



Article

A new cryptic species allied to *Plestiodon japonicus* (Peters, 1864) (Squamata: Scincidae) from eastern Japan, and diagnoses of the new species and two parapatric congeners based on morphology and DNA barcode

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Abstract

A new species of scincid lizard allied to *Plestiodon japonicus* (Peters, 1864) was described as *P. finitimus* **sp. nov.**, from the eastern part of Honshu and Hokkaido, Japan. A previous DNA study reported the taxonomic status of the eastern Japanese populations of *Plestiodon* as an undescribed species on the basis of their collective genetic distinctness from a parapatric congener *P. japonicus* sensu stricto from the western part of mainland Japan. We present the diagnostic features of *P. finitimus* compared to *P. japonicus* and *P. latiscutatus* Hallowell, 1861, the other parapatric species occurring in the Izu Peninsula and Izu Islands of central Japan, on the basis of morphological characteristics and DNA barcode patterns. Both *P. finitimus* and *P. japonicus* have a small postnasal and large anterior loreal that contacts the supralabials. In contrast, the Izu Peninsular populations of *P. latiscutatus*, which had no known diagnostic features relative to the other two species, usually have a large postnasal and small anterior loreal, with the latter separated from the supralabials by the former, or may otherwise lack a postnasal. In most populations of *P. finitimus*, the right and left prefrontals are usually isolated from each other, whereas they exhibit medial contact in most populations of *P. japonicus*. Although all the above characters are variable both within and between populations, 60–90% of the specimens from each locality on mainland Japan were correctly identified using a combination of these characters. Based on these characters, the Russian Far East population of *Plestiodon* was also identified as *P. finitimus*. The interspecific sequence differences in the standard DNA barcode region (a 658 base pair fragment of the cytochrome *c* oxidase subunit I gene of mitochondrial DNA) were distinct, and each of the three species was exclusively clustered in a neighbor-joining tree. The limited hybridization among the three species indicated by previous studies suggests that DNA barcodes could provide a reliable key for their correct identification. The implications for the biogeography and speciation of the three parapatric lizard species are briefly discussed.

Key words: mainland Japan, *Plestiodon finitimus* **sp. nov.**, *Plestiodon latiscutatus*, *Plestiodon okadae*, redescription

Introduction

The scincid genus *Plestiodon* Duméril et Bibron (formerly a part of *Eumeces* Wiegmann *sensu lato*) includes approximately 40 species distributed in North America and East Asia (Lieb 1985; Taylor 1936; Uetz 1995–2010). The East Asian members are classified into four or five endemic species groups (Brandley *et al.* 2012; Hikida 1993). One of these, the *P. latiscutatus* group, consists of six species distributed in mainland Japan (the four large islands, Kyushu, Shikoku, Honshu, and Hokkaido) and several adjacent islets, the Russian Far East, the Ryukyus, Taiwan, and eastern continental China. Monophyly of this species group was confirmed by recent molecular phylogenetic studies (Brandley *et al.* 2011, 2012). Two species of the *P. latiscutatus* group are currently recognized in mainland Japan and several adjacent islets: *P. latiscutatus* Hallowell, 1861, from the Izu Peninsula and the Izu Islands of central Japan (type locality: Shimoda, the Izu Peninsula, site 32 in Fig. 1), and *P. japonicus* (Peters,