

# Delimiting Species without Nuclear Monophyly in Madagascar's Mouse Lemurs

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Speciation begins when populations become genetically separated through a substantial reduction in gene flow, and it is at this point that a genetically cohesive set of populations attain the sole property of species: the independent evolution of a population-level lineage.

The comprehensive delimitation of species within biodiversity hotspots, regardless of their level of divergence, is important for understanding the factors that drive the diversification of biota and for identifying them as targets for conservation.

However, delimiting recently diverged species is challenging due to insufficient time for the differential evolution of characters—including morphological differences, [reproductive isolation](#), and gene tree monophyly—that are typically used as evidence for separately evolving lineages.

In this study, University of Kentucky researchers assembled multiple lines of evidence from the analysis of [mtDNA](#) and nDNA sequence data for the delimitation of a high diversity of cryptically diverged population-level mouse [lemur](#) lineages across the island of Madagascar. The study uses a multi-faceted approach that applies phylogenetic, population genetic, and genealogical analysis for recognizing lineage diversity and presents the most thoroughly sampled species delimitation of mouse lemur ever performed.

The resolution of a large number of geographically defined clades in the

mtDNA gene tree provides strong initial evidence for recognizing a high diversity of population-level lineages in mouse lemurs. Researchers find additional support for lineage recognition in the striking concordance between mtDNA clades and patterns of nuclear [population structure](#). Lineages identified using these two sources of evidence also exhibit patterns of population divergence according to genealogical exclusivity estimates. Mouse lemur lineage diversity is reflected in both a geographically fine-scaled pattern of population divergence within established and geographically widespread taxa, as well as newly resolved patterns of microendemism revealed through expanded field sampling into previously poorly and well-sampled regions.

**More information:** Weisrock DW, Rasoloarison RM, Fiorentino I, Ralison JM, Goodman SM, et al. (2010) Delimiting Species without Nuclear Monophyly in Madagascar's Mouse Lemurs. PLoS ONE 5(3): e9883. [doi:10.1371/journal.pone.0009883](https://doi.org/10.1371/journal.pone.0009883)

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