



Absence of Genetic Relatedness within Maternity Colonies of Big Brown Bats in Flagstaff: Implications for Rabies Transmission

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Background

The big brown bat (*Eptesicus fuscus*) is one of the most common bats in northern Arizona. These bats are generalists and use a variety of sites as roosts, including human structures. In Flagstaff, big brown bats act as a vector for a strain of rabies that has jumped to other species. In the past decade there have been three outbreaks of rabies, which has important implications to human health.

Objectives

- To estimate genetic relatedness among individuals of maternity roosts in order to infer whether females select roosts based on kinship.
- To use findings to understand spatial disease transmission.

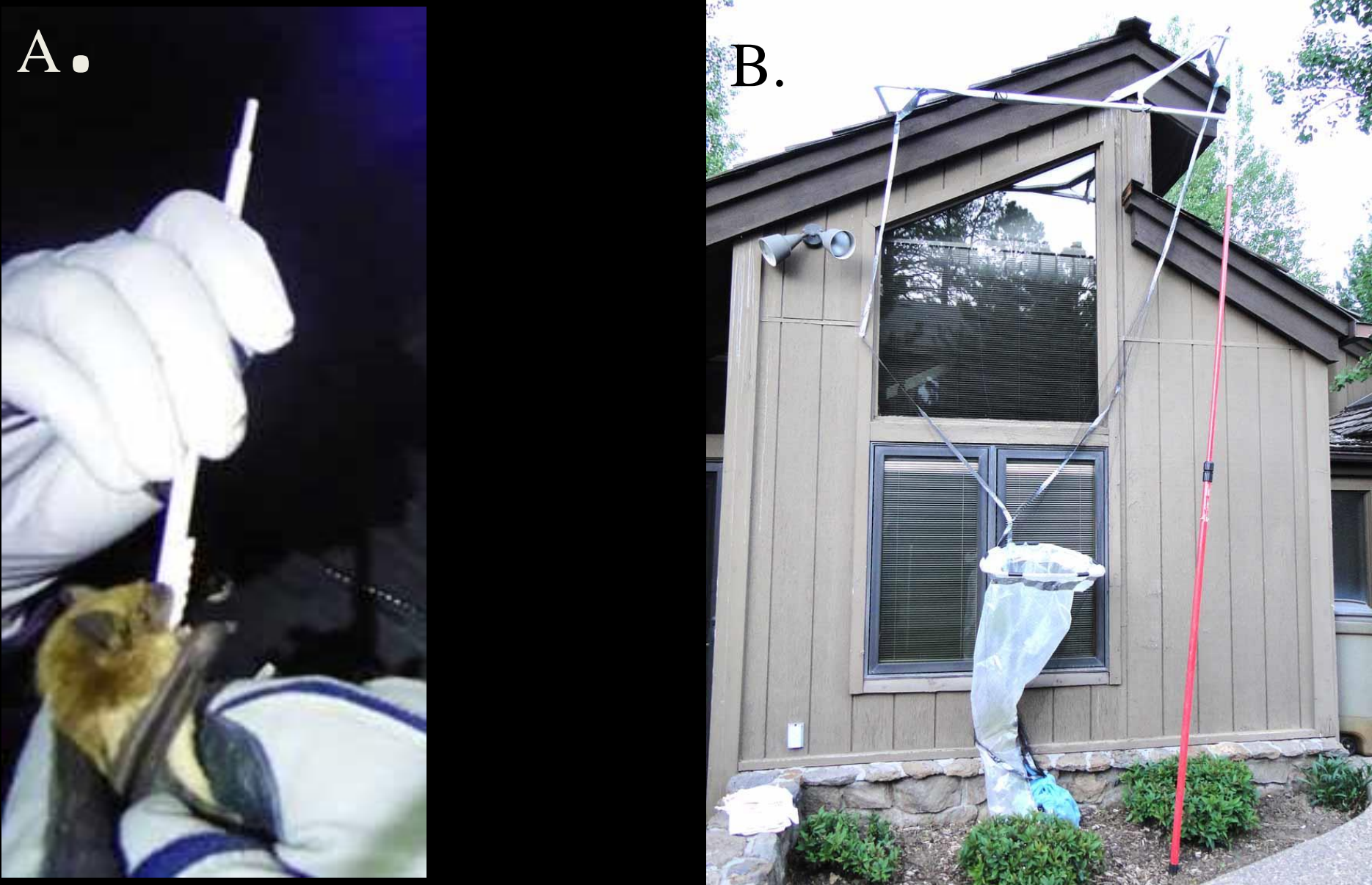


Fig. 1 A. Collecting DNA via buccal swabs. B. Net apparatus at a house roost.

Methods

- Collected 88 genetic samples via buccal swabs (Fig. 1A) from female big brown bats captured from 4 separate maternity roosts in northern Arizona during summer of 2013.
- PCR-amplified 5 microsatellite loci (Maarten et al. 2008; Walker et al. 2014). With genetic data we examined:
 - Locus behavior: Genepop 4.2 (Raymond & Rousset 1995, Rousset 2008)
 - Genetic relatedness: Queller & Goodnight's *R* (GenAlEx 6.5, Peakall & Smouse 2006, 2012; Resampling Stats 5.0.2, Simon 1990)
 - Genetic structure: AMOVA (GenAlEx 6.5) and program STRUCTURE (Pritchard et al. 2000)
 - Parentage: Cervus 3.0 (Marshall et al. 1998)
 - Recaptures: GenAlEx 6.5

References

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Results

Captures: Females were in various reproductive conditions of gestating (N= 38), lactating (N=30), and non reproductive (N=14); 6 were unknown.

Locus behavior: Mean heterozygosity was 0.835 ± 0.19 .

Genetic relatedness and structure: Mean pairwise genetic relatedness was no higher within than among maternity roosts ($P > 0.12$). We found no genetic structure among the three largest maternity roosts (79 bats) (AMOVA, Figure 3; R_{st} , Table 1; STRUCTURE, K=1).

Parentage: We detected two mother-adult daughter pairs: one pair was captured at the same roost, and members of the other pair were captured at different roosts.

Movement: Three females in varying reproductive condition were recaptured at multiple roosts (identified via molecular and telemetry data; Figure 2).

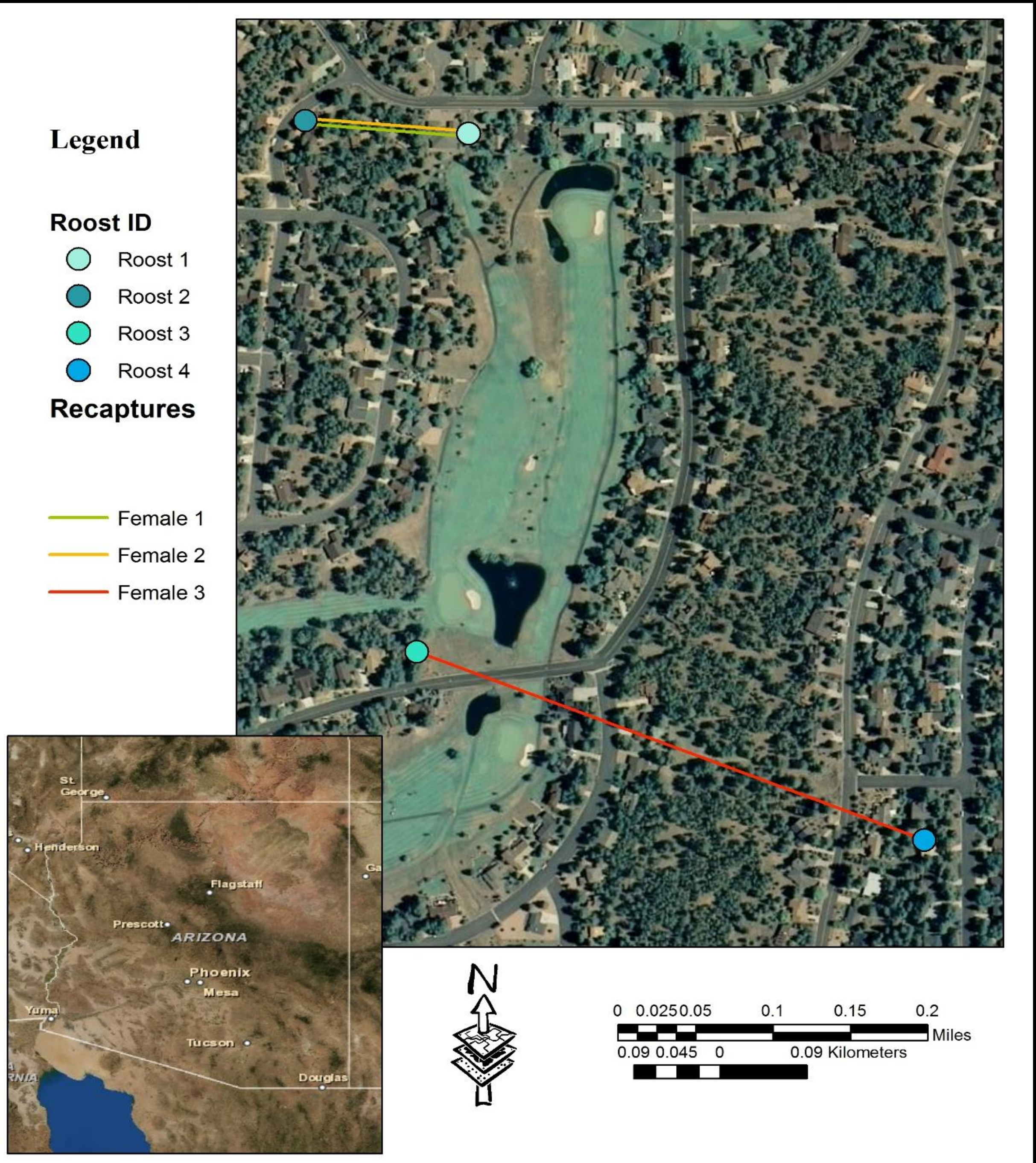


Fig. 2. Study location in Flagstaff, Arizona. Maternity roost locations were in houses within 500 m of golf course water sources. Three female bats switched roosts during the study.

Percentages of Molecular Variance

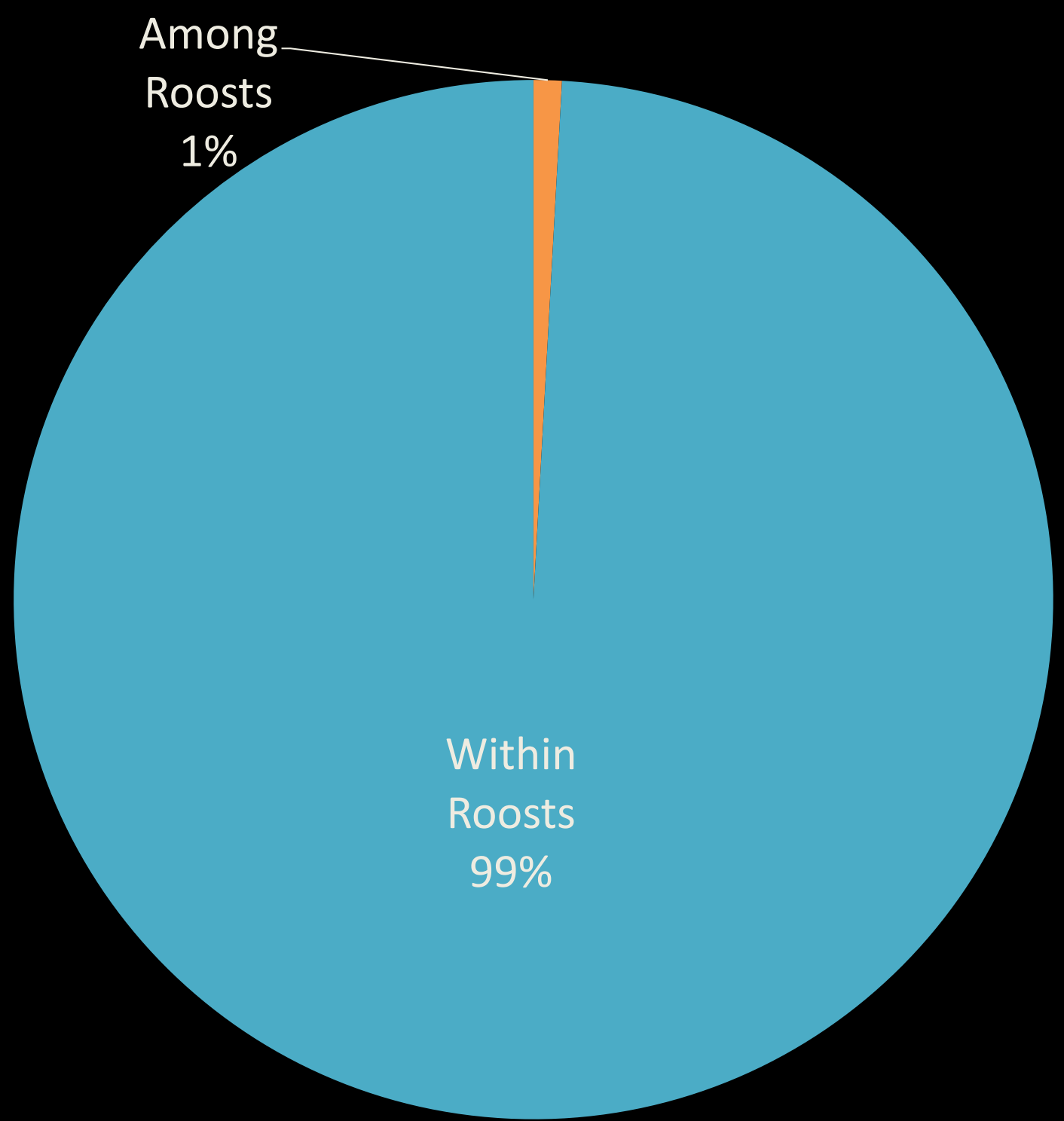


Fig. 3. Lack of genetic structure among roosts, as indicated by Analysis of Molecular Variance.

Roost ID	Roost 2	Roost 3	Roost 4
Roost 2		0.420	0.371
Roost 3	0.000		0.390
Roost 4	0.000	0.000	

P(rand >= data) based on 999 permutations

Table 1. Pairwise population R_{st} values (below diagonal), with P-values (above diagonal).

Summary AMOVA Table							
Source	df	SS	MS	Est. Var.	%	Statistic	P-value
Among Pops	2	10.658	5.329	0.039	1%	PhiPT	0.158
Within Pops	65	289.342	4.451	4.451	99%		
Total	67	300.000		4.491	100%		

Conclusions

- Females are not selecting roosts based on kinship and there are high amounts of movement among roosts, evidenced by:
 - No genetic structure found within maternity colonies
 - Observations of roost switching, and mothers and their adult daughters at both the same and different roosts
- With this high degree of interaction and geographic mobility of females, there is an increased risk of spread of diseases like rabies at a larger geographic level instead of a more centralized area.

Acknowledgments

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