

## 猕猴属中的基因流研究\*

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**摘要** 本文以我们修改的方法从猕猴肝脏组织中提取mtDNA。用限制性片段长度多态分析为手段研究恒河猴 (*Macaca mulatta*)、台湾省的台湾猴 (*M. cyclopis*)、日本猴 (*M. fuscata*) 和食蟹猴 (*M. fascicularis*) 的mtDNA多态。根据mtDNA遗传距离计算了4个种间的分歧年代, 其范围为1.8—3.2百万年。结合化石、行为、动物地理等方面的资料, 我们的结果提示: 在猕猴属的进化过程中, 恒河猴、食蟹猴、日本猴和台湾省的台湾猴的祖先群体间存在长时间大量的基因流, 降低了这些种的核基因组分歧速度, 导致核基因组和线粒体基因组分歧程度的显著差异。这四个种中, 食蟹猴首先分离。在食蟹猴、台湾省的台湾猴和日本猴迁移到相应的岛屿后, 它们与恒河猴间仍存在基因流, 进一步降低了其核基因组间的分歧程度。

**关键词** [猕猴属](#), [mtDNA](#), [蛋白质多态](#), [基因流](#)

分类号

## Gene Flow in Macaques\*

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### Abstract

Mitochondrial DNA was purified from liver tissue of macaques with the method modified in our laboratory. Mitochondrial DNA polymorphism among *Macaca mulatta*, *M. cyclopis*, *M. fuscata* and *M. fascicularis* were investigated by using restriction enzyme analysis. Combining the earlier study of protein electrophoresis, divergence time of the four species was estimated on the basis of mtDNA and protein genetic distance, and the result ranged from 1.8—3.2 and 0.4—1.5 Myr, respectively. Integrate information on fossil record, behavior and zoogeography of macaques, our results indicate that there existed long time gene flow among the ancestral populations of *M. mulatta*, *M. cyclopis*, *M. fuscata* and *M. fascicularis*, which slowed down divergence of nuclear genome. This may be the reason why there were great differences between the estimated divergence times based on mtDNA and protein genetic distance. *M. fascicularis* may dispersed earliest among the four species. There also existed gene flow between species even after *M. fascicularis*, *M. fuscata* and *M. cyclopis* had been isolated on their habitat islands.

**Key words** [Macaques](#) [Mitochondrial DNA](#) [Protein polymorphism](#) [Gene flow](#)

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