

LANDSCAPE HETEROGENEITY INFLUENCES GENE FLOW IN THE CENTRAL AMERICAN SQUIRREL MONKEY

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Central American Squirrel Monkeys (*Saimiri oerstedii*) are restricted to a fragmented, heterogeneous habitat in the Central Pacific region of Costa Rica. Since landscape heterogeneity is hypothesized to play a central role in primate evolution, studies of primate ecology and evolution should explicitly consider landscape heterogeneity. We examined the effects of landscape heterogeneity on gene flow in *S. oerstedii*. 350 fecal samples were collected from 22 *S. oerstedii* troops and genotyped for 17 microsatellite loci. Data were analyzed using landscape genetics methods (least-cost paths and circuit network theory) to characterize localized gene flow patterns for *S. oerstedii* and correlate those patterns with measures of landscape heterogeneity. Our results show that large, commercial palm plantations represent barriers to gene flow but not smaller plantations or residential areas. We recommend ways to develop and refine landscape genetics methods for primates in order to inform future studies of the influence of heterogeneous landscapes on primate ecology, population divergence, and evolution. We also discuss the importance of landscape genetics studies in informing primate conservation management. This study was funded by NSF Award No. BCS-0847912, Columbia University, the International Primatological Society, the American Society of Primatologists, and the Margot Marsh Biodiversity Foundation.

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