Genetic diversity of longtail macaques (Macaca fascicularis) on the island of Mauritius: an assessment of nuclear and mitochondrial DNA polymorphisms

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Abstract

Background Individuals from an introduced population of longtail macaques on Mauritius have been extensively used in recent research. This population has low MHC gene diversity, and is thus regarded as a valuable resource for research.

Methods We investigated the genetic diversity of this population using multiple molecular markers located in mitochondrial DNA and microsatellite DNA loci on the autosomes and the Y chromosome. We tested samples from 82 individuals taken from seven study sites.

Results and conclusions We found this population to be panmictic, with a low degree of genetic variability. On the basis of an mtDNA phylogeny, we inferred that these macaques' ancestors originated from Java in Asia. Weak gametic disequilibrium was observed, suggesting decay of non-random associations between genomic genes at the time of founding. The results suggest that macaques bred in Mauritius are valuable as model animals for biomedical research because of their genetic homogeneity.

Keywords: bottleneck • introduction • microsatellite • mtDNA