Abstract
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Biodiversity in Southeast Asia has been decreasing as a result of human activities. The findings of the Millennium Ecosystem Assessment, reported in 2005, demonstrated that environmental change, such as deforestation, has resulted in recent major loss of biodiversity at the species level and increased rates of extinction; however, it is unknown whether a similar deficit has occurred at the level of genetic diversity within species. This study aims to understand how the past has shaped the current pattern of genetic diversity, the impact of recent forest loss on genetic diversity and how this information can be used to develop effective conservation strategy.

To achieve this aim, microsatellites were developed by sequencing genomic libraries and from comparisons of database sequences. The utility of these markers for population genetics studies has been tested and confirmed for the three main study taxa and across a broad range of other squirrel species. These microsatellites and mitochondrial sequence data (cytochrome b gene) were utilized to determine the genetic diversity and population structure of three squirrel taxa with varying degrees of forest dependency on Thailand’s tropical forests. The most forest dependent taxon is Phayre’s flying squirrel (*Hylopetes phayrei*). The second taxon is the moderately forest-dependent tree squirrel, the Grey-bellied squirrel (*Callosciurus caniceps*). The third, and least forest dependent taxon, is the Indochinese ground squirrel, *Menetes berdmorei*.

Our data revealed far more biodiversity in these taxa than previously recognized; there were three genetically distinct lineages in *H. phayrei* and *M. berdmorei* and two lineages in *C. caniceps*. This demonstrates that biodiversity in this region has been underestimated. In the two most forest dependent taxa lineage divergence dated to the Pleistocene indicating that this biodiversity was generated by isolation in allopatric forest refugia during the cool, dry periods of the Pleistocene. In *H. phayrei*, the most forest-dependent taxon, at least two of the lineages were distinct species occurring sympatrically in Thailand on the border with Myanmar. This taxon supported the biogeographical hypothesis developed in forest dependent mosquitoes of allopatric isolation in northwest and northeastern Pleistocene refugia. *Callosciurus caniceps* had evidence of a southern refugium in peninsular Thailand or Malaysia. The lower levels of structuring in the least forest dependent taxon *M. berdmorei* suggest a limited impact of Pleistocene environmental change. All three taxa had eastern lineages which may have been due to Pleistocene forest fragmentation in some of the species. These eastern populations typically had lower levels of microsatellite and mtDNA genetic diversity. This is likely due to the recent loss of genetic diversity as in recent decades these forests have been highly fragmented and reduced in size due to human activity.

Our finding that the northern Thai-Myanmar border region is a suture zone in highly dependent forest species and has high within lineage/species diversity makes this region a priority for conservation. The distinct genetic lineages in the east and south should also be managed as separate conservation units. Further efforts are required to assess the impact of loss of genetic diversity in Thailand’s fragmented forests and how this may be remedied.