Comparison of the genetic structure of two forest bats across Eastern Cape forests

Miss Monika Moir
PhD Candidate
Department of Botany and Zoology
Stellenbosch University

Supervisors: Dr V. Rambau, Dr L. Richards, Prof. M. Cherry
<table>
<thead>
<tr>
<th></th>
<th><strong>Pipistrellus hesperidus</strong></th>
<th><strong>Rhinolophus swinnyi</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>Forest associated</td>
<td></td>
<td>Forest dependent</td>
</tr>
<tr>
<td>Forest and riparian vegetation</td>
<td></td>
<td>Forest and savanna woodland</td>
</tr>
<tr>
<td>Low wing loading (5.4 N/m²)</td>
<td>Intermediate aspect ratio (8.5)</td>
<td>Low wing loading (6.3 N/m²) Low aspect ratio (6.6)</td>
</tr>
<tr>
<td>LD-FM, intermediate peak frequency echolocation (50 kHz)</td>
<td></td>
<td>HD-CF, high peak frequency (106 kHz)</td>
</tr>
<tr>
<td>Clutter-edge forager</td>
<td></td>
<td>Clutter forager</td>
</tr>
</tbody>
</table>

(Monadjem et al., 2010)
Hypotheses

- *Pipistrellus hesperidus* will display gene flow between forest study areas and a lesser degree of genetic sub-structuring as it is a clutter-edge, forest associated species.

- *Rhinolophus swinnyi* will display population structuring between forest study areas as they are forest specialists, and have a low dispersal ability.
Transkei Mistbelt
Eastern Mistbelt
Amatole Mistbelt
Pondoland Scarp
Transkei Coastal Scarp

Mistbelt Forest Groups
- Transkei Mistbelt
- Eastern Mistbelt
- Amatole Mistbelt

Scarp Forest Groups
- Pondoland Scarp
- Transkei Coastal Scarp

(Von Maltitz et al., 2003)
**Pipistrellus hesperidus**

Cytochrome b (1 140 bp)  
N = 55

Sequence divergence 0.01 – 1.4 %  
\( h = 0.903 \pm 0.024 \)  
\( \pi = 0.00416 \pm 0.00029 \) (DnaSP v6 Rozas et al., 2017)

27 % variation among groups  
\( P = 0.01 \pm 0.004 \) (Arlequin 3.5.2.2 Excoffier et al., 1992)

Figure 1: NJ (Kimura 2-parameter model) and ML (Tamura-Nei model) phylogenetic tree (MEGA7 Kumar et al., 2017)

Figure 2: Median-joining haplotype network (PopART Bandelt et al., 1999)
**Rhinolophus swinnyi**

Cytochrome b (1 140 bp)

N = 16

Sequence divergence 0.01 – 0.7 \%

h = 0.7 ± 0.127

π = 0.00167 ± 0.00057 (DnaSP v6 Rozas et al., 2017)

82 \% variation among groups

P = 0.02 ± 0.005 (Arlequin 3.5.2.2 Excoffier et al., 1992)

Figure 3: NJ (Kimura 2-parameter model) and ML (Tamura-Nei model) phylogenetic tree (MEGA7 Kumar et al., 2017)

Figure 4: Median-joining haplotype network (PopART Bandelt et al., 1999)
Conclusion

- *Pipistrellus hesperidus*: Genetic structuring between study areas is not evident due to generalist utilization of wooded habitats and clutter edge adaptations

- *Rhinolophus swinnyi*: Low level structuring between mistbelt and scarp forests due to reduced dispersal ability and forest dependence

- Next step: Microsatellites
Thank you
References


