

Executive summary

The tokay gecko *Gekko gecko* is distributed in the mainland and islands of Southeast Asia, South Asia and extreme southern part of China. The two morphotypes i.e., “Red tokay” and “Black tokay” are found in different geographical regions and are recognized as different subspecies. In Thailand, Laos and Vietnam, only “Red tokay” has been recorded for its habitats which are forests and commensal areas. However, the populations of the tokay gecko in Thailand have been exploited for human consumption and tend to decrease population sizes in some areas and could affect to genetic diversity of the tokay gecko. Therefore, this study aimed to investigate genetic diversity and relationships among populations of *G. gecko* in Thailand. Population genetic analyses were conducted using mitochondrial cytochrome-*b* gene (1127 bp). Genetic analyses showed 44 haplotypes, containing 28 unique haplotypes. The phylogenetic analyses showed two major lineages, clades A and B. The clade A consists of most Thai populations i.e., East, Northeast, Central, West and South populations whereas the clade B contains populations from two localities i.e., Phitsanulok and Chanthaburi. The populations from Phitsanulok and Chanthaburi are closely related with the populations from China, Laos and Vietnam. The genetic divergence among clades was 8.1-9.9%, indicating high level of genetic differentiation among these two clades. Considering relationships with clade A, genetic structuring was found and divided into 2 subclades i.e., subclade A1 and A2, indicating the limit of gene flow between populations in Thailand and this could be a result of geographic barrier. However, the population structure of *G. gecko* might affect from translocation by human.