

Molecular Systematics and Conservation Genetics of Gliding Petaurids (Marsupialia, Petauridae)

Abstract

The gliding petaurids are small sized arboreal and nocturnal marsupials restricted to Australia and the New Guinean region. They have suffered range contractions since European settlement, and most of the species are of conservation concern, either nationally or at a state level. This study applied molecular approaches to investigate several questions involving *Petaurus* species which may provide valuable insights for the conservation and management of species. The objectives of this study included an examination of phylogenetic and evolutionary relationships among *Petaurus* species, an assessment of phylogeographic structure within *P. breviceps* and an investigation of genetic diversity, social structure and mating system of *P. breviceps* in fragmented habitats.

A broad molecular systematics study of the genus *Petaurus* was first undertaken. Two mitochondrial genes (*ND2* and *ND4*) and a nuclear gene marker (*ω -globin*) were screened for sequence variation in samples obtained from across the distribution of petaurid species, including Australia, New Guinea and its surrounding islands. Phylogenetic analyses confirmed the monophyly of the genus *Petaurus* and revealed that, with the exception of *P. gracilis*, the currently recognised species were associated with divergent mtDNA clades. It also revealed considerable mtDNA diversity within the widely distributed species *P. breviceps*. The existence of at least seven distinct and divergent mtDNA lineages within *P. breviceps* was supported, with two lineages located in Australia and at least five lineages in New Guinea. However, the distribution of these evolutionary lineages did not correspond with current morphological subspecies boundaries. Analyses of *ω -globin* sequence provided support for a number of these distinct populations, suggesting the possible presence of cryptic species within *P. breviceps*. Molecular analyses also suggested that squirrel gliders, *P. norfolcensis*, may occur in both South Australia and the Northern Territory, extending the current known range of the species. The presence of *P. norfolcensis* in SA was further verified by examining museum skins.

Population structure and current pattern of gene flow within *P. breviceps* in Australia was examined further to elucidate phylogeographic structure within the species, and explore potential causes of geographic variation. Evidence for significant phylogeographic structuring across the range of the species in Australia was provided from population genetic (AMOVA) and phylogenetic analyses of both mitochondrial DNA and the ω -globin gene. In particular, there was evidence for the existence of two divergent clades that were distributed over distinct geographical regions. Divergence dates calculated for the two major mtDNA clades suggested that environment and climate changes which occurred during the Pliocene may have facilitated this diversification.

Habitat fragmentation is generally considered to be a major factor threatening the viability of forest dependent species such as gliders. Effects of habitat fragmentation were therefore investigated in *P. breviceps* in the highly disturbed landscape of south-eastern South Australia. Genetic mating system and social structure of the species in these fragmented habitats was explored in 13 populations, using nine polymorphic microsatellite loci. Social groups consisted of two to seven gliders, and these were often close relatives, including parents with their offspring. Parentage analyses provided some evidence for a polygamous mating system, with a number of males found to have fathered offspring from multiple female partners. Some direct evidence of inbreeding was also found within a small isolated patch. Genetic diversity within *P. breviceps* populations was moderate compared to the range reported in other marsupial species. Population structure analyses indicated that gene flow between some patches was restricted. Small patches surrounded by a matrix of pine were more likely to show inbreeding and potentially suffer from inbreeding depression, although further data are required to verify this result. Overall, results suggest that, although the species is still present in these small and isolated patches, it may face threats from a lack of dispersal and inbreeding. Maintaining the size of patches and establishing corridors between isolated populations needs to be considered in conservation and management of species in these fragmented habitats.