



Project description

Molecular phylogeny and evolutionary history of Mentawai macaques and their close relatives

In order to elucidate the evolutionary history and taxonomy of the Mentawai macaques, we sequenced a 567 base pairs (bp) long fragment of the mitochondrial cytochrome b gene from 39 individuals representing pigtailed macaque populations from Siberut, Sipora, South Pagai, and Sumatra. Pairwise difference analyses carried out within and among populations have shown, that: (1) variation within populations is relative low, (2) variation among populations is increased, and (3) pairwise differences within and among the populations from Sipora and South Pagai are in the same range. From phylogenetic tree reconstructions including further macaque species, we detected a paraphyletic origin of Mentawai macaques with the Siberut population being more closely related to *Macaca nemestrina* from Sumatra, than it is to the populations from the Southern islands. Based on these results, we favour a scenario in which macaques entered the Mentawai islands by two independent colonisation events. Taking together the paraphyletic origin of Mentawai macaques and the genetic differences detected among pigtailed macaque populations, which are comparable with those observed among the seven Sulawesi macaque species, we propose to separate macaques from Siberut and Sipora, North and South Pagai into two distinct species, *Macaca siberu* and *Macaca pagensis*, respectively.