

**CONSERVATION GENETICS OF THE ENDANGERED SKY ISLAND  
LIZARD, *Ceratophora stoddartii***

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The global decline in biodiversity necessitates urgent conservation action, with genetic diversity being vital for species survival and adaptation, underscoring conservation genetics as crucial tool in biodiversity preservation. *Ceratophora stoddartii* (Rhino-horned lizard) is an endangered arboreal agamid lizard species endemic to Sri Lanka's montane cloud forests. The species is highly vulnerable to habitat fragmentation and isolation within these 'sky island' habitats. This study presents the first population genetic analysis of a montane lizard species in Sri Lanka, evaluating genetic structure and diversity across the distribution range of *C. stoddartii* to inform conservation strategies. Tail tissue samples were collected from six montane forest sites spanning the species' distribution range. DNA was extracted and mitochondrial ND2 gene region was successfully amplified and sequenced in 17 individuals. Population genetic structure was assessed using phylogenetic analysis (Bayesian and Maximum Likelihood) and haplotype network analysis. Spearman's correlation analysis examined the relationship between genetic divergence and geographic distance. Molecular diversity indices estimated genetic diversity among populations. Phylogenetic analyses identified two major clades corresponding to the Raxawa Mountain population and Central Highlands populations indicating two distinct evolutionary lineages. Uncorrected pairwise genetic distances ranged between 0.00 – 4.89%, with Raxawa showing the highest divergence (3.53 – 4.89%). Within Central Highlands populations, divergence ranged from 0.00% to 3.80%. Haplotype analysis revealed eight unique haplotypes; none shared among sites. Spearman's correlation indicated significant positive relationship between genetic and geographic distance. Overall nucleotide diversity was moderate ( $\pi = 0.02613$ ) while Raxawa population exhibited the highest nucleotide diversity ( $\pi = 0.00212$ ). These results indicate that *C. stoddartii* comprises genetically distinct, geographically structured populations, with long-term isolation contributing to divergence. The deep divergence between the Raxawa Mountain and Central Highland lineages supports their recognition as separate conservation management units. Future studies integrating whole-genome sequencing and expanded geographic sampling are essential for refining conservation strategies and investigating historical drivers of population subdivision.

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