

Molecular phylogenetics of the Asian striped squirrels (genus *Tamiops*) based on paternal, maternal, and biparental markers

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Current classification of the genus *Tamiops* is mainly based on pelage color pattern that is prone to seasonal variation or convergent adaptation to environmental selection. The arrangement of four species, *Tamiops mcclellandii*, *T. rodolphii*, *T. swinhoei* and *T. maritimus*, is regarded as tentative due to difficulty delineating species, especially the latter two species. Multi-locus phylogenies of all four *Tamiops* species were constructed based on paternal (Y-chromosomal *SRY* and *SMCY7*), maternal (mitochondrial cytochrome *b* gene), and biparental (autosomal *IRBP*, *RAG1*, and *PRKCI*) sequences. Maximum likelihood and Bayesian tree-constructing methods resulted in phylogenies with

similar topologies. All genetic markers supported diversification of three main lineages: (1) *T. mcclllandii*, (2) *T. rodolphii*, and (3) *T. swinhoei-maritimus* complex. On the basis of 24 *T. maritimus* from 5 localities and 10 *T. swinhoei* from 4 localities, *Tamiops swinhoei* and *T. maritimus* were not reciprocally monophyletic. The six populations of the *T. swinhoei-maritimus* complex were monophyletic in all loci except for autosomal loci in one *T. maritimus* population from Tam Dao, Vietnam. Autosomal phylogenies were more similar to Y-chromosomal than to mitochondrial phylogenies. Incongruence between nuclear and mitochondrial phylogenies indicates that either *T. maritimus* from Taiwan or *T. maritimus* from Phu Yen, Vietnam was probably descended from ancient hybridization. Diversification of the three main *Tamiops* lineages was estimated to occur 8.8–6.7 million years ago and may have been affected by rapid uplift of the Himalayan Mountains in the western part of their range. Multiple divergences from 5.8 to 1.7 million years ago likely led to formation of modern *Tamiops* species. All six populations of *T. swinhoei-maritimus* complex could be regarded as distinct species. Divergence in mitochondrial DNA among *T. rodolphii* populations was also at the interspecies level. Our analyses highlight the underestimation of species diversity in the genus *Tamiops*.