

Kornsorn Srikulnath 2010: Cytogenetic Characterization and Mitochondrial Genome Analysis in the Butterfly Lizard (*Leiolepis reevesii rubritaeniata*, Agamidae, Squamata). Doctor of Philosophy (Genetics), Major Field: Genetics, Department of Genetics. Thesis Advisor: Associate Professor Somsak Apisitwanich, Ph.D.
168 pages.

Cytogenetic characterization of the butterfly lizard (*Leiolepis reevesii rubritaeniata*) was determined by conventional Giemsa staining, Ag NOR-banding, FISH with the 18S-28S and 5S rRNA genes and telomeric (TTAGGG)₂₀ sequences. The karyotype was composed of two distinct components, macrochromosomes and microchromosomes, and the chromosomal constitution was $2n=2x=36$ ($L_4^m + L_2^{sm} + M_2^m + S_4^m + 24$ microchromosomes). NORs and the 18S-28S rRNA genes were located at the secondary constriction of the long arm of chromosome 1, and the 5S rRNA genes were localized at the pericentromeric region of chromosome 6. Comparison to other two Thai butterfly lizards, *L. belliana belliana* and *L. boehmei*, showed similar major and minor ribosomal gene positions. However, hybridization signals of (TTAGGG)₂₀ sequences were observed at the telomeric ends of all chromosomes and interstitially at the same position as the 18S-28S rRNA genes in *L. reevesii rubritaeniata* and *L. boehmei*, suggesting that in the Leiolepidinae tandem fusion probably occurred between chromosome 1 and a microchromosome where the 18S-28S rRNA genes are located. Homologues of six chicken Z-linked genes (*ACO1/IREBP*, *ATP5A1*, *CHD1*, *DMRT1*, *GHR*, *RPS6*) were all mapped to *L. reevesii rubritaeniata* chromosome 2p in the same order as that on the snake chromosome 2p. The complete mitochondrial genome of these three butterfly lizards showed twenty-two tRNA genes, two rRNA genes, thirteen protein-coding genes and a control region in their mitochondrial genomes. The deletion of sequences approximately 47 bp in 12S rRNA gene has been revealed in *L. reevesii rubritaeniata* and *L. boehmei*, suggesting that it might occur in the lineage of *Leiolepis* spp. before the divergence of *L. reevesii rubritaeniata* and *L. boehmei*. Molecular phylogenetics comprising nuclear gene (*RAG1*, *C-mos*, *α-Enol* and *GAPD* genes) and concatenate 12 proteins coding mitochondrial gene also suggested that the most primitive among three butterfly lizards might be *L. belliana belliana*, which was more related to *L. reevesii rubritaeniata* while *L. boehmei* was the most recent species.

Student's signature

Thesis Advisor's signature

___ / ___ / ___