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**Chromosome evolution in the gekkonid genus *Gekko*
(Reptilia: Squamata) in East Asia**

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The lizard genus *Gekko* consists of over 30 species distributed in Asia and Oceania. From Japan, eight species, *G. japonicus*, *G. yakuensis*, *G. tawaensis*, *G. hokouensis*, *G. shibatai*, *G. vertebralis* and two undescribed species (*Gekko* sp.1 from western Kyushu and *Gekko* sp.2 from the Okinawa Island Group), are currently recognized on the basis of morphological and allozyme data. We analyzed karyotypes of all these species together with those of *G. hokouensis* from Taiwan and eastern continental China and another undescribed species (*Gekko* sp.3) from northeastern Taiwan. The C-banding, G-banding, and Ag-NOR techniques were adopted besides the standard Giemsa-staining. All *Gekko* species examined here shared a number of features in the standard karyotype, such as the diploid chromosome number (38) and the presence of two large metacentric autosome pairs. However, substantial variations were observed in the presence/absence of one heteromorphic sex chromosome pair and in the shape of W-chromosome, when present, among the *G. hokouensis* populations: heteromorphic pair was not detected by any means in samples from eastern continental China (type locality of the species), northern Taiwan, and Yonagunijima Island of the Southern Ryukyus; one distinct heteromorphic pair, consisting of relatively large telocentric (Z) and submetacentric (W) chromosomes, was observed only in females from the Central and Northern Ryukyus (ZZ in males); one indistinct heteromorphic pair (corresponding to the heteromorphic pair in the former karyotype), whose components were similar with each other in shape (relatively large telocentric) but differed in G-banding pattern, was observed in females from the Southern Ryukyus exclusive of Yonagunijima Island. *Gekko hokouensis* populations showed variation also in the shape of another relatively large homologous pair, which was telocentric in the eastern continental sample, but subtelocentric in the others including the northern Taiwan and Yonagunijima samples. Sex chromosome heteromorphisms were not recognized for karyotypes of all other *Gekko* species. *Gekko* sp.1 from western Kyushu shared all chromosomal features examined with the continental *G. hokouensis*, whereas karyotypes of *G. yakuensis*, *G. tawaensis*, *G. shibatai*, and *Gekko* sp.3 from northeastern Taiwan were apparently identical with those of *G. hokouensis* from northern Taiwan and Yonagunijima Island. Karyotypes of *G. vertebralis* and *Gekko* sp.2, while seemingly identical with each other, differ from the others in having fewer telocentric macrochromosomes, fewer microchromosomes, and more submetacentric or subtelocentric macrochromosomes. The karyotype of *G. japonicus* was similar to that of the continental *G. hokouensis*, but differed from the latter, as well as from all remaining karyotypes, in having a pair of relatively small subtelocentric (instead of telocentric) chromosomes. In the East Asian *Gekko*, ZW sex chromosome system seems to have evolved in the Ryukyu Archipelago from the state, in which heteromorphic sex chromosomes were absent, through the stage at which the heteromorphisms were recognizable only in the banding pattern. The present results also suggest cryptic taxonomic diversity in *G. hokouensis* in the current definition.