Understanding the evolutionary drivers of diversification

Reconstructing the diversification of cryptic lemurs in a biodiversity hotspot - bridging the gap from evolution to conservation

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In Short

- Lemurs are a diverse radiation of Malagasy mammals and an excellent model system to study the drivers of evolutionary diversification processes.

- We will reconstruct the evolutionary history of mouse lemurs (*Microcebus* spp.) to understand the role of different factors driving speciation.

- We will infer phylogeny, divergence times and species limits across the entire genus *Microcebus* and study population structure on a smaller spatial scale in a region in northeastern Madagascar.

- Our findings will shed light on the general principles underlying Malagasy adaptive radiations and will help to inform conservation priorities.

Understanding the processes that are responsible for the diversification and distribution of species is a central focus of evolutionary biology. Speciation, the process that leads to formation of distinct, reproductively isolated evolutionary lineages (i.e., species), is governed by a variety of factors, including geography, climate, genome architecture, and a species' ecology. The relative importance of these factors and how they interact to drive reproductive isolation remains debated.

An ideal model region to understand the drivers of evolutionary diversification processes is the Island of Madagascar [1]. It has been isolated from other land masses for at least 80 million years and large parts of its flora and fauna are endemic (i.e., they occur nowhere else). It is believed that its unique biota evolved through adaptive radiations after founder individuals were released from competition and predation, reaching the island from mainland Africa [2]. The largest radiation of Malagasy mammals are the lemurs. They exhibit exceptional diversity in morphology and behavior and comprise more than 100 existing species across 15 genera. The number of recognized lemur species has increased by more than three-fold during the last 30 years, which is partly due to the identification of many cryptic species (i.e., similar in outer appearance) using genetic markers. At the same time lemurs are the world's most endangered mammals, as about 95 % of the currently described species are threatened by extinction primarily because of rapid habitat loss and degradation [3,4].

The present project aims to reconstruct the evolutionary history of mouse lemurs (*Microcebus* spp.), a cryptic radiation of lemurs comprising 24 described species distributed all over Madagascar, as a model to understand the role and importance of different factors driving reproductive isolation and ultimately speciation in Malagasy terrestrial mammals. We will use restriction site associated DNA (RAD) markers in hundreds of individuals and bioinformatic tools to explore patterns of diversification on different spatiotemporal scales. First, we will infer phylogeny, divergence times, species limits and potential introgression across the entire genus *Microcebus*. Second, we will model population structure, patterns of gene flow, and demography (population size changes, migration, etc.) of mouse lemur species on a smaller spatial scale in a biodiversity hotspot in northeastern Madagascar (Fig. 1) in comparison to medium-sized lemurs of the genus *Avahi*. Because of its high lemur diversity and special geography, the study region is particularly well suited to understand the role of a variety of speciation factors such as river chronology, altitude, paleoclimatic oscillations, forest fragmentation, vegetation, and habitat plasticity.
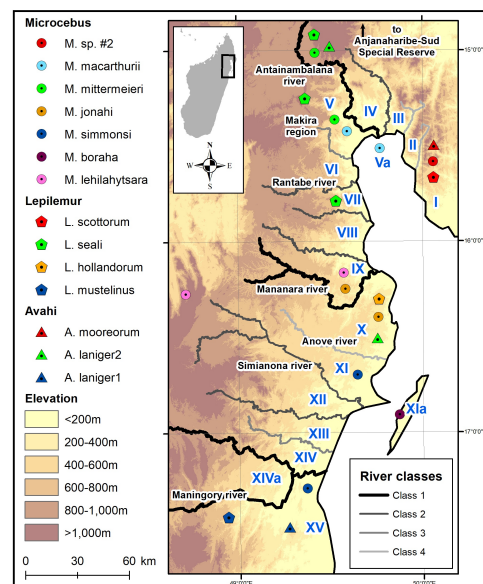

Figure 1: *Study region in northeastern Madagascar with known distributions of Avahi, Lepilemur and Microcebus species. Roman numerals indicate inter-river systems that will be sampled.*

So far, our assessments of mouse lemur diversity in the study region resulted in the discovery and description of the species *M. jonahi* (Fig. 2), revealed signals of ongoing diversification, and showed that mouse lemur evolutionary history and population structure were shaped by paleoclimatic events and anthropogenic factors. [5–8], which shall be investigated further.

Figure 2: Microcebus jonahi. Photo by D. Schüßler.

Our findings will shed light on the general principles and factors underlying (Malagasy) adaptive radiations. In addition, they will further understanding of the diversification of mouse lemurs and provide a high-confidence, divergence-dated phylogeny, that is based on genome-scale markers and covers all described *Microcebus* species. By studying evolutionary relationships, species limits, population structure and barriers to gene flow, our results will also make an important contribution to lemur conservation.

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More Information

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