in shrub spread. These studies indicated a prominent role for *Cortinarius* spp. in the response of *B. nana* to warming and the existence of mycorrhizal networks (MN) that are involved in inter plant C-transfer but only among conspecific *B. nana*. Here, I describe a novel combination of stable isotope probing (SIP) of microbial phospholipid fatty acids (PLFA) and fungal DNA, which we used to identify the ECM fungi involved in C transfer among *B. nana* plants in the field. PLFA-SIP revealed 7 times the <sup>13</sup>C enrichment of



fungal than bacterial PLFAs, confirming a dominant role for a direct MN pathway in C transfer among plants. Our DNA-SIP-pyrosequencing data indicate *Cortinarius* spp. were unique among rhizosphere fungi in being highly enriched in the <sup>13</sup>C-SIP-DNA fractions, providing strong evidence that MNs of *Cortinarius*, potentially involving several species, facilitate C transfer among *B. nana*. Our data suggest that symbiosis with *Cortinarius* spp. provides *B. nana* with a competitive advantage over co-occurring species facilitating its expansion in Arctic tundra as climate warms.

#### PS 4-8 Fire, fungi, and the changing boreal forest

DEVAN, M.R.<sup>1</sup> and D.L. Taylor<sup>1</sup>

<sup>1</sup>Department of Biology, University of New Mexico, Albuquerque, NM 87131 USA, raedevan@unm.edu.

**Abstract:** Soil microbes have indisputably strong influences on ecosystem properties and functions, and likely serve as biological filters during recolonization of aboveground vegetation following forest fires. There are only six species of trees native to interior Alaska, and all are dependent on ectomycorrhizal fungi. Black spruce is the most abundant tree species in interior Alaska, and has historically undergone self-replacement after fire. However, severe fires, which are becoming more frequent under warmer and drier conditions, favor dominance of deciduous species such as paper birch and aspen at the expense of black spruce. Various types of mycorrhizae (ecto-, endo-, arbutoid, etc.) confer a spectrum of benefits to host plants, which can be further divided by plant-fungal species combinations; however, few of these relationships have been elucidated, especially in the field. In 2005, native seedlings (*Picea. mariana*, *Picea glauca*, *Populus tremuloides*, *Betula neoalaskana*) and non-native *Pinus contorta* were outplanted at sites established in 2004 following the largest burn year on record in Interior Alaska. Aboveground biomass and roots were simultaneously harvested in 2011 and 2013. Data were collected on wet and dry biomass, basal diameter, diameter at breast height, height, new wood, old wood, and foliar nutrient concentrations. Over 10,000 colonized root tips have been subsampled from the 1,200 seedlings and are currently undergoing DNA extraction, PCR, and ITS sequencing. Here we present preliminary results on the composition of EMF communities on these seedlings as a function of host species and fire severity. Additionally we analyze differences in host tree growth characteristics associated with particular species of mycorrhizal fungi.

#### LT 2-5 Plant growth promoting fungi-PGPF associate with the ectomycorrhizal fungi *Rhizopogon luteolus* and *Pinus caribaea* roots

DÍAZ-ARIZA, L.A.<sup>1</sup>, A.L. García Prieto<sup>1</sup>, W.H. Sandoval<sup>1</sup>, J.C. Duque Yate<sup>1</sup> and A.M. Pedroza-Rodríguez<sup>2</sup>

<sup>1</sup>Grupo de Investigación en Agricultura Biológica, Departamento de Biología, Facultad de Ciencias, Pontificia Universidad Javeriana, Bogotá, D.C., Colombia, luciaana@javeriana.edu.co; <sup>2</sup>Grupo de Biotecnología Ambiental e Industrial, Departamento de Microbiología, Facultad de Ciencias, Pontificia Universidad Javeriana, Bogotá, D.C., Colombia.

**Abstract:** The aims of this work were to determine the occurrence of PGPF inside carpophores of the ectomycorrhizal fungi *Rhizopogon luteolus* and the short roots of *Pinus caribaea*, and to evaluate their effect individually or in combination with a bacteria consortium on the growth of the plant. The sampling site and greenhouses were located in a Caribbean pine commercial plantation in Casanare Colombia (4°39'10.73"N; 72°54'58.76"W). Closed *R. luteolus* sporocarps were collected from plots of 10-year-old trees and the pine roots from the pine greenhouses. Twenty-two fungal isolates were obtained on BAF, MNM, and malt extract agars, twelve from sporocarps and 10 from roots. *Pinus caribaea* seedlings were inoculated with 14 different fungal isolates. *Amanita muscaria* ATCC62932 was used as a control. All plants were fertilized with Kristasol® at 6mL/plant (0.75g/L). Two 81-day-old plants of each treatment were sown in the field. Treatments with *N. glabra*, *Penicillium brasilianum*, and *Eupenicillium* sp. significantly increased shoot length (p=0.009). Overall, survival rate was not significantly different among treatments after 53 days. *N. glabra* were selected as the PGPF for the next study with bacteria on pine. One month after sowing the seeds, the seedlings were inoculated with 10 mL of a mixed plant growth promoting bacteria-PGPB inoculum (10<sup>8</sup>cell/mL) previously isolated from teak (*Stenotrophomonas* sp., *Enterobacter* sp., *Pseudomonas* sp., TgLGBER275), 10 mL of the PGPF, and two ectomycorrhizal fungi, *Laccaria bicolor* ATCC MYA4686 and *Pisolithus tinctorius* ATCC MYA4688, and distributed in five treatments with a non-treated control and fertilized seedlings. Plants receiving the *N. glabra* inoculum were significantly larger than those inoculated with the other microorganisms, followed by the treatment with the mix of *P. tinctorius*, *L. bicolor* and the PGPB consortium. Under the conditions used in the present study, the application of the native PGPF *N. glabra*, a naturally associate with ectomycorrhizal fungi has considerable potential in forestry.

## CS 5-4 The co-invasion of ectomycorrhizal plants and fungi: complex interactions with fungi, animals, plants, and soil biota

DICKIE, I.A.<sup>1</sup>, J.R. Wood<sup>2</sup>, H.V. Moeller<sup>3</sup>, T. Fukami<sup>3</sup> and D.A. Peltzer<sup>2</sup>

<sup>1</sup>Bio-Protection Research Centre, Lincoln University, Box 85084 Lincoln 7647, New Zealand, [ian.dickie@lincoln.ac.nz](mailto:ian.dickie@lincoln.ac.nz);

<sup>2</sup>Landcare Research, Lincoln 7640, New Zealand; <sup>3</sup>Department of Biology, Stanford University, Stanford, CA 94305, USA.

**Abstract:** Ectomycorrhizal fungi occur in a complex interaction network with plant hosts and non-hosts, other soil decomposer biota (including fungi, bacteria, and animals), and aboveground animals that may disperse fungal spores. The complexity of these interactions presents a challenge to understanding their function. One system for better understanding these interactions are invasive ectomycorrhizal trees. We show that many ectomycorrhizal trees in New Zealand co-invade with non-native fungi. Intriguingly, this co-invasion of North American trees and fungi also involves novel interactions with invasive European and Australian mammals, which act as dispersal agents for the major fungal invaders, *Rhizopogon* and *Suillus*. Other trees, such as *Pseudotsuga menzeisii*, have more context dependent interactions, forming novel associations with native fungi when invading forests but co-invading with exotic fungi in grasslands. The net effects of tree-fungal co-invasions on soil ecosystems are complex and include interactions with soil bacteria, fungi, and nematodes. In particular, pine-fungal co-invasion into native grass/shrub-lands results in the release of recalcitrant N and P, increases in available nutrients, and greatly increased bacterial dominance of soil food-webs. These changes in ecosystem function can generate long-lasting legacies including facilitating invasion by non-native grasses. These results highlight that complex interaction networks are involved in both determining ectomycorrhizal invasions and their effects in ecosystems. Further, we believe they demonstrate that biological invasions are ideal systems for better understanding the multi-kingdom interactions of mycorrhizas and their effects on ecosystems.

## LT 1-2 Preliminary observations of diversification of mycorrhizal plant response - island versus continent populations

DUCHICELA J.<sup>1,2</sup>, J. Bever<sup>2</sup> and P. Schultz<sup>2</sup>

<sup>1</sup>Universidad de las Fuerzas Armadas – ESPE, Sangolqui, Ecuador, [jiduchicela@espe.edu.ec](mailto:jiduchicela@espe.edu.ec); <sup>2</sup>Indiana University, Biology Department, USA

**Abstract:** Arbuscular mycorrhizal fungi (AMF), widespread soil fungi that colonize the majority of plant species in terrestrial ecosystems, influence plant growth, local biodiversity, and ecosystem function, in particular, the stabilization of soil aggregates. In this study, we sought to understand the variation in the responses to AMF inoculation of 12 native and 8 introduced plant species from the highlands of Santa Cruz Island, Galapagos. We also related those responses to soil properties of fields dominated either by native or introduced plant communities. The results revealed that, when compared to the native flora, a greater proportion of introduced plant species are from plant families that are typically associated with AMF. This result is consistent with the findings of the plant growth experiment, which revealed that introduced plants are more responsive to mycorrhizal inoculation than are native species. Further, field sites dominated by introduced species had a greater proportion of stable soil aggregates compared to field sites with native species which appears to result from introduced plants being more associated with AMF. Our study provides a first evaluation of AMF associations with native and introduced hosts and the potential ecosystem effects at the island. It is crucial to acknowledge the difficulty in discerning introduced versus indigenous fungi at the island, and understand their respective contributions to terrestrial biodiversity. Therefore, the next question needs to be assessed at a continental scale. We present preliminary results of an analysis of the mycorrhizal status of the local flora on the continent compared with the island. We also discuss a greenhouse experiment used to assess the response of *Psidium guajava*, which is native to the continent but was introduced to the island, to AMF isolates from the continent and the island.

## CS 4-4 Mycorrhizal plant facilitation: a promising key tool for nickel mine site ecological restoration in Madagascar and New Caledonia

**DUCOUSSO, M.**<sup>1</sup>, C. Henry<sup>2</sup>, A. Houlès<sup>1,3</sup>, A. Razafimamonjy<sup>4</sup>, P. Andrianaivomahefa<sup>4</sup>, A. Leveau<sup>3</sup>, L. Hannibal<sup>5</sup>, F. Carriconde<sup>6</sup>, H. Ramanankierana<sup>7</sup>, M. Lebrun<sup>8</sup>, M.A. Selosse<sup>9</sup> and P. Jourand<sup>5</sup>

<sup>1</sup>CIRAD, Laboratoire des Symbioses Tropicales et Méditerranéennes, TA A-82/C Campus International de Baillarguet, 34398 Montpellier cedex 5, France, marc.ducouso@cirad.fr; <sup>2</sup>AgroParisTech, Laboratoire des Symbioses Tropicales et Méditerranéennes, TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, France; <sup>3</sup>Koniambo Nickel SAS, BP 696, 98860 Koné, Nouvelle-Calédonie; <sup>4</sup>Ambatovy, Immeuble Tranofitaratra - 7ème étage, Rue Ravoninahitriniarivo – Ankorondrano, Antananarivo 101 – Madagascar; <sup>5</sup>IRD, Laboratoire des Symbioses Tropicales et Méditerranéennes, TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, France; <sup>6</sup>Institut Agronomique néo-Calédonien, BPA5, 98848 Noumea, New Caledonia; <sup>7</sup>Centre National de Recherches sur l'Environnement, Laboratoire de Microbiologie de l'environnement, Antananarivo, Madagascar; <sup>8</sup>Université de Montpellier, Laboratoire des Symbioses Tropicales et Méditerranéennes, TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, France; <sup>9</sup>MNHN, Origine, Structure et Evolution de la Biodiversité, UMR 7205, 57 Rue Cuvier, 75005 Paris, France.

**Abstract:** In most terrestrial ecosystems, mycorrhizal symbiosis plays a key role in plant growth and development, especially in harsh contexts where it may intervene in the facilitation process between plants. Madagascar and New Caledonia are considered hot spots of biodiversity, and ecological restoration in these unique environments is challenging. In such contexts, facilitation is a promising tool that may assist in ecosystem reclamation. As mycorrhizal fungi can be associated with several plant species, one plant can facilitate the establishment of another by providing fungal inoculum in the form of already established and supported mycelia. Facilitation implies that plants share a large proportion of their ectomycorrhizal fungal partners. We characterized ectomycorrhizal communities on nickel and cobalt mining sites in Madagascar and New Caledonia to identify facilitator plants that may be used in ecological restoration technical itineraries. In Madagascar, four ectomycorrhizal tree species, *Asteropeia mcphersonii*, *Leptolaena* sp., *Rhodolaena bakeriana*, *Sarcolaena* sp., and *Uapaca* sp., locally dominate the canopy. We demonstrate that these trees share most of their ectomycorrhizal partners and could be considered as generalists and they remain stable independent of tree age (e.g., adult or seedling). Following original ecosystem destruction, the only species spontaneously regenerating is *A. mcphersonii*, making this species a candidate for its use as a facilitator. In New Caledonia, extreme soil constraints such as heavy metal toxicities (Ni, Co, Mn, Cr), Ca/Mg unbalance by Mg excess, paucity of nutrients (N, P, K), and an excess of iron oxides (>90%) enable only a few planted species to grow after ecosystem destruction. Among them, we demonstrate that *Acacia spirorbis* shares most of its ectomycorrhizal fungal partners with the endemic *Tristaniaopsis* spp. (Myrtaceae), a dominant species in some maquis and is now tested as a facilitator in a set of field trials on the Koniambo massif. Facilitation is a promising process to assist in the successful ecological restoration of mine sites.

## LT 4-2 Aboveground and belowground responses of native and invasive prairie grasses to elevated temperatures and drought

**DUELL, E.B.**<sup>1</sup>, G.W.T. Wilson<sup>1</sup> and K.R. Hickman<sup>1</sup>

<sup>1</sup>Department of Natural Resource Ecology Management, Oklahoma State University, Stillwater, Oklahoma 74075 USA, eric.duell@okstate.edu.

**Abstract:** Global-scale anthropogenic alterations include intense and prolonged droughts, increases in atmospheric temperatures, and invasion of native ecosystems by non-native species. Climate change may increase success of non-natives directly as these species often possess traits that are favored by variable climates, or indirectly through negative impacts on native vegetation or alterations in soil microbial communities. Understanding how native and non-native grasses tolerate drought and elevated temperatures is essential for projecting native species competitive success. To determine the effects of elevated temperature and reduced soil moisture on plant performance at early growth stages, we assessed germination and seedling growth of an invasive warm-season grass (*Bothriochloa ischaemum*), compared with a functionally similar native (*Schizachyrium scoparium*), and an invasive cool-season grass (*Bromus inermis*), compared to functionally similar native (*Pascopyrum smithii*). Direct effects of climate change on seedling growth were assessed by

determining plant biomass and indirect effects were determined through assessment of intra- and inter-radical mycorrhizal fungal abundance. Germination and biomass production of both invasive species were substantially greater across all temperature and moisture regimes, compared to their paired native species indicating increased germination, growth rate, and biomass production may be primary mechanisms of successful invasibility for non-native grasses and that elevated temperatures and intense drought may further exacerbate successful invasion of non-native grasses. Because associations with mycorrhizal fungi may aid in host water acquisition and thermal tolerance, we hypothesized both intra- and inter-radical hyphal abundance would be greater when plants were exposed to adverse conditions. Inter-radical hyphal abundance was greater in rhizospheres of the invasive warm-season grass, compared to the paired native, potentially providing the invasive species with an edge over native species when grown under adverse conditions.

#### LT 1-10 **Assessment of Illumina MiSeq dual end sequencing of arbuscular mycorrhizal fungal communities using mock communities of known DNA quantity**

**EGAN, C.P.<sup>1</sup>**, Y. Lekberg<sup>2,3</sup>, A. Cornell<sup>2</sup>, M. Settles<sup>4</sup>, J.N. Klironomos<sup>1</sup> and M.M. Hart<sup>1</sup>

<sup>1</sup>Biology University of British Columbia Okanagan, Kelowna, BC, Canada, cameron.egan@ubc.ca; <sup>2</sup>MPG Ranch, Missoula, MT, USA; <sup>3</sup>Department for Ecosystems and Conservation Sciences, University of Montana, Missoula, MT, USA; <sup>4</sup>Institute for Bioinformatics and Evolutionary Studies, Department of Biological Sciences, University of Idaho, ID, USA.

**Abstract:** Methods used to characterize arbuscular mycorrhizal fungal (AMF) communities are rapidly changing. Accurate identification, delineation, and quantification of AMF taxa is essential for ecological studies. With the advent of next generation sequencing (NGS), there has been an increase in the number of ecological studies on AMF using sequencing technology. These techniques present both unprecedented challenges and opportunities for AMF community ecologists. With NGS technology, there is potential for biases, either during amplification or sequencing, which can potentially alter taxa abundances, thereby reducing the usefulness of quantitative metrics and cross study comparisons. In this study, we developed a dual end sequencing/indexing technique for AMF taking advantage of the Illumina MiSeq platform with the goal of reducing costs to researchers. We tested the accuracy of this technique for detecting identities and abundances of AMF taxa within samples using mock communities of varying taxa dominance from spore isolates spanning 6 families using the primers Wanda and AML2. We found a highly significant correlation ( $r > 0.90$ ,  $p < 0.001$ ) between observed and expected communities in which relative abundances were accurately reflected across families. Consistency among replicates was also very high based on Bray-Curtis distances ( $R^2 = 0.98$ ,  $p < 0.001$ ). Our data suggests that this technique does not introduce bias during the amplification and sequencing and can provide AMF researchers with a tool to accurately identify and quantify AMF taxa within samples at a reduced cost.

#### PS 2-49 **Montane orchids steal from their neighbors, but are they harmful?**

**ENRIQUEZ, A.C.<sup>1</sup>** and D.L. Taylor<sup>1</sup>

<sup>1</sup>Department of Biology, University of New Mexico, Albuquerque, New Mexico 87131 USA, nitatina@unm.edu.

**Abstract:** The Orchidaceae houses 50% of all plants that have lost photosynthetic machinery. This adaptation is likely facilitated by the unusual and exploitative mycorrhizal relationship that orchids have with fungi called mycoheterotrophy. Mycorrhizal symbioses are ubiquitous in the plant kingdom and impact the growth, community composition, and responses to stress and climate change of vegetated terrestrial ecosystems. *Corallorhiza striata* is an obligately mycoheterotrophic orchid that possesses no chlorophyll and is reliant upon fungi for nutrients and carbon products siphoned from a neighboring tree. Upon “tricking” the fungus into infecting the rhizome, the orchid dismantles the fungus allowing access to the fungal resources. Does mycoheterotrophy in orchids negatively impact its host fungus or tree? Orchid rhizomes and seedpods were collected in two New Mexico mountain ranges. Fungi were cultured directly from *C. striata* pelotons on agar and then in broth for inoculation onto conifer seedlings growing in small glass microcosms. Once ectomycorrhizae are established, viable orchid seeds will be sown directly into half of the microcosms, and autoclaved orchids seeds will be sown into the remaining half. Aboveground and belowground conifer biomass and fungal abundance will be compared across systems with and without orchids to determine the fitness impact of mycoheterotrophy on the trees and fungi. Orchids possess a unique ability to lure and destroy fungi. This knowledge could be applied to fighting fungal pathogens in plants, animals, and humans.



**PS 4-9 Interaction between *Washingtonia robusta* and root endophytes modify overall plant physiology and metabolism to alleviate drought stress**

**ESTRADA-LUNA, A.A.**<sup>1,2</sup>, V. Olalde-Portugal<sup>2</sup>, H.C.M. Torres<sup>2</sup>, J.M. Torres<sup>2</sup> and E.R. Chávez<sup>2</sup>

<sup>1</sup>School of Agronomy, Universidad De La Salle Bajío, León, Guanajuato 37150 Mexico, aestradaluna@yahoo.com;

<sup>2</sup>CINVESTAV-IPN. Km. 9.6 Libramiento Norte Carretera Irapuato-León. Apartado Postal 629, Irapuato, Gto., 36821, México.

**Abstract:** Water stress is one of the major constraints that terrestrial plants face. Because of this, it is clear that they have evolved intricate physiological and molecular mechanisms to perceive and respond to this common environmental situation, in which the interaction with some bacteria and mutualistic associations with mycorrhizal fungi seem to play an important role. We ran a glasshouse study and report the effects of water stress and two selected endophytes on growth, physiology and metabolism of young *Washingtonia robusta* plants. Data on root colonization indicated that *W. robusta* was able to establish mycorrhizas and interact with beneficial bacteria. However, water stress reduced the percentage of fungal vesicles, arbuscules and the bacteria population, which was also affected by the presence of mycorrhizas. The nutrient status of the plants was enhanced by the fungi, which increased concentrations of P and K. In general, the water limitation promoted drastic changes in plant functioning, growth and metabolite profile of both shoots and roots. Plants suffering water stress closed the stomata and a substantial reduction in the efficiency of the photosynthetic machinery and the rate of CO<sub>2</sub> fixation was observed. Overall plant growth was increased by endophytes, especially by mycorrhizal fungi. Chlorophyll *a*, *b* and total chlorophyll content were reduced by water stress. In contrast, sucrose, galactose and amino acid concentrations dramatically increased in the whole plant. Our observations suggest that *W. robusta* is genetically resistant to water stress, however, the interaction between the roots and the two endophytes attenuate all negative effects. The establishment of mycorrhizas seemed to have a critical role in plant response and survival, in contrast, to a secondary role that the bacteria seem to play. Data on plant recovery will be discussed.

**SY 2-1 Towards a comprehensive understanding of the molecular mechanism of phosphate acquisition through the mycorrhizal pathway**

**EZAWA, T.**<sup>1</sup>, Y. Kikuchi<sup>1</sup>, N. Hijikata<sup>1</sup>, K. Yokoyama<sup>1</sup>, R. Ohtomo<sup>2</sup>, M. Kawaguchi<sup>3</sup>, K. Saito<sup>4</sup> and C. Masuta<sup>1</sup>

<sup>1</sup>Graduate School of Agriculture, Hokkaido University, Sapporo 0608589, tatsuo@res.agr.hokudai.ac.jp; <sup>2</sup>National Agriculture and Food Research Organization, Hokkaido Agricultural Research Center, Sapporo 0628555; <sup>3</sup>Division of Symbiotic Systems, National Institute for Basic Biology, Okazaki 4448585; <sup>4</sup>Faculty of Agriculture, Shinshu University, Minamiminowa 3994598 Japan.

**Abstract:** Mycorrhizal plants take up a significant part of inorganic phosphate (Pi) through the mycorrhizal pathway, but the underlying physiological and molecular mechanisms are largely unknown. Arbuscular mycorrhizal (AM) fungi take up Pi from the soil through hyphal networks, accumulate a massive amount of polyphosphate for long-distance translocation to arbuscules in the roots, and then release Pi to the periarbuscular space. In this project, dynamics of transcriptome and inorganic and organic nutrients are being investigated in conjunction with a novel gene silencing technique to provide a comprehensive understanding of the physiological and molecular mechanisms of the pathway. *Rhizophagus clarus* HR1 (MAFF502276) was grown in a two-compartment mesh bag culture system in association with *Lotus japonicus* or *Nicotiana benthamiana*, and the roots and extraradical mycelia were harvested. Levels of polyphosphate, inorganic cations, and amino acids were measured, and RNA-Seq was performed on the Illumina platform. AM fungal genes were knocked down by virus-induced gene silencing. Pi application to Pi-starved hyphae triggered not only polyphosphate accumulation but also near synchronous and equivalent uptake of Na<sup>+</sup>, K<sup>+</sup>, Ca<sup>2+</sup>, and Mg<sup>2+</sup> with Pi, while the genes that are responsible for Pi uptake, polyphosphate biosynthesis, cation uptake, and maintenance of cellular homeostasis were up-regulated. These results indicate that inorganic cations play a major role in neutralizing the negative charge of polyphosphate and, further, that these processes are achieved by the orchestrated regulation of gene expression. Further detailed analysis of the fungal transcriptomes allowed us to identify several candidate genes involved in subsequent Pi delivery processes such as long-distance polyphosphate translocation and Pi transfer from the fungus to the host. Functional analysis of these genes is currently being conducted via knockdown experiments.



## PS 2-23 Distance effects of green-tree retention in conservation of ectomycorrhizal fungal diversity

FELDMAN, E.C.<sup>1</sup>, S. Berch<sup>2</sup>, J.M. Kranabetter<sup>3</sup>, V. Ward<sup>1</sup>, D. Durall<sup>1</sup> and M.D. Jones<sup>1</sup>

<sup>1</sup>Biology Department, University of British Columbia, Okanagan Campus, Science Building, 1177 Research Road, Kelowna, B.C. Canada, V4V 1V7, erin.feldman.82@gmail.com; <sup>2</sup>British Columbia Ministry of Environment, North Road Lab, 4300 North road, Victoria BC V8W 9C4; <sup>3</sup>British Columbia Ministry of Forests, Lands and Natural Resource Operations, P.O. Box 9536, STN PROV GOVT, Victoria, B.C. Canada V8W 9C4.

**Abstract:** Green-tree retention has been gaining popularity as a forestry practice over the last 25 years as a way to retain and re-establish biodiversity in adjacent harvested areas. Retention cuts have been shown to support higher richness and abundance of forest species than clear-cuts, though certain forest interior species may not be supported by smaller islands, and the positive effects of this practice are proportional to the number of retained trees and time since harvest. British Columbia's Forest Practices Act, Canada's National Forest Strategy, and Canada's Biodiversity Strategy all emphasize the importance of maintaining forest biological diversity, the ecological integrity of forests, and ensuring sustainable use of forest resources. Current policies, regulations, and guidelines do not adequately consider the significance of soil organisms to the preservation of ecological functions, and yet, soil microbes play an indispensable role in nutrient cycling, so conservation of a healthy, functioning soil biotic community is critical for total ecosystem function. We examined species composition and abundance of ectomycorrhizal fungi (EMF) colonizing young Douglas-fir (*Pseudotsuga menziesii*) seedlings from 0 to 20 m from retention islands into cut blocks. Seedlings were planted shortly after harvest in the spring of 2009 and collected after eight months for examination of ectomycorrhizae. We used molecular analysis of ITS sequences to which OTUs were assigned and sequences were BLASTed against NCBI and UNITE databases. Seedlings in cut blocks maintained comparable levels of total EMF species diversity to seedlings within retention patches. Variation in species composition between sampling sites will be discussed.

## SY 3-5 AM fungal hyphae exudates can prime a bacterium mediated phytate mineralization in hyphosphere

Zhang, L.<sup>1</sup>, F. Wang<sup>1</sup>, F. Zhang<sup>1</sup> and G. FENG<sup>1</sup>

<sup>1</sup>College of Resource and Environmental Science, China Agricultural University, Beijing 100193, China, fenggu@cau.edu.cn.

**Abstract:** A main subject in ecology is to understand how cooperative strategies evolve and are maintained in species networks. Here, we focus on the three-partner relationship between plants, arbuscular mycorrhizal (AM) fungi, and hyphosphere bacteria to ask if the interaction between AM fungi and bacteria can pay back the resource (phosphorus here) to host plants by consuming the plants derived carbon (C). Two microcosm experiments that separate the plant roots, mycorrhizal hyphae, and bacteria were conducted to demonstrate the direct effects of hyphal exudates on the growth and activity of bacteria in organic phosphorus (P) mobilization and the direct effects of bacteria on the growth and activity of the AM fungus in P uptake which were transferred to plants. Results showed that AM fungi released substantial C to the environment, triggering bacterial growth and stimulating their activity on organic P mineralization and turnover. <sup>13</sup>C-DNA stable isotope probing was used to track C flow through hyphae exudates and to the hyphosphere bacteria community. We found *Pseudomonas alcaligenes*, which has been previously identified to mineralize phytin, was labeled with <sup>13</sup>C derived from maize photosynthate via extraradical mycelium of *R.irregularis*, indicating the P-solubilizing bacteria strain used hyphae exudates. The bacteria enhanced hyphal proliferation, by which the fungus has more access to available P. Our results suggest that AM fungi and bacteria share host photosynthates, and as reciprocation, the AM fungi-bacteria interaction repays the plant with P by jointly mobilizing soil organic P.

Zhang, Q.<sup>1</sup> and H. FENG<sup>1</sup>

<sup>1</sup>School of Life Sciences, Key Laboratory of Cell Activities and Stress Adaptations, Lanzhou University, Lanzhou 730000, China, fenghy@lzu.edu.cn.

**Abstract:** The Qinghai-Tibet Plateau is a very unique and fragile alpine ecosystem, where permafrost degradation and loss of vegetation are becoming more and more serious due to increasing human activities and global warming. To effectively restore the damaged ecosystem on the Qinghai-Tibet Plateau, the government and researchers have conducted a series of revegetation programs and restoration studies. To date, the restoration dynamics of aboveground vegetation in this region is well studied, but little is known about the restoration of below-ground arbuscular mycorrhizal (AM) fungi, which are essential for nutrient cycling and ecosystem stability. This study was conducted in an artificial vegetation restoration site, which is located in Tuotuohe, the frozen soil engineering corridor of Qinghai-Tibet Plateau. Vegetation restoration was conducted in 2002 by planting monocultures of *Elymus nutans*, *Leymus secalinus*, *Roegneria thoroldiana*, and *Poa crymophila* in separate plots in the pit, or mixed sowing of *E. nutans* + *P. crymophila*. Natural recovery plots (no seeding) and native plots (without vegetation destruction) were set at the same time (7 treatments in total). In 2013, the community structure and function of AM fungi under different treatments were analyzed using clone libraries and other state-of-the-art techniques. AM fungal colonization rate and spore communities showed significant differences among varied restoration treatments. *R. thoroldiana* seeding led to the highest AM fungal colonization rate, indicating that this recovery method is beneficial to the symbiotic relationship between plants and AM fungi. Twenty phylotypes of AM fungi were identified from all root samples (5 families, 6 genera). Native plots had the highest number of phylotypes. Although the diversity and species composition of AM fungi showed no significant differences among treatments, the community structure of AM fungi in *R. thoroldiana* plots was most similar to native plots.

#### PS 1-13 The community of arbuscular mycorrhizal fungi and its correlation with plant phylogeny from south-facing to north-facing slope

Chai, Y.<sup>1</sup>, W. Guo<sup>1</sup>, J. Pan<sup>1</sup>, S. Jiang<sup>1</sup>, M. Qin<sup>1</sup>, Y. Liu<sup>1</sup> and H. FENG<sup>1</sup>

<sup>1</sup>MOE Key Laboratory of Cell Activities and Stress Adaptations, School of Life Sciences, Lanzhou University, Lanzhou 730000, China, fenghy@lzu.edu.cn.

**Abstract:** Knowledge of the distribution of arbuscular mycorrhizal fungal communities in ecosystems is key to understanding their potential functions. Here we compare AM fungal communities on south-facing and north-facing slopes of Qilian Mountain in China. Thirty sampling sites on south-facing slopes and 15 in north-facing slopes were studied. The plant species richness in north-facing slopes is significantly higher than on south-facing slopes. However, the root length colonization and AM fungal extraradical hyphal length density in south-facing slope are significantly higher than that on north-facing slopes. A total of 25 AM fungal phylotypes were recovered from all root samples based on clone and sequencing with the primer pairs NS31-AML2. The phylotypes belong to following seven genera: *Glomus*, *Rhizophagus*, *Funneliformis*, *Septoglomus*, *Claroideoglomus*, *Diversispora*, and *Gigaspora*. There were 17 phylotypes observed on north-facing slopes and 19 phylotypes observed on south-facing slopes. The species composition of the AM fungal communities was significantly different in the different slopes. The phylogenetic signal detection results show that the plant water content, the plant height and plant N:P have strong phylogenetic signal, indicating that these plant properties has a significant correlation with plant phylogeny. In addition, a total of 35 AM fungal phylotypes are found in 42 plant species and belong to 6 families (9 genera, *Glomus* has the highest abundance, and it exists in all plant species). The AM fungal species richness in different plant species are significantly different and changes from  $1.00 \pm 0.57$  to  $6.67 \pm 1.86$ . The Mantel Test shows that the phylogenetic distance of the 42 plant species in our sampling sites have a significant positive correlation with community distance of AM fungi. The plant phylogeny and functional traits could explain 43.68% of the variation of community structure of AM fungi, showing that the host plant genetic relationship is the major factor influencing AM fungal community structure.

## CS 7-1 Carbon quality and N concentration control the decomposition dynamics of ectomycorrhizal fungal necromass

FERNANDEZ, C.W.<sup>1</sup>, P.G. Kennedy<sup>1</sup> and R.T. Koide<sup>2</sup>

<sup>1</sup>Department of Plant Biology, University of Minnesota, cwfern@umn.edu; <sup>2</sup>Department of Biology, Brigham Young University.

**Abstract:** In forest ecosystems, tree hosts allocate a considerable amount of carbon to ectomycorrhizal (EM) fungi. The necromass resulting from the death of EM fungi represents a large input into forest carbon and nutrient cycles. Understanding what controls the fate of this carbon has recently become a major focus of mycorrhizal ecology. Given the tremendous diversity in morphological, anatomical, and chemical traits among EM fungi, our central goal has been to identify traits of EM fungi that determine necromass quality in order to gain a more mechanistic understanding of what controls their decomposition. For this talk, I will focus on knowledge gained from a series of litterbag studies and a minirhizotron study, which examined the influence of biochemistry on the decomposition of EM fungal necromass. Species identity is a significant determinant of the decomposability of fungal necromass. This is largely due to the variation in biochemistry found across EM fungi. Like the decomposition of plant litter, the decomposition rate of EM fungal necromass was governed by both N concentration and the carbon quality. The N concentration of necromass was positively correlated with decomposition rate. Contrary to what has been speculated throughout the literature, chitin was found to be labile relative to other compounds present in the necromass, and initial chitin concentration was positively correlated with decomposition (% mass loss) suggesting that chitin concentration has a positive effect on necromass quality. Conversely, the production of melanin, a group of dark cell wall polymers, which vary widely in concentration among fungi, appears to be a biochemical trait that greatly reduces the carbon quality of EM fungal necromass. This is likely due to the complex aromatic structure of these polymers, which are impervious to hydrolytic breakdown. Together, these findings will be discussed in the context of potential effects on carbon sequestration in forest soils.

## CS 9-2 *Arabidopsis*-AM fungi, impossible relationship?

FERNANDEZ, I.<sup>1</sup>, M.J. Pozo<sup>2</sup>, S.C.M. van Wees<sup>1</sup>, C.M.J. Pieterse<sup>1</sup> and M.G.A. van der Heijden<sup>1,3</sup>

<sup>1</sup>Plant-Microbe Interactions, Utrecht University, Utrecht 3508 TB The Netherlands, I.M.FernandezLopez@uu.nl;

<sup>2</sup>Department of Soil Microbiology and Symbiotic Systems, Estación Experimental del Zaidín (CSIC), Granada 18008 Spain;

<sup>3</sup>Ecological Farming Systems, Agroscope Reckenholz-Tänikon Research Station ART, Zürich 8046 Switzerland.

**Abstract:** The 450 million-year-old symbiosis between the majority of land plants and arbuscular mycorrhizal (AM) fungi is one of the most ancient, abundant, and ecologically important mutualisms on Earth. Recent developments in mycorrhizae research revealed novel insights into the functioning of this symbiosis, identifying key genes and signals responsible for nutrient uptake and symbiosis establishment. However, approximately 18% of all land plants, including important crop species, do not form a symbiosis with AM fungi and can even be antagonized by them. Recently, we demonstrated that the non-host *Arabidopsis thaliana* becomes heavily infected by AM fungi when exposed to mycorrhizal networks that are nursed by neighboring host plants, resulting in strong growth reduction. In this study, we investigated the tripartite interaction between an AM fungus (*Rhizophagous irregularis*, formerly known as *Glomus intraradices*), its host (*Medicago truncatula*), and a non-host plant (*A. thaliana*). We aim to unravel mechanisms that explain the biological basis of AM fungal incompatibility and to analyze whether AM fungi act as pathogens on *Arabidopsis* roots. In addition, we study the early recognition events during the *Arabidopsis*-mycorrhiza interaction by using monoaxenic cultures, and we compare the results obtained with the early recognition events observed in other *Arabidopsis* beneficial and pathogenic interactions.

### CS 6-3 Comparative evolutionary physiology of Mucoromycotina and Glomeromycota symbionts in basal land plants

FIELD, K.J.<sup>1</sup>, M.I. Bidartondo<sup>2,3</sup>, W.R. Rimington<sup>2,3,4</sup>, J.G. Duckett<sup>4</sup>, D.D. Cameron<sup>5</sup>, J.R. Leake<sup>5</sup> and S. Pressel<sup>4</sup>

<sup>1</sup>School of Biology, Faculty of Biological Sciences, University of Leeds, LS2 9JT, UK, k.field@leeds.ac.uk; <sup>2</sup>Jodrell Laboratory, Royal Botanic Gardens, Kew, TW9 3DS, UK; <sup>3</sup>Department of Life Sciences, Imperial College London, London SW7 2AZ, UK; <sup>4</sup>Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK; <sup>5</sup>Department of Animal and Plant Sciences, University of Sheffield, S10 2TN, UK.

**Abstract:** The discovery that members of Mucoromycotina, an ancient and partially-saprotrophic fungal lineage, associate with the basal liverwort lineage Haplomitriopsida, casts doubt on the widely-held view that Glomeromycota formed the sole ancestral plant-fungus symbiosis. New evidence has shown that representatives of all extant early branching lineages of land plants actually harbor members of both fungal lineages, sometimes simultaneously. Whether these dual associations with both Glomeromycota and Mucoromycotina fungi, or indeed those between liverworts and Mucoromycotina fungi alone, are mutualistic or how their functioning may have been affected by the fall in atmospheric CO<sub>2</sub> concentration ([CO<sub>2</sub>]) following plant terrestrialization remains unknown. We measured carbon-for-nutrient exchanges between the early-branching liverwort genera *Haplomitrium*, *Treubia*, *Neohodgsonia*, and *Allisonia* and their symbiotic fungal partners. By supplying <sup>14</sup>CO<sub>2</sub> to the plants and <sup>33</sup>P-orthophosphate and <sup>15</sup>N-ammonium chloride to the fungal associates, we quantified nutrient uptake and efficiency of each symbiosis at both a replicated Paleozoic [CO<sub>2</sub>] of 1,500 ppm and a modern lower [CO<sub>2</sub>] of 440 ppm. We compared our findings to those from identical experiments investigating liverwort-Glomeromycota relationships, showing that plant-Mucoromycotina and dual fungal-plant symbiotic associations are both mutualistic and mycorrhiza-like. Further, we demonstrate greater nutrient benefit for reduced carbon outlay in plants with Mucoromycotina and dual fungal associations compared to non-vascular plants colonized solely by Glomeromycota fungi at 440 ppm [CO<sub>2</sub>]. Our findings suggest a more versatile and shifting evolutionary scenario in early plant-fungal symbioses than has previously been assumed and demonstrate the pressing need for further functional studies across land plant and fungal phylogenies.

### CS 7-3 Mycorrhizal fungi and coupled biogeochemical cycles at plot-to-global scales

FINZI, A.<sup>1</sup>

<sup>1</sup>Department of Biology, Boston University, afinzi@bu.edu.

**Abstract:** Mycorrhizal fungi differ in form and function with very well defined differences in their ability to degrade soil organic matter. As such, mycorrhizas affect soil carbon storage and the response of ecosystems to global change via direct (e.g., decomposition) and indirect (e.g., nutrient retention with hyphae) effects on decomposition and primary production. Over the last decade our research group has examined plant-mycorrhizal interactions in the hope of gaining a better understanding patterns of belowground plant C allocation, how this C affects the costs of nutrient acquisition, and the role of mycorrhizal versus saprotrophic microbial activity in regulating decomposition and the provisioning of nutrients to host plants. The objective of this talk is to present research beginning with local-scale observations in a mid-latitude forest in central Massachusetts, USA where we use in-growth cores to study soil organic matter decomposition. I then discuss our research from other sites and the results of a meta-analysis of belowground C allocation to make the case that the costs of nutrient acquisition varies inversely with climate (e.g., high latitude = high cost, low latitude = low cost) because of changes in the composition of mycorrhizal communities and plant-mycorrhizal competition for those nutrients. An emergent property of this interaction is vast storages of C at high latitudes despite exceptionally low rates of primary production.

**FIRESTONE, M.K.**<sup>1</sup>, A. Karkourdis<sup>1</sup>, E. Nuccio<sup>1,2</sup>, D. Herman<sup>1</sup>, T. Whitman<sup>1</sup>, A. Hodge<sup>3</sup>, R. Neurath<sup>1,2</sup> and J. Pett-Ridge<sup>2</sup>

<sup>1</sup>Department of Environmental Science Policy and Management, University of California, Berkeley, CA 94720 USA, mkfstone@berkeley.edu; <sup>2</sup>Chemical Sciences Division, Lawrence Livermore National Laboratory, Livermore CA USA;

<sup>3</sup>Department of Biology, University of York, York, YO10 5DD, UK.

**Abstract:** The interactions of arbuscular mycorrhiza (AM) with plant roots are central to the functioning of most terrestrial ecosystems. However, in addition to their “direct” effects on the survival, growth, and fitness of plants, AM also interact with other members of the soil ecosystem, particularly bacteria and fungi, and thereby impact belowground nutrient transformation and availability. Research has shown that the presence of arbuscular mycorrhizal fungi (AMF) can accelerate decomposition of plant detritus, even though AMF do not have significant saprotrophic capabilities. AMF can impact decomposition and N-mineralization processes by providing substrates for decomposers or by altering the composition or functionality of hyphosphere microbial communities. We have evidence that both of these potential mechanisms appear to be in play during decomposition of plant litter. Another critically important soil process is the stabilization of carbon through interaction with soil mineral components. While there has been much historical interest in how AMF contribute to soil carbon pools, the actual interactions of living AMF hyphae or AMF hyphal necromass with soil mineral components is poorly understood. The identity of microbes involved in the localization of plant root carbon on mineral surfaces can be explored by molecular analysis of microbes developing on minerals in the presence of roots. The microscopy and DNA evidence we will present gives a first glimpse of the roles of AMF and non-AMF hyphal interactions with mineral surfaces in soil.

#### PS 3-31 Acclimatization of arbuscular mycorrhizal fungi to heavy metal stress

Cuong, B.V.<sup>1</sup> and **P. FRANKEN**<sup>1</sup>

<sup>1</sup>Leibniz Institute of Vegetable and Ornamental Crops Großbeeren/Erfurt e.V., 99090 Erfurt, Germany, franken@igzev.de.

**Abstract:** One important character of arbuscular mycorrhizal (AM) fungi is their general ability to confer heavy metal (HM) tolerance to their host plants. Numerous studies showed that AM fungal strains isolated from HM-contaminated sites perform much better in this aspect than taxonomically-related strains which have never been in contact with these toxic metals. However, AM fungi lose this character if propagated under HM-free conditions. Based on these observations, we raised two hypotheses: (1) HM tolerance of the AM fungus is a prerequisite for the ability to confer HM tolerance to plants and (2) If AM fungi are propagated under HM stress, they are able to gain HM tolerance. The model AM fungal strain *Rhizophagus irregularis* DAOM-197198 was cultivated for over five generations in root organ cultures harboring moderate Zn or Pb concentrations. The final generation of newly developing spores was used for inoculating carrot root organ cultures and maize plants in pot cultures, both treated with high amounts of Zn and Pb. The results showed that AM fungi can be acclimatized to HM stress. Hyphal density or the number of spores was higher if the strains were propagated either on Zn or on Pb compared to the non-acclimatized control strains. The process of acclimatization was also reflected by AM fungal gene expression patterns. RNA of particular genes accumulated earlier or to increased amounts in the acclimatized strain. This phenomenon could be also transferred to pot cultures, where plants inoculated with acclimatized strains formed higher biomass, if soils were contaminated with Pb or too high amounts of Zn. How this process of acclimatization, accompanied with gene expression analyses, could be transferred to a commercial directed inoculum production process with quality control adapted to particular customer needs will be discussed.



## PS 2-6 Exudation of organic acids and transcriptome analyses of change in gene expression in *Piloderma fallax* in response to organic and inorganic nitrogen

Bent, E.<sup>1</sup>, M. Elfstrand<sup>1</sup>, J. Söderberg<sup>1</sup>, S. Norström<sup>2</sup>, D. Bylund<sup>2</sup> and P. FRANSSON<sup>1</sup>

<sup>1</sup>Uppsala BioCenter, Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden, petra.fransson@slu.se; <sup>2</sup>Mid Sweden University, Faculty of Science, Technology and Media, Department of Natural Sciences, Sundsvall, Sweden.

**Abstract:** Ectomycorrhizal (EM) fungi produce low molecular weight (LMW) organic compounds, which support soil microbial communities and nutrient mobilisation and uptake. This exudation is important for soil carbon and nutrient cycling. Increasing anthropogenic inputs of inorganic nitrogen (N) may alter EM fungal exudation patterns and impact terrestrial ecosystems. We aimed to determine how exudation of LMW organic acids and gene expression is affected by N source and level to better understand the functional response of EM fungi to changes in N availability. We used *Piloderma fallax*, a commonly occurring species in boreal forests, as our model species. Colonised *Pinus sylvestris* L. seedlings were grown under axenic conditions in a glass bead Petri dish systems containing a sterile liquid nutrient solution with either L-alanine (0.1 mM and 1 mM) or NH<sub>4</sub>Cl (0.1 mM and 5 mM). After five weeks pre-growth, the nutrient solution was replaced with fresh solutions and incubated for another seven days. We sampled exudates and harvested mycorrhizal root tips and extraradical mycelia separately from each system. Eleven pooled samples per treatment were collected, of which a total of 15 were subjected to global transcriptome profiling and chemical analysis of organic acids. For 15 out of 18 LMW organic acids analysed, there was a significant effect of N source on exudation. Generally, exudation was highest in the high alanine treatment and lowest in the high NH<sub>4</sub>Cl treatment. We performed RNAseq using the Illumina HiSeq platform. On average, the sequencing yielded 2 Gbp quality filtered reads per library, and the reads were mapped to the gene catalogue from the recently released genome of *P. croceum* F 1598. We found 1,214 predicted gene models that were differentially expressed between N treatments or between mycorrhizal root tips and extraradical mycelia in response to the N treatments. These results will be discussed in relation to exudation data.

## PS 3-62 Ontogenetic and histochemical study of the ectomycorrhiza formed by *Suillus brevipes* with *Pinus hartwegii*

GALINDO-FLORES, G.L.<sup>1</sup>, J. Álvarez-Sánchez<sup>2</sup>, J. Márquez Guzmán<sup>3</sup> and A.L. Anaya Lang<sup>4</sup>

<sup>1</sup>Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Centro de Investigaciones en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, México, gemagalindo@msn.com; <sup>2</sup>Departamento de Ecología y Recursos Naturales, Facultad de Ciencias, Universidad Nacional Autónoma de México; <sup>3</sup>Departamento de Biología Comparada, Facultad de Ciencias, Universidad Nacional Autónoma de México; <sup>4</sup>Instituto de Ecología, Universidad Nacional Autónoma de México.

**Abstract:** In Mexico, there are many studies about the ectomycorrhizal interaction, which include physiological and molecular issues, inoculation, and the effect on host plant growth. However, there are few studies about the ontogeny of native ectomycorrhizal fungi based on structure and histochemical characteristics. The aim of this study was to investigate the ontogenetic and histochemical characteristics of ectomycorrhiza formed by *Suillus brevipes* (Peck) Kuntze and *Pinus hartwegii* Lindl. *In vitro* synthesis was induced and after 6 and 12 months the root system was extracted. Mycorrhizal tips were classified into four development stages and these were fixed in FAA and glutaraldehyde. Subsequently, tips were embedded in paraffin and LR white resin, and sections of 8 and 1.5 µm were obtained. We used light microscopy, interferential contrast of Normaski, scanning electron microscopy, and transmission microscopy. The histochemical characterization was carried out with vanillin for determining phenolic compounds and phloroglucinol for lignin. The non-mycorrhizal tips were reddish-brown with simple branching and abundant meristematic cells. The mycorrhizal tips were yellowish-brown with bifurcated to dichotomous branches and, finally, formed a coralloid mycorrhiza with the apices rounded. The mantle surface was smooth with plectenchymatous type F and occasionally type B, according to the Agerer's classification. Emanating hyphae and embedded crystals were observed. The Hartig network had two to three epidermal cell layers of type A. The cortical cells of the mycorrhizal tips that were found in contact with the inner mantle presented a dark brown color due to tannin production. Histochemical results indicate that the early stages of ectomycorrhiza formation contain a higher amount of lignin, which decreased with the colonization stage. Phenolic compounds increased in the later stages of the ectomycorrhiza formation.

### PS 3-1 Mycorrhizal-dependent potassium nutrition of *Medicago truncatula*

GARCIA, K.<sup>1</sup> and J.M. Ané<sup>1</sup>

<sup>1</sup>Department of Agronomy, University of Wisconsin-Madison, Madison, WI 53706, USA, kgarcia5@wisc.edu.

**Abstract:** Potassium (K) is the most abundant element in soil, but its very low availability limits plant growth and the productivity of ecosystems. This cation participates in various crucial processes such as plasma membrane polarization, growth, stomatal aperture, and adaptation to environmental changes. Thus, understanding mechanisms involved in K nutrition is an important topic in plant science. In various model plants, many genes involved in K acquisition were identified such as the high-affinity K transporter 5 (*HAK5*) of *Arabidopsis thaliana* which is upregulated by K deprivation. Mycorrhizal associations occur between the root system of around 80% of land plants, and the mycelium of various fungi improve hydro-mineral nutrition of the majority of terrestrial plants. Recent data assumed that mycorrhizal fungi have a positive effect on plant K uptake mainly at low K and under stressful conditions, which is the rule in natural ecosystems. However, very little is known about the molecular mechanisms governing this fungal K allocation. Using the model arbuscular mycorrhizal (AM) association between *Medicago truncatula* and *Rhizophagus irregularis*, we showed a higher K content in AM plants than non-mycorrhizal ones under K-limiting conditions. Moreover, we found that one orthologous gene of *HAK5* in *Medicago* (*MtHAK5.4*) is upregulated only in non-mycorrhizal plants at low K, supporting the presence of an AM pathway for K acquisition. In addition, non-mycorrhizal plants display a reduction of biomass and iron content and an increase in sodium concentration compared to AM plants. All these results indicate better adaptation of mycorrhizal *Medicago* to K deprivation and confirm a buffering role of *R. irregularis* to prevent sodium toxicity. Finally, we performed RNAseq analysis on AM and non-colonized *Medicago* roots growing at high or low K in order to identify the molecular basis of AM-dependent plant K nutrition.

### PS 2-50 Arbuscular mycorrhizal fungi communities, functional diversity, and the resilience of ecosystem functions in a dynamic tropical dry forest ecosystem

GAVITO, M.E.<sup>1</sup> and S.M. Carrillo-Saucedo<sup>1</sup>

<sup>1</sup>Instituto de Investigaciones en Ecosistemas y Sustentabilidad. Universidad Nacional Autónoma de México-campus Morelia, 58090, Morelia, Michoacán, México, mcarrillo@cieco.unam.mx.

**Abstract:** Tropical dry forests are under continuous transformation and land cover change. The high environmental heterogeneity resulting from this ongoing process likely shapes arbuscular mycorrhizal fungi (AMF) community composition according to the conditions of each environment. However, in order to prevail, ecosystem functions need to be maintained and be performed by the resulting AMF communities. The prevalence of ecosystem functions like nutrient cycling and water and organic matter storage, the basis for the provision of critical ecosystem services, relies on the existence of substantial functional redundancy within the organisms that perform those functions. Such redundancy, among other factors, confers resilience. The sensitiveness of ecosystem functions to disturbance and the speed of the recovery after disturbance are two indicators of functional resilience and thereby of the maintenance of ecosystem functions and the derived services. We hypothesized that, despite the changes in AMF composition originated by land cover change, 1) functional redundancy would be high in the AMF communities but would not completely overlap, and 2) functional diversity would originate differential sensitiveness of ecosystem functions to disturbance but, when affected, rapid recovery from it. Support to these hypotheses would thus suggest resilience. We described the composition of AMF communities in field sites with different land cover and measured mycelium traits related to nutrient cycling and water and organic matter storage (hyphal length, hyphal allocation to diameter categories, soil aggregation capacity, and enzymatic activities). Data from experiments and from field measurements were combined to test our hypotheses. We then explored the relation between community composition, mycelium traits, and ecosystem functions. We found high functional redundancy and remarkably high resilience of the ecosystem functions evaluated and performed, or mediated, by AMF communities within this ecosystem.

GAZIS, R.<sup>1</sup> and D.S. Hibbett<sup>1</sup>

<sup>1</sup>Clark University, Biology Department, 950 Main Street, Worcester, Massachusetts 01610, USA, rgazis@clarku.edu.

**Abstract:** Constructing a phylogenetic tree with all fungal species represents a Holy Grail of mycology. To this end, fungal systematists have gathered and analyzed morphological and molecular data for hundreds of thousands of species yielding phylogenetic trees that have been reported in thousands of publications. However, these research products have never been combined into an accessible, comprehensive fungal tree of life, and complete phylogenies for large clades are rare. Challenges to constructing comprehensive phylogenies include computational requirements and low overlap in the molecular markers used among phylogenetic studies. In the absence of phylogenetic knowledge, taxonomic information can provide a species hierarchy that can be combined with trees based on molecular analyses. By using taxonomy as a backbone, and resolving shallower relationships among taxa with phylogenies, we can detect areas in the tree where taxonomic revisions are needed. As part of the Open Tree of Life project (<http://blog.opentreeoflife.org/>), we are working toward a draft of the most comprehensive fungal tree to date by combining phylogenetic and taxonomic sources. While this tree is far from complete, it is an important first step to a comprehensive fungal tree of life that can be updated and will provide a foundation for comparative mycology.

PS 3-13 **Influence of drought and different nitrogen:phosphorus ratios on the distribution of recently assimilated carbohydrates from <sup>13</sup>CO<sub>2</sub> to mycorrhizae of *Populus maximowiczii* x *P. nigra***

GEPPERT, U.<sup>1</sup>, B. Winkler<sup>2</sup> and K. Pritsch<sup>1</sup>

<sup>1</sup>Helmholtz Zentrum München, Institute of Biochemical Plant Pathology, Environmental Mycology and Allergies, Ingolstädter Landstraße 1, D - 85764 Neuherberg, uwe.geppert@helmholtz-muenchen.de; <sup>2</sup>Helmholtz Zentrum München, Research Unit Environmental Simulation, Ingolstädter Landstraße 1, D - 85764 Neuherberg.

**Abstract:** Ectomycorrhizae (ECM) are considered to play a significant role in resistance and resilience mechanisms of trees during and after drought. Concomitantly, the nutritional status of the plant influences their fitness. So far, most experiments on nutrient stoichiometry have been conducted with arbuscular mycorrhizal fungi. In a greenhouse experiment, poplars were grown under low and high N and P fertilization regimes (↑N and ↓P, ↓N and ↑P, both↑, and both↓) and subject to drought followed by rewatering and continuous irrigation (control), respectively. Our main focus was on the recovery phase following the drought period. We studied carbon allocation to poplar ECM using <sup>13</sup>C and the dynamics of extracellular enzyme activities involved in carbon and nutrient release. According to the stress gradient hypothesis, we assumed that the benefit of ECM for trees would be highest under low nutrient availability (N, P) in soil. A reduction of carbon supply to the ECM was hypothesized to increase degrading enzyme activities more under high nutrient conditions due to altered C:N:P stoichiometry. During the drought period, photosynthesis was reduced due to stomatal closure compared to controls. After rewatering, photosynthesis of drought treated plants was higher than of continuously irrigated control plants. Accordingly, ECM received considerably more photosynthate in the recovery phase after rewatering than the ECM of the continuously irrigated control plants in the same time period. In agreement with our hypothesis, carbon allocation to ECM was highest where neither N nor P was added and lowest where both nutrients were added. Exoenzyme activities were highest in N-fertilized treatments and did not differ significantly due to drought. This indicates promotion of mycorrhizal growth and mobilization of C, N, and P when enough available N (e.g., from decaying microorganisms) is present during recovery after drought.

**PS 4-66 A combined morphological, biochemical and molecular approach for diversity analysis of arbuscular mycorrhiza fungal obtained from sub Himalayan regions of Mukteshwar, India**

**GHORUI, M.<sup>1</sup>, K. Sunar<sup>1</sup>, B. Sashidhar<sup>1</sup> and A. Adholeya<sup>1</sup>**

<sup>1</sup>Centre for Mycorrhiza Research, Biotechnology and Management of Bioresources Division, The Energy and Resources Institute (TERI), New Delhi, India, maunata.ghouri@teriuniversity.ac.in.

**Abstract:** Representative rhizosphere soil samples including the root bits were collected from sub Himalayan regions of Mukteshwar, India and were assessed for arbuscular mycorrhizal fungi (AMF) spore density and species diversity. AMF trap cultures were raised with *Sorghum sudanense* and *Zea mays* in greenhouse and monosporels were established from spores isolated from these traps. A total of 216 monosporel cultures were obtained which were further characterized. Light and scanning electron microscopy based morphotaxonomic analysis, fatty acid methyl ester (FAME) profile based biochemical profiling and nuclear encoded ITS-LSU based molecular identification of each single AMF isolate obtained from this region was carried out. Morphological analysis of AMF spores revealed a significant diversity when analyzed in terms of spore shape, size colour, subtending hyphal attachments, wall layers and spore wall ornamentations. FAME profiles of successful monosporels showed presence of marker fatty acid for fungal species i.e., C16:1. Over all, a total of 25-30 types of fatty acids were detected. Unweighted numerical analysis of the FAME profiles revealed relatively tight clusters at intraspecific, specific, and generic levels, which suggested that it could be used as a measure of fungal diversity that might have taxonomic and diagnostic applications. For molecular identification, rDNA locus consisting of entire ITS and partial long subunit (LSU) sequences were amplified to obtain the DNA sequence by nested PCR and was cloned using pGEM-T vector. These sequences were successfully tested by BLAST query and multiple sequence alignments followed by phylogenetic analysis for species identification and characterization. A vast AMF diversity was enumerated representing the families Glomeaceae, Acaulosporaceae, Diversisporaceae, Claroideoglomeraceae, and Gigasporaceae. One isolate of *Acaulospora* sp. (UTMU 128 BM24/11) and *Claroideoglossum* sp. (UTMU 128 BM9/11) were found to possess unique morphological and molecular characters and can possibly be designated new species categories.

**PS 4-11 Ectomycorrhizal fungal spore bank recovery after a severe forest fire: some like it hot**

**GLASSMAN, S.I.<sup>1</sup> and T.D. Bruns<sup>1</sup>**

<sup>1</sup>Department of Environmental Science Policy Management, University of California, Berkeley, CA 94720 USA, sglassman@berkeley.edu.

**Abstract:** Fires in western North America have transitioned from frequent, low intensity events to infrequent stand-replacing events. After severe wildfires, pine recovery depends on ectomycorrhizal (ECM) fungal spores surviving and serving as partners for regenerating forest trees. We took advantage of a large, severe natural forest fire that burned our long-term study plots to test the response of ECM fungi to fire. We sampled the ECM spore bank using pine seedling bioassays and high throughput sequencing before and after the California Rim Fire, which killed most or every tree in both plots. We found that ECM spore bank fungi survived the fire and dominated the colonization of in situ and bioassay seedlings, but there were specific fire fungi such as *Rhizopogon olivaceotinctus* that increased in abundance after the fire. The frequency of ECM fungal species colonizing pre-fire bioassay seedlings, post-fire bioassay seedlings, and in situ seedlings were strongly positively correlated. While the most abundant taxa remained the same, fire reduced the ECM spore bank richness and density: fewer species were detected in the spore bank after the fire and fewer of the samples had colonized seedlings. Our results show that although there is a reduction in ECM inoculum, the ECM spore bank community largely remains intact, even after a severe “mega-fire.” Furthermore, simple greenhouse bioassays can be used to determine which fungi will colonize after fires. Similar to plant seed banks, a specific suite of ruderal, spore bank fungi take advantage of open niche space after fires.

## PS 2-24 Mycorrhizal fungal communities associated with *Arbutus unedo* and the potential for the formation of common mycelial networks with *Pinus pinaster*

Dinis, D.<sup>1</sup>, N. Mesquita<sup>1</sup>, J. Martins<sup>1</sup>, J.M. Canhoto<sup>1</sup>, **M.T. GONÇALVES<sup>1</sup>** and S.C. Gonçalves<sup>1</sup>

<sup>1</sup>Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, 3000-456 Coimbra, Portugal, mtgoncal@ci.uc.pt.

**Abstract:** In Portugal, *Arbutus unedo* is a common understory shrub in *Pinus pinaster* dominated forests and plays an important role in ecosystem recovery after disturbance. This positive effect has been related to mycorrhizal fungi, but there are few molecular-based studies of the mycorrhizal fungal communities associated with *A. unedo* and the potential for the formation of common mycelial networks with *P. pinaster*. We examined the mycorrhizal fungal communities associated with *A. unedo* shrubs during two consecutive growing seasons in a field site that has been clear-cut following pine nematode infection *ca.* 7 years ago and that shows natural pine regeneration. Because spores and other resistant fungal propagules play an important role after a severe disturbance, we conducted a greenhouse experiment to examine the mycorrhizal colonization of *A. unedo* seedlings in bioassays. Also, *A. unedo* seedlings were planted in the field to compare mycorrhizal communities between shrubs and seedlings. Finally, we addressed the question of whether mycorrhizal fungi can mediate pine regeneration through the identification of fungal species shared between *A. unedo* shrubs and *P. pinaster* saplings growing at the site. From the various experiments, we collected representative samples of mycorrhizal roots from each plant and used ITS sequencing to identify the fungi. After the first season of sampling, we identified 10 fungal taxa, dominated by the genus *Tomentella*, in association with *A. unedo*. Results are discussed in relation to the role of *A. unedo* in maintaining mycorrhizal fungal inoculum to support the later establishment of *P. pinaster* seedlings.

## LT 4-3 Potential distribution and identity of introduced *Amanita muscaria* worldwide

**GONÇALVES, S.C.<sup>1</sup>**, N. Mesquita<sup>1</sup>, L. Bittleston<sup>2</sup>, N. Vargas<sup>3</sup>, I.A. Dickie<sup>4</sup>, J. Geml<sup>5</sup> and A. Pringle<sup>2</sup>

<sup>1</sup>Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, 3000-456 Coimbra, Portugal, scgoncal@uc.pt; <sup>2</sup>Departments of Botany and Bacteriology, University of Wisconsin, Madison, USA; <sup>3</sup>Laboratory of Mycology and Plant Pathology, University of Los Andes, Bogotá, Colombia; <sup>4</sup>Bio-Protection Research Centre, Lincoln University, New Zealand; <sup>5</sup>Naturalis Biodiversity Center, 2333CC Leiden, The Netherlands.

**Abstract:** *Amanita muscaria sensu lato* is an eye-catching and easily noticed fungus, the red-and-white spotted mushroom of fairy tales. However, it comprises multiple clades that are considered different species according to the phylogenetic species concept. Members of this northern hemisphere species complex have been introduced to many locations in the southern hemisphere, and south of its native range in the northern hemisphere. The species seems confined to plantations in Tanzania, Zimbabwe, and South Africa but in Colombia it appears to be associating with native *Quercus humboldtii*, and in Australia and New Zealand, the species is considered invasive and associates with native *Fuscospora cliffortioides* (formerly *Nothofagus solandri* var. *cliffortioides*). Which phylogenetic species are introductions, and whether more than one phylogenetic species of the *A. muscaria* complex has been introduced to new ranges, is unclear. Nor do we know if multiple species co-occur in introduced ranges. In this study we hypothesized that the cryptic species of *A. muscaria* possess distinct environmental niches, and that environmental niche models of the different clades would predict which species are introduced to different parts of the world. We also used ITS sequencing of *A. muscaria* from across its introduced ranges to ascertain the identity of the occurring species. Species distribution modeling predicts that both clade I (North America) and clade II (Eurasia, Alaska) can grow in parts of the introduced ranges, in places including Chile, southern Brazil, Uruguay, New Zealand, and southern Australia. But sequence data from many populations demonstrates that across its introduced ranges *A. muscaria* is mainly (perhaps solely) represented by clade II, the originally described *A. muscaria* from Eurasia. Results are discussed in relation to the current knowledge of the ecology of each cryptic species, as well as in relation to historical information about co-introductions with exotic hosts.



### PS 1-36 Analysis of PCR-DGGE technique to design molecular markers for arbuscular mycorrhizal fungi species detection

GONZÁLEZ, D.<sup>1</sup>, D.M. Morales-Londoño<sup>1</sup>, R.D. Armas<sup>1</sup>, S. Stoffel<sup>2</sup>, C.R.F.S. Soares<sup>2</sup> and S.L. Stürmer<sup>3</sup>

<sup>1</sup>Universidade Federal de Santa Catarina, Program of Plant Genetic Resources, Florianópolis, SC, 88040-900, Brazil, dandresgr@hotmail.com; <sup>2</sup>Universidade Federal de Santa Catarina, Departamento de Microbiologia, Imunologia e Parasitologia, Florianópolis, SC, 88040-900, Brazil; <sup>3</sup>Universidade Regional de Blumenau, Departamento de Ciências Naturais, Cx.P. 1507, Blumenau, SC, 89012-900, Brazil.

**Abstract:** Classical identification of arbuscular mycorrhizal fungi (AMF) relies on the analysis of spore wall structure. This approach imposes difficulties during analysis of AMF field communities as characters might be absent from spores, and cryptic species may not be sporulating during sampling time. A molecular approach allows for the analysis of microbial community structure using the large subunit (LSU) of the rRNA gene associated with denaturing gradient gel electrophoresis (DGGE) because the 28S region is a highly conserved DNA region, but with enough variability to distinguish among AMF species, even those of *Glomus*. This study aimed to make a molecular marker to identify AMF species based on band arrangement obtained with the PCR-DGGE technique from amplified sequences of the LSU. Isolates obtained from the International Culture Collection of Glomeromycota (CICG) included *Rhizophagus clarus* RJN102A, *Acaulospora morrowiae* SCT400A, *A. colombiana* SCT115A, and *Gigaspora albida* SCT200A. Five spores of each isolate were used to extract DNA that was amplified with a nested-PCR technique. Primers LR1 and FLR2 were used for the first amplification. The PCR product was then amplified for a second time using the FLR3 and FLR4 primers. These primers are specific for AMF and amplify the LSU region. Amplicons were analyzed by the DGGE technique, and the band patterns obtained for each species were tested with Bionumerics 7.5 software. All isolates tested yielded evidence of more than one band, probably due to the polymorphism of the studied region or because of the presence of several nuclei in each spore, but the pattern of the bands was unique for each species. Our results provide evidence that the species tested herein can be separated from each other using the LSU as molecular marker associated with the DGGE technique, which can be useful during the analysis of AMF communities under field conditions.

### PS 3-32 Effect of organic soil amendments and continuous tomato monoculture on arbuscular mycorrhizal fungal communities

Smith, M.M.<sup>1</sup>, E.G. Johnson<sup>1</sup>, D.O. Chellemi<sup>2</sup> and J.H. GRAHAM<sup>1</sup>

<sup>1</sup>Department of Soil and Water Sciences, Citrus Research and Education Center, University of Florida, Lake Alfred, FL 33850 USA, jhgraham@ufl.edu; <sup>2</sup>USDA-ARS-USHRL, Fort Pierce, FL 34945 USA.

**Abstract:** As interest in crop management alternatives to conventional high input farming increases, understanding the impacts of organic soil amendments and crop rotations on microbial components of the agroecosystem is desirable, especially for arbuscular mycorrhizal (AM) fungi. Soil amendments are thought to be more conducive for the activity of AM fungi, depending on nutrient supply. The effects of broiler litter and urban plant debris on infectivity and community structure of AM fungi were evaluated in a tomato (*Solanum lycopersicum*) microplot study. Tomato plants were cultivated under conventional methods for two years, and then transitioned for three years with alternative organic soil amendment treatments and rotation with cover crops (sunn hemp [*Crotalaria juncea*] and Japanese millet [*Echinochloa crusgalli*]). Mycorrhizal inoculum potential (MIP) of rhizosphere soil was assayed using maize (*Zea mays*) to assess infectivity of AM fungi. Soil DNA was assayed using real-time quantitative PCR for the presence of three key rDNA phylotypes in an attempt to track changes in the AM fungal community over time at different stages of management transition. Despite high levels of soil disturbance, and excess supply of phosphorus and nitrogen to insure plant nutrient sufficiency, AM fungal colonization was not suppressed. A significant effect of tomato on the incidence of one of the phylotypes suggests a host mediated community shift, and evidence for differing AM fungal biological characteristics. High AM fungal infectivity and incidence supports previous findings of their resilience despite repeated disturbance and plant nutrient inputs. These conditions may favor AM fungi that colonize and/or sporulate rapidly, altering community structure and functioning in the transition to an organic agroecosystem.

## LT 1-11 Diversity and distribution of native truffle species (*Tuber* spp.) in Europe

GREBENC, T.<sup>1</sup>, G.M.N. Benucci<sup>2</sup>, M. Karadelev<sup>3</sup>, M.P. Martin<sup>4</sup> and H. Kraigher<sup>1</sup>

<sup>1</sup>Slovenian Forestry Institute, Večna pot 2, SI-1000 Ljubljana, Slovenia, tine.grebenc@gozdis.si; <sup>2</sup>Department of Plant, Soil and Microbial Sciences, Michigan State University, 1066 Bogue Street 48825 East Lansing, MI, USA; <sup>3</sup>Mycological Laboratory, Institute of Biology, Faculty of Natural Science and Mathematics, Ss. Cyril and Methodius University, Arhimedova 5, 1000 Skopje, The Republic of Macedonia; <sup>4</sup>Jardín Botánico, CSIC, Plaza de Murillo 2, 28014 Madrid, Spain.

**Abstract:** Truffles (genus *Tuber*) are a diverse group of ectomycorrhizal hypogeous fungi with mostly a temperate distribution. Knowledge about their diversity is mainly limited to commercial species, while many others remain understudied. Using ITS gene ribotypes, we attempted to correlate the intraspecific diversity observed in several *Tuber* species with their distribution, and discuss potential limits of different species concepts. The selection of European collections, with a stress on the Balkan Peninsula, revealed a high number of different ribotypes in the study area. For *T. excavatum*, *T. fulgens*, *T. brumale*, and *T. rufum*, considerable “intraspecific” variability was observed if the species concept followed the morphological concept. *Tuber melanosporum*, *T. magnatum*, and *T. macrosporum* are morphologically and molecularly stable and are well-defined species/ribotypes. For some of the variable morpho-species, the geographic distribution followed well the ribotype distribution while others, for example *T. rufum*, appear to be a complex of a high number of closely related ribotypes with no clear geographic distribution and follow the nomenclature of the species hypothesis concept. Based on the high number of truffle ribotypes found in Southeastern Europe (mainly the Dinaric Alps), this area appears to a hot spot of diversity, and in the northern part, there is also a convergence zone of two postglacial migration routes.

## CS 4-5 Forest restoration following exotic plant invasion: the role of ectomycorrhizal fungi at forest edges

GROVE, S.<sup>1</sup>, N.P. Saarman<sup>2</sup>, G.S. Gilbert<sup>3</sup>, K.A. Haubensak<sup>4</sup> and I.M. Parker<sup>1</sup>

<sup>1</sup>Ecology and Evolutionary Biology, University of California, Santa Cruz CA 95064 USA, sgrove@ucsc.edu; <sup>2</sup>Ecology, Evolution and Marine Biology, University of California, Santa Barbara CA ZIP USA; <sup>3</sup>Environmental Studies, University of California, Santa Cruz CA 95064 USA; <sup>4</sup>Biological Sciences and Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, AZ 86011 USA.

**Abstract:** Even after the removal of the invasive shrub *Cytisus scoparius*, standard reforestation efforts in previously invaded areas often fail. In previous greenhouse studies, we found that soils invaded by *Cytisus* harbor less ectomycorrhizal fungi, and growth of Douglas-fir seedlings is linked to the abundance of these fungi. We implemented a field experiment in five *Cytisus*-invaded clearcuts to assess two strategies to maximize ectomycorrhizal fungal colonization and improve Douglas-fir seedling success: planting near intact Douglas-fir forest edges, and inoculation with uninvaded forest soils. We planted Douglas-fir seedlings along paired transects: an ‘edge’ transect within five meters of the forest edge and an ‘interior’ transect 15-25 m into the *Cytisus*-invaded clearcut. Along each transect we planted seedlings into three liters of soil collected from either an adjacent Douglas-fir forest or from within the *Cytisus*-invaded clearcut. After two years, we used Illumina sequencing to identify the assemblages of ectomycorrhizal fungi on these seedlings. We compared ectomycorrhizal fungal communities and the relative abundances of ectomycorrhizal fungal species at the edge relative to the interior of *Cytisus*-invaded clearcuts, and we examined the resilience of local ectomycorrhizal fungi to transplantation into the invaded sites. ‘Edge’ Douglas-fir seedlings had more than 2.5 fold higher survival and 32% more ectomycorrhizal fungi than ‘interior’ seedlings. Our findings suggest that ectomycorrhizal fungal abundance is important to Douglas-fir survival. Transplanting forest soil into the invaded areas did not result in increased ectomycorrhizal fungal colonization or Douglas-fir success, suggesting inoculation of invaded areas is not sufficient to reintroduce ectomycorrhizal fungi. Surprisingly, there was no difference in ectomycorrhizal fungal species richness between the forest edge and interior of the invaded clearcut. Species diversity was, however, much greater at the edge. This work provides some insights into which ectomycorrhizal fungi are important for reforestation, and suggests that, where *Cytisus* invasion limits reforestation success, planting near existing forest edges may be a beneficial forestry strategy.

**GUERRA SIERRA, B.E.<sup>1</sup>**

<sup>1</sup>Faculty of Physical and Natural Sciences. Microbiology school-Agro environmental Biotechnology Research Laboratory, MICROBIOTA Group Street 70, number 55-210, University of Santander (UDES) Cacique's Lake, Santander, Bucaramanga, Colombia, bguerra@udes.edu.co.

**Abstract:** The most important production-limiting factor in acidic soils is soluble aluminum in the form of  $Al^{+3}$ . 85% of Colombia's soil is acidic with pH below 5.5, low fertility, and high concentrations of aluminum. In this assay, oil palm roots, with and without arbuscular mycorrhiza (AM), were exposed for 72h at 50, 100, or 200 ppm  $Al^{+3}$  in aerated liquid solutions at pH  $4.4 \pm 0.1$ . A seedling control that was not exposed to Al was also considered. The goal of this work was to determine the ability of mycorrhizal and non-mycorrhizal roots to capture Al. The distribution and Al uptake by root tissue were evidenced in roots embedded in low density agarose, sectioned in longitudinal cuts to 100  $\mu m$ , and the sections stained with DAPI (4',6-diamino-phenylindole) and lumogallion dye (3-[2,4 dihydroxyphenylazol]-2-hydroxy-5-chlorobenzenesulfonic acid]) to determine the uptake of Al bound to DNA in nuclei and in AM-infected root tissue and non-AM root tissue. A series of controls for autofluorescence were used, such as non-AM roots exposed to Al + lumogallion, AM roots exposed to Al but not stained with lumogallion, and other roots not exposed to Al and stained with lumogallion. The fluorescence intensity obtained in each root image under confocal microscopy were processed using MATLAB® software. Emitted fluorescence intensity by roots was measured by transforming the image to gray scale and using the histogram equalization. Using ANOVA to compare means ( $n=45$ ), significant differences ( $p<0.0001$ ) were found for the average fluorescence intensity of mycorrhizal and non-mycorrhizal root structures. The results show for the first time in the mycorrhizal roots of oil palm, that the fungal hyphae emit a higher fluorescence signal followed by the nuclei of the root tissue, and this can be interpreted as higher Al uptake in comparison with the structures of non-mycorrhizal oil palm roots. These findings may indicate the important contribution of mycorrhizal fungi in the cultivation of oil palm and their contribution in reducing aluminum toxicity in acidic soils.

PS 4-67 **A potential strategy of mangrove associates to reduce the stress of tide flooding, mediated by arbuscular mycorrhizal fungus and dark septate endophytes**

**GUO, J.<sup>1</sup>, X. Peng<sup>1</sup>, G. Xin<sup>1</sup> and W. Hu<sup>1</sup>**

<sup>1</sup>State Key Laboratory of Biocontrol, School of Life Sciences, Sun Yat-sen University, Guangzhou, China, lssxgr@mail.sysu.edu.cn.

**Abstract:** Mangrove forests are an important, but fragile ecosystems disturbed by the integrated stresses of flooding, salt, and tides. Previous studies have proved the common presence of arbuscular mycorrhizal fungi (AMF) and dark septate endophytes (DSE) in the roots of mangroves and their associates. However, it is unknown whether AMF and DSE reduce the stress that mangrove communities suffer from tidal flooding as they do on land. Given that mangrove associates have no or few structural adaptations to tides compared to true mangroves, which may result in increased stress due to tidal flooding, we predict higher colonization rates of AMF and DSE in the roots of mangrove associates. In the field investigation, plant communities were grouped into three categories: (1) true mangroves (TM), which grew at the high tide level, (2) mangrove associates (MA), which grew with TM and were swamped by high tide, and (3) other plants (OP), including some mangrove associates and terrestrial plants, which were not swamped by high tide. Both roots and soil samples were collected for determination of AMF and DSE colonization rates, AMF spore density, and soil chemical and physical properties. We found that AMF colonization rates of MA were significantly higher than the other two groups, while there was no difference between TM and OP. However, DSE colonization rates of MA were only significantly higher than TM, while the rates of OP were not significantly different from the other two groups. AMF spore density was similar among the three groups. Our work demonstrates that the higher colonization rates of both AMF and DSE in mangrove associates, which suffer from being swamped by high tide, is a potential strategy to reduce the integrated stresses of flooding, salt, and tides. Additionally, AMF in this strategy may play a more important role than DSE.

#### SY 4-6 Responses of AM fungal community to warming, nitrogen addition and increased precipitation in a semiarid steppe ecosystem

Kim, Y.C.<sup>1</sup>, C. Gao<sup>1</sup>, Y. Zheng<sup>1</sup> and L.D. GUO<sup>1</sup>

<sup>1</sup>State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China, guold@sun.im.ac.cn.

**Abstract:** Arbuscular mycorrhizal (AM) fungi form mutualistic symbioses with most plant species and play important roles in ecosystems. Knowledge of the response of AM fungi to environmental variation will improve our understanding of the function of AM fungal communities under global change scenarios in ecosystems. In this study, we examined AM fungal communities in asymmetrical warming, nitrogen (N) addition and increased precipitation treatments in a semiarid steppe in northern China. AM root colonization was significantly increased by day-time and 24-hour warming, but not by night-time warming and N addition. AM fungal spore density was significantly increased by day-time warming, 24-hour warming and increased precipitation, but not by night-time warming and N addition. AM fungal extraradical hyphal density had a positive response to increased precipitation, neutral response to all three regimes of warming, and a negative response to N addition. A high diversity of AM fungi was recovered by 454 pyrosequencing of SSU rDNA. AM fungal operational taxonomic unit (OTU) richness was significantly increased by all three regimes of warming, but not by N addition and increased precipitation. Some AM fungal OTUs occurred preferentially in different treatments. The AM fungal community composition was significantly affected by all three regimes of warming and N addition, but not by increased precipitation in the semiarid steppe. Our findings provide insights into the role of AM fungi under global change scenarios in the semiarid steppe ecosystem.

#### PS 4-36 Spatial distribution of AM fungi in the rhizospheres of *Ammopiptanthus mongolicus* associated plants in Inner Mongolia, northwest China

GUO, Q<sup>1</sup>, C. Hu<sup>1</sup>, X. Wang<sup>1</sup> and X. He<sup>1</sup>

<sup>1</sup>College of Life Sciences, Hebei University, Baoding 071002, P.R.China, qinghua6062@163.com.

**Abstract:** *Ammopiptanthus mongolicus* (Leguminosae) is a broad-leaved evergreen plant, which has significant effects in windbreak and sand fixation. Its community has a large preponderance in shrub layer, with the character of low species richness and diversity, while plants of Chenopodiaceae, Asteraceae and Leguminosae are associated with *A. mongolicus*. This study assesses the spatial distribution of AM fungi associated with *A. mongolicus* plants. Soil and root samples (0–50 cm depth) were collected in three sites, such as Dengkou, Wuhai, Alxa, and northwest China in June 2013. A total of 4 genera and 25 AM fungal species were isolated from the rhizosphere of four associated plants such as *Haloxylon ammodendron*, *Artemisia ordosica*, *Caragana korshinskii*, and *Amygdalus mongolica*. Of these, 14 species belong to *Glomus*, 7 to *Acaulospora*, 3 to *Funneliformis*, and 1 to *Scutellospora*. *Glomus reticulatum* was the dominant species, and AM fungal species distribution and symbiotic status had spatial heterogeneity. The greatest colonization and spore density found in 10-30 cm and in 10-20 cm soil layer, respectively. Hyphal colonization was positively correlated with soil organic C ( $P < 0.01$ ) and negatively correlated with EEG ( $P < 0.05$ ). Spore density was negatively correlated with soil organic C and alkaline phosphatase ( $P < 0.01$ ) and positively correlated with soil available N ( $P < 0.01$ ). Principal component analysis showed that soil available P, acid phosphatase, alkaline phosphatase and TEG can reflect the nutritional status of desert soil. From the comparing with previous testing result, the total colonization and spore density of *A. mongolicus* are higher than that of its associated plants, which demonstrates that AM symbiont facilitates the *A. mongolicus*' adapting to the absolute rigid desert environment. Basing on symbiont relationship of plant and AM fungi, screening nice resistance kind and using mycorrhizal biotechnology have an important scientific significance and application value to improve the desert plant growth and vegetation recovery.

## PS 1-14 Do AM fungi show biogeographic patterns in India?

**GUPTA, M.M.**<sup>1</sup>, V.K. Singh<sup>1</sup>, R. Dev<sup>1</sup>, H. Verma<sup>1</sup>, O. Muyal<sup>1</sup>, P. Kumari<sup>1</sup>, Ankit<sup>1</sup>, A. Aggarwal<sup>1</sup>, M. Dandodiya<sup>1</sup>, V. Goyal<sup>1</sup>, M. Kumar<sup>1</sup>, A. Bisht<sup>1</sup> and P. Jindal<sup>1</sup>

<sup>1</sup>University of Delhi, Sri Aurobindo College, Malviya Nagar, Delhi 110017 India, mbansalsac@outlook.com.

**Abstract:** Three main questions are addressed in the present work: (1) How many species of arbuscular mycorrhizal fungi (AMF) exist in India, and which are common. (2) Do AMF show biogeographic patterns? (3) What controls fungal community composition, and how is diversity maintained? The study was conducted in two phases. Phase I generated a searchable biodiversity database ([www.amfungi.aurobindo.du.ac.in](http://www.amfungi.aurobindo.du.ac.in)) using MS access and visual basic applications. A consolidated regional checklist of 148 species of AMF belonging to 20 genera was developed, which can be searched by either species or state to retrieve information about latest consensus classification, type specimen description, apart from occurrence and abundance. Phase II estimated AMF diversity in terms of abundance, species richness and evenness in 99 samples from 11 different sites in Aravali forests of the Delhi ridge area. Spores were quantified and characterized after one trap culture cycle. Single spore cultures could only be raised for 5 species for which the identification based on morphological characters was confirmed with signature molecular sequences for these species. We found *Funneliformis mosseae* to be the most widely distributed species of Glomeromycota in India, being present in largest number of states which is in dissent with earlier reports of *Glomus fasciculatum* and *G. macrocarpum* as the most widely distributed. The genus *Glomus* is represented by highest number of species (i.e. 65) followed by *Acaulospora* and *Scutellospora*. Further the states falling in the Western Ghats region i.e. Karnataka, Goa and Maharashtra contain more than 68.9% of all AMF reported to be present in India. Spore abundance and distribution of AMF in Delhi region followed almost the same trend except the number of spores isolated (g/soil) was much less. We hope that our checklist serves as a quick reference for Glomeromycota in India.

## LT 4-16 Arbuscular mycorrhiza and *Fusarium oxysporum* f.sp. *lycopersici* interactions in intercropping systems

**HAGE-AHMED, K.**<sup>1</sup>, J. Kramer<sup>1</sup> and S. Steinkellner<sup>1</sup>

<sup>1</sup>Division of Plant Protection, Department of Crop Sciences, University of Natural Resources and Life Sciences Vienna, Konrad-Lorenz-Strasse 24, A-3430 Tulln, Austria, karin.hageahmed@boku.ac.at.

**Abstract:** Soilborne pathogens such as *Fusarium oxysporum* f.sp. *lycopersici* are difficult to control and, thus, cause serious yield losses in tomato production worldwide. The use of arbuscular mycorrhizal fungi (AMF) with their bioprotective aspects and their combination with plant species diversity shows great promise for the management of plant diseases in environmentally compatible agriculture. In the present study, AMF were tested against *Fusarium oxysporum* f. sp. *lycopersici* with tomato intercropped with either leek, cucumber, basil, fennel or tomato itself. The intercropping partner affected the arbuscular mycorrhizal (AM) root colonization of tomato. Tomato intercropped with leek showed a 20% higher AM colonisation rate than tomato intercropped with tomato. Positive effects of AMF expressed as an increase of tomato biomass compared to the untreated control treatment could be observed in root as well as in shoot weights. The intercropping partners leek, cucumber, basil and tomato had no effect on *F. oxysporum* f. sp. *lycopersici* disease incidence or disease severity. Nonetheless, bioprotective effects of AMF resulting in the decrease of *F. oxysporum* f. sp. *lycopersici* disease severity were evident in treatments with AMF and *F. oxysporum* f. sp. *lycopersici* co-inoculation in the tomato/leek and tomato/basil combination. In conclusion, the effects of the intercropping partner on AMF colonisation of tomato are of great interest for crop plant communities and for the influences on each other. The outcome of the bioprotective effects of AMF resulting in the decrease on *F. oxysporum* f.sp. *lycopersici* disease severity and/or compensation of plant biomass does not depend on the degree of AM colonization but more on the intercropping partner.



## CS 7-4 Production and turnover of extramatrical mycelium in a nemo-boreal Scots pine chronosequence

HAGENBO, A.<sup>1</sup>, A. Ekblad<sup>3</sup>, J. Kyiashchenko<sup>2</sup>, K. Clemmensen<sup>1</sup>, B.D. Lindahl<sup>2</sup>, R.D. Finlay<sup>1</sup> and P. Fransson<sup>1</sup>

<sup>1</sup>Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden, andreas.hagenbo@slu.se; <sup>2</sup>Department of Soil and Environment, Swedish University of Agricultural Sciences, Uppsala, Sweden;

<sup>3</sup>School of Science and Technology, Örebro University, Örebro, Sweden.

**Abstract:** In boreal forest ecosystems, belowground allocation of photosynthetically fixed carbon to roots and mycorrhizal fungi may contribute considerably to the soil carbon pool via the production of mycorrhizal extramatrical mycelium (EMM). Typically, this production exceeds several hundreds of kg ha<sup>-1</sup> per growing season, and may result in a large carbon pool compromised of fungal biomass. However, the size of this biomass pool is not regulated by EMM production alone. Turnover of EMM is an equally important component, which directly affects carbon cycling within the EMM biomass and influx of carbon to the soil organic matter pool. The close association of EMM production and turnover with belowground carbon fluxes calls for incorporating EMM dynamics into models of ecosystem carbon cycling. However, in order to do so we need accurate estimates of both EMM production and turnover. These are both poorly understood processes, and this lack of knowledge currently represents a critical bottleneck restricting the development of forest carbon flux modeling. In the present study we separately quantified EMM production and turnover by combining modeling with measurements of the temporal EMM biomass dynamics in a nemo-boreal Scots pine chronosequence. Our results suggest that approximately 1-3 kg of EMM is produced per hectare per day, and that turnover of EMM is strongly negatively correlated with forest age, highlighting EMM turnover as a highly important factor regulating EMM biomass in forest soils. Results of this study could be used to increase the predictive power of forest carbon flux models.

## CS 7-5 Mycorrhizas: pipeline or director of belowground C fluxes?

HAMMER, E.C.<sup>1</sup>, M.C. Rillig<sup>2,3</sup> and I. Jakobsen<sup>4</sup>

<sup>1</sup>Institute of Biology, Microbial Ecology, Lund University, Sölvegatan 37, 22362 Lund, Sweden, edith.hammer@biol.lu.se; <sup>2</sup>Institute of Biology, Plant Ecology of Freie Universität Berlin, Altensteinstr. 6, 14195 Berlin, Germany; <sup>3</sup>Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB), D-14195 Berlin, Germany; <sup>4</sup>Department Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark.

**Abstract:** Roots direct resources to nutrient patches and both their biomass and exudates add carbon compounds to the soil spaces they are exploring. What role do their root symbionts, mycorrhizal fungi, play? Do arbuscular mycorrhizal (AM) fungi constitute a nutrient patch for the plant on a root cellular level? Can AM fungi be viewed as the extended phenotype of the root, or do they give additional attributes to the carbon distribution in soil? We found that AM fungi, or roots via AM fungi, directed 5-fold more <sup>13</sup>C to OM patches compared to plain soil in a field experiment. While in a pot experiment, AM fungal colonization did not alter the total amount of <sup>14</sup>C allocated belowground by *Brachypodium distachyum*, but there was a strong preferential allocation of C to the part of split-root systems colonized by AM fungi, which received double the amount of C than the uncolonized side of the root system. This preferential carbon allocation to mycorrhizal roots stopped abruptly when P limitation of the plant was lifted demonstrating the differential, targeted belowground allocation of C during nutrient foraging by the plant. While these results point to a plant-directed C flux to nutrient patches via AM fungi on a centimeter scale, we also found evidence that, on a micrometer scale, there may be processes in C allocation which are special to AM fungi. We found that the <sup>13</sup>C coming from a donor plant to an AM fungus was substantially allocated to the intraradical mycelium in a neighboring, C-starved root. This could be interpreted as using a C-starved root as a safe storage space. We also found that hyphae colonize remote pore spaces of black carbon particles, which are inaccessible for plant roots. Such carbon compounds may become 'protected' against decomposers, and may be more recalcitrant simply due to its location in soil space.

HARROWER, E.<sup>1</sup>, N.L. Bougher<sup>2</sup>, T.W. Henkel<sup>3</sup>, E. Horak<sup>4</sup> and P.B. Matheny<sup>1</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, 569 Dabney Hall, University of Tennessee, Knoxville, TN 37996, USA, eharrowe@vols.utk.edu; <sup>2</sup>Department of Parks and Wildlife, Science and Conservation Division, Western Australian Herbarium, Bentley Delivery Centre, Kensington, WA 6151, Australia; <sup>3</sup>Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA; <sup>4</sup>Schlossfeld 17, A-6020 Innsbruck, Austria.

**Abstract:** We present a multi-gene phylogeny (partial nuc rDNA and *RPB2*) of *Cortinarius* sect. *Cortinarius* (i.e., the *C. violaceus* group) which reveals eight species distributed in Europe, Australasia, South America, Central America, and North America. Relaxed molecular clock analyses suggested that diversification began during the Miocene, thus rejecting more ancient Gondwanan origin scenarios among the taxa currently occurring in the Northern and Southern Hemispheres. There was strong support for an Australasian origin of the *C. violaceus* group with initial dispersal to the Neotropics, followed by migration into North America and Europe. A dispersal-extinction cladogenesis model that includes a parameter for founder effects was the most highly supported biogeographic model in the program BioGeoBEARS. A maximum likelihood analysis showed the most recent common ancestor of sect. *Cortinarius* was an angiosperm ectomycorrhizal associate. Ancestral associations at the plant family level, however, were ambiguous. Of eight recovered species-level lineages, *C. violaceus* is the only one that associates with Pinaceae and the only species to associate with both Pinaceae and angiosperms. This analysis showed that long-distance dispersal and founder event speciation have been important factors during evolution of the *C. violaceus* group.

PS 2-25 Fire in the future, lessons from the past: perspectives from forest fire reduction treatment impacts on ectomycorrhiza diversity

HART, B.T.<sup>1</sup>, J.E. Smith<sup>2</sup> and D.L. Luoma<sup>1</sup>

<sup>1</sup>Department of Forest Ecosystems and Society, College of Forestry, Oregon State University, Corvallis, OR 97330 USA, ben.hart@oregonstate.edu; <sup>2</sup>Pacific Northwest Research Station, USDA Forest Service, Corvallis, Oregon 97330 USA.

**Abstract:** Severe wildfires are an increasing risk as the western United States becomes hotter and dryer for longer periods annually due to the changing climate. Reduction of historically uncharacteristic woody fuels that drive large, severe forest fires is an increasing priority for forest managers. Traditionally, fuel reduction has been achieved with mechanized thinning of over-crowded trees and low-intensity prescribed fire to reduce woody fuels near the forest floor. However, the long-term impact of these fuel reduction treatments is poorly understood with respect to ectomycorrhizal fungi (EMF). We quantified EMF biodiversity associated with ponderosa pine (*Pinus ponderosa*) in four randomly assigned, replicated restoration treatments (thinned, burned, thinned and burned, and untreated) applied over a decade ago. Molecular methods were employed to assign operational taxonomic units. Preliminary results indicate that species richness was similar across treatment types and among sample units, and that fire effects on community composition was smaller than anticipated. Furthermore, EMF commonly associated with fire treatments (*Piloderma*, *Wilcoxina*, and *Lactarius deliciosus*) were under-represented in terms of their frequency in sample units that were burned. *Wilcoxina* is commonly associated with fire treatments while *Piloderma* and *L. deliciosus* are more characteristic of mature forests. Our results provide evidence that a 10+ year interval allows EMF to disseminate and re-colonize areas from which they may have been removed or reduced by disturbance treatments. Our findings will also be related to results from a 2-year post-disturbance study in the same study area. Knowledge of the long-term impacts of forest restoration treatments on EMF will aid in understanding the outcomes of management designed to produce stands with large-tree retention and low fuel loads.

HART, M.<sup>1</sup>

<sup>1</sup>University of British Columbia Okanagan, Miranda.hart@ubc.ca.

**Abstract:** Understanding the factors shaping arbuscular mycorrhizal (AM) fungal communities is important for understanding terrestrial systems in general. Whether these fungal communities are driven by fungal vs. host plant constraints (Driver/Passenger Hypothesis) or environmental factors (Habitat Hypothesis) has not been resolved. One reason for this is that most studies are based on disturbed landscapes and short-lived hosts. Given that AM fungi exist in all ecosystems with a variety of plants, we may be underestimating their diversity and functioning. In particular, AM fungal communities in old ecosystems may represent late seral AM fungal communities. If so, understanding AM fungal community dynamics across successional stages may help us understand the relative importance of fungal/plant /environmental controls on AM fungal communities. I examined AM fungal communities associated with 'old growth' sites across a variety of ecosystems ranging from grasslands to ancient forests. Across systems, I found that old ecosystems had significantly different AM fungal communities from comparable younger systems. Within systems, there was evidence that AM fungal communities shift from younger to older host plants. In addition, variation among communities was explained by different factors across seral stages. I found no evidence to support prevailing theories of phylogenetically conserved life history strategies in AM fungi. These results force us to reconsider what we mean by 'life history strategies' in the Glomeromycota, and whether this concept is meaningful when applied to AM fungi. Understanding natural AM fungal community assembly is essential if we are to preserve the immeasurable services they provide. Because old ecosystems and large trees are threatened globally, we must quickly work to identify and understand the role of these 'old growth' microbial communities, before they are gone.

PS 3-63 **Root endophytes in *Miscanthus sinensis* promote the Al-tolerance mechanism via increasing Fe absorption and producing siderophores**

HARUMA, T.<sup>1</sup>, K. Yamaji<sup>1</sup> and H. Masuya<sup>2</sup>

<sup>1</sup>Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-0005 Japan, s1530278@u.tsukuba.ac.jp; <sup>2</sup>Tohoku Research Center, Forestry and Forest Products Research Institute, Morioka, Iwate 020-0123 Japan.

**Abstract:** Under acidic soil conditions, *Miscanthus sinensis* is known as an aluminium (Al) tolerant plant which accumulates and detoxifies high concentrations of Al in the roots via producing citric and malic acids. Root endophytes are known to promote plant growth and nutrient absorption into plant tissue and to produce siderophores, including organic and phenolic acids which detoxify Al by chelating. The objective of this study was to clarify the mechanism of Al tolerance in *M. sinensis*, considering the interaction with root endophytes. We collected *M. sinensis* growing in an old mine site with high acidity and containing high concentrations of Al and heavy metals. Root endophytes were isolated from *M. sinensis* and their siderophore productions were evaluated via chrome azurol S assay. We isolated well-known root endophytic fungi such as *Phialocephala fortinii*, and *Chaetomium cupreum* was a common isolate. In addition, *C. cupreum* showed high siderophore production. In the inoculation test of *C. cupreum*, we examined the growth, Al absorption, and nutrient absorption of *M. sinensis* seedlings growing in sterile study site soil, with or without root endophytes, and detected Al-detoxicants in the roots by HPLC-DAD and GC-MS. *Chaetomium cupreum* increased root growth and Fe concentration and even seemed to increase Al concentration in the roots compared with the control treatment. However, endophytes did not induce plant-derived Al-detoxicants, chlorogenic acid, malic acid, or citric acid in the roots. Our results indicate that *C. cupreum* might alleviate Al toxicity via increasing Fe, which is a constituent element in superoxide dismutase, to cancel superoxides and via producing siderophores to detoxify Al. It was reported that some microbes could detoxify harmful elements via a sequestration mechanism. Although a species of *Chaetomium* is known to be a root endophyte and an opportunistic colonizer of plant roots, *C. cupreum* would produce siderophores to detoxify Al and might accumulate Al in the hyphae.

### SY 3-3 Greater carbon allocation to mycorrhizal fungi reduces tree nitrogen uptake in a boreal forest

HASSELQUIST, N.J.<sup>1</sup>, D.B. Metcalfe<sup>1,2</sup>, E. Inselsbacher<sup>1,3</sup>, Z. Stangl<sup>4</sup>, R. Oren<sup>1,5</sup>, T. Näsholm<sup>1,4</sup> and P. Höglberg<sup>1</sup>

<sup>1</sup>Department of Forest Ecology and Management, Swedish University of Agricultural Sciences (SLU), Umeå 90183 Sweden, nils.hasselquist@slu.se; <sup>2</sup>Department of Physical Geography and Ecosystem Science, Lund University, Lund 22362, Sweden; <sup>3</sup>Department of Geography and Regional Research, University of Vienna, Vienna 1090 Austria; <sup>4</sup>Department of Forest Genetics and Plant Physiology, Umeå University, Umeå 90185 Sweden; <sup>5</sup>Division of Environmental Science and Policy, Nicholas School of the Environment, Duke University, Durham, North Carolina 27708 USA.

**Abstract:** The central role that ectomycorrhizal (EM) symbioses play in the structure and function of boreal forests pivots around the prevailing dogma that carbon (C) and nitrogen (N) are exchanged at rates favorable for plant growth. It is therefore commonly assumed that increasing C allocation to mycorrhizal fungi results in greater N transfer to host trees. However, this may not always be the case. It has been hypothesized that the benefits mycorrhizal fungi convey to host plants is strongly dependent on the availability of C and N to mycorrhizal fungi. Using large-scale shading and N addition treatments, we tested how changes in C and N supply alter the transfer of N in intact mycorrhizal associations with ~15 year old Scots pine trees. To assess the dynamics of N transfer in EM associations, we added trace amounts of highly enriched <sup>15</sup>NO<sub>3</sub><sup>-</sup> label to the EM-dominated mor-layer and followed the fate of the <sup>15</sup>N label in plant foliage and fungal chitin isolated from EM root tips. Shading resulted in reduced tree C uptake and allocation to EM fungi but greater N transfer to tree foliage than in the unshaded control, where more <sup>15</sup>N label was found in fungal biomass on colonized roots. Despite no change in below-ground tree C allocation, short-term addition of N shifted the incorporation of <sup>15</sup>N from EM fungi to tree foliage. Contrary to the prevailing dogma, our results show that under N-limited conditions greater C allocation to EM fungi results in reduced, not increased, N transfer to host trees. Moreover, our results highlight the likely effects of changes in the availability of C and N in intact mycorrhizal associations in the field and stress the need to incorporate mycorrhizal dynamics into process-based ecosystem models to better predict forest C and N cycles in light of global climate change.

### PS 4-12 Native shrub management effects on soil arbuscular mycorrhizae: optimization and adaptation to simulated climate changes in Sahelian agroecosystems

HASSNA, F.M.<sup>1,2</sup>, D. Sidy<sup>1,2</sup>, B.N.N. Yacine<sup>1,2</sup>, D. Sally<sup>1,4</sup>, M. Dominique<sup>2</sup>, C.L. Lydie<sup>3</sup> and P.D. Richard<sup>5</sup>

<sup>1</sup>Institut Sénégalais de Recherches Agricoles, Laboratoire National de Recherches sur les Productions Végétales (ISRA-LNRPV), Dakar, Sénégal, fhassna@yahoo.fr; <sup>2</sup>LMI IESOL Intensification Ecologique des Sols cultivés en Afrique de l'Ouest, Dakar, Sénégal; <sup>3</sup>Institut de Recherche pour le Développement, IRD, UMR Eco&Sols, Place Viala Bat 212 Montpellier, France; <sup>4</sup>Université Cheikh Anta Diop, Dakar, Sénégal; <sup>5</sup>The Ohio State University, Columbus, Ohio, USA.

**Abstract:** In the Sahel, current projections by the International Panel for Climate Change, predict water scarcity and higher temperatures, affecting food production in Sub-Saharan Africa (SSA). Two indigenous shrub species (*Piliostigma reticulatum* and *Guiera senegalensis*) have the ability to lift water from wet sub to dry surface soil and likely will alter biological soil functioning to the benefit of associated food crops. The goals of this study were to understand: (1) how arbuscular mycorrhizal fungi (AMF) react to water and heat stresses in the presence or absence of shrubs? (2) if it is possible to improve crop productivity by inoculation of selected strains of AMF in stressful conditions. Our study was based on lab experiments in a climate chamber to generate climate scenarios that mimic climate change predictions. For that, soil samples were collected from an experimental field design where pearl millet (*Pennisetum glaucum*) was cultivated alone or with *P. reticulatum* stands. To assess the role of AMF in water deficit, a greenhouse experiment was conducted in a pot with 10 kg of soil collected and cultivated by pearl millet. Three different levels of irrigation were applied; (1) 80% WHC (as a control); (2) 40% WHC; (3) 20% WHC. The diversity of AMF was analyzed to determine the predominant groups in each treatment. For heat stress, the same experimental design was used at two temperature associated with water stress. These analyses are ongoing and will be presented. The predominant group of AMF will be inoculated with the millet to study their impact on crop productivity in the condition of heat and water stresses. The main expected outcome the development of fundamental information towards the development of optimized shrub-crop systems that will assist subsistence farmers to withstand climatic change.

## PS 4-13 Cheatgrass invasion alters the arbuscular mycorrhizal fungal community composition of sagebrush shrublands

HAYER, M.<sup>1,2</sup>, E. Schwartz<sup>1,2</sup>, C. Gehring<sup>1</sup>, L. Flores-Renteria<sup>1</sup>, A. Krohn<sup>1</sup> and P. Dijkstra<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA, mh45@nau.edu; <sup>2</sup>Center for Ecosystem Science and Society, Northern Arizona University, Flagstaff, Arizona 86011 USA.

**Abstract:** The success of introduced plant species is partly affected by interactions with local soil microbial communities. Suppression of arbuscular mycorrhizal fungi (AMF) or shifts in AMF community structure in the presence of invasive plant species can result in reductions in nutrient uptake and growth in native plants. However, these relationships have been rigorously explored in only a few study systems. We aimed to identify the AMF community associated with sagebrush (*Artemisia* spp.) and cheatgrass (*Bromus tectorum*) in sagebrush dominated (native) and cheatgrass dominated (invaded) areas. Cheatgrass is an introduced annual grass that is widespread in sagebrush steppe communities of the Intermountain West where it alters natural fire regimes and influences plant community composition and ecosystem function. We sampled roots from sagebrush and cheatgrass at native and invaded sites in Utah, Idaho, and Arizona. The AMF community associated with sagebrush roots differed from the community associated with cheatgrass roots; the sagebrush root community was more diverse than the cheatgrass root community, which was dominated by a single species of *Glomeraceae*, regardless of invasion history or location. The presence of cheatgrass also influenced the AMF community associated with sagebrush roots. In invaded soils, sagebrush root communities were less diverse than in the native soils. Co-occurrence network analysis showed that sagebrush in native soil formed significant associations with more fungal species than sagebrush in invaded habitats. Sagebrush co-occurred with AMF and also with fungal species from the Mucoromycotina that have been shown to form symbioses with plants, or synergistic relationships with AMF. In contrast, cheatgrass associated with fungal species thought to be pathogenic to AMF and with dark septate endophytes. Taken together, our results indicate that cheatgrass invasion significantly alters AMF communities and suggest that adding AMF and other plant symbionts common in intact sagebrush shrublands to invaded areas may aid restoration.

## PS 3-64 Phylogenetically driven partner choice in the ectomycorrhizal symbiosis

HAYWARD, J.<sup>1</sup> and N.A. Hynson<sup>1</sup>

<sup>1</sup>Department of Botany, University of Hawaii Manoa, Honolulu, HI 96822, haywardj@hawaii.edu.

**Abstract:** Consistent, nonrandom patterns of association between fungal species or genera and their plant hosts are a feature of many ectomycorrhizal systems. A small number of ectomycorrhizal plants and fungi have previously been reported to associate with a phylogenetically restricted set of partners. For example, suilloid fungi preferentially associate with host lineages within the family Pinaceae, while members of the *Pisoniae* (Nyctaginaceae) associate with a phylogenetically restricted group of thelephoroid symbionts. However, it remains unclear to what extent these patterns represent exceptions to a more general rule of phylogenetically unpatterned associations, or whether phylogenetic signal in the ectomycorrhizal symbiosis is widespread. We analyzed tens of thousands of publicly available ectomycorrhizal fungal DNA sequences and associated plant hosts and geographic metadata in a comparative phylogenetic context. We used newly developed methods to integrate across phylogenetic and taxonomic uncertainties and to correct for phylogeographic bias. We report that many ectomycorrhizal plant and fungal lineages exhibit phylogenetically nonrandom patterns of association, including many not previously known to exhibit nonrandom host associations, such as interactions between Ericaceae plant hosts and several ectomycorrhizal fungal genera and between thelephoroid fungi and most host plant species. We discuss these results in the context of mycorrhizal specificity and diffuse coevolution.



PS 1-16 **Genotypic diversity matters: examining the diversity-ecosystem function relationship with ectomycorrhizal fungi**

HAZARD, C.<sup>1,2</sup>, A.F.S. Taylor<sup>3</sup> and D. Johnson<sup>1</sup>

<sup>1</sup>Institute of Biological and Environmental Sciences, Cruickshank Building, University of Aberdeen, Aberdeen AB24 3UU, UK, Christina.Hazard@ec-lyon.fr; <sup>2</sup>Environmental Microbial Genomics Group, Laboratoire Ampère, Ecole Centrale de Lyon, Université de Lyon, Ecully cedex 69134, France; <sup>3</sup>The James Hutton Institute, Craigiebuckler, Aberdeen AB15 8QH, UK.

**Abstract:** The relationship between biodiversity and ecosystem function is a hotly debated topic in ecology and yet little is known about the nature of the relationship with respect to ectomycorrhizal (ECM) fungal communities. Furthermore, even less is known about the relative importance of within-species versus between-species diversity. To bridge this gap in knowledge, the following hypotheses were tested: 1) richness and identity of ECM fungal genotypes (intraspecific), relative to species (interspecific), regulate plant and fungal productivity, and have quantifiable effects on ecosystem processes (soil CO<sub>2</sub> flux and nutrient dynamics), and 2) the effects of genotypic ECM diversity on productivity are greatest when the chemical composition of nutrient resources in soil are complex, due to niche complementarity. To test for ecosystem responses, microcosms containing pine seedlings colonized by a diversity gradient, from monocultures to mixtures of ECM genotypes or species, were utilized. Significant genotypic identity effects on plant and fungal productivity, and nutrient loss in leachate were found. There was a weak positive genotypic richness effect with root biomass, root length and ECM root-tips per root length, and nutrient loss generally decreased with increasing genotypic richness. Genotype mixtures outperformed the monocultures in only half of the cases, suggesting that complementarity and selection effects are both in operation. In contrast, species monocultures mostly outperformed the mixtures. Overall, genotypic effects were as significant as species effects. Contrary to expectation, genotypic effects were less significant under complex versus simple soil nutrient resources. Stable isotopes labelling studies in microcosm and fungal culture experiments were utilised to further elucidate genotypic identity effects. Genotypes were found to vary in growth rate and nitrogen source uptake and utilization. Results highlight the importance of ECM fungi and intraspecific genotypic level of diversity in the regulation of ecosystem functioning.

PS 1-46 **Two-way nitrogen transfer between *Eucalyptus* and *Casuarina* via a common ectomycorrhizal network linkage is evidenced by <sup>15</sup>N natural abundance ( $\delta^{15}\text{N}$ ) signature**

HE, X.<sup>1,2</sup>, G. Stewart<sup>2</sup> and C. Critchley<sup>2</sup>

<sup>1</sup>Centre of Excellence for Soil Biology, College of Resources and Environments, Southwest University, Beibei, Chongqing 400716, China, xinhua.he@uwa.edu.au; <sup>2</sup>School of Agriculture and Food Sciences, University of Queensland, St Lucia, Brisbane 4072, Australia.

**Abstract:** Plant roots are often linked by common mycorrhizal networks (CMNs) that are pathways for nutrient transfers between plants. Two-way nitrogen (N) transfers between mycorrhizal plants have been evidenced by <sup>15</sup>N enrichment labeling, but not by <sup>15</sup>N natural abundance ( $\delta^{15}\text{N}$ ) studies. In mixed Australian native *Casuarina* and *Eucalyptus* communities, both mycorrhization and N cycling are extensive. We addressed two questions. First, does two-way N transfer occur between the non-leguminous, actinorhizal, N<sub>2</sub>-fixing *Casuarina* and the non-N<sub>2</sub>-fixing *Eucalyptus*? Second, is N transfer affected by mycorrhization and/or N<sub>2</sub>-fixation? *Eucalyptus maculata* and *C. cunninghamiana* were grown in 3-compartment boxes (300 × 12 × 150 cm, separated by a 37 µm mesh). A middle, 10 mm, narrow compartment acted as the air gap bridge for hyphal linkages, and excluded root contact and water movement. Three 'N-donor' seedlings (*Casuarina* or *Eucalyptus* (6 month and 1-year-old), with or without external <sup>14</sup>N supplement) were planted on one outside compartment and three 'N-receivers' on the other. We observed bi-directional N transfers between *Eucalyptus*-*Casuarina* pairs (linked by a CMN with the fungus *Pisolithus tinctorius*) by detecting the variation in their  $\delta^{15}\text{N}$  values. The results suggested that N<sub>2</sub>-fixing capacity was not a prerequisite for two-way N transfers, but might affect the intensity of such mycorrhiza-mediated N transfers. If *Casuarina* was not nodulated, N-transfer to *Casuarina* or *Eucalyptus* was similar. If *Casuarina* was nodulated, more N (2-4 times) was transferred in nodulated mycorrhizal pairs than in non-nodulated mycorrhizal pairs, whether *Casuarina* or *Eucalyptus* was the N-donor. Surprisingly, *Eucalyptus* (non-N<sub>2</sub>-fixer) donated 1.5 times more N to *Casuarinas* (N<sub>2</sub>-fixer) than the reverse, especially when adequate external N was accessible.

Growth of *Casuarina* was significantly increased by interspecific N transfer relative to *Eucalyptus*. We postulate a ‘myco-centric’ N transfer mechanism to account for these differences. The magnitude of mycorrhiza-mediated N transfer and N movement may be determined by dynamic four-way interactions among plant roots, mycorrhizal fungi, N<sub>2</sub>-fixing bacteria, and soil N resource availability.

#### LT 4-12 Hosts, niches, and resources – drivers of ectomycorrhizal fungal diversity in tropical rainforests

HENKEL, T.W.<sup>1</sup> and M.E. Smith<sup>2</sup>

<sup>1</sup>Department of Biological Sciences, Humboldt State University, Arcata, California 95521 USA, twh5@humboldt.edu;

<sup>2</sup>Department of Plant Pathology, University of Florida, Gainesville, Florida 32611 USA.

**Abstract:** Ectomycorrhizal (ECM) fungi are diverse in higher latitude forests dominated ECM plant families such as the *Pinaceae* and *Fagaceae*. In contrast, previous mycorrhiza surveys in low latitude, tree-diverse tropical rainforests indicated a preponderance of arbuscular-mycorrhizas. The resulting dogma that ECM fungi are impoverished in tropical forests led to a recent “reverse latitudinal diversity gradient” hypothesis for the guild. However, tropical forests are increasingly documented with abundant ECM canopy trees and high ECM fungal diversities. Forests dominated by ECM *Fabaceae* and *Dipterocarpaceae* in South America’s Guiana Shield have ECM fungal alpha-diversities of up to 300 species. In Guineo-Congolian Africa, a recent single-site, single-season survey recovered ~225 species of ECM fungi in association with monodominant forests of the fabaceous, ECM canopy tree *Gilbertiodendron dewevrei*. Ecological factors shaping these “anomalous” ectotrophic tropical forests and their fungal assemblages, and implications for a global understanding of ECM fungal biogeography, systematics, and ecology will be discussed.

#### PS 4-37 Habitat disturbance affects communities of arbuscular mycorrhizal fungi of coastal sand dunes and tropical dry forest at Ría Lagartos Biosphere Reserve, Mexico

Salinas-Escobar, L.A.<sup>1</sup>, A.M. González-Flores<sup>2</sup>, A.M. Montiel-González<sup>1,3</sup>, A. Estrada-Torres<sup>1,3</sup>, J.A.R. Zapata<sup>4</sup>, P. Guadarrama-Chavez<sup>5</sup>, I. Sánchez-Gallen<sup>6</sup>, F.J. Álvarez-Sánchez<sup>6</sup> and L.V. HERNÁNDEZ-CUEVAS<sup>1,2,3</sup>

<sup>1</sup>Centro de Investigación en Ciencias Biológicas, fungicuevas@hotmail.com; <sup>2</sup>Cuerpo Académico “Ciencias Biológicas”;

<sup>3</sup>Licenciatura en Biología, Universidad Autónoma de Tlaxcala; <sup>4</sup>Cuerpo Académico “Ecología Tropical”, Universidad Autónoma de Yucatán; <sup>5</sup>Unidad Multidisciplinaria de Docencia e Investigación Campus-Sisal, Facultad de Ciencias;

<sup>6</sup>Departamento de Ecología y Recursos Naturales, Facultad de Ciencias, Universidad Nacional Autónoma de México.

**Abstract:** Habitat disturbance effects on arbuscular mycorrhizal fungi (AMF) communities have been poorly assessed in tropical ecosystems. Our goal was to evaluate changes in AMF community structure and composition in coastal sand dunes (CSD) and tropical dry forest (TDF), under two contrasting disturbance conditions at the Ría Lagartos Biosphere Reserve, Yucatan, Mexico. We place six plots (100 m<sup>2</sup>) on each ecosystem, three in disturbed sites and three in conserved sites. We extracted AMF spores and identified them through morphological traits, and calculated species richness, diversity, dominance, and frequency. Soil and root samples from CSD were used from DNA extraction and identification of AMF through analysis of the ITS region (ITS1JF and ITS4 primers). Disturbed CSD sites had the highest AMF species richness (17 species) vs. conserved sites (8 species). AMF species richness at TDF was similar between disturbed (12 species) and conserved sites (13 species); only four species were common in both conditions. *Funneliformis badius* was the most common species in both ecosystems and conditions; *Septoglomus constrictum* was only present in disturbed TDF. *Funneliformis mosseae* and *Claroideoglossum etunicatum* spores were extremely infrequent at CSD, but its presence in soils and roots was detected through molecular analysis, they could be some of the predominant soil and roots inhabiting but poorly sporulating species in this ecosystem. Overall diversity was low, but without significant differences among disturbance conditions or ecosystems (Bootstrap analysis, p=5%). Species composition is more sensitive than species richness or diversity to habitat disturbance, while community structure is resistant to environmental variation. Species in conserved sites can be replaced by others more tolerant which can have consequences on AMF functional role.

## PS 1-47 Mycorrhizal fungal abundance and ecosystem-level dynamics following woody plant encroachment into grasslands

HESS, K.M.<sup>1</sup>, L. Mino<sup>1</sup>, P. Coppick<sup>1</sup> and G.W.T. Wilson<sup>1</sup>

<sup>1</sup>Department of Natural Resources Ecology and Management, Oklahoma State University, Stillwater, Oklahoma 74077 USA, Kayla.hess@okstate.edu.

**Abstract:** Woody plant encroachment refers to a native species that is expanding its range into the native community through displacement and subsequent competition of native plant species. Rough leaf dogwood (*Cornus drummondii*) is an encroaching species throughout the Great Plains of North America. This species is expanding primarily due to anthropogenic removal of fire. One hypothesis for the competitive success of *C. drummondii* entails that this woody species disrupts soil microbial communities, including symbiotic relationships with arbuscular mycorrhizal fungi (AMF). Most native grasses are obligate symbionts with AMF, requiring the symbiosis for nutrient and water uptake for completion of their life cycle. Therefore, alterations in the abundance of AMF may have severe negative ramifications to the success of the dominant native grasses. Therefore, we assessed soil biotic (e.g., AMF abundance) and abiotic (e.g., soil aggregate stability, SOC) factors associated with native plant communities (i.e., *Andropogon gerardii* and *Sorghastrum nutans*) and *C. drummondii*. Our results show that *C. drummondii* has greater abundance of AMF, less root biomass (gram per m<sup>3</sup>), greater soil aggregate stability, and greater soil organic carbon. While these results may indicate *C. drummondii* has a positive effect on grassland soils, the loss of important ecosystem services must also be taken into account. An important woody species encroaching into these grasslands is *C. drummondii* (dogwood) with multi-scale effects including loss of plant and animal biodiversity and loss of habitat for wildlife species. These grasslands provide primary resources for livestock production in North America and habitat for a wide variety of wildlife. Therefore, conservation of the remaining tallgrass prairie is essential.

## LT 3-10 Large-scale field application of mycorrhiza-based inoculants, a sustainable solution for global food security

HIJRI, M.<sup>1</sup>

<sup>1</sup>Institut de recherche en biologie végétale, Département de sciences biologiques, Université de Montréal, 4101 Rue Sherbrooke Est, Montréal, QC, H1X 2B2, Canada, mohamed.hijri@umontreal.ca.

**Abstract:** The global population is expected to reach 9.6 billion people by 2050 implying more food production in nutrient-efficient systems will be required to simultaneously meet global food needs while reducing the environmental agricultural footprint. This represents a great challenge for the future of agriculture, because millions of people currently die annually of malnutrition. Plant breeding has increased the genetic potential for yield, but this has leveled off for some crops. Beneficial soil microbes such as mycorrhizal fungi have the potential to enhance crop yield, but their efficiency has yet to be demonstrated in large-scale crop production systems. Here, I analyzed a dataset consisting of 231 field trials in which mycorrhiza-based inoculants were applied in potato fields over a period of four years in North America and Europe. Farmers themselves performed these trials through an international incentive program. Overall, I found a highly significant increase of potato yield (ANOVA,  $P < 0.0001$ ) for inoculated fields (41.8 tons/hectare) compared to the non-inoculated control (38.3 tons/hectare), regardless of the trial year. The average yield increase was 3.92 tons/hectare, 9.5 % of total yield. Importantly, the application of mycorrhiza-based inoculant is profitable at 0.49 tons/hectare yield increase, a threshold reached for almost 80% of the trials. This finding clearly demonstrates the benefits of mycorrhizal-based inoculation on crop yield using potato as a case study, and similar inoculants are also available for other important crops. Further improvements of these beneficial inoculants, combined with controlled or slow release fertilizers, could thus help solve crop production needs and sustainability problems.

### LT 3-13 A phylogenetic meta-analysis of biotic and abiotic factors affecting plant response to mycorrhizal fungi

**HOEKSEMA, J.D.**<sup>1</sup>, J.D. Bever<sup>2</sup>, S. Chakraborty<sup>3</sup>, V.B. Chaudhary<sup>4</sup>, E.A. Housworth<sup>5</sup>, W. Kaonongbua<sup>6</sup>, M.J. Lajeunesse<sup>7</sup>, J.F. Meadow<sup>8</sup>, B. Milligan<sup>9</sup>, B.J. Piculell<sup>1</sup>, M.A. Rúa<sup>1</sup>, J. Umbanhowar<sup>10</sup>, W. Viechtbauer<sup>11</sup> and P.C. Zee<sup>12</sup>

<sup>1</sup>Department of Biology, University of Mississippi, University, MS, hoeksema@olemiss.edu; <sup>2</sup>Department of Biology, Indiana University, Bloomington, IN; <sup>3</sup>Department of Statistics, University of Missouri; <sup>4</sup>Institute of Environmental Sustainability, Loyola University Chicago; <sup>5</sup>Departments of Mathematics and Biology, Indiana University; <sup>6</sup>King Mongkuts University of Technology Thonburi, Thailand; <sup>7</sup>University of South Florida; <sup>8</sup>Biology and the Built Environment Center, Institute of Ecology and Evolution, University of Oregon, Eugene, OR; <sup>9</sup>Department of Biology, New Mexico State University; <sup>10</sup>Biology Department, University of North Carolina, Chapel Hill, Chapel Hill, NC; <sup>11</sup>Department of Psychiatry and Psychology, Maastricht University; <sup>12</sup>Department of Biology, Stanford University, Stanford, CA.

**Abstract:** Plant growth response to mycorrhizal fungi varies among plant and fungal taxa, but it is unknown whether this variation is driven by deep or recent evolutionary divergence in fungal or plant lineages. Moreover, we do not know whether this evolution has progressed independently in plant and fungal lineages, or has evolved interactively between plant and fungal phylogenies. To investigate these questions, we conducted dual-phylogenetic meta-analysis to model phylogenetic heritability of plant response to mycorrhizal fungi in host plant lineages, fungal lineages, and interactions between them, i.e., the evolution of specificity. We also tested for the influence of key environmental variables on plant response to mycorrhizal fungi, while controlling for the influence of plant and fungal phylogenies. In arbuscular mycorrhizal (AM) symbioses, plant responsiveness exhibited heritable specificity as a result of the interaction between fungal and host plant phylogenies, as well as substantial variability among host plant species unrelated to phylogeny, suggesting recent, rapid evolution of this trait in plants. In contrast, ectomycorrhizal (EM) symbioses exhibited substantial heritability of plant responsiveness in the host plant phylogeny, suggesting deeper divergence of this trait among EM host plant lineages. Ectomycorrhizal symbioses showed no evidence of heritable specificity, and neither symbiosis showed evidence of heritability in fungal lineages for plant responsiveness. When controlling for plant and fungal phylogeny in the AM symbiosis, plant responsiveness varied according to the Trade Balance Model of mycorrhizal function, which predicts that a high ratio of nitrogen (N) to phosphorus (P) availability in soils should result in the largest benefits of AM fungi for the growth of their host plants. Overall, contemporary variability in outcomes of AM and EM symbioses results from a combination of heritable phylogenetic influences in plant and fungal lineages and variation in environmental context.

### PS 4-14 Spore dispersal in ectomycorrhizal Basidiomycota with implications for the invasive success of suilloids fungi

**HORTON, T.R.**<sup>1</sup>, M.A. Nuñez<sup>2</sup>, S. Ashiglar<sup>3</sup>, T.E. Lewandowski<sup>4</sup>, J. Hayward<sup>1,7</sup>, D.P. Swaney<sup>5</sup> and M.K.N. Sørensen<sup>6</sup>

<sup>1</sup>Department of Environmental and Forest Biology, SUNY-ESF, Syracuse, NY, USA, trhorton@esf.edu; <sup>2</sup>Conicet, Inibioma, Universidad Nacional Del Comahue, Bariloche, Argentina; <sup>3</sup>Rocky Mountain Research Station, USDA Forest Service, Moscow, ID, USA; <sup>4</sup>Department of Forest and Wildlife Ecology, University of Wisconsin, Madison, WI, USA; <sup>5</sup>Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY, USA; <sup>6</sup>Department of Ecology and Evolution, University of Copenhagen, Copenhagen; <sup>7</sup>Current address: Department of Botany, University of Hawaii, Honolulu, HI, USA

**Abstract:** We summarize our investigations of ectomycorrhizal Basidiomycete spore dispersal with a focus on early successional Pinaceae communities where spores are the primary source of inoculation. Ectomycorrhizal fungi are epigeous taxa that fruit close to the ground or hypogeous taxa that fruit belowground. Approximately 90% of spores of epigeous taxa observed on traps after dropping to the ground near source sporocarps fall within a one meter horizontal radius. A similar pattern is observed in spore dispersal with vertical distance above the cap. We have not yet measured the total number of spores released per sporocarp and the percentage of spores dispersed over large distances remains unclear. The nuclei in spores of many species are binucleate products of post-meiotic mitosis and are still haploid. Secondary homothallism appears to be rare. Following wind dispersal, haploid germinants in uncolonized areas must form a dikaryon with a compatible germinant, the probability of which may be low given that aerially dispersed spore rain is increasingly diffuse with distance. However, suilloids (epigeous *Suillus* and hypogeous *Rhizopogon* spp.) have several life history traits that override these dispersal limitations, contributing to their success in early successional and invasive Pinaceae communities. For instance, large mammals such as deer and boar eat suilloid sporocarps, dispersing compatible mating types by the millions in fecal pellets over long distances. Suilloid spores are apparently longer lived than spores from most



other species and may accumulate to high levels as resistant spore banks. Unlike the spores of most species, suilloids spores can easily be used to inoculate seedlings under nursery conditions. These features contribute to making suilloids keystone mutualistic species for invasive Pinaceae. This is especially true when mycophagist mammals from the invasive tree's natural geographic range are also introduced to the new location, contributing to a biological meltdown.

#### PS 3-65 Effect of $^{137}\text{Cs}$ on the symbiosis between *Clethra barvinervis* and root endophytes

HOSHI, M.<sup>1</sup>, K. Yamaji<sup>1</sup> and H. Masuya<sup>2</sup>

<sup>1</sup>Graduate School of Life and Environmental Sciences, University of Tsukuba, s1521194@u.tsukuba.ac.jp; <sup>2</sup>Tohoku Research Center, Forestry and Forest Product Research Institute.

**Abstract:** Due to the accident at the Fukushima Daiichi nuclear power plant caused by a tsunami in March 2011, large amounts of radioactive materials have been released into the atmosphere. In particular,  $^{137}\text{Cs}$  contamination might have serious environmental impacts because its half-life (30.2 years) is longer than other radionuclides such as  $^{131}\text{I}$  (8.04 days) and  $^{134}\text{Cs}$  (2.06 years). It has been reported that soil fungal communities have been altered by ionizing radiation, resulting in simpler community structures such as the high dominance of melanized fungi. Generally, fungi play major roles in forest ecosystems, and root endophytes have been demonstrated to alleviate environmental stress to plants. Therefore, changes to endophyte communities may affect the symbiosis. A *deciduous tree*, *Clethra barvinervis*, is known to be tolerant of high concentrations of heavy metals with root endophytes controlling excess absorption of heavy metals into roots. The purpose of this study is to evaluate effect of  $^{137}\text{Cs}$  and heavy metals on species and chemical characteristics of root endophytes in *C. barvinervis*. We isolated root endophytes from seedlings growing in five different study sites exhibiting different concentrations of  $^{137}\text{Cs}$  and heavy metals. The following genera were isolated from all study sites: *Phialocephala*, *Acephala*, *Colletotrichum*, *Leptodontidium*, *Rhizoscyphus*, *Lachnum*, *Rhizodermea*, and *Cryptosporiopsis*. We analyzed  $^{137}\text{Cs}$  and heavy metal concentrations in root-zone soil to evaluate the effect of  $^{137}\text{Cs}$  and heavy metals on root endophyte frequency. The frequency of *Acephala* and *Colletotrichum* was positively correlated with  $^{137}\text{Cs}$  concentration in root-zone soil. In contrast, the frequency of *Cryptosporiopsis* was negatively correlated with  $^{137}\text{Cs}$  concentration. Our results may suggest that melanized root endophytes are tolerant to high concentrations of  $^{137}\text{Cs}$ , and their frequencies may increase compared with other species. On the basis of heavy metal detoxicant production by root endophytes, we discuss whether the symbiosis between *C. barvinervis* and root endophytes can be maintained under high  $^{137}\text{Cs}$  concentration.

#### PS 3-14 The central role of arbuscular mycorrhizal fungi in enhancing soil aggregation and organic C sequestration under no-tillage and residue retention

HU, J.<sup>1</sup>, J. Dai<sup>1</sup>, A. Yang<sup>2</sup>, X. Cui<sup>1</sup>, J. Wang<sup>1</sup>, A. Zhu<sup>1</sup> and X. Lin<sup>1</sup>

<sup>1</sup>State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing 210008, PR China, jlhu@issas.ac.cn; <sup>2</sup>Provincial Key Laboratory of Biotic Environment and Ecological Security in Anhui, College of Life Sciences, Anhui Normal University, Wuhu 241000, PR China.

**Abstract:** The mechanisms of soil organic C sequestration in response to no-tillage (NT) and residue retention are unclear. Three experiments were conducted to investigate the role of arbuscular mycorrhizal (AM) fungi in influencing soil processes in cultivated fields. First, a four-year field experiment established in North China elucidated the prominent role of NT in maintaining external hyphae growth rather than in promoting spore density, species richness, and diversity of AM fungi. Additionally, NT enhanced soil aggregation and increased organic C accumulation by macroaggregates (>50  $\mu\text{m}$ ), and the greatest change of AM fungal community composition revealed by PCR-DGGE was observed with 250-50  $\mu\text{m}$  aggregates. Furthermore, NT played a vital role in maintaining AM fungal population growth and glomalin-related soil protein (GRSP) production, binding soil aggregates and increasing organic C sequestration. Second, a greenhouse pot experiment using sterilized soil showed the interactive and/or additive influences of AM fungi and residue on the soil-crop system. The application of maize straw resulted in lower soil pH and higher relevant soil enzyme activity, while AM fungal inoculation further decreased soil pH in straw-applied soil, and elevated wheat grain yield and soil organic C content compared to the control, suggesting the potential exploitation of AM fungi in residue-retained fields. Third, a three-year field experiment carried out in North China again indicated that, being different from tillage systems, residue retention



under NT increased GRSP and thereby increased organic C contents in all size aggregates except for 50-2  $\mu\text{m}$ . Additionally, half of the total amount of residue retention was more feasible than the full amount of residue retention in maintaining/elevating microbial functional diversity in aggregates because excess residue on the topsoil under NT may induce worse soil conditions resulting in a decrease in heterotrophic microbial activities. In conclusion, NT with half of the total residue retention obviously improved soil physical, chemical, and microbiological properties, and could be an appropriate management practice in North China.

#### PS 4-68 A survey into the mycorrhizal fungal diversity of *Dendrobium devonianum*: an endangered Chinese endemic orchid in Xishuangbanna's tea plantations

HUANG, H.<sup>1,2</sup>, S.C. Shao<sup>1</sup> and J.Y. Gao<sup>1</sup>

<sup>1</sup>Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, The Chinese Academy of Sciences, Mengla, Yunnan 666303, China, haunghui@xtbg.ac.cn; <sup>2</sup>Graduate University of Chinese Academy of Sciences, Beijing 100049, China.

**Abstract:** The epiphytic orchid *Dendrobium devonianum*, used in traditional Chinese medicine, became locally endangered in recent years due to over-collection. To get a comprehensive understanding of the mycorrhizal fungi of *D. devonianum* for future development of conservation strategies, we used next generation sequencing technologies and applied diversity indices to determine the diversity of mycorrhizal fungi. We confirmed the presence of Basidiomycetes. Tulasnellaceae, Tomentella, and Ceratobasidiaceae were occasionally distributed within the roots. Other sporadically associated mycorrhizal fungi include *Coprinu*, *Mycena*, and *Clavulina*. Sebaciniales (94%) and Agaricales (5%) were the dominant mycobiont taxa and are possible supplements for orchid mycorrhizal fungi. Diversity index analysis revealed a relatively high diversity in the fungal association of this epiphytic orchid. This suggests some flexibility in adaptation to environmental degradation and the potential for successful reintroduction in natural habitats for plants. These findings offer important information for conservation and reintroduction of *D. devonianum* in tea plantations.

#### PS 4-69 Wheat yield, phosphorus and nitrogen uptake as affected by inoculation of arbuscular mycorrhizal fungi and composts of different organic materials

HUMAIRA, S.<sup>1</sup>, B. Jan<sup>1</sup>, M. Sharif<sup>1</sup>, F. Wahid<sup>1</sup> and F. Khan<sup>1</sup>

<sup>1</sup>The University of Agriculture, Peshawar, sarwarhumaira@yahoo.com.

**Abstract:** A pot experiment was conducted under natural conditions to determine wheat yield, phosphorus and nitrogen uptake as affected by inoculation with arbuscular mycorrhizal fungi (AMF) and composts of different organic materials. The experiment was laid out in a completely randomized design (CRD) with three replications. Wheat variety Atta Habib was grown in The University of Agriculture, Peshawar research farm during Rabi 2013-14. Initially ten seeds were grown and then thinned to five per pot and harvested at maturity. The results of the experiment indicate that the maximum wheat grain yield of 3,300 kg ha<sup>-1</sup> was found in the treatment where half dose of farm yard manure compost (C-1) with commercial AMF inoculation (AMF-II) was used and a significant increase of 30% was noted. It is evident from the data that the maximum shoot dry matter yield of 8,360 kg ha<sup>-1</sup> was obtained from the treatment of half dose of C-I + AMF -II and full half dose of C-I + AMF -II, which was significantly ( $P \leq 0.05$ ) increased by 30% and 28%, respectively over control and N and K fertilizers. The data showed that the maximum N uptake of 175 kg ha<sup>-1</sup> was found in the treatment of half dose of C-II + AMF-I, which was significantly ( $P \leq 0.05$ ) higher by 78% over control. The highest P uptake of 13 kg ha<sup>-1</sup> was recorded in the treatment where half dose of C-II + AMF-I was used and was significantly ( $P \leq 0.05$ ) higher by 209% and 158%, respectively over control and N and K fertilizers. The spore density of AMF of 26 spores per pot and their root infection intensity 39% were maximum in the treatment full dose of C-II + AMF-I, which was 73% and 95% respectively over control. These results suggest that inoculation of AMF with different compost has the potential to improve wheat yields and plant nutrient uptake under given soil conditions.

### PS 3-15 Phenology-mediated enzyme secretion of aspen ectomycorrhizas in the boreal forest

HUPPERTS, S.<sup>1</sup>, J. Karst<sup>1</sup>, K. Pritsch<sup>2</sup> and S.M. Landhäusser<sup>1</sup>

<sup>1</sup>Department of Renewable Resources, University of Alberta, Edmonton, Alberta T6G 0X6 Canada, hupperts@ualberta.ca;

<sup>2</sup>Institute of Biochemical Plant Pathology, Helmholtz Zentrum München, D-85354 Neuherberg Germany.

**Abstract:** Trees reserve sugar and starch for metabolism when photosynthetically-derived carbon is limited. Carbon reserves fluctuate in response to seasonality, which induces changes in source-sink dynamics in trees. Carbon, predominantly in the form of glucose, fuels growth and metabolism of ectomycorrhizal (EM) fungi. Though primarily dependent on living trees for this resource, some research indicates that EM fungi may mobilize carbon from soil organic matter when highly limited by photosynthetically-derived carbon. We tested whether phenological shifts in carbon reserves in roots of mature aspen (*Populus tremuloides*) affect the activity of EM-derived carbon-degrading enzymes. Specifically, we predicted the activity of  $\beta$ -glucosidase,  $\beta$ -glucuronidase, *N*-acetylglucosaminidase, and laccase to be highest when root carbon reserves are lowest, and to also be mediated by invertase, an enzyme that converts sucrose to glucose. Across four phenological stages, i.e., dormancy, leaf flush, full leaf expansion, and leaf abscission, we sampled EM roots of three mature ( $\geq 60$  years old) aspen trees at each of eight stands dominated by aspen in northeastern Alberta, Canada. Collectively, EM-derived carbon-degrading enzymes were negatively associated with fine root sugar concentration; however, this relationship was driven by one enzyme,  $\beta$ -glucosidase, although most EM-derived enzymes exhibited positive correlations with each other. Moreover, root invertase activity was positively associated with fine-root sugar concentrations, indicating that glucose availability underlies the shift to saprotrophic behavior. Our results demonstrate that a temporary shift to potential saprotrophic behavior by aspen ectomycorrhizas, as measured by  $\beta$ -glucosidase, coincides with phenologically-driven low root carbon reserves and corresponding low root invertase activity.

### PS 2-39 Host herbivory and fertilization impacts on soil and root fungal communities in a controlled field experiment

HUUSKO, K.<sup>1</sup>, A.L. Ruotsalainen<sup>1</sup>, T. Andersson<sup>2</sup>, H. Koivuniemi<sup>1</sup>, K. Saravesi<sup>1</sup>, M. Suokas<sup>1</sup>, O. Suominen<sup>2</sup>, P. Wäli<sup>1</sup> and A. Markkola<sup>1</sup>

<sup>1</sup>Department of Ecology, University of Oulu, FI-90014 University of Oulu, Finland, maija.huusko@oulu.fi; <sup>2</sup>Kevo Subarctic Research Institute, University of Turku, FI-20014 University of Turku, Finland.

**Abstract:** During past decades, autumnal moth (*Epirrita autumnata*) and winter moth (*Operophtera brumata*) outbreaks have resulted in severe defoliation of about 400 km<sup>2</sup> of mountain birch (*Betula pubescens* ssp. *czerepanovii*) forests in northern Fennoscandia. Moth outbreaks in the forest-tundra ecotone cause drastic vegetation changes both in terms of extensive deaths of birch trees in large areas but also in the understorey vegetation. Soil microbial communities and soil nutrient and carbon cycles are strongly affected by moth outbreaks. Mycorrhizal fungi play an essential role in carbon and nutrient cycling in boreal and subarctic forest ecosystems, and changes in the availability of these resources greatly affect ecosystem functioning. As microbes in forest soils are generally considered as carbon limited, decline in carbon availability after moth defoliation may have a major impact on mycorrhizal and soil fungal communities. We studied effects of moth-feeding and artificial defoliation (including defoliation of mountain birch and mechanical shoot damage of understorey vegetation) and fertilization on soil fungal and root-associated ectomycorrhizal communities in a controlled field experiment near Kevo Subarctic Research Station (69°N) in 2011-2013. Fungal rDNA from ITS2 region was amplified both from soil and roots of transplanted mountain birch seedlings and sequenced with Ion Torrent PMG in BioSer Oulu laboratory. Preliminary results on fungal community composition show, that in the moth-feeding experiment, fungal diversity in birch roots was lower in plots exposed to three years of moth feeding compared to the two-year moth-feeding treatment or control. In soil, fungal diversity seemed to be higher in moth-feeding treatments compared to control. In the defoliation and fertilization experiment, soil fungal diversity and evenness were lower in the fertilization treatment compared to the defoliation treatment or control, but no differences were found in root fungal diversity. Differences between functional groups will be discussed.

## CS 9-5 Mycorrhizal specificity can lead to ecophysiological plasticity in plants living off fungi

HYNISON, N.A.<sup>1</sup>, M.I. Bidartondo<sup>2</sup> and D.J. Read<sup>3</sup>

<sup>1</sup>Department of Botany, University of Hawaii Manoa, 3190 Maile Way Room 101, Honolulu, HI 96822 USA, nhynson@hawaii.edu; <sup>2</sup>Department of Biological Sciences, Imperial College London and Royal Botanic Gardens, Kew TW9 3DS, UK; <sup>3</sup>Department of Animal and Plant Sciences, University of Sheffield, Sheffield S10 2TN, UK.

**Abstract:** Many symbiotic interactions are specific where hosts and symbionts fine-tune their physiologies to receive the most benefit from their partners. Fully mycoheterotrophic plants that have lost the ability to photosynthesize and rely completely on symbiotic interactions with fungi to meet all of their carbon and nutrient demands have been touted as prime examples of mycorrhizal specialists. However, the question remains whether this fine-scale fungal partner specialization among mycoheterotrophs leads to the fixation of traits that also increase plant fitness, or if mycorrhizal specificity is an evolutionary dead end. To address this question, we focus on partial mycoheterotrophy, the ability of plants to meet a portion of their carbon demands via symbiotic fungi, and fungal partner specificity as forms of local adaptation. Local adaptation is a concept used to describe how species allocate resources in order to survive in their environments. Here, using DNA sequencing and the analysis of carbon and nitrogen stable isotopes, we examine the fungal partnerships and ecophysiology of a putatively partially mycoheterotrophic species, *Moneses uniflora* (Ericaceae), across two continents. We reveal that, while this species remains highly specific in its mycorrhizal partnerships across a large portion of its natural range, its ability to derive carbon from similar fungi varies among populations. This finding indicates that environment rather than interactions with fungal partners may be a stronger determinant for mycoheterotrophy, and partial mycoheterotrophy is a plastic trait within some plant species. We conclude that partial mycoheterotrophy should be considered a local adaptation rather than a fixed functional trait, and fungal partner specificity does not necessarily lead to a decrease in plant fitness.

## PS 4-38 Diversity of arbuscular mycorrhizas associated with saffron in the Kashmir valley, India

ITOO, Z.A.<sup>1</sup>, M.A. Shah<sup>1</sup> and Z.A. Reshi<sup>1</sup>

<sup>1</sup>Biological Invasions Research Lab, Department of Botany, University of Kashmir, Srinagar 19006, zahooritoo151@gmail.com.

**Abstract:** Saffron is one the most valuable spices in the world and the valley of Kashmir is well known globally for the quality of saffron grown. The best quality of saffron has been found to be a function of the ideal corm size, which is very important for flowering and yield, and depends on efficient nutrient cycling. In view of the role of mycorrhizas in nutrient acquisition and other benefits to saffron, the present study was undertaken to isolate and characterize the arbuscular mycorrhizal fungi (AMF) associated with saffron. We tackled this objective through molecular phylogenetic analysis using highly conserved nuclear ribosomal DNA sequences. The genomic DNA extracted from Saffron roots was amplified by PCR using ITS1 and ITS4 primers. The PCR amplicons in all species, ranging from 650-750 bp, were sequenced and the sequences were aligned and BLAST searched using NCBI database for confirmation of their identity by comparing the sequences of these species with respective species present in GenBank. Ten different AMF species belonging to 3 genera and 6 species were identified from saffron growing in Pampore belt of Kashmir valley, India. The species identity was further confirmed by performing phylogenetic analysis using MEGA and Phylip software. Studies on the impact of these AMF on growth and yield of saffron are underway to identify the most elite species or their consortia for mass multiplication and large-scale use by the saffron farmers.

### PS 3-34 N fertilizer effects on arbuscular-mycorrhizae fungi abundance and function in a perennial grass cropping system

JACH-SMITH, L.C.<sup>1,2</sup> and R.D. Jackson<sup>1,2</sup>

<sup>1</sup>Nelson Institute for Environmental Studies, University of Wisconsin, Madison, Wisconsin 53706 USA, lcsmith4@wisc.edu; <sup>2</sup>DOE Great Lakes Bioenergy Research Center, University of Wisconsin, Madison, Wisconsin 53706 USA.

**Abstract:** Nitrogen (N) amendments are a common agricultural practice to increase crop productivity, but they exacerbate environmental pollution and decrease soil microbial diversity and function. To understand the effects of N fertilizer on AMF abundance and function in a cellulosic bioenergy production system, we measured the extra-radical hyphae biomass, plant biomass, and plant  $\delta^{15}\text{N}$  at two field sites growing *Panicum virgatum* (switchgrass), a native perennial grass, subjected to varying levels of N fertilizer. While above- and below-ground biomass did not respond to fertilizer, early results from one site show that extra-radical hyphae were reduced by 87% in the high-N treatment and 24% in the low-N treatment compared to the unfertilized treatment. The plant proportional allocation to AMF was also significantly higher in the unfertilized treatment compared to the high-N treatment indicating that plants invested significantly more resources to AMF symbioses than fertilized counterparts. We hypothesized that extra-radical hyphae biomass would be negatively correlated to plant  $\delta^{15}\text{N}$ , assuming there is significant fractionation upon transfer of N molecules if AMF are contributing to plant N nutrition. Plant  $\delta^{15}\text{N}$  was correlated to hyphae biomass ( $r^2 = -0.6$ ), but this relationship was driven primarily by differences between fertilizer treatments. Our results indicate that high rates of applied N significantly decrease AMF abundance and function, but moderate rates may not affect AMF in these systems. However, since not fertilizing supports greater AMF symbioses without yield losses in most instances, reducing N fertilizer to encourage AMF may be a more sustainable route for perennial grass cropping systems.

### PS 3-66 Composition of arbuscular mycorrhizal fungal communities as plant adaptation to environmental conditions?

JANOŠKOVÁ, M.<sup>1</sup>, J. Jansa<sup>2</sup>, D. Püschel<sup>1,2</sup>, A. Voříšková<sup>1</sup>, M. Krüger<sup>1</sup> and M. Vosátka<sup>1</sup>

<sup>1</sup>Institute of Botany, Czech Academy of Sciences, Zámek 1, 25243 Průhonice, Czech Republic, martina.janouskova@ibot.cas.cz; <sup>2</sup>Institute of Microbiology, Czech Academy of Sciences, Vídeňská 1083, 14220 Praha 4, Czech Republic.

**Abstract:** Under most natural conditions, plant roots are colonized by complex arbuscular mycorrhizal fungal (AMF) communities rather than by fungal monocultures. The structure of these communities is supposed to be influenced by various factors including plant species identity, relative infectivity of the different fungal genotypes, and environmental conditions. We know that different fungi are functionally different, and host plants have the capacity to promote a specific mycosymbiont through targeted reward mechanisms. Thus, the question arises if the plant actively shapes the composition of its symbiont community in response to changing or fluctuating environmental conditions in order to maximize its benefits from the symbiosis. In such a case, the composition of AMF communities would play an important part for the plant to adapt to specific environmental conditions. We present our study that experimentally targets the theoretical concept of AMF community composition as a tool of plant adaptation. First, we monitor abundance ratios of AMF species in communities established from the same inoculum pool under different environmental conditions, manipulating water, light, and phosphorus availability. Second, we test whether divergence from conditions-specific AMF abundance ratios alters the plant response to mycorrhiza. Additionally, we compare the response of individual AMF to environmental conditions in monoculture and in community. Our findings will improve the understanding of how AMF community composition is related to the functioning of mycorrhiza.

### PS 3-2 Mycorrhizal costs and benefits in C3 and C4 grasses at different P availabilities

Slavíková, R.<sup>1</sup>, M. Gryndler<sup>1</sup>, D. Püschel<sup>1</sup>, O. Beskid<sup>1</sup>, M. Hujšlová<sup>1</sup>, H. Gryndlerová<sup>1</sup> and J. JANSÁ<sup>1</sup>

<sup>1</sup>Institute of Microbiology, Czech Academy of Sciences, Vídeňská 1083, 14220 Prague 4, Czech Republic, jansa@biomed.cas.cz.

**Abstract:** In contrast to often recorded mycorrhizal benefits, carbon (C) balance of mycorrhizal plants has only rarely been assessed, and a whole C budget of a C4 plant has not been assembled yet. Here, we used two closely related *Panicum* spp. with different types of photosynthesis (*P. bisulcatum* with C3 type and *P. maximum* with C4 type) to minimize the phylogenetic bias of the comparison. Plants were inoculated with a synthetic arbuscular mycorrhizal (AM) fungal

community and grown for 9 weeks at two levels of phosphorus (P) availability. Shortly before harvest, they were pulsed with  $^{13}\text{CO}_2$  and a whole-plant C balance including aboveground and belowground respiration was assembled. Within three days after labeling, a large share (33%) of  $^{13}\text{C}$  was allocated to aboveground respiration, 14% to the roots, 5% to belowground respiration, and 4% to the soil. Growth of the grasses was unaffected by the inoculation. In contrast, plant P uptake generally improved due to the inoculation, with strong benefits (+40%) recorded for the C4 host at both P levels and for the C3 host at low P only. In contrast to the C3 plants, C4 hosts remained strongly colonized even at high P, with the composition of AM fungal communities being strongly affected by both host identity and P availability. The  $^{13}\text{C}$  was quickly transferred belowground in mycorrhizal plants, with a measurable enrichment of the soil C pool in mycorrhizal pots as early as 1 hour after  $^{13}\text{C}$  labeling. The inoculation induced C reallocation from aboveground to belowground respiration in the C3 hosts, whereas the AM fungi associated with the C4 hosts retained a greater portion of  $^{13}\text{C}$  in the soil. Little impact of mycorrhizal inoculation on other C pools in the C4 plants suggest a greater compensation of the mycorrhizal C costs in C4 as compared to the C3 hosts.

#### CS 9-1 Plant preferential allocation and fungal reward decline with soil phosphorus: implications for evolution of the mycorrhizal mutualism

Ji, B.<sup>1</sup> and J.D. Bever<sup>2</sup>

<sup>1</sup>Research Center of Grassland Resources and Ecology, College of Forestry, Beijing Forestry University, Beijing 100083 China, baomingji@bjfu.edu.cn; <sup>2</sup>Department of Biology, Indiana University, Bloomington, Indiana 47405 USA.

**Abstract:** Explaining the persistence of mutualisms in nature has been a major challenge in ecology and evolutionary biology. The evolutionary stability of arbuscular mycorrhizae, one of the most widespread and ancient mutualistic associations, is particularly intriguing because plants lack apparent mechanisms to prevent cheaters from gaining competitive advantages over cooperators. Recent evidence suggests that preferential allocation may prevent the breakdown of mycorrhizal symbiosis by non-beneficial fungal cheaters, but the resource base of preferential allocation has never been demonstrated with natural plants. We developed a triple isotopic labeling method ( $^{14}\text{C}$ ,  $^{32}\text{P}$ , and  $^{33}\text{P}$ ) within a split-root design to measure the exchange of carbon and phosphorus between the host plant (*Allium vineale*) and two mycorrhizal partners (*Claroideoglomus candidum* and *Gigaspora margarita*) across a soil P gradient. Our results demonstrate that plants can preferentially allocate fixed C to roots that host the fungus delivering more soil P to the shoots. The strength of preferential allocation declines with soil P. At low soil P, 35% of labelled C is allocated to roots infected with the beneficial fungus, and at high P this declines to approximately 10%, a level not different from that allocated to roots infected with the non-beneficial fungus. The host plant gets more P per unit of allocated C from the more beneficial fungus, and this advantageous exchange rate does not depend upon P availability. As a result, the level of preferential allocation is correlated with the differential uptake of P from the two fungi. These findings suggest that plant preferential allocation to better mutualists can stabilize mutualisms in environments limiting in the traded resource, but as the availability of this resource increases, plant preferential allocation declines. This environmental dependence of preferential allocation generates predictions of declining levels in relative abundance of mutualistic fungi in high resource environments.

#### CS 6-4 The arbuscular mycorrhizal fungi colonising root nodules of New Zealand kauri (*Agathis australis*)

Padamseem, M.<sup>1</sup>, R. JOHANSEN<sup>1,2</sup>, A. Stuckey<sup>2</sup>, S.E. Williams<sup>3</sup>, J.E. Hooker<sup>2</sup>, B. Burns<sup>2</sup> and S.E. Bellgard<sup>1</sup>

<sup>1</sup>Landcare Research Ltd Private Bag 92170, Auckland 1142, New Zealand, rjoh103@aucklanduni.ac.nz; <sup>2</sup>The University of Auckland, Private Bag 92019, Auckland 1142, New Zealand; <sup>3</sup>University of Wyoming, 1000 E University Avenue, Laramie, WY 82071, USA.

**Abstract:** As the only endemic member in New Zealand of the ancient coniferous family, Araucariaceae, *Agathis australis* is an ideal species to study putatively long-evolved mycorrhizal symbioses. However little is known about *A. australis* root and nodular endophytes, the function of the root nodules, and how mycorrhizal colonization occurs. We use light, scanning and transmission electron microscopy, and 454-sequencing to characterize colonization, and identify the arbuscular mycorrhizal fungi (AMF) endophyte(s) associated with *A. australis* roots and nodules. Representatives of five families of Glomeromycota were identified via high-throughput pyrosequencing. Imaging studies showed that there is abundant, but not ubiquitous, colonization of nodules, which suggests that nodules are colonized by horizontal transmission. Roots were also found to be colonized by AMF. This study is the first to demonstrate the multiple Glomeromycota lineages to colonize *A. australis* including some that may be specific to this host species.



PS 2-51 **The biogeography of the arbuscular mycorrhizal fungi of the invasive dune grass, *Ammophila arenaria***

**JOHANSEN, R.B.**<sup>1</sup>, P. Johnston<sup>2</sup>, R. Vilgalys<sup>3</sup> and B. Burns<sup>1</sup>

<sup>1</sup>School of Biological Sciences, The University of Auckland, Auckland, New Zealand, rjoh103@aucklanduni.ac.nz;

<sup>2</sup>Landcare Research, Auckland, New Zealand; <sup>3</sup>Department of Biology, Duke University, Durham, NC27708 USA.

**Abstract:** Native to Europe, the coastal dune grass marram (*Ammophila arenaria*) has been shipped around the world for erosion control. This study tracks the movement of the plant from the United Kingdom to the United States, Australia, and New Zealand. Next generation sequencing on the Illumina MiSeq platform is being used to explore the biogeography of the arbuscular mycorrhizal fungi (AMF) within marram roots in these countries at multiple spatial scales. Host species influence over fungal community structure is also being examined, with the AMF from an alternative host grass in each country being sequenced. Our results show a wide range of AMF are able to tolerate the harsh, frequently disturbed environment presented by sand dunes and occupy the roots of marram in its native and introduced ranges. While some taxa are widely shared amongst marram growing in different dune systems, spatial heterogeneity occurs within and between countries. Host species influence appears to be contextual, with the US native grass *Leymus mollis* sharing largely the same AMF community with marram, while communities are different in alternative host plant species in other locations. Non-AMF taxa in roots are also being sequenced, and their biogeographic patterns will be compared and contrasted with those of AMF.

CS 2-3 **Mycorrhizal networks as conduits of inter-plant signals and drivers of multi-trophic interactions**

**JOHNSON, D.**<sup>1</sup>, Z. Babikova<sup>1,2,3</sup>, J.A. Pickett<sup>3</sup>, T. Bruce<sup>3</sup> and L. Gilbert<sup>2</sup>

<sup>1</sup>Institute of Biological and Environmental Sciences, University of Aberdeen, Aberdeen AB243UU UK, d.johnson@abdn.ac.uk; <sup>2</sup>James Hutton Institute, Craigiebuckler, Aberdeen AB158QH UK; <sup>3</sup>Rothamsted Research, Rothamsted, Harpenden, AL52JQ UK.

**Abstract:** Plants mediate indirect ‘apparent’ effects between above-ground herbivores and below-ground mutualistic mycorrhizal fungi. Here, we show that the herbivore-plant-mycorrhiza continuum is further complicated because signals produced by plants in response to herbivores can be transmitted to other plants via shared fungal networks below-ground. We also show that insect herbivores, such as aphids, affect the functioning of mycorrhizal fungi, probably by changing the supply of recent photosynthate from plants to mycorrhizas, but the timing of colonisation of roots and leaves is critical. We also present evidence that mycorrhizas affect aphid fitness by changing plant signalling pathways, rather than only through improved nutrition. New knowledge of the transfer of signals through fungal networks between plant species means we now need a better understanding of how this process occurs in relation to the feeding preferences of herbivores and the consequences for plant community composition and herbivore behavior in nature.

PS 1-17 **Using high-throughput sequencing to study a hemiepiphytic orchid, *Vanilla planifolia*, at four Mexican farms**

**JOHNSON, L.**<sup>1</sup>, Ma. del C.A. González-Chávez<sup>2</sup>, R. Carrillo-González<sup>1</sup>, A. Porras-Alfaro<sup>3</sup> and G.M. Mueller<sup>4</sup>

<sup>1</sup>Northwestern University, 2205 Tech Drive, O.T. Hogan Hall, Room 2-144, Evanston, IL, 606208, USA, Lynnaunjohnson2018@u.northwestern.edu; <sup>2</sup>Colegio de Postgraduados, Campus Montecillo, 56230 Carretera México, Texcoco, km 36.5, Montecillo, Estado de México, México; <sup>3</sup>Western Illinois University, Biological Sciences, Waggoner Hall 372, 1 University Circle, Macomb, IL, 61455, USA; <sup>4</sup>Chicago Botanic Garden, Conservation Science, 1000 Lake Cook Road, Glencoe, IL, 60022, USA.

**Abstract:** Orchid mycorrhizal fungi are phylogenetically diverse, occurring primarily in the Basidiomycota. Challenges such as culturing techniques and limited sequencing depth have restricted rigorous investigations of these mycorrhizal fungi. Moreover, 70% of the family Orchidaceae is epiphytic, but investigations have focused primarily on the fungi in terrestrial roots, especially *Rhizoctonia*-like group. This study addresses mycorrhizal fungal diversity and specificity within epiphytic and terrestrial roots of *Vanilla planifolia*, an economically important crop that is hemiepiphytic, using high-throughput (Miseq) sequencing. We examined epiphytic and terrestrial roots from 20 individuals. These individu-

als were collected from four farms, each with different agricultural practices that ranged from a wild natural system to a highly managed farm. We hypothesized that mycorrhizal fungal diversity and community varies between agricultural practices and root niche. Using primers for the ITS region 2, optimized for Cantharellaceae, we recovered 6 million quality filtered reads and identified 431 OTUs (at 97% similarity) of which 34 were considered as putative mycorrhizal. Within the *Rhizoctonia* complex we recovered different teleomorphs including *Ceratobasidium*, *Sebacina*, and *Thanatephorus*. Additionally our results suggest that *V. planifolia* associates with a wide variety of mycorrhizal fungi. This research was conducted in the states of Veracruz and Puebla and is part of an International project to enhance the production of Mexican vanilla.

#### LT 1-6 Functional differences of Douglas-fir ectomycorrhizae along a natural nitrogen gradient

Hawkins, B.J.<sup>1</sup>, J.M. Kranabetter<sup>2</sup>, T. Li<sup>3</sup> and M.D. JONES<sup>4</sup>

<sup>1</sup>Centre for Forest Biology, University of Victoria, P.O. Box 3020, STN CSC, Victoria, B.C. Canada V8W 3N5; <sup>2</sup>British Columbia Ministry of Forests, Lands and Natural Resource Operations, P.O. Box 9536, STN PROV GOVT, Victoria, B.C. CANADA V8W 9C4; <sup>3</sup>Laboratory of Conservation and Utilization for Bioresources, Yunnan University, Kunming, China; <sup>4</sup>Biology Department, University of British Columbia, Okanagan Campus, Sci-385, 1177 Research Road, Kelowna, B.C. Canada V4V 1V7, melanie.jones@ubc.ca.

**Abstract:** Nitrogen (N) availability is hypothesized to be a strong abiotic filter for ectomycorrhizal (ECM) fungi, directly affecting the composition and diversity of ECM communities. N-related functional trait differences among ECM fungal species may therefore be a key adaptation for both the fungal and plant partners in the symbiosis. We investigated whether uptake of ammonium and nitrate differed among Douglas-fir (*Pseudotsuga menziesii*) ectomycorrhizae from three sites of contrasting fertility (~0.09–0.28% N) and N form availability (~10–65% inorganic N) in May/June and again in September/October. Net fluxes of ammonium, nitrate and protons were measured on root tips colonized by representative ECM fungi and on non-mycorrhizal roots using a microelectrode ion flux measurement system (MIFE™) (n=13–20 roots per site). Species turnover (cf. beta diversity) in the ECM fungal communities over the gradient was high, with many more *Tomentella* and *Clavulina* species on high-N soils in contrast to the *Cortinarius* and *Piloderma* species associated with the low-N soils. ECM root tips had up to five times greater rates of ammonium uptake than non-mycorrhizal roots, and ammonium uptake was much greater than nitrate uptake for most ectomycorrhizae. Ammonium uptake peaked in the spring, at over 200 nmol m<sup>-2</sup> s<sup>-1</sup>, for a number of *Tomentella*, *Russula*, *Tylospora*, and *Lactarius* species from the high- and medium-N sites. The lowest uptake rates of ammonium were generally by *Cortinarius* species. Proton efflux, indicating acidification of the rhizosphere, was greatest in roots from the high-N site and lowest for the low-N site. These results suggest that ammonium uptake capacity may be a particularly important functional trait differentiating the niches of ECM fungal species. Important questions remain as to the phenotypic plasticity of ECM fungi in NH<sub>4</sub><sup>+</sup> and NO<sub>3</sub><sup>-</sup> uptake capacity, and the effect of season, root age, and host demand on ion fluxes.

#### PS 2-7 Ectomycorrhizal *Pisolithus albus* from ultramafic soils in New Caledonia: diversity, tolerance to nickel, and the role in plant host adaptation to harsh soil conditions

JOURAND P.<sup>1</sup>, C. Majorel<sup>2</sup>, H. Hannibal<sup>1</sup>, M. Lebrun<sup>3</sup> and M. Ducousso<sup>4</sup>

<sup>1</sup>IRD, Laboratoire des Symbioses Tropicales et Méditerranéennes (LSTM UR040), TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, France, philippe.jourand@ird.fr; <sup>2</sup>Université de la Nouvelle-Calédonie, Laboratoire Insulaire du Vivant et de l'Environnement, BPR4, 98851 Nouméa Cedex, Nouvelle-Calédonie; <sup>3</sup>Université Montpellier II, Laboratoire des Symbioses Tropicales et Méditerranéennes (LSTM UR), TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, France; <sup>4</sup>CIRAD, Laboratoire des Symbioses Tropicales et Méditerranéennes (LSTM UR082), TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, France.

**Abstract:** The ectomycorrhizal fungus *Pisolithus albus* from New Caledonia was investigated for its biodiversity, mechanisms involved in tolerance to nickel, and the role in plant host adaptation to soil constraints, especially ultramafic conditions. Phylogenetic and AFLP analyses confirmed that all isolated and herbarium samples collected in the frame of this study in New Caledonia are correctly named as *P. albus* with a very close relationship with Australian specimens. Isolates coming from ultramafic soils constitute a separated homogeneous group when compared to other isolates. Ultramafic isolates can be split into two groups for their *in vitro* Ni-tolerance with Ni-tolerant (average EC<sub>50</sub>=576 µM) and Ni-sensi-

tive (average  $EC_{50}=30\text{ }\mu\text{M}$ ) isolates. In the presence of high Ni concentration (1 mM), no Ni accumulation was observed in the mycelium of Ni-tolerant isolates due to a metal efflux mechanism. Pyrosequencing and qPCR approaches showed that 30% of the Ni-tolerant *P. albus* genome is modulated by nickel. Some genes are exclusively expressed *in vitro* in Ni-tolerant isolates and also *in situ* in ectomycorrhizae and mycelium. Genes putatively involved in metal efflux were identified from the fungal transcriptome; they encode for a metal transporter as P-ATPase, MFS, or ABC transporter. Cloning these genes in yeast provided significant advantages in terms of nickel tolerance (+31% Ni  $EC_{50}$ ) and growth (+83%  $\mu$ ) when compared to controls. Furthermore, a nickel efflux mechanism was also detected in the transformed yeast cells. Enhanced plant growth and biomass, improved plant mineral nutrition (N, P, K), and reduced metal transfer (including Ni) to plant tissue was found when individuals from a model host plant in the Myrtaceae were inoculated with Ni-tolerant isolates of *Eucalyptus globulus* and placed a nickel dose-response experiment or in an ultramafic substrate. Altogether, these data suggest a large fungal contribution to plant adaptation through an adaptive physiological response to Ni toxicity or ultramafic edaphic constraint.

**PS 3-67 Arbuscular and ectomycorrhiza colonization of *Coccoloba uvifera* L. in a coastal dune in the Ria Lagartos Biosphere Reserve, Yucatan, Mexico**

**JUÁREZ-BARRADAS, R.**<sup>1</sup>, G.L. Galindo-Flores<sup>1,2</sup>, A. Estrada-Torres<sup>1,3</sup>, I. Sánchez-Gallen<sup>4</sup>, C. Lara-Rodríguez<sup>1,3</sup>, L. Hernández-Cuevas<sup>2</sup>, A. Kong-Luz<sup>1,3</sup> and R. Garibay-Origel<sup>5</sup>

<sup>1</sup>Posgrado en Ciencias Biológicas y Laboratorio de Micorrizas, Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, México, Shalimar\_rfa@hotmail.com; <sup>2</sup>Laboratorio de Micorrizas, Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, México; <sup>3</sup>Laboratorio de Biodiversidad, Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, México; <sup>4</sup>Departamento de Ecología y Recursos Naturales, Facultad de Ciencias, Universidad Nacional Autónoma de México; <sup>5</sup>Laboratorio de Sistemática y ecología de micorrizas, Instituto de Biología, Universidad Nacional Autónoma de México.

**Abstract:** *Coccoloba uvifera* is a pioneer plant of coastal dunes with the ability to tolerate adverse conditions, such as high salinity and water stress, because of its mycorrhizal symbiosis. However, it is unknown what mycorrhizal species *C. uvifera* is associated with or if *C. uvifera* associates with more than one type of mycorrhiza. Our objective was to evaluate ectomycorrhizal (ECM) and arbuscular mycorrhizal (AM) colonization and the mycorrhizal fungal diversity associated with *C. uvifera* in the Ria Lagartos Biosphere Reserve. One transect was established along the dune coastline in the El Cuyo, Yucatan to collect rhizospheric soil and root samples of *C. uvifera* juveniles and adults. The ECM colonization and species identity were determined by morphological and molecular characterization of mycorrhizal tips. The presence of arbuscular mycorrhizae on roots was determined by the trypan blue staining technique and colonization estimation method of McGonigle *et al.* (1990) Arbuscular mycorrhizal fungal species diversity was estimated through the extraction and morphological identification of spores. Ectomycorrhizal colonization percentages were statistically different between morphotypes and stages of plant development. We have identified three ECM morphotypes on the roots of juvenile and adult plants; one of them corresponds to *Scleroderma bermudense*. For AM colonization, there were no differences between juveniles (12.48%) and adult plants (9.31%); vesicles were the more abundant structure. Furthermore, thirteen species of AM fungi were identified, and *Acaulospora kentinensis* was the most abundant species. Our study contributes to evaluating the mycorrhizal community in the coastal dunes and is the first record of dual mycorrhizal colonization in *C. uvifera*, which could be a critical aspect for the establishment and managing of this key species for the conservation of this ecosystem.

**SY 1-5 Diversity and function of dark septate endophytes**

Mandyam, K.<sup>1</sup> and **A. JUMPPONEN**<sup>2,3</sup>

<sup>1</sup>Department of Agriculture, Alcorn State University, Lorman, MS 39096, USA; <sup>2</sup>Division of Biology, Kansas State University, Manhattan, KS 66506; <sup>3</sup>Ecological Genomics Institute, Kansas State University, Manhattan, KS 66506, ari@ksu.edu.

**Abstract:** Mycorrhizal fungi and endophytes may be equally abundant as judged by the proportion of hosts colonized or by the extent of colonization in sampled root systems. Comparisons across arid and mesic grasslands suggest that the diversity and composition of root endophyte communities may be biome specific and that communities of fungal endophytes are often unique to a biome and overlap only marginally. Data suggest high beta-diversity on a biome level:

arid grasslands are distinct from mesic grasslands and grasslands are distinct from forested (boreal) biomes. Despite the high frequency and suspected ecological importance of the root endophytes, the effects of root endophyte colonization on plant growth and performance remain still unclear. Experiments that exploit the model plant *Arabidopsis thaliana* and many native plants indicate similarly distributed host responses and, on average, endophytes suppress host growth, although populations include strains that promote host growth. These results highlight the context dependency: responses to conspecific endophytes vary among plant species, but also among ecotypes of near homozygous lines of model plants suggesting possible genotype-specific interactions or responses. Analyses of transcriptional responses to endophyte colonization suggest that fungal endophytes may modulate host nutrient metabolism, defenses, or responses to pathogens and stress. Much remains to be learned about the root endophyte symbioses, the diversity of endophytic fungi, as well as their effects on colonized hosts. Modern era of expedient and inexpensive deep sequencing of communities and transcriptomes likely permit testing specific hypotheses emerging from studies focusing on comparable mycorrhizal or other endophyte systems.

### SY 3-1 Exploring the transfer of recent plant photosynthates to soil microbes via the mycorrhizal pathway

**KAISER, C.**<sup>1</sup>, M.R. Kilburn<sup>2</sup>, P.L. Clode<sup>2</sup>, J.B. Cliff<sup>2</sup>, Z.M. Solaiman<sup>3</sup>, M. Koranda<sup>1</sup>, L. Fuchslueger<sup>1</sup> and D.V. Murphy<sup>3</sup>

<sup>1</sup>Department of Microbiology and Ecosystem Science, University of Vienna, Austria, Christina.kaiser@univie.ac.at; <sup>2</sup>Centre for Microscopy, Characterisation and Analysis, The University of Western Australia, Australia; <sup>3</sup>Soil Biology and Molecular Ecology Group, School of Earth and Environment, The University of Western Australia, Australia.

**Abstract:** Root exudation of recently assimilated plant carbon (C) is known to accelerate microbial decomposition of soil organic matter (rhizosphere priming effect). However, much less is known about an analogue short-term transfer of recent photosynthates to soil microbes via mycorrhizal fungal hyphae. Do mycorrhizal fungal hyphae enhance soil nutrient availability by ‘priming’ surrounding soil microbes with recent plant C? To tackle this question, it is necessary to understand mechanisms of C and nutrient exchange between plant roots, mycorrhizal fungi, and soil microbes. We use nano-scale secondary ion mass spectrometry (NanoSIMS) to visualize <sup>13</sup>C and <sup>15</sup>N flow across the plant-fungus interface within mycorrhizal roots at the subcellular level. We further traced *in situ* flows of photoassimilated <sup>13</sup>CO<sub>2</sub> from wheat (*Triticum aestivum*) through both root and arbuscular mycorrhizal pathways into associated soil microbial communities using <sup>13</sup>C phospholipid fatty acid analysis (<sup>13</sup>C-PLFAs). <sup>15</sup>NH<sub>4</sub> was added to either root- or hyphae-associated soil to elucidate whether changing soil N availability affects belowground C transfer in the short-term. Four hours after the start of <sup>13</sup>CO<sub>2</sub> labeling, 13% of plant photoassimilated C was allocated to roots and soil microbes. NanoSIMS analysis revealed that, within roots, <sup>13</sup>C was almost exclusively located in the vascular bundle and in mycorrhizal intraradical hyphae. <sup>13</sup>C-PLFAs showed that different microbial groups utilized recent plant C in root- and hyphae-associated soil. The addition of NH<sub>4</sub> to either root- or hyphae-associated soil significantly increased <sup>13</sup>C in mycorrhizal biomarkers. Our results suggest that mycorrhizal hyphae may be an important pathway for the delivery of recent photosynthates to soil microbial communities. Plants may be able to rapidly respond to changing soil nitrogen availability along the hyphal network by short-time adjustment of C transfer to mycorrhizal intraradical hyphae. Based on our results, we speculate that hyphal exudations may play a well-defined role for the priming effects of microbial decomposition.

### PS 1-48 Early effect of host genotype, soil moisture, and soil pollution on mycorrhizal colonization of poplar roots

**KARLIŃSKI, L.**<sup>1</sup>, M. Rudawska<sup>1</sup> and T. Leski<sup>1</sup>

<sup>1</sup>Institute of Dendrology Polish Academy of Sciences, ul. Parkowa 5, 62-035 Kórnik, Poland, leszekk@man.poznan.pl.

**Abstract:** Poplars (*Populus*) are recognized as fast-growing tree species with substantial commercial importance, planted in marginal agricultural lands and abandoned farmlands, often used in reforestation programs of riparian areas, and used in the reclamation of polluted industrial regions. In natural conditions, *Populus* is known to form both ectomycorrhizal (ECM) and arbuscular mycorrhizal (AM) associations, and this dual colonization is an important factor in poplar management. The objectives of the presented studies were to analyze the impact of poplar genotype, soil moisture, and soil origin on ECM and AM colonization of roots. Seedlings of four different clones (originated from cuttings) were grown for six months in pot cultures filled with soils from polluted and unpolluted poplar stands. Pots were watered to 10% and 50% soil moisture. All poplars were colonized by ECM (0.01-5.3%) and AM fungi (0.8-62.2%). Multifactor



analysis of variance revealed a significant effect of soil moisture, soil pollution, and host genotype on the colonization of poplar roots by ECM and AM fungi. Soil moisture was the strongest factor positively stimulating ECM colonization of roots, while AM colonization was the most negatively impacted by trace metal soil pollution. Host genotype significantly differentiated ECM and AM colonization in both soil moisture treatments and at individual polluted/unpolluted soils. The highest ECM colonization was found in the fast growing clone NE42 in the 50% soil moisture treatment, irrespective of soil pollution. In contrast to ECM colonization level, species richness of ECM fungi was not influenced by soil moisture. Furthermore, biometric parameters (biomass, length, volume, etc.) of roots were modified by poplar genotype and soil moisture. In conclusion, this study suggests the contribution of host genotype and soil conditions in establishing mycorrhizal associations in the early stage of poplar growth, and indicates the need for further research in the poplar selection program.

#### SY 4-4 Ectomycorrhizal fungi mediate transgenerational cascades in beetle-killed pine forests

**KARST, J.**<sup>1,2</sup>, N. Erbilgin<sup>1</sup>, G.J. Pec<sup>2</sup>, P.W.Cigan<sup>1,2</sup>, A. Narjar<sup>1</sup>, S.W. Simard<sup>3</sup> and J. Cahill, Jr.<sup>2</sup>

<sup>1</sup>Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada T6G 2E3, justine.karst@ualberta.ca; <sup>2</sup>Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9; <sup>3</sup>Department of Forest and Conservation Sciences, University of British Columbia, Vancouver, British Columbia V6T 1Z4.

**Abstract:** Forest die-off caused by mountain pine beetle (*Dendroctonus ponderosae*) is rapidly transforming western North American landscapes. We studied cascading effects of this insect outbreak on fungal diversity and function, stand biogeochemistry, and forest regeneration. We found a reduction in the abundance and diversity of ectomycorrhizal fungi occurring above and belowground, coupled with a variety of changes in stand conditions linked to the death of the dominant canopy species, lodgepole pine (*Pinus contorta*). Here, I will demonstrate that shifts in the community composition of ectomycorrhizal fungi caused by beetle-induced mortality of mature trees have surprisingly far-reaching consequences for the next generation of pine seedlings. To demonstrate transgenerational cascades on pine seedlings, we tested the effects of fungal inoculum origin (beetle-killed or undisturbed stands), light level, and litter (origin and presence) on seedling secondary chemistry and growth in a greenhouse. Abundance and richness of monoterpenes in particular, are critical for defense against insect and pathogen attack as well as mediating complex plant-insect interactions. We also tracked survival of seedlings over two growing seasons in the same stands from which fungi and litter was collected. In agreement with our previous research, we found that fungal communities in potted field soils differed by inoculum origin. Moreover, seedlings grown with fungi collected from beetle-killed stands had lower monoterpene concentrations and fewer monoterpene compounds present compared with seedlings grown with fungi collected from undisturbed stands. Seedling survival in the field was lower in beetle-killed than undisturbed stands. Taken together, our results demonstrate that seedlings colonized by fungi from beetle-killed stands express defense characteristics of stressed trees, suggesting they may be prone to successful insect attacks. The legacy of the mountain pine beetle extends far beyond a single cohort of trees; transgenerational cascades influence subsequent generations likely through disrupted belowground mutualisms.

#### PS 3-35 Mycorrhizal fungi improve resistance to *Fusarium subglutinans* f. sp. *ananas* in micropropagation-derived pineapple plantlets

**KASUYA, M.C.M.**<sup>1</sup>, B.C. Moreira<sup>1</sup>, P. Prates Júnior<sup>1</sup>, T.C. Jordão<sup>1</sup>, S.L. Sturmer<sup>2</sup> and L.C.C. Salomão<sup>3</sup>

<sup>1</sup>Universidade Federal de Viçosa, Departamento de Microbiologia/BIOAGRO, Viçosa, Minas Gerais, 36579-900, Brazil, mkasuya@ufv.br; <sup>2</sup>Fundação Universidade Regional de Blumenau, Departamento de Ciências Naturais, Blumenau, Santa Catarina, 89012-900; <sup>3</sup>Universidade Federal de Viçosa, Departamento de fitotecnia, Viçosa, Minas Gerais, 36579-900, Brazil.

**Abstract:** Pineapple has great economic importance for various tropical countries. *Fusarium subglutinans* f. sp. *ananas* is the agent of a major disease, which may reduce fruit production 30-40% and approximately 20% loss of propagative material. Arbuscular mycorrhizal fungi (AMF) and *Piriformospora indica* are known as growth-promoting and biological control agents in plants, and they also aid micropropagated plants to better tolerate the acclimatization by alleviating the stressful conditions. So, the effect of inoculation with AMF and *P. indica* on inducing antioxidant enzyme activity



in plantlets of pineapple 'Imperial' (fusariosis-resistant) and 'Pérola' (fusariosis-susceptible) in the presence of *F. subglutinans* f. sp. *ananas* was investigated to evaluate the induction of plant resistance to the pathogen. The experiment was a completely randomized design in factorial arrangement (2x5x2), comprising two cultivars, with or without mycorrhizal fungal (MF) inoculation (*Claroideoglomus etunicatum*, *Rhizophagus clarus*, *P. indica*, a mixture of all the fungi (Mix), and the control with absence MF), and also with or without applying *F. subglutinans* f. sp. *ananas* conidia, with four replicates. Mycorrhizal colonization and activities of superoxide dismutase (SOD), catalase (CAT) and glutathione reductase (GR) were evaluated. Inoculation with MF or the pathogen affected antioxidant enzyme activity in the shoot and root system. MF increased the activities of SOD, CAT and GR, indicating that MF inoculation may increase resistance to pathogen attack. Additionally, mycorrhized plantlets developed better than the control even in the presence of *F. subglutinans* f. sp. *ananas*. MF can induce systemic resistance and mycorrhizal association is a potential strategy for managing this crop. The aim is to explore biological control as an alternative to reduce environmental and health impacts by decreasing the use of fungicides.

#### PS 4-70 Nitrogen acquisition by ectomycorrhiza

KAUR, A.<sup>1</sup>

<sup>1</sup>Biodiversity and Climate Change Division, Indian Council of Forestry Research and Education, Dehradun, India, ajeetkaur2000@yahoo.com.

**Abstract:** Soil nitrogen normally exceeds plant nitrogen by many times but only a small fraction of total soil nitrogen is available to plants at any given time as most of it is sequestered in organic compounds. A very small fraction (3-7%) gets converted into accessible inorganic forms (nitrate and ammonium) after mineralization. Low availability of nitrogen is a characteristic feature of many soil ecosystems dominated by ectomycorrhizal plants, better equipped to compete with decomposers and nitrifying bacteria for efficient uptake and recycling of nitrogen. It is now believed that ectomycorrhizae (ECM) help plants acquire nitrogen through different pathways *i.e.* fixation of atmospheric elemental nitrogen and acquisition of organic and inorganic (mineral) forms from soil. Significant nitrogenase activity (acetylene reduction activity) has been estimated in ectomycorrhizae *viz.* *Laccaria laccata*, *Suillus breviceps*, *Pisolithus tinctorius*, *Cenococcum geophilum*, *Rhizopogon luteolus*, and *Thelephora terrestris* in pure culture. Significant activity was also reported in *Suillus tomentosus* forming tuberculate ectomycorrhizae with *Pinus contorta* and in the mycorrhizal systems of *P. caribaea*, *P. patula*, and *P. radiata*. Nif genes have been detected in pine roots colonizing ectomycorrhizae *Suillus variegatus* and *Tomentellopsis submollis*. Another ectomycorrhiza, *Laccaria bicolor* has been shown to possess genetic potential for both mineral and organic nitrogen compound utilization. ECM fungi help in mineral weathering and mobilization of nitrogen (and other nutrients) from organic complexes by secreting enzymes such as chitinases, phosphatases and proteases extracellularly and thereby, allow the organic residues to be tapped directly for nutrients. The ability of ECM fungal hyphae to exploit resources is far greater than that of roots due to their innate physiological and morphological plasticity, extended (by 100 fold or more) effective root length and ability to reach into smaller pores than roots can.

#### PS 3-3 Root and arbuscular mycorrhizal exudation under different global change scenarios

KAZANSKI, C.E.<sup>1</sup>, S.E. Hobbie<sup>1</sup> and P.B. Reich<sup>2</sup>

<sup>1</sup>Department of Ecology, Evolution, and Behavior, University of Minnesota-Twin Cities, St. Paul, MN 55108 USA, ckazansk@umn.edu; <sup>2</sup>Department of Forest Resources, University of Minnesota-Twin Cities, St. Paul, MN 55108 USA.

**Abstract:** In addition to their influences on plant growth, arbuscular mycorrhizae (AM) also add to soil carbon (C) through their own growth and turnover. However, whether AM release soluble C into the soil (*i.e.*, exudation), as has been shown for roots and ectomycorrhizae, is poorly understood and could represent an important pathway for inputs of C to soil. Because AM could increase in abundance under elevated atmospheric CO<sub>2</sub> (eCO<sub>2</sub>), particularly with low nitrogen (N) availability, it is important to understand this potential pathway of C. Our objectives were to test 1) whether AM contribute to exudation and 2) whether roots and AM hyphae release more exudates at eCO<sub>2</sub> and low N (*i.e.*, when plants are especially nutrient-limited) compared to conditions when plants are less nutrient-limited. We conducted a pot study within the Biodiversity, CO<sub>2</sub> and N Experiment (BioCON) at the Cedar Creek Ecosystem Science Reserve in

Minnesota. Briefly, plants were grown from seed with or without an AM inoculum in sterilized sand and exposed to a full factorial of CO<sub>2</sub> and N treatments. Exudation was measured after one growing season. Exudate samples were analyzed for DOC, and plants were harvested to assess root and shoot biomass. After accounting for shoot biomass, plants with AM added produced significantly higher DOC than non-inoculated controls (ANCOVA,  $P < 0.05$ ), suggesting AM increase exudation and C release into soil. There was no effect of eCO<sub>2</sub>, N, or their interaction on shoot biomass or DOC content, despite other work from BioCON showing effects of eCO<sub>2</sub>, N, and their interaction on plant growth. Overall, this work suggests that AM contribute to soil C inputs via exudation. More work is needed to determine whether the effect is via an AM-induced increase in root exudate production or from AM exudation.

#### PS 4-71 Survey of ericoid mycorrhizae in the Pacific Northwest

KELLER-PEARSON, M.<sup>1,2</sup> and S.M. Schwab<sup>2</sup>

<sup>1</sup>Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI 53706 USA, michelle.keller-pearson@wisc.edu; <sup>2</sup>Department of Biology, Eastern Washington University, Cheney, WA 99004 USA.

**Abstract:** Most land plants form symbiotic relationships with mycorrhizal fungi. Ericoid mycorrhizae (ERM) are a group of highly specialized fungi that grow in symbiosis with ericaceous plants, which include wild huckleberry (*Vaccinium* spp.). Huckleberries have substantial market value, despite requiring labor-intensive wild collection. Demand for huckleberries is great, yet they remain non-domesticated. Huckleberries have potential to be a significant commercial crop but have yet to be successfully cultivated. Growing at high elevations in soils with exceptionally low pH (3-5) and high in iron and aluminum, huckleberries thrive in conditions toxic to many plants. ERM species are thought to mitigate some of the abiotic factors affecting plants, including drought, soil acidity, and heavy metal concentrations. The ERM species associated with wild huckleberry species are mostly unknown, and a better understanding of these fungi may contribute to huckleberry's domestication. To characterize the fungal associates of huckleberries, roots were collected from various huckleberry species at sites in Eastern Washington and North Idaho, and fungi were isolated and described. ERM fungi were present in all roots and differed by collection locations and host species.

#### LT 4-9 Guild-specific links between soil fungal diversity and plant phylogenetic diversity in a field-based tree experiment

Nguyen, N.H.<sup>1</sup>, L. Williams<sup>2</sup>, J.B. Vincent<sup>1</sup>, J. Cavender-Bares<sup>2</sup>, P.B. Reich<sup>3</sup> and P.G. KENNEDY<sup>1,2</sup>

<sup>1</sup>Department of Plant Biology, University of Minnesota; Department of Ecology, Evolution, and Behavior, University of Minnesota, kennedyp@umn.edu; <sup>3</sup>Department of Forest Resources, University of Minnesota, 1445 Gortner Ave. St. Paul, MN 55108.

**Abstract:** Exploring the link between above- and belowground biodiversity has been a major theme of recent ecological research, due in large part to the increasingly well-recognized role that soil microorganisms play in driving plant community processes. In this study, we utilized a field-based tree experiment in Minnesota, USA to assess the effect of changes in plant community richness and phylogenetic diversity on the richness and composition of both ectomycorrhizal (ECM) and saprotrophic fungal communities. We found that ECM fungal species richness was significantly positively influenced by both increasing plant phylogenetic diversity, while saprotrophic fungal species richness was affected by plant leaf nitrogen content and specific root length. Although the species composition of ECM and saprotrophic fungal communities changed in response to changes in plant species composition, the effect was much stronger for ECM fungi. In addition, ECM but not saprotrophic fungal species composition was significantly influenced by both plant phylum (angiosperm, gymnosperm, both) and origin (Europe, North America, both). The increasing ECM fungal richness associated with increasing plant phylogenetic diversity was driven by the combined presence of ECM fungal specialists in plots with both gymnosperm and angiosperm hosts. Similarly, the significant effect of plant origin of ECM composition appeared to be caused by ECM species specialized on hosts from different geographic origin. Taken together, this study indicates that aboveground effects on soil fungal communities are highly guild-specific and provides the first experimental-based results demonstrating a strong positive link between ECM fungal richness and composition and aboveground plant phylogenetic diversity.

## CS 3-1 The early evolution of roots and soils

KENRICK, P.<sup>1</sup>, C. Strullu-Derrien<sup>1,2</sup> and R. Mitchell<sup>1</sup>

<sup>1</sup>Department of Earth Sciences, The Natural History Museum, Cromwell Road, London SW7 5BD, United Kingdom, p.kenrick@nhm.ac.uk; <sup>2</sup>UMR 1136, Interactions Arbres-Microorganismes, Labex ARBRE, INRA-Nancy, 54280 Champenoux, France.

**Abstract:** Evidence from fossils and living plants demonstrate that roots evolved on land, that they were an early innovation of plant life, and that they were a prerequisite for the evolution of trees. The fossil record of plants documents a continuum of variation in the evolution of rooting systems that began with simple rhizoid-bearing stems and developed over a period of 40 million years into a broad range of complex multicellular organs specialised in anchorage and nutrient acquisition. Here, we review this fossil evidence prior to the evolution of forest ecosystems. Rooting systems evolved in a piecemeal fashion independently in several different clades of plants, rapidly acquiring and extending functionality and complexity. Mycorrhizal associations were an integral early development evolving from a general systemic relationship within photosynthetic aerial systems to a root specific role in the vascular plants. Prior to the evolution of forests, plants had evolved organ systems with multiple adaptations to rooting functions, including physiological adaptations to growth in soils, the capacity to absorb and translocate nutrients, anatomical modifications of the epidermis, and highly integrated symbiotic relations with fungi. Sites of exceptional preservation, such as the 407 million year old Rhynie chert, have the capacity to yield information at a cellular, and even subcellular level, on the infection process and the plants' responses. These early rooting systems evolved in the context of ecosystems that are thought to have had many of the characteristics of modern cryptogamic ground covers. In addition to investigating the evolution of plant-fungal symbioses, we are seeking to develop approaches to understand their broader impact on the early development of soil ecosystems.

## PS 1-18 Arbuscular and ectomycorrhizal root colonization in soil exposed to extreme freezing temperatures

KILPELÄINEN, J.<sup>1</sup>, M. Vestberg<sup>2</sup>, T. Repo<sup>3</sup> and T. Lehto<sup>1</sup>

<sup>1</sup>School of Forest Sciences, University of Eastern Finland, 80100 Joensuu, Finland, jouni.kilpelainen@uef.fi; <sup>2</sup>Green Technology, Natural Resources Institute Finland (Luke), 41330 Vihtavuori, Finland; <sup>3</sup>Natural resources and Bioproduction, Natural Resources Institute Finland (Luke), 80100 Joensuu, Finland.

**Abstract:** The widely accepted theory by D.J. Read explains the dominance of mycorrhiza types in global vegetation zones in terms of the most limiting nutrient, which is determined by climatic factors – not as much directly, but through soil formation in each zone. We suggest that temperature and water have also direct roles in the success of arbuscular mycorrhizas (AM) and ectomycorrhizas (EM): we suggest that AM are more tolerant to drought than EM, and EM are more tolerant to low temperatures and frost. Here, the focus is in the tolerance of mycorrhizal propagules in soil to very low temperatures. We collected and homogenized surface soil from sites with diverse EM and AM vegetation in Eastern Finland in late autumn. Soil batches were exposed to a range of temperatures: +5°C (control), -12°C, -25°C, -48°C and -130°C. Seeds of silver birch (*Betula pendula*), grey alder (*Alnus incana*) or white clover (*Trifolium repens*) were sown in the treated soils. Plants were grown in similar, favourable conditions in a growth room. Mycorrhizal colonization rates were determined after 11 weeks. EM were not affected by the treatments significantly in either birch or alder. Regarding AM in clover, arbuscule formation was not significantly affected, but vesicle formation was reduced as well as the occurrence of hyphae and spores. The occurrence of AM hyphae was reduced also in alder. The growth and nutrition of the plants were not strongly affected by the treatments. In conclusion, EM propagules were able to survive even the lowest temperature without any reduction in the ability to colonize roots, as expected. The reduced vesicle, spore and hypha formation by AM may be either due to delayed colonization because of mortality of vegetative mycelium, or the survival of only some species.

## PS 2-26 Wood ash, liming, and pH effects on ectomycorrhizal fungal abundance, diversity, and community composition

KJØLLER, R.<sup>1</sup>, C.C. Paredes<sup>1</sup>, H. Wallander<sup>2</sup> and K. Clemmensen<sup>3</sup>

<sup>1</sup>Terrestrial Ecology Section, University of Copenhagen, Denmark, rasmusk@bio.ku.dk; <sup>2</sup>Department of Microbial Ecology, Lund University, Sweden; <sup>3</sup>Forest Mycology and Plant Pathology, SLU, Sweden.

**Abstract:** Liming or wood ash amendments are common practices to counteract acidification in forests. Additionally, wood ash also returns some of the nutrients removed after harvest or clear cutting. There is a concern that wood ash may also introduce toxic elements such as Cd, Ni, and Cr. Here, we review and synthesize previous work on liming and wood ash effects on ectomycorrhizal fungal abundance, diversity, and community composition. We show that while species richness is most often not influenced, community composition, in contrast, is changed. The community changes are, to some extent, predictable with certain genera decreasing (e.g., *Lactarius* and *Russula*) or increasing (e.g., *Tuber* and *Amphinema*) in abundance with treatment. Whether the changes are caused directly, by increased pH, or indirectly, by improved N availability because of the pH change, is discussed. Finally, we report new results showing how wood ash influences ectomycorrhizal fungal mycelial production in soil and investigate if elemental composition of mycelia and fruiting bodies differs after amendment, with a special focus on Cd.

## PS 4-15 Contribution of legumes to the production of sustainable forage and plant nitrogen and to increase soil AM fungal diversity in grassland communities

KLABI, R.<sup>1,3</sup>, H.B. Terrence<sup>1</sup>, C. Hamel<sup>2</sup>, A. Iwaasa<sup>2</sup>, M. Schellenberg<sup>2</sup>, A. Raies<sup>3</sup> and M. St-Arnaud<sup>1</sup>

<sup>1</sup>Biodiversity Centre, Institut de recherche en biologie végétale, Université de Montréal and Jardin botanique de Montréal, 4101 rue Sherbrooke est, Montreal, Québec H1X 2B2 Canada, rim.klabi@umontreal.com; <sup>2</sup>Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-food Canada, P.O. Box 1030, Airport Road, Swift Current, Saskatchewan S9H 3X2 Canada; <sup>3</sup>Département de Sciences Biologique, Faculté des Sciences de Tunis, Université Tunis El-Manar, Campus universitaire, Tunis 1060, Tunisia.

**Abstract:** The addition of legumes and phosphorus to pastures seeded with native grasses are important for increasing soil fertility and forage production. However, these practices may also shape the structure and diversity of soil fungal communities and as a result plant fungal interactions. The aim of this study was to demonstrate the effect of legumes (*Medicago sativa* or *Dalea purpurea*) and soil P fertility (addition of 0 or 200 P<sub>2</sub>O<sub>5</sub> kg ha<sup>-1</sup> at seeding) on the forage yield and nutrient content of native grasses mixes or the introduced grass *Bromus biebersteinii* and on the structure and diversity of the soil AM fungal community, and to determine the relationship between AM fungal diversity and forage and nutrients yields. Plant harvests were performed twice at the end of the growing season, over two years 2008 and 2009, and once during the vegetative growth phase, in July 2009. We used 454-pyrosequencing to analyse soil fungal communities over the two years. Our results shown that the mixtures containing *M. sativa* produced forage yields that were similar to, or higher than the native grasses grown in the absence of a legume. In addition, *M. sativa* increased the nitrogen yield and concentration of the entire plant mixture. This legume also increased AM fungal diversity in the mixture containing native grass mixes and this shift was positively correlated with the productivity and nitrogen nutrition of the entire mixture, but only at the vegetative growth of 2009. Our study shown that *M. sativa* contrary to *D. purpurea*, augments or sustains the yield and nitrogen yield of plant mixtures containing the native grasses mixes or *B. biebersteinii*. Moreover, the inclusion of *M. sativa* within native grass mixes contributes to promote functionally beneficial AM fungi taxa that were involved in plant productivity and nitrogen nutrition.

## LT 1-3 Diversity of pleosporalean dark septate endophytic (DSE) fungi of semiarid areas

**KNAPP, D.G.**<sup>1</sup>, P.J. Berek-Nagy<sup>1</sup>, P.W. Crous<sup>2</sup>, J.Z. Groenewald<sup>2</sup>, I. Imrefi<sup>1</sup>, G. Herczeg<sup>3</sup> and G.M. Kovács<sup>1</sup>

<sup>1</sup>Eötvös Loránd University, Institute of Biology, Department of Plant Biology, Hungary, knappdani@gmail.com; <sup>2</sup>CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT, Utrecht, The Netherlands; <sup>3</sup>Eötvös Loránd University, Institute of Biology, Department of Systematic Zoology and Ecology, Behavioural Ecology Group, Hungary.

**Abstract:** In addition to multiple mycorrhizal fungi, several endophytic fungi often colonize plant roots. Dark septate endophytes (DSEs) comprise a form-group of root colonizing fungi common in environments with strong abiotic stress, such as arid and semiarid ecosystems. DSEs are present in several ascomycetous orders; one of those is Pleosporales, to which the majority of root-associated fungal communities of semiarid areas belong. Although there is an increasing interest in DSEs, our knowledge on their function in ecosystems is still limited. During a compositional diversity study of the DSE community of semiarid sandy areas, three unidentified DSE lineages were found in the Pleosporales. Here we present the results of their formal description: they represent three new genera (*Aquilomyces*, *Flavomyces*, and *Darksidea*) with eight new species based on morphology and multilocus phylogenetic analyses. For functional diversity studies we used two of those species (*D. alpha* and *F. fulophazii*), and *Periconia macrospinosa*, another widespread pleosporalean DSE fungus. To characterize also intraspecific diversity eight isolates per species were studied and compared. Intraspecific variability was studied by means of DNA sequence data (ITS) and inter-simple sequence repeat analyses. The symbiotic characteristics of the isolates were studied by screening the effect on growth of *Zea mays*. Saprobiotic features were characterized by the growth rate on cultural medium. Enzymatic activities were evaluated by enzyme assays, and carbon source utilization by means of BioLog FF. Our results indicate a high functional diversity of these DSE fungi, which are distributed worldwide, as common members of root associated fungal communities in arid and semiarid grasslands.

## SY 2-2 The mycorrhizal genome initiative (MGI): exploring the transcriptomes of mycorrhizal fungi to understand the functioning of symbiosis

**KOHLER A.**<sup>1</sup>, C. Veneault-Fourrey<sup>1</sup>, E. Morin<sup>1</sup>, Y. Daguerre<sup>1</sup>, S. Wittulsky<sup>1</sup>, J. Ruytinx<sup>1</sup>, C. Murat<sup>1</sup>, J.M. Plett<sup>2</sup>, E. Lindquist<sup>3</sup>, K. Barry<sup>3</sup>, A. Kuo<sup>3</sup>, I.V. Grigoriev<sup>3</sup>, F. Martin<sup>1</sup> and the Mycorrhizal Genome Initiative Consortium

<sup>1</sup>INRA, UMR 1136 INRA-Université de Lorraine, Interactions Arbres/Microorganismes, Laboratoire d'Excellence ARBRE, INRA-Nancy, 54280 Champenoux, France, kohler@nancy.inra.fr; <sup>2</sup>Hawkesbury Institute for the Environment, University of Western Sydney, Richmond NSW 2753, Australia; <sup>3</sup>US DOE-JGI, Walnut Creek, CA 94598, United States.

**Abstract:** To better understand the evolutionary origin of mycorrhizal symbiosis and to elucidate the molecular mechanisms involved, the Joint Genome Institute and the Mycorrhizal Genome Initiative (MGI) started a large genome and transcriptome sequencing project including species from different taxa, phylogenetic clades, and symbiotic lifestyles (ectomycorrhiza, ericoid, and orchid mycorrhiza). The analysis of a dozen mycorrhizal transcriptomes revealed the involvement of both conserved and clade-specific genes. Induced are genes coding for the same functions but without orthology, like (often clade-specific) small-secreted proteins, transporters, redox metabolism, or carbohydrate active enzymes, suggesting convergent evolution. Of special interest for further functional analyses are mycorrhiza-induced small-secreted proteins (MiSSPs) that have been identified in all interactions studied so far. They are likely used to manipulate their hosts during colonization as it has been shown for *Laccaria bicolor* MiSSP7. This effector protein is able to control plant immunity by interacting with the *Populus* protein PtJAZ6 and to stabilize it from jasmonate-induced degradation.



#### LT 4-4 I'll scratch your back and you scratch mine: plant introductions as drivers and passengers of global ecology and geography of mycorrhizal fungi

KOHOUT, P.<sup>1,2,3</sup>, K. Štajerová<sup>2,3</sup>, M. Hejda<sup>2</sup>, R. Sudová<sup>2</sup>, Z. Sýkorová<sup>2</sup>, L. Tedersoo<sup>1</sup> and P. Pyšek<sup>2,3</sup>

<sup>1</sup>Institute of Ecology and Earth Sciences, University of Tartu, 50411 Tartu, Estonia, petr.kohout@natur.cuni.cz; <sup>2</sup>Institute of Botany, Academy of Sciences of the Czech Republic, 252 43 Průhonice, Czech Republic; <sup>3</sup>Faculty of Science, Charles University in Prague, 128 44 Prague 2, Czech Republic.

**Abstract:** Many plant species have been introduced to new habitats throughout the world, and some also spread and grow in abundance and extend beyond their original points of introduction. Plant species that spread extensively in their novel habitats are termed invasive. Many invasive plants affect populations of native species, resident communities and influence ecosystem properties. To effectively manage invasive plants, it is important to understand the mechanisms involved in the invasion process. Surprisingly, only a few studies considered that an introduced species might lack its specialized mutualists in the new environment, yet there is growing evidence that the absence of mutualists in the new range can be of the same importance as that of enemies. Despite the salient role of ubiquitous arbuscular mycorrhizal fungi (AMF) in plant interactions, studies exploring the role of such symbionts in invasiveness of non-native species and invasibility of communities are limited, in part because of limited understanding of AMF ecology and role in ecosystems. To better understand the role of AMF in plant invasions, we conducted a cross continental study focused on AMF community comparisons among invasive (*Cirsium arvense*, *Tanacetum vulgare*, and *Leucanthemum vulgare*) and indigenous plant species in invaded (USA: Wyoming, Montana, and Minnesota; Canada: Ontario) sites as well as comparisons of AMF communities of invasive species (the same as before) in their novel (USA and Canada) and native (Czech Republic, Poland, and Switzerland) sites. Pyrosequencing of ITS region of rDNA was used for characterisation of the AMF communities.

#### LT 1-13 Arbuscular mycorrhizas increase resource competition within a model plant community

KONVALINKOVÁ, T.<sup>1</sup>, H. Gryndlerová<sup>1</sup>, D. Püschel<sup>1,2</sup>, V. Procházková<sup>1</sup>, M. Gryndler<sup>1</sup> and J. Jansa<sup>1</sup>

<sup>1</sup>Laboratory of Fungal Biology, Institute of Microbiology, Czech Academy of Sciences, Prague, 14220 Czech Republic, konvalinkova@biomed.cas.cz; <sup>2</sup>Department of Mycorrhizal Symbioses, Institute of Botany, Czech Academy of Sciences, Průhonice, 25243 Czech Republic.

**Abstract:** Most natural plant communities encompass more than one closely interacting plant species. If different plant species are hosts of arbuscular mycorrhizal (AM) fungi they often share a common mycorrhizal network (CMN) due to the low specificity of the symbiosis. There is great and dynamic spatial heterogeneity in such systems with respect to the availability of resources such as light, water, and mineral nutrients. For example, plants sharing a CMN could be, at times, differentially shaded by other plants or exposed to grazing, spot contamination, or other types of stress influencing their potential inputs into shared AM mycelium. Does the mycorrhiza redistribute nutrient resources according to hard trading rules (where the richer get more), or does it relax competition by supporting the weaker partner? We tested this question by exposing two plant species (*Medicago truncatula* alone, *Allium porrum* alone, or both species together) to temporary shading. The shading was applied to one or both of species within a pot. We tracked P fluxes from the soil into the different plant species by using <sup>33</sup>P isotope labeling. Our results showed that the presence of mycorrhizal fungi increased the competition for resources between the two plant species, and that a strong reward mechanism was obviously at play causing dramatically more P to be supplied to a host with temporarily more available C resources. We thus found no support for socialism in the CMN in terms of redistribution of resources to the weaker partner. Instead, our results demonstrate that AM fungi, probably in their own interest, are able to distinguish and promote the better host within a plant community sharing the same rooting zone.

#### SY 4-5 Plants are expanding their range: does this affect their association with arbuscular mycorrhizal fungi?

KOOREM, K.<sup>1</sup>, O. Kostenko<sup>1</sup>, B. Snoek<sup>1</sup>, S. Geisen<sup>1</sup>, K.S. Ramirez<sup>1</sup>, R. Wilschut<sup>1</sup>, M.M. Freixa<sup>1</sup> and W.H. van der Putten<sup>1</sup>

<sup>1</sup>Netherlands Institute of Ecology, Droevendaalsesteeg 10, 6708 PB Wageningen, The Netherlands, k.koorem@nioo.knaw.nl.

**Abstract:** Current climate warming has brought about range expansion of plants, animals, and microorganisms to higher altitudes and latitudes. Range shifts of plant species are well documented, but we know little about the ecological consequences of this expansion. As plants disperse faster than soil organisms, range-expanding plants may in their new range be released from their natural enemies, but also from symbionts and decomposer organisms. To test this expectation, we characterized fungal communities (targeting the ITS region) associated to range expanding plant species (*Centaurea stoebe*, *Solanum nigrum*, *Rorippa sylvestris*) in their original and new range. We detected differences in fungal community composition associated to these plants in the two ranges. Fungal community dynamics, focusing on arbuscular mycorrhizal fungi, will be discussed in the presentation. With time, soil organisms may also disperse over long distances and expand their ranges but the effects of this possible event has never been tested. We established a greenhouse experiment to examine how range expansion of soil organisms influences the establishment of range expanding plants in the new range. Eight plant individuals, consisting of plants from distinctive ecological strategies (range-expanding plants, native plant species, and their combination), were grown in mesocosms, which were inoculated with different soil communities (sterile soil, soil community from original range, new range, or a mixture of original and new range). Our results show that the range-expanding plant species, which do not have closely related plant species in native plant communities, suppress the growth of native plants, whereas range-expanders with closely related species in the native plant community have no negative effect. Interestingly, the effect of soil communities differed also between these two types of range-expanding plants, being clearly distinctive between plants that commonly form arbuscular mycorrhizas and plants that do not.

#### LT 2-6 Diminished successional pathway or novel trajectory? Boreal ectomycorrhizal fungal communities 20 years after harvest-related disturbances of compaction and organic matter removal

KRANABETTER, J.M.<sup>1</sup>

<sup>1</sup>B.C. Ministry of Forests, Lands and Natural Resource Operations, Victoria, British Columbia, V8Z 5J3 Canada, marty.kranabetter@gov.bc.ca.

**Abstract:** Ectomycorrhizal fungal (EMF) communities are significantly altered by tree mortality and undergo community succession over the decades following logging. However, other harvesting-related disturbances to soils, such as compaction and organic matter removal, may compound upon the initial effects of logging and have progressively negative impacts on EMF community recovery. Community composition and species diversity of EMF might be diminished because of the severity of these combined soil disturbances, leading to losses in ecological integrity. Alternatively, the altered habitat might create novel trajectories for EMF succession, leading to new but equally viable EMF communities. I tested these questions regarding ecosystem recovery and resilience by sampling EMF roots of 20 year-old lodgepole pine (*Pinus contorta*) and white spruce (*Picea glauca*) trees across three Long-term Soil Productivity Study sites in the northern interior of British Columbia, Canada. The study has a factorial design, with three levels of organic matter removal (bole-only harvest, whole-tree harvest, and forest floor removal) combined with three levels of soil compaction (no compaction, light compaction, and heavy compaction). All roots were colonized by EMF with almost 50 species detected (via Sanger sequencing) from the two hosts. Moderate soil disturbances (compaction with forest floor retained) primarily led to differences in EMF community composition, suggesting some degree of novel trajectory in EMF succession. The most negatively impacted soils (compaction with forest floor removed) had more notable reductions in species richness and diversity, with few unique taxa, suggesting a loss in ecological integrity. The removal of forest floors was a primary factor in this response but may represent only a successional lag if the diminished EMF community recovers over time with organic matter accumulation. EMF communities were generally sensitive to harvest-related soil disturbances, but the large species pool within these boreal landscapes likely contributes to considerable resilience for the ecosystem.

## PS 4-16 Host tree genetics influences rhizosphere total fungal and ectomycorrhizal fungal communities in pinyon pine

KROHN, A.L.<sup>1</sup> and C.A. Gehring<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA, alk224@nau.edu;

<sup>2</sup>Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, Arizona 86011 USA.

**Abstract:** Populations of pinyon pine (*Pinus edulis*) have experienced high mortality during drought events in the US southwest, and many models predict a significant range contraction in this species. However, a northern Arizona population of *P. edulis* shows dramatic variation in drought tolerance that has been associated with particular communities of root-associated ectomycorrhizal (EM) fungal communities. The relationship between host genetics, drought tolerance, and EM fungi has yet to be rigorously explored in the field using modern molecular tools. We used high throughput ITS2 amplicon sequencing of the rhizosphere to examine total fungal and EM fungal communities among pinyon pine seedlings in a common garden derived from drought tolerant and drought intolerant maternal trees. For both total fungal and EM fungal communities, we observed differences in beta diversity but not alpha diversity between the rhizospheres of seedlings of drought tolerant and intolerant trees. EM fungi were major constituents of the total fungal community, with taxa identified in proportions similar to data collected using more traditional methods that targeted colonized roots. A non-mycorrhizal genus, *Penicillium*, was the most abundant taxon overall and had not previously been observed in this system. Dominant EM fungal genera included members of *Geopora*, *Rhizopogon*, and *Tricholoma*. *Cenococcum* and *Astraeus*, taxa known to participate in EM associations but not previously found within this system, were also observed. The ectomycorrhizal fungal communities associated with the offspring of drought tolerant trees possessed higher proportions of *Geopora* and *Rhizopogon* and decreased proportions of members of the *Thelephoraceae*. Our results demonstrate that pinyon pine rhizosphere fungal community beta diversity is under partial genetic control and provide the most detailed view to date of the total rhizosphere fungal communities associated with this drought-adapted population.

## PS 1-19 Arbuscular mycorrhiza fungal community succession and seasonality on post-mining sites

KRÜGER, C.<sup>1</sup>, M. Janoušková<sup>1</sup>, D. Püschel<sup>1</sup>, J. Frouz<sup>1</sup> and J. Rydlová<sup>1</sup>

<sup>1</sup>Institute of Botany, Academy of Sciences of the Czech Republic, 25243 Průhonice, Czech Republic, claudia.kruger@ibot.cas.cz.

**Abstract:** Post-mining areas offer excellent opportunities for the study of primary succession of vegetation, soil and microbial communities. We investigated communities of arbuscular mycorrhizal fungi (AMF) at two chronosequences of 12, 20, 30 and 50 year old sites (3 sites per age) at a spoil bank of the Sokolov brown-coal mining district in the Czech Republic. One chronosequence consisted of sites left to spontaneous succession, the second chronosequence comprised sites reclaimed by plantings of *Alnus* trees. The AMF communities were described by pyrosequencing of an rDNA fragment in field-collected root samples of *Calamagrostis epigejos*, the most frequent AMF host plant along both chronosequences and two dual host trees - *Salix caprea* at the spontaneous succession sites and *Alnus glutinosa* at the reclaimed sites. The sites left to spontaneous succession had higher AMF diversity than the reclaimed sites, especially at the youngest site age. For example, several *Diversispora* and *Rhizophagus* spp. were found at the spontaneous succession sites, sharing solely one species per genus with the reclaimed sites. The dynamics of diversity along the chronosequences depended not only on the reclamation regime but also on the season in which roots were sampled. Thus, our results show that a specific seasonality is an important characteristic of a successional stage of AMF community.

KRÜGER, M.<sup>1,2</sup>, M. Janouskova<sup>1</sup>, K. Krak<sup>1</sup> and H. Storchova<sup>2</sup>

<sup>1</sup>Institute of Botany, The Czech Academy of Sciences, Zamek 1, 25243 Průhonice, Czech Republic, manuela.kruger@ibot.cas.cz; <sup>2</sup>Institute of Experimental Botany, The Czech Academy of Sciences, Rozvojová 313, 16502 Lyosaje, Prague, Czech Republic.

**Abstract:** Arbuscular mycorrhizal (AM) fungi are key drivers in ecosystems as about 80% of all land plants form AM symbioses. Despite their importance, their biology is still enigmatic. There is ongoing progress in obtaining the complete genome of the AM model fungus *Rhizophagus irregularis* DAOM197198, which resulted in a draft genome of this fungus with about 101 megabases (Mb) obtained from *in vitro* cultures. Recently, genome data of single nuclei of DAOM197198 were published, enlarging the knowledge of the gene repertoire of this AM fungus resulting in an even more comprehensive draft genome. In our study, we used the combined genome datasets for DAOM197198 as a reference genome for genome-guided mapping with the RNA-Seq assembler, Trinity, for the analyses of differential expressed genes within roots of *Medicago truncatula*, either inoculated with *R. irregularis* DAOM197198, *Claroideoglomus claroideum*, or both AM fungi. Expression analyses and subsequent gene annotation was done with the Trinotate and PASA pipeline to obtain a comprehensive transcriptome dataset. This approach was used to address the question of which symbiotic genes are expressed in AM fungi, with one AM fungus or two AM fungi, and how competition during root colonisation might affect their gene expression. The resulting data will advance our knowledge about the genes expressed in AM fungi for the model fungus *R. irregularis* DAOM197198 and the non-model AM fungus *C. claroideoglomus*.

#### LT 4-10 Community patterns of arbuscular mycorrhizal fungal spores in the Serengeti

KRZNARICH, S.<sup>1</sup>, A. Antoninka<sup>2</sup>, B.M. Stevens<sup>3</sup> and N.C. Johnson<sup>1,3</sup>

<sup>1</sup>School of Earth Sciences and Environmental Sustainability, Northern Arizona University, Flagstaff, Arizona 86011 USA, slkrznarich@gmail.com; <sup>2</sup>School of Forestry, Northern Arizona University, Flagstaff, Arizona 86011 USA; <sup>3</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA.

**Abstract:** Arbuscular mycorrhizal (AM) fungi are abundant in natural grasslands, yet the factors that structure their communities are not well understood. We studied the influence of soil properties, precipitation, and grazing on the abundance and diversity of AM fungal spores in the Serengeti grassland in Tanzania. Spores were extracted from soils collected from 42 experimental plots at seven sites that form antiparallel gradients of soil phosphorus and precipitation. In 1999, half of the experimental plots were fenced to eliminate grazing by large herbivores. Spores were analyzed in the dry season (2006) and the wet season (2012). An exceptionally high density of spores was observed, ranging from 326 to 1,757 spores/g dry soil in the wet season and 315 to 742 spores/g dry soil in the dry season. To our knowledge, these are the highest spore densities ever reported from any natural ecosystem. Spore diversity was very high in both seasons (64 species/morphotypes). Five different morphotypes of auxiliary cells of Gigasporaceae were also observed. Interestingly, grazing only affected the abundance of Glomeraceae spores, with more spores in fenced areas. Precipitation, soil phosphorus, pH, texture, and organic matter were all predictors of spore community composition. For example, Acaulosporaceae spores were most abundant in coarse textured soils. Glomeraceae and Gigasporaceae spores were most common at the driest sites with high soil pH, phosphorus and organic matter. In contrast, the auxiliary cells of Gigasporaceae were most abundant in soils with low pH, phosphorus, and organic matter. This supports the hypothesis that auxiliary cells function as phosphorus storage structures in low phosphorus soils. These findings contribute to our knowledge of the environmental requirements of Glomeromycota and indicate that different families have different niche requirements. These discoveries help us to better understand the factors that structure the Serengeti grassland.

## PS 3-4 The plant cell wall, where sugar is transferred, filtrated, and absorbed by arbuscular mycorrhizal fungi

KUGA, Y.<sup>1</sup>, N. Sakamoto<sup>2</sup>, K. Nagata<sup>3</sup>, T.-D. Wu<sup>4,5</sup>, H. Yurimoto<sup>3</sup> and J.-L. Guerquin-Kern<sup>4,5</sup>

<sup>1</sup>Graduate School of Integrated Arts and Sciences, Hiroshima University, Higashihiroshima, Hiroshima 739-8521 Japan, ykuga@hiroshima-u.ac.jp; <sup>2</sup>Isotope Imaging Laboratory, Creative Research Institute, Hokkaido University, Sapporo 001-0021, Japan; <sup>3</sup>Department of Natural History Sciences, Hokkaido University, Sapporo 060-0810, Japan; <sup>4</sup>Institut Curie, Centre de Recherche, F-91405 Orsay, France; <sup>5</sup>INSERM, U1196; CNRS, UMR9187, F-91405 Orsay, France.

**Abstract:** Exchanges of carbon and inorganic elements define mycorrhizal mutualisms. Arbuscular mycorrhizal fungi (AMF) are obligate symbionts; colonization of plant roots is essential for obtaining carbon. Intraradical structures of Arum-type AMF are morphologically divided into intercellular hyphae, vesicles, and arbuscules. The objective of this study was to elucidate the site(s) of carbon transfer to AMF by imaging of a <sup>13</sup>C tracer at the subcellular level based on secondary ion mass spectrometry (SIMS). *Allium cepa* plants colonized by *Gigaspora margarita*, a species that does not produce vesicles, were labeled with <sup>13</sup>CO<sub>2</sub>. Shoot and root tissues were processed in the same way as conventional TEM samples. Isotope imaging of resin sections were then conducted by dynamic SIMS (IMS1270-SCAPS and TEM-nanoSIMS50), and ratio images of <sup>13</sup>C/<sup>12</sup>C (r13C) were produced. In shoot parenchyma cells, higher r13C than the natural ratio was found in chloroplasts, nuclei, and cell walls. r13C of cell walls was elevated in phloem, but not in xylem. In the roots, r13C of host structures were higher than those of the shoots. Fungal structures and host cytoplasm and nuclei associated with arbuscules showed higher r13C than that of host cell walls, except for xylem vessel walls. This study suggests that the plant cell wall may act as a platform for sugar transport. At the same time, vessel cell walls of roots seem to play a role as a filter to prevent backflow of sugar. AMF intercellular hyphae were appressed to the cell walls of intercellular spaces, whereas arbuscules are adjacent to the cell periphery. Together, these characteristics, suggest that intercellular hyphae absorb sugar directly from the cell wall, but arbuscules absorb sugar indirectly but more efficiently through host cytoplasm by contacting a wider area of the cell wall from inside the cell.

## PS 2-52 Arbutoid mycorrhizas of the genus *Cortinarius* from Costa Rica

KÜHDORF, K.<sup>1</sup>, B. Münzenberger<sup>1</sup>, D. Begerow<sup>2</sup>, J. Gómez-Laurito<sup>3</sup> and R.F. Hüttel<sup>4</sup>

<sup>1</sup>Institute of Landscape Biogeochemistry, Leibniz Centre for Agricultural Landscape Research (ZALF), 15374 Müncheberg, Germany, Katja.Kuehdorf@zalf.de; <sup>2</sup>AG Geobotany, Ruhr-University of Bochum, 44780 Bochum, Germany; <sup>3</sup>Escuela de Biología, University of Costa Rica, CP 11501-2060, San José, Costa Rica; <sup>4</sup>Chair of Soil Protection and Recultivation, Brandenburg University of Technology Cottbus-Senftenberg, 03013 Cottbus, Germany and German Research Centre of Geosciences Potsdam (GFZ), 14473 Potsdam, Germany.

**Abstract:** Arbutoid mycorrhizas of *Comarostaphylis arbutoides* (Ericaceae) from neotropical montane forests are rarely described. To date, only associations with the fungal species *Leccinum monticola*, *Leotia lubrica*, and *Sebacina* sp. are known from literature. The genus *Cortinarius* is one of the most species-rich ectomycorrhizal taxa with over 2000 assumed species. In this study two sampling sites in the Cordillera de Talamanca of Costa Rica were chosen, where *C. arbutoides* is endemic and grows together with *Quercus costaricensis*. Using a combined method of rDNA sequence analysis and morphotyping thirty-three sampled mycorrhizal systems of *Cortinarius* were assigned to the subgenera *Dermocybe*, *Lustrati*, *Phlegmacium*, and *Telamonia*. Specific plant primers were used to identify the host plant. Here, we describe four arbutoid morphotypes of *Dermocybe*, *Phlegmacium*, and *Telamonia* morphologically and anatomically and present the molecular phylogenetic data.



**PS 3-36 Effect of *Glomus fasciculatum* on antioxidant enzyme responses in tomato plants infested with root-knot nematode**

**KULKARNI, M.V.**<sup>1</sup> and M.P. Dudhane<sup>2</sup>

<sup>1</sup>Division of Biochemistry, Department of Chemistry, Savitribai Phule Pune University, Pune 411007, India, drmvkulkarni@gmail.com; <sup>2</sup>Department of Botany, Savitribai Phule Pune University, Pune 411007, India.

**Abstract:** Tomato (*Lycopersicon esculentum* Mill.) is one of the most important commercial and widely grown vegetable crops, which is often susceptible to attack by Root-Knot Nematode (RKN). The present study was undertaken in an attempt to resist RKN infestation and improve the survival and growth of tomato plants by using *Glomus fasciculatum* species reported to be resistant against RKN. The experimental strategy consisted of three controls including mycorrhizal and RKN (C, Gf, and RKN) and treatment including combination of mycorrhizal and RKN (Gf+RKN). Gall index per plant was significantly suppressed in *Glomus fasciculatum* treated plants after 30, 60 and 90 days of *Meloidogyne incognita* infestation. The percent increase in shoot peroxidase (POD) activity was more with Gf+Nm treatment, as compared to control plants, up to 118%, 129%, and 84% after 30, 60 and, 90 days of AM inoculation respectively. Percent increment in root superoxide dismutase (SOD) was up to 158%, 128%, and 113% in Gf+Nm treated plant after 30, 60 and 90 days of AM inoculation respectively. Also, proline content was significantly enhanced in Gf+Nm plants. AM colonization significantly increased antioxidant enzyme activities like SOD and POD activity in mycorrhizal tomato plants, as compared to non-AM inoculated plants, under RKN infestation, which could help protect the plants from the oxidative damage caused by biotic stress. Therefore, such mycorrhizal inoculants will have an application in tomato cultivation as a means of RKN resistance.

**PS 3-57 Examining the effect of an entomopathogenic fungus on the age demographic of Acrididae species**

**KUMAR, S.**<sup>1</sup> and R. Sultana<sup>1</sup>

<sup>1</sup>Department of Zoology, University of Sindh, Jamshoro, Pakistan, santoshsonu@hotmail.com.

**Abstract:** An important debate about how pathogens affects grasshopper species has been going on for the past few decades. For confirmation of this fact, an investigation has been carried out under laboratory conditions and many species of grasshoppers and locusts were directly inoculated with *Aspergillus*, an important bio-pesticide. During the present study, it was observed that the insect population response to disease may depend upon age demographic. Mostly the earlier developmental stages (i.e., 1<sup>st</sup> to 3<sup>rd</sup>) were found to be more susceptible to pathogen, and the possible reason might be due to inferior resistance of the nymphs. In contrast, other advanced stages (i.e., 4<sup>th</sup> onwards, including adults) were far less susceptible. Our study suggests that age demographics may need to be considered when predicting how grasshoppers species will response to disease.

**PS 3-16 The effect of soil fertility on fungal communities, enzyme activities, and soil carbon dynamics in unmanaged forests**

**KYIASHCHENKO, I.**<sup>1</sup>, K.E. Clemmensen<sup>2</sup>, E. Karlton<sup>1</sup> and B.D. Lindahl<sup>1</sup>

<sup>1</sup>Department of Soil and Environment, Swedish University of Agricultural Sciences Box 7014, SE-75005 Uppsala, Sweden, iuliia.kyiashchenko@slu.se; <sup>2</sup>Department of Forest Mycology and Plant Pathology, Uppsala BioCenter, Swedish University of Agricultural Sciences, Box 7026, SE-75005 Uppsala, Sweden.

**Abstract:** Boreal forest is one of the largest biomes in the world and constitutes a persistent terrestrial carbon sink with a major fraction of the carbon stored in the soil. Mycorrhizal and saprotrophic fungi are dominant components of the boreal ecosystem and play important, yet fundamentally different, roles in nutrient and carbon cycling. Saprotrophic fungi are considered to be the main wood and litter decomposers, while mycorrhizal fungi mine for nutrients in more processed soil organic matter. By producing extracellular enzymes, mycorrhizal fungi may act to decrease organic matter stocks, but may also contribute substantial amounts of organic matter in the form of mycelium. In this study, we aim to investigate the interplay between soil fertility, fungal communities, enzyme activities, and soil carbon dynamics in unmanaged boreal forests. In order to investigate influences of fungal communities on organic matter dynamics across

a soil fertility gradient, stable isotopes, C:N ratio, and extracellular enzyme activities were measured throughout fine-scale soil depth profiles. In contrast to our expectations, we found that organic matter was more actively processed on nutrient rich sites, while divergent C:N and  $^{15}\text{N}$  depth gradients indicate impaired decomposition and nitrogen retention on nutrient poor sites. Higher activities of manganese-dependent peroxidases on richer sites correlated well with lower stocks of total organic matter, indicating a negative effect on carbon sequestration. Higher Mn-peroxidase activity on richer sites is expected to be connected to a higher abundance of cord-forming ectomycorrhizal fungi (e.g., certain *Cortinarius* species), while lower Mn-peroxidase activity on poorer sites is expected to be linked to increased dominance by stress tolerant ascomycetes that may promote high carbon sequestration.

#### **CS 5-5 Tree genotype mediates covariance among disparate communities, from ectomycorrhizal fungi to lichens, arthropods and more**

**LAMIT, L.J.**<sup>1</sup>, P.E. Busby<sup>2</sup>, M.K. Lau<sup>3</sup>, Z.G. Compson<sup>4,5,6</sup>, T. Wojtowicz<sup>4,5</sup>, A.R. Keith<sup>4,5</sup>, M.S. Zinkgraf<sup>7</sup>, J.A. Schweitzer<sup>8</sup>, S.M. Shuster<sup>4,5</sup>, T.G. Whitham<sup>4,5</sup> and C.A. Gehring<sup>4,5</sup>

<sup>1</sup>School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI, USA, [llamit@mtu.edu](mailto:llamit@mtu.edu); <sup>2</sup>Department of Biology, University of Washington, Seattle, WA, USA; <sup>3</sup>Harvard Forest, Harvard University, Petersham, MA USA; <sup>4</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, USA; <sup>5</sup>Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, AZ, USA; <sup>6</sup>Center for Ecosystem Science and Society, Northern Arizona University, Flagstaff, AZ, USA; <sup>7</sup>US Forest Service, Pacific Southwest Research Station, Davis, CA, USA; <sup>8</sup>Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN, USA.

**Abstract:** Community genetics studies frequently focus on individual communities associated with plant genotypes, but little is known about the genetically based relationships among disparate communities. We first show that ectomycorrhizal fungal (EMF) communities vary among *Populus angustifolia* genotypes. We then integrate EMF with a range of data from other communities (endophytes, pathogens, lichens, arthropods, soil microbes) living in association with the same plant genotypes to understand how the ecological and evolutionary dynamics of one community may be constrained or modulated by its underlying genetic connections to another community. Specifically, we test the hypothesis that the composition of pairs of distinct communities covary across tree genotypes, such that individual plant genotypes that support a unique composition of one community are more likely to support a unique composition of another community. Finally, we evaluate whether physical proximity, taxonomic similarity, time between sampling, and interacting foundation species explain the strength of correlations. Three main results emerged. First, Mantel tests between communities revealed moderate to strong ( $\rho=0.25$  to  $0.85$ ) community-genetic correlations in almost half of the comparisons. Second, physical proximity determined the strength of community-genetic correlations, supporting a physical proximity hypothesis. However, ectomycorrhizal fungi and leaf pathogens were strongly correlated in two comparisons; because these communities are associated with distinct tree tissues, their connection represents an exception to the physical proximity hypothesis. Third, consistent with the interacting foundation species hypothesis, the most abundant species drove many of the stronger correlations. The field of community genetics demonstrates that the structure of communities varies among plant genotypes; our results add to this field by showing that disparate communities covary among plant genotypes. Eco-evolutionary dynamics between plants and associated organisms may therefore be mediated by the shared connections of different communities to plant genotype, indicating that the organization of biodiversity in this system is genetically based.

#### **SY 2-3 Pathogenic versus mycorrhizal fungi: functional genomics tools to investigate fungal responses to strigolactones**

Belmondo, S.<sup>1</sup> and **L. LANFRANCO**<sup>1</sup>

<sup>1</sup>Department of Life Sciences and Systems Biology, University of Torino, Torino, Italy, [luisa.lanfranco@unito.it](mailto:luisa.lanfranco@unito.it).

**Abstract:** Strigolactones (SLs) as components of root exudates induce hyphal branching of arbuscular mycorrhizal fungi (AMF) which is thought to favor root colonization. Little is known on how AMF detect and respond to SLs. AMF are poor model systems due to the obligate biotrophism and the lack of genetic transformation protocols. Moreover, SLs are widely distributed in the plant kingdom and this supports the hypothesis that SLs also have other important roles possibly affecting both beneficial and pathogenic microorganisms. It has been shown that a number of phytopathogenic fungi,

including the well-studied *Botrytis cinerea*, are sensitive to GR24, a synthetic SLs analog. With the aim to identify the molecular determinants involved in SLs response in AMF and assuming conserved mechanisms of SLs response in the fungal kingdom, we exploited *B. cinerea*, for which genomics data and mutant collections are available. Exposure of *B. cinerea* to GR24 led to a reduction in radial growth and slightly increased branching. We, therefore, set up the screening of a collection of *B. cinerea* knock-out mutants defective in genes mainly involved in signaling to isolate genotypes with altered responses to SLs. Among the 40 mutant strains analysed, three turned out to be less responsive to GR24: one mutant is defective of a G gamma subunit of heterotrimeric GTPases, the second strain is defective of a thioredoxin reductase (trr), and the third is defective of a GATA transcription factor. One feature shared by the three mutants is the overproduction of ROS (reactive oxygen species) suggesting that the response to GR24 requires changes of the redox status. Homolog gene sequences in the AMF *Gigaspora margarita* are under investigation, and data from a large-scale gene expression study after short exposure to GR24 will be presented.

### PS 3-37 Arbuscular mycorrhizal fungi pre-inoculation for improving the growth and health of strawberry (*Fragaria x ananassa*) planting materials

LANGENDORF, B.<sup>1,2</sup>, X. Xu<sup>1</sup>, A. Hodge<sup>2</sup> and P. Young<sup>2</sup>

<sup>1</sup>East Malling Research, New Road, East Malling ME19 6BJ, Kent, UK, benjamin.langendorf@emr.ac.uk; <sup>2</sup>Department of Biology, University of York, Wentworth Way, York YO10 5DD, UK.

**Abstract:** Control of soil-borne pathogens is a major problem in several horticultural crops since the withdrawal of several effective broad-spectrum chemical fumigants. Pre-colonisation of plants with arbuscular mycorrhizal fungi (AMF) before trans-planting has been proposed as a method for protecting crops against biotic stresses. Strawberry (*Fragaria x ananassa*) is an ideal production system to study such control methods as planting materials (micro-propagated or runners derived plug plants) can be easily pre-inoculated with AMF. We investigated (1) whether AMF could colonise strawberry under high moisture during the weaning process, and (2) whether AMF pre-colonised plants could reduce *Verticillium dahliae* incidence. Strawberry plants of different popular cultivars susceptible to *Verticillium* ('Elsanta', 'Malling Centenary', 'Red glory', 'Vibrant') and one new cultivar (EM-1996) were inoculated with each of the following AMF species: *Funneliformis mosseae*, *F. geosporum*, *Glomus microagregatum*, *Rhizophagus irregularis*, and *Claroideoglomus claroideum*. Controls were un-inoculated. The growth substrates used were peat/perlite mix, vermiculite or attapulgit clay. Several published studies have suggested that certain types of peat and compost had a negative effect on AMF symbiosis and that AMF colonisation may be limited under prolonged periods of damp conditions. Four experiments were undertaken in growth chambers or glasshouses at East Malling Research, UK. In all experiments, AMF colonisation was high (65-94%) in both types of strawberry planting material after 6-8 weeks. Non-specific associations were observed among the strawberry cultivars and AMF species tested. Colonisation by AMF did not however, result in a significant improvement in growth of runner tips derived plants. In contrast, AMF inoculation significantly reduced overall total fresh weight but increased crown diameter of *in-vitro* derived plantlets. These results show that AMF can colonise strawberry plants under a prolonged period of damp conditions in soil-less substrates. Further studies will be conducted to assess whether AMF pre-inoculated strawberry plug plants could reduce *Verticillium* incidence.

### PS 2-27 Inoculation with mycorrhizal fungi on street planted trees: impact at time of planting and 10 years later

LANTHIER, M.<sup>1</sup>, S. Peters<sup>1</sup> and S. Harel<sup>1</sup>

<sup>1</sup>CropHealth Advising & Research, Kelowna BC, Canada, www.crophealth.com, mario@crophealth.com.

**Abstract:** Four replicated, controlled experiments were initiated in 2004 to verify the impact on root colonization and plant growth for trees planted in urban settings. Bare-root trees of three genera (*Acer*, *Gleditsia*, and *Zelkova*) were installed in sidewalk planters at four different locations in two cities. A commercial formulation of mycorrhizal fungi, containing *Glomus intraradices* and *Pisolithus tinctorius*, was applied at label rate by spreading a dry formulation over the roots on the day of planting. One year after planting (2005) and ten years after planting (2015), soil was excavated to expose the root systems. A sample was collected for examination in the laboratory for mycorrhizal colonization. Trees growing in urban situations are exposed to supplementary stress because of the location. Planting sites in sidewalks or roadsides often have poor soil quality, inadequate watering after planting, and excess deicing salts after winter. Inoculation with mycorrhizal fungi should provide benefits in stress situations. Our company has successfully inoculated con-

tainer grown plants in commercial nursery production. Our efforts have not been successful in urban environments. The quality of the soil in the rhizosphere, and the related microbial activity may prevent successful application of mycorrhizal fungi in urban areas.

#### PS 1-20 Diversity and richness of AMF in a wheat monoculture parasitized with *Fusarium* spp.

**LARA-CHÁVEZ, Ma.B.N.**<sup>1</sup>, M. Vargas-Sandoval<sup>1</sup>, M. Gutiérrez-Contreras<sup>1</sup>, S. Aguirre-Paleo<sup>1</sup>, T. del C. Avila-Val<sup>1</sup>, J.M. Magdaleno-Torres<sup>1</sup> and C.E. Figueroa-Araujo<sup>1</sup>

<sup>1</sup>Universidad Michoacana de San Nicolás de Hidalgo, Facultad de Agrobiología "Presidente Juárez", Paseo Lázaro Cárdenas Esquina con Berlín S/N. Uruapan, Michoacán, México, chavez12001@yahoo.com.mx.

**Abstract:** Agricultural practices such as tillage, fertilization and no crop rotation affect the composition of the arbuscular mycorrhizal fungal community. In addition certain decline diseases of crops may be related to a shift from beneficial to non-beneficial or even parasitic fungi in continuous monocultures under high fertility conditions. The richness and diversity of arbuscular mycorrhizal fungi (AMF) were investigated in a wheat monoculture parasitized with *Fusarium* spp and managed with high inorganic fertilization. The study area is located in Jose Sixto Verduzco Municipality, Michoacan, Mexico. At the time of soil collection, the climatic conditions were: temperature 31°C, and no rainfall. During the dry season (March of 2014), soil cores were sampled from the uppermost 15 cm horizon under winter wheat crops with symptoms of dryland foot rot. Spores were isolated from 30 g samples and morphologically identified. Diversity was calculated using the Shannon Wiener index. Total species richness was nine. *Claroideoglomus etunicatum*, *Glomus tortuosum*, *Diversispora spurca*, *Entrophospora infrequens*, *Funneliformis mosseae*, *Rhizophagus intraradices*, *Sclerocystis sinuosa*, and *Septoglomus constrictum*. Our results show a low diversity in the study field with a loss of non glomoid spores and increase on population of *F. mosseae* and *R. intraradices*. We suggest that the uniform nature of the agricultural practices in this place strongly selects for dominance of few AMF species.

#### CS 3-4 Evolution and functioning of mycorrhizas from liverworts to forests, pedogenesis to global impacts

**LEAKE, J.R.**<sup>1</sup>, J. Quirk<sup>1</sup>, K.J. Field<sup>1</sup>, J.G. Duckett<sup>2</sup>, M.I. Bidartondo<sup>3</sup>, R. Thorley<sup>1</sup>, J.L. Morris<sup>1</sup>, W.E. Stein<sup>4</sup>, C.M. Berry<sup>5</sup> and D.J. Beerling<sup>1</sup>

<sup>1</sup>University of Sheffield, Department of Animal and Plant Sciences, Sheffield S10 2TN, UK, j.r.leake@sheffield.ac.uk;

<sup>2</sup>Department of Life Sciences, Natural History Museum, London SW7 5BD, UK; <sup>3</sup>Department of Life Sciences, Imperial College London, London SW7 2AZ, UK; <sup>4</sup>Department of Biological Sciences, Binghamton University, New York, 13902-6000, USA; <sup>5</sup>Cardiff University, School of Earth and Ocean Sciences, Cardiff, CF10 3AT, UK.

**Abstract:** The co-evolution of mycorrhizal fungi with liverworts was a pivotal first step in the greening of the continents. Plants of increasing biomass and nutrient demand eventually lead to the rise of forest ecosystems, which are major drivers of the formation of pedogenic clays and global biogeochemical cycles. We present experimental and observational evidence in support of four linked hypotheses: (1) that high atmospheric CO<sub>2</sub> concentrations of the early Palaeozoic strongly favoured the establishment of mycorrhiza-like associations in basal land plants to increase nutrient uptake, (2) as plants evolved in stature, biomass, and rooting depth, their mycorrhizal fungal partnerships received increasing amounts of plant photosynthate, (3) this enabled intensification of plant-driven fungal weathering of rocks to release growth-limiting nutrients such as the element P from calcium phosphates, (4) in turn, this has transformed biogeochemical cycles of Ca and P with impacts on the carbon cycle affecting biosphere-geosphere-ocean-atmosphere interactions over the past 410 million years. These hypotheses are examined using laboratory mesocosms to determine the carbon-for-nutrient exchange efficiency of extant basal liverworts that form mycorrhiza-like associations with Mucoromycota and Glomeromycota, and to quantify rates of mineral weathering under liverworts and trees under ambient and early Palaeozoic atmospheric CO<sub>2</sub> concentrations. Rates of photosynthate allocation to mycorrhizal fungi is shown to control their weathering rates. In field experiments, weathering of Ca from silicate and carbonate minerals increased with evolutionary advancement from liverworts to gymnosperm and angiosperm trees and from arbuscular to ectomycorrhizal fungal partners. Our complementary geochemical analysis of Middle Devonian palaeosol cores, preserving the root traces of one the Earth's earliest forest ecosystems with cladoxyloids and archaeophytalean progymnosperms, confirms the importance of rooting depth in pedogenesis and weathering. Our findings support an over-arching hypothesis that evolution has selected plant and mycorrhizal partnerships that have intensified mineral weathering rates of global biogeochemical cycles.



## PS 1-21 Orchid mycorrhizal fungi isolated from eight species of native orchid in Korea

LEE, B.H.<sup>1</sup>, S.J. Kim<sup>1</sup> and A.H. Eom<sup>1</sup>

<sup>1</sup>Department of Biology Education, Korea National University of Education, Cheongju, Chungbuk 363791, Korea, sdonate62@gmail.com.

**Abstract:** Orchidaceae is the most diverse and widespread family of flowering plants, with 25,000 species currently recognized. In Korea, more than 100 species have been reported in the wild. Most orchids depend on orchid mycorrhizal fungi (OMF) to enhance nutrient absorption by the roots and prevent infection by pathogens. In this study, we investigated the diversity and host-symbiont relationship of OMF associated with native orchid plants in Korea. We collected 8 species of native orchids; *Calanthe discolor*, *Cephalanthera falcata*, *Cephalanthera longibracteata*, *Gymnadenia conopsea*, *Habenaria flagellifera*, *Habenaria linearifolia*, *Platanthera japonica*, and *Platanthera mandarinorum* var. *brachycentron*. We confirmed OMF colonization by observation of pelotons in stained roots under a light microscope. OMF were isolated from surface-sterilized roots and identified using morphological characteristics of the fungal hyphae and DNA sequence analysis. A total of 10 fungal strains were isolated, wherein 8 strains belonged to the family Tulasnellaceae, identified as mostly *Tulasnella calospora* and 2 strains belonged to the family Ceratobasidiaceae. The results suggested that most orchids identified in this study belonged to the Tulasnellaceae family. OMF diversity and their relationship with Korean native orchids are discussed.

## PS 4-39 Freezing tolerance of mycorrhizal and non-mycorrhizal Scots pine seedlings

Korhonen, A.<sup>1,2</sup>, T. Repo<sup>1</sup> and T. LEHTO<sup>2</sup>

<sup>1</sup>Natural resources and bioproduction, Natural Resources Institute Finland (Luke), 80100 Joensuu, Finland; <sup>2</sup>School of Forest Sciences, University of Eastern Finland, 80100 Joensuu, Finland, tarja.lehto@uef.fi.

**Abstract:** Boreal forests and other cold regions are mostly dominated by ectomycorrhizal trees. Although soil temperatures are not generally as low as air temperatures, soil frost occurs in forests, and the topsoil may freeze and thaw repeatedly during a winter. We studied for the first time, whether ectomycorrhizal structure can improve the freezing tolerance of tree roots and whole seedlings. We grew Scots pine (*Pinus sylvestris*) in a growth room with and without *Hebeloma* sp. or *Suillus luteus*. At the end of the growth period there was additionally a hardening treatment with short day and low temperature (+5°C) (SDLT) while non-hardened plants continued in the long day high temperature (LDHT) regime. Freezing tolerance was assessed after exposure to seven different temperatures. In one experiment, root samples were exposed to frost and freezing tolerance was determined using a relative electrolyte leakage test. In another experiment, seedlings were exposed to frost intact in their pots, and they were incubated in LDHT for three weeks. Their condition was assessed visually (browning of needles), and root hydraulic conductance was measured. The mycorrhizal status of the seedlings did not make any difference in the freezing tolerance of roots or whole plants in either SDLT or LDHT. Although ectomycorrhizal fungi have been found to survive much lower temperatures than tested here, they did not offer protection to the host. The recovery processes after non-lethal frost remain to be studied, as well as the possible survival of the fungus after the death of the host.

## LT 1-5 Should we expect a positive relationship between plant and AMF richness?

LEKBERG, Y.<sup>1,2</sup>

<sup>1</sup>MPG Ranch, 1001 S. Higgins Ave, Suite A3, Missoula MT, 59801, yleberg@mpgranch.com; <sup>2</sup>Department of Ecosystem and Conservation Sciences, University of Montana, Missoula, MT 59812.

**Abstract:** AMF richness and diversity can influence plant community diversity and productivity, yet factors that drive AMF richness are not well understood. While it is intuitive that a more species-rich plant community would host more AMF taxa, this may only occur if co-occurring plants generate more AMF niches. Because different AMF taxa occupy the same space (roots) to access the same resource (carbon), arguably the two most important niche dimensions created by the plants are associated with root characteristics and seasonality. These do not necessarily differ among plant species,



which may help explain the lack of consistent patterns between plant and AMF species in previous studies. The effect of resources has not been considered extensively in AMF community ecology, but the intermediate resource hypothesis posits that AMF richness should be greatest at intermediate resource levels, regardless of plant richness. We found a greater AMF richness in monodominant plant communities that provided more resources to AMF relative to more species-rich, but host-quality poor plant communities. We also found the greatest phylogenetic dispersal among host plants that had the lowest AM colonization, suggesting a more competitive environment for AMF. Using previously published work and our own data, I will discuss the relative importance of plant richness and resources for driving AMF richness, and demonstrate the utility of phylogenetic dispersal estimates to assess strengths of competitive interactions and habitat filters for AMF.

#### SY 1-2 Fungi associated with a Hawaiian ericoid host across a 4 million year chronosequence

LEOPOLD, D.R.<sup>1</sup>

<sup>1</sup>Department of Biology, Stanford University, Stanford, CA, 94305 USA, devin.leopold@gmail.com.

**Abstract:** Ericoid mycorrhizal fungi (ERM), which form mycorrhizas with Ericaceous plants, were once believed to be restricted to a narrow phylogenetic range. More recently, a wide range of taxa have been recognized as ERM, yet the factors influencing ERM community composition are poorly defined. To examine the role of nutrient availability as a driver of ERM community composition, I used Illumina metabarcoding of the ITS1 region of rDNA to identify fungi associated with hair roots of a single ERM host species, *Vaccinium calycinum*, in Hawaii, USA. Samples were collected in replicated, long-term (25+ yr) nutrient addition plots and across the Long Substrate Age Gradient (LSAG), a 4 million year chronosequence characterized by a natural soil fertility gradient. *Vaccinium calycinum* root-associated fungi identified across the LSAG included both ascomycetes and basidiomycetes (181 and 56 OTUs at 97% similarity, respectively) with many matches in clades known to include ERM (*Rhizoscyphus* spp., *Odiodendron* spp., *Melinomyces* spp., and Sebaciniales), along with other potential mycorrhizal fungi and root endophytes. Communities of root-associated fungi varied significantly between LSAG sites, with a clear distinction between nitrogen-limited and fertile or phosphorus-limited sites. Analysis of fungal community composition from nutrient addition plots revealed a divergence in community composition under nitrogen vs. phosphorus additions; however, this effect depended on the underlying nutrient status of the unfertilized soil. These findings demonstrate the dramatic range of potential ERM species associated with a single host plant across a soil fertility gradient and demonstrate that both nitrogen and phosphorus availability can influence ERM community composition.

#### PS 1-49 AM fungi in roots of hemiparasitic *Pedicularis*: friends or foes?

LI, A.R.<sup>1</sup>, K.Y. Guan<sup>1</sup>, X.L. Sui<sup>1</sup>, X.Y. Huang, Y. Chen, R. Stonor<sup>2</sup>, S.E. Smith and F.A. Smith<sup>2</sup>

<sup>1</sup>Key Laboratory of Economic Plants and Biotechnology, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, 650201 China, airongli@mail.kib.ac.cn; <sup>2</sup>Soil Group, School of Agriculture, Food and Wine, The University of Adelaide, Adelaide, SA 5005 Australia.

**Abstract:** Arbuscular mycorrhizal (AM) fungi and parasitic plants are two ubiquitous and important components in terrestrial ecosystems. Both groups impose direct impacts on their host plants, as well as consequent influences on community structure of their ecosystems, though in very different ways. Despite their opposite influence on host plants (with parasitic plants often being parasitic and AM fungi mostly mutualistic), recent findings suggest that colonization by AM fungi and infection by root parasitic plants may be modulated by similar molecular mechanisms, and interesting parallels between plant parasitism and AM associations have been indicated. In addition, a limited but growing number of studies have found that the AM status of host plants significantly influences growth of parasitic plants. However, most root parasitic plants do not form mycorrhizal associations, and studies experimentally addressing interactions between parasitic plants and AM fungi are very limited. As a consequence, roles of AM fungi for plant communities in which root parasitic plants occur remain largely unknown. Using root hemiparasitic plant species in the genus *Pedicularis* (Orobanchaceae) that harbor AM fungi in their root systems, we investigated possible roles of these fungi in the root hemiparasites, as well as in the plant communities where both partners occur. The results showed that AM fungi had significant influence on survival and biomass of the root hemiparasites, though robust variation was observed in terms of

the outcomes of AM inoculation, which depended on plant and fungal identity as well as growing conditions. In addition, AM fungi played important roles in regulating interactions between the root hemiparasites and their host plants. Damage to host plants by parasitism of the root hemiparasites was generally alleviated by inoculation with AM fungi. However, the mechanisms involved in the alleviation were quite different between different host-parasite pairs.

**PS 4-72 The colonization and species diversity of dark septate endophytes in roots of *Ammopiptanthus mongolicus* of desert ecosystem in Inner Mongolian, China**

LI, B.<sup>1</sup>, C. He<sup>1</sup>, Y. Chen<sup>1</sup>, B. Chen<sup>1</sup> and X. He<sup>1</sup>

<sup>1</sup>College of Life Sciences, Hebei University, Baoding 071002, P.R. China, libaoku@hbu.cn.

**Abstract:** Improved understanding of the ecological significance of dark septate endophytes (DSE) associations in semi-arid and arid lands. The colonization, diversity, and ecological distribution were surveyed in three sites located in desert, such as WuHai, Urad Back Banner, and Alxa Left Banner, in Inner Mongolian, northwest China. Roots samples of *Ammopiptanthus mongolicus* (Leguminosae) were collected in June 2013. The study was carried out by acid fuchsin staining, analysis of pure culture isolates, analysis of morphological characteristics, and ITS sequencing. The results indicated that *A. mongolicus* could form strong symbiotic relationships with DSE fungi. It could be highly infected by DSE, which formed typical dark septate hyphae and "microsclerotia". The main distribution type of microsclerotia are discrete and polymerization. The colonization and distribution of DSE were significantly different, and have obvious spatial heterogeneity among the three studied sites. A total of 206 isolates from roots of *A. mongolicus* were obtained. Of 206 DSE strains, 88 strains were isolated from WuHai site, 90 strains were isolated from Urad Back Banner site, and 28 strains were isolated from Alxa Left Banner site. The length of ITS fragment is 525 bp to 617 bp. 7 genera and 11 species were identified by using online tools for sequence alignment BLAST (e.g., *Cladosporium*, *Phialocephala*, *Exophiala*, *Phialophora*, *Paraphoma*, *Phoma*, and *Pleosporales*). The sequence similarity was 97%-99% between isolated DSE strains and similar strains. Species diversity index was significantly difference among the three sites with altitude changing. These indicate that *A. mongolicus* roots contain an abundant and more diverse community of DSE fungi, thus offering a potential bioresource for establishing a novel model of plant-fungal mutualistic interactions in desert ecosystem. The specific DSE fungi also represent a novel system for exploring mutualistic plant-fungus interactions.

**LT 3-9 Impact of arbuscular mycorrhizal fungi on crop and weed growth: potential for conservation biocontrol of weeds**

LI, M.<sup>1</sup> and A. Davis<sup>1,2</sup>

<sup>1</sup>Department of Crop Sciences, University of Illinois at Champaign-Urbana, Urbana, IL 61801 USA, mengli5@illinois.edu;

<sup>2</sup>USDA-ARS Global Change and Photosynthesis Research Unit, University of Illinois at Champaign-Urbana, Urbana, IL 61801 USA.

**Abstract:** Effects of arbuscular mycorrhizal fungi (AMF) on plants are context-dependent and vary from positive to negative. If AMF have differential effects on agricultural weeds and crops, they may potentially contribute to the control of weeds. To understand this, we asked two questions: 1) can AMF directly suppress some weeds, especially non-host weed species, and 2) can AMF indirectly suppress some weeds by improving the competitive ability of crops against weeds? Five weed species, including host and non-host species, were planted side by side with corns in an agricultural field along with a two-factor factorial treatment: tillage (low disturbance vs. high disturbance) and cover crop (cover crop vs. no cover crop). Our results showed that 1) non-host weeds neither showed much AMF colonization in their roots nor differences in growth between low and high disturbances. 2) The low disturbance treatment significantly increased the AMF colonization rate of corn and one of the host weed species than the high disturbance treatment. This increase of colonization was companied with the increase of the plant biomass. In addition, the increase of biomass was more pronounced in corn plants than non-host weeds and host weeds. Thus, AMF may benefit more on the growth of corn than weeds under the low disturbance condition, and indirectly suppress weeds by improving the competitive ability of crops against weeds. 3) AMF community compositions in plant roots varied according to plant identities and treatments and explained a large variation in plant growth. In conclusion, our results indicated that AMF have the potential to indirectly suppress weeds through increasing the crop-weed inferences. In addition, AMF community composition varied from plant species and disturbance intensities and explained a large proportion of variation in weed and crop growth.

**PS 1-50 Coexpression of the D-*myo*-inositol-3-phosphate synthase gene and the 14-3-3 gene in maize roots is favorable for crosstalk between host plants and arbuscular mycorrhizal fungi, and between the aboveground and belowground under drought stress**

LI, T.<sup>1</sup> and B.D. Chen<sup>1</sup>

<sup>1</sup>State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, 100085 China, qq2006\_tom@126.com.

**Abstract:** The arbuscular mycorrhizal (AM) symbiosis is known to stimulate plant drought tolerance. However, the mechanisms underlying the synergetic resistance of AM associations are largely unknown. As a primary stress hormone, abscisic acid (ABA) helps to maintain plant water status by activating downstream stress-responsive genes. By considering the specific role of ABA in the development of the complete arbuscule and its functionality during AM symbiosis, we aim to reveal the regulatory roles of AM fungi (AMF) in ABA distribution and its influence on drought tolerance through the ABA signaling pathway. Additionally, we were interested in detecting the potential cross-talk between host plants and AMF under drought stress. In this study, we applied a split-root system where each part of the maize root system was subjected to drought stress and/or mycorrhizal inoculation with *Rhizophagus intraradices*. Based on GeneChip data and other studies, we selected 15 maize genes involved in ABA-mediated drought tolerance and cloned three genes from *R. intraradices*. Expression of the drought-tolerance related genes was analyzed by quantitative real-time PCR. The results showed that AMF down-regulated the expression of the aldehyde oxidase gene and decreased root ABA content. Consequently, induction of genes encoding D-*myo*-inositol-3-phosphate synthase (IPS) and 14-3-3-like protein GF14 (14-3GF), respectively, led to the up-regulated expression of the plasma membrane intrinsic protein genes and the superoxide dismutase gene in maize roots which was positively correlated with improved plant-water relations. Furthermore, the coordination of *IPS* and *14-3GF* expression evoked significant alterations in shoot growth and the expression of AM fungal stress-responsive genes. These findings suggest that coexpression of *IPS* and *14-3GF* serves as a key regulator to mediate AM-associated systemic drought tolerance as a result of conferring crosstalk between host plants and AMF and between shoots and roots, and it may also play an important role in signaling transduction in AM symbiosis in response to abiotic stress.

**LT 2-3 Integrated proteomics/metabolomics reveals carbon source, nitrogen source, and potential pathogenicity of an endobacterium of an endophytic fungus associated with *Populus***

LI, Z.<sup>1</sup>, S. Dearth<sup>2</sup>, Q. Yao<sup>1</sup>, J. Uehling<sup>3</sup>, H. Castro-Gonzalez<sup>2</sup>, S. Campagna<sup>2</sup>, G. Hurst<sup>1</sup>, J. Labbé<sup>1</sup> and C. Pan<sup>1</sup>

<sup>1</sup>Oak Ridge National Laboratory, Oak Ridge, TN, liz1@ornl.gov; <sup>2</sup>University of Tennessee, Knoxville, TN; <sup>3</sup>Duke University, Durham, NC.

**Abstract:** The mycorrhizal fungus *Mortierella elongata* plays an important role in forest ecosystems. Interestingly, this fungus hosts a bacterial endosymbiont, *Candidatus Glomeribacter* sp. Molecular interactions between them and whether the symbiosis is commensal, mutualistic, or parasitic are largely unknown. Here, this symbiotic system was treated with antibiotics to decrease endosymbiont populations and grown in media differing in nitrogen content. Mass spectrometry-based proteomics and metabolomics were used to investigate changes in protein abundances, post-translational modifications (PTMs), and metabolites. We identified over 6,000 proteins. Particularly, in nitrogen-limited conditions, fungal growth was significantly suppressed; however, proteomic data suggested the endosymbiont was actively dividing and had higher abundance than in normal conditions. Several gluconeogenesis-related proteins in the endosymbiont were identified, including the key enzyme fructose-1,6-bisphosphatase, suggesting gluconeogenesis was used to synthesize carbohydrates. We identified a few enzymes involved in synthesizing lipopolysaccharide in the endosymbiont, particularly those for synthesizing lipid A, an extremely potent toxin. Some amino acid transporters in the endosymbiont were identified, such as those for glutamate/aspartate which could be the nitrogen source imported from the host. These data suggest the endosymbiont may take on a pathogenic lifestyle under nitrogen-limited conditions. Over 10,000 PTMs were identified and quantified. Changes in the abundance of many PTMs were not correlated with the changes in the abundance of the associated proteins. For example, the abundance of a di-methylation on a fungal fructose-biphosphate aldolase increased by 4.2-fold in nitrogen-limited conditions compared to the normal condition, but this protein's abundance did not change. Our data indicate dynamic PTMs may regulate metabolic activities in this symbiotic system. Finally, 92 metabolites

were identified and quantified. While the abundance of 15 metabolites changed significantly when the abundance of the endosymbiont was reduced, nitrogen limitation prompted abundance changes of 70 metabolites, implying drastic rewiring of the metabolic network. Overall, our multi-omics data provide functional insights into this mycorrhizal fungus-endobacterium symbiotic system.

### CS 9-3 Common and unique (host-specific) interactomes control ectomycorrhizal symbiosis between *Pinus* and *Suillus*

**LIAO, H.L.**<sup>1</sup>, Y. Chen<sup>2</sup>, T.D. Bruns<sup>3</sup>, K.G. Peay<sup>4</sup>, J.W. Taylor<sup>3</sup>, S.Branco<sup>3</sup>, J.M. Talbot<sup>5</sup>, I. Grigoriev<sup>6</sup>, K. Barry<sup>6</sup>, D.W. Hoyt<sup>7</sup>, C.D Nicora<sup>7</sup>, S.O. Purvine<sup>7</sup>, K.H. Chen<sup>1</sup> and R. Vilgalys<sup>1</sup>

<sup>1</sup>Departments of Biology and <sup>2</sup>Department of Medicine, Duke University, Durham, NC, sunny.liao@duke.edu;

<sup>3</sup>Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA; <sup>4</sup>Department of Biology, Stanford University, Stanford, CA; <sup>5</sup>Department of Biology, Boston University, Boston, MA; <sup>6</sup>US Department of Energy Joint Genome Institute, Walnut Creek, CA 94598; <sup>7</sup>Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, WA.

**Abstract:** *Suillus* species are members of the boletes (Suillaceae) that form host-specific ectomycorrhizal (EM) associations with conifer tree species in the family Pinaceae. We investigated the genetics of ectomycorrhizal host specificity by cross inoculation of different *Pinus* hosts with basidiospores of different *Suillus* species with varying natural host ranges. We assessed the outcome of these interactions using comparative metatranscriptomics, metabolomics, and proteomics. Several *Suillus* spp., including *S. granulatus*, *S. pictus*, and *S. americanus*, readily form ectomycorrhizae (compatible reaction) with plant hosts belonging to the *Pinus* subgenus *Strobus* (*P. strobus* and *P. monticola*), but were incompatible with other ‘2-needle pine’ hosts belonging to subgenus *Pinus* (*P. taeda* and *P. banksiana*). Metatranscriptomic analysis of inoculated roots revealed that both plants and fungi express distinctive transcriptional responses during incompatible versus compatible mycorrhizal pairings. Using RNA-Seq, we identified common and unique patterns of plant-fungal gene expression (interactomes) for compatible/incompatible *Pinus*-*Suillus* pairings. Compatible mycorrhizal interactions are further characterized by distinct metabolomic signatures for trehalose, mannitol, and arabinol. Functional annotation of highly expressed genes reveals that the *Suillus*-*Pinus* interactomes respond via similar highly conserved gene regulatory networks involving coordinated responses by both fungal and plant genomes, including G-protein signaling and secretory pathways. *Pinus* spp. activate a core set of gene products that mediate *Suillus*-specific recognition, including leucine-rich repeat and pathogen resistance proteins. We are developing the *Pinus*-*Suillus* symbiosis as a model for understanding plant-fungal communication and other aspects of EM function. Further studies will employ genome sequencing, transcriptomics, and metabolomics to study the mechanisms of adaption and coevolution of *Suillus* with their *Pinus* hosts.

### PS 2-40 AMF and PGPR improve strawberry fruit quality and modulate element and volatile concentrations

Todeschini, V.<sup>1</sup>, N. Ait-Lahmidi<sup>2</sup>, E. Mazzucco<sup>1</sup>, F. Marsano<sup>1</sup>, F. Gosetti<sup>1</sup>, E. Robotti<sup>1</sup>, E. Bona<sup>1</sup>, N. Massa<sup>1</sup>, L. Bonneau<sup>2</sup>, **G. LINGUA**<sup>1</sup>, E. Marengo<sup>1</sup>, D. Wipf<sup>2</sup> and G. Berta<sup>1</sup>

<sup>1</sup>Dipartimento di Scienze ed Innovazione Tecnologica, Università del Piemonte Orientale, viale T. Michel, 11 – 15121 Alessandria, Italy, guido.lingua@uniupo.it; <sup>2</sup>Université de Bourgogne, UMR Agroécologie/INRA 1347/AgroSup/Université de Bourgogne, Plant Microorganism Interactions Dpt – ERL 6300 CNRS, 17 rue Sully, 21000 Dijon, France.

**Abstract:** In this study, three arbuscular mycorrhizal fungal species (*Funneliformis mosseae*, *Septoglomus viscosum*, and *Rhizophagus irregularis*) were used in combination with three strains of *Pseudomonas* sp. (19Fv1t, 5vm1K, and Pf4) to inoculate plantlets of *Fragaria x ananassa* Duch var. Eliana F1. Uninoculated plants were kept as controls. The effects of the different fungus/bacteria combinations (9 treatments) were assessed both on plant growth parameters and fruit production and quality. Plants were maintained in a greenhouse for 4 months and irrigated weekly with a Long Ashton solution at two different levels of phosphate, half of control plants (C) were fed with 32µM of phosphate, while the remaining controls (C-P) and all the inoculated plants were irrigated with 16µM of phosphate. Flower and fruit production were recorded weekly. Mature fruits were collected, weighed, measured, frozen in liquid nitrogen, and stored at -80°C before biochemical analysis. At harvest, fresh and dry weights of roots and shoots, mycorrhization, and the concentration of leaf photosynthetic pigments were measured. The following fruit parameters were evaluated:



pH, concentration of organic acids, soluble sugars, vitamin C, anthocyanins, the profile of volatile compounds, and the mineral content (55 elements). Data were analyzed with ANOVA, and principal component analysis methods were used to draw a general profile of strawberry plants. Mycorrhizal colonization was highest in plants inoculated with *R. irregularis* followed by *F. mosseae* and *S. viscosum*. Inoculations enhanced root and shoot biomass and increased fruit yield and quality. In particular, inoculation with Pf4 increased flower and fruit production and malic acid content while decreasing the pH regardless of the fungus used. Sugar and anthocyanin concentrations were increased. Sixty volatile molecules were detected. The factor “fungus” mostly affected the parameters associated with the vegetative portion of the plant, while the factor “bacterium” was especially relevant for fruit yield and quality.

## PS 1-22 Chinese truffle biodiversity and their conservation

LIU, P.G.<sup>1,5</sup>, C. Juan<sup>1,2</sup>, D. Xiao-Juan<sup>1,3</sup>, Q. Peng<sup>1,4</sup> and Z. Fenglan<sup>1</sup>

<sup>1</sup>Key Laboratory for Plant Biodiversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming, 650204, Yunnan, China, pglu@mail.kib.ac.cn; <sup>2</sup>Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100194, P. R. China; <sup>3</sup>College of Biological Science and Engineering, Northern University of Nationalities, Yinchuan 750021, P. R. China; <sup>4</sup>Sericultural Research Institute, Shandong Academy of Agricultural Sciences, Yantai, Shandong 264002, China; <sup>5</sup>Haiyan Engineering and Technology Center, Kunming Institute of Botany, Chinese Academy of Science, Zhejiang Province, China.

**Abstract:** South-western China is an area with complicated geography, vertical climate condition, luxuriant plant species, and diversified forest vegetation. These environmental and biologic factors provide abundant and wide variety of favourable habitats and symbiotic host for the growth and reproduction of the ectomycorrhizal macrofungi, such as the renowned truffles in the world. A total 41 species of Chinese truffles have been discovered and identified up to now, among of them 16 are new species to science recently decennium, with 26 taxa are endemic species to China. The Chinese black truffle covered 6 species, among of them, *Tuber indicum* is a most common commercial species, the sister relationship with European species *T. melanosporum*. The Chinese summer truffle, *T. sinoaestivum*, is another popular species, and is a new species identified by classification characters and molecular analysis, and is also a sister taxon with the European summer truffle, *T. aestivum*. These ectomycorrhizal symbiotic fungi show similar or approximately coincident distributed patters with their host trees. *Tuber indicum* complex is always separated into two branches in molecular evolutionary trees (such as NJ, MP trees et al.) and with their genetic structure analysis (such as microsatellite genetic structure SSR, PCO, and Bayesian analysis). Base upon these analyses, they should be two different species in science, one distributed on the north part of Yangzi river upstream (Jinsha river), another is distributed primarily on the southern part. The truffle-infected seedlings of *Castanea mollissima*, *Pinus armandii*, *P. massoniana*, *P. tabuliformis*, *P. thunbergii*, *Quercus acutissima*, *Q. pannosa*, *Corylus heterophylla*, *Populus yunnanensis*, etc. had been obtained successfully by inoculation on the axenic seedlings with *T. indicum*, *T. sinoaestivum*, *T. pseudohimalayense*, *T. panzhihuanese*, and *T. melanosporum* and then transplanted in suitable field (limestone area). Some truffle plantations have been set up since 2008, and the first truffle fruit-bodies were produced in a plantation at end of 2012. By the method, we can achieve the purposes of truffle conservation and the development of truffle plantations.

## PS 4-17 Phylogenetic structure of arbuscular mycorrhizal community shift in response to increasing soil fertility

LIU, Y.<sup>1,2</sup>, N.C.Johnson<sup>3</sup>, M. Lin<sup>1</sup>, G. Shi<sup>1</sup>, S. Jiang<sup>1</sup>, X. Ma<sup>1</sup>, G. Du<sup>1</sup>, L. An<sup>1</sup> and H. Feng<sup>1</sup>

<sup>1</sup>School of Life Sciences, Lanzhou University, Lanzhou 730000, China, yjliu@lzu.edu.cn; <sup>2</sup>Cold and Arid Regions Environmental and Engineering Research Institute, Chinese Academy of Sciences, Lanzhou, 730000, China; <sup>3</sup>School of Earth Sciences and Environmental Sustainability, Northern Arizona University, Flagstaff, AZ 86011, USA.

**Abstract:** Understanding the underlying mechanisms driving the responses of belowground communities to increasing soil fertility will facilitate our prediction of ecosystem sustainability in response to anthropogenic eutrophication of terrestrial systems. Here, we studied the impact of fertilization of an alpine meadow on arbuscular mycorrhizal (AM) fungi, a group of root-associated microorganisms that are important in maintaining sustainable ecosystems. Species and phylogenetic composition of AM fungal communities in soils were compared across a soil fertility gradient generated by 8 years of combined nitrogen and phosphorus fertilization. Phylogenetic patterns were used to infer the ecological



processes structuring the fungal communities. We identified 37 AM fungal virtual taxa mostly in the genus *Glomus*. High fertilizer treatments caused a dramatic loss of *Glomus* species, but a significant increase in genus richness and a shift towards dominance of the lineage of *Diversispora*. AM fungal communities were phylogenetically clustered in unfertilized soil, random in the low fertilizer treatment and over-dispersed in the high fertilizer treatment, suggesting that the primary ecological process structuring communities shifted from environmental filtering (selection by host plants and fungal niches) to a stochastic process and finally to competitive exclusion across the fertilization gradient. Our findings elucidate the community shifts associated with increased soil fertility, and suggest that high fertilizer inputs may change the dominant ecological processes responsible for the assembly of AM fungal communities towards increased competition as photosynthate from host plants becomes an increasingly limited resource.

#### CS 7-6 Mycorrhizal fungi as drivers for soil carbon and nitrogen accumulation on the volcanic island Surtsey, Iceland

LIU, Z.F.<sup>1,2</sup> and H. Wallander<sup>1</sup>

<sup>1</sup>Section of Microbial Ecology, Department of Biology, Lund University, Lund SE-223 62 Sweden, liuzf@scbg.ac.cn; <sup>2</sup>Key Laboratory of Vegetation Restoration and Management of Degraded Ecosystems, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650 China.

**Abstract:** Mycorrhizal fungi play an important role in distributing carbon (C) and nitrogen (N) in soils, which is critical to reveal the underlying microbial mechanism of soil development. However, the information about how different mycorrhizal types affect soil C and N accumulation is still not fully understood. Pristine volcanic islands offer a unique opportunity to estimate the contribution of different mycorrhizal types in C and N accumulation during soil development. In 2014, soils were sampled under plants associated with different mycorrhizal types (nonmycorrhizal (NM), arbuscular mycorrhizal (AM) fungi, ectomycorrhizal (ECM) fungi, and ericoid mycorrhizal (ERM) fungi) on the volcanic island Surtsey, Southern Iceland, which was formed during an eruption between 1963 and 1967. Soil C and N, natural abundance of  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$ , and SOM chemistry were characterized to investigate how mycorrhizal fungi mediate soil C and N accumulation during soil development. The results showed that the amounts of soil C and N that had been accumulated under ECM and ERM plants were significantly higher than those under NM and AM plants. Soil  $\delta^{13}\text{C}$  varied inversely with soil C concentration and C: N ratio and slightly decreased under ECM and ERM plants. Compared to NM plants, soil  $\delta^{15}\text{N}$  was greatly enriched under mycorrhizal plants and positively associated with soil C: N ratio. Fourier-transform infrared (FTIR) spectroscopy analysis demonstrated that SOM chemical composition also greatly varied with mycorrhizal types. Significant relative increases of the main lipid markers (2,906 and 2,843  $\text{cm}^{-1}$ ) were observed in the soils under ECM and ERM plants, and significant increases of main lignin markers (1,615, 966, and 855  $\text{cm}^{-1}$ ) in the soils under NM plants. Our study highlights the importance of mycorrhizal fungi in mediating C and N accumulation and SOM chemistry during soil development.

#### PS 3-68 Breaking out of a specific host lineage: *Suillus subaureus* on angiosperm hosts in the Great Lakes region, USA

LOFGREN, L.<sup>1</sup>, N.H. Nguyen<sup>1</sup> and P.G. Kennedy<sup>1,2</sup>

<sup>1</sup>Department of Plant Biological Sciences, University of Minnesota, St. Paul MN, 55108 USA, lofgr080@umn.edu;

<sup>2</sup>Department of Ecology Evolution and Behavior, University of Minnesota, St. Paul MN, 55108 USA.

**Abstract:** Determining the evolutionary and ecological drivers of mycorrhizal host specificity can be greatly facilitated by comparisons of closely related fungal species with distinctly different host associations. For ectomycorrhizal (ECM) fungi, however, contrasting specificity on phylogenetically diverse hosts is relatively uncommon in closely related species, which tend to cluster into lineage-specific host associations. In this study, we demonstrate a novel ECM association within the genus *Suillus*, a lineage otherwise known to associate exclusively with hosts in the family Pinaceae. Sporocarp collections of *Suillus subaureus*, a rare species known from the Great Lakes region of the United States, have been reported in *Quercus*- and *Populus*-dominated forests where coniferous hosts are absent. In 2014, we made a series of collections of *S. subaureus* from a forest site in Minnesota in which conifer trees were locally absent (>50 m away). Molecular phylogenetic analyses confirmed the sporocarp collections were clearly nested within the genus *Suillus*, being related to species known to associate with 2 and 5 needle pines as well as *Larix* hosts. Co-analyses of fungal (ITS rRNA) and plant (*trnL* cDNA) DNA from ECM root tips collected directly under the sporocarps showed that *S. subaureus* ectomycorrhizas

are formed with *Q. rubra* tree roots *in situ*. An *in vivo* seedling bioassay is currently underway to quantify the colonization success of *S. subaureus* on *Quercus*, *Populus*, and *Pinus* hosts from spore. The confirmation of this novel association within an otherwise specific host lineage provides a model system for investigating the mechanisms mediating ECM host specificity and has broad ecological implications related to global change-induced shifts on host ranges and ECM fungal species persistence.

**PS 3-69 Comparing ectomycorrhizal fungus communities of understory giant chinquapin (*Chrysolepis chrysophylla*) and overstory Pinaceae in a mixed conifer forest in central Oregon**

**LONGWAY, L.<sup>1</sup>**, J.E. Smith<sup>2</sup> and D. Luoma<sup>1</sup>

<sup>1</sup>College of Forestry, Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon 97331 USA, Lucas.Longway@oregonstate.edu; <sup>2</sup>Forest Service, Pacific Northwest Research Station, Corvallis, Oregon 97331 USA.

**Abstract:** Giant chinquapin (*Chrysolepis chrysophylla*) is an evergreen hardwood often found as an understory shrub in coniferous forests of the Pacific Northwestern United States. Forest managers often view it as a competing species for site resources due to its ability to quickly sprout after disturbances, such as fire and thinning of overstory conifers. Like its associated overstory conifers, giant chinquapin forms ectomycorrhizae. However, the ectomycorrhizal fungal communities associated with giant chinquapin have received little investigation. We compared the ectomycorrhizal communities associated with giant chinquapin and co-occurring overstory Pinaceae hosts in the Lookout Mountain unit of the Pringle Falls Experimental Forest within the Deschutes National Forest. We sampled 16 plots of co-occurring giant chinquapin and Pinaceae trees growing along an elevation gradient. Our data show that the ectomycorrhizal fungal communities on Pinaceae hosts had a greater species richness than those found associated with giant chinquapin. However, 69% (9 of 13) of the dominant taxa (those found ten times or more on Pinaceae hosts) were also found on giant chinquapin. Additionally, the most frequently found taxon on Pinaceae hosts, a *Cenococcum geophilum* strain, was the fifth most frequently found taxa on giant chinquapin. Nearly 50% (25 of 56) of the ectomycorrhizal taxa found on giant chinquapin were also found associated with Pinaceae hosts. Based on these results, giant chinquapin is likely supporting a subset of the Pinaceae ectomycorrhizal community. Giant chinquapin's ability to maintain its presence on the landscape by re-sprouting may benefit conifer seedlings by providing a source of ectomycorrhizal inoculum should overstory conifers be severely damaged.

**PS 2-9 Dense genome sampling of the ectomycorrhizal lineage Russulaceae (Russulales)**

**LOONEY, B.P.<sup>1</sup>**, J. Labbé<sup>2</sup> and P.B. Matheny<sup>1</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA, blooney@vols.utk.edu; <sup>2</sup>Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831, USA.

**Abstract:** Recent evidence suggests that some ectomycorrhizal (ECM) fungi have retained the capability to degrade complex plant biopolymers, thus contributing to carbon cycling in new and unexpected ways. The family Russulaceae, including the genera *Russula*, *Lactarius*, *Lactifluus*, and *Multifuraca*, is one of the most widespread and species rich ECM lineages. Preliminary evidence suggests that members of this family have retained genes responsible for the degradation of the most recalcitrant class of plant biopolymers, lignin. This group has also been implicated as the dominant producer of laccases, enzymes involved in lignin degradation, in leaf litter of hardwood temperate forests. In addition, nitrophilic species of Russulaceae are vital players in the transport of nitrates to ECM plant partners. Here we will present an overview of a project that seeks to utilize dense genome sampling within the family to investigate to what extent genes involved in plant biopolymer degradation have been maintained within a single, diverse ECM lineage. We will present progress and issues involved in sample preparation for genome sequencing, which is considered a major bottleneck towards genome-enabled mycology. Preliminary results and plans for utilizing genomic information in an experimental system investigating the ectomycorrhizome of *Populus* will also be presented.

### PS 3-38 Importance of natural communities of arbuscular mycorrhizal fungi on maize growth in different mineral N and P fertilization scenarios

LOPEZ-CARMONA, D.A.<sup>1</sup>, E. Martínez-Romero<sup>2</sup>, A. Alarcón<sup>3</sup>, J.J. Peña-Cabriaes<sup>4</sup> and J. Larsen<sup>1</sup>

<sup>1</sup>Instituto de investigaciones en Ecosistemas y Sustentabilidad, Universidad Nacional Autónoma de México, Morelia, México, lopezcarda@hotmail.com; <sup>2</sup>Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, México; <sup>3</sup>Colegio de Postgraduados campus Montecillo, Texcoco, México; <sup>4</sup>Centro de Investigación y de Estudios Avanzados, Irapuato, México.

**Abstract:** The importance of natural communities of arbuscular mycorrhizal fungi (AMF) on maize growth was examined in a green house pot experiment with different N and P mineral fertilization scenarios. Natural communities of AMF was obtained from three contrasting maize agroecosystems (low, medium and high input of agrochemicals) and propagated with maize as trap plant in a low P soil. The experiment had a fully factorial design with three main factors: 1) AMF communities (without, low input, medium input and high input), 2) mineral fertilizers (without, complete except P, complete except N and complete) and 3) harvest (3, 6 and 9 weeks after sowing). Each treatment had 4 replicates giving a total of 192 experimental units. Sterile soil mixed with sand (1:1, w/w) was used as growth substrate. Inoculum of natural communities of AMF was mixed into the soil corresponding to 10% of the growth substrate. Plants were grown in 2-liter pots and watered to 80% of the field capacity on a daily basis. At each harvest shoot and root dry weight, N and P shoot content, and AMF root and soil colonization were measured. Strong plant growth promotion and depression was observed for all types of AMF communities in maize grown without mineral P fertilizers and fully fertilized soil, respectively. The AMF communities had no effect on maize growth in treatments without mineral N. As expected AMF root colonization was highest in plants where no P fertilizers were added and lowest in fully fertilized plants. Information on AMF soil colonization in terms of biomarker fatty acids and shoot N and P content are in progress. In conclusion, natural communities of AMF seem to be important in maize growth mainly linked with P nutrition, but the benefits from these natural biological resources depend on the type of fertilization strategy applied.

### PS 3-39 Colonization extent and mycorrhizal responsiveness in genetically modified (Bt) maize using near isogenic lines and a landrace line

Morales-Londoño, D.M.<sup>1</sup>, E. Meyer<sup>2</sup>, D. González<sup>1</sup>, A. González-Hernández<sup>1</sup>, S. Stofel<sup>2</sup>, R.D. Armas<sup>1</sup>, C.R.F.S. Soares<sup>3</sup> and P.E. LOVATO<sup>4</sup>

<sup>1</sup>Plant Genetic Resources Program,, Universidade Federal de Santa Catarina, SC. (Brazil), CEP: 88040-900; <sup>2</sup>Agricultural Science student, Universidade Federal de Santa Catarina, SC. (Brazil); <sup>3</sup>Soil Microbiology Laboratory, Department of Microbiology, Immunology and Parasitology, Universidade Federal de Santa Catarina, SC. (Brazil), CEP: 88040-900; <sup>4</sup>Department of Rural Engineering, Center of Agricultural Sciences, Universidade Federal de Santa Catarina, SC. (Brazil), CEP: 88040-900, paulo.lovato@ufsc.br.

**Abstract:** Genetically modified Bt (modified with *Bacillus thuringiensis* genes) maize is widely grown worldwide, covering 12.9 million hectares in Brazil. Those plants express Cry recombinant proteins in all organs, including roots, and could therefore cause changes in symbiotic microorganism of the rhizosphere such as arbuscular mycorrhizal fungi. Two greenhouse experiments were carried out aiming to assess mycorrhizal root colonization and plant responsiveness in transgenic maize (events: TC1507, BT11 and MON89034), their near isogenic lines, and one landrace widely used by farmers in Santa Catarina (Southern Brazil). In the first experiment, plants of TC1507 maize and its near isogenic line were inoculated with *Rhizophagus clarus* or *Gigaspora albida*. In the second experiment, a landrace called Pixurum 5, BT11 and MON89034 maize and their respective near isogenic lines were inoculated with *Rhizophagus clarus*, *Gigaspora margarita*, or a mixture of those fungi. In both experiments, there were control plants without inoculation. Mycorrhizal colonization frequency, hyphae, arbuscules, storage cells (vesicles or auxiliary cells), as well as plant height, shoot diameter, biomass, and phosphorus content were measured periodically for 60 days. There were transient differences in colonization frequency between each pair of transgenic and its near isogenic line. Mycorrhizal responsiveness was dependent on maize genotype and environmental factors that seem to modulate gene expression. Our results show higher growth and greater accumulation of phosphorus in inoculated landraces, as compared to non-inoculated plants, while in hybrids (genetically modified and their near isogenic lines) this difference was less pronounced. In some cases, non-inoculated plants had greater biomass and presented higher shoot phosphorus contents. In conclusion, genetic plant identity and fungus type were more relevant than introduction of Br genes in determining colonization extent and mycorrhizal responsiveness in maize.

LUOMA, D.L.<sup>1</sup> and J.L. Eberhart<sup>1</sup>

<sup>1</sup>Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR 97331 USA, luomad@fsl.orst.edu.

**Abstract:** Swiss needle cast (SNC) is a disease specific to Douglas-fir (*Pseudotsuga menziesii*) caused by *Phaeocryptopus gaeumannii*. Here we examine characteristics of the EM fungus community that are potentially useful in predictive models that would monitor forest health. We found that mean EM density (number of colonized root tips/soil core) varied nearly 10-fold among sites of varying levels of SNC, while mean EM fungus species richness (number of species/soil core) varied by about 2.5 times. Strong relationships were found between EM and SNC parameters: EM species richness was positively correlated with both Douglas-fir needle retention ( $R^2=0.93$ ) and EM density ( $R^2=0.65$ ); EM density also was significantly correlated with Douglas-fir needle retention ( $R^2=0.70$ ). These simple characteristics of the EM fungus community could be used to monitor forest health and generate predictive models of site suitability for Douglas-fir. Based on previous findings that normally common EM types were reduced in frequency on sites with severe SNC, we also hypothesized that some EM fungi would be stress-tolerant dominant species. Instead, we found that various fungi were able to form EM with the stressed trees, but none were consistently dominant across samples in the severely diseased areas. The 31 EM species obtained from 20 soil cores in the severely diseased areas contrasts with an expected number of 60–65 species found in 20 soil cores from mature Douglas-fir stands in the Cascade Range not affected by SNC. Others have noted that winter temperature increases predicted for the Pacific Northwest correlate with an increased severity and distribution of SNC as a result of changing climate. It appears that anthropogenic disturbance has interacted with regional climate change to perturb the health of forest ecosystems in northern coastal Oregon engendering subsequent impacts on EM fungus diversity.

PS 1-23 Biodiversity of arbuscular mycorrhizal fungi in the Balkan Peninsula

MAČEK, I.<sup>1,2</sup>, Ž.S. Marjanović<sup>3</sup> and F. Oehl<sup>4</sup>

<sup>1</sup>Biotechnical Faculty, University of Ljubljana, Jamnikarjeva 101, 1000 Ljubljana, Slovenia, irena.macek@bf.uni-lj.si;

<sup>2</sup>Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Glagoljaška 8, 6000 Koper, Slovenia; <sup>3</sup>Institute for Multidisciplinary Research, University of Belgrade, Kneza Višeslava 1a, 11 000 Beograd, Serbia; <sup>4</sup>Agroscope, Federal Research Institute of Sustainability Sciences, Plant-Soil Interactions, Reckenholzstrasse 191, CH-8046 Zürich, Switzerland.

**Abstract:** Arbuscular mycorrhizal (AM) fungi are plant root endosymbionts and important, ubiquitous organisms in soils belonging to the phylum Glomeromycota. Despite the fact that they have been proven as an important component of terrestrial ecosystems worldwide, the Balkan Peninsula represents an unstudied geographical region regarding research on any aspect of AM fungal community ecology or biodiversity. The Balkan Peninsula, alongside Iberia, however, harbours the richest flora in Europe, possessing not only the largest number of species but also hosting most endemics. This is also the area where the main Pleistocene refugia for the postglacial colonisation of Europe took place. Within a SCOPES (Scientific Co-operation between Eastern Europe and Switzerland) project, we study biodiversity and community ecology of AM fungi in selected biodiversity hot-spots in Slovenia and Serbia based on concomitant morphological and molecular analyses. Simultaneously, high resolution amplicon sequencing of AM fungal DNA from plant roots and morphologically and molecular-based surveys of AM fungal spores from soil and trap cultures is used in order to study the changes in AM fungal community composition across a range of different ecosystems (e.g., different types of pristine forests, dry grasslands, secondary succession areas). We will test if the observed patterns in AM fungal communities are seasonally stable, and try to determine the main predictors of the spatial and temporal AM fungal community compositional shifts and its stability. Research into this valuable genetic pool is not only important from a biodiversity view point, but also represents a resource for site-directed reclamation of disturbed soils (ecosystems), sustainable forestry, agriculture, and nature conservation that has not been used as such in Balkans so far.

### PS 3-5 Investigating defense-related information transfer between Douglas-fir trees via ectomycorrhizal networks

MADDISON, J.H.A.<sup>1</sup> and S. Simard<sup>1</sup>

<sup>1</sup>Department of Forest and Conservation Sciences, University of British Columbia, Vancouver, BC, Canada, joules53@gmail.com.

**Abstract:** Mycorrhizal fungi link multiple plants together belowground in what are often called “common mycorrhizal networks” (CMNs). Resources such as nutrients, water, and carbon travel between plant neighbors via CMNs. Recent work, particularly in arbuscular mycorrhizal systems, has suggested that defense-related information may also travel between plants via CMNs. While further work in arbuscular mycorrhizal systems has indicated the involvement of the jasmonate pathway in defense-related information transfer, little is known about the potential for this transfer in ectomycorrhizal systems or the specific defense pathways involved. To further explore this area, three main questions were addressed. (1) Are there similar patterns of defense-related information transfer in ectomycorrhizal systems as in arbuscular systems? (2) Does defense-related information transfer happen when eliciting a response using a plant defense hormone, methyl jasmonate (MeJA), as opposed to “natural” pathogens or herbivores? (3) What defense pathways are involved in this process, especially in seedlings potentially “receiving” the defense-related information? Greenhouse-grown microcosms of paired Douglas-fir trees were grown in wild soil containing mycorrhizal inoculum from multiple species. Mycorrhizal network connectivity (controlled by mesh bags of different pore sizes) was crossed with defense-stimulus (MeJA application versus control). Stems from each 11-month-old seedling were harvested either 24 or 48 hours after defense-stimulus treatment, and real-time PCR of selected defense genes was performed on stem tissue to test for the presence and nature of defense responses in both directly-treated and neighboring “receiver” seedlings. Root systems were also harvested and morphotyping of root tips was completed to characterize the mycorrhizal colonization and potential for a CMN between paired seedlings. I will be presenting the data from the morphotyping work as well as selected defense-related gene expression in seedling stem tissues.

### PS 3-40 Indigenous arbuscular mycorrhizal fungi alleviate salt stress and promote growth of cotton and maize in saline fields

Liu, S.<sup>1</sup>, X. Guo<sup>1</sup>, B. MAIMAITILI<sup>2</sup>, X. He<sup>3,4</sup> and G. Feng<sup>1</sup>

<sup>1</sup>College of Resources and Environmental Sciences, China Agricultural University, Beijing, China; <sup>2</sup>Institute of Nuclear Technology and Biotechnology, Xinjiang Academy of Agricultural Science, Urumqi, China, baidengsha@sohu.com; <sup>3</sup>Department of Environmental Sciences, University of Sydney, Eveleigh, NSW 2015, Australia; <sup>4</sup>School of Plant Biology, University of Western Australia, Crawley WA 6009, Australia.

**Abstract:** The functioning of indigenous arbuscular mycorrhizal (AM) fungi for crops is not well addressed because of methodology limitations. In this study, we determined the effects of the indigenous AM fungal community on growth responses and salt tolerance of cotton and maize by a two-year field trial with in-growth microcosms, which were constructed by polyvinylchloride (PVC) tube cores and 30 µm nylon mesh and buried in different saline soils. Two core treatments, including static (allowed AM fungal colonization freely) and vibrating (patted the top core edge to prevent AM fungal colonization), were applied under field conditions. Results showed that vibrating did not affect the growth of non-mycorrhizal sugar beet, but significantly affected the growth of mycorrhizal cotton and maize. Mycorrhizal colonization of cotton and maize were significantly lower under vibrating than under static in all saline soils. Phosphorus uptake and biomass production of cotton and maize were significantly higher in static treatment. AM fungi promoted leaf proline accumulation in cotton and regulated a higher K<sup>+</sup>/Na<sup>+</sup> ratio by selective uptake of more K<sup>+</sup> and less Na<sup>+</sup>. Our results demonstrated that the core systems presented in this study were promising to evaluate the contribution of indigenous AM fungi to crop salt tolerance *in situ*.



## PS 2-40 The Mycological Society of America Student Section

Adams, C.<sup>1</sup>, T. Cheeke<sup>2</sup>, D. Haelewaters<sup>3</sup>, S. Lee<sup>4</sup>, **M. MALTZ**<sup>5</sup>, K. Scharnagl<sup>6</sup>, C. Smyth<sup>7</sup> and J.K. Uehling<sup>8</sup>

<sup>1</sup>University of California, Berkeley, Plant and Microbial Biology Department, 321 Koshland Hall, Berkeley, CA, 94720, USA, miarosequarts@gmail.com; <sup>2</sup>Indiana University, Department of Biology, 1001 East Third Street, Bloomington, IN 47405-7005; <sup>3</sup>Harvard University, Farlow Reference Library and Herbarium of Cryptogamic Botany, 22 Divinity Avenue, Cambridge MA, 02138, USA; <sup>4</sup>Rutgers, The State University of New Jersey, Plant Biology and Pathology, 59 Dudley Road, New Brunswick, NJ, 08901, USA; <sup>5</sup>University of California, Irvine, Ecology and Evolutionary Biology, 321 Steinhaus Hall, Irvine, CA, 92604, USA; <sup>6</sup>Michigan State University, Plant Biology, 612 Wilson Rd, East Lansing, MI 48824; <sup>7</sup>Penn State University, Department of Plant Pathology and Environmental Microbiology, 324 Buckhout Lab, University Park, PA 16802, USA; <sup>8</sup>Duke University, University Program in Genetics and Genomics, 354 Bio Sci, Durham, NC, 27708, USA.

**Abstract:** The Mycological Society of America (MSA) Student Section is a student-run group within MSA, which aims to, (1) facilitate communication among all students of the Society, (2) provide opportunities for students to network with other individuals in their own research fields and beyond, and (3) connect student members of MSA with scientists performing cutting edge mycological research providing the possibility for future collaborations. For the 2014 annual meeting in East Lansing, MI, the Student Section organized the symposium “Fungal functional traits in a changing world,” which discussed both the evolution of selected traits and how key attributes of fungal taxa influence their environment and stress response. In 2015, the Student Section initiated a Mycology Skill Share database that enables students beginning new projects or learning new techniques to easily contact fellow students and other mycologists in specific areas for guidance and/or potential collaboration. For the 2016 MSA meeting in Berkeley, the Student Section is organizing a professional development workshop that will be geared towards preparing graduate students and postdocs for a career in science. The Student Section is open and inclusive, welcoming the participation of graduate students, postdoctoral researchers, and faculty(!) in building and pioneering this group. We hope you can join us at our future events.

## PS 4-19 Sources of inocula influence mycorrhizal colonization of plants in restoration projects: a meta-analysis

**MALTZ, M.R.**<sup>1</sup> and K.K. Treseder<sup>1</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697 USA, mmaltz@uci.edu.

**Abstract:** Inoculation may increase mycorrhizal colonization and provide benefits to plants in restoration projects. However, it is unclear whether inoculation has consistent effects across ecosystem types, if it has long-term effects on colonization, and whether types of inocula differ in their effectiveness. To address these issues, we performed a meta-analysis of published restoration studies across a variety of ecosystems to examine the effects of mycorrhizal inoculation on mycorrhizal establishment and plant growth under field conditions. Across ecosystem types, we found that inoculation consistently increased the abundance of mycorrhizal fungi in degraded ecosystems ( $P < 0.001$ ), and thus improved the establishment of plants ( $P < 0.001$ ). These benefits did not significantly attenuate over time. Moreover, inocula from different sources varied in their effects on mycorrhizal colonization ( $P = 0.047$ ). Inocula sourced from reference ecosystems and inocula with specific fungal species yielded higher increases in mycorrhizal colonization than did inocula from commercial sources. These results suggest that inocula source matters, and that an initial investment into mycorrhizal inoculation could provide lasting benefits for facilitating the establishment of the below- and aboveground components of restored ecosystems.

MANOHARACHARY, C.<sup>1</sup>

<sup>1</sup>Department of Botany, Osmania University, Hyderabad-500007, Telangana state, cmchary@rediffmail.com.

**Abstract:** Soils support varied plant and microbial communities in different climatic and geographic zones with diverse soil conditions. Arbuscular mycorrhizal (AM) fungi are obligate biotrophs belonging to the phylum Glomeromycota forming mutualistic symbiosis with the roots of around 80% of plants. During AM symbiosis, extra-radical hyphae disperse outside the roots to have access to a greater quantity of water and soil minerals for the host plant. In return, the mycobiont receives carbohydrates from plants for the completion of life cycle. The main function is to provide phosphorus and other nutrients to their host plants. AM fungi also help in plant growth, increasing root surface for absorption of water, enhancing flowering and fruiting, optimizing fertilizer use, increasing tolerance to salinity, maintaining soil fertility, and nutrient cycling.

Data pertaining to the following aspects will be presented in this paper:

1. Diversity of arbuscular mycorrhizal fungi – Indian scenario.
2. Discovery of three new AM fungi by the author (*Glomus hyderabadensis*, *G. indica*, and *Acaulospora terricola*).
3. Results pertaining to the impact of AM fungi inoculation under glasshouse conditions on sesame, castor and sunflower. The results indicate increased levels of biomass, NPK, yield, and oil content.
4. Data on the association of AM fungi with some medicinal plants and xerophytes.
5. Role of *Pisolithus tinctorius* in the establishment *Pinus* sp. Seedlings are also discussed.
6. Data on the distribution of AM fungi in polluted and unpolluted soils.
7. Issues related to taxonomic implications of AM fungi in light of the Melbourne Code-2013 will be discussed.

PS 3-41 **Why white truffles (*Tuber magnatum*) cannot be cultivated: isolation and characterization of microorganisms that may play a role in truffle mycorrhization and fruitbody production**

MAROZZI, G.<sup>1</sup>, B. Turchetti<sup>1</sup>, D. Donnini<sup>1</sup>, G.M.N. Benucci<sup>1,2</sup>, G. Bonito<sup>2</sup> and E. Albertini<sup>1</sup>

<sup>1</sup>Department of Agricultural, Food and Environmental Science, University of Perugia, 06121 Perugia, Italy, giorgio.marozzi@studenti.unipg.it; <sup>2</sup>Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing MI 48825.

**Abstract:** Truffles are ascomycetes produced from ectomycorrhizal ascomycetes belonging to *Tuber* spp. Among all truffles, *Tuber magnatum* Pico is the most appreciated because of its peculiar taste and aroma. However, basic aspects of the biology of this *Tuber* species have not been fully elucidated. To date, cultivation of *T. magnatum* (white truffle) is still challenging, and the reason is still unclear. In fact, both the life cycle and soil/environmental conditions stimulating mycorrhizae and ascomycetes formation in *T. magnatum* remain unknown. Several studies have suggested a role played by bacteria, fungi, and yeasts in the development of truffle fruitbodies and aromas, but data are lacking for white truffle. The aim of this study was to describe the whole microbial composition present in two different natural orchards. The analysis was carried out on nine ascomycetes and on soil samples collected at four distances (from 0.20 to 2 meters) from the place where each ascomycete was retrieved. Microorganisms were isolated both from the inside and the outside of each ascomycete as well as from each soil sample. DNA was isolated from all colonies and used for molecular characterization using ITS (internal transcribed spacer rDNA) for fungi (including yeasts) and 16S for bacteria. Our analyses revealed a high level of microbial diversity in these samples, which increased proportionally with the distance from the fruitbody. In contrast, a low but distinct fungal and bacterial diversity level was found inside ascomycetes, indicating that truffle fruitbodies select for a distinct microbiome. For instance, Hypocreales dominated, but Sarcoscyphaceae and Pyrenomataceae were also isolated from the peridium, while Herpotrichiellaceae and Cladosporiaceae were isolated mostly from the gleba. These results will be discussed in more detail pertaining to the autecology and microbiology of *T. magnatum*.

**PS 3-42 Nutritional, physiological and hormonal activity of *Glomus iranicum tenuihypharum* var *nova* a promising species of arbuscular mycorrhiza fungus for intensive agriculture**

**MARTÍN, F.F.<sup>1</sup>**

<sup>1</sup>Symborg.sl. Campus de Espinardo No 7. Edificio CEEIM: CP 30100, Murcia. Spain, felixfernandez@symborg.com.

**Abstract:** Nutritional, physiological, hormonal, and plant productivity responses associated with arbuscular mycorrhizal fungi in different agronomic crops was assessed. *Glomus iranicum tenuihypharum* var *nova* increased absorption of major and minor elements, except for potassium, including a marked increase in iron uptake. Water use efficiency was higher at different time points after inoculation. Hormonal responses and gene expression were related to symbiont activity. Examples of practical applications and production increases in vegetable and fruit crops will be discussed.

**PS 1-51 Distribution of surface-bound phosphatase (SPB) in different parts of mycorrhizal fungi**

Štraus, I.<sup>1</sup>, T. MARTINOVIĆ<sup>1</sup>, T. Mrak<sup>1</sup>, T. Grebenc<sup>1</sup>, M. Kreft<sup>2</sup> and H. Kraigher<sup>1</sup>

<sup>1</sup>Slovenian Forestry Institute, Večna pot 2, 1000 Ljubljana, Slovenia, hojka.kraigher@gozdis.si; <sup>2</sup>Biotechnical Faculty, Department of Biology, and Institute of Pathophysiology, Faculty of Medicine, University of Ljubljana, Večna pot 111, 1000 Ljubljana, Slovenia; Celica Biomedical, Tehnološki park 24, 1000 Ljubljana, Slovenia.

**Abstract:** Root colonization with ectomycorrhizal (ECM) fungi results in increased exploration of the forest soil for P compounds through extramatrical mycelium. Phospho-monoesterases have been extensively studied in terrestrial ecosystems. The determination of surface-bound phosphatase (SBP) activity is based on the hydrolysis of *p*-nitrophenyl phosphate (pNPP) to *p*-nitrophenol phosphate (pNP) and phosphate (P). The present study indicates the distribution of SBP in different parts of ECM tissue (ECM mantle, rhizomorphs, hyphae) of *Scleroderma* sp., which is classified as a long-distance (LD) exploration type (ET). *Scleroderma* species were identified on beech seedlings (*Fagus sylvatica* L.) that were grown for three years in glass rhizotrons (internal size 28x49x2 cm) and had native nursery-derived mycorrhizal colonization. Seedlings were grown at 15–20°C (air temperature) under artificial light (90 ± 5 μmol m<sup>-2</sup>s<sup>-1</sup>). Substrate moisture was automatically regulated to 8%. Occurrence of SBP was investigated with image processed two photon confocal laser scanning microscopy (LSM 7 MP, Zeiss) using the fluorogenic substrate ELF-97 (enzyme-labelled fluorescence), and computer analysis of images was based on the programme ImageJ 1.35j. The threshold was set to be at least 10% of maximal fluorescence intensity. We found active SBP enzymes on the ectomycorrhizal mantle and on the surface of rhizomorphs and hyphae. The distribution of SBP on different parts of ectomycorrhizal structures is discussed with respect to their function in the soil.

**PS 1-24 Mycorrhizal specificity of the partially mycoheterotrophic Ericaceae *Pyrola japonica* (Ericaceae)**

**MATSUDA, Y.<sup>1</sup>**, T. Uesugi<sup>1</sup>, C-F. Chen<sup>2</sup>, M.K. Huh<sup>3</sup>, T. Tanikawa<sup>4</sup>, Y. Hashimoto<sup>5</sup>, T. Yagame<sup>6</sup>, M-A. Selosse<sup>7</sup>, M. Murata<sup>8</sup> and K. Nara<sup>8</sup>

<sup>1</sup>Graduate School of Bioresources, Mie University, Kurimamachiya 1577, 514-8507, Japan, m-yosuke@bio.mie-u.ac.jp; <sup>2</sup>Division of Botanical Garden, Taiwan Forestry Research Institute, 53 Nanhai Road, Taipei, Taiwan; <sup>3</sup>Department of Molecular Biology, Dongeui University, 614-714, Korea; <sup>4</sup>Kansai Research Centre, Forestry and Forest Products Research Institute, Nagai-kyutaro, Momoyama, 612-0855, Japan; <sup>5</sup>Agro-environmental Science, Obihiro University of Agriculture and Veterinary Medicine, Inada-cho, Obihiro, 080-8555, Japan; <sup>6</sup>Tsukuba Botanical Garden, National Museum of Nature and Science, 1-1 Amakubo 4, Tsukuba, 305-0005, Japan; <sup>7</sup>Institut de Systématique, Evolution, Biodiversité (UMR 7205) CP 50, 45 rue Buffon, 75005 Paris, France; <sup>8</sup>Graduate School of Frontier Sciences, the University of Tokyo, 5–1–5 Kashiwanoha, 277-8563, Japan.

**Abstract:** Mixotrophic green plants that obtain carbon sources from both their own photosynthesis and associated mycorrhizal fungi are called partially mycoheterotrophic (PMH) plants. Although fully mycoheterotrophic plants often have a high specificity towards certain mycorrhizal fungal species, limited studies on PMH plants revealed such the specificity. Members of the PMH genus *Pyrola* (Ericaceae) distribute around the Northern Hemisphere and harbor rather a

wide range of fungal associates. However, our previous studies indicated that Asian *P. japonica* from a deciduous forest showed a high specificity towards members of the genus *Russula*. The aim of this study was to identify mycorrhizal associations of *P. japonica* by covering more largely natural distribution of the plants. We hypothesized that *Russula* groups were major mycorrhizal fungi in *P. japonica*, irrespective of the site. Thirty-four adult *P. japonica* plants were collected at 5 sites in 3 countries, including Japan, Korea and Taiwan. Colonized root samples were used for PCR, cloning, RFLP typing and direct sequencings. Although the abundance pattern of detected mycorrhizal fungal taxa varied among study sites, members of ectomycorrhizal Russulaceae and Thelephoraceae consistently occurred at all study sites. These results suggested that Asian *P. japonica* showed a higher specificity to rather limited members of ectomycorrhizal fungi. We discuss the factor affecting the mycorrhizal fungal community in this plant species.

#### **PS 2-28 Isolation of arbuscular mycorrhizal fungi from forest soils in Indonesia and its effect on the growth of *Paraserianthes falcataria***

**MAULANA, A.F.**<sup>1,2</sup>, W. Cheng<sup>2</sup> and K. Tawaraya<sup>2</sup>

<sup>1</sup>United Graduate School of Agricultural Science, Iwate University, Japan, akado\_soul@yahoo.co.id; <sup>2</sup>Faculty of Agriculture, Yamagata University, Japan.

**Abstract:** *Paraserianthes falcataria* is a fast-growing tree species that is economically important and expected to be used for forest rehabilitation of degraded forests in Indonesia. Arbuscular mycorrhizal (AM) fungal colonization of this species and its effect on the growth of this species are not known. The objective of this study was to isolate effective AM fungi from forest soils in Indonesia and to clarify its effect on *P. falcataria* growth. Soils were collected from five different forests (*Tectona grandis* monoculture, *Swietenia macrophylla* monoculture, dipterocarp dominated, *Macaranga* sp.-dominated secondary forest, and a mix forest with *Arthocarpus* sp., *Gmelina* sp., and dipterocarps) and replicated five times. *Paraserianthes falcataria* was grown in each forest soil type in growth chamber (28°C, 16 hours photoperiod) for three months. In total, 32 or 16 morphotypes were collected from soil and used for multi-spore or single spore propagation, respectively, using the same plant species. *Paraserianthes falcataria* or *Trifolium repens* were then inoculated with the spores. One mg P L<sup>-1</sup> nutrient solution was applied as the water and nutrient source. Plant height, fresh shoot and root weight, and root colonization were measured. Number of pots of propagated spores were 3 from 72 pots (multi-spore) or 1 from 124 pots (single spore). There were no significant differences in plant height, leaf number, or root fresh weight between inoculated and non-inoculated *P. falcataria*. Shoot fresh and dry weight of *P. falcataria* inoculated with isolate S6-4 was significantly higher than that of other inoculated and non-inoculated *P. falcataria*. Shoot fresh and dry weight and root fresh weight of all inoculated *T. repens* were significantly higher than that of non-inoculated plants. *Trifolium repens* inoculated with isolate S6-4 exhibited the highest value of those parameters. These findings suggest that AM fungal inoculation for *P. falcataria* can be used for rehabilitation of degraded forests in Indonesia.

#### **PS 3-70 Effects of mycorrhizal fungi on tree seedling growth: quantifying the parasitism-mutualism transition along a light gradient**

Ibáñez, I.<sup>1</sup> and S. MCCARTHY-NEUMANN<sup>2</sup>

<sup>1</sup>School of Natural Resources and Environment, University of Michigan, Ann Arbor, Michigan 48109 USA; <sup>2</sup>Department of Biology, Alma College, Alma, Michigan 48801 USA, neumannsm@alma.edu.

**Abstract:** Mycorrhizal fungi colonize most tree seedlings shortly after germination, and the nature of this relationship (positive, neutral, or negative) has been reported to vary as a function of resources available to the seedlings. Although critical for recruitment success, this transition from parasitism to mutualism has rarely been quantified. In this study, using a light gradient, we planted germinated seeds of eight tree species in soils that varied in resources and that were cultivated by several coexisting species of adult trees. We used data on mycorrhizal fungi colonization of the roots to quantify colonization along the gradient of light levels commonly found in temperate forests. We then analyzed plant performance, i.e., growth, as a function of both the light gradient and extent of mycorrhizal fungi colonization. Finally, we documented the negative/neutral to positive shifts in the tree seedling-mycorrhizal fungi interaction along light levels. The probability of mycorrhizal fungi colonization varied among species but was not correlated with the species' seed sizes or shade tolerances. Within a species, colonization varied among soil sources, but those differences followed neither

the conspecific versus heterospecific dichotomy, nor the soil host's arbuscular mycorrhizal fungi versus ectomycorrhizal fungi associations commonly reported. There were species differences on the level of light at which mycorrhizal fungi colonization started and on how colonization rates responded to an increase in light levels. At high light, seedling growth rates increased with increasing levels of mycorrhizal colonization for seven species. At low light levels, the effect of mycorrhizal colonization was negative for five species. Our analytical framework allowed us to quantify the light threshold at which the plant-mycorrhizal fungi relationship shifted from neutral to positive (four species), negative to neutral (one species), and neutral to negative (one species), documenting differences among species that could exacerbate competitive interactions during the recruitment stages.

#### PS 3-71 Genetic and temporal variation in resource prices of a mycorrhizal market

MEACHUM, M.K.<sup>1</sup> and J.D. Hoeksema<sup>1</sup>

<sup>1</sup>Department of Biology, University of Mississippi, University, Mississippi 38677 USA, mkhornby@go.olemiss.edu.

**Abstract:** Multiple economic theories have been adapted to explain the evolutionary persistence of resource exchange mutualisms such as mycorrhizae. The ratio of resources exchanged between plants and fungi is an important variable common to all these models, and thus measuring resource exchange ratios is the first step in testing the hypotheses generated by these models. We examined how the C:N and C:P exchange ratios established between *Pinus radiata* and an ectomycorrhizal fungus, *Rhizopogon occidentalis*, varied temporally and between native populations of *P. radiata* using a microcosm approach. Exchange ratios were measured at 8, 16, 32, and 64 weeks after inoculation for two genetic families from each of two *P. radiata* native populations. The C:N and C:P exchange ratios varied significantly between the two host populations and varied over time in a manner predicted by theory. Such variation in resource exchange ratios may allow future tests of economic models of mutualisms and may constitute the mechanism behind variation in mycorrhizal fungal compatibility between populations of host plants.

#### PS 1-25 A map of the dominant mycorrhizal associations of the United States of America

MICHAEL, H.E.<sup>1</sup>, R.L. Swaty<sup>2</sup> and C.A. Gehring<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA, hem63@nau.edu; <sup>2</sup>The Nature Conservancy's LANDFIRE team, 101 S. Front Street, Marquette, MI 49855 USA.

**Abstract:** Environmental changes such as warming temperatures, land-use change, invasive species, drought and stand-replacing wildfires have significantly altered the distribution of vegetation communities around the world. Some of these changes may be large enough to alter the type of mycorrhizal fungal association that dominates an ecosystem. However, our ability to document these changes and predict their consequences is poor because we do not have a detailed map that integrates data on dominant vegetation with type of mycorrhizal association. We combined data on mycorrhizal associations from the literature with detailed Biophysical Settings (BpS) data from LANDFIRE for the conterminous U.S. LANDFIRE is a program shared between the wildland fire management programs of the U.S. Department of Agriculture Forest Service and U.S. Department of the Interior that provides landscape scale geo-spatial products, including vegetation mapped using extensive field-referenced data, satellite imagery and biophysical gradient layers. The BpS data represents vegetation on the landscape prior to Euro-American settlement, based on the biophysical environment and natural disturbance regimes. We found that most areas of the United States were dominated by vegetation associated with arbuscular mycorrhizal fungi. However, large tracts of land in several parts of the US were dominated by ectomycorrhizal fungi and many areas had several types of mycorrhizal associations in nearly equal abundance. The map we have developed establishes a baseline of mycorrhizal associations against which the consequences of vegetation shifts with climate change and other stressors can be compared. LANDFIRE maps have been used previously to model conservation risk associated with land conversion. The addition of data on mycorrhizal associations will improve predictions of the types of vegetation that will establish post-disturbance and allow more detailed modeling of the differential functions of varying types of mycorrhizal fungi such as soil carbon storage.



MINO, L.A.<sup>1</sup> and G.W.T. Wilson<sup>1</sup>

<sup>1</sup>Department of Natural Resource Ecology and Management, Oklahoma State University, Stillwater, Oklahoma 74074 USA, l.ann.mino@gmail.com.

**Abstract:** Historically, vast areas of Great Plains grasslands were lost due to conversion to row-crop agriculture. Currently, it is estimated that as little as 1% of the historical range is still intact, and these tracts are threatened by a variety of global change phenomena. One of the greatest current threats to grasslands worldwide is the expansion of woody species. While many studies have documented aboveground consequences of encroachment, little research exists on belowground ecosystem-level effects, such as arbuscular mycorrhizal fungi (AMF) abundance and soil aggregate stability, following woody plant establishment. Mycorrhizal interactions have previously been shown to play a critical role in native plant species dominance and contribute to soil function of tallgrass prairie ecosystems. Woody species expanding their native ranges may competitively engage in mycorrhizal interactions, but the potential competitive interactions between native grasses and encroaching woody species has not yet been determined. Our study assesses abiotic and biotic soil characteristics of native tallgrass prairie and adjacent areas with established stands of the following woody species: *Juniperus virginiana*, *Cornus drummondii*, and *Gleditsia triacanthos*. Our results indicate woody encroachment and establishment of these species may result in species-specific alterations in biotic and abiotic soil characteristics. Alteration in soil characteristics may be one mechanism facilitating the rapid conversion of grasslands to woodland species, and may be a challenge to restoration following removal of the woody species.

PS 1-26 Ectomycorrhizal symbionts of *Dryas octopetala* L., an arctic-alpine plant, along an altitudinal gradient – species diversity and host specificity

MLECZKO, P.<sup>1</sup>, A. Ronikier<sup>2</sup> and M. Ronikier<sup>2</sup>

<sup>1</sup>Institute of Botany, Jagiellonian University in Krakow, Krakow, Poland, piotr.mleczko@uj.edu.pl; <sup>2</sup>Institute of Botany, Polish Academy of Sciences, Krakow, Poland.

**Abstract:** Mountain avens, *Dryas octopetala*, is one of the key arctic-alpine vascular plants of circumpolar distribution forming ectomycorrhizal symbioses with fungi. In Europe, apart from the (sub)arctic tundra, it inhabits alpine zones of temperate mountain ranges, including the Carpathians. Low-elevation populations of this plant are also known and considered post-glacial relicts. We have investigated the mycorrhizal symbionts of *D. octopetala* in the Carpathians to determine: (1) presence of host-specific fungal symbionts of *D. octopetala* at different altitudinal localities, (2) changes of fungal diversity and identity with altitude and (3) presence of arctic-alpine fungal species at low-elevation localities of *D. octopetala*. The last issue in particular will allow us to assess the nature of arctic-alpine ectomycorrhizal fungi and determine whether their distribution is driven by climatic factors or specificity to the plant host. Intact soil cores with plant root systems were collected from populations growing in three climatic-vegetation belts: alpine belt – typical area of the species occurrence, subalpine belt – the area to which the species descends naturally, forest belt – the area of the relict populations occurrence (two sites per category and 5 samples per site, two sampling seasons). Morphotype analysis and molecular barcoding (ITS sequencing) were applied to compare ectomycorrhizal communities of *D. octopetala*. Our results indicate that: (1) *D. octopetala* forms symbioses with a wide variety of fungi, possibly over 50 species, in the investigated area, (2) altitude does not influence the diversity of its ectomycorrhizal fungal symbionts, (3) the identity of fungal partners differs considerably between localities, regardless of climatic-vegetation zone, indicating no clear host specificity between symbionts.

**MOLINIER, V.**<sup>1,2</sup>, D. Wipf<sup>2</sup>, C. Murat<sup>3,4</sup>, R. Splivallo<sup>5,6</sup>, S. Egli<sup>1</sup> and M. Peter<sup>1</sup>

<sup>1</sup>Swiss Federal Institute for Forest Snow and Landscape Research (WSL), 8903 Birmensdorf, Switzerland, virginie.molinier@wsl.ch; <sup>2</sup>Université de Bourgogne, UMR Agroecologie INRA /Agrosup/u. Bourgogne, Pole Interactions Plantes Microorganismes ERL 6300CNRS, BP 86510, 21065 Dijon Cedex, France; <sup>3</sup>Université de Lorraine, UMR1136 Interactions Arbres-Microorganismes, F-54500 Vandoeuvre-les-Nancy, France; <sup>4</sup>INRA, UMR1136 Interactions Arbres-Microorganismes, F-54280 Champenoux, France; <sup>5</sup>Goethe University Frankfurt, Institute for Molecular Biosciences, 60438 Frankfurt am Main, Germany; <sup>6</sup>Integrative Fungal Research Cluster (IPF), Georg-Voigt-Str. 14-16, 60325 Frankfurt am Main, Germany.

**Abstract:** *Tuber aestivum* (Vittad.) is an ectomycorrhizal fungus found throughout Europe. Whether natural populations consist of different genetic ecotypes and how the fungus completes its life cycle is still largely unknown. Genome sequencing and development of microsatellites markers allowed us to obtain a deep insight into its genetic structure. Here we present data from several hundreds of fruitbodies collected all over Europe as well as within single forest stands. At the European scale, our purpose was to identify possible genetic clusters. At smaller scales, our aims were to study temporal and spatial dynamics of genets, to assess the distribution of mating type strains of this heterothallic ascomycete and to understand how genetic structuring along with fruitbody maturation and geographical origin influence truffle aromas. In Europe, we could identify four genetic clusters suggesting the existence of different ecotypes of *T. aestivum*. With the exception of one cluster, which was exclusively present in South-Eastern France, Italy, and Spain, the other clusters did not show a clear geographical separation. A significant deficit of heterozygosity indicated population expansion in Europe. At smaller scales, genetic diversity was high and an important yearly turnover was found. The genet sizes were generally small but some could reach up to 150 m. Genetic differentiation could be detected between and within forest sites indicating the existence of ecotypes among which gene flow might be limited by biological or ecological barriers. Unlike to what has been observed for *T. melanosporum*, the mating type distribution was not clearly clustered. Finally, geographical origin or maturity only had minor effects on aroma profiles but genetic structuring had a pronounced influence on the concentrations of some odorants. Results presented give a pioneering vision about the genetic structure of *T. aestivum* which allows for a better understanding of the biology and life history of this natural forest resource.

Tuesday Banquet Lecture **International Culture Collection of Arbuscular Mycorrhizal Fungi (INVAM): A 25 year perspective**

**MORTON, J.B.**<sup>1</sup>

<sup>1</sup>West Virginia University, 1090 Agricultural Sciences Building, Morgantown, WV 26506-6108, USA, jbmorton@mail.wvu.edu.

**Abstract:** Considerable knowledge has been gained from the management of an International Culture Collection of Arbuscular Mycorrhizal Fungi (INVAM) for 25 years. Notable advances have been made through reliable maintenance of diverse fungal stocks and a wide range of collaborations. Sustainability of cultures has been achieved by making use of low host and ecological specificity and standardizing host plant (sudangrass) and a low nutrient sand soil mix, all grown for <5 months and then stored. Under these conditions, <8% of stocks have been lost and more than 70% have been productive for longer than 10-15 years. Inoculum potential assays have provided an indispensable tool to test quality of inoculants and other products, to screen stocks for soil or host compatibility, and to establish equivalent between stocks with disparate life history traits. Morphological studies have provided criteria for maintaining purity and quality of ca. 1,100 strains of 112 species representing all but two genera. Support from LSU and TUB2 sequences, as well as expressed protein profiles, is helping to clarify relationships at all scales. Intraspecific variation is especially important; 22 species are represented by >10 strains, six of which have >50 widely distributed strains. These stocks are clarifying species grouping and ranking criteria, biogeographic distribution, ranges of adaptation, and patterns of transmission by endosymbionts. Species are broadly classified as “r” versus “k” based on rate of mycorrhizal development and proportionality between colonization and sporulation to assist in germplasm choices. As a public resource, the number of annual users and stock usage has averaged 62 and 340, respectively. Future plans include transitioning to a new curator in 2017, investing in metagenomic analyses, expanding web-based approaches for education and training, and improving networking with other major collections to establish standard best practices.

## PS 2-41 Identification of mycorrhizal partners in heterogeneous samples

**MRÁK, T.**<sup>1</sup>, J. Gričar<sup>1</sup> and H. Kraigher<sup>1</sup>

<sup>1</sup>Slovenian Forestry Institute, Večna pot 2, 1000 Ljubljana, Slovenia, tanja.mrak@gozdis.si.

**Abstract:** Sampling of mycorrhiza in natural stands where multiple tree and bush species grow together is inevitably connected to a problem of tree root identification. Without the possibility to define exactly which mycorrhizal species belongs to which partner species, a lot of information about a host range of mycorrhizal fungi is lost. Compared to the molecular tools, which are still costly, time consuming, and are not appropriate for quantification of tree species occurrence, morphological-anatomical identification of tree roots can provide swift results. To develop the most effective approach, we selected twelve common temperate European tree species, eight broadleaf and four conifers. From each species, roots of diameters 5, 3 and 1 mm as well as the most distal fine roots from three to five individuals were sampled. Anatomy was studied on transversal and longitudinal sections with a light microscope, and for morphological investigation, roots were observed under a dissecting microscope and photographed. In cases where morphological investigation (colour and texture of the bark, pattern of ramification) does not provide reliable results (e.g., due to pieces of roots too small for investigation, similarity between some species), anatomical study is necessary. We already found that 1 mm thick roots can be identified reliably based on anatomical characteristics. However, for anatomical identification of roots, specific determination keys are needed because the anatomy of roots does not correspond exactly to the anatomy of stem. In particular, characteristics of radial root sections differ significantly from the characteristics of radial stem sections. In all investigated broadleaf species, we were consistently able to observe different patterns in porosity and growth rings and the smaller size of root wood vessels compared to the stem wood.

## PS 3-72 Host species drives arbuscular mycorrhizal fungal community structure in a Mexican tropical seasonally dry forest

Morgan, B.<sup>1,2</sup>, **G.M. MUELLER**<sup>1,2</sup> and L. Egerton-Warburton<sup>1,2</sup>

<sup>1</sup>Chicago Botanic Gardens, Glencoe, IL 60022, USA; <sup>2</sup>Northwestern University, Evanston, IL 60208, USA, gmueller@chicagobotanic.org.

**Abstract:** Tropical seasonally dry forests are highly threatened by anthropogenic global climate change and rapid urbanization. Arbuscular mycorrhizal fungi (AMF) are the dominant fungal symbionts of plants in these systems, and are essential drivers of plant individual fitness and community properties, including diversity and resilience. Despite this, the diversity, host specificity, and functional roles of AMF remain poorly resolved, particularly in tropical systems. In this study, we address this challenge in a Mexican tropical seasonally dry forest system by sampling AMF communities from the roots and surrounding soil of five ecologically important tree species (*Brosimum alicastrum*, *Bursera simaruba*, *Ceiba pentandra*, *Metopium brownei*, and *Vachellia cornigera*) from two minimally managed sites in the Yucatan Peninsula. Using ultra-high-throughput Illumina sequencing of a ribosomal DNA fragment, we identified 188 molecular taxa, over 98% of which were identified to genus or species with at least 80% confidence, and documented significant effects of both host species and site on AMF community structure. While the majority of AMF taxa were assigned to the genus *Glomus*, distinct communities hosted by different tree species were primarily differentiated by the abundance of *Diversispora* species. These results indicate that communities of these essential plant symbionts are highly diverse and variable across this ecosystem, suggesting that conservation and restoration efforts cannot assume that small, protected areas adequately protect regional AMF biodiversity, and there is a need to specifically account for AMF to promote resilience of dominant plant communities. Our study finds the highest single-site diversity of AMF reported to date, and identifies host species-specific communities, while the methods established in this study provide an avenue for further investigating the drivers of AMF community assembly.

## PS 1-27 Phylogeny and diversification of *Laccaria*

Wilson, A.W.<sup>1</sup>, K. Hosaka<sup>2</sup> and G.M. MUELLER<sup>1</sup>

<sup>1</sup>Chicago Botanic Garden, Glencoe, Illinois, 60022 USA, gmueller@chicagobotanic.org; <sup>2</sup>Department of Botany, National Museum of Nature and Science (TNS) Tsukuba-shi, Ibaraki 305-0005, Japan.

**Abstract:** *Laccaria* has been used as a model for understanding the evolution, distribution, and ecology of fungi that form ectomycorrhizas. The ability of a number of its species to grow in axenic culture is one of the reasons for this. This ability to form sterile cultures in vitro without a host suggests that the group has retained some free-living, saprobic capabilities. However, the age of the most recent common ancestor for all ECM *Laccaria* is not known, making it problematic to assess the evolution of either ECM or saprobic metabolism in the clade. A multigene phylogeny encompassing the taxonomic and geographic diversity of the group was generated to resolve phylogenetic relationships within the clade and produce a more accurate estimation of the group's diversity and geographic patterns. Molecular dating and diversification analyses provided a better understanding of *Laccaria*'s evolutionary history. Numerous undescribed species were uncovered, and all species in the genus have discrete distribution patterns. Species from temperate South America and Australasia form a basal paraphyly while North Hemisphere taxa form a well-supported clade nested within the austral paraphyly. We detect a vicariance signal, but dispersal and subsequent radiations are responsible for the current distribution patterns. While most species display some degree of host specificity or host preference, evidence of host driven distribution patterns was not evident and the distribution patterns of *Laccaria* species are the result of evolutionary histories independent of their hosts. The split between *Laccaria* and its presumed sister group, represented by *Mythicomyces corneipes*, has a median age of 68 MYBP (HPD 63.5-77.3 MYBP). Major diversification occurred 12-20 MYBP, with the Northern Hemisphere showing an increased diversification rate. We observe a strong correlation between diversification in the clade and the evolution of the ectomycorrhizal habit.

## PS 4-41 What drives mycorrhizal community structure? Using orchids as a study model

MUJICA, M.I.<sup>1,2</sup>, F. Pérez<sup>1,2</sup> and M.A. Selosse<sup>3</sup>

<sup>1</sup>Departamento de Ecología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Alameda 340, Santiago, Chile; <sup>2</sup>Institute of Ecology and Biodiversity (IEB), Alameda 340, Santiago, Chile, mujisa@gmail.com; <sup>3</sup>Institut de Systematique, Evolution, Biodiversite (ISYEB - UMR 7205-CNRS, MNHN, UPMC, EPHE), Museum national d'Histoire naturelle, Sorbonne Universites, 57 rue Cuvier, CP50, 75005 Paris, France.

**Abstract:** One of the major questions in mycorrhizal ecology is what determines the structure of mycorrhizal communities. In order to answer this question, several conceptual and mathematical models have emerged. However, the development of a general theoretical basis for the study of mycorrhizas, with predictive models of the relationship between mycorrhizal fungal communities and environment, is still needed. The Orchidaceae is an extremely diverse and globally distributed family of plants that associates with a relatively narrow group of mycorrhizal fungi in comparison to other plant families. In this presentation, we aim to show that orchids have unique features that position them as an ideal system to answer general questions of mycorrhizal ecology. We reviewed all the hypotheses and models that have been proposed to understand what determines the structure, in terms of species richness, abundance and composition, of mycorrhizal communities, and classify them into what are, in our opinion, the main drivers that structure those communities. We assess how these different ecological and evolutionary drivers affect mycorrhizal assemblages, what is known for the case of orchid mycorrhizal associations, and what contributions can be made from this study model. We hope this proposal promotes theoretical progress in the study of plant-mycorrhizas, motivates empirical research, encourages the formulation of hypotheses and predictions, and stimulates the use of orchid mycorrhizal system as a model to understand what drives the structure of mycorrhizal communities.

Kühndorf, K.<sup>1</sup>, B. MÜNZENBERGER<sup>1</sup>, D. Begerow<sup>2</sup>, J. Gómez-Laurito<sup>3</sup> and R.F. Hüttl<sup>4</sup>

<sup>1</sup>Institute of Landscape Biogeochemistry, Leibniz Centre for Agricultural Landscape Research (ZALF), 15374 Müncheberg, Germany, [bmuenzenberger@zalf.de](mailto:bmuenzenberger@zalf.de); <sup>2</sup>AG Geobotany, Ruhr-University of Bochum, 44780 Bochum, Germany; <sup>3</sup>Escuela de Biología, University of Costa Rica, CP11501-2060 San José, Costa Rica; <sup>4</sup>Chair of Soil Protection and Recultivation, Brandenburg University of Technology Cottbus-Senftenberg, 03013 Cottbus and German Research Centre of Geosciences Potsdam (GFZ), 14473 Potsdam, Germany.

**Abstract:** Arbutoid mycorrhizal plants are commonly found as understory vegetation in forests worldwide where ectomycorrhiza-forming trees occur. *Comarostaphylis arbutoides* (Ericaceae) is a tropical woody plant and common in tropical Central America. This plant forms arbutoid mycorrhiza, whereas only associations with *Leccinum monticola* as well as *Sebacina* sp. are described so far. We collected arbutoid mycorrhizas of *C. arbutoides* from the Cerro de la Muerte (Cordillera de Talamanca), Costa Rica, where this plant species grows together with *Quercus costaricensis*. We provide here the first evidence of mycorrhizal status for the Ascomycete *Leotia* cf. *lubrica* (Helotiales) that was so far under discussion as saprophyte or mycorrhizal. This fungus formed arbutoid mycorrhiza with *C. arbutoides*. The morphotype was described morphologically and anatomically. *Leotia* cf. *lubrica* was identified using molecular methods, such as sequencing the internal-transcribed spacer (ITS) and the large subunit (LSU) ribosomal DNA regions, as well as phylogenetic analyses. Specific plant primers were used to confirm *C. arbutoides* as the host plant of the leotioid mycorrhiza.

### CS 3-5 Comparative genomics of ectomycorrhizal basidiomycetes and ascomycetes provides new insights into the symbiosis evolution

MURAT, C.<sup>1</sup>, A. Kohler<sup>1</sup>, E. Morin<sup>1</sup>, T. Payen<sup>1</sup>, B. Henrissat<sup>2</sup>, P. Wincker<sup>3</sup>, A. Kuo<sup>4</sup>, I.V. Grigoriev<sup>4</sup>, D.S. Hibbett<sup>5</sup>, Mycorrhizal Genome Initiative Consortium and F. Martin<sup>1</sup>

<sup>1</sup>INRA, UMR 1136 INRA-Université de Lorraine, Interactions Arbres/Microorganismes, Laboratoire d'Excellence ARBRE, INRA-Nancy, 54280 Champenoux, France, [claud.murat@nancy.inra.fr](mailto:claud.murat@nancy.inra.fr); <sup>2</sup>UMR7257, Aix-Marseille Université, 13288 Marseille, France; <sup>3</sup>Genoscope, 91057 Evry Cedex, France; <sup>4</sup>US DOE-JGI, Walnut Creek, CA 94598, United States; <sup>5</sup>Department of Biology, Clark University, Worcester, MA, USA.

**Abstract:** To elucidate the genetic basis of the evolution of the mycorrhizal lifestyle, we have sequenced a large set of fungal genomes, including ectomycorrhizal (ECM), orchid (ORM) and ericoid (ERM) species, and saprotrophs, which we analyzed along with other publicly available fungal genomes. In our first analysis, we focused on Agaricomycotina genomes showing that the ECM symbiosis evolved several times over the last 180 million years from white-rot, brown-rot, and litter decayers. Ectomycorrhizal fungi in the Agaricomycotina present a reduced complement of genes encoding plant cell wall-degrading enzymes (PCWDEs) as compared to their ancestral wood decayers. Nevertheless, they have retained a unique array of PCWDEs playing a role in the symbiosis development. On the other hand, ERM and ORM fungal species have a strikingly large arsenal of genes coding for PCWDE, confirming their significant saprotrophic ability. Of the induced genes in symbiotic tissues, 7–38% are orphan genes, including genes that encode secreted effector-like proteins. Convergent evolution of the ECM habit in Agaricomycotina occurred via the repeated evolution of a ‘symbiosis toolkit’ with reduced numbers of PCWDEs and lineage-specific suites of mycorrhiza-induced genes. In a second study, we aimed to investigate genome evolution and gene repertoire idiosyncrasies in Pezizomycetes, an early diverging class in Ascomycotina, having different lifestyles (mycorrhizal, such as truffles, versus saprotroph). Similar to basidiomycetous ECM species, Tuberaceae have a reduced content of PCWDE genes, although the cellobiohydrolase GH6 is found in these symbiotic species. Species-specific secreted effector-like proteins were not detected in *Tuber melanosporum*. These studies provided new insights into the ECM symbiosis evolution highlighting divergence and convergence between Basidiomycetes and Pezizomycetes species.



**NASRABADI, S.E.<sup>1</sup>**, C.N Guppy<sup>1</sup>, O.G.G Knox<sup>1</sup>, D Backhouse<sup>1</sup> and R.E Haling<sup>1,2</sup>

<sup>1</sup>School of Environmental and Rural Science, University of New England, Armidale NSW 2351, Australia, seskanda@une.edu.au; <sup>2</sup>CSIRO Plant Industry, Canberra ACT 2601, Australia.

**Abstract:** The majority of cotton growing regions in Australia are sodic. Cotton is a reputedly mycorrhizal dependent plant, but physical and chemical properties of sodic soils could affect mycorrhizal colonization of cotton. We investigated the development of arbuscular mycorrhizas on cotton in a low phosphorus, sodic soil (ESP=21%) in a series of glasshouse experiments. Initially three inoculum sources, two commercial inoculums and a field soil known to cause good colonisation (83%), were added at 10% w/w and mixed throughout the pot. An uninoculated control was included and colonisation assessed after 3 weeks. In the second experiment, cotton plants with one of the commercial inoculants were grown for 6 weeks. In the third experiment, cotton was grown for 6 weeks in the presence of a root based inoculum source, which comprised 20 g of soil and highly colonised (91%) maize (*Zea mays* L.) root pieces placed 3 cm below the seeds. Control treatments received either the same amount of autoclaved soil and root inoculum or no inoculum. No mycorrhizal cotton roots were detected in sodic soil without inoculum after 3 or 6 weeks. Similarly, both commercial inoculums and field soil when added to a sodic soil at 10% of the volume failed to colonize cotton roots. In the third experiment, percentage of root length colonized in control sodic soils was 1%, which increased significantly to 18 % with inoculum. The autoclaved non-sodic soil with inoculum resulted in 37% colonisation, which was significantly higher than in the sodic soils, whilst fresh non-sodic soil with inoculum had 83% colonisation. These experiments imply a reduction in the ability of cotton to form mycorrhizal symbioses in highly sodic soils. If cotton is mycorrhizally dependant, the chemical, physical or biological changes in soil reducing colonisation require further investigation.

LT 1-9 **FUNGuild: an open annotation tool for parsing high-throughput fungal molecular data by ecological guild**

**NGUYEN, N.H.<sup>1</sup>**, Z. Song<sup>2</sup>, S.T. Bates<sup>2</sup>, S. Branco<sup>3</sup>, L. Tedersoo<sup>4</sup>, J. Menke<sup>1</sup>, J. Schilling<sup>5</sup> and P.G. Kennedy<sup>1,6</sup>

<sup>1</sup>Department of Plant Biology, University of Minnesota, St. Paul, MN, USA, nhnguyen@umn.edu; <sup>2</sup>Department of Plant Pathology, University of Minnesota, St. Paul, MN, USA; <sup>3</sup>Department of Plant and Microbial Biology, University of California Berkeley, Berkeley, CA, USA; <sup>4</sup>Natural History Museum, University of Tartu, Tartu, Estonia; <sup>5</sup>Department of Bioproducts and Biosystems Engineering, University of Minnesota, St. Paul, MN, USA; <sup>6</sup>Department of Ecology, Evolution, and Behavior, University of Minnesota, St. Paul, MN, USA.

**Abstract:** Fungi typically live in highly diverse communities composed of multiple ecological guilds. Although high-throughput sequencing has greatly increased the ability to quantify the diversity of fungi in environmental samples, researchers currently lack a simple and consistent way to sort large sequence pools into ecologically meaningful categories. We address this issue by introducing FUNGuild, a tool that can be used to taxonomically parse fungal OTUs by ecological guild independent of sequencing platform or analysis pipeline. Using a database and an accompanying bioinformatics script, we demonstrate the application of FUNGuild to three high-throughput sequencing datasets from different habitats: forest soils, grassland soils, and decomposing wood. We found that guilds characteristic of each habitat (i.e., saprotrophic and ectomycorrhizal fungi in forest soils, saprotrophic and arbuscular mycorrhizal fungi in grassland soils, and saprotrophic, wood decomposer, and plant pathogenic fungi in decomposing wood) were each well represented. The example datasets demonstrate that while we could quickly and efficiently assign a large portion of the data to guilds, another large portion could not be assigned, reflecting the need to expand and improve the database as well as to gain a better understanding of natural history for many described and undescribed fungal species. As a community resource, FUNGuild is built for open sourcing and annotation, so we invite researchers to populate it with new categories and records as well as refine those already in existence.

**LT 3-1 Influence of mineral nitrogen sources ( $\text{NO}_3^-$ -N vs.  $\text{NH}_4^+$ -N) on arbuscular mycorrhiza development and N transfer in a *Rhizophagus irregularis* symbiosis**

**NGWENE, B.**<sup>1</sup>, J. Mertens<sup>1</sup>, T. Splettstößer<sup>1</sup>, E. Gabriel<sup>2</sup> and E. George<sup>1</sup>

<sup>1</sup>Leibniz-Institute of Vegetable and Ornamental Crops Grossbeeren and Erfurt e.V., Theodor-Echtermeyer-Weg 1, 14979 Grossbeeren, Germany, ngwene@igzev.de; <sup>2</sup>Department of Aridland Agriculture, Faculty of Food and Agriculture, UAE University, P.O. Box 17555, Al Ain, United Arab Emirates.

**Abstract:** Labeled nitrogen ( $^{15}\text{N}$ ) was applied to a soil-based substrate in order to study the uptake of N by *Rhizophagus irregularis* extraradical mycelium (ERM) from different mineral N ( $\text{NO}_3^-$  vs.  $\text{NH}_4^+$ ) sources and the subsequent transfer to plants. Fungal compartments (FCs) were placed within the plant growth substrate to simulate soil patches containing root-inaccessible, but mycorrhiza-accessible, N. The fungus was able to take up both N-forms,  $\text{NO}_3^-$  and  $\text{NH}_4^+$ . However, at a low N supply level, the amount of N transferred from the FC to the plant was higher when  $\text{NO}_3^-$  was applied to the FC. Analysis of ERM harvested from the FC showed a higher  $^{15}\text{N}$  enrichment when the FC was supplied with  $^{15}\text{NH}_4^+$  compared with  $^{15}\text{NO}_3^-$ . The  $^{15}\text{N}$  shoot/root ratio of plants supplied with  $^{15}\text{NO}_3^-$  was much higher than that of plants supplied with  $^{15}\text{NH}_4^+$ , indicative of a faster transfer of  $^{15}\text{NO}_3^-$  from the root to the shoot and a higher accumulation of  $^{15}\text{NH}_4^+$  in the root and/or intraradical mycelium. In contrast, at a higher N supply level,  $^{15}\text{NH}_4^+$  was transferred preferably as compared to  $^{15}\text{NO}_3^-$ . This study further showed an interaction between the two N forms as there was a tendency for the presence of  $\text{NH}_4^+$  to enhance  $^{15}\text{NO}_3^-$  uptake under high  $\text{NH}_4^+$   $\text{NO}_3^-$  supply, whereas the presence of  $\text{NO}_3^-$  depressed  $^{15}\text{NH}_4^+$  uptake under high  $\text{NH}_4^+$   $\text{NO}_3^-$  supply. It was concluded that the hyphae of the arbuscular mycorrhizal fungus may absorb  $\text{NH}_4^+$  preferentially over  $\text{NO}_3^-$  but that export of N from the hyphae to the root and shoot may depend on the amount of N supplied or available for uptake. The influence of the substrate CEC and the need for N to be assimilated into organically bound forms prior to transport into the plant is discussed.

**SY 4-3 The role of ectomycorrhizal fungi in Pinaceae invasions: evidence from Isla Victoria, Argentina**

**NUÑEZ, M.A.**<sup>1</sup>, T.R. Horton<sup>2</sup>, J. Hayward<sup>3</sup>, R.D. Dimarco<sup>4</sup>, M. Sorensen<sup>5</sup> and D. Simberloff<sup>6</sup>

<sup>1</sup>INIBIOMA, CONICET-Universidad del Comahue, Bariloche, 8400, Argentina, Nunezm@gmail.com; <sup>2</sup>Department of Environmental and Forest Biology SUNY-ESF, Syracuse, NY 13210, USA; <sup>3</sup>Department of botany, University of Hawaii at Manoa Honolulu, HI 96822, USA; <sup>4</sup>INTA-CONICET, Bariloche 8400, Argentina; <sup>5</sup>The university of Copenhagen, Copenhagen, Denmark; <sup>6</sup>Department Of EEB, University of Tennessee, Knoxville 37996, USA.

**Abstract:** Mycorrhizal fungal invasion and the role of mycorrhizal fungi in plant invasions were historically ignored. There is now enough evidence to show how complex and important belowground interactions in plant invasions are. Here we describe work conducted on Isla Victoria in Nahuel Huapi National Park. During the last 10 years we have conducted research on Pinaceae invasions, a major problem in the Southern hemisphere, with a focus on the role of ectomycorrhizal fungi. We used a series of greenhouse, field, and lab studies. We have found that mycorrhizal fungi can be a major factor limiting Pinaceae invasion, with seedling establishment and growth far from plantations being limited by a lack of mycorrhizal inoculum. Also, results from inoculation studies with animal feces showed that animals seem to be the main dispersal vectors of compatible mycorrhizal fungi in the area since field experiments showed that wind dispersal of propagules from sporocarps is limited. With a large field experiment (320 pots under different treatments, 10 liters each of intact soil monolith), we have found that mycelial networks associated with exotic Pinaceae seem to be promoting invasion fronts of Pinaceae. When seedlings grew connected to a network of exotic trees, they grew significantly bigger than when isolated from such networks. However, in native forest areas distant from any exotic trees, isolation from the native networks was an advantage. This suggests a new mechanism for biotic resistance, where the fungal network of the native trees can reduce the establishment of exotic trees, perhaps through competitive interactions between the native and exotic networks. These results from Isla Victoria suggest that mycorrhizal fungi can play a complex and important role in tree invasion. It is clear from these results that studying ectomycorrhizal tree invasion without studying their mycorrhizal symbionts can lead to an incomplete understanding of the invasion process.

**PS 4-73 Responses of potato (*Solanum tuberosum*) to *Glomus* sp. combined with *Pseudomonas diminuta* at different rates of NPK fertilizers**

**NURBAITY, A.<sup>1</sup>**, E.T. Sofyan<sup>1</sup> and J.S. Hamdani<sup>1</sup>

<sup>1</sup>Faculty of Agriculture, Universitas Padjadjaran, Bandung 40600, Indonesia, annenurbaity@unpad.ac.id.

**Abstract:** Conventional farming for potato production in Indonesia has been using NPK fertilizers at high application rates. Any adverse environmental effects that might arise through this fertilizer use should be avoided. Application of bio-inoculants consisting of arbuscular mycorrhizal fungi (*Glomus* sp.), isolated from a potato farming area, and mycorrhizal helper bacteria (*Pseudomonas diminuta*) have been tested in an effort to reduce the use of NPK rates in the production of potato crops. The inoculant was pot-cultured prior to its application on potato crops. The controlled-field site experiment used mixtures of *Glomus* sp. spores and an inoculant of *P. diminuta* applied at different rates of NPK fertilizer. Results of the experiment showed that application of *Glomus* sp. and *P. diminuta* reduced the use of NPK by up to 50%, while the growth, nutrient uptake (N, P, K), and the potato tubers responded in similar way to the highest recommend rate of NPK fertilizer (being applied by the farmers). Findings from this experiment confirmed that the application of arbuscular mycorrhizal fungi and mycorrhizal helper bacteria could reduce the use of chemical fertilizers, which is beneficial for sustainable farming systems. Further steps have been taken to scale up the production of inoculations for the wider use by local farmers.

**PS 4-74 Vegetative growth and yield response of five *Amaranthus cruentus* accessions to poultry manure (PM), arbuscular mycorrhizal fungus (AMF), combination of AMF-PM, and inorganic fertilizer**

**NWANGBURUKA, C.C.<sup>1,2</sup>**, R. Adeleke<sup>1</sup>, K. Oyekale<sup>2</sup>, O. Denton<sup>2</sup>, D.S. Daramola<sup>2</sup> and A.W. Olugbenga<sup>2</sup>

<sup>1</sup>Agricultural Research Council-Institute for Soil, Climate and Water, 600 Belvedere street, Arcadia, Pretoria, 0001, South Africa, Nwangburukac@arc.agric.za; <sup>2</sup>Department of Agriculture, Babcock University, Ilishan-Remo, PMB, 21244 Ikeja, Lagos, Nigeria.

**Abstract:** Although poultry manure (PM) promotes and enhances the growth and yield of vegetable plants, not all macro nutrients are readily available for plant intake, and this could bring about slow growth and poor yield. Arbuscular mycorrhizal fungi (AMF) help plants to capture nutrients such as phosphorus, sulphur, nitrogen, and micronutrients from the soil. The effect of combining AMF and poultry manure (AMF-PM) in different concentrations has been tested recently as a new way of guaranteeing efficiency in soil productivity. This work evaluated the vegetative growth and yield response of five accessions of *Amaranthus cruentus* to treatments of PM (400kg/ha<sup>-1</sup>), AMF (400kg/ha<sup>-1</sup>), AMF-PM (200kg/ha<sup>-1</sup>AM plus 200kg/ha<sup>-1</sup>PM), NPK fertilizer (400kg/ha<sup>-1</sup>), and a control. Data were collected on five vegetative and yield related characteristics. The experiment used a randomised complete block design with five treatments and three replicates, each replicate consisting of five single row plots. The combined analysis of variance showed significant treatment, accession, and accession X treatment interaction effects on all the characters evaluated (at 0.001 and 0.005 probabilities). The PM treatment yielded the highest total leaf weight per plant (24.83g), total root weight per plant (5.68g), and plant weight at six weeks (16.22g). Additionally, the AMF-PM treatment resulted in the highest plant height at six weeks (29.48) and produced a mean leaf size that was not significantly different than the NPK treatment, suggesting that AMF-PM could be an alternative to NPK. Furthermore, the accession BUAM 004 performed best for all yield characteristics and should be considered for yield improvement in *Amaranthus*. BUAM 005 was the lowest performing accession. Treatment of *Amaranthus* with 400kg/ha<sup>-1</sup> of PM provided a better leaf weight yield as well as higher root weight and total plant weight. These characteristics constitute the bulk of *Amaranthus* economic yield. Combination of AMF-PM performed adequately better than the treatments of AMF alone or inorganic fertilizer alone, and therefore could be considered as a possible alternative to inorganic fertilizer.

## PS 1-28 Phylogenetically distinct cryptic species within ectomycorrhizal fungus *Cenococcum geophilum* sensu lato

OBASE, K.<sup>1</sup>, G.W. Douhan<sup>2</sup>, Y. Matsuda<sup>3</sup> and M.E. Smith<sup>1</sup>

<sup>1</sup>Department of Plant Pathology, University of Florida, 2517 Fifield Hall, Gainesville FL 32611-0680, USA, oba-suke@hotmail.co.jp; <sup>2</sup>Department of Plant Pathology and Microbiology, University of California, Riverside, CA, 92521, USA; <sup>3</sup>Laboratory of Forest Pathology and Mycology, Graduate School of Bioresources, Mie University, Kurimamachiya 1577, Tsu, Mie 514-8507, Japan.

**Abstract:** The anamorphic fungus *Cenococcum geophilum* Fr. (Dothideomycetes, Ascomycota) is one of the most common ectomycorrhizal fungi in boreal to temperate regions. A series of molecular studies have demonstrated that *C. geophilum* sensu lato is monophyletic but is a heterogeneous species or species complex. Here, we revisit the phylogenetic diversity of *C. geophilum* from a regional to intercontinental scale by using new data from Florida (USA) with existing data in Genbank. In total, 768 isolates of *C. geophilum* were obtained from ectomycorrhizal roots (n=207) and sclerotia (n=561) from 15 forest sites in Florida and Georgia, USA. Sequence data from 208 representative isolates were subjected to phylogenetic analysis with reference data from Japan, Europe and North America (34 isolates in total). The combination of ITS and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) genes resolved six well-supported lineages (234 isolates) that were closely related to each other and one lineage that was distinct from the others (8 isolates from Florida). A multi-locus analysis (SSU, LSU, TEF, RPB1, and RPB2) revealed that the divergent lineage is monophyletic and was resolved as the sister group to all other known isolates of the *Cenococcum* lineages. Isolates of the divergent lineage grow faster on nutrient media than the other isolates of the *C. geophilum* and did not form ectomycorrhizas on seedlings of several pine and oak species. The results indicate that *C. geophilum* includes more phylogenetically distinct cryptic species than have been reported and that the divergent cryptic lineage is a putatively non-ectomycorrhizal sister group. We discuss the phylogenetic diversity of *C. geophilum* sensu lato and consider the necessity of species delimitation based on ecological and molecular attributes along with morphological characteristics. Therefore, we are proposing to erect this newly discovered divergent lineage as a new species within *Cenococcum*.

## PS 1-53 Soil aggregation, glomalin content, and organic carbon in arid soils of the Costa de Hermosillo, Sonora

Armenta, A.D.<sup>1</sup>, E.F. Gomez<sup>2</sup>, S.F. Moreno-Salazar<sup>3</sup> and A. OCHOA-MEZA<sup>3</sup>

<sup>1</sup>Departamento de Investigaciones Científicas y Tecnológicas. Universidad de Sonora. Blvd. Luis Encinas y Rosales; C.P. 83000, Hermosillo, Sonora, México, aochoa@guayacan.uson.mx; <sup>2</sup>Instituto de Ecología y Sistemática, Carretera Varona 11835 e/Oriente y Lindero, La Habana 19, CP 11900, Calabazar, Boyeros, La Habana, Cuba; <sup>3</sup>Departamento de Agricultura y Ganadería. Universidad de Sonora, Carr. a Bahía Kino km 21. Hermosillo, Sonora, México.

**Abstract:** Among soil fungi, the arbuscular mycorrhizal fungi (AMF) are the most important to soil structure due to their role in the formation of aggregates. The principal mechanism involved in this process is the production of glomalin, a recalcitrant and hydrophobic glycoprotein that possess cementing properties and binds soil particles. Because of this, aggregate stability is directly related to the concentration of glomalin. It is also considered that the formation of this substance results in high demands of carbon for AMF, and therefore, for the associated plant. In this paper, the content of organic C, water stable aggregates (WSA), and glomalin content were associated in the rhizosphere of native plants such as *Jatropha cuneata*, *Parkinsonia microphylla*, *Olneya tesota*, *Prosopis juliflora*, and *Larrea tridentate* in the Costa de Hermosillo, Mexico. Aggregate stability was measured on air-dried soil, rewetted for 10 minutes by capillarity, and then subjected to wet sieving for 5 minutes using 0.5, 0.25, and 0.063 mm sieve openings. Total soil protein was solubilized with 50 mM citrate (pH 8.0, autoclaved at 121°C for 60 minutes) and then determined by the Bradford method. Percent organic carbon was determined by combustion at 500°C. Results indicate statistical differences among plants for organic C, glomalin, and WSA (below 0.25 mm diameter), but no correlation between variables was found except for organic C and glomalin ( $r^2=0.92$ ), which means a great quantity of C is in a protein form. The highest organic C value was founded associated with *Olneya* (2.7 %), whereas the lowest (0.98%) were associated with *Parkinsonia*. Glomalin values ranged from 184 to 1,258 mg kg<sup>-1</sup>, with *Olneya* having highest value and *Larrea* the lowest. The means for WSA were 4.4, 5.6, and 8.7% for the 0.5, 0.25, and 0.063 mm openings, respectively, but was only different for the 0.063 mm class in *Prosopis* soils.

## PS 4-20 Bio-fortification with mycorrhizae: a treatment to extend yam cultivation to the low rainfall semi-arid zone of West Africa

ODOH, N.<sup>1,2</sup>, K. Oluwasemire<sup>1</sup>, A. Lopez-Montes<sup>2</sup>, R. Abaidoo<sup>2</sup> and R. Asiedu<sup>2</sup>

<sup>1</sup>Department of Agronomy, University of Ibadan, Ibadan, Nigeria, irukaodoh@yahoo.com; <sup>2</sup>International Institute for Tropical Agriculture, Ibadan, Nigeria; <sup>3</sup>Department of Soil Science, University of Abuja.

**Abstract:** Yam is a food security crop in Africa, considering its food, commercial and sociocultural value. Among the six economically important staple yam species, *Dioscorea rotundata* (white guinea yam) is the most common. Yam requires water throughout its active growth stage. With global climate change, rainfall patterns are highly unreliable and erratic, making yam cultivation zones prone to seasonal moisture deficit. Arbuscular mycorrhizal fungi (AMF) symbiosis can play a major role in enhancing plants' drought tolerance. The yield response of *D. rotundata* plants inoculated with mycorrhizae under moisture stress conditions was investigated in a greenhouse and field studies. The field trial was conducted under well watered and water stress treatment, and setup in a randomized complete block design (RCBD) with 3 replicates. The greenhouse evaluation was conducted using three moisture regimes of 75 Field Capacity (FC) at 11 Weeks after planting (WAP), 25% FC at 15 WAP and 25% FC at 11 WAP in a RCBD with three replicates. Yield data were collected on the field and in the greenhouse and subjected to analysis of variance. Results showed significant ( $p < 0.001$ ) difference among genotypes both in the field and in the greenhouse. Moisture stress imposition in both field and greenhouse significantly decreased the yield of yam ( $p \leq 0.05$ ). In the greenhouse stress imposition at 25% FC at 11 WAP led to 69.6% decline while imposition at 25% FC at 15 WAP resulted in 44.4% decline in yield. Mycorrhizal inoculation in the greenhouse significantly increased the yield by 31.4% while the mycorrhizae treatment showed no significant effect in the field. Variation was observed among the studied genotypes in their response to moisture stress. Mycorrhizal inoculation could be used to improve yam production under moisture stress.

## PS 2-29 Successful fruiting body formation of the edible ectomycorrhizal *Cantharellus* in pot culture with host trees

OGAWA, W.<sup>1</sup>, N. Endo<sup>1</sup> and A. Yamada<sup>1</sup>

<sup>1</sup>Faculty of Agriculture, Shinshu University, Minami-minowa, Nagano 399-4598, Japan, 13st551j@shinshu-u.ac.jp.

**Abstract:** Chanterelles are globally renowned as some of the most popular wild, edible, mycorrhizal mushrooms. Recently, the authors succeeded in producing pure cultures of *Cantharellus cibarius* sp. l. and establishing their fruiting bodies in pot culture with mycorrhizal hosts. However, suitable conditions for fruiting, i.e., factors that trigger fruiting body development, were undefined. The objective of this study was to specify factors that induce the fruiting of Japanese *C. cibarius* under controlled conditions. Five strains of *C. cibarius* sp. l. (EN51, EN52, EN53, EN60, and EN61) were used, all of which were isolated from basidiomata or mycorrhizas and identified phylogenetically to their taxonomic position. First, mycorrhizas with *Pinus densiflora* seedlings were established by *in vitro* mycorrhizal synthesis and acclimatized as open-pot mycorrhizal seedlings under laboratory conditions. Second, oak hosts were prepared by co-culture with mycorrhizal pine hosts. All established mycorrhizal seedlings were grown in open pots that were filled with granite-based mineral soil or organic soil. These seedlings were grown at 20 or 25°C with 24 hour continuous lighting. Fruiting was observed with pine seedlings inoculated with isolates EN60 and EN61 and with oak seedlings inoculated with isolate EN51. Fruiting was observed only in mineral soil pots incubated at 25°C. Irrigation conditions were not specified, but fruiting body formation was observed when the seedlings were covered with another pot, and humidity in the pots was sustained at approximately 100%. When mycorrhizal seedlings were transplanted to pots with a large volume and incubated under the same conditions, larger basidiomata occurred continuously. It is suggested that increased photosynthetic carbon flow to roots contributes to better fruiting.



**PS 2-54 Observations of field-collected fern gametophyte mycorrhizae: arbuscular mycorrhizal colonization in terrestrial cordate gametophytes of pre-polypod leptosporangiate ferns, Cyatheaceae, Plagiogyriaceae, Gleicheniaceae, and Osmundaceae**

**OGURA-TSUJITA, Y.**<sup>1</sup>, Y. Hirayama<sup>2</sup>, A. Sakoda<sup>2</sup>, A. Suzuki<sup>2</sup>, A. Ebihara<sup>3</sup>, N. Morita<sup>4</sup> and R. Imaichi<sup>2</sup>

<sup>1</sup>Faculty of Agriculture, Saga University, 1 Honjyo-machi, Saga 840-8752, Japan, ytsujita@cc.saga-u.ac.jp; <sup>2</sup>Department of Chemical and Biological Sciences, Japan Women's University, 2-8-1 Mejirodai, Tokyo 112-8681, Japan; <sup>3</sup>National Museum of Nature and Science, 4-1-1 Amakubo, Tsukuba, Ibaraki 305-0005, Japan; <sup>4</sup>Mie Prefectural Museum, isshinden-kouzubeta, Tsu, Mie 514-0061, Japan.

**Abstract:** To determine the mycorrhizal status of pteridophyte gametophytes in diverse taxa, the mycorrhizal colonization of wild gametophytes was investigated in terrestrial cordate gametophytes of pre-polypod leptosporangiate ferns, i.e., four species of Cyatheales including tree ferns (*Cyathea podophylla*, *C. lepifera*, *Plagiogyria japonica*, *P. euphlebia*), two species of Gleicheniaceae (*Diplazium glaucum* and *Dicranopteris linearis*), and one species of Osmundaceae (*Osmunda banksiifolia*). Microscopic observations revealed that 58–97% of gametophytes in all species were colonized with arbuscular mycorrhizal (AM) fungi. Fungal colonization was limited to the multilayered midrib (cushion) tissue in all gametophytes examined. Molecular identification using fungal SSU rDNA sequences indicated that the fungal sequences obtained from gametophytes primarily belonged to the Glomeraceae but also included the Claroideoglomeraceae, Gigasporaceae, Acaulosporaceae, and Archaeosporales. Our results provide the first evidence for AM colonization in wild gametophytes in Cyatheaceae and Plagiogyriaceae. We found that taxonomically divergent photosynthetic gametophytes are similarly colonized with AM fungi, suggesting that mycorrhizal association with AM fungi could widely occur in terrestrial pteridophyte gametophytes.

**PS 3-44 Seed coating with inoculum of arbuscular mycorrhizal fungi as a sustainable approach for large-scale agriculture**

**OLIVEIRA, R.S.**<sup>1,2,3</sup>, I. Rocha<sup>1</sup>, Y. Ma<sup>1</sup>, A. Látr<sup>4</sup>, M. Vosátka<sup>5</sup> and H. Freitas<sup>1</sup>

<sup>1</sup>Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal, rsoliveira@uc.pt; <sup>2</sup>CBQF - Centro de Biotecnologia e Química Fina—Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Porto, Portugal; <sup>3</sup>Department of Environmental Health, Research Centre on Health and Environment, School of Allied Health Sciences, Polytechnic Institute of Porto, Vila Nova de Gaia, Portugal; <sup>4</sup>Symbiom Ltd., Lanskrout, Czech Republic; <sup>5</sup>Institute of Botany, Academy of Sciences of the Czech Republic, Průhonice, Czech Republic.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are soil microorganisms known to form symbiotic associations with plants, improving their performance. The exploitation of these beneficial microorganisms has become of great interest in agriculture due to their potential roles in sustainable crop production. Nevertheless, the use of AMF inoculum on large-scale agricultural fields is not feasible because non-targeted spreading of inoculum over large areas results in a high cost per plant. Seed coating has the potential to reduce the amount of inoculum needed, resulting in cost reduction and increased efficiency. The aim of this study was to assess whether coating seeds with AMF inoculum is a feasible delivery system for large-scale agriculture. Maize seeds were coated with inoculum of *Rhizophagus intraradices* BEG140 and germinated in agricultural soil under controlled conditions. A treatment using uncoated seeds with direct soil inoculation of *R. intraradices* was included as a positive control. Plants had percentages of root length colonization of higher than 60% either after direct soil inoculation or with coated seeds, with no significant difference between the treatments. Results indicate that seed coating can be used for a targeted application of inoculum. Seed coating is an innovative approach for large-scale application of AMF, which may result in economic and environmental benefits.

### PS 3-17 Soil organic matter degradation by ectomycorrhizal fungi

OP DE BEECK, M.<sup>1</sup>, C.N. Cuevas<sup>1</sup>, P. Persson<sup>1</sup> and A. Tunlid<sup>1</sup>

<sup>1</sup>Microbial Ecology Group, Department of Biology, Lund University, Ecology Building, SE-22 362 Lund, Sweden, michiel.opdebeeck@outlook.com.

**Abstract:** Ectomycorrhizal (ECM) fungi play a key role in nutrient cycling in boreal forests. In particular, nutrients limiting plant growth, such as nitrogen (N) and phosphorus (P), are known to be taken up efficiently by ECM fungi and transferred to their plant hosts. However, most N and P in soils are not readily available for uptake by mycelia because they are mostly present in organic molecules, such as amino acids, proteins, and chitin, or they are enclosed in, bound to, or embedded in intact cell walls, lignin, etc. Hence, in order for ECM fungi and plants to gain access to these mineral nutrients, a broad spectrum of more or less complex organic molecules must be broken down. Recent studies suggest the involvement of Fenton-type reactions in the degradation mechanisms of soil organic matter (SOM) employed by ECM fungi. To investigate the chemical modifications introduced by ECM fungi to SOM in more detail, modifications of the main SOM components, lignin, cellulose, proteins (BSA), chitin, and pectin, were studied with Fourier-Transform Infrared Spectroscopy (FTIR) in degradation experiments with the ECM fungi, *Paxillus involutus* and *Suillus luteus*.

### SY 1-3 Biodiversity and diversity patterns of arbuscular mycorrhizal fungi

ÖPIK, M.<sup>1</sup>

<sup>1</sup>Department of Botany, University of Tartu, 40 Lai St., 51005 Tartu, Estonia, maarja.opik@ut.ee.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) occur in the majority of terrestrial and some aquatic habitats on the globe. They have important roles in the functioning of individual plants and entire ecosystems. Research on AMF biodiversity (species recognition, phylogenetic relationships, autecology) and diversity patterns (community ecology) has flared up since the easier access of the molecular biology methods. In this talk I aim to highlight some of the current trends and recent novel understandings in these areas of research. The species of Glomeromycota have traditionally been recognised and identified mostly on the basis of morphological traits. Recently, DNA sequence traits have supported delimitation of new species, genera, and higher taxa, sometimes hard to distinguish morphologically. The development of understanding of the higher-level phylogenetic relationships within the phylum has also lead to substantial recent reorganisations in the classification of Glomeromycota. Community ecologists tend to consider species as “set” entities and use them to describe communities. Molecular community ecology of AMF, and of other microbes, has had to make some amendments into the existing “known” species lists and uses operational, pragmatic taxonomies to incorporate “unknown” species and describe communities in natural and man-made habitats. The drivers of the patterns of AMF communities are sought at multiple spatial and temporal scales, both in individual case studies and meta-analyses, in relation to edaphic, climatic and geographic factors as well as host diversity or other biotic factors. The wish to interpret community patterns (re)directs researchers to the questions of diversification, dispersal, autecology and functional traits of AMF. Understanding the taxonomic and functional diversity of AMF along natural gradients from local to global scales, and how AMF respond to pressing global processes such as climate change and changing land use is of ever increasing importance. How close to the answer are we?

### PS 4-75 Quantitative assay of ectomycorrhiza of *Pinus caribaea* in a nursery in Uganda

OPIRO, K.L.<sup>1</sup>

<sup>1</sup>Mycorrhiza Centre, P. O. Box 23250, Kampala, Uganda, kopiro2000@yahoo.com.

**Abstract:** Quantitative assay is numerical examination or analysis of a given substance in a particular sample. Keeping in view the undeniable role ectomycorrhiza play in the establishment and growth of pine seedlings in the field, it is possible to grade the seedlings and establish the most suitable planting-out age of the seedlings through quantitative assay of ectomycorrhiza. This was carried out in order to find out at what age of the seedlings ectomycorrhizal intensity is highest. Seedlings planted out at this age will have the greatest chance of good establishment, growth and survival. The study

was carried out in Katugo nursery. The sampled seedlings were 10, 11, 12, 13, 14, 15, 16, 18, 21, 23, and 25 months old. Thirty seedlings of each age were picked randomly from each nursery bed. They were transported to the laboratory for ectomycorrhizal root counts. Each seedling was soaked in water so as to remove soil from it. The roots of pines consist of short and long roots, the former being ectomycorrhizal and the later non-ectomycorrhizal. Ectomycorrhizal root tips are yellowish in colour with swollen end. Non-ectomycorrhizal roots tips are dark brown and not swollen. Both root tips were counted from each seedling and the averages recorded. Average percentage of ectomycorrhizal root tips was calculated. On the basis of percentage of ectomycorrhizal root tips, seedlings should be planted out when they are 13 months old. However, it is recommended that similar study be carried out for seedlings that are 3, 4, 5, 6, 7, 8, and 9 months old.

#### PS 1-54 Changes in *Rhizophagus* sp. populations after inoculation of cassava with *in vitro* *R. irregularis* under field conditions

ORDOÑEZ, M.<sup>1</sup>, L. Villard<sup>2</sup>, F. Masclaux<sup>2,3</sup>, I.R. Sanders<sup>2</sup> and A. Rodriguez<sup>1</sup>

<sup>1</sup>Department of Biology, Faculty of Sciences, National University of Colombia, Cra. 30 45-03, Bogotá, Colombia, ymordonezc@unal.edu.co; <sup>2</sup>Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland, <sup>3</sup>Swiss Institute of Bioinformatics, Vital-IT Group, Lausanne, Switzerland.

**Abstract:** The positive effect of arbuscular mycorrhizal fungal (AMF) inoculation on cassava plants has been reported in terms of yield. However, it is still unclear whether non-native AMF inoculum has an effect on local AMF communities in terms of diversity. Therefore, we aimed to establish whether commercial inoculation of cassava leads to changes in the AMF community. A cassava crop was inoculated with commercial *in vitro*-produced *Rhizophagus irregularis* and grown under three phosphate fertilizer levels. Glomeromycota taxa outside (rhizospheric soil) and inside cassava roots were described using SSU rDNA region, and it showed complementary information about the AMF community. Samples were taken 12 months after inoculation. Rhizospheric soil was used to establish trap cultures. Spores from trap cultures were sequenced by Sanger to describe active the AMF community. Cassava roots were sequenced using MiSeq Illumina. Assembly of AMF species inside the roots was affected by inoculation, but not by the level of phosphate fertilization. Some species that were present in the rhizosphere (e.g., *Claroideoglomus* sp.) were not found by high throughput sequencing inside the roots. This study revealed that *Rhizophagus* sp. was the dominant genus colonizing cassava roots in field. *Rhizophagus intraradices*, *R. irregularis*, and *R. manihotis* were represented by 22 of the 34 AMF OTUs. Some *Rhizophagus*-OTUs were either excluded or their abundance decreased in cassava that was inoculated with *R. irregularis*. This result suggests that inoculation of cassava with *R. irregularis* generates changes in the AMF community structure in the roots of cassava, particularly populations of *Rhizophagus* spp. Future studies are needed to understand the mechanisms behind this community change.

#### PS 2-42 Linking above and belowground interactions in agro-ecosystems: an ecological network approach

ORRELL, P.<sup>1,2</sup>, A.E. Bennett<sup>1</sup>, D. Evans<sup>2</sup> and M. Nijnik<sup>3</sup>

<sup>1</sup>The James Hutton Institute, Dundee, Scotland, peter.orrell@hutton.ac.uk; <sup>2</sup>The University of Hull, Hull, England; <sup>3</sup>The James Hutton Institute, Aberdeen, Scotland.

**Abstract:** Ecological networks are formed from the species present within communities and the interactions between them with the structure of these networks able to determine the nature of services provided to the ecosystem. Until recently, few aboveground-belowground studies have focused on commercially important crop species, the cascading effects of altered network structures, or how the inherent traits of plant genotypes shape the resulting network. Arbuscular mycorrhizal fungi (AMF) have the potential to influence both plant floral traits, which may impact the attraction of pollinators and shape the resulting plant-pollinator network, as well as plant reproductive factors, which may influence the quantity and quality of crop yields. The influence of AMF and plant genotype on pollinator visitation rates, community structure, and yield were examined using three genotypes of strawberry plants and four AMF treatments and mirrored between the field and glasshouse over two years. Plant genotype significantly affected strawberry yield with a trend for AMF to influence yield. Neither AMF community nor plant genotype affected the overall number of visits by *Bombus terrestris* in the glasshouse; however, both AMF community and plant genotype influenced foraging behaviour (number and duration of visits solely for nectar/pollen foraging). Strawberry yield and the number

of pollinator visits were correlated for two of the three plant genotypes. In the field, both AMF community and plant genotype influenced the composition and structure of the plant-pollinator network with the specific combination of AMF community and plant genotype influencing the interactions between species. Plant floral traits were influenced most strongly by plant genotype with the influence of AMF depending on the combination of AMF community and plant genotype. These results indicate that plant-pollinator interactions can be influenced by the belowground community with these interactions mediated by the inherent traits of the plant genotype.

#### LT 4-8 Effect of different mycorrhizae species with and without biochar application on plant growth

**ORTAS, I.<sup>1</sup>**, I.A.M. Ahmed<sup>1</sup>, F. Göl<sup>1</sup> and G. Koskeroglu<sup>1</sup>

<sup>1</sup>Department of Soil Science and Plant Nutrition, University of Çukurova, Faculty of Agriculture, Adana, Turkey, iortas@cu.edu.tr.

**Abstract:** Agricultural soils can be both a sink and source of atmospheric CO<sub>2</sub>, which has a direct effect on climate change. Soil organic matter (SOM) is an important component of soil fertility, productivity, and quality because of its crucial role in soil chemical, physical, and biological properties. Because of its high carbon stability, biochar is a potential tool in our fight against climate change and plays significant roles in bioenergy and soil fertility. Recently, biochar has been used for carbon sequestration to mitigate climate change, increase crop yields, and mitigate atmospheric CO<sub>2</sub> levels. At the present time, it is not easy to accumulate soil organic carbon; however, it is reasonable to use biochar as a soil additive promoting crop growth and carbon storage. Additionally, mycorrhizae utilize fixed CO<sub>2</sub> gained through the photosynthesis of their hosts, and it may be a useful strategy to investigate the synergistic effects of biochar and mycorrhizae on soil quality and plant health. Our aim is to review the effects of the biochar-mycorrhizae interaction on crop growth, nutrient uptake, mycorrhizal development, and soil quality. Several pot experiments were conducted to compare the effect of mycorrhizae and biochar on plant growth and carbon fixation. Several mycorrhizal species were treated with 40 ton ha<sup>-1</sup> of biochar produced from *Phragmites* feedstock, and the effects on citrus and sorghum plant growth were evaluated. At harvest, plant height, fresh and dry shoot weight, and root dry weight were measured. Sour orange plants inoculated with mycorrhizal fungi had significantly higher plant height and fresh and dry weight than the uninoculated control and biochar only treatment. Under greenhouse conditions, sour orange seedlings were either inoculated with *Glomus mosseae* mycorrhiza inoculated or not and treated with 10 ton ha<sup>-1</sup> or 20 ton ha<sup>-1</sup> of biochar made from *Eucalyptus* feedstock. At harvest, plant responses to mycorrhizae and biochar were determined. The inoculated plants produced more shoot fresh and root dry weight than the uninoculated plants. In another experiment, *Eucalyptus*- and *Phragmites*-derived biochar were used with three mycorrhizae species, *G. mosseae*, *G. etunicatum*, and *G. intraradices*, on sorghum (*Sorghum bicolor*) host plants to investigate the effects of biochar and mycorrhizae inoculation on plant growth. *Eucalyptus* biochar produced more dry matter than *Phragmites* biochar. In general, the contribution of mycorrhizae seems to be higher than that of biochar. In particular, *G. mosseae*-inoculated plants produced more shoot dry weight than other *Glomus* species. The combined mycorrhizae and biochar application increased sorghum plant growth. These findings are very important for future agricultural applications.

#### PS 4-76 Phosphorus and mycorrhizae inoculation effect on wheat yield and nutrient uptake under field conditions

Akpınar, Ç.<sup>1</sup>, **I. ORTAS<sup>1</sup>** and A. Demirbas<sup>1</sup>

<sup>1</sup>Department of Soil Science and Plant Nutrition, University of Çukurova, Faculty of Agriculture, Adana, Turkey, iortas@cu.edu.tr.

**Abstract:** Because soil pH in Çukurova soils (Eastern Mediterranean region, Turkey) is over 7.5 due to high CaCO<sub>3</sub> content, wheat plants are suffering from insufficient P and Zn uptake. Soil organic matter content and soil biological fertility is also low. Farmers sometimes complain about having to use so much phosphate fertilizer. As the world fertilizer sources, especially P, are very limited and costly, it is reasonable to use natural organic sources such as mycorrhizal inoculation and compare them to manufactured fertilizers. To test ecological and sustainable farming methods, several experiments were conducted under field conditions. A field experiment was carried out on Menzilat soil series (Typic Xerofluvents), which is located in the Research Farm, Faculty of Agriculture, University of Çukurova (Eastern Mediterranean region), Turkey in the years of 2001, 2003, 2005, and 2009. For phosphorus placement, band and broadcast methods were used

and phosphorus fertilizer was applied at the rate of 0, 50, 100, and 150 kg/P<sub>2</sub>O<sub>5</sub>/ha. At harvest, yield, leaf and grain P and Zn content, and root colonization were determined. The results show that application of mycorrhizal fungi significantly increased wheat yield, root infection and P and Zn uptake. Positive responses to mycorrhizal inoculation were found at lower phosphorus levels. In the highest P level, root colonization significantly decreased. In the four years of the experiment (2001, 2003, 2005, and 2009) band application of P outperformed broadcast application as measured by wheat yield and nutrient uptake.

#### LT 2-7 Long-term effects of high-severity wildfires on ectomycorrhizal fungal communities

OWEN, S.M.<sup>1,2</sup>, L.C. Cottingham<sup>3</sup>, C.A. Gehring<sup>3</sup>, C.H. Sieg<sup>2</sup> and P.Z. Fulé<sup>1</sup>

<sup>1</sup>School of Forestry, Northern Arizona University, Flagstaff, Arizona 86011 USA, smn25@nau.edu; <sup>2</sup>USDA Forest Service, Rocky Mountain Research Station, Flagstaff, AZ 86001; <sup>3</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA.

**Abstract:** Altered disturbance regimes due to high fuel loads and recent drought conditions threaten the sustainability of native forests in the southwestern US. Managers are concerned about the future of ponderosa pine (*Pinus ponderosa*) forests because of increases in high-severity fires that remove large patches of mature forests and alter the underlying soil. Ponderosa pine is adapted to low-severity fires with regenerating pine seedlings often relying on mature trees as sources of ectomycorrhizal (EM) inoculum. We set up mycorrhizal inoculum potential experiments at two stand-replacing fires to address these questions: 1) Does fire severity (high- and moderate-severity) or 2) distance from unburned forest influence the inoculum potential and community composition of EM fungi? Soil was collected near regenerating ponderosa pine seedlings across different fire severities and unburned areas in the 2000 Pumpkin Fire, and along transects that extended from unburned ponderosa pine trees out 400 m into high-severity areas of the 2002 Rodeo-Chediski Fire. Preliminary results show that EM colonization and community composition were similar in unburned and moderately or severely burned sites, and with distance from the unburned forest. There was significant variation among sites within the Rodeo-Chediski fire. One site was dominated by post-fire re-sprouting alligator juniper (*Juniperus deppeana*), which does not form mycorrhizal associations with EM fungi. This site had significantly less EM colonization and a unique EM community composition compared to two other sites that had more regeneration of EM-associated trees. Our results suggest that reduced access to EM fungal inoculum from mature trees did not limit inoculum availability. Other sources of inoculum, such as spores, likely dispersed in these areas over the ten+ years since the fire. Structural changes to EM communities after high-severity wildfires were site specific and could be a function of the dominant post-fire vegetation type.

#### PS 1-29 Temporal changes in ectomycorrhizal fungal community: case study in disturbed Dipterocarp forest, Thailand

PACHIT, P.<sup>1</sup>, J. Piapukiew<sup>2</sup> and N.R. Disyatat<sup>3</sup>

<sup>1</sup>Biological Sciences Program, Faculty of Science, Chulalongkorn University, Phayathai Rd., Wang Mai, Pathumwan, Bangkok 10330, Pawara.P@student.chula.ac.th; <sup>2</sup>Department of Botany, Faculty of Science, Chulalongkorn University, Phayathai Rd., Wang Mai, Pathumwan, Bangkok 10330; <sup>3</sup>Department of Biology, Faculty of Science, Chulalongkorn University, Phayathai Rd., Wang Mai, Pathumwan, Bangkok 10330.

**Abstract:** One of the important deciduous forest types in Thailand is dry dipterocarp forest (DDF), which is the fire climax community dominated by tree species in Dipterocarpaceae. Because of the infertile soil in this forest, the mutualistic association between Dipterocarpaceae and ectomycorrhizal (ECM) fungi is commonly found. Under the forest floor, ECM communities can change throughout the year due to the interactions between ECM fungi, host plant and the environment. This study proposes to investigate the temporal variation in the ECM fungal community in disturbed DDF in Saraburi Province, Thailand. Only one dominant dipterocarp species, *Shorea siamensis* Miq., was found in this forest. Soil samples were collected from three sites every three months from December 2013–September 2014, covering dry and wet seasons. Sites 1 and 3 were burned by forest fires in January 2014. ECM root tips were sorted into morphotypes and relative frequency of each morphotype was calculated. The highest number of total ECM root tips was observed in December 2013 and the lowest in March 2014 (site 2) and September 2014 (site 1 and 3). The same overall temporal pattern was observed in all sites. These results might be explained by soil moisture and fine root production. According to twenty-one morphotypes, the largest number of ECM morphotypes was found in site 1 while the lowest was found in site 2. The similarity coefficient between ECM morphotypes in the two burned sites was the highest. Thus, forest fires



seemed to affect the diversity of ECM morphotypes. Moreover, the different patterns of temporal change were found in each ECM morphotype and there was only one dominant morphotype in each site of disturbed DDF. These results emphasize that ECM fungal species, the vegetation and the environmental factors especially soil properties and forest fires can cause temporal changes of ECM community in disturbed DDF.

#### PS 4-77 Higher salt tolerance of *Rhizophagus irregularis* inoculated pigeonpea plants is reflected in terms of more efficient symbioses and trehalose turnover in nodules

PANDEY, R.<sup>1</sup> and N. Garg<sup>1</sup>

<sup>1</sup>Department of Botany, Panjab University, Chandigarh-160014, INDIA, rekhaphulara@gmail.com.

**Abstract:** Association with arbuscular mycorrhizal fungi (AMF) usually enhance nodulation and N<sub>2</sub> fixation in legumes and impart salt tolerance, but the extent of these effects depends on the AMF species. Studies on the *Rhizobium*-legume symbiosis have shown that trehalose content in nodules under salt stress correlates positively with an increase in plant stress tolerance. Few reports describe trehalose accumulation in mycorrhiza under stress conditions, where it serves not only as the main storage carbohydrate but also as an abiotic stress protectant. However, trehalose dynamics in the mycorrhiza-rhizobium-legume tripartite symbiosis are largely unknown. The present investigations were thus carried out to compare the effectiveness of a native inoculum from saline soil and two exotic isolates, *Funneliformis mosseae* and *Rhizophagus irregularis*, on growth, N<sub>2</sub> fixation, and nodule trehalose turnover in two genotypes of pigeonpea (*Cajanus cajan*, Paras genotype (salt sensitive) and Pusa 2002 genotype (salt tolerant)) grown under salt stress conditions (0-100 mM NaCl). AMF inoculated plants not only overcame the negative effects of salinity on plant growth and N<sub>2</sub> fixation but also had higher trehalose content in nodules. Pusa 2002 was more responsive to all AMF inoculations and recorded higher N<sub>2</sub> fixing potential than Paras. Amongst the AMF, *R. irregularis* performed better by promoting higher biomass accumulation, improved nodulation, enhanced N<sub>2</sub> fixation, and N and P uptake which correlated with higher AMF colonization displayed by this AMF as compared to *F. mosseae* or the native saline mix. *Rhizophagus irregularis* inoculated plants accumulated higher trehalose in nodules due to decreased trehalase and increased trehalose-6-P synthase and trehalose-6-phosphatase activities. Mixed AMF inoculum (*F. mosseae* + *R. irregularis*) did not provide any additional benefits over single species AMF applications. These results indicate that the higher stability of the *R. irregularis*-pigeonpea-rhizobium symbiosis under salt stress (possibly due to increased trehalose) makes it an effective salt stress ameliorator in pigeonpea plants.

#### PS 4-78 Efficacy of arbuscular mycorrhizal fungi (AMF) as a biofertilizer and biocontrol agent in wheat crop

PANWAR, V.<sup>1</sup>, A. Aggarwal<sup>2</sup>, I. Sharma<sup>1</sup> and M.S. Saharan<sup>1</sup>

<sup>1</sup>Indian Institute of Wheat and Barley Research, Karnal, Haryana, India, panwar\_vipin2008@rediffmail.com; <sup>2</sup>Mycology and Plant Pathology Laboratory, Kurukshetra University Kurukshetra, India.

**Abstract:** Wheat (*Triticum* spp. L) is one of the most important food crops in the world. The current global wheat production is 724.9 million tons. But, in the year 2050, the world population is estimated to be 9 billion and the demand for wheat is likely to reach more than 900 million tones. A high population growth rate and unpredictable climate change would pose a challenge to wheat workers for enhanced production to meet the targeted need. Application of chemicals play a major role in wheat production in many countries. But, the hazardous effects on human health lessen their attractiveness. Arbuscular mycorrhizal (AM) fungi, which form symbiotic associations with a wide range of plant species, have been successfully used as a growth enhancer and biocontrol agent in many crops. *Fusarium* head blight (FHB), also known as scab, is a destructive disease and reduce the quantity and quality of wheat worldwide. Current study was conducted to find an effective and eco-friendly strategy to control the FHB and enhance the yield of wheat. In pot study, we used two AMF species [*Glomus intraradices* (Gi) and *Gigaspora margarita* (Gm)] single and integrated with *Trichoderma harzianum* (Th), *Pseudomonas* sp. (pf) and low doses (0.05% and 0.03%) of fungicide (Tebuconazole) for managing FHB of wheat. All treatments significantly increased 100 grain weight as compared to control (uninoculated). Nevertheless, the combinations of Gi+Th and Gi+pf with low dose of fungicides (0.05% and 0.03%) significantly reduced the disease severity nearly equal to the recommended dose of fungicides (0.075%) and there was no negative effect on the growth promoting activity of bioagents. In conclusion, integrated bioagents like AMF and low dose of fungicide reduced the disease severity and improve the yield of wheat.

## PS 3-6 Wood ash effects on ectomycorrhizal fungal mycelial production and N retention capacity

PAREDES, C.C.<sup>1</sup>, H. Wallander<sup>2</sup> and R. Kjølner<sup>1</sup>

<sup>1</sup>Terrestrial Ecology Section, University of Copenhagen, Denmark, carla.paredes@bio.ku.dk; <sup>2</sup>Department of Microbial Ecology, Lund University, Sweden.

**Abstract:** The external mycelia (EM) of ectomycorrhizal (ECM) fungi exploit the soil for nutrients such as N and P. Granulated wood ash has been proposed as a way to return nutrients to forests after the harvest of forest residues or clear cutting. Even though wood ash does not contain high amounts of N, it has been shown that it can increase N mineralization due to enhancing pH, which increases microbial activity and decomposition rates, enhancing the risk of N leaching. The effect of wood ash on ECM fungi is not well established. Some studies have shown that there is no significant effect of ash on the amount of EM biomass or nutrient uptake. However, some ECM fungal species showed a tendency to increase in abundance in plots treated with ash because they colonized ash patches and, as a result, enhance the weathering/solubilizing of hardened wood ash. The aim of this study was to analyze wood ash effects on ECM fungi, EM production, and N retention capacity. The experiment was placed in a Norway spruce monoculture stand in Denmark. Different concentrations of wood ash were applied and in-growth mesh bags were installed. After six months, they were either labeled with <sup>15</sup>NO<sub>3</sub>, <sup>15</sup>NH<sub>4</sub>, or used for natural abundance measurements and evaluated for 15N/14N. EM production was measured by visual estimation, microscopic examination (frequency of hyphae), and ergosterol extraction and weight. There were large differences in EM growth between seasons with the growth between June and November being 45 times higher than between November and June. There was significantly higher mycelial <sup>15</sup>N uptake of NH<sub>4</sub> than NO<sub>3</sub>. A positive correlation was found between EM production and the percent of <sup>15</sup>N added to the pool. There were no significant differences in mycelial growth or N-retention between the different treatments with ash.

## PS 1-30 Arbuscular mycorrhizal fungal diversity in coastal areas and islands of Western Korea

PARK, H.<sup>1</sup>, J.Y. Lee<sup>1</sup>, K.H. Ka<sup>2</sup> and A.H. Eom<sup>1</sup>

<sup>1</sup>Department of Biology Education, Korea National University of Education, Cheongju, Chungbuk 363791, Korea, hawknike5780@gmail.com; <sup>2</sup>Division of Wood Chemistry and Microbiology, Korea Forest Research Institute, Seoul 130712, Korea.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are one of the most widespread symbionts globally. Due to their enhanced nutrient absorption capacity and pathogen resistance, AMF significantly contribute to the survival of individual plants and the ecosystem. Coastal areas and islands adjacent to the sea comprise of an environment where growth of plants is a challenge, due to high salinity, low nutrients, and sandy soil. Therefore, symbiosis between plants and AMF is an essential biological factor in these areas. The purpose of this study was to investigate the diversity of AMF communities in forest soils near coastal areas and islands in Western Korea. We collected samples of soil and roots from 3 coastal and 6 islands. We identified AMF spores using morphological characteristics and 18S rDNA sequence analysis. In this study, 21 species from 13 genera were discovered in coastal areas and islands. *Acaulospora* was the most abundant genus and *A. mellea* was the dominant species found in this study. These results showed that the distribution and diversity of AMF communities in forest soils around coastal area and islands are significantly different from communities in inland forest areas.

## PS 4-21 Plant genetic versus environmental determinants of ectomycorrhizal fungal community composition and growth in Colorado pinyon pine (*Pinus edulis*)

PATTERSON, A.M.<sup>1</sup>, L. Flores-Renteria<sup>1</sup> and C.A. Gehring<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA, amp399@nau.edu;

<sup>2</sup>Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, Arizona 86011 USA.

**Abstract:** Climate change has resulted in significant tree mortality throughout the world with models predicting further mortality and large-scale vegetation shifts. However, intraspecific genetic variation and interactions with fungal mutualists may alter these projections. We examined interactions between plant genetics, ectomycorrhizal fungi and drought in

pinyon pine (*Pinus edulis*) a species with known sensitivity to climate. Previous studies have identified drought tolerant and drought intolerant mature trees growing side by side in the field. Drought tolerant trees had significantly higher survival and growth than drought intolerant trees during the past two decades of drier than average conditions. The communities of ectomycorrhizal fungi that occurred on the roots of these two pinyon types also differed dramatically, with drought intolerant trees colonized mainly by basidiomycetes, and drought tolerant colonized mainly by ascomycetes. To test if these patterns had a genetic basis, we grew seedlings from drought tolerant and drought intolerant mothers in a common garden in northern Arizona in which soil moisture was manipulated. As with adult pinyons in the field, seedlings from drought tolerant mothers had significantly higher growth and survival rates and different ectomycorrhizal fungal communities on their roots than seedlings from drought intolerant mothers. Significant plant genetic by environment interactions were also observed. Seedlings from drought tolerant mothers showed a strong positive growth response to even low levels of supplemental water while retaining a similar ascomycete dominated community of ectomycorrhizal fungi regardless of water treatment. In contrast, a significant shift in ectomycorrhizal fungal community composition was associated with a small growth response to watering in seedlings from drought intolerant mothers. These results show that ectomycorrhizal fungal communities vary among host genotypes grown in a common environment and that this variation is associated with responses to changes in the environment and corresponding host plant performance.

#### SY 1-1 Patterns and drivers of ectomycorrhizal fungal diversity across scales

PEAY, K.G.<sup>1</sup>, J.M. Talbot<sup>2</sup>, J.W. Taylor<sup>3</sup>, R. Vilgalys<sup>4</sup> and T.D. Bruns<sup>3</sup>

<sup>1</sup>Department of Biology, Stanford University, Stanford, CA, USA, kpeay@stanford.edu; <sup>2</sup>Department of Biology, Boston University, Boston, MA, USA; <sup>3</sup>Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA;

<sup>4</sup>Department of Biology and Molecular Genetics and Microbiology, Duke University, Durham, NC, USA.

**Abstract:** Ectomycorrhizal fungi are a critical component of the diversity and function of terrestrial ecosystems. While ecologists have long recognized the importance of scale on ecological processes, ectomycorrhizal communities have traditionally been studied at small-scales, focusing on deterministic processes. Understanding the spatial hierarchy of biological processes that shape ectomycorrhizal communities is in part hindered by the lack of datasets spanning large spatial-scales and the absence of distributional data for most fungi. To rectify this knowledge gap we used next generation sequencing to survey ectomycorrhizal dominated soil fungal communities across North American pine forests, spanning a diverse range of climates from Florida to Alaska. At each site we took 26 soil samples arranged in a nested grid and stratified into organic and mineral soil horizons. With this spatially explicit sampling design we examine patterns of diversity from very small to large spatial scales and across steep local environmental gradients. Using this data we demonstrate that ectomycorrhizal communities show strong patterns of regional differentiation, likely driven by dispersal limitation and climate. By contrast, patterns of alpha-diversity and functional variation appear to be driven primarily by local scale environmental variables. These results demonstrate that ectomycorrhizal fungal communities are shaped by biological processes acting at both large- and small-spatial scales and reinforce the importance of understanding scale in ectomycorrhizal ecology.

#### CS 2-5 Access to ectomycorrhizal fungal networks following a mountain pine beetle outbreak: effects on pine seedling growth and survival

PEC, G.J.<sup>1</sup>, J. Karst<sup>1,2</sup>, S.W. Simard<sup>3</sup> and J.F. Cahill, Jr.<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9, gpec@ualberta.ca;

<sup>2</sup>Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada T6G 2E3; <sup>3</sup>Department of Forest and Conservation Sciences, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4.

**Abstract:** The recent mountain pine beetle (*Dendroctonus ponderosae*) outbreak has disturbed pine-dominated landscapes across western North America. Regeneration of these forests relies on seedlings replacing trees killed by these beetles, thus identifying limitations on seedling establishment will be critical for predicting future forest trajectories. Toward this goal, we tested the importance of access to ectomycorrhizal (EcM) fungal networks for the establishment (survival, growth, and nutrition) of lodgepole pine (*Pinus contorta*) seedlings along a gradient of beetle-induced tree mortality. We predicted that EcM networks degrade with stand-level tree mortality and, in turn, seedling establishment is reduced. For two years, we tracked 660 seedlings sowed across eleven stands varying in beetle-induced tree mortal-

ity (0-80% basal area killed), and manipulated mycorrhizal network access via mesh. We found that seedling survival decreased with beetle-induced tree mortality, though along this gradient, our previous research has shown that light, soil moisture, and nutrients are more readily available. Access to EcM fungal networks did not affect seedling survival along the tree mortality gradient; however, seedling growth and nutrition increased. Seedlings with access to EcM fungal networks were taller, and had higher biomass and foliar N and P in stands with high tree mortality than in undisturbed stands. The increase in seedling height with tree mortality was the same in the presence or absence of roots, reflecting either the insensitivity of height to competition or the consistency in the strength of root competition. Our results demonstrate that access to EcM fungal networks is important to regeneration success in beetle-killed stands.

## CS 8-6 The key role of the inoculation by arbuscular mycorrhizal fungi on field crops in the Mediterranean basin

PELLEGRINO, E.<sup>1</sup>, Bonari E.<sup>1</sup>, Ercoli, L.<sup>1</sup>

<sup>1</sup>Institute of Life Sciences, Sant'Anna School of Advanced Studies, 56127 Pisa, Italy.

**Abstract:** To meet the projected demand for food, world production must increase up to 50% by 2030. Since agricultural production might level off or even decline in many regions for the strong decrease of soil organic matter, filling the gap between actual and potential yield is crucial. In degraded and low fertility Mediterranean soils, the theoretical yield potential can be achieved reducing the effects of the yield-limiting factors by the use of arbuscular mycorrhizal fungi (AMF). Here, the role of single and mixed native or exotic AMF inocula in enhancing food and feed yield and in ameliorating their nutrient and nutraceutical quality was studied on bread and durum wheat, maize, soybean, chickpea, lucerne, and Egyptian clover. Field experiments of inoculation and seed coating were carried out in a Mediterranean area. Performances of the AMF inoculated field crops were compared to those from mock inoculation using a multivariate approach based on yield and yield components, macro- and micro- nutrients and nutraceutical parameters such as concentrations of free and bound phenols and flavonoids, folic and lipoic acids and polyunsaturated fatty acids in grain or shoot. Additionally, in bread and durum wheat, the interaction of AMF inoculation and nitrogen fertilization and genotypes (old versus modern varieties) was studied, while in soybean the interaction with irrigation was taken into consideration. Finally, the field persistence of the AMF inocula in crop rotations with annual and polianual crops was studied using molecular genetic tracing and morphological approach.

## PS 2-30 Atheliaceae fungi are potential keystone species building up the belowground growth of Norway spruce

PENNANEN, T.<sup>1</sup>, S.M. Velmala<sup>1</sup> and T. Rajala<sup>1</sup>

<sup>1</sup>Natural Resources Institute Finland (Luke), Bio-based Business and Industry, Jokiniemenkuja 1, FI-01370 Vantaa, Finland, taina.pennanen@luke.fi.

**Abstract:** Our studies focus on the relationships of ectomycorrhizal (ECM) fungi and the genetic and phenotypic traits of Norway spruce (*Picea abies*), which is one of the most dominating tree species in boreal forests of Northern Europe. High ECM species richness, that may provide increased nutrient mobilization potential due to functional complementarity of the fungal community, was associated with well-growing spruce phenotypes. In particular, the ECM fungal species belonging to the family Atheliaceae were found to abundantly colonize the well growing spruce origins. These ECM fungal species also seem effective in the production of exoenzymes related to N and P uptake. Atheliaceae are inconspicuous sporocarp-forming basidiomycetes which have, for a long time, been merely associated with decomposer communities inhabiting decaying wood in old-growth forests. Furthermore, we have found *Tylospora*, *Amphinema*, and *Piloderma* sp. to be the dominant fungal lineages in roots of very young, naturally regenerated, and vital spruce seedlings. Other common lineages were *Tomentella*, *Meliniomyces*, *Russula*, *Lactarius*, *Cenococcum*, *Thelephora*, and *Amanita* sp. These ECM strains were isolated and inoculated to the seedlings. Modification of seedling growing conditions by altering nutrients and growing media enabled successful colonization of the isolated ECM, and also promoted the dispersal of Atheliaceae fungi from the surrounding environment. In inoculation studies, ECM fungal species belonging to *Tylospora* and *Piloderma* sp. increased seedling performance, especially their root/shoot (R/S) ratio, more than other ECM species. *Piloderma* sp. colonization was also found to alter root system structure towards less ramified with longer lateral roots. Atheliaceae dominated seedlings possessing high R/S ratio also grew fast after outplanting to the field. In conclusion, our ECM community studies on Norway spruce suggest that Atheliaceae are important players in the ecology of Norway spruce in boreal forests because of their good nutrient uptake potential and because they may promote the host resource allocation towards roots.



## PS 2-10 The transcriptional landscape of the *Pisolithus microcarpus* basidiocarp

PEREIRA, M.F.<sup>1,2</sup>, T.C. Anastácio<sup>1</sup>, M.D. Costa<sup>1</sup>, F. Martin<sup>2</sup> and A. Kohler<sup>2</sup>

<sup>1</sup>Departamento de Microbiologia, Campus Universitário, Universidade Federal de Viçosa, 36570-000 Viçosa, Minas Gerais, Brazil, mairadefreitaspereira@gmail.com; <sup>2</sup>Institut National de la Recherche Agronomique, Unité Mixte de Recherche 1136, Interactions Arbres/Microorganismes, Centre de Nancy, Université de Lorraine, 54280 Champenoux, France.

**Abstract:** The basidiomycete fungus *Pisolithus microcarpus* is a gasteromycete of wide distribution in eucalypt plantations worldwide. This fungus produces a complex basidiocarp composed of peridioles at different developmental stages. Inside the basidiocarps, a large number of spores are produced that can be routinely used for seedling inoculation in eucalypt nurseries. The use of ectomycorrhizal fungi in eucalypt nurseries is paramount for achieving sustainable forestry production. Despite the progress achieved in the understanding of basidiosporogenesis in this species, nothing is known about the transcriptional patterns that occur along basidiocarp development and the identity of the RNA molecules stored inside the basidiospores soon after basidiosporogenesis. Taking advantage of the recently sequenced *Pisolithus microcarpus* genome and by using RNA-Seq technology, we analyzed the transcriptome of all compartments of the *Pisolithus microcarpus* basidiocarp: unconsolidated, young and mature peridioles, and internal and mature spores. A set of 737 transcripts grouped in seven clusters was significantly regulated in a minimum of one of the compartments. Several genes involved in cell cycle, replication, transcription, and sugar transporters were strongly regulated in all the peridioles. However, in internal spores and mature spores, genes related energy production were expressed. These results will be important for the understanding of *Pisolithus* biology and ecology and for its use in forestry production.

## PS 4-42 Spatial distribution of arbuscular mycorrhizal fungi in apple root systems

PETERSON, K.A.<sup>1,2</sup> and D.M. Eissenstat<sup>1,3</sup>

<sup>1</sup>College of Agricultural Sciences, Pennsylvania State University, State College, PA 16801, kapeterson126@yahoo.com; <sup>2</sup>Department of Plant Science, Pennsylvania State University, State College, PA 16801; <sup>3</sup>Department of Ecosystem Science and Management, Pennsylvania State University, State College, PA 16801.

**Abstract:** Spatial distribution of arbuscular mycorrhizal fungal (AMF) colonization was investigated within root systems of mature apple (*Malus domestica*) to examine colonization patterns in a common horticultural crop. Root samples were obtained from an orchard in south-central Pennsylvania and were examined on a modular basis by identifying root modules consisting of third-order roots and all associated first- and second-order roots. Modules were stained and presence of AMF structures was quantified microscopically; distances between fine roots within modules were measured in order to assess spatial relationships among colonized and uncolonized roots. Evidence was found to show spatial variation within the root system. First-order roots were more likely to be colonized when located near other colonized roots than when located further away. Absolute measures of AMF structures within second-order roots showed that colonization of second-order roots was positively correlated with colonization of associated first-order roots.

## PS 3-7 How do mycorrhizal symbiosis and organic matter influence metal(loid) (Cd, Pb, Sb) transfer from soil to edibles? Special focus on health threats of urban and periurban soils

PIERART, A.<sup>1,2</sup>, C. Dumat<sup>2</sup> and N. Sejalón-Delmas<sup>1,2</sup>

<sup>1</sup> EcoLab (Laboratoire d'Ecologie Fonctionnelle et Environnement), UPS-INP-ENSAT, Castanet Tolosan, France, antoine.pierart@ensat.fr; <sup>2</sup>EcoLab, CNRS, Castanet Tolosan, France; <sup>3</sup>CERTOP UMR 5044, Université Jean Jaurès, Toulouse, France.

**Abstract:** Cadmium (Cd) and lead (Pb) are trace elements accumulating in the environment because of intense human activities. Emerging pollutants, such as antimony (Sb), appear through the development of new technologies, and its environmental and health risks are often ignored or overshadowed. These three elements are used in car manufacturing processes, leading to their accumulation in urban and peri-urban environments through road dust and aerial deposition. Metal(loid) behavior has been studied in the environment, but knowledge on the role of arbuscular mycorrhizal fungi



(AMF) are still scattered (especially for Sb) even though various studies highlight their potential to sequester metal(loid) in soils or enhance phytoremediation. In recent years, a conflict has arisen between (i) an increasing willingness to garden in urban and peri-urban areas and (ii) the soil sanitary state as influenced by anthropogenic impacts. Gardeners usually want to grow organic food and so can be willing to use biofertilizers such as AMF and composted OM. Consequently, because these cultivated areas are often OM-rich, studies are needed on the influence of the AMF and OM interaction in metal(loid) speciation and uptake by edible plants. Our research project is part of a national program for urban gardens (ANR JASSUR) and focuses on these issues. A greenhouse experiment has been set up to study the role of AMF and OM in metal(loid) speciation, transfer, and the compartmentation from the soil to leafy vegetables grown on peri-urban metal-rich soils. Total and bioaccessible concentrations have been measured by ICP MS; compartmentation and transfer mechanisms were studied through MEB-EDX imagery analysis. Initial results show that AMF and OM influenced (i) metal(loid) uptake and translocation from root to leaf and (ii) the human bioaccessible fraction. However, the response of each metal(loid) varied, suggesting a selective metabolism reaction of the plant-fungal couple. Further analyses are in progress to explain Cd, Pb, and Sb speciation and uptake mechanisms.

#### PS 4-43 Ectomycorrhizal fungus assemblages on Douglas fir and American white pine outside natural range

PIETRAS, M.<sup>1</sup>

<sup>1</sup>Institute of Dendrology Polish Academy of Sciences, Parkowa Str. 5, 62-035 Kórnik, Poland.

**Abstract:** Introductions and spread of foreign and invasive organisms is one of the most important problems in nature conservation. Existing studies of fungi invasion biology mostly concentrate on pathogens, probably because the direct effect of pathogenic organisms occurring in novel ranges is easily perceptible and the negative economic consequences can be remarkable. The invasion ecology of non-pathogenic fungi has attracted much less attention. Thus the main objective of this study was to evaluate if co-invasion of ectomycorrhizal fungi is common phenomenon during introduction of foreign trees such as Douglas fir (*Pseudotsuga menziesii*) and American white pine (*Pinus strobus*) growing outside natural range. Altogether, 15 study sites were surveyed: six old growth forests of Douglas fir and American white pine, eight 20 years old plantations of Douglas fir and one site located in Kórnik Arboretum. Morphological assessment and molecular approach based on PCR and sequencing of the fungal ITS rDNA were performed to identify ectomycorrhizas distinguished on roots of Douglas fir and White pine. Sixty-one and seventy-three ectomycorrhizal fungal taxa were found on Douglas fir and American white pine, respectively. The most frequent ectomycorrhizal taxa associated with both tree species were *Lactarius rufus*, *Meliniomyces variabilis*, Russuloid and Thelephoroid fungi. Generally novel mutualisms and cosmopolitan associations were the most common assemblages of Douglas fir and American white pine in invasion range. Taxa co-invading with Douglas fir and American white pine detected in study sites were *Suillus lakei* and *Rhizopogon salebrosus*, respectively. This study shows, that North American ectomycorrhizal partners of Douglas fir and American white pine in Europe should be regarded more as a fare dodgers, than as partners in a good deal.

#### CS 9-6 Picking partners: how transcriptomic, metabolomics, and proteomics work is shaping our understanding of ectomycorrhizal host specificity

PLETT, J.M.<sup>1</sup>, A. Kohler<sup>2</sup>, K.L. Plett<sup>1</sup>, A. Livio<sup>3</sup>, T. Tschaplinski<sup>4</sup>, N. Engle<sup>4</sup>, S. Piller<sup>3</sup>, I.C. Anderson<sup>1</sup> and F. Martin<sup>2</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, University of Western Sydney, Richmond NSW 2753, Australia, j.plett@uws.edu.au; <sup>2</sup>INRA, UMR 1136 INRA-University of Lorraine, Interactions Arbres/Microorganismes, Laboratory of Excellence ARBRE, INRA-Nancy, 54280 Champenoux, France; <sup>3</sup>School of Science and Health, University of Western Sydney, Campbelltown NSW, Australia; <sup>4</sup>Plant Systems Biology Group, Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831-6445, USA.

**Abstract:** Within forest ecosystems, the roots of most trees and shrubs are colonized by mutualistic ectomycorrhizal (ECM) fungi. Little is understood concerning the host or fungal cellular reprogramming that favors the formation of ECM colonized root tips in compatible plant-fungal interactions and what prevents the formation of ECM root tips in incompatible interactions. In recent years, using model ECM fungi, such as *Laccaria bicolor* and *Pisolithus microcarpus*, we have seen a large step forward in our understanding of the mechanistic molecular events underpinning compatible and incompatible ECM relationships. These findings include the identification of specific metabolic pathways favored during com-

patible relationships, the definition of core transcriptional responses of the plant and fungus during symbiosis, and the characterization of proteomic modification necessary for mycorrhizal formation. I will discuss some of our most recent advances in understanding what molecular events are necessary during ECM host colonisation with specific emphasis on host gene regulation and post-translational modification of proteins. Further, I will compare how ECM fungal lineages from Northern and Southern hemispheres are similar and how they contrast in their cooperation with host plants.

**PS 4-22 Large compositional shifts in mycorrhizal fungal communities in a *Eucalyptus saligna* plantation due to fertilisation, irrigation, and stochastic community assembly**

**POWELL, J.R.<sup>1</sup>, Y. Zheng<sup>1,2</sup> and I.C. Anderson<sup>1</sup>**

<sup>1</sup>Hawkesbury Institute for the Environment, University of Western Sydney, Richmond NSW 2753, Australia, jeff.powell@uws.edu.au; <sup>2</sup>State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China.

**Abstract:** A typical approach to study mycorrhizal responses to environmental change is to compare the average composition of communities in changing environments to those under control conditions, and to determine whether these differences are statistically significant. To demonstrate the limitations of this approach, we studied fungal responses to fertilisation and irrigation in a nutrient- and water-limited *Eucalyptus saligna* plantation and observed significant effects of both treatments and their interactions on soil and root-associated fungal communities. These effects were observed for fungi in general and a subset of ectomycorrhizal (ECM) fungal taxa (using 454 sequencing), and for arbuscular mycorrhizal (AM) fungi (using TRFLP). While the treatments significantly affected community composition, they accounted for <30% of variation. We then used null model analysis to test the hypothesis that unexplained variation was due to processes associated with demographic stochasticity and immigration, based on parameters estimated using the neutral theory of biodiversity. In some cases we found evidence consistent with predictions assuming neutrality (functional equivalence among taxa). However, other cases provided strong evidence for non-neutral dynamics but with outcomes indicating that communities were more dissimilar than the model predicted. This high degree of stochasticity could be due to substantial variation in environmental properties at a small-scale (niche-based assembly). Alternatively, strong interactions among taxa within fungal communities could lead to high levels of stochasticity if colonisation patterns are variable (priority effects). For AM and ECM fungi, especially associated with roots, compositional patterns were more stochastic in fertilised and irrigated plots, suggesting that the treatment could lead to even more unpredictable shifts in composition. These results highlight the limitations of relying solely on statistical tests of within- and between-group estimates of beta diversity and the additional inferences that are possible by focussing on effect sizes while making comparisons to model-based predictions.

**PS 3-45 Community of arbuscular mycorrhizal fungi is affected by management system in coffee plantations**

**PRATES JÚNIOR, P.<sup>1</sup>, B.C. Moreira<sup>1</sup>, M.C.S. Silva<sup>1</sup>, K. Kemmelmeier<sup>2</sup>, R.B.A. Fernandes<sup>3</sup>, S.L. Stümer<sup>4</sup>, M.C.M. Kasuya<sup>1</sup> and E.S. Mendonça<sup>4</sup>**

<sup>1</sup>Universidade Federal de Viçosa, Departamento de Microbiologia, Viçosa, MG, 36570-900, Brazil, junior\_prates2005@yahoo.com.br; <sup>2</sup>Fundação Universidade Regional de Blumenau, Departamento de Ciências Naturais, Blumenau, SC, 89012-900; <sup>3</sup>Universidade Federal de Viçosa, Departamento de Solos, Viçosa, MG, 36570-900, Brazil; <sup>4</sup>Universidade Federal do Espírito Santo, Departamento de Produção Vegetal, Alegre, ES, 29500-000, Brazil.

**Abstract:** Agroecology aims to reduce the impact of farming systems and to promote the use of biological potential. Arbuscular mycorrhizal fungi (AMF) form mutualistic symbioses with plants and increase soil quality. This study evaluated the effects of management practices and temporal variation on the AMF community in coffee production systems (agroecological and conventional) and forest fragments. In three sites with the three systems, soil samples associated with coffee were collected at different phenological stages of the coffee plant (flowering, grain filling, and harvesting) as well as in the forest fragment. Spores were extracted by the wet sieving technique for morphological identification and molecular community analysis by PCR–DGGE of DNA. Forty-two AMF morphospecies, distributed in nine genera and six families and pertaining to the Glomeromycota phylum were identified. Most species recovered were *Acaulospora* (17 sp.), mainly *A. mellea*, *A. morrowiae*, *A. scrobiculata*, *A. sp. 1*, and *A. sp. 2*, and *Glomus*, mainly *G. glomerulatum*, *G. magnicaule*, *G. sp. 5*, *G. sp. 6*, and *G. sp. 7*. This result is to be expected because both genera are widely distributed in natural and agri-

cultural systems. Very few morphospecies of *Ambispora* (1 sp.), *Archeospora* (1 sp.), *Dentisculata* (2 sp.), *Gigaspora* (1 sp.), *Paraglomus* (1 sp.), *Rhizophagus* (1 sp.), and *Scutellospora* (3 sp.) were detected. The average species richness was 9.4, 10.8, and 11.2 in the agroecological, conventional, and forest fragment, respectively, yet, the morphological analyzes were insufficient to distinguish variation among the three ecosystem types. However, the molecular analysis showed that the agroecological system was more similar to the forest than the conventional system at certain periods during the evaluation. We can conclude that management systems and phenological period of the plant affect the AMF community in the soil.

## CS 6-5 The biology of fungal symbioses in lower land plants

PRESSEL, S.<sup>1</sup> and J.G. Duckett<sup>1</sup>

<sup>1</sup>Life Sciences Department, The Natural History Museum, Cromwell Road, London SW7 5BD, UK, s.pressel@nhm.ac.uk.

**Abstract:** Lower land plants, in particular the bryophyte clades, which are the most basal lineages of embryophytes, represent a unique window into the conquest of land by plants from fresh water origins, some 490 million years ago. The evolution of fungal symbioses is considered a key innovation that drove plant terrestrialization, and the notion of Glomeromycota as the sole fungi responsible for the ancestral plant-fungus symbiosis has driven research into these partnerships over the last four decades. However, our recent discovery that early divergent clades of liverworts and hornworts form associations not only with Glomeromycota fungi but also with members of an earlier fungal lineage, the Mucoromycotina, now points to a multifaceted evolutionary scenario. Molecular, functional, and ultrastructural data show that associations involving members of the Mucoromycotina are widespread in bryophytes. These relationships range from obligate and highly host specific to facultative with a broad host range, and also occur, albeit sporadically, in lycopods and ferns. The latest results from our ongoing *in vitro* experiments, coupled with ultrastructural analyses, point to major differences in the morphological responses of lower land plants to Mucoromycotina colonization. However, they also suggest possible structural similarities between Mucoromycotina- and Glomeromycota-plant partnerships. I will discuss our latest findings in the light of current phylogenetic hypotheses and their implications for understanding the origin and evolution of this key attribute of land plants.

## PS 4-44 Hard to compete: mycorrhizal versus wood-decaying fungi in deadwood across highly diverse subtropical forest ecosystems

PURAHONG, W.<sup>1</sup>, F. Buscot<sup>1,2</sup> and T. Wubet<sup>1,2</sup>

<sup>1</sup>UFZ-Helmholtz Centre for Environmental Research, Department of Soil Ecology, Theodor-Lieser-Str. 4, D-06120 Halle (Saale), Germany; <sup>2</sup>German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Deutscher Platz 5e, D-04103 Leipzig, Germany.

**Abstract:** Deadwood is a crucial structural component of natural forest ecosystems, which harbors millions of wood-inhabiting species in the world. Studies in central and northern Europe reported the presence of arbuscular mycorrhizal (AMF) and ectomycorrhizal fungi (EMF) in deadwood. Though mycorrhizal fungi are assumed not to directly decompose deadwood, they are known to interact and compete with wood-decay fungi. Recent evidence also shows that the presence of AMF could significantly reduce wood decomposition rate. Despite the possible importance of mycorrhizal fungi as one of the members of the deadwood microbiome, there is a limited knowledge on their occurrence and community composition in deadwood of tree species in subtropical forest ecosystems. Here, we investigated total and mycorrhizal fungal communities in two deadwood species (*Pinus massoniana* and *Schima superba*) in a subtropical forest ecosystem using pyrotag sequencing of the fungal internal transcribed spacer rRNA genes. Overall, we detected 1,062 fungal OTUs (excluding singleton to tripletons), which includes 24 EMF OTUs. We found no AMF in any of the deadwood samples. Most of EMF OTUs detected have low abundances (except *Hysterangium* OTU00521). We also found a high preference of EMF toward *P. massoniana* which hosted 96% of all EMF detected. In contrast, *Schima superba* only hosted 3 EMF OTUs. The clear variation on the deadwood EMF colonization of the ectomycorrhizal *Pinus massoniana* as compared to the arbuscular mycorrhizal *S. superba*, implies that EMF colonization of deadwood depends on the mycorrhizal status of the tree species. Though we found that the wood-decaying fungi as a dominant component of the deadwood mycobiome, the functional role of EMF in deadwood decomposition and/or flow of decomposition byproducts to the neighboring tree species needs further research.

### LT 3-2 Mycorrhizal benefits to *Andropogon gerardii* are greatly promoted by N fertilization

PÜSCHEL, D.<sup>1,2</sup>, M. Janoušková<sup>1,2</sup>, M. Hujslová<sup>1</sup>, R. Slavíková<sup>1</sup>, H. Gryndlerová<sup>1</sup> and J. Jansa<sup>1</sup>

<sup>1</sup>Institute of Microbiology, Czech Academy of Sciences, Vídeňská 1083, 14220 Prague 4, Czech Republic, david.puschel@ibot.cas.cz; <sup>2</sup>Institute of Botany, Czech Academy of Sciences, Zámek 1, 25243 Průhonice, Czech Republic.

**Abstract:** Mycorrhizal symbiosis is thought to have established as a response to plant transition to terrestrial environments where availability of nutrients such as phosphorus was constrained. Indeed, it has been repeatedly demonstrated that establishment of the arbuscular mycorrhizal symbiosis results in significant improvements in uptake of poorly mobile elements such as P or Zn in many plant species under a variety of environmental conditions, with C4 plants often showing a greater mycorrhizal responsiveness than C3 grasses. More recently, it has been demonstrated that relative, rather than absolute resource limitations, govern mycorrhizal responsiveness with severe limitations in nitrogen or light availability negating the positive growth responses observed under other conditions. Therefore, we tested whether variation in resource (N and P) inputs affects the growth, nutritional responses, root colonization, and carbon redistribution within a model C4 grass (*Andropogon gerardii*) inoculated or not with a field AM fungal community. In a non-fertilized substrate, mycorrhizal plants grew poorer than their nonmycorrhizal counterparts. P acquisition to the plants was not affected, but N uptake was hampered by the presence of AM fungi. With increasing N inputs, the mycorrhizal growth response dramatically improved, and the presence of AM fungi caused biomass production to more than double at high N supply, while the non-mycorrhizal plants exhibited severe P limitation (N:P ratio in the shoots being up to 50.9). Along the same N input gradient, we also observed a much-improved mycorrhizal P uptake response and an increase in root colonization by mycorrhizal structures, particularly arbuscules. Our results demonstrating that significant N inputs greatly improve mycorrhizal benefits, in terms of both biomass production and P uptake, of this C4 grass are surprising when aligned with the observed shifts in plant species composition drifting from C4- to C3-dominated communities following anthropogenic N inputs into prairies and elsewhere.

### PS 4-23 Use of the arbuscular mycorrhizal symbiosis as a biological tool to improve plant growth and tolerance to drought and poor soils: date palm as a model

Benhiba, L.<sup>1</sup>, A. Essahibi<sup>1</sup>, F.M. Oussoufi<sup>1</sup> and A. QADDOURY<sup>1</sup>

<sup>1</sup>Plant Biotechnology and Agrophysiology of Symbiosis, University of Cadi Ayyad, Faculty of Sciences and Techniques, Abdelkerim AlKhattabi Street PO Box 549 Marrakesh, Morocco, qadahmed@gmail.com.

**Abstract:** One of the main challenges for the sustainable management of agricultural land, especially in arid and semi-arid areas, is the combination of the proper use of plant biotechnologies and the management of soil microorganisms as providers of key ecological services that has been at the forefront of generating and promoting agricultural production. These organisms, often referred to as 'ecosystem engineers', 'biocontrol agents', 'biofertilizers', or 'bioenhancers', can participate in improving plant growth and nutrition, strengthening plant performance, restoring ecosystems, and combating pests and pollution. The most important providers of these ecological services are arbuscular mycorrhizal (AM) fungi, which can form a symbiotic association with roots of most land plants including horticultural and forestry species. In this presentation, we will discuss the main results of our recent investigations that have been conducted to assess the ability of arbuscular mycorrhizal fungi to increase date palm tolerance to drought and poor soils. We will discuss the most persuasive mechanism of the contribution of arbuscular mycorrhizal fungi, including water status, nutrient level, antioxidant defense system, osmotic adjustment, and alleviation of cell damage.

#### LT 4-6 Long-term fertilizer application effects on the soil, root arbuscular mycorrhizal fungi, and community composition in rotation agriculture

QIN, H.<sup>1,2</sup>, H.L. Wang<sup>1,2</sup> and Q.F. Xu<sup>1,2</sup>

<sup>1</sup>School of Environmental and Resource Sciences, Zhejiang A & F University, Lin'an, Hangzhou 311300 China, [sagi.qinhua@gmail.com](mailto:sagi.qinhua@gmail.com); <sup>2</sup>Zhejiang Provincial key Laboratory of Carbon Cycling in Forest Ecosystems and Carbon Sequestration, Zhejiang A & F University, Lin'an, Hangzhou 311300 China.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) play key roles in plant growth, ecosystem sustainability, and stability. However, it is still unclear how the soil, root AMF growth and community composition are affected by fertilizer application in subtropical wheat-rice rotation agro-ecosystems. We investigated the impact of different organic and/or inorganic fertilizers on AMF growth and community composition in a long-term experiment field in Zhejiang Province, east China. AMF biomass was determined using 16:1ω5 phospholipid fatty acids (PLFAs) and neutral lipid fatty acids (NLFAs) content. Soil and root AMF community compositions were determined by DGGE analysis, cloning, sequencing and phylogenetic analyses. The root colonization rate was not significantly affected by different fertilizer regimes. Manure amendment significantly enhanced both AMF hyphal (i.e., 16:1ω5 PLFA) and spore (i.e., 16:1ω5 NLFA) biomass content, while inorganic fertilizer only increased the AMF spore biomass. A total of 10 and 11 Glomeromycota phylotypes were detected in soil and root samples, respectively. *Glomus* was the dominant genus in both soil and root samples, while *Acaulospora* genus occurred in roots only. Although the different fertilizers altered soil AMF communities, the root AMF community structure was not significantly altered. Soil pH ( $F=5.695$ ,  $P<0.01$ ) and available K ( $F=4.888$ ,  $P<0.01$ ) contributed to both soil and root AMF community composition, while the C/P ratio ( $F=3.893$ ,  $P<0.01$ ) only contributed to soil AMF community. The data suggests that high soil organic C content benefits AMF growth, while soil pH and available K concentration strongly influence AMF community. The root AMF community was much more resilient to the changes caused by long-term fertilizer application than the soil community.

#### PS 1-55 Desert plants and mycorrhizae: need for mycorrhizal research in a Kuwait desert ecosystem

QUORESHI, A.M.<sup>1</sup> and M.K. Suleiman<sup>1</sup>

<sup>1</sup>Desert Agriculture and Ecosystems Program, Environment and Life Sciences Research Center, Kuwait Institute for Scientific Research, P.O. Box 24885, Safat, Kuwait 13109, [aquoreshi@kisir.edu.kw](mailto:aquoreshi@kisir.edu.kw).

**Abstract:** Kuwait is a small desert country located in the northeastern part of the Arabian Peninsula. The native vegetation of Kuwait includes scant herbaceous perennials, woody shrubs, herbs, and spring ephemerals. Kuwait desert land is characterized by minimal density of vegetation cover, scarce precipitation, limited moisture availability, and high temperatures for most of the year. In arid environments, mycorrhizal associations are common and a crucial factor for the survival of plants and may play an essential role in ecosystem dynamics and productivity. However, very little effort has been made in Kuwait to conduct comprehensive studies of soil microbial communities, particularly mycorrhizal fungal associations, to link biodiversity, ecological processes and structure, and functions. There is no report currently available on the Kuwait desert areas concerning native plants and mycorrhizal association, and their relationship for sustainable community structure and function. The functioning of arbuscular mycorrhizal (AM) fungal symbioses may be affected by the local biotic and abiotic factors of the surrounding rhizosphere and the ecosystem. In recent decades, land degradation and desertification have become a severe problem in Kuwait. An understanding of land reclamation, revegetation, and plant growth and survival might be better attained if knowledge of the presence AM propagules in soil and the association of AM fungi with these native desert plants could be determined. Therefore, there is a need in Kuwait for the evaluation of the mycorrhizal inoculum potential of desert landscapes and a precise understanding of the effects of local environmental changes on AM fungal association and functioning to direct remediation and revegetation programs in Kuwait.



**PS 3-46 Conjoint application of arbuscular mycorrhizal fungi, *Azotobacter chroococcum* and *Trichoderma viride*, in solarised soil for the management of Fusarium wilt of carnation**

**RAJ, H.**<sup>1</sup> and S. Verma<sup>1</sup>

<sup>1</sup>Department of Plant Pathology, Dr. Y.S.Parmar University of Horticulture and Forestry, Nauni-173230, Solan, Himachal Pradesh, India, hrg\_mpp@yahoo.com.

**Abstract:** Fusarium wilt (*Fusarium oxysporum* f. sp. *dianthi*) of carnation is a serious disease found in different parts of India, resulting in up to 79% plant mortality. Studies were conducted to evaluate the effect of different treatment combinations of arbuscular mycorrhizal (AM) fungi, *Azotobacter chroococcum* and *Trichoderma viride*, in soil solarized for 5 weeks with transparent polyethylene mulch (25 µm thick), on the incidence of the wilt in carnation, growth of the plants, and on the quality characteristics of the flowers. Conjoint application of native isolates of AM fungi (5g of inoculums/plant, raised on *Vigna radiata*), *A. chroococcum* (5g slurry/plant as root inoculation of cuttings) and *T. viride* (0.5g talc based formulation mixed in 25g of farmyard manure/5kg of pot soil), as soil application before transplantation of the cuttings was found most effective, with 91% reduction in disease incidence in comparison to non-solarized control. This treatment combination also proved most effective in improving various plant quality parameters with an increase of 242, 45, 43, and 150% in the number of flowers per plant, flower size, length of flowering stem, and stem strength with 'A' grade flowers, respectively, in comparison to non-solarized control. The effect of conjoint application of AM fungi, *A. chroococcum* and *T. viride*, was also quite effective in non-solarized soil as it resulted in an increase of 131, 53, 43, and 130% in number of flowers per plant, flower size, length of flowering stem, and stem strength with 'A' grade flowers, respectively, in comparison to non-inoculated control. This treatment resulted in 23.8 times higher spore count of AM fungi in solarized soil in comparison to non-solarized control and also resulted in 21.6 per cent root colonization.

**PS 2-43 The influence of arbuscular mycorrhizal fungi and plant genetic variation on a natural plant-enemy interaction**

**RASMUSSEN, P.U.**<sup>1</sup>, T. Amin<sup>2</sup>, A.E. Bennett<sup>3</sup>, K.K. Green<sup>4</sup> and A.J.M. Tack<sup>1</sup>

<sup>1</sup>Department of Ecology, Environment and Plant Sciences, Stockholm University, SE-106 91 Stockholm, Sweden, Pil.Rasmussen@su.se; <sup>2</sup>Department of Agricultural Sciences, University of Helsinki, P.O. Box 27, FI-00014 University of Helsinki, Finland; <sup>3</sup>The James Hutton Institute, Invergowrie, Dundee DD2 5DA, Scotland UK; <sup>4</sup> Department of Plant Protection Biology, Swedish University of Agricultural Sciences, Box 102, SE-230 53 Alnarp, Sweden.

**Abstract:** Arbuscular mycorrhizal fungi can influence plant performance, but details on how they affect the plant's interaction with natural enemies are less well studied. Here, we set out to investigate how a natural community of arbuscular mycorrhizal fungi affects the growth of the perennial herb *Plantago lanceolata* as well as its interaction with the herbivore *Melitaea cinxia*. To test this, *P. lanceolata* individuals originating from multiple plant populations in the Åland Islands were selected and grown either with or without mycorrhizal fungi. After 20 days, *M. cinxia* larvae were placed on a subset of plants and allowed to feed for 12 days. Plant morphology and growth rate as well as caterpillar growth rate, developmental time, weight at diapause, and fat content were measured. Results showed that mycorrhizal inoculation did not affect the average plant growth rate; instead, plant genotypes showed striking variation in their response to arbuscular mycorrhizal inoculation. Likewise, caterpillar growth rate, weight at diapause, and developmental time were affected by the interaction between treatment and plant genetic variation. Overall, our findings illustrate that genetic variation in response to mycorrhizal fungi may play a key role in the ecology of plant-insect interactions with consequences for their evolutionary dynamics.

### PS 3-73 Studies on the role of the LysM receptor kinase family in plant root symbiosis with arbuscular mycorrhizal fungi

**RASMUSSEN, S.R.**<sup>1</sup>, W.S.G. Füchtbauer<sup>1</sup>, M.H. Asmussen<sup>1</sup>, M. Novero<sup>2</sup>, A. Genre<sup>2</sup>, P. Bonfante<sup>2</sup>, J. Stougaard<sup>1</sup> and S. Radutoiu<sup>1</sup>

<sup>1</sup>Center for Carbohydrate Recognition and Signalling, Department of Molecular Biology and Genetics, Aarhus University, Gustav Wieds vej 10, 8000 Aarhus C, Denmark, sheena@mbg.au.dk; <sup>2</sup>Department of Life Science and Systems Biology, University of Turin, Viale Mattioli 25, 10125 Torino, Italy.

**Abstract:** Nod-factor (NF) receptors NFR1 and NFR5 are the key molecular components required for perception of the lipochito-oligosaccharide (LCO) signaling molecules produced by rhizobia and for the initiation of signaling events leading to symbiotic nitrogen fixation. Recent studies revealed that arbuscular mycorrhizal (AM) fungi also produce LCOs and short-chain chitin oligomes that are recognized by the legume host and lead to activation of a calcium oscillatory response in the roots similar to the Nod factors. However, so far the receptors for these AM produced signaling molecules remain unknown, and based on the knowledge from NF perception, it is believed that a LysM-containing protein represents the likely receptor. In the model legume *Lotus japonicus*, a large family of LysM receptor-like kinases has been identified. The expression pattern of these genes has been analyzed in various conditions and plant organs; however, their functions remain unknown. We have combined reverse genetics approaches together with genetic complementation, transcript analyses, and promoter studies to investigate the role of *Lotus* LysM receptor kinase genes in plant root symbiosis with AM fungi. TILLING and LORE1 (*L. japonicus* retrotransposon 1) insertion mutants in the various genes have been obtained and characterized for their symbiotic phenotype in the presence of AM. Furthermore, their ability to mount a downstream symbiotic response at the cellular and molecular level in the presence of AM fungi has been investigated. These analyses have been further investigated in detail for specific members of the family using genetic complementation and promoter fusions. The results from our analyses on these prospective candidate genes will be presented.

### PS 2-44 A metagenomics approach to characterizing the soil microbiome of two endangered orchids

**RAVELO, A.V.**<sup>1</sup>, S. Buback<sup>2</sup>, G. Conant<sup>3</sup> and J.C. Pires<sup>1</sup>

<sup>1</sup>Division of Biological Sciences, University of Missouri-Columbia, avrkt6@mail.missouri.edu; <sup>2</sup>Missouri Department of Conservation; <sup>3</sup>Division of Animal Sciences, University of Missouri-Columbia.

**Abstract:** Orchids are obligate dependents on mycorrhizae for the successful germination of their seeds resulting in a relationship that has a significant impact on the orchid life cycle. The presence and distribution of orchid mycorrhizae have been pinpointed as possible limiting factors in the establishment and abundance of orchid populations highlighting the importance of identifying the influence of mycorrhizal fungi on the success of species that are of conservation concern. The western and eastern prairie fringed orchids (*Platanthera praeclara* and *P. leucophaea*, respectively) had historic ranges throughout most of North America, but with the cultivation of the prairie, these orchids suffered great habitat loss and fragmentation. Consequently, their populations were adversely affected and they are now federally listed as threatened. In Missouri, the only known populations of these orchids have been monitored for over twenty years by the Department of Conservation, but there are still many unknowns regarding the biotic and abiotic factors that affect them. This study aimed to characterize the microbial communities associated with the orchids by analyzing soil samples obtained from each of the orchid sites as well as from sites of high-quality prairie but without known populations. To obtain a more complete picture of the microbial communities a two-pronged approach was used for DNA sequencing. To inform on the microbial diversity across the different samples, we used amplicon sequencing targeting the 16S rRNA gene (bacteria and archaea) as well as ITS (fungi). A shotgun metagenomics approach was used to gain insights on the functional characteristics of the microbiome through the deep sequencing of three samples. Additionally, a comparative metagenomics approach was used for 12 samples. This study hopes to establish a baseline representation of the biotic soil characteristics that should be taken into account when evaluating potential habitat for species reintroduction and management.

**LT 2-14 A novel delivery system for the root symbiotic fungus *Sebacina vermifera* and consequent effects on growth of five different cultivars of wheat in two field locations**

**RAY, P.<sup>1</sup>**, Y. Guo<sup>1</sup>, M. Chi<sup>1</sup> and K.D. Craven<sup>1</sup>

<sup>1</sup>Plant Biology Division, The Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401, pray@noble.org.

**Abstract:** *Sebacina vermifera*, first isolated from the Australian orchid *Cyrtostylis reniformis*, has been reported to show beneficial effects on plant growth that includes growth promotion, increased nutrient uptake, enhanced seed production and increased resistance against different biotic and abiotic stresses. Despite these promising results, no products are currently on the market that incorporate this fascinating mycorrhizae. Wheat (*Triticum aestivum*) is a cereal grain grown on more land area than any other commercial food. In terms of total production tonnage, it is currently second to rice as the main human food crop. Here, we describe the development of a carrier-based delivery method for *S. vermifera*, by impregnating the fungus onto bentonite clay particles. Bentonite is a naturally occurring clay mineral composite that has been commonly used in agriculture as a soil preservative and also as carrier for bio-inoculants. With this method, we documented significantly enhanced root development in winter wheat under *in vitro* conditions. Consequently, we tested the effect of *S. vermifera* (MAFF305830) on yield and persistence of five different wheat cultivars in two different locations in Southern Oklahoma, comprised of highly diversified soil types in terms of soil nutrition and pH. The plants were inoculated using bentonite clay coated with or without *S. vermifera*. We found that the fungus remained viable throughout the winter growing season and effectively colonized the root systems in diverse field conditions. Further, in one (OK09125) of the five cultivars tested, *S. vermifera* colonization increased biomass and grain yield in both the field locations, in two cultivars (Duster and OK08328) colonization increased biomass and grain yield in marginal soil type only, whereas in the remaining two cultivars (Gallagher and OK1059016) fungal colonization had no effect on plant fitness. This demonstrates how *S. vermifera* might differentially affect plant genotypes and such effect may predominate over differing soil conditions.

**PS 4-79 Potential involvement of *Pisolithus albus* metallothionein in heavy metal tolerance during mycorrhizal symbiosis**

**REDDY, M.S.<sup>1</sup>**, M. Kour<sup>1</sup>, R. Marmeisse<sup>2</sup> and L. Fraissinet-Tachet<sup>2</sup>

<sup>1</sup>Thapar University, Department of Biotechnology, Bhadson Road, Patiala 147 004, India, msreddy@thapar.edu;

<sup>2</sup>Microbial Ecology, CNRS UMR 5557, USC INRA 1364, Université Lyon1, Université de Lyon, F-69622 Villeurbanne, France.

**Abstract:** Metallothioneins (MTs) are small, cysteine-rich peptides involved in intracellular sequestration of heavy metals in eukaryotes. We examined the role in metal homeostasis and detoxification of a MT in the ectomycorrhizal fungus *Pisolithus albus* (*PaMT*). *Pisolithus albus* (*PaMT*) encodes a 35 amino acid-long polypeptide with seven cysteine residues, most of them part of a C-x-C motif found in other known basidiomycete MTs. The expression levels of *PaMT* increased as a function of increased external Cu and Cd concentrations; the expression levels were higher with Cu than with Cd. Heterologous complementation assays in metal-sensitive yeast mutants indicated that *PaMT* encodes a polypeptide capable of conferring higher tolerance to both Cu and Cd. *Eucalyptus tereticornis* plantlets colonized with *P. albus* grown in presence of Cu and Cd exhibited better growth compared to nonmycorrhizal plants. Higher *PaMT* expression levels were recorded in mycorrhizal plants grown in the presence of Cu and Cd compared to control mycorrhizal plants not confronted with heavy metals. These data, to the best of our knowledge, provide the first evidence that *PaMT* could provide protection against heavy metals while in an ectomycorrhizal symbiosis.

## CS 1-3 Phylogeny of the Glomeromycota: advances and perspectives

REDECKER, D.<sup>1</sup>

<sup>1</sup>Université de Bourgogne, UMR 1347 Agroécologie, BP 86510, F-21000 Dijon, France, dirk.redecker@dijon.inra.fr.

**Abstract:** The Glomeromycota are a monophyletic group within the true fungi comprising arbuscular mycorrhizal fungi and *Geosiphon pyriformis*. Phylogenies obtained based on ribosomal rDNA data alone, or in combination with protein-coding genes, have consistently indicated a position of the glomeromycotan clade between the Dikarya and other “zygomycotan” lineages. Protein-coding gene phylogenies have consistently challenged this view and placed the Glomeromycota close to the Mucoromycotina. Molecular phylogenies have played a crucial role in establishing a natural classification for the phylum, as in many cases the scarce morphological characters of glomeromycotan spores have been shown to be inadequate for defining genus- to order-level taxa. Thus, phylogenetic data have also become important in studies of the ecology of these fungi, many of which are based on high-throughput sequencing surveys. However, in spite of genome data becoming available for a few members of the phylum, sequence data are still lacking for the construction of comprehensive multilocus datasets from a larger subset of taxa, which would be useful to better understand the relationships among major lineages in the phylum. The presentation will highlight recent advances and perspectives in this area of research.

## PS 1-37 The International Bank for the Glomeromycota

REDECKER, D.<sup>1</sup>, V. Monfort-Pimet<sup>2</sup>, J. Michel<sup>2</sup> and D. Wipf<sup>1</sup>

<sup>1</sup>Université de Bourgogne, UMR 1347 Agroécologie, ERL 6300 CNRS IPM, BP 86510, F-21000 Dijon, France, dirk.redecker@dijon.inra.fr; <sup>2</sup>INRA, UMR 1347 Agroécologie, ERL 6300 CNRS IPM, BP 86510, F-21000 Dijon, France.

**Abstract:** The International Bank for the Glomeromycota was founded in 1993 as the “Banque Européenne des Glomales” (BEG) within the framework of a European COST action. The establishment of this culture collection of arbuscular mycorrhizal fungi (AMF) was incited by the evident urgent need for standardized biological material of these obligate biotrophs. Its mission has been to keep and distribute reference cultures of AMF for research and industry. A large number of culture aliquots have been distributed since then and the use of these cultures is reflected in a large number of citations in the scientific literature. The core collection has been at INRA Dijon since its inception by V. Gianinazzi-Pearson, with permanent staff assuring maintenance and renewal of fungal cultures. Changes in the curator and organization of the collection in 2012 have resulted in refocusing on the core collection and its improved genetic and functional characterization. A nominal fee was introduced for requests from developed countries to partly cover the cost of culture handling and sending. BEG isolate codes were given to fourteen fungal cultures which were previously cultivated only for internal use. These cultures will be made publicly available in the near future. Currently, 41 isolates from 33 species are permanently grown in about 250 open-pot cultures. Among them are reference cultures for industrial production and for AMF taxonomy (isotypes). The establishment of root organ cultures for the five *Rhizophagus irregularis* isolates has been initiated to be able to provide material of state-of-the-art purity in the future. As is obvious from the constant flow of culture requests we receive, there is still a clear need for this culture collection. Our strategy for the future will rely on thoroughly characterized isolates, while intensifying coordination with our partner AMF collections. We intend to improve molecular genetic and genomic analysis of these isolates and have initiated work to facilitate molecular purity control of AMF cultures.

## LT 3-11 Mycorrhiza effects on semiarid grassland community structure and species in the Northern Great Plains

REINHART, K.O.<sup>1</sup>

<sup>1</sup>USDA-Agricultural Research Service, Fort Keogh Livestock and Range Research Laboratory, Miles City, Montana, USA, kurt.reinhart@ars.usda.gov.

**Abstract:** Little is known about the importance of arbuscular mycorrhizal fungi (AMF) to plants in expansive, temperate, and semiarid grasslands of the Northern Great Plains. I compared the plant community structure of pairs of plots treated with either fungicide (to suppress AMF) or no fungicide from 2010 to 2014. I also used a growth room experiment to

quantify the mycorrhizal growth responses (MGRs) of 69 regional plant species, including 14 invasive plants. Unlike tallgrass prairie, plant community diversity indices for northern mixed-grass prairie were not appreciably affected by AMF suppression. Plant community composition, however, did vary over time between plots with AMF suppression vs. controls. This was attributed to AMF mediating shifts in abundance of two co-dominant C<sub>3</sub> grasses but were not detectable after a 2012 drought. Across 69 plant species, MGRs were varied and typically lower (log response ratio [LRR] mean=0.12 and standard deviation=0.36) than values reported for (mesic) tallgrass prairie plant species (MGR LRR mean=1.58 and standard deviation= 1.54) of the Central Plains. Unlike tallgrass prairie, MGRs were not phylogenetically conserved. Similar to tallgrass prairie, invasive status was phylogenetically conserved indicating that invasive plants tended to be related and from a few plant clades. For the Northern Great Plains, invasive taxa exhibited wide variation in MGRs (LRR range: -0.21 to 0.68). MGRs did not differ appreciably among invasive versus non-invasive plant taxa. While most regional plant species are mycorrhizal, the plants were relatively unresponsive to AMF based on routine field and greenhouse tests of AMF effects. Other data indicate that this and other semiarid regions are more limited by nitrogen than phosphorus. In these systems, AMF effects may be subtle and/or mainly detectable with alternative experimental designs (e.g., AMF affects drought tolerance or plant-plant interactions).

**PS 4-24 The role of mycorrhizae and soil organism communities in restoring a native grass, *Bouteloua gracilis*, in the face of a dynamic climate and exotic species invasion**

**REMKE, M.J.**<sup>1</sup>, M. Bowker<sup>1</sup> and N.C. Johnson<sup>2</sup>

<sup>1</sup>School of Forestry, Northern Arizona University, Flagstaff, Arizona 86011 USA, mr2237@nau.edu; <sup>2</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA.

**Abstract:** On the Colorado Plateau, land use changes and prolonged drought are negatively impacting native plants. *Bouteloua gracilis* is a perennial grass that is obligately associated with soil organisms, such as mycorrhizal fungi. Plants and soil organisms may be locally adapted to one another suggesting that benefits from soil organisms are site specific. In this experiment, we conducted a greenhouse study to examine whether novel soil organisms would provide equal benefits to *B. gracilis* populations as natal soil organisms. We also examined the lasting effects of exotic plant invasion on soil organism communities, and how such alterations affect native grass growth. We used soil inocula and *B. gracilis* individuals from two sites and an area invaded by *Bromus tectorum* to determine the benefits received from novel versus natal soil organisms. We found that plants grown in association with soil organisms from their natal site were the tallest (p=0.0184). We also found that plants grown in association with *B. tectorum* invaded soil had the lowest establishment rates and were the smallest (p=0.0022). In addition, plant roots were more colonized by arbuscular mycorrhizal fungi when paired with their natal soil organisms. These data suggests the symbiosis that occurs between *B. gracilis* and its soil organisms is site specific. In addition, *B. tectorum* appears to manipulate soil organism communities in a way that inhibits establishment of *B. gracilis*. This could be due to a reduction of mycorrhizal fungal density, or due to an accumulation of parasitic organisms. Land managers should then be interested in preparing soil inoculum from seed collection sites to enhance performance of restoration projects in disturbed or invaded sites. In doing so, land managers should be able to enhance plant productivity and resilience in restoration and conservation projects.

**PS 1-56 Arbuscular mycorrhizal fungal colonization modulates phenolic acids secretion and enhances resistance of watermelon roots to *Fusarium* pathogen**

**REN, L.X.**<sup>1</sup> and G.H. Xu<sup>1</sup>

<sup>1</sup>Department of Plant Nutrient, Nanjing Agricultural University, Nanjing, 210095, China, lxren@njau.edu.cn.

**Abstract:** Arbuscular mycorrhizal fungal (AMF) colonization can affect secretion of allelopathic substances of host plant roots that defend against soilborne pathogens. Watermelon (*Citrullus lanatus*) is susceptible to *Fusarium oxysporum* f. sp. *niveum* (FON) infection, which causes wilt disease. We investigated the response of watermelon's phenolic acid secretion to AMF colonization when FON-caused wilt disease occurred and analyzed the correlation between watermelon resistance to FON pathogen and exogenous phenolic acid application. The results showed that colonization by the AMF species *Glomus mosseae* reduced the wilt disease index by 89.3% as indicated by suppressing pathogen development in the roots and rhizosphere of watermelon. Inoculation with both the AMF and FON decreased the number of colony forming units of FON by 58.1% and 47.7% in watermelon roots and the rhizosphere, respectively. By contrast, *p*-coumaric acid se-



cretion increased by 62.1% upon double inoculation with AMF and FON. The FON infection triggered phenolic acids especially *p*-coumaric acid production. The AMF colonization alleviated watermelon wilt disease and increased allelopathic substance of *p*-coumaric acid exudation of root in response to FON infection. The FON inoculation decreased expression of *CIPR3* gene for encoding chitinase in watermelon leaves, which was remedied by exogenous *p*-coumaric acid application. In contrast, exogenous application of *p*-Coumaric acid upregulated *CIPR3* expression in watermelon roots. Chitinase activity of watermelon roots was enhanced by exogenous *p*-coumaric acid addition, while it tended to be decreased by FON inoculation. The decreased chitinase activity due to FON inoculation was remedied by exogenous *p*-coumaric acid application. These results demonstrated that AMF colonization increased allelopathic *p*-coumaric acid secretion, enhanced plant resistance to wilt disease, and alleviated watermelon wilt disease.

#### PS 4-45 **Comparative genomics and population genetics provide new insights on the life cycle of the black truffle of Périgord (*Tuber melanosporum* Vittad.)**

**RICCIONI, C.**<sup>1</sup>, C. Murat<sup>2</sup>, H. De La Varga<sup>2</sup>, F. Todesco<sup>2</sup>, A. Rubini<sup>1</sup>, B. Belfiori<sup>1</sup>, T. Payen<sup>2</sup>, F. Le Tacon<sup>2</sup>, C. Robin<sup>3</sup>, F. Paolocci<sup>1</sup> and F. Martin<sup>2</sup>

<sup>1</sup>IBBR-CNR, 06128 Perugia, Italy, claudemurat@nancy.inra.fr; <sup>2</sup>INRA, UMR 1136 INRA-Université de Lorraine, Interactions Arbres/Microorganismes, Laboratoire d'Excellence ARBRE, INRA-Nancy, 54280 Champenoux, France; <sup>3</sup>INRA, UMR1121, 54518 Vandoeuvre les Nancy, France.

**Abstract:** Truffles are ectomycorrhizal fungi living in symbiosis with many trees and shrubs. Inoculated seedlings with truffles are available since forty years and the interest in truffle cultivation is increasing worldwide. However, novel management guidelines for sustainable truffle orchards, in which the production is less unpredictable even in the climate change context, are needed. A better understanding of the biological and ecological mechanisms driving the truffle life cycle is one of the approaches to reach these goals. The genomic resources available for *Tuber melanosporum* allowed us to unravel its sexual reproduction mode by identifying mating type genes and to characterize new polymorphic markers allowing population genetics analyses. The study of genet distribution in truffle orchards showed a non-random spatial distribution of ectomycorrhizas formed by both *T. melanosporum* mating types, as well as a rapid yearly turnover of these genets. This analysis revealed a striking competition between genets based on their mating-type genes to colonize plant root system and questioned the localization of both parents in the initiation of the sexual cycle. To gain additional information on *T. melanosporum* genetic diversity, we re-sequenced the nuclear genome of six geographic accessions. A total of 442,326 single nucleotide polymorphisms (SNPs) corresponding to 3,540 SNPs/Mbps were identified. Based on their SNP density, samples clustered according to their geographic origin and the putative role of the last glaciation in *T. melanosporum* phylogeography is confirmed. Additionally, genomic regions and genes potentially subjected to positive or purifying selection were identified. Finally, a large-scale analysis of *T. melanosporum* populations at European scale using highly polymorphic simple sequence repeats (SSR) is also in progress.

#### SY 2-4 **Linking genomes, transcriptomes, and spectroscopy provides insights into the litter decomposing mechanisms in ectomycorrhizal fungi**

**RINEAU, F.**<sup>1</sup>, F.H. Shah<sup>2</sup>, P. Persson<sup>2</sup>, J.V. Colpaert<sup>1</sup>, J. Vangronsveld<sup>1</sup> and A. Tunlid<sup>2</sup>

<sup>1</sup>Centre for Environmental Sciences, Environmental Biology Group, Universiteit Hasselt, 3590 Diepenbeek, Belgium, francois.rineau@uhasselt.be; <sup>2</sup>Microbial Ecology, Department of Biology, Lund University, Ecology Building (Sölvegatan 37) SE-223 62 Lund, Sweden.

**Abstract:** Since Frank's "mycorrhizal decomposition" theory, there has been a lot of debate on the role of ectomycorrhizal fungi (ECM) on C and nutrient cycles. The generally accepted view was that ECM fungi were depending on the degradation of lignocellulose by saprophytic fungi to access organic nitrogen. This assumption was supported the facts that ECM had much lower enzyme activities than saprophytes, and that drastic reductions of gene families involved in lignocellulose degradation were observed in ECM genomes. Several recent studies shed a new light on this postulate. A set of various approaches (genomics, transcriptomics, secretomics, enzyme assays, and advanced substrate chemical characterization) was combined to examine in a more comprehensive way the involvement of ECM in soil organic matter decomposition. Initial results on a model ECM species showed that it had a significant capacity to depolymerize polysaccharides and oxidize lignin building blocks while retrieving N from soil organic matter. These processes involved mecha-

nisms similar to what we know from saprophytic brown-rot fungi and were generated, at least to some extent, by redox cycling of a pigment. However, contrary to their saprotrophic counterparts, the ECM fungus lacked the genes to convert the degraded carbohydrates into energy. Moreover, the degradation of soil organic matter by this ECM species was dependent on the presence of a simple sugar source. Extension of this experiment to an array of supplementary ECM and saprotrophic fungi showed that all species were able to degrade the organic matter to a significant extent, but that they were doing so using a large variety of enzyme combinations. Altogether, these results make us reconsider the role ECM fungi play in the recycling of the organic matter.

#### LT 4-15 Time of inoculation determines the success of arbuscular mycorrhizal fungal symbiosis in oil palm (*Elaeis guineensis* Jacq.) seedlings

RINI, M.V.<sup>1</sup> and M. Faria<sup>1</sup>

<sup>1</sup>Department of Agrotechnology, Faculty of Agriculture, University of Lampung, Lampung, Indonesia, vatrin66@yahoo.com.

**Abstract:** Our previous study showed that inoculating germinated oil palm seeds with arbuscular mycorrhizal fungi (AMF) by either placing 10 spores of AMF on the surface of the radicle tip or by placing AMF inoculum containing 300 spores 5 cm below radicle tip resulted in no AMF infection in the root 3 months after inoculation. Therefore, in this experiment, we studied in more detail the oil palm seedling root system and its relation to AMF infection. For the first study, we inoculated germinated seeds by placing 300 spores of *Glomus* sp. or *Entrophospora* sp. 5 cm below the radicle tip. The seeds were planted in 15 x 20 cm polybags containing sterilized sand as media. Twelve polybags were prepared for each AMF type and another 12 polybags served as the control (without AMF inoculation). Three polybags for each treatment were harvested at 2, 3, 4, and 5 weeks after inoculation (WAI) to observe root system development and AMF infection in the primary and secondary roots. The second experiment was the same as the first, except we used one-month-old oil palm seedlings. The results showed that, using germinated seeds, secondary roots in all treatments developed at 2 WAI (24-32), and the number increased with an increase in sampling time (134-182 at 5 WAI). The number of primary roots also increased from two at 2 WAI to four at 5 WAI. However, no AMF infection was observed at the primary or secondary roots 2-5 WAI. In the one-month-old seedling experiment, AMF infection was observed at 3 WAI for both *Glomus* sp. (9.2%) and *Entrophospora* sp. (13.4%) with the number of secondary roots at 110 and 156, respectively. However, no infection was observed at the primary roots 2-5 WAI.

#### PS 4-25 Arbuscular mycorrhiza *Rhizophagus irregularis* and *Funneliformis mosseae* does not ameliorate *Arundo donax* plantlets response to short time salinization

ROMERO-MUNAR, A.<sup>1</sup>, C. Cabot<sup>1</sup>, E. Baraza<sup>1</sup>, J. Cifre<sup>1</sup> and J.C. Gulías<sup>1</sup>

<sup>1</sup>Biology Department, University of Balearic Islands, Palma de Mallorca, Balearic Islands 07122 Spain, antonia.romero@uib.cat.

**Abstract:** An increase in P assimilation as the mechanism for arbuscular mycorrhizal (AM) to increase plant tolerance to stress has been suggested. With the aim of determining whether AM inoculation could ameliorate salinity stress, a growth chamber experiment was carried out with giant reed (*Arundo donax*) growing at different levels of salinity and phosphorus availability. Plantlets were grown in sand culture with nine treatments: Control 1 (C1), 0,25 mM Pi+1 mM NaCl; Control 75 (C75), 0,25 mM Pi+75 mM NaCl; Control 150 (C150), 0,25 mM Pi+150 mM NaCl; low Pi 1 (LP1) 0.025 mM Pi+1 mM NaCl; low Pi 75 (LP75) 0.025 mM Pi+75 mM NaCl; low Pi 150 (LP150) 0.025 mM Pi+150 mM NaCl; AM low Pi 1 (AMLP1) 0.025 mM Pi+1 mM NaCl; AM low Pi 75 (AM LP75) 0.025 mM Pi+75 mM NaCl; AM low Pi 150 (AMLP150) 0.025 mM Pi+150 mM NaCl. Plant growth rate, biomass, nutrient allocation, soluble leaf protein and chlorophyll concentrations, and gas exchange parameters were measured. Severe salt stress affected all plants equally, regardless of phosphorus concentration or the presence or absence of AM. This lack of effect of AM in salt-stressed plants could be due to the non-specific fungi used, *Rhizophagus irregularis* and *Funneliformis mosseae*. However, without salinity stress, total biomass was higher in AM plantlets, in spite of being grown at low P concentration. Even though no differences in CO<sub>2</sub> assimilation were found amongst treatments, under these culture conditions, AM plantlets produced more leaves, heavier stems, and greater root biomass. These results suggest that AM could increase carbon use efficiency and affect biomass allocation, which can be crucial for the beneficial effect of AM in early plant growth stages.

## LT 1-7 Colonization of new land by arbuscular mycorrhizal fungi

ROSENDAHL, S.<sup>1</sup>, K.B. Nielsen<sup>1</sup>, R. Kjølner<sup>1</sup>, H.H. Bruun<sup>1</sup> and T.K. Schnoor<sup>2</sup>

<sup>1</sup>Department of Biology, University of Copenhagen, Universitetsparken 15, DK-2100 Copenhagen Ø, Denmark, soerenr@bio.ku.dk; <sup>2</sup>Department of Biology, Lund University, Ecology Building, SE-22362 Lund, Sweden.

**Abstract:** The study describes the primary assembly of arbuscular mycorrhizal (AM) communities on the newly formed artificial island Peberholm constructed as part of the Øresund connection between Denmark and Sweden. The structure of arbuscular mycorrhizal communities was assessed through 454 pyrosequencing. Internal community structure was investigated through fitting the rank-abundance of Operational Taxonomic Units to different distribution models. Heterogeneity of communities within islands was assessed by analysis of group dispersion. The mean OTU richness per sample was significantly lower on the new artificial island than on the neighboring natural island, indicating that richness of the colonizing AM fungal community is restricted by limited dispersal. The AM fungal communities colonizing the new island appeared to be a non-random subset of communities on the natural and much older neighboring island, which points to high colonization potential of certain, probably early successional, mycorrhizal fungi, likely assisted by migratory birds.

## CS 1-6 Speciation by hybridization in the Glomeromycota – *Claroideoglossum candidum*

ROSLING, A.<sup>1</sup>, G. House<sup>2</sup>, W. Kaonongbua<sup>3</sup> and J. Bever<sup>2</sup>

<sup>1</sup>Evolutionary Biology, Uppsala University, Uppsala Sweden, anna.rosling@ebc.uu.se; <sup>2</sup>Biology department, Indiana University, Bloomington IN, USA; <sup>3</sup>Department of Microbiology, King Mongkut's University of Technology, Thon Buri, Thailand.

**Abstract:** Arbuscular mycorrhizal fungi have a unique genomic and reproductive organization. They reproduce asexually by forming large multinucleate spores, and thus, have no single nucleate stage in their life cycle. Within organismal rDNA, gene polymorphism is high. Hyphal fusion and nuclear mixing in genetically identical strains are common and can also occur between genetically dissimilar strains, and result in heterokaryosis. Therefore, arbuscular mycorrhizal fungi have a mechanism for hybridization between species, but, until now, there is no evidence that such hybrids form or that they can be stable in nature. Here, we use three different techniques to sequence rDNA genes from single spore extracts and find evidence consistent with between species hybridization in *Claroideoglossum candidum*. From replicate single spore extracts, 11-21 unique genotypes were recovered using cloning and Sanger sequencing of 1500 bp rDNA fragments. Variation detected in the LSU was recovered with both 454 and Illumina sequencing. In *C. candidum*, the majority of rDNA sequences show high homology with other *Claroideoglossum* sequences. However, 10-15% of the recovered sequences are of *Rhizophagus intraradices* origin. This study is part of a larger one where over fifty single spore extracts, representing species across the Glomeromycota, were sequenced. No cultures of *R. intraradices* were in the lab at the time of the sequencing, and sequences from this species were not detected from any other isolates examined in the larger study. We thus conclude that *C. candidum* is a species formed by hybridization of distantly related taxa.

## SY 2-6 The biology of arbuscular mycorrhizal fungi in the light of genomics

Malbreil, M.<sup>1,2</sup>, N. Tang<sup>1,2,3</sup>, F. Martin<sup>4</sup>, J.M. Ane<sup>5</sup>, P.M. Delaux<sup>5</sup> and C. ROUX<sup>1,2</sup>

<sup>1</sup>Université de Toulouse, UPS, UMR5546, Laboratoire de recherche en Sciences Végétales, BP42617, F-31326 Castanet-Tolosan CEDEX, France, roux@lrsv.ups-tlse.fr; <sup>2</sup>CNRS, UMR5546, BP 42617, F-31326 Castanet-Tolosan CEDEX, France; <sup>3</sup>College of Life Science and Technology, Huazhong Agricultural University, WuHan, HuBei province, 430070, China; <sup>4</sup>Institut National de la Recherche Agronomique, Unité Mixte de Recherche 1136, Interactions Arbres/Microorganismes, Centre de Nancy, Université de Lorraine, 54280 Champenoux, France; <sup>5</sup>Rothermel-Bascom, Department of Agronomy, University of Wisconsin Madison, 1575 Linden Drive, Madison, WI 53706-USA.

**Abstract:** Arbuscular mycorrhizal (AM) fungi, Glomeromycota, can associate with non-vascular plants (liverworts, hornworts), early diverging vascular plants (ferns), or seed plants. Such broad host spectrum is unique among plant-interacting fungi. Previous works in comparative phylogenomics showed that mycotrophic plants (i.e., plants hosting AM fungi) share conserved genes that seem to be required for AM symbiosis. By contrast, the AM fungal “symbiotic gene toolkit”

remains poorly characterized, mostly due to the absence of related genetic tools. This is why the release of genome assemblies from the AM fungus *Rhizophagus irregularis* strain DAOM197198 represents an important step forward in the study of AM fungal biology. Different points of these data will be presented. First, the karyotic status of these fungi will be discussed; in contrast with previous works suggesting a heterokaryotic organisation of AM fungi (different nuclei in each individuals), DAOM197198 is homokaryotic with a haploid genome of approximately 154 Mb. As expected for such a large fungal genome, transposable elements are strongly represented, at least one third of the genome. Ongoing work deals with the dynamics of TE activity and their incidence on genome plasticity. Based on the designed gene repertoires, we then compared the transcriptomes of two AM fungal species, *Rhizophagus irregularis* and *Gigaspora rosea*, in association with flowering plants (monocot and dicot) and a liverwort. Interestingly, the obtained gene patterns, including nutrient transporters, metabolic genes, and a panel of secreted proteins potentially involved in host manipulation, were highly conserved whatever the host. How these genes can be considered as remnant of the ancient AM fungal symbiotic gene network will be discussed.

#### CS 9-4 Diversity, distribution, and specificity of ectomycorrhizal fungi in the Amazonian lowlands

**ROY, M.**<sup>1</sup>, H. Schimann<sup>2</sup>, R. Braga-Neto<sup>3</sup>, L. Fernandez<sup>1</sup>, J. Hackel<sup>1</sup>, S. Manzi<sup>1</sup>, R.A.E. Da Silva<sup>4</sup>, J. Duque<sup>4</sup>, D. Frame<sup>5</sup>, C. Decock<sup>6</sup> and M.A. Neves<sup>4</sup>

<sup>1</sup>Université Paul Sabatier – CNRS, Laboratoire Evolution et Diversité Biologique, UMR5174, 118 route de Narbonne, 31062 Toulouse cedex, France, melanie.roy@univ-tlse3.fr; <sup>2</sup>INRA - UMR Ecologie des Forêts de Guyane, Campus agronomique - BP 316 - F-97379 Kourou cedex, France; <sup>3</sup>INPA, Instituto Nacional de Pesquisas da Amazônia, Av. André Araujo 2936, Manaus, AM, CEP: 69060-000, Brazil; <sup>4</sup>MICOLAB, Universidade Federal de Santa Catarina, Departamento de Botânica, Trindade - Florianópolis, SC, CEP: 88040-900, Brazil; <sup>5</sup>Herbier IRD de Guyane, UMR AMAP, Route de Montabo - BP165 - 97323 Cayenne, France; <sup>6</sup>Mycothèque de l'Université catholique de Louvain (MUCL, BCCMTM), Earth and Life Institute - Microbiology (ELIM), Université catholique de Louvain (UCL), B-1348, Louvain-la-Neuve, Belgium.

**Abstract:** Ectomycorrhizal fungi are said to be rare in the Amazonian lowlands outside of the monodominant forests from the Guyana highlands. Indeed, root tip screenings handled on the Amazonian *terra firme* soils have revealed only few ectomycorrhizal hosts associated with fairly low diversity and specific fungal communities. However, based on the numerous fruiting body collections made by Rolf Singer in the lower Rio Negro in the late 1970s, some habitats, like white-sand forests, are thought to host many ectomycorrhizal fungi. More recently, numerous Russulaceae and Amanitaceae have been described from coastal habitats in Brazil, and some species like *Cantharellus guyanensis* have been recorded from Colombia to Brazil. All these records and descriptions of ectomycorrhizal fungi suggest these symbioses are diverse and widespread in the Neotropics, which raises questions about their host specificity in these hyper-diverse plant communities. To draw a first sketch of their distribution and diversity, we gathered fruiting body inventories of ectomycorrhizal specimens in Brazil and French Guiana, and specimens deposited in Brazilian herbaria. In French Guiana, after a three-year survey on ten distinct sites, ectomycorrhizal fungi were detected in diverse non-monodominant forests. Sequencing of fungal communities associated with several co-occurring ectomycorrhizal hosts (belonging to Polygonaceae and Nyctaginaceae) allowed us to investigate the diversity and specificity of these ectomycorrhizal symbioses in non-monodominant forests. Our results highlight the wide distribution of EM fungi all over Brazil and French Guiana, not exclusively in white-sand forests. Fungal specificity was variable, depending on hosts, but was low when several hosts species were co-occurring. By identifying favorable habitats for EM symbioses in non-monodominant forests, our results call for a new investigation of EM fungi diversity and specificity in the Neotropics.



### LT 3-14 Home-field advantage. Does the geographic origin of plants, mycorrhizal fungi and soil determine plant responses to mycorrhizal symbioses?

RÚA, M.A.<sup>1</sup>, A. Antoninka<sup>2</sup>, P.M. Antunes<sup>3</sup>, V.B. Chaudhary<sup>4</sup>, C. Gehring<sup>5</sup>, L.J. Lamit<sup>6</sup>, B.J. Piculell<sup>1</sup>, J. Bever<sup>6</sup>, C. Zabinski<sup>8</sup>, J.F. Meadow<sup>9</sup>, M.J. Lajeunesse<sup>10</sup>, B.G. Milligan<sup>11</sup>, M. Gardes<sup>12,13</sup>, J. Karst<sup>14</sup> and J.D. Hoeksema<sup>1</sup>

<sup>1</sup>Department of Biology, 214 Shoemaker Hall, University of Mississippi, University, MS, 38677, marua@olemiss.edu; <sup>2</sup>University of Colorado, Department of Ecology and Evolutionary Biology, Boulder, CO 80309; <sup>3</sup>Department of Biology, Algoma University, 1520 Queen Street East, Sault Ste. Marie, Ontario P6A 2G4, Canada; <sup>4</sup>Institute of Environmental Sustainability, Loyola University Chicago, 1032 W. Sheridan, Chicago, IL 60660; <sup>5</sup>Department of Biological Sciences, Northern Arizona University 617 S. Beaver Street, Flagstaff, AZ 86011-5640; <sup>6</sup>Michigan Technological University, School of Forest Resources and Environmental Science, 1400 Townsend Dr., Houghton, MI 49931-1295; <sup>7</sup>Department of Biology, Indiana University, Bloomington, IN 47405; <sup>8</sup>Department of Land Resources and Environmental Sciences, 344 Leon Johnson Hall, Montana State University, Bozeman, MT 59717; <sup>9</sup>Institute of Ecology and Evolution, University of Oregon, 335 Pacific Hall, Eugene, OR, 97403; <sup>10</sup>Department of Integrative Biology, University of South Florida, 4202 East Fowler Avenue, Tampa, Florida 33620; <sup>11</sup>Department of Biology, New Mexico State University, Las Cruces, New Mexico 88003; <sup>12</sup>Université Toulouse 3 Paul Sabatier, CNRS, ENFA ;UMR5174 EDB (Laboratoire Évolution & Diversité Biologique), 118 route de Narbonne, F-31062 Toulouse, France; <sup>13</sup>CNRS, Université Paul Sabatier ; UMR5174 EDB, F-31062 Toulouse, France; <sup>14</sup>Department of Renewable Resources, University of Alberta, 442 Earth Sciences Building, Edmonton, Alberta, T6G 2E3.

**Abstract:** Higher fitness of genotypes in their native environment relative to a foreign environment, or local adaptation, can drive the maintenance of genetic diversity in a species, and can also lead to population divergence and even speciation. Mycorrhizal fungi can play an important role in mediating a plant's interaction with the local abiotic and biotic environment. Therefore, studies examining local adaptation of plants that do not take mycorrhizal fungi into account may be missing an important factor in the ability of a plant population to adapt to the environment. Using meta-analysis on a dataset comprising 1,659 studies (from 183 papers), we explored whether the geographic origin of the plant, mycorrhizal inoculum, and/or soil influenced plant biomass response to mycorrhizal fungi. Regardless of whether plant, fungus, and/or soil originated in sympatry or allopatry, the mean effect size of mycorrhizal inoculum on host biomass was positive. The effect was larger when plant and soil origin were sympatric but allopatric to the fungus, or when plant and fungus origin were sympatric but allopatric to the soil. However, the statistical significance of these trends was marginal. Overall, these results strongly support mutualism in the mycorrhizal symbiosis, but provide little support that the relative geographic origin of plants, fungi and soil alters the nature of the interaction. This lack of support may be an artifact of our study, which is limited in two ways. First, our study defined 'local' relative to geographic distance, assuming it would be correlated with ecological distance. Second, while these analyses represent one of the most comprehensive meta-analyses to date, we were greatly limited by the number of papers that reported origin of the soil, fungi, or plant. As such, this meta-analysis provides a first brushstroke to address the impact of local adaptation on mycorrhizal relationships.

### PS 1-57 Nutrient limitation drives the response of *Calamagrostis epigejos* to AMF across a chronosequence of post-mining sites

RYDLOVÁ, J.<sup>1</sup>, M. Dostálová<sup>1,2</sup>, D. Püschel<sup>1</sup> and M. Janoušková<sup>1</sup>

<sup>1</sup>Institute of Botany, Czech Academy of Sciences, Zámek 1, 252 43 Průhonice, Czech Republic, jana.rydlova@ibot.cas.cz;

<sup>2</sup>Department of Experimental Plant Biology, Charles University, Viničná 5, 128 44 Prague 2, Czech Republic.

**Abstract:** Due to significant effects on the acquisition of mineral resources by plants, arbuscular mycorrhizal fungi (AMF) have been shown to substantially affect primary succession of vegetation. However, little is known on how the role of AMF changes during long-term development of newly created man-made ecosystems. Using a greenhouse pot experiment, we studied the growth response of *Calamagrostis epigejos*, a grass that commonly colonizes disturbed habitats, to either native or reference AMF isolates. The plants were grown in sterilized soils originating from four different post-mining sites with spontaneously established vegetation cover (either 12, 20, 30, or 50 years old). Although native AMF colonized the roots less intensively, including having lower arbuscule abundance, the effectiveness of both fungal groups almost did not differ. In soils from the two younger successional stages, AMF significantly increased P uptake and the



plants reached several fold larger biomass than their non-mycorrhizal counterparts. Although AMF decreased shoot N concentrations, total N uptake to the shoots was still enhanced by AMF. The positive effect of mycorrhiza on plants diminished in soils from the two older sites. Despite AMF increasing P uptake by plants, N uptake was not influenced and plant biomass was either not affected (50 year site) or even decreased (30 year site) by AMF. A positive correlation between plant shoot N:P and mycorrhizal growth response was found for the tested model plants. However, the soil at the post-mining sites changes from P to N limited during the chronosequence, as indicated by shoot N:P of the control plants ( $>16$  and  $<14$  in the two younger and two older sites, respectively). Given that AMF show higher N demands than their hosts, they did not confer host plants with any growth benefit once N becomes the limiting resource in older succession stages.

### **PS 3-47 Intercropped pigeon pea and finger millet profit from each other via arbuscular mycorrhizal fungi (AMF) and plant growth promoting rhizobacteria (PGPR) under drought conditions by “bioirrigation”**

**SAHARAN, K.<sup>1</sup>**, L. Schütz<sup>1</sup>, A. Wiemken<sup>1</sup>, T. Boller<sup>1</sup> and M. Natarajan<sup>1</sup>

<sup>1</sup>Department of Environmental Sciences - Botany, University of Basel, Hebelstrasse 1, 4056-Basel, Switzerland, krishna.saharan@unibas.ch.

**Abstract:** Legume-cereal intercropping is well known in traditional dryland agriculture, but little is known about the processes by which nutrient and water resources are shared between legumes and cereals. We tested the hypothesis that finger millet, a shallow rooted cereal, profits from neighboring pigeon pea, a deep rooted legume, by “bioirrigation”, where pigeon pea lifts water from deep soil layers to the top. We also tested whether this “bioirrigation” improves the positive effect of “biofertilization” with arbuscular mycorrhizal fungi (AMF) and plant growth promoting rhizobacteria (PGPR), which may mobilize and distribute mineral nutrients for their host plants. We conducted a greenhouse experiment using compartmented microcosms. Pigeon pea was grown in a deep compartment with access to ground water, even under drought conditions, through a layer of gravel which prevented water movement via capillary rise. Finger millet was grown in an adjacent shallow compartment, separated by 25  $\mu$ m nylon mesh, with no access to ground water. Inside the shallow compartment, we placed small 25  $\mu$ m nylon mesh bags filled with <sup>33</sup>P + <sup>15</sup>N labeled soil. Both pigeon pea and finger millet were inoculated with AMF (*Glomus irregulare*) and PGPR (a fluorescent pseudomonad), providing “biofertilization”. While the nylon mesh excluded roots, it did not restrict the passage of AMF and PGPR. The microcosms were well watered initially, but after two months, water was only provided as ground water to the deep soil layers accessible exclusively to pigeon pea. Under these conditions, growth and nutrient uptake were significantly improved in both biofertilized plants, compared to plants without biofertilizers. This indicates that the “bioirrigation” effect of pigeon pea is enhanced by “biofertilization”, probably because the hydraulically lifted water helps the common AMF-fungal network and the PGPRs to mobilize nutrients in the shallow compartment, making them available to both pigeon pea and finger millet in this model intercropping system.

### **PS 2-11 Transcriptome changes in arbuscular mycorrhizal roots after phosphate application**

**Sugimura, Y.<sup>1</sup>**, Y. Honma<sup>1</sup> and **K. SAITO<sup>1</sup>**

Faculty of Agriculture, Shinshu University, Minamiminowa, Nagano 399-4598 Japan, saitok@shinshu-u.ac.jp.

**Abstract:** Gene expression during arbuscular mycorrhizal (AM) development is highly orchestrated in both plants and AM fungi. Transcriptome analysis using microarrays and oligoarrays have been used for identifying plant genes induced in AM symbiosis. Differentially expressed genes (DEGs) detected by the transcriptome analysis include genes required for AM development, maintenance, degradation, and functioning. Moreover, gene expression changes have arisen in response to the secondary effects of AM fungal infection, such as improved plant nutrition. In our preliminary experiment of *Lotus japonicus*, application of a high concentration of phosphate (Pi) to *Rhizophagus irregularis*-inoculated roots provoked a rapid decline in AM colonization, especially in arbuscule formation. In this study, we performed RNA-seq analysis in which AM roots harvested at 0 h, 3 h, 6 h, 12 h, 24 h, and 7 days after application of 500  $\mu$ M Pi were used to detect candidates for genes regulating AM development. A total of 2,189 DEGs were detected in *L. japonicus* during the Pi application. Expression profiles of the DEGs were divided into five categories by the k-means method. A category in which gene expression was repressed monotonically by the Pi application contained many AM-induced genes, suggesting that the DEGs in the category may be involved in AM development. These genes include fatty acid and cutin synthesis-related

genes, transporter genes, and transcription factor genes. Transcripts of several cutin synthesis-related genes accumulated in arbuscule-containing cortical cells by qRT-PCR using laser microdissection. Cutin-like fatty acids produced by plants in arbusculated cells may be released to the extracellular spaces and play significant roles in AM development.

**PS 3-48 Effect of arbuscular mycorrhizal fungal inoculation on the growth of Welsh onions in soil rich in available phosphate, and characterization of indigenous arbuscular mycorrhizal fungi isolated from the soil**

Suzuki, T.<sup>1</sup>, R. Tajima<sup>1</sup>, S. Hara<sup>1</sup>, T. Shimizu<sup>1</sup>, T. Uno<sup>1</sup>, T. Ito<sup>1</sup> and **M. SAITO**<sup>1</sup>

Field Science Center, Graduate School of Agricultural Science, Tohoku University, Osaki, Miyagi, 989-6711 Japan, msaito@bios.tohoku.ac.jp.

**Abstract:** The objective of the present study was to explore the arbuscular mycorrhizal (AM) fungi adapted to soil rich in available phosphate. (1) An inoculation experiment with the commercial inoculum containing AM fungus R-10 on Welsh onion was conducted over 2 years under field conditions. Welsh onion was pre-inoculated during a nursery period and transplanted to a field rich in available phosphate. Growth, yield, and AM colonization of the inoculated Welsh onion were compared with those of non-inoculated Welsh onion. To examine the indigenous AM fungi, DNA was extracted from the roots of non-inoculated Welsh onion, and rRNA genes of AM fungi were amplified and analyzed. (2) AM fungi were isolated from an area adjacent to the experimental field and identified based upon spore morphology and partial rRNA gene sequences. (3) Effects of the isolated AM fungus on Welsh onion were examined in comparison with those of R-10 by an in-pot experiment in a growth cabinet. The results were as follows: (1) the growth and yield of the plants inoculated with R-10 were not significantly different from those of non-inoculated ones. Although the phosphate availability in the soil was very high, indigenous AM fungi colonized the roots in the non-inoculated plants. Sequences of *Gigaspora margarita* and *Claroideoglomus etunicatum* were detected. (2) An isolated AM fungus was identified as *C. etunicatum*. (3) The isolated *C. etunicatum* increased the growth of Welsh onion to a greater extent than did R-10 and also showed a high colonization rate under high phosphate conditions. Thus, the ability of the indigenous AM isolate to colonize Welsh onion plants under high-phosphate conditions of soil was confirmed, suggesting the presence of AM fungi adapted to soil rich in phosphate. The isolated *C. etunicatum* was effective even in soils rich in available phosphate.

**PS 4-80 Screening of indigenous mycorrhizal fungi for increasing the growth, yield, and nutrient status of *Capsicum annuum* and *Solanum melongena* in red lateritic soil**

**SAMANTA, S.**<sup>1</sup>, J. Adhikary<sup>2</sup> and N. Verma<sup>3</sup>

<sup>1</sup>Department of Botany, Sabang SK Mahavidyalaya, Lutunia, Paschim Medinipur, West Bengal, India, 721166, sudhansusamanta@yahoo.com; <sup>2</sup>Manikpara Forest Range office, Manikpara, Paschim Medinipur, Directorate of Forest, West Bengal India, 721507; <sup>3</sup>Department of Botany and Forestry, Vidyasagar University, West Bengal, India, 721102.

**Abstract:** The vesicular arbuscular mycorrhizal (VAM) symbiosis is now widely accepted as an essential component of any plant community, and this symbiosis has a unique role in the uptake of nutrients and water, particularly in nutrient poor, dry soils. Plants inoculated with indigenous VAM fungi can mobilize P from rock phosphate more efficiently and create a favourable environment for the development of ecosystem processes. Seven experiments were conducted to investigate the seasonal variation of indigenous VAM status in the rhizosphere of *Capsicum annuum* and *Solanum melongena*. The effects of selected VAM fungal species alone and in combination, along with soil amendments, were studied to observe their impacts on the performance on the two solanaceous crop species. The VAM species selected for inoculation were *Acaulospora dilatata*, *Glomus mosseae*, and *G. fasciculatum*. The study indicated that the three indigenous VAM species had enough potential to improve the productivity of *C. annuum* and *S. melongena* in red lateritic soil, which has an inherently poor nutrient status. The efficiency of VAM species was reflected not only in the pot study but also in the field. Over all, *A. dilatata* improved plant biomass, NPK content, ascorbic acid content, protein content, acid phosphatase activities, and VAM infection. Mixed inoculum was more effective in increasing the yield and fruit nutrient quality compared to a single VAM species. Among single species inoculations, *G. mosseae* performed better than *A. dilatata* in terms of the yields of both crops. All VAM treatments amplified growth, nutrition, and yield of the two vegetable crops. Plant growth improved with all VAM inoculations with NPK fertilizer and rock phosphate amendments. Application of VAM with rock phosphates appeared to be a viable alternative bio-fertilizer combination in nutrient poor red lateritic soil when yield, nutrition, quality, and economic feasibility are taken in to consideration.

## PS 2-32 Studies on the preparation of native AM biofertilizer for coastal bio-shield plantations in India

SAMBANDAN, K.<sup>1</sup> and P. Raja<sup>2</sup>

<sup>1</sup>P.G. Department of Plant Science, Avvaiyar Government College for Women, Karaikal 609602, U.T. of Puducherry, India, sambandhan@gmail.com; <sup>2</sup>Biotrack Technology (M) Sdn., Bhd., No.18-1 Jalan Indah 2/8, Taman Univerisiti Indah, 43300 Seri Kembangan, Selangor, Malaysia.

**Abstract:** Coastal soils are generally low in nutrients, sandy, and salt-affected due to frequent inundation with seawater. Coastal topographic slope and poor vegetation are some of the factors that determine vulnerability to coastal hazards. Naturally occurring plants in coastal areas act as bio-shields, shielding regions from the ferocity of storms, tsunamis, and other natural calamities. A natural bio-shield is an eco-friendly approach and can be made by growing mangroves, as well as non mangrove trees like *Azadirachta indica*, *Casuarina equisetifolia*, *Calophyllum inophyllum*, *Pongamia pinnata*, *Thespesia populnea*, etc. along the coastline. Bio-shield plantations are normally grown in linear patches between a coastal village and the sea, and it acts as a barrier to dissipate the energy of sea waves and thus diminish their damage. It is known that most of the plants used for bio-shield plantations have symbiotic associations with arbuscular mycorrhizal (AM) fungi in normal conditions and have improved their drought and salt tolerance. In the present study, bio-shield trees in three study sites were analyzed for arbuscular mycorrhizal status in coastal soils. Among the eight coastal tree species, six were found to be mycorrhizal in the present study. A total of five species of AM fungi belong to *Glomus*. *Scutellospora* and *Gigaspora* were isolated from coastal soils of Karaikal District. Mass propagation was carried out using native dominant AM fungi with pot culture techniques. A sand-vermiculite-coal powder mixture was used as the substrate for the biofertilizer in the present study. Pot and field studies using *Casuarina equisetifolia* and native AM fertilizer influenced growth and biomass consistently. The potential adaptation of this indigenous biofertilizer shows the ability to colonize bio-shield trees in the coastal conditions and improve their nutrient status. Native mycorrhizal fertilizer will be highly useful for the growth and development of coastal bio-shield plantations.

## PS 4-81 Ectomycorrhizal garden as fruiting body provider

SAMBODO C.<sup>1</sup>, F.E. Astanti<sup>1</sup> and Sukarsono<sup>1</sup>

<sup>1</sup>Research and Development Center, Perhutani, corrysambodo@yahoo.com.

**Abstract.** As we know, pine seedlings require the ectomycorrhizal symbiosis for root development and growth. Perhutani is a forestry organization that plants pine and has built ectomycorrhizal gardens since 2000 in several locations near pine plantations on Java Island. These gardens are pine plantations (*Pinus merkusii*), which have been inoculated with ectomycorrhizal fungi (*Scleroderma* sp. and *Pysolithus* sp.). Every year the fungi are harvested, and the fruiting bodies are used to produce ectomycorrhizal tablets. These tablets are effective with pine seedlings, and the seedlings growing better with the tablets than without them. A detailed paper will be delivered about management of the garden, production of ectomycorrhizal fruiting bodies, and the effectiveness of ectomycorrhizal tablets with pine seedlings.

## LT 1-8 Community of arbuscular mycorrhizal fungi and landscape fragmentation in a Mexican tropical rain forest

SÁNCHEZ-GALLEN, I.<sup>1</sup>, A. Antoninka<sup>2</sup>, L.V. Hernández-Cuevas<sup>3</sup> and J. Álvarez-Sánchez<sup>1</sup>

<sup>1</sup>Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad Universitaria, México, D.F. 04510 México, irene\_sgallen@ciencias.unam.mx; <sup>2</sup>School of Forestry, Northern Arizona University, Flagstaff, Arizona 86011 USA; <sup>3</sup>Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, San Felipe Ixtacuixtla, Tlaxcala 90120 México.

**Abstract:** Effects of habitat fragmentation on several groups of organisms has been assessed over the past three decades, results clearly demonstrate that severely fragmented landscapes have populations of native species with low densities, communities with low species richness and diversity, and not healthy ecosystems. However, most of these studies focus on aboveground organisms, little is known about soil organisms' responses to these environmental changes. Our main goal was to analyze tropical rain forest fragmentation in terms of the structure and composition of arbuscular mycorrhizal fungi (AMF) community and its relation with seedling species richness, fragment size, and edaphic variables. We

carried out our study at the Los Tuxtlas Biosphere Reserve, located in the Veracruz state, Mexico. In seven fragments of different sizes (from 3 to 640 ha), we studied a total of 82 plots (25 m<sup>2</sup>) where we collected soil and identified all tree seedlings. From each sample, we separated AMF spores and identified them by their morphological traits. We analyzed soil samples for pH, organic matter, total nitrogen, labile phosphorous, and texture. We applied NMDS ordination to identify the main factors explaining AMF composition, and structural equation models to elaborate a general model to explain our AMF community structure. We found, contrary to what we expected, that fragment size negatively explained seedling species richness, AMF composition, and spore abundance, and edaphic variables explained very little of AMF structure. On the other hand, AMF spore abundance was positively related to AMF species composition. Our results indicate that AMF presence and composition depend upon multiple factors others than the fragment size. We propose that the AMF community has not been strongly affected by the fragmentation of Los Tuxtlas ecosystem and it has still the potential to contribute to this tropical rain forest natural regeneration.

#### PS 3-49 Variation in the population of arbuscular mycorrhizal fungi in an agricultural soil irrigated with tequila vinasse

**SANCHEZ-LIZARRAGA, A.L.<sup>1</sup>**, E.N. Marino-Marmolejo<sup>2</sup>, D. Davila-Vazquez<sup>1</sup>, L. Hernández-Cuevas<sup>3</sup> and S.M. Contreras-Ramos<sup>1</sup>

<sup>1</sup>Unidad de Tecnología Ambiental, Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco A.C. (CIATEJ), Guadalajara, Jalisco, México, CP 44270, analorenasl22@gmail.com; <sup>2</sup>Unidad de Biotecnología Médica y Farmacéutica, CIATEJ; <sup>3</sup>Centro de Investigaciones en Ciencias Biológicas, Laboratorio de Micorrizas, Universidad Autónoma de Tlaxcala, km 10.5 Autopista Tlaxcala-Tezmelucan, San Felipe Ixtacuixtla, Tlaxcala, México, CP 90120.

**Abstract:** Tequila vinasse irrigation of soils is a common practice. These vinasses are characterized by high organic matter content, acidic pH, high concentration of suspended solids, and the presence of K<sup>+</sup>, Ca<sup>2++</sup>, and Mg<sup>2++</sup> ions. Because of these qualities, it is thought that the application of vinasses could be beneficial to soil. There are very few papers in the literature about the effect of vinasses in soils, and there is no information about its effect on populations of beneficial organisms such as arbuscular mycorrhizal fungi (AMF). The aim of this research was to determine if the presence and variation of AMF in an agricultural soil was affected by the addition of different concentrations of tequila vinasse. In the first stage of this research, vinasse soil (VS) was compared to a soil that was not irrigated with tequila vinasse (CS). Sixteen AMF species were identified with a predominance of *Acaulospora mellea*, *A. scrobiculata*, *Funneliformis geosporum*, *F. mosseae*, and *Paraglomus occultum*. Some species were found in VS but not in CS, such as *Clareidoglomus etunicatum*, *Septoglomus constrictum*, and *Racocetra gregaria*. In contrast, *A. morrowiae* and *Scutellospora reticulata* were found in CS but not in VS. No significant differences were found in abundance, richness, or biodiversity in either soil treatment. In the second research stage, the propagation of CS AMF was carried out with a spore mean of 236 ± 79. Additionally, an experiment was initiated where CS soil was irrigated with different concentrations (0, 25, 50, 75, and 100%) of tequila vinasse for four months. Data so far include the number of spores of the initial day (mean of spores in all concentrations: 319 ± 3) and the first month (289 ± 5) of the experiment. This is the first report of AMF findings in soils irrigated with tequila vinasses.

#### CS 1-5 Scaling macro- and micro-evolutionary dynamics of ectomycorrhizal fungi in space and time: the Caesar's mushrooms case

**SANCHEZ-RAMIREZ, S.<sup>1</sup>** and J.M. Moncalvo<sup>1,2</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Ontario M5S 3B8, Canada, santiago.snchez@gmail.com; <sup>2</sup>Department of Natural History, Royal Ontario Museum, Toronto, Ontario M5S 2C6, Canada.

**Abstract:** Biological diversity is the product of evolutionary and ecological factors that operate at different spatial, temporal, organismal, and genomic scales. Phylogenies and genomes have the potential to uncover the mechanisms leading to such diversity, with clues imprinted throughout the evolution of DNA sequences. Mycologists face several challenges in their quest to study fungal evolution, some of which include inaccurate species delimitations, unknown distributions, sampling biases, and a poor fossil record. However, most fungi have small genomes and short generation times, which make them more amenable for studying evolutionary genomics. This work consists of four empirical studies in the Caesar's mushrooms (*Amanita* sect. *Caesareae*) that exemplify the use of phylogenies and genomes to approach specific



evolutionary questions. The first two sections show how diversification and historical biogeographical models explain the distribution, geographic disjunctions, and diversity of temperate and tropical taxa worldwide. Results indicate that land-mediated dispersal and high diversification rates in the New World and in the temperate region have played important roles. This explains, in part, “shifted” latitudinal diversity gradients within the group. The last two sections focus on species-population level processes and the interrelationships between past climate change, regional geography, species richness, genetic diversity, and historical demography. Genealogy and coalescent-based multi-locus species delimitations reveal high levels of cryptic diversity. Higher speciation rates in climatically stable areas and recent population expansions highlight the importance Pleistocene glacial dynamics in shaping diversity patterns within the North American *Caesar’s mushroom* complex. Finally, both natural selection on coding DNA and demography explain genome-wide diversity across 500 single-copy genes and eight species from a recently diverged species complex.

#### PS 4-26 **Mycorrhiza Network at TERI New Delhi since 1988 to date: a journey of progress and achievements**

Adholeya, A.<sup>1</sup>, R. Singh<sup>1</sup>, C. Manoharacharya<sup>1</sup> and **T.P. SANKAR**<sup>1</sup>

<sup>1</sup>The Energy and Resources Institute, India Habitat Centre, Lodhi Road, New Delhi 110 003, tpsankar@teri.res.in.

**Abstract:** Mycorrhiza, the symbiotic association, plays an important role in nutrient uptake, soil stabilization, plant growth, and productivity. In this context, a Mycorrhiza Network was set up with the objective to strengthen research, encourage cooperation, promote exchange of information and germplasm, and facilitate transfer of technology to the field. The Network functions as a specialized centre for the collection, compilation and dissemination of databases and publications on mycorrhiza. The Network’s **Literature Abstracts Database** has 4,000 refereed and classified references; it serves the main purpose of assisting research scientists who are looking for different aspects of mycorrhizal research, besides being useful for formulating research projects. The **Database of Mycorrhiza Culture Collection:** Wide diversity exists within the AM fungi, which have over 210 species within the order Glomerales; this diversity shows up in morphology, physiology, and functionality. The database helps researchers obtain information on specific cultures of interest. It has a collection of over 600 different isolates of which 257 are ectomycorrhizal and 350 are arbuscular mycorrhizal. The Network’s **Directory of Mycorrhizologists** has created a network of scientists associated directly with research on mycorrhizas and also identifies centers and institutions where mycorrhizal research is being carried out. The Network’s **Mycorrhiza Newsletter** provides a forum for dissemination, interaction and communication of scientific information on mycorrhizal research. It contains state-of-the-art papers covering the biology, ecology, and other related aspects of mycorrhizas including biodiversity and conservation. Other databases being developed by the Mycorrhiza Network include (i) Gene Bank database of mycorrhizal fungi including published data on gene sequence, EST and microarray analysis; and (ii) Genes identified from mycorrhizal fungi. Data pertaining to keys, monographs, probes and primers used for identification of mycorrhizal fungi are among other databases the Network has developed.

#### PS 2-55 ***Rhizophagus* sp. nov. (accession CMCC/AM-1106) isolated from soils polluted with fly ash and heavy metals on the Deccan Plateau of the Indian subcontinent**

**SASHIDHAR**, B.<sup>1</sup>, D.K. Joshi<sup>1</sup>, K. Sunar<sup>1</sup>, M. Ghroui<sup>1</sup> and A. Adholeya<sup>1</sup>

<sup>1</sup>Centre for Mycorrhiza Research, Bioethnology and Bioresources Division, The Energy and Resources Institute, New Delhi, India, b.sashidhar@teri.res.in.

**Abstract:** An undescribed species of arbuscular mycorrhizal (AM) fungus was isolated from fly ash dumped, heavy metal polluted soils of Durshed, Telangana, India (18°27'27"N 79°10'58"E). The novel AM fungal characteristics were based on spore morphology, FAME analysis, and molecular analyses of both monospore-grown material *in situ* pot cultures (*Sorghum bicolor* as host plant) and *in vitro* carrot ROC. In both culture types, spores occurred in aggregates developing basally at hyphal tips from parent hyphae, secondary branches of parent hyphae (multiparous), or intercalarily along dichotomously branched coenocytic to sparsely septate extraradical hyphae. Spores are globose to sub-globose, hyaline to pale yellow in color, with one subtending hyphae, and 100 to 220 µm in diameter. The subcellular structures of the spore exhibited two wall layers. Layer one of the outer wall of *in situ*-raised spores was composed of a hyaline mucilaginous layer that degenerated with age and stained red in Melzer’s reagent; this layer was absent in ROC raised spores. Layer two was smooth, laminated, and hyaline to pale yellow in color. The inner wall was smooth, thin, and flexible, which



wrinkles in spores crushed in PVLG. The subtending hyphae were straight or recurvate, rarely constricted at spore base, and hyaline. Phylogenetic analyses based on entire ITS and partial LSU region of nuclear encoded rDNA placed the species into the Glomeraceae (group A) without closely related homology with known described AM fungal species. Several characters that separate this *Rhizophagus* sp. nov. from closely related known species of group A include the presence of two laminate spore wall layers (*R. clarus*, which forms three layers), formation of globose or sub-globose spores (*R. irregularis*, which forms irregular spores), formation of hyaline to pale yellow colored spores (*R. proliferus*, which forms only hyaline spores), as well as the formation of spores in aggregates developing blastically (*R. intraradices*, which forms terminal spores).

#### PS 3-8 Release of acid phosphatase from extraradical hyphae of the arbuscular mycorrhizal fungus *Rhizophagus clarus* under low P condition

SATO, T.<sup>1</sup>, T. Ezawa<sup>2</sup>, W. Cheng<sup>1</sup> and K. Tawaraya<sup>1</sup>

<sup>1</sup>Faculty of Agriculture, Yamagata University, Tsuruoka 997-8555 Japan, abr18085@tds1.tr.yamagata-u.ac.jp; <sup>2</sup>Graduate School of Agriculture, Hokkaido University, Sapporo 060-8589 Japan.

**Abstract:** Arbuscular mycorrhizal (AM) fungi increase phosphate (P) uptake of plants. Organic P comprises 30%-80% of the total P in most agricultural soils. Some plants can utilize organic P by the secretion of acid phosphatase (ACP) from the roots, especially under low P conditions. However, little is known about the secretion of ACP from the extraradical hyphae of AM fungi. The objective of this study was to detect ACP activity from hyphal exudates of AMF under low P conditions. *Allium fistulosum* plants were inoculated or not with the AM fungus *Rhizophagus clarus* and grown in two-compartment pots. The soil solution was collected by using mullite ceramic tubes. Hyphal extracts were extracted from extraradical hyphae grown in sand culture and in *in vitro* monoxenic culture. Root exudates of *A. fistulosum* were collected from hydroponic culture. The soil solution, hyphal extracts, root extract, and root exudates were subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis. *Linum usitatissimum* was inoculated with *R. clarus* and grown on a solid minimal media with three P levels (3, 15, and 30  $\mu$ M). The extraradical hyphae and hyphal exudates were collected and subjected to analysis of ACP activity by using *p*-nitrophenylphosphate. P concentration, P content, and the dry weight of shoots were higher in the inoculated treatments than in the uninoculated treatments. Activity staining of the gel revealed that ACP activity at 187 kDa was observed in the soil solution of the inoculation treatment and in the hyphal extract collected from sand culture and *in vitro* monoxenic culture, but not in the root exudates of non-mycorrhizal plants grown in the hydroponic culture nor in the root extracts, irrespective of mycorrhizal status. ACP activity of extraradical hyphae and hyphal exudates were higher in the 3  $\mu$ M treatment than in the 30  $\mu$ M treatment. These findings suggest that the fungus releases ACP from extraradical hyphae into the hyphosphere under low P conditions.

#### LT 4-14 Clades of mycorrhizal fungi differentiate isotope abundance patterns of partially mycoheterotrophic species in the orchid genus *Epipactis*

SCHIEBOLD, J.M.I.<sup>1</sup>, M.I. Bidartondo<sup>2</sup>, P. Karasch<sup>3</sup>, B. Gravendeel<sup>4</sup> and G. Gebauer<sup>1</sup>

<sup>1</sup>BayCEER – Laboratory of Isotope Biogeochemistry, University of Bayreuth, 95440 Bayreuth, Germany, Julienne. Schiebold@uni-bayreuth.de; <sup>2</sup>Imperial College London and Royal Botanic Gardens, Kew TW9 3DS, UK; <sup>3</sup>German Mycological Society, Kirch 78, 94545 Hohenau, Germany; <sup>4</sup>Naturalis Biodiversity Center, Leiden, The Netherlands.

**Abstract:** The orchid genus *Epipactis* contains 49 terrestrial species distributed throughout the northern hemisphere. Until now, information about fungal partners and trophic strategies such as autotrophy and partial or full mycoheterotrophy is available for only five *Epipactis* species. In this study, we took leaf samples of another eight *Epipactis* species growing in forest habitats, and the accompanying autotrophic plant species as references, to elucidate the orchids' nutritional type with stable isotope natural abundance analyses. Root samples were taken from the same individuals at 11 sites in NE Bavaria and on the North Sea coastline of the Netherlands for identification of fungal partners using ITS sequencing. Analyses of fungal partners separate *Epipactis* species into three clusters: species mostly associated with obligate ectomycorrhizal (ECM) ascomycetes (*Tuber*, *Wilcoxina*), ones that form mycorrhiza with obligate ECM basidiomycetes (*Entoloma*, *Hebeloma*, *Hygrophorus*, *Russula*, *Thanatephorus*, *Tomentella*), and rhizoctonia *E. gigantea* and *E. palustris*. Stable isotope abundances showed that all *Epipactis* species in this survey were significantly enriched in <sup>13</sup>C and <sup>15</sup>N towards the autotrophic references indicating partial mycoheterotrophy as the nutritional mode, whereas the type of fungal partner

drives the degree of isotopic enrichment to distinctive clusters. The cluster of *Epipactis* species associated with ECM basidiomycetes showed an intermediate enrichment in both  $^{13}\text{C}$  and  $^{15}\text{N}$  compared to the clusters of species forming orchid mycorrhiza with ECM ascomycetes and rhizoctonias. *Epipactis* species that were mycorrhizal with ECM ascomycetes exhibited an especially high enrichment in  $^{15}\text{N}$  with an average of 20‰. Stable  $^{15}\text{N}$  isotope profiles of the sporocarps of ECM ascomycetes (*Tuber*) and ECM basidiomycetes (*Inocybe*, *Russula*, *Thelephora*) corresponded to the  $^{15}\text{N}$  enrichment of the *Epipactis* clusters that were mycorrhizal with ECM ascomycetes and ECM basidiomycetes, respectively. Our results allow for the drawing of conclusions about food-web interactions. Ectomycorrhizal *Epipactis* species obviously obtain carbon simultaneously from photosynthesis and their mycorrhizal fungi while their complete nitrogen requirements might be gained from the fungal source.

#### SY 2-5 Plant-secreted LysM proteins may play a role in defense suppression for maintaining symbiosis in arbuscular mycorrhizas

SCHMITZ, A.M.<sup>1,2</sup> and Harrison, M.J.<sup>1</sup>

<sup>1</sup>Boyce Thompson Institute for Plant Research, Ithaca, NY, USA, ams629@cornell.edu; <sup>2</sup>Department of Pathology and Plant-Microbe Biology, Cornell University, Ithaca NY, USA.

**Abstract:** Arbuscular mycorrhizal (AM) fungi are obligate biotrophs that provide their host plant with mineral nutrients in return for carbon. Throughout the relationship, the fungus maintains an intimate intracellular lifestyle inside plant roots. Typically, plants respond to the presence of microbes through recognition of molecular patterns, leading to the induction of pattern-triggered immunity (PTI). Chitin is an elicitor of PTI and can be found in the cell walls of all fungi. How AM fungi are able to avoid this first level of plant defense is still unknown; however, lessons may be learned from plant-pathogen effectors that bind and sequester chitin through their lysin motif (LysM) domains to inhibit PTI. The LysM domain is implicated in binding peptidoglycans and related molecules and can also be found in at least five different plant protein families, one of which consists of a small, secreted protein with a single LysM domain. Due to their similarities to fungal effectors, these plant-secreted small LysM (SLM) proteins may play a role in masking fungal chitin from the plant's own receptors for the maintenance of the symbiosis. Through analysis of transcriptome data, we have identified three *Medicago truncatula* SLM genes that are expressed only during AM symbiosis. SLM promoter-GUS fusions reveal that these SLM genes are expressed specifically in cells containing arbuscules, the intracellular fungal structure where nutrient exchange takes place during the symbiosis. Furthermore, using fluorescent protein fusions, we have shown SLM proteins localize around arbuscules. Initial experiments suggest that ectopic expression of AM-specific SLM genes results in an increase in AM fungal colonization, which led us to investigate if SLM proteins can inhibit chitin-elicited ROS production. We are currently working to determine if SLM proteins bind chitin or other molecules. Our work attempts to uncover a mechanism for suppression of defense during AM symbiosis.

#### PS 4-46 Soil fungal diversity and community composition in the rhizosphere mycobiome of grassland ecosystems along land use gradients

SCHÖPS, R.<sup>1,2</sup>, T. Wubet<sup>1,3</sup>, H. Bruehlheide<sup>3,4</sup> and F. Buscot<sup>1,3</sup>

<sup>1</sup>UFZ-Helmholtz-Centre for Environmental Research, Department of Soil Ecology, Theodor-Lieser-Straße 4, 06120 Halle/Saale, Germany, ricardo.schoeps@ufz.de; <sup>2</sup>University of Leipzig, Department of Biology II, Johannisallee 21 04103 Leipzig, Germany; <sup>3</sup>German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig Deutscher Platz 5e, 04103 Leipzig, Germany; <sup>4</sup>Martin Luther University Halle Wittenberg, Department of Biology and Geobotany, Halle/Saale, Germany.

**Abstract:** As decomposers, mutualists, and pathogens, soil fungi play a crucial role in the functioning of terrestrial ecosystems. Particularly, arbuscular mycorrhizal fungi may have an important effect on plant diversity in grassland ecosystems. The microbial abundance and activity e.g., of mycorrhizal fungi, in turn, is highly influenced by plants via the release of root exudates. This plant-microbe relationship is greatest in the rhizosphere. However, it is not well known to which extent plant traits, plant identity and other co-varying factors such as land-use influence the fungal community in the rhizosphere in species-rich grasslands. Therefore, we will investigate the fungal community composition in the rhizosphere of grassland phytometer plants to disentangle the effects of plant species, plant traits and land-use intensity on the rhizosphere mycobiome. To test the plant-microbe interaction in the rhizosphere we set up 54 permanent study plots across

three different German regions within the framework of the Biodiversity Exploratories (a large research platform for biodiversity and ecosystem research). In each region 18 plots with different land-use intensities (hardly managed grasslands to highly fertilized and intensively used meadows and pastures) have been chosen. Within each study plot, 20 different phytometer species were planted randomized in 5 blocks. From these 20 species, three herbs and three grasses were selected for our analysis. We will harvest the phytometer plants (one block per year) at three time points (2014, 2015, and 2016). The plants will be dug out and divided in to three compartments (bulk soil, rhizosphere soil and roots). These compartments will be used for fungal ITS-DNA paired-end amplicon sequencing using Illumina MiSeq. The statistical analysis will be made with respect to the compartments, plant identities and land-use intensity. The study will be carried out in close collaboration with other projects dealing with the plant traits, exudation patterns and bacterial diversity.

#### PS 2-12 Self-assembling proteins from arbuscular mycorrhizal fungi: are they unique to *Rhizophagus irregularis*?

SCHULTZ, C.J.<sup>1</sup>, Y. Wu<sup>1</sup>, R.G. Creasey<sup>2</sup> and U. Baumann<sup>3</sup>

<sup>1</sup>School of Agriculture, Food and Wine, The University of Adelaide, Waite Research Institute, PMB 1, Glen Osmond, SA, 5064, Australia, carolyn.schultz@adelaide.edu.au; <sup>2</sup>School of Pharmacy, University of Nottingham, Nottingham, NG7 2RD, UK; <sup>3</sup>Australian Centre for Plant Functional Genomics, The University of Adelaide, PMB 1, Glen Osmond, SA, 5064, Australia.

**Abstract:** The ability of arbuscular mycorrhizal (AM) fungi to colonise the root apoplast and, in coordination with the plant, develop specialised plant–fungal interfaces is key to successful symbioses. *Rhizophagus irregularis* (previously *Glomus intraradices*) is considered an aggressive species because it rapidly colonises roots. We are investigating the role of three AM fungal genes, *AGL1-3*, encoding arabinogalactan protein-like (AGL) proteins to determine if they contribute to the aggressiveness of *R. irregularis*. To address this question we are: 1) characterising AGL proteins, 2) comparing gene expression changes in roots displaying *Arum*- and *Paris*-type morphologies, and 3) identifying orthologous AGL genes in other AM fungi. We used circular dichroism spectroscopy to show that recombinant proteins and synthetic peptides for AGL1 and AGL3 form polyproline II helices (triangular prisms), giving them three distinct surfaces for self assembly. Atomic force microscopy and scanning electron microscopy revealed that recombinant proteins and peptides of AGL1 and AGL3 can self-assemble into fibers and microtubes with different properties. To determine if AGL genes are differentially regulated in roots showing *Arum*- and *Paris*-type morphologies, we compared colonised roots from two plant species that display *Arum*-type when colonised by *R. irregularis* (*Medicago truncatula* and *Allium porrum*) and from *Asphodelus fistulosus* that exhibits *Paris*-type. Quantitative PCR revealed a 3-fold increase in one of the AGL genes in the roots of *A. fistulosus* with *Paris*-type mycorrhizal structures compared to *M. truncatula* and *A. porrum* roots with *Arum*-type structures. Lastly, we identified putative orthologues of *AGL1-3* from *R. clarus*. We will discuss the potential effects of different amino acid repeats in orthologous AGL proteins and their impact on self-assembly. Results are evaluated in the context of several alternate hypotheses for AGL function and provide new information on the uniqueness of *R. irregularis*.

#### SY 1-4 Functional and taxonomic diversity of orchid mycorrhizal fungi

SELOSSE, M.A.<sup>1</sup>

<sup>1</sup>Institut de Systématique, Evolution, Biodiversité (UMR 7205), Muséum national d'Histoire naturelle, Paris, ma.selosse@wanadoo.fr.

**Abstract:** Orchid evolved a specific mycorrhizal association with three apomorphic features: first, hyphae form intracellular pelotons that undergo a final lysis within living host cells; second, their fungal associates are not (or rarely) mycorrhizal in other plants; last, small and reserveless orchid seeds receive all nutrients (including carbon) from the future mycorrhizal fungus, resulting in a heterotrophic germination. This talk highlights some of the current trends and recent novel understandings on this mycorrhizal association. The main orchid mycorrhizal fungi (ORM) are often called 'rhizoctonias', a taxonomically incorrect name that encompasses a polyphyletic assemblage of Sebaciales and Cantharellales (Ceratobasidiaceae and Tulasnellaceae). These fungi turn out to be widespread throughout orchid phylogeny and ecosystems worldwide. Interestingly, they accompanied orchids in their repetitive radiation in the epiphytic niche in tropical forests. Beyond 'rhizoctonias', other ORM taxa were serendipitously found, e.g. Atractiellomycetes, (Pucciniomycotina), suggesting that some ORM diversity awaits discovery. Some terrestrial orchids associate to non-'rhizoctonia' ectomycorrhizal taxa (including truffles) or saprotrophic taxa (mainly in tropical forests, e.g., Psathyrellaceae or Polyporaceae): this

is linked to a particular physiology, where adult orchid obtain part (mixotrophy in green species) or all (mycoheterotrophy in achlorophyllous species) of their carbon from the mycorrhizal fungus. Whereas isotopic methods have helped to decipher the later associations and understand the dynamic of carbon in the plant, exchanges between orchids and classical 'rhizoctonias' remains unclear. First, whether carbon is moving to heterotrophic seedlings before or at peloton lysis is unknown. Second, the persistence of a C flow in adult 'rhizoctonia'-associated orchids is debated, based on conflicting evidences: does the plant reward the fungus after leaves expansion, or still recover fungal C? The raising evidence that beyond well-known saprotrophic abilities 'rhizoctonias' are endophytic in non-orchid plants suggests that orchid mycorrhizas evolved from root endophytism, and are not strictly required for 'rhizoctonias'.

**PS 4-47 Diversity and genetic structure of *Scleroderma bermudense* population associated with *Coccoloba uvifera* (L.) L. in these origin and introduction regions**

**SENE, S.**<sup>1,2</sup>, A. Geoffroy<sup>3</sup>, J. Lambourdière<sup>2</sup>, M. Sauve<sup>3</sup>, A.G. Diédhiou<sup>1</sup>, S.N. Sylla<sup>1</sup>, M.A. Selosse<sup>2</sup> and A. Bâ<sup>4,5</sup>

<sup>1</sup>Laboratoire Commun de Microbiologie, IRD/UCAD/ISRA, BP 1386 Dakar, Sénégal, senseynabou@gmail.com; <sup>2</sup>UMR 7205 CNRS OSEB Muséum national d'Histoire naturelle, Département Systématique et Evolution, CP 5045 rue Buffon 75005 Paris, France; <sup>3</sup>UMR 5175 CNRS/CEFE, Centre d'Ecologie Fonctionnelle et Evolutive, 1919 Route de Mende 34293 Montpellier Cedex 5; <sup>4</sup>Laboratoire de Biologie et Physiologie Végétales, Faculté des Sciences Exactes et Naturelles, Université des Antilles, BP 592, 97159, Pointe-à-Pitre, Guadeloupe, France; <sup>5</sup>Laboratoire des Symbioses Tropicales et Méditerranéennes, UMR113 INRA/AGRO-M/CIRAD/IRD/UM2-TA10/J, Campus International de Baillarguet, 34398 Montpellier cedex 5, France.

**Abstract:** *Coccoloba uvifera* tree is a *Polygonaceae*, native to tropical America, where it forms ectomycorrhizae (ECM) with a diversity of fungal species including *Scleroderma bermudense*. *Coccoloba uvifera* was introduced into several regions including Senegal where it is only associated with *S. bermudense*. To verify if this plant is associated with the same species in other introduction regions, we sequenced ITS of sporocarps and ECM from regions of origin (Guadeloupe, Martinique, and Puerto Rico), and of introduction (French Guiana, Senegal, Reunion, Japan, and Malaysia). Subsequently, sporocarps and ECMs identified to *S. bermudense* were genotyped with 6 microsatellite markers to verify if genets of *S. bermudense* recruited in introduction regions are co-introduced. The species *S. bermudense* identified with *C. uvifera* in original regions is identical to that sampled in Guiana, Senegal, and Reunion. However, in Japan and Malaysia, another *Scleroderma* (*Scleroderma* sp.) is associated with *C. uvifera*. This tree would therefore have preference for *Scleroderma* spp. in all introduction regions. Isolation by distance was observed between *S. bermudense* populations of origin and introduction regions, suggesting gene flow limited by the oceans. However, high gene flow was noted within regions suggesting large spore dispersal in *S. bermudense*. Low genetic diversity was noted within *S. bermudense* populations of introduction regions compared to those of origin, with private alleles in Puerto Rico, suggesting a founder effect in regions of introduction. Marked genetic differentiation ( $F_{st}=0.27$ ) was observed between the genetic population of *S. bermudense* in Senegal and those in Reunion, supporting independent introductions in these two regions. Genets of *S. bermudense* identified in introduction regions would probably have been co-introduced with *C. uvifera*. We have evidence that dried fruits can aggregate soil particles, including *Scleroderma* spore bank, and may have been involved in this process.

**LT 4-7 Using symbiotic seed germination to restore over-collected medicinal orchids: the practice of "restoration-friendly cultivation" in Southwest China**

**SHAO, S.C.**<sup>1,2</sup>, H. Huang<sup>2,3</sup>, J. Gao<sup>1,2</sup>, L. Qiang<sup>1,2,3</sup> and Y. Hu<sup>4</sup>

<sup>1</sup>Key Laboratory of Tropical Plant Resources and Sustainable Use, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan 666303, China, gjy@xtbg.org.cn; <sup>2</sup>Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, The Chinese Academy of Sciences, Mengla, Yunnan 666303, China; <sup>3</sup>Graduate University of Chinese Academy of Sciences, Beijing 100049, China; <sup>4</sup>Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla 666303, Yunnan, PR China.

**Abstract:** More than 1/3 of Chinese native orchids are used as traditional Chinese medicine including many species of *Dendrobium* (known as Shihu, in Chinese). Xishuangbanna is one of the hotspots of orchid species richness in China with 48 *Dendrobium* species. Most of these species were widely distributed in the area but have been massively collected



during 1990s. In recent years, Shihu industry developed rapidly in South China via massive commercial cultivation, but this mode does not seem to offer an alleviation of wild harvest pressure, likely because there are few local people involved in and benefitted from the industry. In addition, Chinese people believe that wild plants are of much better quality than cultivated products. The restoration-friendly cultivation model (i.e., planting targeted species in natural settings) is considered a new conservation tool for Chinese epiphytic medicinal orchids, especially for *Dendrobium* species. We set out to test this model. Using seed baiting techniques, we successfully isolated symbiotic fungi from protocorms of *D. devonianum* with high medicinal merits. The fungi have been experimentally tested to be effective for seed germination and seedling development of the species. We sowed seeds of this *Dendrobium* species with its specific fungi directly on tree trunks in natural forests and traditional tea gardens. Generally, seeds started to germinate in about 6 weeks, and seedlings developed very well. Our experiments show that the restoration-friendly cultivation could be an effective way to alleviate rural poverty and protect wild medicinal orchids in tropical area of China. Equally significant, the symbiotic seed germination methods that we developed during this research can be used for reintroduction of endangered orchids in more strictly protected natural areas.

### PS 1-31 Diversity of arbuscular mycorrhizal fungi in undisturbed forest, slash-and-burn field, and monoculture forest of Indo-Burma megadiverse region

SHARMAH, D.<sup>1</sup> and D.K. Jha<sup>2</sup>

<sup>1</sup>Department of Plant Science, Jawaharlal Nehru Rajkeeya Mahavidyalaya, Port Blair 744104, Andaman and Nicobar Islands, India, dsharmah@yahoo.com; <sup>2</sup>Microbial Ecology Laboratory, Department of Botany, Gauhati University, Guwahati 781014, Assam, India.

**Abstract:** Conversion of pristine forests to agricultural lands is one of the leading causes of biodiversity loss worldwide. To assess the impact of such forest disturbance on microbial diversity, we investigated the diversity of arbuscular mycorrhizal fungi (AMF) in the rich forests of Karbi Anglong hills of Assam, a biodiversity hotspot part of Indo-Burma region. AMF spore diversity was assessed in distinct sites with different intensities of disturbances that encompassed a pristine undisturbed forest (UF), slash-and-burn field (SBF), and monoculture forest (MF), located adjacently in a hilly slope. Soil was sampled between June 2009 and January 2011 in rainy (June 2009/2010 and September 2009/2010) and dry (November 2009/2010 and January 2010/2011) seasons. Altogether, 35 AMF species belonging to 9 genera were identified. Species forming glomoid spores comprised *Glomus* sensu lato, *Rhizophagus* and *Claroideoglomus* were the predominant genera followed by acaulosporoid spores. The AMF community structure in MF was significantly different from UF and SBF by ordination (correspondence analysis) and statistical (MANOVA) method. UF and SBF harboured higher spore population and identical Shannon-Wiener and Simpsons diversity indices. These parameters were lower in MF, possibly due to the dominating presence of single tree species, *Tectona grandis*. Also, hierarchical cluster analysis showed identical arbuscular mycorrhizal status in UF and SBF. Seasonality had a strong influence on AMF community composition with greater species richness and spore abundance in the dry season. We observed similar and higher AMF species richness and diversity in UF and SBF, suggesting diversity was not adversely affected for at least one key functional group of soil microbiota by the slash-and-burn agricultural land use practiced by the ethnic hilly tribes. Also because of the high generic and species diversity found, the semi-evergreen forests of this region can be considered a storehouse of Glomeromycota and a priority place for conservation.

### PS 3-74 The responses of mycoheterotrophic plants and their arbuscular mycorrhizal fungal symbionts to long-term fertilisation in a tropical forest

SHELDRAKE, M.<sup>1,2</sup>

<sup>1</sup>Department of Plant Sciences, University of Cambridge, Downing Street, CB2 3EA; <sup>2</sup>Smithsonian Tropical Research Institute, Roosevelt Ave., Building 401 Balboa, Ancon, Panamá, Rep. of Panamá, merlinsheldrake@gmail.com.

**Abstract:** In a symbiosis based on the mutual exchange of resources, fertilisation alters the degree to which plants and mycorrhizal fungal partners depend on each other. Using a long-term fertilisation experiment in a lowland tropical forest, I investigated the effect of fertilisation on the relationship between arbuscular mycorrhizal fungi (AMF) and two species of mycoheterotrophic plants, a symbiosis based on the one-way transfer of resources, from fungus to plant. Given that mycoheterotrophs depend on AMF, and AMF depend on autotrophic plants, I hypothesised that changes in the distribu-



tion of mycoheterotrophs reflect underlying changes in the balance of exchange between autotrophic plants, mycoheterotrophic plants, and their AMF symbionts. I found that soil nutrients have strong effects on the abundance of mycoheterotrophs. In a long-term factorial NPK addition experiment, P addition completely eliminated both species of mycoheterotroph. In plots along a natural P gradient, mycoheterotroph abundance sharply declined with increasing P; numbers fell from 300-600 plants per 40 x 40 m plot (under 2 ppm P) to zero plants per plot (over 2 ppm P). P addition reduced the total abundance of AMF in the soil, as indicated by a neutral lipid biomarker, and reduced the relative abundance (in the overall soil pool) of the AMF taxa found in the roots of the mycoheterotrophs, as revealed by 454 sequencing. However, these reductions in AMF abundance were not large enough to explain the complete elimination of mycoheterotrophs from plots with added P. My results suggest that P addition changes the symbiotic behaviour of AMF and their photosynthetic plant partners, such that the AMF are less susceptible to parasitism by mycoheterotrophs. I discuss these findings in light of current opinions on the regulation and stability of plant-AMF mutualisms.

#### PS 4-82 Drought stress does not impact arbuscular mycorrhizal community structure

SHI, N.<sup>1</sup>, R. Cao<sup>1</sup> and G. Feng<sup>1</sup>

<sup>1</sup>College of Resources and Environmental Sciences, China Agricultural University, Beijing, 100193, People's Republic of China, b1202219@cau.edu.cn.

**Abstract:** Different species of arbuscular mycorrhizal fungi (AMF) can affect each other when they lived together in one root system. The aim of this study is to determine whether the interaction between AMF species affects maize grown with different water levels. Using a pot experiment with a completely randomized design, maize was grown with a single AMF species (*Rhizophagus intraradices*, *Funneliformis mosseae*, or *Gigaspora margarita*) or a mixture of AMF species under two water levels and using two harvest times. Real-time PCR was used to determine the composition of AMF communities in the roots using the number of large ribosomal subunit (LSU) genes. The effects on stomatal conductance and water use efficiency depended on the different mycorrhizal communities in the drought stress treatment. Additionally, intense competition occurred among AMF species in the drought stress treatment. High efficiency fungal communities benefited their plant symbionts, although there was fierce competition between the different AMF species. *Rhizophagus intraradices* promoted plant growth, but had fewer LSU genes present in the communities. Low efficiency *F. mosseae* and *F. margarita* benefited maize, and there were a larger number of LSU genes in a single inoculation, but they were decreased significantly when combined with *R. intraradices*.

#### CS 4-6 Toward production of salt-tolerant hybrid strains of the ectomycorrhizal fungus *Rhizopogon roseolus* (= *R. rubescens*)

SHOTA, N.<sup>1</sup>, G. Qi<sup>1</sup>, A. Tadanori<sup>2</sup> and S. Norihiro<sup>2</sup>

<sup>1</sup>The United Graduate School of Agricultural Sciences, Tottori University, 4-101 Koyama, Tottori 680-8553 Japan, D13A2002M@edu.tottori-u.ac.jp; <sup>2</sup>Faculty of Agriculture, Tottori University, 4-101 Koyama, Tottori 680-8553 Japan.

**Abstract:** *Rhizopogon roseolus* (Corda) Th. M. Fr. is an ectomycorrhizal symbiont of *Pinus thunbergii* (Parl.) in coastal areas, and this fungus is known to be a salt tolerant species. Our previous study revealed that spore germination and subsequent colony formation was inhibited in the presence of NaCl, indicating that the addition of NaCl could be used as a selective pressure during the phase of spore germination producing salt tolerant hybrid strains. On the basis of these results, our present study evaluated the salt tolerance of basidiospore isolates obtained under selective pressure conditions, and of hybrid strains generated by crossing basidiospore isolates. For this study, the criterion for salt tolerance was determined as mycelial growth on agar plates. Fungal inoculum was grown on a diluted MMN agar medium containing different concentrations of NaCl, and radical mycelial growth after incubation was measured. Variability in salt tolerance was observed among basidiospore isolates, and some isolates showed salt tolerance; in contrast, other isolates exhibited salt sensitivity. Variation in salt tolerance was also evident among the generated hybrid strains, and some strains exhibited higher salt tolerant than their parental wild strains collected from natural forests. These results showed the possibility of the production of salt tolerant hybrid strains by using a crossbreeding technique. However, this present study only evaluated mycelial growth on agar plates. Evaluation of the salt tolerance of these strains is now being undertaken in soil conditions to develop a practical method.

## LT 2-12 Overlapping network structure between arbuscular mycorrhizal fungi, flowering plants, and their pollinators

SIKES, B.A.<sup>1,2</sup>, O.N. Lynch<sup>1</sup>, B.L. Foster<sup>1,2</sup> and K.A. Roccaforte<sup>1</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, Kansas 66047 USA, ben.sikes@ku.edu;

<sup>2</sup>Kansas Biological Survey, Lawrence, Kansas, 66047 USA.

**Abstract:** Network analyses can describe the structure and specificity of interactions between mutualistic partners, such as mycorrhizal fungi and their host plants. Nearly all research in this field has focused on pollination and dispersal mutualisms with plants, although recent work has started to explicitly map plant-mycorrhizal networks. A pervasive feature of mutualistic networks appears to be their nestedness or asymmetric specialization, where generalists of one trophic group interact with most of the rare specialist species in the other trophic group. To date, all explored networks incorporate only two trophic groups (bipartite), yet nestedness implicitly predicts links occurring between different mutualists on the same hosts such as the mycorrhizal fungi and insect pollinators on which plants rely. In a remnant tallgrass prairie, we observed pollinators on flowering, insect-pollinated plant species, then sampled their roots, and assessed communities of arbuscular mycorrhizal (AM) fungi. Twenty-four insect pollinators were identified on five different plant species at a single date and preliminary analyses using all fungal primers (NL1-NL4) identified 39 distinct AM fungal OTUs on the same plants. Analyses using the R package bipartite show that both bipartite networks are nested and that the most abundant plant species interacts with the lion's share of specialist species in both networks. Ongoing work using AMF-specific primers, a broader time window, and analyses of the structure of the tri-trophic mutualistic network will be presented. Our current data indicate that plant abundance and community structure may predict indirect linkages between rare mycorrhizal fungi and rare pollinators, all of which specialize on generalist, and often most-abundant plant species.

## PS 1-32 Arbuscular mycorrhizal fungi community in *Eucalyptus urograndis* plantations

SILVA, M.C.S.<sup>1</sup>, I.R. Mendes<sup>1</sup>, T.A. Paula<sup>1</sup>, B.C. Moreira<sup>1</sup>, D.M.S. Bazzolli<sup>1</sup> and M.C.M. Kasuya<sup>1</sup>

<sup>1</sup>Departamento de Microbiologia, Universidade Federal de Viçosa, Av. P. H. Rolfs, s/n, Campus UFV, Viçosa, Minas Gerais, 36570-000, Brazil, telephone: (+55) 31 3899-2967, e-mail: mcassiabio@yahoo.com.br.

**Abstract:** *Eucalyptus* is a very economically important species in Brazil, occupying more than 4.5 million hectares. This plant receives many benefits through interactions with microorganisms, including arbuscular mycorrhizal fungi (AMF), which benefit the plant by increasing the absorption of nutrients and protecting it against pathogens and heavy metals. Given this important symbiotic relationship, the aim of this study was to evaluate and identify AMF groups in a *Eucalyptus urograndis* plantation, in the eastern region of Minas Gerais State, Brazil, where eucalypt occupies 30% of the cultivated area. This community associated with eucalypt, after N addition and by the seasons changing, were evaluated, using two DNA extraction techniques for further analyses by DGGE technique. The DGGE proved satisfactory in the evaluation of AMF community *Eucalyptus* plantations in eastern Minas Gerais. The diversity of AMF and the profile of the AMF community were influenced both by season and by nitrogen fertilization. The greatest AMF diversity was found in samples extracted directly from the soil than extracted from soil spores. Understanding the community structure of AMF in the soil is important for adequate management, particularly in acidic soils with low availability of P and other nutrients, like in Brazil, where the soils of the most of eucalypt plantations present low fertility.

**PS 4-48 Arbuscular mycorrhizal fungal diversity in high-altitude hypersaline Andean wetlands studied by 454 pyrosequencing metagenomic and morphological approaches**

Colombo, R.P.<sup>1</sup>, **V.A. SILVANI**<sup>1</sup>, M.V. Scorza<sup>1</sup>, L.F. Bidondo<sup>1</sup>, C.P. Rothen<sup>1</sup>, M.E. Benavidez<sup>1</sup>, A. Scotti<sup>2</sup>, M. Pégola<sup>1</sup>, S. Fracchia<sup>3</sup> and A.M. Godeas<sup>1</sup>

<sup>1</sup>Departamento de Biodiversidad y Biología Experimental, Facultad de Ciencias Exactas y Naturales Universidad de Buenos Aires, Ciudad Universitaria, 4to piso Pabellón 2, 1428, Buenos Aires, Argentina, vanesasilvani@gmail.com;

<sup>2</sup>International Center for Earth Sciences, Regional Mendoza, Comisión Nacional de Energía Atómica, Padre Contreras 1300, 5500, Mendoza, Argentina; <sup>3</sup>Centro Regional de Investigaciones Científicas y Transferencia Tecnológica La Rioja (CRILAR- CONICET), Entre Ríos y Mendoza s/n. 5301, Anillaco, La Rioja, Argentina.

**Abstract:** The Laguna Brava wetland is a stressful habitat in the Andean Mountains (Argentina) dominated by extreme abiotic factors: high altitude (4300 m above sea level) and UV radiance, hypersalinity, alkalinity, and high heavy metal content in soils. Organisms have evolved in order to survive under these extreme conditions. The sparse vegetation that inhabits this wetland is frequently colonized by arbuscular mycorrhizal (AM) fungi. However, it is unknown which AM species can survive in such a harsh environment and how it may affect the structure of AM community. To answer these questions, 454 amplicon pyrosequencing and morphological (based on spore traits) approaches were used for assessing fungal diversity. Physical and chemical soil analyses were also performed. A total of 22 molecular operational taxonomic units (MOTUs) and 29 morphospecies of AM fungi were identified. *Glomeraceae* and *Claroideoglomeraceae* were the dominant families. AM community composition differed significantly between sampled sites. AM fungi were not detected in two sites with high electrical conductivity, Na, Sr, U, Pb, and As content in soils. Some MOTUs were found in all the remaining three sites, while others were specific of each site. Plant and AM communities were more diverse and equitable in soils with high organic matter, N, and P. Spore density dramatically decreased with salinity. In the most saline soils, *Rhizophagus* af. *intraradices-irregularis* and *Claroideoglossum* species were the most abundant taxa. Both methodologies showed that cosmopolitan AM species that occur across a broad range of environments also occurred in this habitat. Our results strongly suggest that presence of AM fungi and their community structure are strongly associated with local environmental variations in Laguna Brava. This study represents the first metagenomic analysis of AM fungal community in high Andean wetland in Argentina, improving the knowledge about these fungi in extreme environments.

**PS 3-50 Mycorrhizae and coupling beneficial organisms, complete package for sustainable agriculture**

**SINGH, R.**<sup>1</sup>, S. Kumari<sup>1</sup>, P. Dey<sup>1</sup>, B. Sashidhar<sup>1</sup>, S.K. Sundari<sup>1</sup> and A. Adholeya<sup>1</sup>

<sup>1</sup>Centre for Mycorrhiza Research, Biotechnology and Bioresources Division, The Energy and Resources Institute (TERI), Darbari Seth Block, IHC Complex, Lodhi Road, New Delhi- 110 003, India, reenaa@teri.res.in.

**Abstract:** In nature, a variety of microbes, including AM fungi, interact in the plant rhizosphere and benefit the plant by enhancing the availability of nutrients and increasing resistance to disease-causing microorganisms. Therefore, it is necessary to develop specific host-strain combinations of both bacteria and AM fungi with a high effectiveness under a wide range of experimental conditions. The present study used selected isolates of plant growth promoting microbes with proven biofertilizer and biocontrol properties and developed a microbial consortium. The choice of candidate microbes (*Rhizophagus irregularis* (*Glomus intraradices*), *Pseudomonas*, *Brevibacillus*, and *Trichoderma* sp.) for developing the consortium was carefully done, taking into consideration the principle attributes of each of microbe with respect to their ability to promote plant growth by increasing the availability of plant nutrients (N, P), increasing tolerance to edaphic factors (e.g., variations in soil pH, temperature, salt concentration, organic/inorganic pollutants), or providing growth promoting substances and increased resistance to disease. The root organ system is well optimized for *R. irregularis* and has been used for interaction studies under *in vitro* systems. The results indicate that these species co-habited successfully, and their population density increased when grown together. Greenhouse experiments were carried out with different carrier combinations. The fly ash based consortium of *B. borstelensis*, *Pseudomonas*, and *R. irregularis* with a dose of 10<sup>9</sup> cfu/g and 200 ppg/pot showed a significant response in tomato plant fresh weight, dry weight, and macronutrients (nitrogen, phosphorus, and potassium) uptake in the *in vivo* pot assay. The fly ash based consortium of *Trichoderma*, *B. borstelensis*, *Pseudomonas*, and *R. irregularis* was found to suppress charcoal rot disease in tomato, which caused by *Macrophomina phaseolina*.

SITOLE, P.<sup>1</sup> and J.F. Dames<sup>1</sup>

<sup>1</sup>Department of Microbiology and Biochemistry, Mycorrhizal Research Laboratory, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa, g011s4227@campus.ru.ac.za.

**Abstract:** Mycorrhizal fungi interact with rhizobacteria colonising roots and the surrounding soil where they work in concert to assist in plant growth promotion and plant protection. The objectives of this research were to compare the arbuscular mycorrhizal (AM) fungal status of *Citrus* under conventional and organic management practices and to investigate the role of mycorrhizal associated bacteria isolated from AM spores and determine whether they have any plant growth promoting potential. Soil and root samples were collected from a selected orchard at the organically managed citrus estates Olifantstokop and Rosedale and the conventionally managed estates at J&B Citrus and Arundel, Eastern Cape, South Africa. AM fungal spores were extracted from the soil using the wet sieving and decanting technique and root samples were cleared and stained with lactoglycerol trypan blue. Mycorrhizal percentage colonisation was assessed microscopically. AM spores were mounted onto slides with PVLG and Melzer reagent in order to observe morphological features. Spores were soaked in sterile saline/tween solution, followed by serially diluting the solution, which was subsequently spread plated onto media. AM fungal spore numbers were low and ranged from 31 to 54/100 g soil. Spores of *Glomus* and *Paraglomus* were dominant. Root percentage colonisation of between 48-70% was recorded with typical Arum colonisation strategy. A total of 19 bacterial isolates were isolated from arbuscular mycorrhizal spores, identified molecularly as mainly *Bacillus* species, and three isolates were selected for a *Citrus* pot trial. *Bacillus cereus* and mycorrhizal inoculation were found to increase shoot and root biomass of *Citrus* rough lemon saplings.

PS 4-27 **Arbuscular mycorrhizal symbiotic functioning along an experimental soil gradient**

SLAVÍKOVÁ, R.<sup>1,2</sup>, J. Jansa<sup>2</sup>, D. Püschel<sup>2</sup>, M.A. Ali<sup>1</sup>, E. Frossard<sup>1</sup> and H.A. Gamper<sup>1</sup>

<sup>1</sup>Department of Environmental Systems Science, Swiss Federal Institute of Technology Zurich, Eschikon 33, 8315, Lindau, Switzerland, renata.slavikova@usys.ethz.ch; <sup>2</sup>Institute of Microbiology, Czech Academy of Sciences, Vídeňská 1083, 14220 Prague 4, Czech Republic.

**Abstract:** Environmental change and range shifts in species distributions have the potential to disrupt or at least considerably change ecosystem functioning. Here we present our first findings on plant biomass and nutrient accumulation in a pot experiment mimicking gradients of simultaneous dispersal of arbuscular mycorrhizal fungi (AMF) and changes in biotic and abiotic soil conditions. The fluxes of carbon, nitrogen, and phosphorus were estimated via <sup>13</sup>CO<sub>2</sub> pulse-labeling of the host plant and injecting <sup>33</sup>P-orthophosphoric acid and <sup>15</sup>N-ammonium chloride into a small root-exclusion/fungus-access soil compartment eleven days prior to harvest, 5.5 months after experimental setup. A nine-step gradient of reciprocal soil dilution was created by mixing a slightly acidic sandy soil with an alkaline clayey soil from geographically disparate, but climatically similar permanent grasslands. Mixtures in which only one or both soil fractions had been gamma-irradiated and re-inoculated with their native microbes, except AMF, were used to control for effects on plant performance by changes to abiotic conditions. Above- and belowground biomass accumulation in the study herb *Plantago lanceolata* was heavily impaired by exposure to the living soils compared to AMF-free control soils. Surprisingly, just 5% of sterilized alkaline soil reduced growth suppression in the acidic living soil, which seems to be explained by soil pH-mediated changes to phosphorus availability. <sup>33</sup>P-radiotracing indicated high AMF uptake and retention in roots, which seems conceivable based on first indications of heavy vesicular colonization of roots of plants grown in mixtures of native soils. Ongoing <sup>13</sup>C and <sup>15</sup>N measurements in shoots, roots, and soil and microbial community fingerprinting are expected to elucidate the observed biomass and nutritional patterns from a mechanistic angle. In short, the study has the potential to reveal phenomenological insights into impacts on ecosystem functioning after major environmental disturbance events and to give first clues about possible mechanisms.

## PS 1-58 Restoring Texas Blackland Prairies: an insight into the effects of management practices on mycorrhizal fungi

SLIFFE, P.<sup>1</sup>, J. Ward<sup>1</sup>, A. Olivo<sup>1</sup>, B.R. Twanabasu<sup>1</sup>, C.M. Smith<sup>2</sup> and K.J. Stevens<sup>3</sup>

<sup>1</sup>Weatherford College, Weatherford, TX 76086 USA, lavueltaalsistema@gmail.com; <sup>2</sup>Austin College, Sherman, TX 75090 USA; <sup>3</sup>Wilfrid Laurier University, Waterloo, ON N2L 3C5, Canada.

**Abstract:** Arbuscular mycorrhizal (AM) fungi, which colonize over 90% of plants, are found in all terrestrial ecosystems. They play a great role in shaping the vegetation of tall grass prairies. The Texas Blackland Prairie, which extends from the Red River to San Antonio, Texas, is a continuation of the North American tall grass prairie to the southern US. Since 1997, Austin College has been involved in the restoration of 100 acres that were previously farmland to its original Blackland Prairie state. The Clinton and Edith Sneed Environmental Research Area is currently examining two management strategies, prescribed burns and controlled grazing with cattle. Treatment plots are managed using fire, grazing, or fire + grazing. To determine the effects of each management technique on below ground symbiotic fungi, we obtained soil samples in August 2013 from each restoration plot and quantified AM fungi and dark septate endophyte (DSE) colonization and AM spore density in the soil. Our goals were to determine how AM and DSE respond to fire and cattle grazing as prairie restoration techniques and to better understand the health of AM in each type of managed plot. We did not find any significant difference in AM hyphal, arbuscular, vesicular colonization, or AM spore density among treatment plots; however, DSE hyphal colonization was greater in the plots treated with fire and grazing ( $29 \pm 19.9$  and  $39.42 \pm 20.22$ , respectively) compared to fire + grazing and remnant plots ( $8.77 \pm 6.77$  and  $6.32 \pm 9.59$ , respectively). We believe this study provides a better understanding of restoration techniques and management practices of prairie ecosystems while considering below ground mycorrhizal fungi.

## PS 4-27 Assessing temperature-related changes to soil fungal communities through next generation sequencing

SMITH, J.E.<sup>1</sup>, A.D. Cowan<sup>2</sup> and A. Jumpponen<sup>3</sup>

<sup>1</sup>USDA-FS, Pacific Northwest Research Station, Corvallis, Oregon 97331 USA, jsmith01@fs.fed.us; <sup>2</sup>Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon 97331 USA; <sup>3</sup>Division of Biology, Kansas State University, Manhattan, Kansas 66506 USA.

**Abstract:** Contemporary fires have created high-severity burn areas exceeding historical distributions in a time of rapid climate change pressures on forest conditions in the western United States. Low intensity fires sustain forest ecosystems by removing dead and accumulated vegetation and releasing nutrients bound in litter. In contrast, high intensity soil heating resulting from the complete combustion of down wood, volatilizes soil nutrients and causes mortality of the beneficial mycorrhizal fungi that are particularly sensitive to fire. At Pringle Falls Experimental Forest in central Oregon, we replicated log-burning conditions and quantified the temperature, duration, and penetration of the soil heat pulse. We are comparing the soil fungal diversity and function in ten high intensity burned (HB) micro-sites paired with adjacent low intensity broadcast burned (LB) areas before, after, and 2 years post-burning and at different soil depths (0-10, 30 cm). In addition to characterizing physical and chemical responses to these burn treatments, we will employ next generation sequencing methods to quantify soil and mycorrhizal biodiversity and investigate how temperature-related changes in fungal communities contribute to the establishment and growth of ponderosa pine seedlings. Our data show that maximum soil surface temperatures ranged from 424 to 1168°C in the HB treatment and from 42 to 360°C in the LB treatment. In the HB treatment, temperatures ( $98 \pm 22^\circ\text{C}$ ) causing root and soil organism mortality penetrated the soil to at least 10 cm, but were not recorded at 30 cm ( $28 \pm 2^\circ\text{C}$ ) permitting the survival of propagule reservoirs at deeper soil horizons. In contrast to the HB treatment, soils in the LB treatment experienced potentially lethal temperatures only at the surface. Knowledge about temperature-related shifts in fungal communities and propagule banks, and how such changes contribute to the establishment and growth of planted pine seedlings, aid in understanding the outcomes and risks of high intensity fires that correlate with changing climate conditions in central Oregon.



### SY 3-4 Unexpected effects of host nitrogen status on nitrogen distribution in a common mycorrhizal network

SMITH, J.M.<sup>1</sup>, M.D. Whiteside<sup>1,2</sup> and M.D. Jones<sup>1</sup>

<sup>1</sup>Biology Department, University of British Columbia Okanagan Campus, Kelowna, British Columbia V1V 1V7 Canada, joshua.smith@ubc.ca; <sup>2</sup>Current Address: Department of Ecological Sciences, Vrije Universiteit, Amsterdam, The Netherlands.

**Abstract:** Ectomycorrhizal fungi commonly form simultaneous mutualistic associations with the root systems of multiple hosts. While mycorrhizal associations are typically examined in a single-host, single-fungus environment, little is known about nutrient flux among a single fungus and multiple host plants. To test the hypothesis that nutrients are differentially allocated in response to disparate host demands, we created ectomycorrhizal networks consisting of an ectomycorrhizal fungus, *Suillus tomentosus*, in symbiosis with two *Pinus contorta* seedlings in microcosms. After the mycorrhizas were formed, 4.7 mM NH<sub>4</sub>Cl was applied to the foliage of one of the seedlings with water applied to the other seedling. The only other nitrogen source in the microcosms was a well accessible only to hyphae. This ensured that the only route of nitrogen acquisition was via the fungus. After 12 weeks, the hyphal well was replenished with an organic (glycine) or inorganic (NH<sub>4</sub>) nitrogen source and harvested after 48 hrs. We found evidence of nitrogen loss from the seedlings in response to the introduction of a fungal supply of nitrogen. Before the well application, N concentration of shoots and roots ranged from 36.6 ± 0.9 to 44.9 ± 8.2 (µg N mg<sup>-1</sup>, ± SD), but 48 hrs after the hyphal nitrogen was applied, tissue N concentrations ranged from 11.2 ± 1.5 to 13.5 ± 2.1. We hypothesize that, contradictory to typical nutrient translocation within mycorrhizal associations, N moved from host to fungus. We speculate that, after a nutrient starvation period, exposure of the fungus to a renewed nutrient source induced a priming effect by the host plant. The N translocated from the plant may have facilitated fungal exploration of the new nutrient source. Further research into bi-directional nutrient exchange between mycorrhizal symbionts is required to determine the frequency and conditions under which this host-to-fungus nutrient transfer occurs.

### LT 2-8 Elucidating biological complexity in pecan truffles (*Tuber lyonii*) and managed orchards of Pecan trees (*Carya illinoensis*) in the Southeastern USA

SMITH, M.E.<sup>1</sup>, Z.W. Ge<sup>1</sup>, M. Reitman<sup>1</sup>, R.H. Healy<sup>1</sup>, T. Brenneman<sup>2</sup>, G. Guevara<sup>3</sup> and G.M. Bonito<sup>4</sup>

<sup>1</sup>Department of Plant Pathology, University of Florida, Gainesville, FL, USA, trufflesmith@ufl.edu; <sup>2</sup>Department of Plant Pathology, University of Georgia, Tifton, GA, USA; <sup>3</sup>Instituto Tecnológico de Victoria, Tamaulipas, Mexico; <sup>4</sup>Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, USA.

**Abstract:** *Tuber lyonii* is one of only a few native truffle species in North America that is tasty, abundant, and widespread enough to be consumed as food. This spiny-spored truffle is commonly referred to as the 'pecan truffle' because it is regularly collected in commercial orchards of pecan trees (*Carya illinoensis*, Juglandaceae). Commercialization of *T. lyonii* is limited by major gaps in our knowledge about this species. To elucidate the biology of pecan truffles we are using molecular techniques to: 1) explore phylogenetic diversity within the *T. lyonii* species complex, and 2) determine the distribution of *T. lyonii* on roots in pecan orchards and nearby natural habitats. We have sampled and sequenced ITS rDNA from >100 pecan truffles from across eastern North America. We detected 10 phylogenetic groups with distinct biogeographic patterns but minimal morphological differences. Only one dominant widespread species was typically found in managed pecan orchards and also in nearby native habitats. In contrast, most other taxa within the species complex were restricted to oak-dominated woodlands. We also sampled ectomycorrhizal roots from 75 pecan trees in 25 orchards across Florida and Georgia, and from *Quercus* and *Carya* species in adjoining woodlands. We used 454 pyrosequencing of ITS rDNA and detected 141 species of ECM fungi. We found *T. lyonii* present on roots in 12 of 25 sites. In three sites that produced truffles, *T. lyonii* was not detected on roots indicating its uneven distribution within orchards and on root systems. Based on DNA sequences, *T. lyonii* was the most abundant and tenth most frequent species on pecan roots. It was also found on native trees nearby orchards at four sites, indicative of dispersal between orchards and native habitats. Future research synthesizing these findings will work to further understand how edaphic and management factors in pecan orchards affect *T. lyonii* growth and fruiting.

## PS 3-18 The role of mycorrhizal fungi in the buildup and breakdown of SOM

SMITS, M.M.<sup>1</sup>, K. Clemmensen<sup>2</sup>, B. Lindahl<sup>2</sup>, D. Wardle<sup>3</sup>, R. Carleer<sup>1</sup> and J. Colpaert<sup>1</sup>

<sup>1</sup>Hasselt University, Diepenbeek, Belgium, mark.smits@uhasselt.be; <sup>2</sup>Swedish University of Agricultural Sciences, Uppsala, Sweden; <sup>3</sup>Swedish University of Agricultural Sciences, Umeå, Sweden.

**Abstract:** In relation to the soil carbon balance, the flow of energy from the plant into the ectomycorrhizal (EcM) fungi has been traditionally considered as a contribution to the soil carbon pool via the production of fungal biomass. Additionally, it has been proposed that EcM fungi reduce the decomposition rate of soil organic matter (SOM) through competition with saprotrophic fungi ("Gadgil" effect). On the other hand, there is growing evidence that this flux of easily metabolized energy catalyzes ("prime") decomposition. Furthermore, recent work demonstrated the ability of EcM fungi to decompose complex SOM. A series of islands with a range of sizes in two Swedish lakes provides an excellent natural experiment to study the contrasting effects of mycorrhizal fungi on SOM. Due to a smaller risk of forest fire, the smaller islands have a much thicker O-horizon (organic horizon) than the larger islands, but they also experience highly reduced primary production because of severe N-limitation. Recent work revealed that root-associated fungi form a major contribution to the SOM pool. Here we present a more detailed study on the chemical changes of the SOM over the chronosequence using pyrolysis GC/MS. The data reveal striking differences in SOM chemistry between smaller and larger islands. It confirms the contribution of fungal tissue to SOM buildup, especially the role of highly pigmented mycorrhizal mycelium. On the other hand, the data also show reduced lignin oxidation rates on the islands with lower primary productivity rates, supporting the mycorrhizal priming hypothesis.

## PS 1-59 Arbuscular mycorrhizal colonization of the dominant plant species at the arid Laguna Salada, Baja California, Mexico

Herrera-Martinez, A.<sup>1</sup>, I.M. Sanchez-Leyva<sup>1</sup>, M.C. Gonzalez-Chavez<sup>2</sup>, S. Romero-Hernandez<sup>3</sup>, J. Lopez-Luna<sup>4</sup>, J.A. Reyes-Lopez<sup>3</sup>, S. Norzagaray-Plasencia<sup>1</sup> and F.A. SOLIS-DOMINGUEZ<sup>1</sup>

<sup>1</sup>Facultad de Ingenieria, Universidad Autonoma de Baja California, Blvd. Benito Juarez s/n. Mexicali B.C. Mexico, C.P. 21280, solisf@uabc.edu.mx; <sup>2</sup>Programa de Edafologia, Colegio de Postgraduados, Texcoco, Mexico; <sup>3</sup>Instituto de Ingenieria, Universidad Autonoma de Baja California, Blvd. Benito Juarez s/n. Mexicali B.C. México, C.P. 21280; <sup>4</sup>Instituto de Estudios Ambientales, Universidad de la Sierra Juarez, Ixtlan de Juarez, Oax., Mexico, C.P. 68725.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are considered to be critical for the survival of many plants in arid environments. This study was conducted to quantify AMF colonization of the roots of predominant plant species at Laguna Salada, a desert ecosystem. Laguna Salada is a vast dry lake surrounded by scarce vegetation and is considered to be an extremely arid zone. It is located in the northwest of Mexico, 30 km southwest from Mexicali city (32°21'56" N, 115°40'20" W; elevation -3 to 7 masl). Annual precipitation varies from 54.9 to 127.4 mm, and the temperature can reach up to 52°C during the summer. Root and soil samples from nine plant species were collected (n=5 for each species). The soil has a sandy loam texture, pH 8.1 to 9.7, EC 9.78 dS/m, and contains 0.18% organic matter and 12 kg ha<sup>-1</sup> of nitrogen. *Pluchea sericea*, *Larrea tridentata*, *Haplopappus* sp., *Prosopis* sp., and *Lycium andersonii* were strongly colonized by AMF (96–98%). *Allenrolfea occidentalis*, *Suaeda divaricata*, *Atriplex canescens*, and *Tamarix ramosissima* were nonmycorrhizal. Spores, sporocarps, and hyphae of AMF were present in soil samples from all plant species studied, even in the nonmycorrhizal species. The number of AMF spores in the soil varied depending on plant species. The number of spores and sporocarps was lower ( $p<0.05$ ) in nonmycorrhizal plants (42-97 spores, 46-172 sporocarps/50 g dry soil) compared to mycorrhizal plants (160-248 spores, 242-377 sporocarps/50 g dry soil). Six spore and four sporocarp morphotypes were observed. Most plants of Laguna Salada live in a symbiosis with AMF. Although some plant species were nonmycorrhizal, their rhizospheres were found to contain abundant AMF hyphae and spores. High colonization of the roots by other fungi was also observed, which could play important roles for the survival of these plants.

## PS 2-13 Applications of *Piriformospora indica* in obviating saline soil conditions and promoting growth of some medicinal plants

Varma, A.<sup>1</sup> and S.K. SRIVASTAVA<sup>2</sup>

<sup>1</sup>Amity Institute of Microbial Technology, Amity University, Uttar Pradesh, Noida, India; <sup>2</sup>Department of Microbiology, Swami Shraddhanand College, University of Delhi, Delhi, India, sun27sri@gmail.com.

**Abstract:** *Piriformospora indica* is a symbiotic mycorrhizal fungus isolated from the rhizospheres of xerophytic woody shrubs growing in the Thar Desert of Rajasthan, India. *Piriformospora indica* not only promotes plant growth, but also confers resistance against both biotic and abiotic stresses. The properties of the fungus were patented. It has a wide host range, colonizing members of Bryophytes, Pteridophytes, Gymnosperms, and Angiosperms. Molecular phylogenetic analyses placed *P.indica* in the order Sebaciales (Basidiomycota: Agaricomycetes). A neighbor joining analysis of partial 18S rDNA sequences (525 nucleotide position) placed *P.indica* close to the *Rhizoctonia solani* group (Ceratobasidiales). Sequencing studies of *P.indica* reported a 25Mb genome size. The genomic features include a 50.68% GC content, 4.68% repeat rate, 11,769 protein coding genes, an average of 5.16 exons per gene, gene density of 471 (no. of genes per Mb), 867 secreted proteins, 386 small secreted proteins (SSP), 3,134 unique gene models, 197 unique SSP, and 58 tRNA genes. Soil salinity hampers the cultivation of crop plants resulting in growth inhibition and even plant death. *Piriformospora indica* has shown promise in overcoming salinity and making these affected lands fit for cultivation. The experimental results in the remediation of degraded saline soils on the GT Karnal Road that stretches in and around Delhi shall be presented. Reclamation of the saline soils by the use of *P.indica* has not only led to successful cultivation of plants of pharmaceutical importance but also a significant enhancement of growth parameters. We shall also be presenting recent studies on solving the crystal structure of Cyclophilin A isolated from *P.indica* (Pi Cyp A) at 1.97 Å<sup>0</sup> resolution (PDB id 4EYV). The high expression levels of this protein under soil stress conditions indicating its role in countering salt stress shall be discussed.

## PS 2-56 Mycorrhiza as an elicitor for rosmarinic acid in a co-culture system with hairy roots of *Ocimum basilicum*

SRIVASTAVA, S.<sup>1</sup>, D. Cahill<sup>2</sup> and A. Adholeya<sup>1</sup>

<sup>1</sup>TERI-Deakin Nanobiotechnology Centre, BB Division, TERI, New Delhi, India, shivani.srivastava@teri.res.in; <sup>2</sup>School of Life and Environmental Sciences, Deakin University, Australia.

**Abstract:** Arbuscular mycorrhizae (AM) are the most ubiquitous plant-fungus endosymbioses found on Earth. They colonize plant roots which are a rich source of secondary metabolites having medicinal importance. Rosmarinic acid (RA) is an ester of caffeic acid and 3,4- dihydroxyphenyllactic acid, and is obtained from *Ocimum basilicum* (basil). It is widely used as an antioxidant, anti-inflammatory, antiviral, and anticancer agent. This study, for the first time, reports development of a co-culture between selected hairy root lines of *O. basilicum* and *Rhizophagus irregularis* *in vitro* for the production of mycorrhiza and rosmarinic acid. We developed a co-culture system to provide insights into interaction mechanism between transformed roots and arbuscular mycorrhizal fungi. The developmental stages were studied using light, confocal, and scanning electron microscopy. All mycorrhizal structures were found to exhibit autofluorescence. Scanning electron microscopy studies showed tree shaped, highly branched arbuscules in the colonized cortical cells. Effect of mycorrhizal colonization was assessed on root traits (length, diameter, number of tips), biomass, total phenolics, and rosmarinic and caffeic acid content. No significant difference was found in root length and root biomass due to mycorrhization. Mycorrhization significantly increased RA levels at all three ages of co-culture in hairy root line. A positive correlation between RA content and phenylalanine ammonia-lyase (PAL) activity was also found. Thus, the potential of mycorrhiza to be an elicitor of rosmarinic acid in mycorrhized hairy root cultures was successfully demonstrated in this study. For utilization of the developed co-cultures as biological and biochemical factories, various green extraction methodologies were also screened, and the results of these studies will be presented.

## CS 1-1 Evolutionary genomics of early branches of the fungal tree

**STAJICH, J.E.**<sup>1</sup>, M.C. Aime<sup>2</sup>, M. Berbee<sup>3</sup>, M. Binder<sup>4</sup>, P. Crous<sup>5</sup>, I.V. Grigoriev<sup>6</sup>, D.S. Hibbett<sup>7</sup>, T.Y. James<sup>8</sup>, F. Martin<sup>9</sup>, L.G. Nagy<sup>10</sup>, J.W. Spatafora<sup>11</sup> and the 1KFG Consortium

<sup>1</sup>Department of Plant Pathology and Microbiology and Institute of Integrative Genome Biology, University of California-Riverside, Riverside, CA, 92521, USA, jason.stajich@ucr.edu; <sup>2</sup>Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN, 47907, USA; <sup>3</sup>Department of Botany, University of British Columbia, Vancouver, BC, V6T1Z4, Canada; <sup>4</sup>CBS Fungal Biodiversity Centre, Royal Netherlands Academy of Arts and Sciences, Utrecht, Netherlands; <sup>5</sup>Fungal Genomics Program, Joint Genome Institute, Walnut Creek, CA, 94598, USA; <sup>6</sup>Department of Biology, Clark University, Worcester, MA, 01610, USA; <sup>7</sup>Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, 48109, USA; <sup>8</sup>INRA, Nancy, France; <sup>9</sup>Biological Research Center, HAS, Synthetic and Systems Biology Unit, Institute of Biochemistry, Szeged, Hungary; <sup>10</sup>Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA.

**Abstract:** The 1,000 fungal genomes (1KFG; <http://1000.fungalgenomes.org/home/>) project and other efforts worldwide have generated a wealth of sequence data supporting studies of evolutionary genomics of kingdom Fungi. Major changes in morphology and trophism have occurred throughout the evolutionary history of Fungi, and some can be traced in the history and gene composition of extant lineages. This includes transitions from a flagellated zoospore life stage seen in chytrid fungi (Cryptomycota, Chytridiomycota, and Blastocladiomycota) to the filamentous and yeast forms observed in the “Zygomycetes” and the multicellular Dikarya lineages. Branching order of the zoosporic lineages has been difficult to resolve with different topologies supporting an early branching Blastocladiomycota and others supporting Chytridiomycota as sister to the Blastocladiomycota + “Zygomycetes” + Dikarya. Data from 300 fungal genomes were used to evaluate the phylogenetic relationships among the early branches and compare gene content in animals, zoosporic fungi, and the Dikarya fungi. Individual gene trees and concatenated analyses from hundreds of orthologous genes were used to assess the phylogenetic conflict for the early branching nodes and provide more confidence in recovered topologies for these clades. Comparison of gene content among the species and their outgroup taxa identified sets of lineage-specific genes and confirmations of gene losses and gains that correspond to the transition from a zoosporic ancestor to filamentous, yeast, and multicellular growth forms. This work provides a new genomic perspective on the evolution of kingdom Fungi including transitions to land and correlation with evolutionary events associated with other major clades (e.g., animals, plants) of life on Earth.

## PS 1-60 *Sphaerospora brunnea* and *Inocybe* sp. naturally dominated microbiome composition and determined growth and Zn uptake of willows introduced to a former landfill

Bell, T.H.<sup>1</sup>, B. Cloutier-Hurteau<sup>2</sup>, F. Al-Otaibi<sup>1,3</sup>, M.C. Turmel<sup>2</sup>, E. Yergeau<sup>4</sup>, F. Courchesne<sup>2</sup> and **M. ST-ARNAUD**<sup>1</sup>

<sup>1</sup>Biodiversity Centre, Institut de recherche en biologie végétale, Université de Montréal and Jardin botanique de Montréal, Montréal, QC, Canada, marc.st-arnaud@umontreal.ca; <sup>2</sup>Département de géographie, Université de Montréal, Montréal, QC, Canada; <sup>3</sup>Department of Soil Science, King Saud University, Riyadh, Saudi Arabia; <sup>4</sup>National Research Council Canada, Energy, Mining and Environment, Montréal, QC, Canada.

**Abstract:** Although plants introduced for site restoration are pre-selected for specific traits (e.g., trace element bioaccumulation, rapid growth in poor soils), the *in situ* success of these plants likely depends on the recruitment of appropriate rhizosphere microorganisms from their new environment. We introduced three willow (*Salix* spp.) cultivars to a contaminated landfill and performed soil chemical analyses, plant measurements, and ion torrent sequencing of rhizospheric fungal and bacterial communities at 4 and 16 months post-planting. The abundance of certain dominant fungi was linked to willow accumulation of Zn, the most abundant trace element at the site. Interestingly, total Zn accumulation was better explained by fungal community structure at 4 months post-planting than 16 months post-planting, suggesting that initial microbial recruitment may be critical. In addition, when the putative ectomycorrhizal fungi *Sphaerospora brunnea* and *Inocybe* sp. dominated the rhizosphere at 4 months post-planting, Zn accumulation efficiency was negatively correlated with fungal diversity. Although field studies such as this rely on correlation, these results suggest that the soil microbiome may have the greatest impact on plant function during the early stages of growth, and that plant-fungus specificity may be essential.



## PS 2-45 Environmental predictors of arbuscular mycorrhizal fungi and soil microbes associated with Serengeti grasses

STEVENS, B.M.<sup>1</sup>, S.L. Krznarich<sup>2</sup>, A. Antoninka<sup>3</sup>, Maarja Õpik<sup>4</sup> and N.C. Johnson<sup>2</sup>

<sup>1</sup>Northern Arizona University, Department of Biological Sciences, Flagstaff, AZ, 86011, bs527@nau.edu; <sup>2</sup>Northern Arizona University, School of Earth Sciences and Environmental Sustainability, Flagstaff, AZ, 86011; <sup>3</sup>Northern Arizona University School of Forestry, Flagstaff, AZ, 86011; <sup>4</sup>Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, 51005 Tartu, Estonia.

**Abstract:** The purpose of this study is to compare the community composition of arbuscular mycorrhizal (AM) fungi (phylum: Glomeromycota), bacteria, and archaea in soil and grass roots of the Serengeti. Arbuscular mycorrhizal fungi are obligate plant symbionts that form structures within the roots of grasses and, along with other microbes, play an important role in plant nutrition. Our study utilizes natural gradients in soil properties and precipitation to test the hypotheses that, along the Serengeti gradients, (1) microbial communities will vary, (2) there are distinct AM fungal communities within the two dominant grass species, and (3) microbial species will correlate with environmental predictors. Our analyses shows microbial community diversity varied across the Serengeti grassland. A diverse community of AM fungal spores (65 spore morphospecies) correlated with resource availability and soil characteristics (phosphorus,  $r = 0.524$ ; silt,  $r = 0.431$ ). Bacterial communities correlate with the Serengeti environmental gradient (phosphorus,  $r = 0.226$ ; silt,  $r = 0.182$ ). This study also revealed that the Serengeti grass roots host a diverse community of AM fungi (128 VT). Surprisingly, we observed no molecular evidence of distinct AM fungal communities within the roots of dominant grasses. Also contrary to expectations, there appears to be no effect of resource availability on AM fungi within plant roots.

## CS 3-2 Combining studies on fossils and genomics to understand mycorrhizal plant relationships

STRULLU-DERRIEN, C.<sup>1,2</sup>, P. Kenrick<sup>1</sup>, J.P. Rioult<sup>3</sup> and F. Martin<sup>2</sup>

<sup>1</sup>Department of Earth Sciences, Plants Division, Natural History Museum, Cromwell Road, London SW7 5BD, UK, c.strullu-derrien@nhm.ac.uk; <sup>2</sup>UMR 1136, Interactions Arbres-Microorganismes, Labex ARBRE, INRA-Nancy, 54280 Champenoux, France; <sup>3</sup>Unité de Recherche Aliments Bioprocédés Toxicologie Environnements EA 4651 - TOXEMAC & Département de Botanique, Mycologie et Biotechnologie, Université de Caen Basse-Normandie, 14032 Caen Cedex, France.

**Abstract:** The ability of fungi to form mycorrhizae with plants is one of the most remarkable and enduring adaptations to life on land. Calibrated molecular phylogenetic trees of fungi indicate that mycorrhiza-forming clades of fungi are ancient. This is also consistent with the known distribution of mycorrhizal relations across the plant tree of life. Remarkably, direct evidence from the fossil record proves that well-developed arbuscular mycorrhizal associations existed in one of the earliest fossil environments known to host land plants. Molecular phylogenetic studies are also providing insights into the evolution of different types of mycorrhizal associations through time, and genomic studies of both plants and fungi are shedding light on how the complex set of interactions evolved. The fossil record, therefore, has a role to play in establishing a chronology of when key mycorrhizal associations evolved and in understanding their importance in ecosystems through time. Here we present a brief review of our current knowledge of the fossil record of mycorrhizae in the context of plant evolution. In addition to providing an overview of what is known, our aim is to identify areas in which the fossil record can be of relevance to genomic works and to recommend an approach that would bridge the two disciplines.

## PS 3-52 International Culture Collection of Glomeromycota (CICG): procedures and services

STÜRMER, S.L.<sup>1</sup>

<sup>1</sup>Universidade Regional de Blumenau, Departamento de Ciências Naturais, Cx.P. 1507, Blumenau, SC, 89012-900, Brazil, sturmer@furb.br.

**Abstract:** A living culture collection of arbuscular mycorrhizal fungi (AMF) was established in 2010 (CICG) at Santa Catarina, Brazil with funding from state and federal agencies. The mission of CICG is to establish, maintain, characterize and document AMF stocks with the goal of conserving diversity and making monospecific experimental isolates available for researchers. A web page ([www.furb.br/cicg](http://www.furb.br/cicg)) was established in Portuguese, Spanish, and English to communicate policies of the collection, information on living stocks, AMF taxonomy, and methodology to work with mycorrhizal fungi, and



accessibility for depositing or requesting fungal isolates. At present, CIGC consists of 96 stocks originating mainly from several habitats and regions of Brazil. The taxonomic composition is 25 species of 10 genera in 7 families of Glomeromycota. Many of the methodological approaches are those that have proven successful at INVAM over the past 25 years. The standard host used to establish and grow AMF monospecific cultures is *Brachiaria brizantha*, a C4 grass that is well adapted to greenhouse conditions. The standard growth medium is a 1:1 mix of quartzite sand:soil with pH 5.3 that is suitable to grow fungal isolates from tropical and subtropical acidic soils. Research has focused on testing fungal isolates for their efficiency in promote plant growth, developing mycorrhizal inocula using the on-farm methodology, assessing intra-specific variability of functional diversity among AMF isolates, characterizing morphological variation, and more recently sampling LSU sequences. Services provided by the CIGC include releasing fungal isolates at no cost (so far) for experimental purposes, providing taxonomic advice, trapping and identification of native fungi, and conducting workshops on taxonomy and applied aspects of arbuscular mycorrhizal fungi biology and ecology. The collection provides a reference center to consolidate research in need of fungal species identification and training of human resources for taxonomy and culture establishment.

### CS 3-6 Phylogenetic perspective of biogeographic patterns in Glomeromycota

STÜRMER, S.L.<sup>1</sup> and J.B. Morton<sup>2</sup>

<sup>1</sup>Departamento de Ciências Naturais, Universidade Regional de Blumenau, Cx.P. 1507, 89012-900 Blumenau, SC, Brazil, sturmer@furb.br; <sup>2</sup>West Virginia University, 1090 Agricultural Sciences Building, Morgantown, WV 26506-6108, USA.

**Abstract:** Fossil evidence from the Rhynie chert and evolutionary patterns of Glomeribacter endosymbionts clearly indicate major clades (Acaulosporaceae, Gigasporaceae, and Glomeraceae) evolved more than 400 million years ago. An extensive 28S rRNA gene tree consisting of more than 560 sequences from stocks of INVAM, together with a comprehensive biogeography database consisting of records from 767 published papers over five decades, 718 accessions from INVAM and CIGC, and 225 species, test hypotheses of dispersal and distribution over geologic time. The geographic data encompassed 87 countries, ten biogeographic realms, ten biomes, and 19 ecoregions. A Venn diagram revealed 92-127 species were shared between any two climatic zones and 79 species were present in all climatic zones. Inadequate sampling limited measurement of distribution to 43% of known species. Despite the smaller taxon sampling pool, all of these species were distributed pandemically using a criterion of presence on at least four of the seven major continents. When these pandemic species are matched with their position in a consensus phylogeny reconstructed from rDNA sequences, they were distributed among all monophyletic clades. At least 14 pandemic virtual taxa from the MaarjAM database of SSU sequences were similarly widespread in the phylogenetic tree. While the possibility of endemism by species about which little is known still is a possibility, the absence of geographic discrimination at any level in phylogenetic history of Glomeromycota suggests it would be rare. The observed pattern supports the hypothesis that most, if not all, of fungal species evolved and dispersed across the supercontinent, Pangea, over at least 180 million years. Dispersal may have been more constrained by bodies of water in the >200 million years of continental migration that followed. However, distribution of taxa across a phylogenetic gradient indicates few if any barriers resulting in vicariance of individual clades.

### LT 4-1 Effectiveness of urban preserves in maintaining biodiversity of mycorrhizal fungi in desert ecosystems

STUTZ, J.C.<sup>1,2</sup> and A.O. Valencia<sup>2,3</sup>

<sup>1</sup>College of Letters and Sciences, Arizona State University, Mesa, Arizona 85212 USA, jstutz@asu.edu; <sup>2</sup>Julie Ann Wrigley Global Institute of Sustainability, Arizona State University, Tempe, Arizona 85287 USA; <sup>3</sup>Swette Center for Environmental Biotechnology, Arizona State University, Tempe, Arizona 85287 USA.

**Abstract:** Urbanization has been associated with reductions in species richness of most biotic communities including mycorrhizal fungi. Preservation of existing natural habitats within urban areas has been proposed as a method of reducing the impact of urbanization on biodiversity. The purpose of this study was to analyze the effectiveness of urban desert preserves in maintaining arbuscular mycorrhizal (AM) fungal diversity and functioning of AM and dark septate endophytes (DSE) fungi with respect to root colonization. Species composition and richness were determined at four study sites, two located in large urban desert preserves in Phoenix, Arizona and two located in the Arizona Uplands subdivision of the surrounding Sonoran desert. Root colonization of native succulent and woody plants by AM fungi and DSE was

also determined. A greater number of AM fungal species was detected at sites in surrounding deserts in comparison to urban preserves sites, but the number of species/samples was not significantly different. There were similarities in the species composition between urban preserve and desert sites with 70% of the same AM fungal species detected at both. The most common species detected were in the Glomeraceae at both urban and desert sites, while species in the Acaulosporaceae were only detected at desert sites. Total root colonization by AM fungi in plants from the urban preserves was 50% less than colonization in plants from surrounding deserts with significantly less hyphae and vesicles ( $p < 0.001$ ) and arbuscules and hyphal coils ( $p < 0.05$ ). Colonization by DSE was not significantly different between the preserves and desert areas. Although many of the same AMF species were detected in both the urban preserve and the surrounding deserts, decreases in AM root colonization and species richness at urban preserves may reduce the ability of preserves to sustain biodiversity.

#### LT 1-15 **New species of ectomycorrhiza *Elaphomyces* associated with dipterocarp tropical rainforest from Indonesia**

**SUKARNO, N.<sup>1</sup>**, S. Listiyowati<sup>1</sup> and K. Nara<sup>2</sup>

<sup>1</sup>Department of Biology, Faculty of Mathematics and Natural Sciences, Bogor Agricultural University, Bogor, Indonesia, nampiahsukarno@yahoo.com; <sup>2</sup>Department of Natural Environmental Studies, Graduate School of Frontier Science, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba 2777-8563, Japan.

**Abstract:** Morphological and molecular characteristics of *Elaphomyces tropicalis* Sukarno & Listiyowati, sp. nov., and *Elaphomyces* sp. collected from a dipterocarps tropical rainforest from Indonesia are described. The characteristics cover macroscopic and microscopic features using light and scanning electron microscopy, habitat, sequence, and phylogenetic analysis of ITS, SSU, and LSU regions. Observations are made strictly on ascomata collected from the rhizosphere of the dipterocarp forest dominated by *Shorea selanica* with scattered *S. leprosula* stands located at 6°32' - 6°33' S and 106°26' W. Soil characteristics of the forest are acidic (pH 4.1), low phosphorus content (3.1 ppm of soluble P), 4.6 C/N ratio, and 11 me/100 g of Al. Ascomata were found in 3-5 cm soil depth. Spore features of *E. tropicalis* Sukarno & Listiyowati, sp. nov. are close to those of *E. virgatosporus*, except for their size and ornamentation. Furthermore, colour and size of ascoma, and sequence of SSU are also different. ITS and LSU sequences of *E. virgatosporus*, however are not available in GenBank. *Elaphomyces* sp. has similar morphological characteristics with *E. tropicalis* but they differ in ITS, SSU, and LSU sequences. This is the first report of ectomycorrhizal *Elaphomyces* species associated with roots of dipterocarps and also the first record of the genus from Indonesian tropical rainforest.

#### PS 4-49 **Spatial distribution of dark septate endophytes in roots of *Ammopiptanthus mongolicus* and its associated plants**

**SUN, Q.<sup>1</sup>**, X. He<sup>1</sup> and L. Zhao<sup>1</sup>

<sup>1</sup>College of Life Sciences, Hebei University, Baoding 071002, P.R.China, 15733205591@163.com.

**Abstract:** *Ammopiptanthus mongolicus* and its associated plants are both live and develop together, with competitive inhibition and co-evolution. The spatial distribution of dark septate endophytes was surveyed in three sites located in desert, such as Yinchuan, Shapotou and Minqin, northwest China. Roots samples of *A. mongolicus* and its associated plants were collected in July 2013. The results showed that the roots of *A. mongolicus* and its associated plants could be highly infected by DSE. Microsclerotia of *A. mongolicus* was compact lumps. However, the associated plants had scattered microsclerotia. In the same site, microsclerotia colonization in *A. mongolicus* and its associated plants showed no significant difference, and colonization intensity, hyphal and total colonization of *A. mongolicus* were much higher than that of its associated plants. In different sites, the changing of colonization intensity and total colonization of DSE in *A. mongolicus* was Shapotou > Yinchuan > Minqin, and the changing of these indexes in associated plants was Yinchuan > Minqin > Shapotou. The principal component analysis indicated that soil organic matter, TEG, phosphatase and available K are the main soil factors. Furthermore, the path coefficient and comparison of 3 plots showed that soil organic C and available N have an effect on the colonization of DSE. Glomalin not only directly affects the colonization of DSE, but indirectly affects the colonization of DSE by soil enzymes and N contents. The paper has analyzed the characters and the colonization of DSE of *A. mongolicus* and its associated plants, expounding the symbiotic relationship between soil fungi with desert plants, so as to provide a base for the growth of host plant and vegetation restoration on desert environment.

#### PS 4-50 Multipronged approaches for characterization of arbuscular mycorrhizal fungal isolates from diverse ecological zones of India and their effect on growth and nutrient uptake in tomato plants

SUNAR, K.<sup>1</sup>, B. Sashidhar<sup>1</sup>, M. Ghorui<sup>1</sup>, P. Ahuja<sup>1</sup>, A. Pandit<sup>1</sup>, V. Ali<sup>1</sup>, S. Saxena<sup>1</sup> and A. Adholeya<sup>1</sup>

<sup>1</sup>Centre for Mycorrhiza Research, Biotechnology and Management of Bioresources Division, The Energy and Resources Institute (TERI), New Delhi, India, kiran.sunar@teri.res.in.

**Abstract:** Arbuscular mycorrhiza fungi obtained from diverse ecological zones of India were characterized and identified through basic morphotaxonomy, biochemical fingerprint-based fatty acid methyl ester profiling (FAME), and nuclear-encoded ribosomal DNA (n-rDNA) sequencing. Morphological studies revealed features like spore wall layers, ornamentations and type of hyphal attachments identical to specific families and genera. A total of 100 AMF were analysed for specific marker fatty acid and were found to contain C 16:1 (C-9) irrespective of their geographic origin. A total of 27-30 different FAMEs were identified out of which C 12:0, C 14:0, C14:1, C16:0, C18:0, and C18:1 was common to all. Unweighted pair group analysis of FAME profiles revealed relatively tight clusters of groups at the intraspecific and specific levels, indicating that FAME profile comparisons could provide a robust measure of similarity below the family level. For molecular identification, ITS-LSU (ITS1–5.8S–ITS2) (~500-600 bp) and partial LSU (~800–900 bp) sequences were initially tested by BLAST query and multiple sequence alignments followed by phylogenetic analysis among the AMF species. Pot experiments were conducted to investigate the potential of selected AMF under three different dose of phosphorous (full, half and quarter of recommended dose) on *Lycopersicon esculentum* L. Inoculation with AMF at half strength of phosphate showed maximum, root and shoot length, fresh and dry root weight, AM root colonization, AM spore count, acidic and alkaline phosphatase activity, and the percent available phosphorus content in the rhizosphere soil. Apart from this, the available micronutrient contents were also found to be significantly higher in these treatments. Among all the tested AMF, *Glomus hoi* RJJS114 SM1/11 and *Diversispora spurca* NC111 EM10/11 showed maximum nutrient acquisition and plant growth. Multipronged approach used to characterize AMF in this study gives a broader picture about the diversity and functionality of species/strain of Glomeromycota.

#### PS 4-51 Mycorrhizal assemblages in pure versus mixed Scots pine plantations in England

SUZ, L.M.<sup>1</sup>, S. Kallow<sup>2</sup>, K. Reed<sup>3</sup>, M.I. Bidartondo<sup>1,4</sup> and N. Barsoum<sup>3</sup>

<sup>1</sup>Comparative Fungal Biology, Royal Botanic Gardens, Kew, TW9 3DS, England, UK, l.martinez-suz@kew.org; <sup>2</sup>Conservation Science, Royal Botanic Gardens, Kew, TW9 3AB, England, UK; <sup>3</sup>Forest Research, Alice Holt Lodge, Farnham, Surrey GU10 4LH, UK; <sup>4</sup>Division of Ecology and Evolution, Imperial College London, SW7 2AZ, UK.

**Abstract:** Generally, plantations of mixed tree species present advantages over monocultures related to disease resistance, wind stability, insect outbreak, greater productivity, and lower disturbance risks. In England, mixed plantations of Scots pine (*Pinus sylvestris*) allow harvesting flexibility in a fluctuating timber market, representing for foresters an alternative to pine monocultures facing future disturbances associated to climate change, like pests or drought. In these plantations, among other factors, host preference is likely to play an important role in shaping ectomycorrhizal (ECM) communities. Changes in interactions among ECM species in mixed versus monoculture stands can influence ecosystem functioning and productivity. However, little is known about the effect on mycorrhizal assemblages of the progressive replacement of pine monocultures with mixtures of pine and oak (*Quercus robur*) in England. In this study we carried out a mycorrhizal survey at 16 Scots pine plantations (either pure or mixed with oak) at two different locations in England, New Forest and Thetford Forest. We aimed to: 1) study the structure and composition of ECM communities colonising pine roots in pure Scots pine and plantations of pine and oak, 2) compare the environmental variables (i.e., ground vegetation, soil chemistry) in both type of plantations, and 3) explore the effect of host composition and the environmental variables on ECM community assemblages. We analysed 640 soil cores and sequenced over 2,500 mycorrhizas. We found ca. 150 ECM taxa associated with pine roots, of which 40% were present in both type of plantations. ECM diversity was higher (30%) in mixed stands. We compared the ECM communities between both pure and mixed plantations, identified dominant and rare species and their main environmental drivers. The information obtained in this study will help to design Scots pine plantation strategies taking into account their ECM communities.

**LT 2-11 Metagenomic analysis of viromes in intercontinental isolates of *Rhizophagus clarus* suggests a long history of coevolution between glomeromycotan fungi and double-stranded RNA viruses**

**SUZUKI, M.**<sup>1</sup>, H. Shimura<sup>1</sup>, C. Masuta<sup>1</sup>, K. Tawaraya<sup>2</sup> and T. Ezawa<sup>1</sup>

<sup>1</sup>Graduate School of Agriculture, Hokkaido University, Sapporo 0608589 Japan, suzumei@res.agr.hokudai.ac.jp; <sup>2</sup>Faculty of Agriculture, Yamagata University, Tsuruoka, Yamagata 997-8555, Japan.

**Abstract:** Fungal viruses, which possess a double-stranded RNA (dsRNA) genome in most cases, do not have an extracellular infection route but are transmissible vertically via asexual spores and horizontally via anastomosis. Infection by dsRNA viruses often alters not only phenotypic expression of the host fungus but also higher order biological interactions. So far, arbuscular mycorrhizal (AM) fungi that belong to the phylum Glomeromycota have been found to harbor a diverse array of dsRNA viruses, including a phylogenetically distinct virus that has a significant impact on a symbiotic phenotype. In this study, dsRNA viruses in intercontinental isolates of an AM fungus were investigated by an unbiased metagenomic approach in order to understand the origin and evolution of dsRNA viruses in glomeromycotan fungi. Two intercontinental isolates of *Rhizophagus clarus*, strains RF1 (Hokkaido, Japan) and CK001 (Central Kalimantan, Indonesia), were grown in a mesh bag open culture system in association with *Lotus japonicus*, and dsRNA was extracted from extraradical mycelia, purified, and sequenced on the Illumina HiSeq platform. The paired-end reads obtained by sequencing were assembled, and contigs longer than 500 bp were subjected to Blastx searches. Maximum-likelihood trees were constructed based on alignments of amino acid sequences of viral replicase RNA-dependent RNA polymerase (RdRp). In total, 17 RdRp genes were identified in the two isolates, which were classified into the three viral families, Totiviridae, Narnaviridae, and Partitiviridae. Detailed phylogenetic analysis revealed that the two isolates harbor six closely related viruses, two mitoviruses in Narnaviridae, two totiviruses and an unclassified virus in Totiviridae, and a gamma-partivirus in Partitiviridae. The results strongly suggest the possibility that these viruses were obtained during the speciation of *R. clarus* and have evolved within their hosts after geographic isolation.

**PS 2-46 Detection of Mollicutes-related endobacteria from putative saprotrophic *Endogone* spp. and *Sphaerocreas pubescens***

**TAKASHIMA, Y.**<sup>1</sup>, K. Yamamoto<sup>2</sup>, K. Seto<sup>3</sup>, Y. Degawa<sup>3</sup> and K. Narisawa<sup>4</sup>

<sup>1</sup>United Graduate school of Agricultural Science, Tokyo University of Agriculture and Technology, 3-5-8 Saiwai-cho, Fuchu-shi, Tokyo 183-8509 Japan, yusuke.takashima.senmu@gmail.com; <sup>2</sup>Department of Bioscience and Food Production Science, Interdisciplinary Graduate School of Science and Technology, Shinshu University, Minami-minowa, Nagano 399-4598 Japan; <sup>3</sup>Sugadaira Montane Research Center, University of Tsukuba, 1278-294 Sugadaira kogen, Ueda, Nagano 386-2204 Japan; <sup>4</sup>College of Agriculture, Ibaraki University, 3-21-1 Chuo, Ami-machi, Ibaraki 300-0393 Japan.

**Abstract:** Mollicutes-related endobacteria (Mre-bacteria) are known to be associated with diverse genera of Glomeromycota and the genus *Endogone* of Mucoromycotina. Nevertheless, Mre-bacteria have not been detected in culturable species of *Endogone*. Therefore, this study attempted to detect and identify Mre-bacteria from culturable *Endogone* spp. (*E. incrassata*, *E. pisiformis*, and *Endogone* sp.) and *Sphaerocreas pubescens* which is related to Endogonales and is culturable. In total, 130 sporocarps consisting of 30 *E. incrassata*, 29 *E. pisiformis*, 16 *Endogone* sp., and 55 *S. pubescens* were collected at Ibaraki, Tochigi, and Nagano prefectures, Japan. In order to obtain pure cultures, the collected sporocarps were incubated on 1% MNC media after surface sterilization. One month after incubation, 21 isolates of *E. pisiformis* were attained from the sporocarps. These pure cultures and uncultured sporocarps (no colonial development remarked) were subjected to PCR with specific primers to detect Mre-bacteria. The results showed that 19% of *E. pisiformis* isolates and 74.5% of uncultured sporocarps harbored Mre-bacteria. Further clone library analysis indicated that most of the Mre-bacteria detected in this study were closely related to those inhabiting previously reported *Endogone* spp. In addition, we successfully confirmed the presence of Mre-bacteria inside the hyphae of *E. pisiformis* isolates using fluorescence *in situ* hybridization (FISH) with the specific probe. The present study indicated Mre-bacteria inhabiting putative saprotrophic *Endogone* spp. and *S. pubescens* which emphasizes that Mre-bacteria are associated with both of Glomeromycota and Mucoromycotina. Moreover, it showed Mre-bacteria can be associated with not only plant-associated fungal hosts but also putative saprotrophic fungal hosts. It is noteworthy that Mre-bacteria was successfully detected in *E. pisiformis* pure cultures which will help in the investigation of the role of Mre-bacteria.



**PS 3-53 PSB highly attached to *Rhizopagus irregularis* hyphae: *in situ* screening, *in vitro* function, and *in vivo* application**

**TAKTEK, S.**<sup>1</sup>, H. Antoun<sup>1</sup>, Y. Piché<sup>2</sup> and J.A. Fortin<sup>2</sup>

<sup>1</sup>Département des Sols et de Génie Agroalimentaire, CRH, Université Laval, Québec, Canada, salma.taktek.1@ulaval.ca;

<sup>2</sup>Département des sciences du bois et de la forêt, Université Laval, Québec, Canada.

**Abstract:** Soluble phosphorus (P) fertilizers added to soil rapidly precipitate, forming sparingly soluble phosphates, not available to plants. Furthermore, the excessive use of chemical fertilizers to compensate soil P deficiency is not considered sustainable and it leads to costly and potentially harmful applications. Many reports confirmed that beneficial soil microorganisms, including phosphate-solubilizing bacteria (PSB), have a significant influence on soil fertility and crop productivity. Indeed, PSB can also improve phosphate rock (PR) efficiency when directly applied to soil. However, most published works on PSB overlooked the possible interaction between PSB and arbuscular mycorrhizal fungi (AMF), which are ubiquitous in cultivated plants. A new approach based on the trapping of PSB strongly attached to the hyphosphere of AMF *Rhizopagus irregularis* (Ri) DAOM 197198, previously inoculated with microbial soil suspensions was developed to isolate relevant PSB able to mobilize P from a low reactive igneous PR more efficiently than those directly isolated from the same rhizosphere soil samples. An *in vitro* study demonstrated that the synergism between hyphobacteria (*Burkholderia anthina* Ba8 and *Rhizobium miluonense* Rm3) and Ri hyphae highly improved the solubilisation of PR. Our results go beyond the existing studies and showed specific mechanisms involved on PSB-AMF interactions. Indeed, hyphobacteria, mainly *B. anthina* Ba8, strongly adhere to Ri hyphal surfaces and PR particles forming a structured biofilm. Under greenhouse conditions, the direct application of PSB and AMF Ri as biostimulants for sustainable corn production showed that these beneficial microorganisms improve growth and P uptake of corn fertilized with superphosphate or Quebec PR.

**PS 1-61 Bacterial communities associated with ectomycorrhizal roots of pioneer dwarf willow in a primary successional volcanic desert**

**TANAKA, M.**<sup>1,2</sup> and K. Nara<sup>2</sup>

<sup>1</sup>Department of Forest Science, Faculty of Regional Environment Science, Tokyo University of Agriculture, 1-1-1 Sakuragaoka, Setagaya, Tokyo 156-8502, Japan, m4tanaka@nodai.ac.jp; <sup>2</sup>Department of Natural Environmental Studies, Graduate School of Frontier Science, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8563, Japan.

**Abstract:** Plants depend on mycorrhizal fungi for soil nutrients, but there is growing evidence that bacteria inhabiting mycorrhizal roots (mycorrhizosphere bacteria) play an important role in the nutrient acquisition processes. While many abiotic and biotic factors may affect mycorrhizosphere bacterial communities, we know very little about how the community of mycorrhizosphere bacteria (MRB) is structured in early primary succession. Here, we studied MRB communities associated either ectomycorrhizal (ECM) roots of a pioneer dwarf willow in a volcanic desert on Mount Fuji, Japan. Soil samples were collected under the pioneer dwarf willow (*Salix reinii*) with different developmental stages (i.e., young and small willow patches, each <1m<sup>2</sup>), edge, and inside of large willow patches. We only selected the most dominant ECM morphotype in each soil sample and collected seven root tips from it. Five of the collected ECM tips per soil sample were used for isolation of MRB by a culture dependent method, and two tips were used for molecular identification of ECM fungi and molecular identification of MRB after cloning. In total, we identified 240 MRB species from 564 sequences obtained from both culture dependent and independent methods. Dominant MRB genera included *Rhodoferrax*, *Rhizobium*, and *Leptothrix*. As the dominant ECM fungal communities changed with willow patch development, MRB communities significantly changed with willow patch development. Although we could not exactly isolate the causal factor for MRB succession, the succession of ECM fungi and soil development may partly account for the observed change of MRB communities.



## PS 3-19 Mycorrhizal resource and its potential contribution to soil carbon sequestration in subtropical forests, southern China

TANG, X.<sup>1</sup>, J. Liu<sup>1</sup>, J. Zhang<sup>1,2</sup>, L. Tong<sup>1,2</sup> and S. Zhong<sup>1,2</sup>

<sup>1</sup>South China Botanical Garden, CAS, 723 Xingke Road, Tianhe District, Guangzhou, Guangdong, 510650 PR China, xltang@scib.ac.cn; <sup>2</sup>Graduate University of CAS, 19A Yuquan Road, Shijingshan, Beijing, 100049 PR China.

**Abstract:** Previous studies have found that more than 60% of NPP was allocated belowground in an old-growth subtropical forest, while 45% was allocated belowground in a young forest with comparable NPP. The old-growth forest was demonstrated to be phosphorus limited as indicated by higher phosphorus use efficiency and acid phosphatase activity compared with the young forest. Because mycorrhizae are believed to be essential for relieving phosphorus limitations and are important for soil carbon conservation, we have conducted research on mycorrhizae since 2012 in subtropical forests by addressing two hypotheses. First, compared to young forests, old-growth forests have more mycorrhizae because of phosphorus deficiency. Second, mycorrhizae promote SOC sequestration in the old-growth forest due to more C being allocated belowground. A preliminary study found that 70% of the plant roots were colonized by mycorrhizae, with arbuscular mycorrhizae accounting for 2/3 of the mycorrhizae in the young forest while ectomycorrhizae and arbuscular mycorrhizae were comparable in the old-growth forest. NPP allocated to mycorrhizae was  $198.1 \pm 61.3$  and  $324 \pm 81.6$  g C m<sup>-2</sup> a<sup>-1</sup> in the young and old-growth forest, respectively. Carbon losses via hyphal respiration, as measured by the micromesh method, was  $118.9 \pm 100.7$  and  $190.6 \pm 125.2$  g C m<sup>-2</sup> a<sup>-1</sup>, respectively, accounting for 60% and 41% of NPP allocated to mycorrhizae. These results suggest that the direct contribution of mycorrhizae to SOC accumulation is negligible. However, we found that GRSP concentrations in the subtropical forests were  $3.34 \pm 0.47$  and  $\sim 5.56 \pm 1.52$  mg g<sup>-1</sup>, and accounted for about 5% of SOC. The contribution of GRSP to SOC is 8-15 times that of microbial biomass C. The chemical structure of GRSP, as detected by NMR, indicated relatively high amount of aromatic compounds (20.6-30.0%) and alkyl carbon (27.7-38.3%) enable GRSP as inactive component that could preserve carbon from decomposing. GRSP is therefore an important way for mycorrhizae to indirectly influence soil carbon sequestration.

## LT 2-2 Protective effects of mycorrhiza helper bacterium against pathogens of pedunculate oak is mediated by induced defenses

TARKKA, M.T.<sup>1</sup>, F. Kurth<sup>1</sup>, M. Bönn<sup>1</sup>, F. Caravaca<sup>2</sup>, L. Feldhahn<sup>1</sup>, H. Maboreke<sup>2</sup>, S. Mailänder<sup>3</sup>, S. Herrmann<sup>4</sup>, L. Ruess<sup>2</sup>, S.D. Schrey<sup>5</sup> and F. Buscot<sup>1</sup>

<sup>1</sup>UFZ - Helmholtz Centre for Environmental Research, Department Soil Ecology, Halle, mika.tarkka@ufz.de; <sup>2</sup>Institute of Biology, Ecology Group, Humboldt-Universität zu Berlin, Berlin; <sup>3</sup>Interfaculty Institute of Microbiology and Infection Medicine, University of Tübingen; <sup>4</sup>UFZ - Helmholtz Centre for Environmental Research, Department Community Ecology, Halle; <sup>5</sup>Forschungszentrum Jülich, Institut für Bio-und Geowissenschaften, IBG-2: Plant Sciences, Jülich, Germany.

**Abstract:** The establishment of a mycorrhizal symbiosis can be stimulated by mycorrhiza helper bacteria (MHB), and it has been suggested that certain MHB do not only promote mycorrhization but may also reduce damage caused by phytopathogens. We first assessed the influence of AcH 505 on the microbial community structure and on the root parasitic nematode *Pratylenchus penetrans* by using a culture system in which the mycorrhizosphere isolate MHB *Streptomyces* sp. strain AcH 505 was grown in a soil-vermiculite substrate with a defined starting microbial community and pedunculate oak as the host plant. Subsequently, we addressed how the oak responds to AcH 505 and how this response is related to the interaction of the oak with the ectomycorrhizal fungus *Piloderma croceum* and a challenge of the oak with the leaf pathogenic powdery mildew *Microsphaera (Erysiphe) alphitoides*. We observed that inoculation with AcH 505 counteracted the damage to the oak caused by the nematodes' parasitism of oak roots. This antagonistic effect of AcH 505 was linked to shifts in the rhizosphere microbial community fostering fungi. Using RNA sequencing, we estimated how the oak responds to AcH 505. In the AcH 505 treatment, oak genes related to disease resistance were up-regulated in both roots and leaves. Co-inoculation of the substrate with the ectomycorrhizal fungus attenuated, in part, the AcH 505-elicited defense gene expression and resulted in faster mycorrhiza formation and increased biomass of AcH 505. In contrast, the oak defense gene expression and phenylalanine ammonia lyase activity were further enhanced in oak leaves upon the challenge with the powdery mildew, and this response resulted in reduced disease symptoms. Our studies show that the presence of MHB affects the structure of the microbial community and offer novel insights into the mechanisms of the priming of plant defenses by mycorrhizosphere associates.

## PS 4-52 Within-field variation and ecosystem function of arbuscular mycorrhiza in agricultural landscape laboratories (AgroScapeLabs)

TAUSCHKE, M.<sup>1</sup>, K. Pirhofer-Walzl<sup>2</sup>, Z. Kayler<sup>1</sup>, M. Glemnitz<sup>2</sup>, M. Müller<sup>1</sup> and A. Gessler<sup>3</sup>

<sup>1</sup>Leibniz Centre for Agricultural Landscape Research (ZALF) e.V. Institute for Landscape Biogeochemistry, Eberswalder Str. 84, 15374 Müncheberg, mtauschke@zalf.de; <sup>2</sup>Leibniz Centre for Agricultural Landscape Research (ZALF) e.V. Institute of Land Use Systems, Eberswalder Str. 84, 15374 Müncheberg; <sup>3</sup>Swiss Federal Institute for Forest, Snow and Landscape Research (WSL), Birmensdorf, Switzerland.

**Abstract:** Climate change, change in biogeochemical cycles, and land use changes cause a reduction in biodiversity with appropriate consequences on ecosystem functions. Studies analyzing these complex interrelations focus mainly on protected areas or extensive used landscapes. Therefore it is important to study the biodiversity and their ecosystem function also outside of protected areas “AgroScapeLabs”- Biodiversity laboratories in agricultural used landscapes in northeast Germany provide this option, combining the dynamic of landscape structures with the dynamic and movement of different populations and the landscape functions as well. The objective of our research was to link the heterogeneity in wheat fields at the “AgroScapeLabs” with the spatial distribution and the ecosystem function of arbuscular mycorrhiza at a landscape scale. Therefore we analyzed in two intensively used agricultural fields the role of mycorrhiza in linking the soil nutrient and water availability on the one hand and the plant growth and biomass production on the other hand in 2012-2014. Following the measurement with a tractor based sensor and a statistical distribution analysis the fields were classified in four different biomass categories with 20 sampling points in each category. The varying nutrient and biotic soil parameter within the fields were associated to these different biomass categories. The wheat yield and the mycorrhizal colonization were positive correlated to the  $C_{org}$ , the  $N_t$ . According to other authors the isotope fractionation showed that the mycorrhiza prefer the  $^{14}N$  isotope compared to the heavier  $^{15}N$  isotope for N uptake in to the plant root. The spatial distribution of the stable isotopes and water use efficiency across the biomass categories will be correlated to the plant yield. To integrate these important agroecological interactions between mycorrhiza, plants, and soil in an economic and ecological sustainable management, we need more temporal and spatial analyses on landscape level.

## PS 1-62 Transfer of nitrogen among three plant species through common mycorrhizal networks

TAWARAYA, K.<sup>1</sup>, A. Sakata<sup>1</sup> and W. Cheng<sup>1</sup>

<sup>1</sup>Faculty of Agriculture, Yamagata University, Tsuruoka, 997-8555 JAPAN, tawaraya@tds1.tr.yamagata-u.ac.jp.

**Abstract:** Arbuscular mycorrhizal (AM) fungi can link neighboring plant root systems through common mycorrhizal networks of extraradical hyphae. Transfer of nitrogen and phosphorus between two plant species through common mycorrhizal networks is well documented. On the other hand, more than two plant species are often growing in mixed cropping systems. However, transfer of nutrient among three plant species is not known. We investigated whether common mycorrhizal networks link three different plant species and if nitrogen is transferred among the three plant species occurs. Three separate pots with plants were separated by a set of two stainless steel screens (34  $\mu m$ ) separated by a 1 cm air gap. Sterilized subsoil from an Andosol was added to the pots. *Medicago sativa* (M), *Allium fistulosum* (A), and *Dactylis glomerata* (D) were grown in the pots (M-D-A and M-A-D). Plants were either inoculated with *Glomus* R-10 or not, and were grown for 84 days in glasshouse. One percent (w/v)  $K^{15}NO_3$  (31.0 atom%) solution was applied to the soil of *M. sativa* 3 and 5 days before harvest. Shoot dry weight, AM colonization, hyphal length, and  $^{15}N$  content were measured. Mycorrhizal colonization and extraradical hyphal length were higher in inoculated plants compared to uninoculated plants.  $^{15}N/^{14}N$  ratio was higher in inoculated *M. sativa* and *D. glomerata* than that of uninoculated plants grown in combination of M-A-D.  $^{15}N/^{14}N$  ratio was not different between inoculated plants and uninoculated plants grown in combination of M-D-A. These results indicate that nitrogen in the fertilizer was transferred among the three plant species through common mycorrhizal networks, and transfer was affected by plant species.

**CS 6-2 Deconstructing mycoheterotrophic networks: narrowly specialized non-photosynthetic *Corallorhiza* orchids target abundant ectomycorrhizal fungi linked to diverse host trees**

**TAYLOR, D.L.**<sup>1</sup>, B. Sedillo<sup>1</sup>, S.L. Fox<sup>1</sup> and A. Enriquez<sup>1</sup>

<sup>1</sup>Department of Biology, University of New Mexico, Albuquerque, New Mexico 87131 USA, [fflt@unm.edu](mailto:fflt@unm.edu).

**Abstract:** Common mycorrhizal networks occur when mycorrhizal fungi interconnect multiple individuals of the same or different plant species. An extreme expression is seen in the case of non-photosynthetic, mycoheterotrophic plants that obtain all carbon and nutrients from their mycorrhizal fungi. In most cases, these fungi are linked to other plants, which are the sources of sugar. A well-established hallmark of mycoheterotrophs is narrow mycorrhizal specificity. However, little information is available on the specificity of the fungi with which mycoheterotrophs associate and, hence, the diversity of plants that serve as indirect hosts to mycoheterotrophs. Recent theories for the structure of symbiotic networks predict that specialists will most often associate with generalists. We tested this prediction for mycoheterotrophs by identifying both fungi and linked trees involved in mycoheterotrophic networks of orchids in the genus *Corallorhiza* using ITS RFLPs and sequencing (fungi) combined with chloroplast trnC-D sequencing (tree roots). We find that the fungal species associated with *Corallorhiza* species are dominant members of the ectomycorrhizal communities on tree roots immediately adjacent to the orchid and that the fungi associate with diverse tree species occurring at these sites. Our findings agree with network theory and suggest that narrow specificity in mycoheterotrophs may be possible due to high abundances of target fungi combined with diverse and abundant indirectly linked host trees.

**PS 4-29 Does plant richness and host identity affect diversity of mycorrhizal fungi? Lessons from local-to-global-scale studies**

**TEDERSOO, L.**<sup>1</sup>

<sup>1</sup>Natural History Museum of Tartu University, 14A Ravila, 50411 Tartu, Estonia, [leho.tedersoo@ut.ee](mailto:leho.tedersoo@ut.ee).

**Abstract:** There has been decades of discussion whether, to what extent, and how plant richness affects fungal richness. On a local scale, various studies suggest that richness of both arbuscular mycorrhizal (AMF) and ectomycorrhizal (EcMF) fungi is positively correlated with plant diversity. For EcMF, we sought to disentangle the roles of productivity, host identity, and richness *per se* in two forestry experiments. EcM fungal richness was correlated with host richness, but the strongest predictors differed among systems. Richness of EcM fungi was negatively affected by *Alnus glutinosa* proportion ( $R^2_{\text{adj}}=0.289$ ) but positively affected by soil pH ( $R^2_{\text{adj,partial}}=0.217$ ) and tree diversity (Shannon index:  $R^2_{\text{adj,partial}}=0.127$ ) in Finland. In Estonia, proportion of *Pinus sylvestris* ( $R^2_{\text{adj}}=0.522$ ) and alder ( $R^2_{\text{adj,partial}}=0.109$ ) had strong negative effects on EcMF richness with no tree diversity effect. AMF richness lacked clear patterns in these experiments. Thus, tree diversity effects are context-dependent and may be driven by both sampling effect and tree diversity directly. On a global scale, EcMF and AMF richness was positively correlated with that of plants. For EcMF, richness was explained by the proportion of hosts ( $R^2_{\text{adj}}=0.1831$ ) up to 60% basal area. In EcM-dominated sites, positive effects of soil pH ( $R^2_{\text{adj}}=0.204$ ), approximate soil moisture ( $R^2_{\text{adj,partial}}=0.068$ ), and host richness ( $R^2_{\text{adj,partial}}=0.068$ ) constituted the strongest determinants. AMF patterns were relatively weak, with strongest effects of vegetation age (negative effect:  $R^2_{\text{adj}}=0.073$ ), soil pH ( $R^2_{\text{adj,partial}}=0.043$ ), and potential evapotranspiration ( $R^2_{\text{adj,partial}}=0.035$ ) but no impact of projected plant richness. Global-scale analyses indicate that the similar climatic effects drive the richness of both plants and fungi with little if any causal relationships among these taxa. Further research accounting for plant identity and environment is required to understand vegetation effects on fungal diversity. Experimental approaches are needed to shed light into biological processes underlying diversity that may include direct genetic compatibility between partners, root or litter chemistry and their patchiness.

### LT 3-4 Resolving the 'nitrogen paradox' of arbuscular mycorrhizas: fertilisation with organic matter brings benefits for plant nutrition and growth

THIRKELL, T.J.<sup>1,2</sup>, D.D. Cameron<sup>2</sup> and A. Hodge<sup>1</sup>

<sup>1</sup>Department of Biology, University of York, Wentworth Way, York, YO10 5DD, UK, [tjt507@york.ac.uk](mailto:tjt507@york.ac.uk); <sup>2</sup>Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield, S10 2TN, UK.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) are known to be able to transfer substantial amounts of nitrogen (N) to partner plants, but the ecological relevance is debated, as total plant N does not always increase. Additionally, and perhaps paradoxically, N fertilisation of arbuscular mycorrhizal plants often suppresses plant and fungal growth. Using a compartmented microcosm experiment, we determined the significance to a mycorrhizal plant of placing a <sup>15</sup>N-labelled, nitrogen-rich patch of organic matter in a compartment to which only the fungal hyphae had access. Control microcosms denied hyphal access to the patch compartment. When permitted access to the patch compartment, the fungus proliferated densely in the organic matter patch and transferred substantial quantities of N to the partner plant. For the first time, we show that allowing hyphal access to an organic matter patch prompted total plant N and phosphorus to increase, with a simultaneous and substantial biomass benefit. Our data show that AMF can be greatly beneficial in plant nutrient capture and thereby improve plant fitness. Moreover, it is demonstrated that organic matter fertilization of arbuscular mycorrhizal plants can foster a mutually beneficial symbiosis based on nitrogen transfer, a phenomenon previously thought irrelevant.

### PS 3-9 The role of forest trees and their mycorrhizal fungi in carbonate weathering and phosphorous biogeochemical cycling

THORLEY, R.M.S.<sup>1</sup>, D.J. Beerling<sup>1</sup>, J.R. Leake<sup>1</sup> and S.A. Banwart<sup>2</sup>

<sup>1</sup>Department of Animal and Plant Sciences, University of Sheffield, Sheffield, S10 2TN, UK, [rachel.thorley@sheffield.ac.uk](mailto:rachel.thorley@sheffield.ac.uk); <sup>2</sup>Kroto Research Institute, University of Sheffield – North Campus, Sheffield, S3 7HQ, UK.

**Abstract:** On timescales of decades-to-centuries, accelerated weathering of carbonate rocks may increase land–ocean alkalinity flux, counteracting ocean acidification. Historical land use change and recent experimental evidence show that trees and their associated mycorrhizal fungi are key players in weathering biogeochemical cycles. Here, we report the effect of evolutionary advancement of trees and their mycorrhizal partnerships in intensifying weathering of carbonate minerals within forests. In a 2-year field experiment at the UK's national pinetum, we buried rock grains from four carbonates (chalk, oolite, marble, and dolomite) and an acid volcanic rock under 65 mature trees from a range of gymnosperm and angiosperm taxa that form arbuscular mycorrhizal (AM) or ectomycorrhizal (EM) fungal partnerships. During the first 3 months, chalk, oolite, and marble weathered significantly faster under EM angiosperm tree species than under AM trees, an effect linked to rhizosphere acidification by EM trees. More extensive weathering after 6 months, especially within EM forest soils, confirms the important role of EM fungi in initial mineral dissolution and nutrient mobilisation. Throughout the study, carbonate dissolution under EM trees was 12 times as fast as that of volcanic rocks. SEM imagery and molecular identification of fungal communities within ingrowth bags provides evidence of mycorrhizal involvement in carbonate weathering. Fungal hyphae preferentially colonised chalk and volcanic rock grains, which were both relatively rich in the plant-growth limiting nutrient, phosphorus, compared to the other minerals. In the volcanic silicate, phosphorus was preferentially removed from the rock grains, especially in EM forests. Contrastingly, carbonates showed net phosphorus accumulation, most likely of biological origin. Carbonate weathering and the resulting alkalinity export are likely to increase with rising atmospheric CO<sub>2</sub> and associated climate change. Our analyses suggest that EM tree species substantially increase weathering, especially of carbonates, so that planting these species on carbonate-rich terrain could help slow rates of ocean acidification.

**PS 4-30 The impact of waterlogged conditions on the development of pedunculate oak (*Quercus robur* L.) seedlings and ectomycorrhizae**

**TIKVIĆ, I.**<sup>1</sup>, D. Ugarković<sup>1</sup>, Z. Zgrablić<sup>2</sup> and N. Pernar<sup>1</sup>

<sup>1</sup>Department of Ecology and Silviculture, Faculty of Forestry, University of Zagreb, Svetošimunska 25, 10 000 Zagreb, Croatia, ivica.tikvic@zg.htnet.hr; <sup>2</sup>Croatian Forest Research Institute, Centre for Forest Ecosystem Goods and Services “Josip Ressel”, 154. brigade Hrvatske vojske 2, 52 000 Pazin, Croatia.

**Abstract:** Pedunculate oak (*Quercus robur* L.) as the principal tree species in lowland forests is adapted to various soil moisture conditions. Recently, disturbances in the natural hydrological features of lowland forests resulting from climate and other changes are increasing. We analyzed the diversity of ectomycorrhizae (ECM) and the impact of waterlogged conditions on the development of one-year-old seedlings of pedunculate oak under controlled conditions. Pedunculate oak seedlings were produced from seed collected in five localities in the pedunculate oak distribution range in Croatia. Different soil concentrations (3, 10, and 100%) from natural pedunculate oak forests were used as an infective soil inoculum for the development of ECM under controlled conditions. Nine (9) morphological ECM types were determined, one was dominant, three showed average presence, and the others were rare. Mean intensity of ECM root tips was 19%. No correlation was found between the percentage of infective soil inoculum and the intensity of ECM development. Pedunculate oak seedlings were inoculated with *Laccaria bicolor* L., and the growth of inoculated and non-inoculated seedlings was analyzed in optimal and waterlogged controlled conditions. The heights of inoculated seedlings in waterlogged conditions were 54% lower than those of inoculated seedlings in optimal moisture conditions. The stem diameters at the root of inoculated seedlings under extreme waterlogged conditions were 12% smaller than those of inoculated seedlings in optimal conditions. Inoculated seedlings under extreme conditions did not develop any ECM, whereas inoculated seedlings in optimal moisture conditions developed ECM on over 70% root tips. Soil waterlogging had a considerable effect on reduced height of pedunculate oak seedlings and lower intensity of ECM. Our results showed that ECM fungi, as the most important symbionts of forest trees, are significantly affected by hydrological disturbances in the forest. Decreased ECM vitality is directly related to decreased tree vitality.

**PS 3-54 The impact of mycorrhiza and plant growth promoting bacteria on phosphorus uptake of wheat (*Triticum aestivum*) from inorganic and organic phosphorus forms**

**TILLE, S.**<sup>1</sup>, D. Engelmoer<sup>2</sup>, J. Ton<sup>1</sup>, T. Kiers<sup>2</sup>, G. Phoenix<sup>1</sup>, J. Leake<sup>1</sup> and D. Cameron<sup>1</sup>

<sup>1</sup>Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK, s.tille@sheffield.ac.uk; <sup>2</sup>Institute of Ecological Science, Vrije Universiteit, Amsterdam, Netherlands.

**Abstract:** Sustainable soil phosphorus (P) management strategies increasingly focus on the prospective use of inoculums of beneficial soil microorganisms due to their ability to mobilize P from organic and inorganic sources naturally occurring in soil. However, many factors including nutrient type and status, plant species and the presence of other microbes have an effect on microbial fitness and activity. In this study, we investigated wheat responsiveness to single and dual inoculation of *Glomus intraradices* and *Pseudomonas putida* and whether both microorganisms improve P assimilation from organic (phytic acid, DNA) and inorganic P (sodium phosphate, hydroxyapatite) forms and subsequent plant tissue formation. Moreover, we examined changes in root metabolite profiles as a result of microbial colonization and due to the presence of different P forms. Our results show that root colonization and performance of *Glomus intraradices* and *Pseudomonas putida* and wheat responsiveness was highly dependent on the prevailing P form as well as the presence or absence of the respective other microbe. Furthermore, root metabolite patterns differed between the various P and microbial treatments.



PS 2-47 **Abundance and community composition of archaea and bacteria in boreal forest pine mycorrhizospheres**

**TIMONEN, S.**<sup>1</sup> and J.M. Rinta-Kanto<sup>1</sup>

<sup>1</sup>Department of Food and Environmental Sciences, University of Helsinki, 00014 University of Helsinki, Finland, sari.timonen@helsinki.fi.

**Abstract:** Ectomycorrhizospheres of trees cover large volumes of the topsoil in boreal forests. Both tree roots and the associated fungi have profound effects on the prokaryotes living in this environment. Tree roots are thought to especially promote bacterial populations, whereas the effect of fungi is more versatile. In this study, the population composition of archaea and bacteria in different *Suillus bovinus*-*Pinus sylvestris* ectomycorrhizal habitats was determined using qPCR and sequencing. The studied habitats included uncolonized short roots, mycorrhizas, external mycelia, *Suillus bovinus* fruiting bodies, and uncolonized soil. Both bacteria and archaea were found in all the studied habitats. The abundance of 16S rRNA gene copies of bacteria and archaea ranged from  $1 \times 10^6$  to  $3 \times 10^9$  copies g<sup>-1</sup> FW in the different habitats. Surprisingly, the number of bacterial gene copies was higher in uncolonized soil than in plant roots. The highest number of archaea was found in external mycelia. In fruiting bodies, archaeal 16S copy numbers outnumbered bacterial 16S copy numbers. Partial 16S rRNA gene sequences showed that Alphaproteobacteria, Actinobacteria, and Acidobacteria were the most common bacterial groups in the ectomycorrhizospheres, whereas Thaumarchaeota dominated the archaeal communities. Thaumarchaeota were the most abundant prokaryotes inside fruiting bodies.

PS 4-31 **Does eutrophication affect the interactions of arbuscular mycorrhizae with tropical dry forest tree seedlings?**

**TIRUVAIMOZHI, Y.V.**<sup>1</sup>, V. Varma<sup>1</sup> and M. Sankaran<sup>1</sup>

<sup>1</sup>National Centre for Biological Sciences, GKVK Campus, Bellary Road, Bangalore, India, yadugirivt@ncbs.res.in.

**Abstract:** Atmospheric nutrient deposition is recognized as an important global change driver that can affect plant composition and performance in various ecosystems. Deposition-mediated increases in plant-available nutrients in the soil are likely to also affect plant investment in nutritional symbionts such as arbuscular mycorrhizal fungi (AMF). Here we present results from an experiment studying the effects of nitrogen (N) and phosphorus (P) addition on AMF densities in dominant dry forest tree species in India. Specifically, we asked two questions. 1) How do N and P addition affect AMF densities in dry forest tree seedlings? 2) Are plant-AMF interaction responses to increased N and P availability different for N-fixing and non-N fixing host plants, given that they differ in their nutrient acquisition strategies, and nutrient requirements? We conducted a factorial experiment using seedlings of 13 dry forest tree species (6 N-fixers and 7 non-N-fixers), with N and P addition (as urea and single super phosphate, respectively); the seedlings were harvested after 6 months of nutrient addition to measure AMF densities and other parameters. Initial results suggest that AMF responses to nutrient addition cannot be generalized at a functional group level, even though the classification of the two plant groups is based on their different nutrient requirements and N acquisition strategies. There are striking differences between host species in the AMF density responses to nutrient addition; contrasting responses were observed in some species belonging to the same genera. Our results point to possible species-level differences in nutrient acquisition strategy, and mycorrhizal investment not driven by the need to acquire any one nutrient. This is in agreement with the growing appreciation of the multiple roles of AMF symbioses of plants.

CS 3-3 **The genome of the widespread *Mycoplasma*-related endobacteria colonizing arbuscular mycorrhizal fungi reveals transkingdom horizontal gene transfer and extreme dependence on the fungal host**

**TORRES-CORTÉS, G.**<sup>1</sup>, S. Ghignone<sup>2</sup>, P. Bonfante<sup>3</sup> and A. Schüssler<sup>1</sup>

<sup>1</sup>Department of Biology, Ludwig-Maximilians-University Munich, 82152 Martinsried, Germany, gloria.torres@bio.lmu.de; <sup>2</sup>Institute for Sustainable Plant Protection (IPSP), UOS Torino, National Research Council (CNR), 10125 Torino, Italy; <sup>3</sup>Department of Life Sciences and Systems Biology, University of Torino, 10125 Torino, Italy.

**Abstract:** For more than 400 million years, arbuscular mycorrhizal fungi (AMF) have formed symbiotic associations with most land plants. The obligate plant-symbiotic AMF hosts the uncultivable *Mollicutes*-related endobacteria (MRE). *Mollicutes*-related endobacteria could be detected in all major evolutionary AMF lineages studied, but their function in arbuscular mycorrhiza (AM) is unknown. 16S rRNA gene sequences of MRE fall in a monophyletic clade in the *Mollicutes* and

are highly polymorphic within a single AMF spore. Thus, MRE represent an unnamed, diverse, but monophyletic higher bacterial taxon. They probably evolved endosymbiotically for more than 400 million years. To uncover putative roles of these widespread MRE and to shed light on MRE evolution, we sequenced the genome of the MRE living in *Dentiscutata heterogama* called *DhMRE*. Multilocus phylogenetic analyses showed that *DhMRE* belong to a previously unknown lineage that is sister to a *Mycoplasma* clade. In addition, the draft annotation indicated an extremely reduced metabolic capacity, a strict dependency on the fungal host, and a large number of unique proteins. Strikingly, several *DhMRE* proteins show similarity to nuclear encoded proteins of AMF, indicating trans-kingdom gene transfer between MRE and AMF. The *DhMRE* genome encodes many proteins with domains predominantly described for eukaryotic proteins involved in bacteria-host interactions. Moreover, we found evidence for gene transfer of MRE with fungi of the *Mucoromycotina*, raising new questions about the role of MRE in the early evolution of fungus-plant associations and the AM symbiosis.

#### PS 4-32 Can mycorrhizal interactions be linked to invasion success of introduced *Eucalyptus* species in New Zealand?

TOURTELLOT, S.G.<sup>1</sup>, P.E. Hulme<sup>1</sup> and I.A. Dickie<sup>1</sup>

<sup>1</sup>Bio-Protection Research Centre, Lincoln University, Lincoln 7647, Canterbury, New Zealand, samuel.tourtellot@lincolnuni.ac.nz.

**Abstract:** Mutualist limitation can be a barrier to the success of plants when introduced to a novel area. Ectomycorrhizal (EM) fungi are a prerequisite for the establishment and spread of introduced *Pinus* and are also important for introduced *Salix* and *Alder*. These genera all associate with introduced fungal species from the plant's native range. There are, however, other possible mechanisms by which an EM plant may overcome ectomycorrhizal mutualist limitation in a novel area. In this study we test the following four mechanisms in a glasshouse soil-bioassay using invasive and non-invasive species of *Eucalyptus* in New Zealand: (i) Reliance on co-introduced EM fungi; (ii) an ability to form effective novel associations with native EM fungi; (iii) an ability to benefit sufficiently from alternative mutualist associations, such as arbuscular mycorrhiza (AM); and/or (iv) simply an ability to prosper in the absence of such mutualists. We expect that if any of these mechanisms influence invasion success it will be reflected in the relative mycorrhizal growth responses of invasive and non-invasive species. Eight plant species were used, three each of invasive and non-invasive *Eucalyptus*; *Pinus contorta*, and *Salix cinerea* were also included for comparison. The latter two are both highly invasive in NZ and are from groups often considered strongly EM dependent and dual AM-EM plants respectively. Plants were grown in soil inocula collected from under *Eucalyptus* (containing EM and AM inoculum) and from an agricultural paddock (AM only). Half of each soil type was pasteurized to make four soil types which were mixed to create EM, AM, EM+AM, and sterile soil treatments. Plant height and root and shoot biomass were used to estimate mycorrhizal growth response. Ectomycorrhizal and AM infection were measured and the EM fungus communities were characterized. The results provide unique insights in the mycorrhizal ecology of invasive *Eucalyptus*.

#### KN 1 How we got where we are: tracking down the giants

TRAPPE, J.<sup>1,2</sup>

<sup>1</sup>Department of Ecosystems and Society, Oregon State University, Corvallis, Oregon 97331; <sup>2</sup>USFS Forestry Sciences Laboratory, 3200 Jefferson Way, Corvallis, Oregon 97331, trappej@onid.orst.edu.

**Abstract:** Beginning with the oldest profession, taxonomy, all sciences have history. Certain scientists stand out for their achievements: the giants. Time passes, early giants fade from memory, many are never even hailed as giants. Yet we can learn the thought processes that made them giants. Scientific progress is independent of technology, except as technology enables increasingly sophisticated hypothesis testing. Tracking down giants entails history and philosophy more than science and is idiosyncratic more than objective. I confined my search to scientists who completed their careers largely before 1960 to avoid disappointing friends and outraging others. Anyhow, history is best understood years after it is made. I focus on two major giants in mycorrhiza research: Albert Bernhard Frank (1839-1900) and Johannes Botvid Elias Melin (1889-1979), both for their own contributions to science and for their students, some of whom become giants in their own right. Frank's publications are occasionally cited in today's literature, Melin's, less so. I also selected less known giants, who profoundly influenced how we think about mycorrhizae, e.g. Vittadini, Gallaud, Peyronel, Hatch, Björkman, Slankis. How did they think, what can we learn from them? They achieved from seeing, not just looking, thinking deeply,

not just accepting. Like the giants, we, too, can follow Henry Wadsworth Longfellow's observation: "Lives of great men all remind us, we can make our lives sublime, and, departing, leave behind us, footprints in the sands of time." In closing, I regret that no women made my giants list. This is mostly because of my 1960 closing date. Few women were involved in mycorrhiza research before then. A future seeker will find many women qualifying as giants for our emulation. Look around this room, they are among us!

### PS 3-55 Large-scale use of commercial mycorrhizal inoculant in agriculture

TRÉPANIÉ, M.<sup>1</sup> and S. Gagné<sup>1</sup>

<sup>1</sup>Premier Tech Biotechnologies, 1 avenue Premier, Rivière-du-Loup, Québec, G5R 6C1, Canada, trem5@premiertech.com.

**Abstract:** Premier Tech Biotechnologies is a Canadian company which has been producing commercial mycorrhizal inoculants (Myke® Pro) for more than 20 years. Granular, powder, and liquid formulations have been developed and adapted to growers' equipments and practices. These inoculants have been used for the last four years in many side-by-side field trials done by growers where yield from inoculated part of a field is compared to an adjacent control part without inoculation. Trials were done mainly with potato, lentil, and wheat crops in different provinces of Canada. The average inoculation rate varies from 0.8 to 2.5 M spores per hectare according to the type of crop, representing a cost of approximately 35 to 110 US \$ per hectare for the end user. For potato, results obtained from 210 sites during 2011 to 2014 indicate an average yield increase of 9.5% (+3100 Kg/ha) when using the commercial inoculant. For lentil, results obtained from a total of 68 sites during 2010 to 2013 showed an average yield increase of 7.3% (+129 Kg/ha) while for wheat, yield increase from 57 sites during 2012 to 2014 is 5.1% (+233 Kg/ha). In 2014, 120,000 ha of field crops were inoculated with mycorrhizae in Canada and forecasts for 2015 are for more than 200,000 ha. Recently, a new formulation of mycorrhizae has been developed for the pre-inoculation of seeds, giving more flexibility to growers and facilitating the inoculation of their crops. Our results in real field conditions show that mycorrhizal inoculants are efficient tools that help growers improve the yield, quality, and profitability of their crops. Use of mycorrhizal inoculants is a sustainable practice that provides higher yields without degrading natural systems and resources, and will contribute to supply food for the growing population.

### KN 5 Mycorrhizal fungi may mitigate ecosystem responses to global change

TRESEDER, K.K.<sup>1</sup> and J.M. Talbot<sup>2</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, University of California Irvine, Irvine, CA 92697 USA, treseder@uci.edu;

<sup>2</sup>Department of Biology, Boston University, Boston, MA 02215.

**Abstract:** Mycorrhizal fungi form symbioses with plant roots in almost every terrestrial ecosystem on Earth. In fact, in many ecosystems they are the most abundant fungal group in the soil. Therefore, their influence on soil carbon could have significant consequences for the global carbon cycle. In this talk, we will synthesize the mechanisms by which mycorrhizal fungi augment versus reduce soil carbon storage, and discuss environmental conditions that might shift the balance between the two. Specifically, mycorrhizal fungi can contribute to soil carbon storage by improving plant growth and thereby increasing the production of plant litter; constructing recalcitrant organic compounds that remain in the soil for years to decades following the death of the mycorrhizal fungus; and competitively inhibiting decomposition by free-living saprotrophs. On the other hand, mycorrhizal fungi can reduce soil carbon storage by directly breaking down soil organic matter to obtain nitrogen and phosphorus or supplement plant-supplied carbon. In this way, they might act as "decomposers in disguise". The net effect of mycorrhizal fungi on soil carbon storage depends on the magnitude of each of these processes, many of which remain unquantified under natural conditions. Finally, global changes such as anthropogenic nitrogen enrichment may alter the relative strengths of these processes, potentially leading to a net increase soil carbon sequestration.

#### PS 4-53 Turkey's diverse geography and climates foster a rich hypogeous mycota

TÜRKÖĞLU, A.<sup>1</sup>, M.A. Castellano<sup>2</sup>, J.M. Trappe<sup>3</sup> and M.Y. Güngör<sup>1</sup>

<sup>1</sup>Biology Department, Science Faculty, Muğla Sıtkı Koçman University, Muğla, 48000 Turkey, aturkoglu@mu.edu.tr;

<sup>2</sup>United States Department of Agriculture, Forest Service, Northern Research Station, Forestry Sciences Laboratory, Corvallis, Oregon 97331, USA; <sup>3</sup>Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon 97331, USA.

**Abstract:** Studies of hypogeous fungi in Turkey, begun by Dr. A. Pilát in 1937, have so far revealed 79 species from 30 genera belonging to 21 families including 5 ascomycete and 16 basidiomycete. This species richness is due to Turkey's combination of phytogeographical and climatic diversity, ranging from arid to wet lowlands to mountains rising well into alpine zones to foster a diversified vegetation and a similarly diversified mycota. Three phytogeographic regions of Euro-Siberian, Mediterranean, and Irano-Turanian intersect on the Anatolian Peninsula. Turkey is divided into seven regions according to the geographical properties, and generally four climate types including Continental climate, Mediterranean climate, Black Sea climate, and Marmara (transition) climate occur over these regions. All three phytogeographic regions and climate types combine to support 12,000 plant species, including 3,000 endemics. The Black Sea region is generally characterized by forests of broadleaf trees (beech, chestnut, linden, oak, maple, and alder) and conifers (larch, fir, pine, spruce, and juniper), whereas the Mediterranean region is dominated by conifers (pine, fir, cedar, and juniper). In the Aegean and Mediterranean regions, both moist and dry coniferous forests occur along with shrub and maquis communities. In central Anatolia the forests areas consist of oak, juniper, and larch. The number of hypogeous fungi discovered in Turkey is increasing every year, often including new species.

#### PS 1-63 Arbuscular mycorrhiza and *Orobanch* interactions in metal rich tailings

TURNAU, K.<sup>1,2</sup>, R. Piwowarczyk<sup>3</sup>, R. Jędrzejczyk<sup>2</sup>, N. Mikołajek<sup>1</sup> and P. Rozpądek<sup>1,2</sup>

<sup>1</sup>Institute of Environmental Sciences, katarzyna.turnau@uj.edu.pl; <sup>2</sup>Malopolska Centre of Biotechnology, Jagiellonian University, Gronostajowa 7, Kraków, Poland; <sup>3</sup>Department of Botany, Institute of Biology, Jan Kochanowski University in Kielce, Świętokrzyska 15, 25-406 Kielce, Poland.

**Abstract:** Industrial waste, although extremely difficult for re-vegetation, may become adequate for rare plants which may be condemned to extinction due to their inability to compete in their natural habitat. At the same time, this may facilitate the colonization of invasive plants such as *Orobanch* species into the environment. In recent years, *Orobanch* have been found in areas degraded as a result of anthropogenic activity. Among them, the most common are host specific *O. lutea*, *O. kochii*, *O. elatior*, *O. arenaria*, and *O. coerulescens*. *Orobanch lutea* is particularly interesting. In Silesia, it forms an extremely rare branched phenotype. The present research aims to explain the role of a host-plant signaling molecule, strigolactone orobanchol, involved in the stimulation of arbuscular mycorrhizal fungi (AMF) but also serves parasitic plants in locating their host. Phosphorus deficiency induces SL synthesis and exudation. The expansion of *Orobanch* sp. may result from the lack of AMF in polluted sites, which are commonly deficient in this nutrient. The interactions between *Orobanch* sp., selected host plants, and AMF have been the focus of our attention. In this study, we have estimated the concentration of heavy metals in plants using the fluorescence of chlorophyll of the host plants and microscopic analysis of mycorrhizae. Understanding relations in this ternary network will allow us to understand the phenomenon of wasteland colonization by different plants and fungi.

#### PS 1-38 Orchid mycorrhizae: the next generation (sequencing)

UNRUH, S.<sup>1</sup>, L. Decker<sup>1</sup>, L. Zettler<sup>2</sup>, P. Shiu<sup>1</sup> J.C. Pires<sup>1</sup>

<sup>1</sup>Division of Biological Science, University of Missouri-Columbia, Columbia, sauvd3@mail.missouri.edu; <sup>2</sup>Biology, Illinois College, Jacksonville.

**Abstract:** Orchids associate with a large diversity of fungal species. Their mycorrhizal relationship is unique because the fungi supply the plants with carbon, and the return on the fungi's investment remains undetermined. Understanding this relationship is important because many of these fungi have other roles in the environment (e.g., decomposers, ectomyc-

corrhizal associations with other plants), and other species in certain orchid fungi genera are plant pathogens. Knowing more about the molecular nature of this partnership may shed light on many more processes involving plant-fungal interactions. To study this orchid-fungal partnership, we will use next-generation sequencing technologies for gene discovery, expression-level analysis, and gene family evolution in the fungi, the orchids, and both in symbiotic culture. We are working with Lawrence Zettler who has isolated more than 400 fungi from wild orchids. These samples have been identified with ITS and belong to three main genera that form orchid mycorrhizas (*Tulasnella*, *Ceratobasidium*, and *Sebacina*). In collaboration with the Shiu lab, we will grow these fungal cultures to extract genetic material. First, we will sequence the genomes of representative fungal species. In addition, we will produce transcriptome data of the same fungal cultures and map those reads onto our genomic sequences to build a more robust genome assembly. The RNAseq data will also be used as a comparison for expression studies of symbiotic orchid seedlings. These “-omics” resources will contribute to our understanding of mycorrhizal associations and their evolution.

#### SY 4-2 Does climate or suitable ectomycorrhizal symbionts constrain pine expansion along an altitudinal gradient?

URCELAY, C.<sup>1</sup>, S. Longo<sup>1</sup>, J. Geml<sup>2</sup>, P. Tecco<sup>1</sup> and E. Nouhra<sup>1</sup>

<sup>1</sup>Instituto Multidisciplinario de Biología Vegetal (CONICET) and Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Argentina, curcelay@imbiv.unc.edu.ar; <sup>2</sup>Naturalis Biodiversity Center, the Netherlands.

**Abstract:** To succeed in habitats where ectomycorrhizal (ECM) fungi are absent, pines need to co-invade with their fungal partners. In mountains from central Argentina there are no native ECM hosts, thus we cannot currently predict if climate and/or lack of compatible fungal symbionts constrain pine expansion from plantations toward distances and altitudes in which there are absent. We combined DNA meta-barcoding of soils and field experiments along an altitudinal gradient that is subjected to an incipient spread of exotic *Pinus elliottii* to assess a) whether fungal partners are present in soils at different altitudes and b) if pines can survive and form ectomycorrhizas at elevations outside of their current range. Three plots were selected at four sites along the altitudinal gradient (900, 1,600, 2,200, and 2,700 masl). They were established at approximately 110, 3,000, 6,000, and 9,000 m from the closest pine plantation, respectively. Eight seedlings were transplanted to each plot soil at each altitude. Plants were harvested in two stages (before and after winter). For soil analyses, a pine plantation close to the lowest site was also selected. Among the 31 ectomycorrhizal OTUs found in the pine plantation, 11 were found at other altitudes, indicating the presence of suitable fungal symbionts in the soil spore bank even at considerable distances from plantations. After five months (before winter), pine seedlings survived at all altitudes. At least one individual from 900, 1,600, and 2,200 was colonized by *Suillus granulatus*. Two individuals at 1,500 m asl were also colonized by *Rhizopogon* sp. and *Thelephora terrestris*. After 11 months, individuals also survived at all altitudes but only one individual at 1,500 masl showed colonization by *Suillus granulatus*. Our results show that pines can survive, find suitable fungal symbionts and form ectomycorrhizas at long distances from plantations and at elevations where they currently do not occur.

#### CS 5-6 Linking soil biodiversity, mycorrhizal fungal diversity, and ecosystem multifunctionality

VAN DER HEIJDEN, M.G.A.<sup>1,2</sup>, C. Wagg<sup>2</sup>, K. Schlaeppi<sup>1</sup>, K. Hartman<sup>1</sup>, S. Pellkofer<sup>1,2</sup>, F. Bender<sup>1</sup>, R. Wittwer<sup>1</sup> and E. Verbruggen<sup>3</sup>

<sup>1</sup>Plant Soil Interactions, Institute for Sustainability Sciences, Agroscope, Reckenholzstrasse 191, CH-8046 Zurich, Switzerland, marcel.vanderheijden@agroscope.admin.ch; <sup>2</sup>Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, CH-8057, Switzerland; <sup>3</sup>Department of Biology, University of Antwerpen, 2610 Wilrijk, Belgium.

**Abstract:** Biodiversity loss has become a global concern as evidence accumulates that it will negatively affect ecosystem services on which society depends. So far, most studies have focused on the ecological consequences of aboveground biodiversity loss, yet a large part of Earth's biodiversity is literally hidden belowground. Whether reductions of biodiversity in soil communities belowground have consequences for the overall performance of an ecosystem remains unresolved. In this talk, we first discuss how intense agriculture influences belowground biodiversity, focusing on communities of arbuscular mycorrhizal (AM) fungi. We show, based on a comparison of conventionally and organically managed fields in Switzerland and the Netherlands, that land use intensification reduces AM fungal abundance and diversity. Using



data from a newly established experiment comparing four major arable farming systems, we show that land use intensification alters microbial communities associated with plant roots (e.g., the plant microbiome). The above-mentioned data were obtained using use molecular identification tools (e.g., 454 sequencing, Illumina sequencing, and single molecule real-time (SMRT) sequencing). Next, we present a series of experiments where we test whether changes in AM fungal diversity and soil biodiversity impact ecosystem functioning and plant performance. We show that reductions in soil biodiversity alter a range of ecosystem functions and that soil biodiversity loss leads to impaired ecosystem functioning. Next, we assessed the effects of different soil communities on plant community dynamics and stability over a one-year time span. Our first results indicate that more complex soil communities, which also contain AM fungi, enhance ecosystem stability by equalizing the performance among competing plant species. We use path-analysis to investigate how different groups of soil biota, including AM fungi, interact to influence ecosystem functioning. Overall, our results indicate that changes in soil communities and the loss of soil biodiversity threaten ecosystem multifunctionality and sustainability.

**PS 1-39 Origin of *Amanita muscaria* introduced to Colombia and a range expansion to tropical *Quercus humboldtii* forests**

**VARGAS, N.<sup>1</sup>**, C. Pardo<sup>1</sup>, S. Gonçalves<sup>2</sup>, S. Restrepo<sup>1</sup> and A. Pringle<sup>3</sup>

<sup>1</sup>Laboratory of Mycology and Plant Pathology, Universidad de Los Andes, Bogotá, Colombia, n.vargas20@uniandes.edu.co; <sup>2</sup>Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, 3000-456 Coimbra, Portugal; <sup>3</sup>Department of Botany and Bacteriology, University of Wisconsin, Madison, USA.

**Abstract:** To meet the global demand for timber, industrial tree plantations were established in South America during the first half of the 20<sup>th</sup> century. Extensive plantations are found in many countries in the tropics and subtropics, for example Brazil and Chile. In Colombia, miscellaneous plantations were established during the 1950s, when industrial activities were at their height, and policies to limit deforestation in native *Quercus humboldtii* forests (considered a main source for charcoal production) were established. One unforeseen consequence of establishing plantations of non-native trees was the subsequent introduction and persistence of fungal symbionts, and spread of introduced fungi to native forests. We review the possible origins of the invasive ectomycorrhizal *Amanita muscaria* found in exotic plantations of *Pinus* spp. and *Eucaliptus* spp., and in *Q. humboldtii* forests in Colombia. This is the first time the spread of an exotic fungal species into native forests has been documented in this country. According to a Bayesian phylogenetic analysis based on the nuclear ribosomal internal transcribed spacer (ITS) and the nuclear large subunit (nLSU) regions, *A. muscaria* individuals associated with *P. patula*, and those colonizing *Q. humboldtii* stands, have origins in the geographic region of Eurasia (clade II), supporting a hypothesis of an Eurasian origin of most southern hemisphere *A. muscaria* invasions. Potential negative effects of *A. muscaria* colonization in Colombian forests are discussed.

**PS 1-64 Land-use change effects on mycorrhizal symbioses in dioecious wild *Carica papaya* (Caricaceae)**

**VEGA-FRUTIS, R.<sup>1</sup>**, F. Puebla-Olivares<sup>1</sup> and G. Luna-Esquivel<sup>1</sup>

<sup>1</sup>Unidad Académica de Agricultura, Universidad Autónoma de Nayarit, Km. 9 Carretera Tepic-Compostela, C.P. 63780, Xalisco, Nayarit, Mexico, rociovegaf@yahoo.com.mx.

**Abstract:** Land-use change and habitat fragmentation are important causes for declining biodiversity and may alter biotic interactions, including belowground interactions with arbuscular mycorrhizal fungi (AMF). Dioecious plants are expected to be more sensitive to habitat fragmentation than self-compatible plants. Recent findings suggest that the frequency of AMF in roots of dioecious plants is higher in females, which is linked to the different costs of reproduction between the two genders. Here, we investigated land-use change effects on the colonization by AMF in the dioecious wild *Carica papaya*, a species known to have suffered loss of genetic diversity as a consequence of habitat fragmentation. We collected fine roots and soil from selected reproductive male and female individuals during the dry and rainy seasons in three sites differing in habitat fragmentation in the Nayarit State, Mexico. Our preliminary results showed no significant differences in AMF colonization between plant sexes nor sites, but higher AMF colonization during the dry season, coinciding with the lower soil fertility parameters observed in the dry season. The lack of sex and land-use change effects on mycorrhizal colonization may be due to *C. papaya*, a pioneer species, being adapted to disturbance conditions (e.g., it grows in main and dirt roads). In addition, a previous study did not find differences between sexes of *C. papaya* when plants were reproductively active for several months compared with seedlings. Further research is needed to determine the role of land-use change and the consequent habitat fragmentation on AMF in other dioecious species.

**VELMALA, S.M.**<sup>1</sup>, T. Rajala<sup>1</sup> and T. Pennanen<sup>1</sup>

<sup>1</sup>Natural Resources Institute Finland (Luke), Bio-based Business and Industry, Jokiniemenkuja 1, FI 01370 Vantaa, Finland, sannakajsa.velmala@luke.fi.

**Abstract:** The means by which trees establish and utilize fungi is intriguing given the lack of host specificity shown by many fungal species. In order to reveal the mechanism by which fungal species richness affects forest productivity, we studied the interaction of Norway spruce (*Picea abies*) seedlings and ectomycorrhizal (EM) fungi. We addressed how susceptibility to EM infection and the composition and functionality of the associated EM fungal communities relate to host genotype and their long-term growth performance. We found that Norway spruce genotype partly controlled EM colonization of seedlings. However, we found no relationship between the future growth performance of the host and the established EM communities or the functional capacity of single ectomycorrhizas; seedlings representing contrasting future phenotypes were equally colonized by EM fungi. Additionally, the activities of potential exoenzymes varied only according to the colonizing EM fungal species, not between host genotypes or phenotypes. Nevertheless, the short root architecture, which was found to be a moderately heritable trait, varied consistently between seedlings of contrasting future phenotypes. One-year-old seedlings known to show fast growth in a later stage had sparse and widespread rootlets compared to seedlings representing the stunted future phenotypes. Norway spruce does not seem to show a strong genetic signal for within-population selection towards its EM fungi at the species level. The superior growth of some spruce phenotypes may be a consequence of resource allocation and optimal root structuring in the juvenile stage rather than the extent of colonization by EM fungi. We accept that root physiological factors may subsequently lead to a higher capacity for symbiotic interactions in heterogeneous forest soil. An adequate and versatile means of nutrient acquisition is an important factor enabling fast growth, but might also provide the basis for positive feedback via enhanced mutualistic fungal interactions.

#### CS 7-2 **Arbuscular mycorrhizal fungi can stabilize root-litter carbon in soil**

**VERBRUGGEN, E.**<sup>1,2,3</sup>, J. Jansa<sup>4</sup>, E.C. Hammer<sup>1,2,5</sup> and M.C. Rillig<sup>1,2</sup>

<sup>1</sup>Dahlem Center of Plant Sciences, Plant Ecology, Freie Universität Berlin-Institut für Biologie, Berlin, Germany, erikverb82@hotmail.com; <sup>2</sup>Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB), Berlin, Germany; <sup>3</sup>current address: Department of Plant and Vegetation Ecology, University of Antwerp, Wilrijk, Belgium; <sup>4</sup>Institute of Microbiology, Academy of Sciences of the Czech Republic, Prague, Czech Republic; <sup>5</sup>Department of Biology, Microbial Ecology/Biodiversity, Lund University, Sölvegatan 37, 22362 Lund, Sweden.

**Abstract:** Fine roots and mycorrhiza often represent the largest input of carbon (C) into soils, and therefore, of primary relevance to soil C balance. Arbuscular mycorrhizal fungi have previously been found to increase litter decomposition which may lead to reduced soil C stocks, but these studies have typically focused on immediate decomposition of relatively high amounts of high-quality litter and, thus, may not hold in many ecological settings over longer terms. Here we assessed the effect of mycorrhizal fungi on the fate of C and nitrogen (N) contained within a realistic amount of highly <sup>13</sup>C/<sup>15</sup>N labelled root-litter in soil. This litter was either added fresh or after a 3-month incubation under field conditions to a hyphal in-growth core where mycorrhizal abundance was modified through rotation. After three months of incubation with a plant under greenhouse conditions, the effect of mycorrhiza on residual <sup>13</sup>C and <sup>15</sup>N inside the cores was measured, as well as <sup>13</sup>C incorporation in microbial signature fatty acids and <sup>15</sup>N incorporation in plants. Mycorrhizal fungi were found to reduce the abundance of decomposers and <sup>13</sup>C loss from cores, while <sup>15</sup>N content of cores and plants was unaffected. The field-incubated litter showed an even lower loss in <sup>13</sup>C left in cores in response to mycorrhizal fungi than “fresh” litter. This suggests that arbuscular mycorrhizas can stabilize C and that this effect is persistent through time. These results will be discussed in the larger framework of current knowledge of direct and indirect effects of mycorrhizal fungi on soil carbon sequestration.

## PS 2-33 Reintroduction of orchid: changing in the mycorrhizal fungi diversity

VIEIRA, C.A.<sup>1</sup>, T.G.R. Veloso<sup>1</sup>, M.F. Bocayuva<sup>1</sup>, D.M.S. Bazzolli<sup>1</sup> and M.C.M. Kasuya<sup>1</sup>

<sup>1</sup>Federal University of Viçosa, Centre of Biological Sciences and Health, Department of Microbiology, Viçosa, MG, Brazil, vieiraca@live.com.

**Abstract:** The great diversity of orchid colors and forms makes them highly economically valuable. Over-collecting, habitat fragmentation, and climate change are increasing the extinction risk of several orchid species and their associated orchidaceous mycorrhizal fungi (OMF). Inoculating orchid seedlings with selected OMF can enhance the success of orchid reintroduction. In this study, we evaluated the changing OMF community of *Hadrolaelia jongheana* using individuals of this species transplanted into Atlantic Forest fragments of the Minas Gerais state, Brazil, where this orchid species occurs naturally. Forty orchid seedlings that were 7-months-old and symbiotically growth *in vitro* were transferred to different fields and affixed to tree trunks. Root samples were collected before reintroduction and at 120 and 240 days post reintroduction. The diversity of mycorrhizal fungi was determined using ITS-PCR-DGGE and evaluated by the Shannon index and PCA analysis incorporating environmental factors. The process of ecological succession occurred naturally with OMF diversity significantly increasing over time. OMF diversity was 1.391 before reintroduction and 1.734 and 2.438 at 120 and 240 days post reintroduction, respectively. These results suggest that the environment promotes dynamic change in the fungal community, and maximum temperature seems to strongly influence changes in diversity. Additionally, our study illustrates that, in the field, other fungi are able to colonize orchid roots. This is part of the first study on the reintroduction of Brazilian orchids.

## PS 2-14 The root microbiome: culturing, sequencing, and functional genomics of fungi from the *Populus* rhizosphere

Bonito, G.<sup>1,2</sup>, K. Hameed<sup>1</sup>, C. Schadt<sup>3</sup>, J.L. Labbé<sup>3</sup>, G. Tuskan<sup>3</sup>, I. Grigoriev<sup>4</sup>, F. Martin<sup>5</sup>, H.L. Liao<sup>1</sup> and R. VILGALYS<sup>1</sup>

<sup>1</sup>Department of Biology, Duke University, Durham, NC 27708, fungi@duke.edu; <sup>2</sup>Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI 48824; <sup>3</sup>Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831; <sup>4</sup>US Department of Energy Joint Genome Institute, Walnut Creek, CA 94598; <sup>5</sup>Interactions Arbres-Microorganismes, INRA-Lorraine University, Nancy, France.

**Abstract:** Plant roots interact and interface with a bewilderingly complex community of microbes. Among these are rhizosphere fungi that are essential in maintaining plant health. To gain a better understanding of rhizospheric fungal diversity, we conducted field and greenhouse studies to sample, isolate, and characterize culturable rhizosphere fungal communities associated with *Populus deltoides*, *P. trichocarpa*, and the co-occurring plant hosts *Quercus alba* and *Pinus taeda*. Using both general and selective isolation media, we isolated more than 1,800 cultures from individual surface sterilized root tips collected from field sites and greenhouse experiments. ITS and LSU sequences from these isolates were compared to 454/Illumina sequence datasets obtained from the *Populus* rhizosphere. While most ectomycorrhizal taxa that associate with *Populus* have evaded isolation, further isolation and identification of key endomycorrhizal fungal taxa has enable more targeted study of plant-fungal interactions of this functional guild. Genome sequencing and targeted metatranscriptome experiments are currently underway for a key set of *Populus* root-associated fungi to aid in the understanding of mechanisms involved in plant-fungal interactions within the rhizosphere. This diverse culture library of fungal root associates will be a valuable resource for future metagenomic research, experimentation, and to further studies on plant-fungal interactions and the *Populus* microbiome.

## PS 1-66 Interactions of arbuscular mycorrhizal and ectomycorrhizal fungi in primary succession on mining spoil banks

VOSÁTKA, M.<sup>1</sup>, T. Lukešová<sup>1</sup>, P. Kohout<sup>1</sup>, J. Rydlová<sup>1</sup>, M. Janoušková<sup>1</sup>, P. Doubková<sup>1</sup>, D. Püschel<sup>1</sup>, C. Krüger<sup>1</sup> and J. Frouz<sup>2</sup>

<sup>1</sup>Institute of Botany, Czech Academy of Sciences, Zámek 1, 252 43 Průhonice, Czech Republic, miroslav.vosatka@ibot.cas.cz; <sup>2</sup>Department of Botany, Charles University, Viničná 5, 128 44 Prague 2, Czech Republic.

**Abstract:** Mining activities in western Bohemia resulted in deposition of excavated material on extensive post-mining heaps that provide unique habitat for studying primary succession. Succession on mining spoil banks follows a distinct path where different vegetation dominates and occurs with various levels of dependence on either ectomycorrhizal

(EcM) or arbuscular mycorrhizal (AM) fungi. However, the roles of symbiotic fungi in forming plant communities and the changes in diversity of mycorrhizal fungi during succession are poorly understood. A chronosequence study was conducted where mining sites of different ages were used to investigate the occurrence, diversity, and changes in mycorrhizal fungal communities. Interactions of AM fungi (associated with grasses, herbs, willows, and alder) with EcM fungi (associated with willows, birch, and alder) have been investigated on a 25-year-old succession site where both types of mycorrhiza are abundant. The interactions between both types of mycorrhizal fungi and their influence on host plant is being studied in mesocosm experiments with indigenous spoil bank substrates. The results show that both types of mycorrhizal symbiosis have distinct patterns related to the interaction of vegetation dominants on mining spoil banks in given chronosequence.

**PS 3-56 Inoculation effect of arbuscular mycorrhizal fungi and *Azospirillum brasilense* on yield and nutrient uptake of maize crop**

**WAHID, F.<sup>1</sup>**, B. Jan<sup>1</sup>, M. Sharif<sup>1</sup> and F. Khan<sup>1</sup>

<sup>1</sup>Department of Soil and Environmental Science, The University of Agriculture, Peshawar, Pakistan, fazliwahid@aup.edu.pk.

**Abstract:** An experiment was conducted to determine the combined effect of arbuscular mycorrhizal fungi (AMF) and *Azospirillum brasilense* on growth and nutrient uptake of maize. The experiment was conducted in pots under natural conditions using a completely randomized design with three replications during Kharif 2013. The maize variety Azam was grown in pots with five seeds initially and was thinned to three plants per pot. Data revealed that the combined inoculation of AMF and *A. brasilense* with a half dose of SSP produced maximum maize dry shoot and root yields of 5,800 and 2,266 kg ha<sup>-1</sup>, respectively, which was a significant ( $P \leq 0.05$ ) increase of 28% and 21%, and 44% and 34% over the shoot and root yields of the control and *A. brasilense* alone, respectively. Maximum N and P uptake by maize plants of 96 and 13.4 kg ha<sup>-1</sup> were observed in the treatments of combined inoculation of AMF and *A. brasilense* with half dose of SSP, respectively, which was a significant ( $P \leq 0.05$ ) increase of 109% and 41%, and 141% and 103% over the N and P uptake of the control and *A. brasilense* alone, respectively. The combined inoculation of AMF and *A. brasilense* with half dose of SSP increased Zn and Cu uptake over the control (by 175% and 167% for Fe and Cu, respectively) and *A. brasilense* alone (by 88% and 84% for Zn and Cu, respectively). Similarly, the combined inoculation of AMF and *A. brasilense* with half dose of SSP increased both Mn and Fe uptake over the control (by 110% and 285% for Mn and Fe, respectively) and *A. brasilense* alone (by 59% and 161% for Mn and Fe, respectively). The AMF spores and root infection intensity were significantly increased by the combined inoculation of AMF and *A. brasilense*. Results indicate that the combined inoculation of AMF and *A. brasilense* has potential to improve shoot and root dry matter yield of maize with enhanced N, P, Zn, Cu, Mn, and Fe uptake of maize plants.

**PS 4-33 Arbuscular mycorrhizal fungi in mountain grassland show altitude and host-plant dependent responses to future climate conditions**

**WAHL, A.-L.<sup>1</sup>**, L. Tillet<sup>1</sup>, G. Niedrist<sup>2</sup>, G.J. Lair<sup>3</sup>, U. Tappeiner<sup>2,3</sup> and T. Spiegelberger<sup>1</sup>

<sup>1</sup>Irstea, Research Unit Mountain Ecosystems (UR EMGR), 2 rue de la Papeterie, BP 76, FR-38402 Saint-Martin-d'Hères, France, anne-lena.wahl@irstea.fr; <sup>2</sup>European Academy of Bozen/ Bolzano (EURAC), Institute for Alpine Environment, Viale Druso 1, I-39100 Bolzano/Bozen, Italy; <sup>3</sup>University of Innsbruck, Institute of Ecology, Sternwartestr. 15, 6020 Innsbruck, Austria.

**Abstract:** Rising temperatures affect all ecosystem compartments, yet the possible response of arbuscular mycorrhizal fungi (AMF) to elevated temperature is rarely studied in the field, especially in mountain regions, which are disproportionately affected by climate change. We investigated AMF colonization of plant roots in grasslands along an altitudinal gradient from the colline to the subalpine belt in the Italian Alps under current and future climate conditions, simulated by downward transplantation of soil monoliths. Simulation of future climate conditions by transplantation from the subalpine to the montane zone (+ 2.8 K) lead to a general decrease in the mean percentage of root length colonized by AMF. However, no changes in average percentage of root length colonized by AMF occurred when species were transplanted from the montane to the colline vegetation belt, thereby equally subjected to a temperature increase of 2.8 K. At his lower transplantation, responses varied among different plant species: One third showed an increase in AMF colonization rate, one sixth a decrease and half of the plant species showed no significant change in colonization rates. Under cur-



rent climate conditions, colonization by mycelium remained similar along the gradient and the plant-fungus relationship stayed mutualistic. Our study provides new insights into the development of arbuscular mycorrhizal root colonization in mountain grassland under current and future climate conditions, assessed in a field experiment along an altitudinal gradient. The results suggest that reaction to warmer temperatures is linked to altitude-dependent evapotranspiration and its hydrological consequences as well as to different and complex plant-fungal interactions of individual plant species. While at higher altitudes warmer temperatures seem to benefit plants and lead to a general decrease in AMF colonization, drought stress at lower altitudes leads to plant species-specific reactions that appear to be linked to different root traits.

## CS 2-2 Mycorrhizal networks are shared by different plants under unequal terms of trade

WALDER, F.<sup>1,2</sup>, P.E. Courty<sup>2,3</sup>, T. Boller<sup>2</sup>, A. Wiemken<sup>2</sup> and M. van der Heijden<sup>1,4,5</sup>

<sup>1</sup>Plant-Soil Interactions, Institute for Sustainability Sciences, Agroscope, 8046 Zürich, Switzerland, florianwalder@gmx.ch; <sup>2</sup>Zurich-Basel Plant Science Center, Department of Environmental Sciences, Botany, University of Basel, 4056 Basel, Switzerland; <sup>3</sup>Department of Biology, University of Fribourg, 1700 Fribourg, Switzerland; <sup>4</sup>Institute of Evolutionary Biology and Environmental Studies, University of Zürich, 8057 Zürich, Switzerland; <sup>5</sup>Plant-Microbe Interactions, Institute of Environmental Biology, Faculty of Science, Utrecht University, 3584 CH Utrecht, the Netherlands.

**Abstract:** The majority of plants associate with arbuscular mycorrhizal (AM) fungi. AM fungi exhibit low host specificity and, therefore, frequently form common mycorrhizal networks (CMNs) interconnecting neighboring plant species. Thus, mycorrhizal plants often share their fungal partners and trade photosynthetic carbon for essential nutrients with a common symbiont. Although substantial amounts of resources are exchanged, the factors that regulate trade in the CMNs are still poorly understood. To study this issue experimentally, we established microcosms of two adjacent plants, flax and sorghum, sharing a CMN. Depending on the AM fungal species, we found strong asymmetry in the symbiotic resource exchange. Flax invested little carbon but gained up to 94% of the nutrients provided by the CMN, which highly facilitated its growth, whereas the neighboring sorghum invested massive amounts of carbon with unsatisfactory returns, but its growth was barely affected. Obviously, the exchange of carbon for nutrients was not tightly linked in the surveyed CMNs. This contrasts with recent findings revealing that resource exchange in the AM symbiosis is based upon reciprocal trade and follows the biological market theory. We discuss our results in the light of the biological market dynamics and we propose an alternative framework explaining plant-fungal coexistence. In our experiments, the extent of nutritional return was determined by the sink strength of the plants and on the identity of the symbionts, and the results do not support predictions under a biological market theory scenario. In conclusion, CMNs are shared under uneven but species-specific terms of trade promoting overall plant growth. Thus, CMNs may contribute to interplant facilitation and enhanced productivity when agricultural plants are intercropped.

## PS 4-34 Environmental drivers of ecto- and endomycorrhizal dynamics in *Eucalyptus* species

WALKER, J.K.M.<sup>1</sup>, I.C. Anderson<sup>1</sup> and J.R. Powell<sup>1</sup>

<sup>1</sup>University of Western Sydney, Hawkesbury Institute for the Environment, Richmond, NSW 2753 Australia, jennifer.walker@uws.edu.au.

**Abstract:** *Eucalyptus* species are primarily colonised by ectomycorrhizal (EM) fungi, but arbuscular endomycorrhizal (AM) fungal colonisation has also been detected in varying proportions. Our objective was to identify potential drivers of reported AM-EM shifts in roots of *Eucalyptus* species. We hypothesised that the timing and extent of these shifts may be constant, and linked to specific growth stages, or flexible, and dependent on environmental conditions. Bioassay seedlings were planted into two existing field experiments to test mycorrhizal community responses to environmental change (fertilisation and irrigation in a reclaimed paddock; elevated CO<sub>2</sub> in native woodland). Root samples were collected from seedlings harvested 4 and 8 months after planting. Plant growth characteristics and soil chemical properties were measured. To date, we have calculated percent colonisation of ectomycorrhizae formed on fine roots, then extracted DNA, amplified and sequenced the fungal ITS region. EM fungal colonisation and species richness increased significantly over time ( $P < 0.01$ ); this was correlated with an increase in above- and below-ground seedling biomass ( $r^2 > 0.70$ ). Seedlings were on average 28% ( $\pm 25$  sd) colonised by EM fungi after 4 months, and 85% ( $\pm 12$  sd) after 8 months. EM fungal spe-



cies richness was lower on younger seedlings ( $1.3 \pm 1.2$  sd) compared to older seedlings ( $4.25 \pm 1.2$  sd), with treatment interactions: the increase was greater in irrigation and in elevated CO<sub>2</sub> plots. *Hydnangium*, *Tomentella*, *Inocybe*, *Sebacina*, Sordariomycetes, and Descomycetes were among the most frequently detected EM fungal groups. Our finding of robust EM fungal colonization on young seedlings was surprising; however, analysis of AM fungal colonisation is still underway. Notwithstanding those analyses, we speculate that AM and EM fungal inoculum potential may be a more important driver of AM-EM shifts than host growth stage, and an experiment to test this hypothesis is also underway.

#### PS 4-54 Succession of ectomycorrhizal fungi in mesh bags over a three year period in a fertilized and unfertilized Norway spruce forest

WALLANDER, H.<sup>1</sup> and N. Rosenstock<sup>1</sup>

<sup>1</sup>Department of Biology, MEMEG, Lund University, 22362 Lund, Sweden, hakan.wallander@biol.lu.se.

**Abstract:** Ingrowth mesh bags are commonly used to estimate ectomycorrhizal production in forest ecosystems. A minor disturbance is caused when inserting such bags, and the bags themselves can be viewed as an empty space in the soil open to fungal colonization. In this study ingrowth mesh bags were incubated in forest soil and harvested after 1, 2, or 3 years to follow succession of fungi over time. Additional bags were harvested after one year of incubation during the same period to follow variation between years. We used three replicate plots in a Norway spruce forest in south-eastern Sweden, which were either unfertilized or fertilized with a complete fertilizer added every second year to maximize forest production. Mesh bags were also placed in trenched plots where the importance of mycorrhizal fungi was reduced. At harvest subsamples were taken for fungal biomass estimates (ergosterol) and 454-sequencing to characterize the fungal community. For comparison, soil samples were taken from the same plots. Fertilization strongly reduced the production of fungal biomass (all three years) and altered the composition of the fungal community during the third year. Sampling time was the most important factor influencing the fungal community with many yeast-like fungi (*Guheomyces*, *Cryptococcus*, *Candida*) dominated during the first year (30%), while ectomycorrhizal fungi (EMF) became more important during the second and especially the third year (80% after 3 years). The most common EMF genera were *Tylospora*, *Piloderma*, and *Amphinema*. *Piloderma olivaceum* was the most common fungus in bags from control plots during year 3 (30%), but totally absent in bags from fertilized plots. Annual variation was the most important factor shaping the fungal community in the present study, but small scale disturbances, nutrient availability and presence of tree roots were also important factors influencing the composition of fungal communities in mesh bags and soil.

#### LT 3-15 Getting to the root of species interactions: can we use plant functional traits to predict interactions with AM fungi?

WALLER, L.P.<sup>1</sup>, H. Maherali<sup>2</sup>, Y. Lekberg<sup>3,4</sup>, J.N. Klironomos<sup>5</sup>, G. Wilson<sup>6</sup> and J.L. Maron<sup>1</sup>

<sup>1</sup>Division of Biological Sciences, University of Montana, Missoula, MT 59812 USA, lauren.waller@umontana.edu;

<sup>2</sup>Department of Integrative Biology, University of Guelph, Guelph, Ontario N1G 2W1, Canada; <sup>3</sup>Department for Ecosystem and Conservation Sciences, University of Montana, Missoula, MT 59812, USA; <sup>4</sup>MPG Ranch, Missoula, MT 59801, USA;

<sup>5</sup>Biology and Physical Geography Unit, University of British Columbia-Okanagan, Kelowna, British Columbia V1V 1V7, Canada; <sup>6</sup>Department of Natural Resource Ecology and Management, Oklahoma State University, Stillwater, OK 74078, USA.

**Abstract:** Interactions between plants and arbuscular mycorrhizal (AM) fungi are largely considered to be mutualistic, although the net benefits exchanged between partners can vary widely. Plant growth responses to AM fungi span a broad continuum from strongly positive to strongly negative, and root colonization by AM fungi, which may reflect benefits offered by plants to fungi, also varies widely among plant hosts. We currently lack a clear, predictive framework for understanding what drives this variation, particularly among non N-fixing forbs. Here, we combined published mycorrhizal data from two different study systems where co-occurring plants were grown under common garden conditions (Konza Prairie Long-term Ecological Research Site and Guelph Long-term Mycorrhizal Research Site) with plant functional trait data from two global repositories (GLOPNET and TRY) to investigate whether plant traits related to resource use can explain variation in mycorrhizal benefits. We also examined whether native species differ from exotics in relationships between functional traits and AM fungal responsiveness. We hypothesize that plant species possessing leaf traits specialized for

resource conservation should benefit more from the symbiosis and have greater colonization than species possessing leaf traits specialized for resource acquisition. When accounting for phylogenetic relationships among species, LMA correlated positively with mycorrhizal responsiveness (MR) and root colonization (RC) among native species (Konza n=42, MR:  $r^2=0.28$ , RC:  $r^2=0.45$ ; Guelph n=82, MR:  $r^2=0.30$ ). Interestingly, there was no relationship between LMA and MR or RC among the exotic species in these datasets. Our results indicate that plant traits that may critically influence resource acquisition can predict how strongly plants benefit from AM fungi. Further, the fact that exotic species do not show these strong relationships suggests a strong role of evolutionary history in shaping how trait evolution influences interactions between plants and AM fungi.

**PS 4-83 Compositions of bacterial community associated with extraradical mycelia of *Funneliformis mosseae* response to phosphorus forms in the leek hyphosphere**

**WANG, F.**<sup>1</sup>, M. Kertesz<sup>2</sup>, R. Jiang<sup>1</sup>, F. Zhang<sup>1</sup> and G. Feng<sup>1</sup>

<sup>1</sup>College of Resources and Environmental Sciences, China Agricultural University, Beijing, 100193, People's Republic of China, wangfei11@cau.edu.cn; <sup>2</sup>Faculty of Agriculture and Environment, The University of Sydney, New South Wales, 2015, Australia.

**Abstract:** In our study, a compartmented cultivation system and molecular microbial ecology techniques (T-RFLP, 454 high-throughput sequencing) were employed to study the response of the bacterial community associated with the extraradical mycelia of *Funneliformis mosseae* when exposed to different forms of phosphorus in the hyphosphere of *Allium porrum*. Through the analysis of 16S T-RFLP combined with non-parametric multivariate ANOVA, it was found that the bacterial community structure in the bulk soil was significantly different from that found in the *F. mosseae* hyphosphere, independent of P application. Moreover, the different forms of phosphorus supplied in the leek hyphosphere significantly altered the composition of the bacterial community associated with *F. mosseae* extraradical mycelia. The predominant phyla in those communities were Firmicutes and Cyanobacteria, as determined by 454 sequencing. Inorganic P treatment increased the relative abundance of Firmicutes compared to the no added P and organic P treatments. However, the relative abundance of Cyanobacteria was increased after organic P supplementation compared to the no added P and inorganic P treatments. The results indicate that the forms of phosphorus change the composition of the bacterial community in the hyphosphere by influencing hyphal growth of *F. mosseae* and the quantity of hyphal exudates.

**PS 1-67 Role of mycorrhizal symbiosis in aluminum and phosphorus interactions in relation to aluminum tolerance in soybean**

Zhang, S.<sup>1</sup>, J. Zhou<sup>1</sup>, G. Wang<sup>1</sup>, **X. WANG**<sup>1</sup> and H. Liao<sup>1</sup>

<sup>1</sup>State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, Root Biology Center, South China Agricultural University, Guangzhou 510642, China, xrwang@scau.edu.cn.

**Abstract:** Arbuscular mycorrhizal (AM) symbiosis contributes to phosphorus (P) acquisition and protects plants against aluminum (Al) toxicity. Understanding the possible mechanisms of Al and P interactions in relation to Al tolerance of mycorrhizal soybean should help facilitate the positive effects of AM fungal inoculants in the field. In this study, a number of Al and P treatments were applied to soybean plants cultivated in the presence or absence of four different AM fungi. The results showed that plants in symbiotic association with *Gigaspora margarita* and *Glomus etunicatum* displayed enhanced tolerance to high Al. The effectiveness of *G. margarita* appeared to be associated with more abundant arbuscules and intraradical hyphae compared to low Al controls. Similarly, the effects of *G. etunicatum* were associated with more abundant vesicles and intraradical hyphae. The highest levels of Al toxicity mitigation were observed with the combination of high P availability and AM fungal inoculation, which was associated with a concomitant increase in the expression of the AM inducible phosphate (Pi) transporter gene *GmPT9*. Taken together, these results suggest that AM symbiosis can alleviate Al toxicity in soybean through enhanced P nutrition, as well as the alteration of the abundance of mycorrhizal structures. These findings highlight the importance of P nutrition status in ameliorating Al toxicity in mycorrhizal plants.

### SY 3-6 Local and distal effects of arbuscular mycorrhizal colonisation on direct pathway Pi uptake and root growth in *Medicago truncatula*

WATTS-WILLIAMS, S.J.<sup>1,2</sup>, I. Jakobsen<sup>2</sup>, T.R. Cavagnaro<sup>3</sup> and M. Grønlund<sup>2</sup>

<sup>1</sup>Boyce Thompson Institute for Plant Research, Tower Rd, Ithaca, NY 14853, USA, sjw266@cornell.edu; <sup>2</sup>Department of Chemical and Biochemical Engineering, Technical University of Denmark, 2800 Kgs. Lyngby, Denmark. Current address: Department of Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, DK-1871 Frederiksberg C, Denmark; <sup>3</sup>School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, Glen Osmond, SA, Australia.

**Abstract:** Two pathways exist for plant Pi uptake from soil: via root epidermal cells (direct pathway of uptake) or via associations with arbuscular mycorrhizal (AM) fungi (mycorrhizal pathway of uptake), and the two pathways interact in a complex manner. This study investigated distal and local effects of AM colonisation on direct root Pi uptake, root growth, and expression of direct and mycorrhiza-induced phosphate transporter-encoding genes at three different soil P levels. *Medicago truncatula* was grown in split-root pots with one, both, or none of the root-halves inoculated with AM fungi, and where one root half grew into soil labelled with <sup>33</sup>P. Plant genotypes included the A17 wild-type and the MtPT4 mutant, which is defective in the mycorrhiza-induced phosphate transporter gene, MtPT4. The MtPT4 mutant plants, which can be colonised by AM fungi but have no functional mycorrhizal pathway for Pi uptake, were included to better understand effects of AM colonisation. Colonisation of the roots by AM fungi decreased expression of direct Pi transporter genes locally, but not distally. In MtPT4 mutant plants, direct Pi transporter genes and the Pi starvation-induced gene *Mt4* were more highly expressed than in wild-type roots. In wild-type plants, less Pi was taken up via the direct pathway by non-colonised roots when the other root half was colonised by AM fungi, compared to non-mycorrhizal plants. Furthermore, root growth in terms of length and biomass, was influenced by AM fungal inoculation status of the plant and by genotype. Colonisation by AM fungi clearly influenced root growth both locally and distally and, to some extent, also influenced direct root Pi uptake activity. The responses to AM colonisation in the MtPT4 mutant suggest that increased P concentration of colonised roots is a major factor driving the effects of AM colonisation on direct root Pi uptake.

### CS 2-6 Common mycorrhizal networks amplify competition through preferential <sup>15</sup>N allocation to large host plants

WEREMIJEWICZ, J.<sup>1</sup>, L. Sternberg<sup>1</sup> and D.P. Janos<sup>1</sup>

<sup>1</sup>Department of Biology, University of Miami, Coral Gables, FL 33124, jweremi@gmail.com.

**Abstract:** Common mycorrhizal networks (CMNs) involving arbuscular mycorrhizal fungi may interconnect and simultaneously distribute mineral nutrients among many neighboring plants. Recent root organ culture work has suggested that CMNs preferentially allocate mineral nutrients such as N and P to those roots that supply the fungi with the most carbon. We tested this hypothesis in a pot experiment with whole *Andropogon gerardii* plants and a suite of field-collected mycorrhizal fungi. We surrounded target individuals with neighbors to whom we provided <sup>15</sup>N while CMNs were kept intact, severed, or not allowed to form. To differentiate plant size *per se* from potential carbon provision to AM fungi, we shaded half of the target plants. We found that target plant dry weight was negatively associated with total neighbor dry weight only when CMNs were intact, demonstrating that CMNs mediated competition between the target and neighbor plants. When CMNs were intact, target plants, on average, were larger and their leaves contained more <sup>15</sup>N than plants with severed CMNs or no CMNs. Moreover, with intact CMNs, the foliar <sup>15</sup>N content of target plants was positively associated with dry weight. Shading target plants precluded the aforementioned significant relationships. Thus, CMNs conferred a competitive advantage to well-insolated, large plants and diminished the growth of small plants by preferentially supplying <sup>15</sup>N to large, networked target plants. These “reciprocal rewards” amplified plant competition and thereby may potentially influence plant community composition.

WHITHAM, T.G.<sup>1,2</sup>

<sup>1</sup>Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, Arizona 86011 USA;

<sup>2</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, Arizona 86011 USA, Thomas.Whitham@nau.edu.

**Abstract.** Large collaborative efforts are needed to understand the principles that produce Darwin's "entangled bank" of complex communities and to mitigate global change. Based on the collaborations of a large group of faculty, students, land managers, and agencies, our interdisciplinary group has explored the genetic basis of community structure and ecosystem processes, which in turn has important consequences for land managers trying to mitigate the impacts of global change. Six key findings have emerged. 1) Different tree genotypes support different communities of soil microbes, mycorrhizae, arthropods, vertebrates, understory plants, lichens, and pathogens. 2) Genetics-based differences in community structure and ecosystem processes represent heritable plant traits. 3) While these findings are common to most ecosystems studied so far, their impacts seem to be greatest on foundation species that largely define their respective ecosystems. 4) Feedbacks of community members on foundation species are likely a major driving factor in community evolution. 5) Because different plant populations and individual genotypes vary predictably in the communities they support, and in their responses to climate change ( $G \times E_{\text{abiotic environment}}$ ) and invasive species ( $G \times E_{\text{biotic environment}}$ ), genetics-based approaches can provide important solutions to help mitigate global change impacts on wildlands. 6) An experimental tool to develop these genetic approaches is the Southwest Experimental Garden Array (SEGA; <http://www.sega.nau.edu>). This facility is an array of replicated common gardens/experimental forests distributed along elevation, latitude, soil and other gradients to quantify gene x environment interactions. Findings from the array allow scientists and land managers to identify specific plant genotypes, populations and key genetics-based interactions (e.g., mycorrhizae/plant) that can be deployed at restoration sites or used in assisted migration to help meet conservation goals in future climates. I describe how land managers in federal, state and private agencies are participating and utilizing these findings in land management.

### LT 2-13 Mycorrhizal characteristics of a rare endemic in a hyper-arid, cryic environment

WILLIAMS, S.E.<sup>1</sup> and B. Heide<sup>1</sup>

<sup>1</sup>Department of Ecosystem Science and Management, University of Wyoming, Laramie 82071, sewms@uwyo.edu.

**Abstract:** Desert yellowhead (*Yermo xanthocephalus*) is a threatened Asteraceae found in a small population (~10,000 individuals) on Cedar Rim (elevation 2,100 m) in central Wyoming. It has very high conservation priority and is ranked as critically imperiled. Desert yellowhead occupies sparsely populated cushion plant communities on rim margins, colluvial fans, and deflation hollows. These plants are found on embryonic soils (silty sand) of low organic carbon (<0.4%), available P (<2 µg/g), and soluble salts (<2 mS/m) but high pH (8.0). The aboveground plant parts are up to 25 cm tall and have taproots that extend down to 50 cm. Annual precipitation is <200 mm/yr (covariance of 70%) with <90 frost-free days per year. A preliminary study of mycorrhizal associations of this plant entailed removing fine roots from herbarium specimens (Rocky Mountain Herbarium). Rehydration, followed by clearing, staining, and light microscopy revealed root fungi with vesicles. A permit from the US Fish and Wildlife Service allowed for the non-destructive excavation and collection of field roots. Processing (as above) revealed considerable but highly variable presence of root fungi with arbuscular regions and vesicles. Hyphae were characteristic of arbuscular mycorrhizal (AM) fungi (aseptate, variable diameter of 5-10 µm, and knobby). Sieving and sucrose flotation showed no soil-borne spores, although adjacent sites (*Artemisia tridentata*) were spore positive. In the roots, however, were thick-walled objects of 60 µm diameter, likely chlamydospores. *Yermo xanthocephalus* is a perennial and dies back to the taproot with regrowth along established root channels. Competition with other biota is low in this environment, which is dominated by abiotic factors. Basic knowledge of AM associations suggests these fungi are key in the survival of this plant in this extreme environment.

### PS 3-75 Genotypic variation among switchgrass cultivars influences mycorrhizal responsiveness

WILSON, G.W.T.<sup>1</sup>, R.M. Miller<sup>2</sup>, Y. Wu<sup>1</sup> and K. Haase<sup>1</sup>

<sup>1</sup>Department of Natural Resource Ecology and Management, Oklahoma State University, Oklahoma, 74078 USA, gail.wilson@okstate.edu; <sup>2</sup>Argonne National Laboratory, Biosciences Division, Argonne, Illinois, 60439, USA.

**Abstract:** Switchgrass (*Panicum virgatum* L.) is a native perennial that shows great promise as a low input biofuel crop. Plant breeders have made progress in selecting for traits that improve its biomass yields, yet the belowground components of this plant are not well understood. Our research extends belowground and assesses switchgrass interactions with mycorrhizal fungi, an important soil microbial group that forms a symbiotic association with most grasses. Although switchgrass is known to be strongly associated with mycorrhizal relationships and these symbioses may increase switchgrass production by increasing nutrient and water uptake, little is known about how genotypic variation among switchgrass cultivars influence mycorrhizal responsiveness. Genetic inheritance and resultant genotypic differences can influence morphology of grass roots, the amount of AM fungi they support, and subsequent production of hyphae in the soil. We find evidence of a strong genetic component for relative mycorrhizal responsiveness ( $rMR = (M_{myco} - M_{nonmyco})/M_{nonmyco}$ ), where  $M$  is total dry mass) in switchgrass populations. Within populations,  $rMR$  is directly related to whether ecotypes were derived from upland or lowland populations, with upland populations expressing a significantly higher  $rMR$  than lowland populations. We also find  $rMR$  maps at a continental scale in a manner similar to the distributions of upland and lowland populations, with highest levels of  $rMR$  being found in the Central Great Plains. Principal coordinate analysis supports the population differences between upland and lowland populations, but also suggest that the lowland populations can be separated into coastal and interior populations based on response to mycorrhizae. Evidence is presented that, through selective breeding,  $rMR$  can be increased in lowland populations to levels usually associated with upland populations. These findings indicate that it is possible to genetically improve a sustainability trait like  $rMR$  in switchgrass.

### PS 3-10 Uptake, translocation, and transformation of chromium by arbuscular mycorrhizal fungi

WU, S.<sup>1,2</sup>, X. Zhang<sup>1</sup> and B. Chen<sup>1</sup>

<sup>1</sup>State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, 100085, People's Republic of China, pine12072006@163.com; <sup>2</sup>University of Chinese Academy of Sciences, Beijing, 100049, People's Republic of China.

**Abstract:** As ubiquitous soil fungi that form symbioses with the majority of terrestrial plants, arbuscular mycorrhizal fungi (AMF) play an important role in plant Cr(VI) resistance. However, the underlying mechanisms, especially the direct influence of AMF on translocation and transformation of Cr(VI) in the soil-plant continuum, are still unresolved. In the present study, we use a three-compartment cultivation system to demonstrate that extraradical mycelium (ERM) could take up and transport Cr to mycorrhizal roots but reduce Cr translocation to shoots. In order to further explore the translocation and deeper biotransformation of Cr(VI) by AMF, we also used a two-compartment root-organ cultivation system coupled with X-ray absorption near-edge spectroscopy (XANES) technology. The results indicate that ERM can actively take up and transport Cr(VI) to plants but retain most of Cr in fungal biomass. XANES of Cr(VI)-treated living or deactivated ERM showed that Cr(VI) in ERM was completely reduced to Cr(III) and subsequently combined with phosphate analogues, probably on the fungal surface, and the living AM fungi can possibly produce histidine analogues to bind Cr(III). Our findings have not only for the first time provided strong evidence of Cr immobilization by ERM *in vitro* without interference from undesirable organisms other than the symbionts, but also elucidated how AMF tolerate Cr(VI) using newly advanced technologies like XANES.



**WU, Z.X.**<sup>1,2</sup>, Z.P. Hao<sup>1</sup> and B.D. Chen<sup>1</sup>

<sup>1</sup>State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China, wuzhaoxiang2004@126.com; <sup>2</sup>University of China Academy of Sciences, Beijing 100049, China.

**Abstract:** Mycorrhizal technology is a green biological technology with wide prospects for application in the cultivation of medicinal plants. An indoor simulation experiment was carried out to study the process and characteristics of arbuscular mycorrhizal (AM) fungal infection and the changes to the growth, nutrient status, and photosynthesis of *Panax notoginseng*. 90 days after inoculation, root samples were preprocessed and observed through microscopic examination. Plant growth indexes, concentration of mineral elements, and leaf chlorophyll fluorescence were measured and compared between the AM inoculation and control treatments. Through a series of steps, including the establishment of an entry point, extension of hyphae, formation of arbuscules, and the generation of spores, AM fungi successfully infected the roots of *P. notoginseng* and mycorrhizal symbiosis was established. AM fungal inoculation improved plant P concentration and enhanced chlorophyll fluorescence significantly, but did not improve the biomass, height, nor root system. AM fungi effectively promoted P absorption in *P. notoginseng* and leaf photosynthesis, improving the quality of *P. notoginseng* seedlings.

LT 2-9 **Co-occurrence network patterns of *Medicago sativa* rhizosphere microbiomes under soil nutrient pressure: cooperation or competition among symbiotic fungi and bacteria?**

Lentendu, G.<sup>1</sup>, J. Schmidt<sup>1</sup>, E. Schulz<sup>1</sup>, F. Buscot<sup>1,2</sup> and **T. WUBET**<sup>1,2</sup>

<sup>1</sup>UFZ-Helmholtz Centre for Environmental Research, Department of Soil Ecology, Theodor-Lieser-Str. 4, D-06120 Halle (Saale), Germany, tesfaye.wubet@ufz.de; <sup>2</sup>German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Deutscher Platz 5e, D-04103 Leipzig, Germany.

**Abstract:** Symbiotic microorganisms are well known for their role in improving plant nutrient uptake in agro-ecosystems through their impact on nutrient availability and transportation. However, the factors governing root symbiotic microbial community assemblages, their response to increased nutrient availability through fertilization, and the co-occurrence network patterns of arbuscular mycorrhizal fungi (AMF; Glomeromycota) and symbiotic bacteria (rhizobia; Rhizobiales and *Burkholderia*) are not well known. Therefore, we studied the diversity of AMF and rhizobia using high-throughput pyrotag sequencing of the fungal and bacterial SSU rRNA genes from the rhizosphere soils of *Medicago sativa* (alfalfa) grown under different management practices in a long-term static fertilization experiment located in Bad Lauchstädt, Germany. Unlike rhizobia, we found a significant decline both in the diversity and relative abundance of AMF with increasing farmyard manure (FYM) and mineral (NPK) fertilization suggesting a loss of mycorrhization due to increased nutrient availability for the plant. The relative abundance of rhizobial OTUs was strongly correlated with C:N ratio ( $p < 0.01$ ) and pH ( $p < 0.001$ ), while AMF showed significant correlation with ammonium ( $p < 0.05$ ), nitrate ( $p < 0.01$ ), total organic carbon ( $p < 0.001$ ), and total nitrogen ( $p < 0.001$ ). A co-occurrence network analysis revealed that AMF OTUs co-occurred more often than expected by chance with other AMF OTUs, which could be explained by their overlapping niche space. In contrast, rhizobial OTUs displayed a trend of lower co-occurrence with AMF OTUs compared to what was observed in randomized networks indicating certain avoidance between AMF and rhizobia. However, no significant exclusion patterns were detected for both AMF and rhizobia refuting the hypothesis of direct competition between and/or among their respective mycorrhizal fungal and rhizobial taxa.

**PS 2-15 A population genomics approach reveals variable levels of heterokaryosis in the arbuscular mycorrhizal fungus *Rhizophagus irregularis***

**WYSS, T.**<sup>1</sup>, F.G. Masclaux<sup>1,2</sup>, P. Rosikiewicz<sup>1</sup>, M. Pagni<sup>2</sup> and I.R. Sanders<sup>1</sup>

<sup>1</sup>Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland, tanja\_wyss@hotmail.com;

<sup>2</sup>Vital-IT Group, Swiss Institute of Bioinformatics, 1015 Lausanne, Switzerland.

**Abstract:** In natural populations, genetic diversity among isolates of arbuscular mycorrhizal fungi (AMF) can be high and structured, with diverse effects on plant growth. Genetic diversity within isolates of AMF, however, is poorly characterized, despite its potentially important consequences on plant growth and communities. The genome of the model AMF *Rhizophagus irregularis* (isolate DAOM197198) exhibits low polymorphism, suggesting that the nuclei in this fungus are the same. Paradoxically, experiments with other *R. irregularis* isolates suggest a population of genetically divergent nuclei. We investigated whether there is evidence for the maintenance of heterokaryosis in *R. irregularis* populations. We genotyped 19 isolates of *R. irregularis* coming from a Swiss population using restriction site-associated DNA sequencing. We developed novel approaches for characterizing polymorphism among haploid nuclei. We observed variable levels of within-isolate SNP densities among isolates, but all isolates had SNP densities higher than in DAOM197198. Some isolates had SNP densities as high as other diploid organisms, but the distribution of allele frequencies within isolates deviated from diploids or tetraploids, indicating a population of diverse nuclei. In addition, we found that SNP densities were similar in non-coding and in coding regions. Because within-fungus genetic diversity in *R. irregularis* is known to lead to large differences in plant growth, characterizing genomic variation within AMF populations where it occurs and how it is maintained is of major ecological importance.

**PS 4-55 Genetic Populations Structure of the fungus *Floccularia luteo-virens* in Qinghai-Tibet Plateau region revealed by SSR markers**

**XIE, Z.**<sup>1</sup>, Y. Li<sup>1</sup>, F. Tian<sup>1</sup>, X. Zhang<sup>1</sup> and J. Zhang<sup>1</sup>

<sup>1</sup>State Key Laboratory Breeding Base-Key Laboratory of Qinghai Province for Plateau Crop Germplasm Innovation and Utilization, Department of Biological Sciences, Qinghai University, 810016 China, xiezhanling2012@126.com.

**Abstract:** *Floccularia luteo-virens* is endemic, ecologically important, and famously delicious mushroom distributed in Qinghai-Tibet Plateau (QTP), western China. Recent over collection because of direct economic benefits has caused a decline in population size of the species. Therefore, we expected to find population structure and differentiation in QTP, an area encompassing 2,572.4×10<sup>3</sup> km<sup>2</sup>. A total of 220 individuals of *F. luteo-virens* from 22 differently populations were analyzed using simple sequence repeat (SSR) markers. UPGMA dendrogram of 22 *F. luteo-virens* based on the Nei's genetic distance and microsatellites data analyses revealed QTP genetic structure with three geographic genetically defined demes: the south deme of QTP included 6 populations of Xizang, 1 population of Sichuan, and 4 populations of Qinghai; while the middle deme included 5 populations of the south part of Qinghai, and the north deme included 3 populations of Qilian area north part of Qinghai and 3 populations from middle of Qinghai. 22 populations from QTP showed evidence of 3 geographic populations. Analysis of molecular variance (AMOVA) results indicated that there was significant difference differentiation among groups ( $\Phi_{CT}=0.1924$ ,  $Pb0.01$ ), among populations within group ( $\Phi_{SC}=0.1277$ ,  $Pb0.01$ ), and great significant genetic differentiations within population ( $\Phi_{ST}=0.4319$ ,  $Pb0.01$ ). In addition, UPGMA dendrogram cluster of 22 *F. luteo-virens* populations based on the Nei's genetic distance and microsatellites data supported the grouping of the population into 3 groups. The proportion of the genetic variation contained by genetic group was 70.15%, 19.24%, and 10.31%, respectively. Genetic relationships among the 22 *F. luteo-virens* populations estimated using structure showed the model with  $K=3$  showed, the highest  $\Delta K$  value. The present genetic structure of *F. luteo-virens* may be limited genetic flow hindered by complex terrains. Tanggula Mountain is the most likely barrier to genetic flow from the north. Its life-history traits, unique biological traits, geological separation, and anthropogenic disturbance may also prevent movement of the north population and the middle populations. These discoveries will shed light on the effects of historical and ongoing population genetic structure and diversity of *F. luteo-virens*, and also provide the foundation for other geographic biology QTP.

PS 4-56 **Species diversity and ecological distribution of arbuscular mycorrhizal fungi of *Hedysarum leave* in Saibei desert steppe**

XU, W.<sup>1</sup>, J. Zhang<sup>1</sup>, J. Yan<sup>1</sup>, L. Zhao<sup>1</sup> and X. He<sup>1</sup>

<sup>1</sup>College of Life Sciences, Hebei University, Baoding 071002, P.R.China, xuweihehaobo1234@163.com.

**Abstract:** To understand the ecological significance of arbuscular mycorrhizal (AM) associations in semi-arid and arid lands, tempo-spatial dynamics of AM fungi were surveyed in Saibei desert steppe, northern China. According to the growth characteristics of *Hedysarum leave* (cloning plant), six surveyed couples of 1 m<sup>2</sup> plots were designed along the extension direction of the rhizomes of *H. leave* in June 2013. The distance between any couple of plots was at least 200 m. Soil and root samples in the rhizosphere of *H. leave* were collected in June, August and October 2013 and 2014, respectively. Three genera and 17 species were isolated from the rhizosphere of *H. laeve*, 9 species belonged to *Glomus*, 7 species belonged to *Acaulospora*, and 1 species belonged to *Funneliformis*. Species richness, Shannon Wiener index, and evenness of AM fungi were significantly lower in June than in August and October. Species diversity and colonization of AM fungi had temporal and spatial heterogeneity. Clonal growth of *H. laeve* had a significant effect on AM fungal colonization and distribution. Correlation analysis showed that spore density exhibited positive correlation with soil temperature and available N ( $P < 0.01$ ). Vesicular colonization was negatively correlated with soil acid and alkaline phosphatase ( $P < 0.01$ ). Total colonization was positively correlated with soil urease ( $P < 0.05$ ). Principal component analysis showed that soil available P, available K, organic C, urease, pH were the main factors affecting AM fungi. The clonal growth of *H. leave* significantly increased the content of soil available nutrition, such as available N and P, which became more suitable for the growth of AM fungi and clonal plants.

PS 1-33 **Diverse lineages of Mucoromycotina and Glomeromycota that colonize in the subterranean axes of the Asian liverwort, *Haplomitrium mnioides* from Japan**

YAMAMOTO, K.<sup>1</sup>, Y. Degawa<sup>2</sup> and A. Yamada<sup>1</sup>

<sup>1</sup>Department of Bioscience and Food Production Science, Interdisciplinary Graduate School of Science and Technology, Shinshu University, Minami-minowa, Nagano 399-4598, Japan, kohei081@yahoo.co.jp; <sup>2</sup>Sugadaira Montane Research Center, University of Tsukuba, 1278-294 Sugadaira kogen, Ueda, Nagano 386-2204 Japan.

**Abstract:** It is widely accepted that the early plant colonization of the terrestrial environment from the hydrosphere was promoted by mycorrhizal symbioses with fungi in the Glomeromycota. On the other hand, Bidartondo and colleagues have revealed that many extant species in the basal lineage of liverworts, i.e., Haplomitriopsida, associate with endophytes phylogenetically included in the mucoromycotinan order Endogonales and its relatives rather than Glomeromycota. These data develop a hypothesis that the symbiont of the earliest land plants is not in Glomeromycota but in Mucoromycotina. However, their data mostly depend on Haplomitriopsida species sampled from Oceanian region, and its Asian species was scarcely included. We collected about 5 cm square of *Haplomitrium mnioides* colonies at Kyoto (Kyoto City) and Tokyo (Hachijo-jima Isl.), Japan. At first, subterranean axes (3-5 mm length) that were colonized by fungal endophytes were longitudinally fragmented. One of the fragments was stained with trypan blue and microscopic observations were conducted. Fungal DNA was extracted from remaining fragments, and PCR amplifications were performed with Mucoromycotina- or Glomeromycota-specific primers on nSSU region. Phylogenetic analyses were subsequently conducted. Glomeromycotan (arbuscules and/or vesicles) and/or mucoromycotinan (hyphal coils and swellings) structures were detected in the most axes. Phylogenetic analyses indicated at least three lineages of Glomeromycota (two in Glomeraceae and one in Archaeosporales) and three lineages of Mucoromycotina (one in *Endogone* and two in *Sphaerocreas-Densospora* group) in subterranean axes of *H. mnioides*. In particular, dual colonization of mucoromycotinan and glomeromycotan symbionts in a liverwort individual was confirmed by both morphological observations and molecular identifications for the first time. It is suggested that Haplomitriopsida liverworts associate with more diverse fungal symbionts than expected.

ZARUBINA, N.<sup>1</sup>

<sup>1</sup>Institute for Nuclear Research of National Academy of Science of Ukraine, 47 Prospekt Nauky, Kyiv, Ukraine, 03680, nataliia.zarubina@gmail.com.

**Abstract:** Mycorrhizal fungi are the maximum accumulators of  $^{137}\text{Cs}$  within forest ecosystems after radiation accidents. Changes in the  $^{137}\text{Cs}$  content of mycorrhizal fungal fruiting bodies during the vegetation season in the Kiev region, the exclusion zone of Chernobyl NPP after the accident in 1986, and the influence of precipitation quantity on those changes have been studied. *Cantharellus cibarius* and *Russula delica* were chosen as the study organisms. During the vegetation season (summer – fall), the maximum values of  $^{137}\text{Cs}$  have been detected in the middle of October followed by a decrease in the specific activity of this radionuclide until December. There are published data about annual intensive growth of fungal mycelium in the fall, which is not connected to year-to-year weather conditions (precipitation quantity). The intensive mycelium growth in soil results in enhanced absorption of water and microelements (e.g.,  $^{137}\text{Cs}$ ), which in turn, could be a reason for  $^{137}\text{Cs}$  radionuclide specific activity level increase in fruiting bodies (up to 10 times), particularly in the middle of the fall. Linear correlations between the quantity of precipitation (2 months, 1 month, 2 weeks, 1 week, 5 days, 3 days, 2 days, and 1 day) and  $^{137}\text{Cs}$  specific activity in *C. cibarius* and *R. delica* during the vegetation period were conducted. The maximum correlation coefficient is 0.64 for the Stayky testing area. A correlation is considered reliable when the linear correlation coefficients are greater than  $|0.75|$ . Basing on the performed correlation coefficient calculations, it could be stated that the amount of precipitation does not directly influence  $^{137}\text{Cs}$  specific activity levels in the fungal fruiting bodies. The amount of precipitation influences the availability of  $^{137}\text{Cs}$  for fungi considerably less than the physiological changes occurring in a fungus body.

PS 1-34 Diversity of dark septate endophytes of clonal plants in Saibei desert

ZHANG, J.<sup>1</sup>, J. Yan<sup>1</sup>, L. Zhao<sup>1</sup> and X. He<sup>1</sup>

<sup>1</sup>College of Life Sciences, Hebei University, Baoding 071002, P.R.China, zhang\_juan87@163.com.

**Abstract:** To elucidate the symbiotic relationship between the dark septate endophytes (DSE) and clonal plants, roots samples were collected under three clonal plant species (*Hedysarum laeve*, *Psammochloa villosa*, *Artemisia ordosica*) in Inner Mongolia, north China in June 2013. The DSE from the three clonal plants were isolated and analyzed using morphological traits and molecular identification. The results indicated that the three clonal plants could be infected by DSE and form typical symbiotic structures, such as septate hyphae, microsclerotia and vesicles. The morphology of DSE differed in the different clonal plants. The colors of hyphae, microsclerotia and vesicle of *P. villosa* were lighter than that of *H. laeve* and *A. ordosica*. The microsclerotia and vesicle of *A. ordosica* were densely distributed. The length of every hyphal septate of *A. ordosica* was shorter than that of *H. laeve* and *P. villosa*. Guerilla clonal plants, such as *H. laeve* and *P. villosa* could invade into the blank spaces. The number of invaded community of *P. villosa* was higher than that of *H. laeve*. The invasion of clonal plants greatly affected DSE colonization, although such effects varied between different clonal plants. DSE colonization in roots of *H. laeve* community declined gradually with the sampling time. In contrast, DSE colonization of *P. villosa* increased with the sampling time. Seven DSE isolates have been obtained from the roots of three clonal plants: *Alternaria arborescens*, *Pleosporales* sp., *Thielaviopsis basicola*, *Paraphoma chrysanthemicola*, *Leptosphaeria* sp., *Phoma radicina*, and *Paraphoma radicina*. *Hedysarum laeve* and *P. villosa* had two common species of DSE. *Psammochloa villosa* and *A. ordosica* had one common species of DSE. This research provides a basis and references for further clarifying the ecological functions of DSE and making full use of DSE to promote vegetation restoration and soil conservation in arid areas.

## PS 4-84 Stocks of glomalin-related soil protein and its potential influences on soil organic carbon sequestration in subtropical forests in China

ZHANG, J.<sup>1,2</sup> and X. Tang<sup>1</sup>

<sup>1</sup>Key Laboratory of Vegetation Restoration and Management of Degraded Ecosystems, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, China, zhangj@scib.ac.cn; <sup>2</sup>University of Chinese Academy of Sciences, Beijing 100049, China.

**Abstract:** Glomalin-related soil protein (GRSP) is a recalcitrant glycoprotein produced by arbuscular mycorrhizal fungi (AMF) that has been repeatedly demonstrated to improve soil structure and to be a substantial contributor to soil carbon. To better understand the potential influence of GRSP on soil C storage, we examined GRSP concentrations in three typical subtropical forests in southern China and under environmental change scenarios such as elevated CO<sub>2</sub>, N addition, and acid rain. Our results show that the mean content of total GRSP (TG) in the top 10 cm of soil is 394.71±108.90 g m<sup>-2</sup>, which accounted for 3.16±0.45% to 4.70±0.78% of the soil organic carbon (SOC) in natural forests. TG is more easily contributed to recalcitrant carbon accumulation because TG has higher aromatic (20.6-30.0%) and alkyl (27.7-38.3%) carbon than SOC (aromatic (2.3-8.7%) and alkyl (22.7-35.3%) carbon). Additionally, we detected a response of GRSP to elevated CO<sub>2</sub> and N addition. The results indicate that elevated CO<sub>2</sub> significantly increased TG by 35.02%, but decreased easily extractable GRSP (EEG) by 5.09% in the top 10 cm of the soil layer. There was a 1.72%-48.49% increase in TG and a slight increase in EEG under N addition, and the marginal increase of T-GRSP indicated that the interaction between elevated CO<sub>2</sub> and N addition offset their independent effects. The response of GRSP to simulated acid rain was also investigated, and acid rain promoted TG concentration and may potentially contribute to SOC sequestration to some degree. Our results indicate that GRSP could be an indicator of SOC change in the long run. Additionally, our study improves the understanding of the functioning of GRSP in soil C sequestration from a C functional group perspective in natural forests and under global environmental change scenarios.

## PS 1-70 Study of the tolerance mechanisms of arbuscular mycorrhizal symbionts under heavy metal contamination

ZHANG, X.<sup>1</sup>, B.D. Chen<sup>1</sup>, S.L. Wu<sup>1</sup>, B.H. Ren<sup>1</sup> and Y.Q. Sun<sup>1</sup>

<sup>1</sup>State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, 100085 P.R. China, xinzhang@rcees.ac.cn.

**Abstract:** Arbuscular mycorrhizal fungi (AMF) can adapt to heavy metal (HM)-contaminated soils and form symbiotic associations with higher plants. Obviously, for potential use of AMF in the alleviation of HM phytotoxicity and remediation of HM contaminated soils, it is important to uncover the mechanisms of HM metabolism and detoxification in mycorrhizal symbionts. We have focused on three HM elements (chromium (Cr), cadmium (Cd), and arsenic (As)) to study the HM transport, distribution, and transformation process in mycorrhiza. Cr uptake by extraradical mycelium (ERM) was investigated utilizing a compartmented cultivation system and using a stable Cr isotope tracer. Our work provides possible evidence of Cr uptake and transport by ERM, and also indicates an enrichment of lighter Cr isotopes in shoots during Cr translocation from roots to shoots in mycorrhizal plants. *In situ* Cd distribution in mycorrhizae was also investigated by synchrotron radiation  $\mu$  X-ray fluorescence (SR- $\mu$ -XRF), indicating that arbuscules accumulated the largest amount of Cd followed by hyphae, then vesicles. Transformation was also investigated in mycorrhizal plants by HPLC-ICP-MS. Mycorrhizal inoculation generally increased the percent of arsenite in total As, and dimethylarsenic (DMA) was detected only in the shoots of mycorrhizal plants, indicating that AMF are most likely involved in the reduction of arsenate to arsenite and in the methylating of inorganic As into the less toxic organic DMA. Our investigations provide deeper insights into the mechanisms of HM uptake, distribution, and transformation in mycorrhizal symbionts and promote the potential use of AMF in bioremediation of HM contaminated environments.



**ZITLALPOPOCA, G.<sup>1</sup>**, M.B. Nájera-Rincón<sup>2</sup>, E. del Val de Gortari<sup>1</sup>, A. Alarcón<sup>3</sup>, T. Jackson<sup>4</sup> and J. Larsen<sup>1</sup>

<sup>1</sup>Research Institute of Ecosystems and Sustainability, National Autonomus University of Mexico, Morelia 58190 Mexico, zitlalh@live.com.mx; <sup>2</sup>National Institute of Forestry, Agriculture and Livestock Research (INIFAP) Uruapan, Michoacan 60150 Mexico; <sup>3</sup>Post graduate College, Texcoco, Mexico State 56230 Mexico; <sup>4</sup>AgResearch, Christchurch 8140, New Zealand.

**Abstract:** Multitrophic interactions between natural communities of arbuscular mycorrhizal fungi (AMF), an entomopathogenic fungus (*Beauveria bassiana*), and a root-feeding insect (*Phyllophaga vetulai*) were studied in a greenhouse pot experiment with a randomized factorial design. The main factors studied included, 1) AMF (with or without), 2) *B. bassiana* (with or without), and 3) *P. vetula* (with or without). Each of the eight treatments had five replicates resulting in a total of 40 experimental units. Plants were grown in a low P sterilized soil from a maize field mixed with sand (1:1, w/w). All plants were fully fertilized except for P, and plants were watered to 80% of field capacity by weight on a daily basis. Three weeks after sowing, two larvae of *P. vetula* were applied to each pot according to the respective treatments. Plants were grown for seven weeks, and, at harvest, the following variables were recorded: shoot and root dry weight, N and P content in shoot and root, population density of *B. bassiana*, AMF root colonization, and biomass of *P. vetula* larvae. Root herbivory by *P. vetula* reduced plant growth and nutrition and reduced AMF root colonization. In contrast, AMF improved plant growth and P nutrition but also reduced the population density of *B. bassiana*. Inoculation with *B. bassiana* caused less than 5% mortality of *P. vetula* larvae and, interestingly, increased biomass of *P. vetula*, which coincided with increased root dry weight and AMF root colonization. On the other hand, inoculation with AMF markedly decreased the soil population density of *B. bassiana*. Dual inoculation with AMF and *B. bassiana* induced plant tolerance to the damage caused by *P. vetula* herbivory. In conclusion, our results emphasize the importance of considering multitrophic plant-microbe-insect interactions when developing biocontrol strategies against root feeding insects.

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