

THE EFFECTS OF HABITAT FRAGMENTATION AND PHYLOGEOGRAPHIC HISTORY ON THE GENETIC STRUCTURE OF A SMALL NOCTURNAL LEMUR

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Habitat fragmentation and historic climate change strongly influence the genetic structure of natural populations, but integrative studies on both aspects are sparse for most primates. Consequently, the genetic structure of a mouse lemur species (*Microcebus murinus*) was analysed at its northern distribution edge in order to detect genetic signals of its colonization history and of recent anthropogenic processes (fragmentation) that can influence genetic diversity and differentiation along with other natural features (e.g., geographic distance, rivers). The analysis of mitochondrial D-loop sequences (195 samples) and multilocus genotypes (186 samples) from forest fragments (N=5) and from sites in a larger continuous forest (N=10), stemming from two adjacent Inter-River-Systems in northwestern Madagascar, revealed that forest fragmentation and the large river Mahajamba restrict gene flow, thereby leading to a loss of genetic diversity in fragments and an increased genetic differentiation between populations beyond the effect of isolation-by-distance. Demographic simulations based on the sequence data detected signals of two successive spatial expansions that could be preliminarily dated to the late Pleistocene and early Holocene. A haplotype network revealed geographic structure and showed deep molecular divergences within and between the IRSs that would be congruent with a two-step colonization scenario. This study supports the hypothesis of a relatively recent spatial expansion of the grey mouse lemur in northwestern Madagascar, but also demonstrates that even the smallest of all lemurs are vulnerable to human interventions and therefore require the attention of conservationists. The study was funded by the German Research Council (DFG) and the DAAD.

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