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Phylogenetic Relationships, Character Evolution and Historical Biogeography of the Subfamily Lygosominae (Reptilia: Scincidae) Inferred from Mitochondrial DNA Sequences

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The subfamily Lygosominae contains 45 genera and over 600 species mainly distributed in temperate and tropical Asia, Australia, central and southern Africa, Madagascar, the western Indian Ocean islands, southeastern North America, and central and South America including the Caribbean islands. Within this subfamily, three evolutionary lineages (i.e., the *Eugongylus* Group, the *Mabuya* Group and the *Sphenomorphus* Group) have been recognized on morphological, karyological and immunological data. However, there still remain a number of debates regarding the phylogeny of those major lineages and generic classification within each of them. Due to the scarcity of informative characters, it is not easy to formulate a sufficiently reliable phylogenetic hypothesis for this subfamily solely on the morphological ground. In collaboration with several colleagues, I have tried to elucidate the phylogenetic relationships of the subfamily on the basis of approximately 1,250 base positions of mitochondrial DNA sequence of 12S and 16S rRNA genes. On this occasion, I give summary of results of this project, and discuss the pattern and process of diversification and the historical biogeography of the subfamily.

Our results supported the monophyly of the Lygosominae, but suggested the presence of five distinct infra-subfamilial lineages. Of these, the *Sphenomorphus* Group appears to have diverged first, followed by the *Lygosoma* Group and the *Egernia* Group, leaving the *Eugongylus* Group and the *Mabuya* Group as sister groups. This negates the monophyly of the *Mabuya* Group in the former definition (i.e., as including the *Lygosoma* Groups and the *Egernia* Group), for which a number of morphological and karyological studies yielded supportive evidence. Morphological and karyological features shared within the *Mabuya* Group in the former definition may actually represent plesiomorphic character states.

In the Australian region (including Papua New Guinea and adjacent islands), the *Egernia* Group, the *Eugongylus* Group and the *Sphenomorphus* Group have their representatives, and so do the *Lygosoma* Group, the *Mabuya* Group and the *Sphenomorphus* Group in the African region (including Madagascar). Because each of these local assemblages does not constitute a monophyletic cluster, the phyletic diversity of lygosomine skinks in both regions is most likely to have increased through multiple colonizations from Southeast Asia, which neighbors both of the former regions and has high lygosomine diversity.

In the New World, only three genera (*Mabuya*, *Sphenomorphus* and *Scincella*), all common to the Old World, occur for this subfamily. Present results, together with the absence of extant or fossil representatives of the *Mabuya* Group from North America, strongly suggest the trans-Atlantic dispersals of *Mabuya* from Africa to Neotropics. Our results also indicated a closer affinity of the New World *Scincella* with the New World *Sphenomorphus* than with the Old World *Scincella*. Such relationships suggest the trans-Beringian dispersal of the common ancestor from Asia and its subsequent divergence into the North American *Scincella* and the Neotropical *Sphenomorphus*.