

猕猴属6个种的rDNA变异及其系统进化关系

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摘要 以人28S、18S rDNA为探针,用15种限制性内切酶构建了猕猴属6个种(*M. mulatta*, *M. fascicularis*, *M. arctoides*, *M. assamensis*, *M. thibetana*, *M. nemestrina*)和滇金丝猴(*Rhinopithecus bieti*)、白颊长臂猿(*Hylobates leucogenys*)核糖体DNA重复单位的限制性内切酶图谱。红面猴(*M. arctoides*)与熊猴(*M. assamensis*)拥有完全相同的限制性内切酶图谱。基于内切酶图谱得到了68个信息位点并计算了各种rDNA重复型间的遗传距离。用PHYLP version 3.5c软件包中的NEIGHBOR和RESTML程序,以滇金丝猴和白颊长臂猿为外群,构建了NJ树和最大似然树。两棵树的拓扑结构不完全一致,但恒河猴(*M. mulatta*)和食蟹猴(*M. fascicularis*)总是位于树的基部,提示它们可能是最早分化出的类群。熊猴-红面猴(*M. assamensis*-*M. arctoides*)虽然与藏猴(*M. thibetana*)共享的限制性位点数更多,在NJ树上两类动物也最为接近,但在最然树中熊猴-红面猴却与平顶猴(*M. nemestrina*)聚在一起。因此,rDNA变异的数据尚不能对猕猴类动物进行有效的分组。这一方面可能是因为我们目前获得的rDNA变异数据有限,另一方面也可能反映了猕猴类动物系统发育关系的复杂性。

关键词 [猕猴属](#) [核糖体DNA](#) [系统进化](#)

分类号

Phylogenetic Relationships Among Six Species of *Macaca* Inferred from Ribosomal DNA Variations

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Abstract

Restriction maps of ribosomal DNA repeating units of six species of *Macaca* (*M. mulatta*, *M. fascicularis*, *M. arctoides*, *M. assamensis*, *M. thibetana*, *M. nemestrina*) and two outgroup species, *Rhinopithecus bieti* and *Hylobates leucogenys*, were constructed with 15 restriction endonucleases and 28S, 18S rDNA probes cloned from human. *M. arctoides* shares a common restriction map with *M. assamensis*. Phylogenetic tree derived from the neighbor-joining was somewhat different that derived from the maximum like lihood methods using the NEIGHBOR and RESTML program in PHYLP version 3.5c. However, the consensus of our phylogenetic trees supports the viewpoint that *M. fascicularis* and *M. mulatta* were maybe diverged first in the genus *Macaca*. Further studies using DNA sequencing method are required to resolve the phylogeny of the genus *Macaca*.

Key words [Macaca](#) [Ribosomal DNA](#) [Phylogenetic relationships](#)

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