



New species of *Gekko* (Squamata: Sauria: Gekkonidae) from China: morphological and molecular evidence

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Abstract

A new species of *Gekko* is described from the south slope of the west Qinling Mts in Gansu, China. *Gekko wenzianensis*, **sp. nov.**, is characterized by its nostril-rostral contact, moderate sized body with dorsal tubercles extending from the occiput and temporal region to the back and tail base, but lacking on the forelimb and thigh, 6–8 precloacal pores in a continuous series in males, and tail generally with two cloacal spurs on each side. Molecular phylogenetic analyses using 1556 bp of mtDNA (825 bp COI and 731 bp *cyt b*) from 7 species of *Gekko* indicate that the new species is the sister taxon of *G. japonicus*. It is the twelfth species of *Gekko* recorded from China.

Key words: *Gekko wenzianensis* **sp. nov.**, Gekkonidae, Northwest China, description, molecular study

Introduction

Gekkonid lizards of the genus *Gekko* Laurenti, 1768, currently comprising about 32 species, are common inhabitants of plains and plateaus across temperate and tropical Asia and the western islands of Oceania. Eleven species of the genus *Gekko* have been reported so far from the Chinese mainland (Kluge 2001; Rösler & Tiedemann 2007; Zhao *et al.* 1999). During a collecting trip to north-western China in 2006, we collected specimens of a species of *Gekko* from the south slope of the west Qinling Mts in Gansu, China, which could not be assigned to any known species. It closely resembled *G. japonicus* Schlegel morphologically, but the presence or absence of tubercles in the limbs and the number of the cloacal spurs of the unidentified specimens were different from those previously reported for *G. japonicus* (Zhou *et al.* 1982; Zhao *et al.* 1999).

Molecular data are useful for understanding relationships among cryptic or sibling species. In particular, mitochondrial DNA sequences have been effectively used in many animal groups to discriminate between closely related species (e.g. Kon *et al.* 2007; Oliver *et al.* 2007; Ljubisavljević *et al.* 2007). DNA-based identification systems have the potential to facilitate both the identification of known species and the discovery of new ones. A 648 bp region near the 5' terminus of the COI gene has been used as the barcode region for members of the animal kingdom (Hebert *et al.* 2003; Savolainen *et al.* 2005). Its efficiency has been validated for various animal groups and more than 94% of the species tested possess distinctive barcode sequences with low intraspecific variation and high divergences from closely allied taxa (Hajbabaie *et al.* 2006).

Comparisons of morphological characters of the unidentified west Qinling Mts specimens with *G. japonicus*, *G. hokouensis* Pope and *G. taibaiensis* Song suggest that they represent a new species. In addition to detailed morphological studies, we examined partial DNA sequences of the mitochondrial *cyt b* gene (731 bp) and COI gene (825 bp) to test our hypothesis that the unidentified specimens were distinct from those of any described species.