

Study on phylogeography and species taxonomy of *Ateuchosaurus pellopleurus*
(Reptilia, Squamata, Scincidae)

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DIGEST

INTRODUCTION

The Ryukyu Archipelago is an island chain located between the Japanese main islands and Taiwan. Its northern, central and southern parts geographically delimited by two sea straits, Tokara and Kerama Gaps, are also called as the Northern, Central, and Southern Ryukyus. The high biodiversity in this archipelago has attracted the interests of taxonomists and biogeographers. Especially, the reptile fauna of the Central Ryukyus shows high endemism, and the major endemics have the late Miocene origin. Many of the endemic reptiles are also known to show the large genetic divergences between the Amami and Okinawa Groups, which sometimes make demands of taxonomic revision. On the other hand, some native reptiles and amphibians have the exceptionally wide distributions including the Northern and Southern Ryukyus and shows continuous or complex geographic pattern of genetic variation.

Ateuchosaurus pellopleurus (Hallowell, 1861) is a scincid lizard distributed in the Northern and Central Ryukyus. This species has been treated as one of the Central Ryukyu endemics because the congener does not occur the adjacent region including the Southern Ryukyus and Taiwan. However, *A. pellopleurus* is distributed in the both sides of Tokara Gap. This distribution pattern of *A. pellopleurus* questions the biogeographic status of this species. In addition, *A. pellopleurus* has been generally considered as a single species since its original description whereas the geographic variation data has not been investigated using genetic data ever. Thus, the taxonomy of this species should also be assessed by molecular information.

In this study, the biogeographic status, geographic variation pattern and taxonomy of *A. pellopleurus* was assessed based on molecular and morphological investigations.

MATERIALS AND METHODS

The *A. pellopleurus* specimens were collected to cover its whole distribution. These specimens were morphologically observed using a stereoscopic binocular microscope. The divergence time among *A. pellopleurus* and the congener was estimated using several outgroups and DNA sequences of seven nuclear loci. The phylogenetic relationship and population genetic characteristics were assessed using DNA sequences of mitochondrial DNA (mtDNA) and one nuclear locus (*RAG1*). In addition, the detailed geographic variation in Okinawa Group was investigated using population genetic analyses on a genome-wide SNP dataset.

RESULTS

Intraspecific mtDNA phylogeny and *RAG1* haplotype network of *A. pellopleurus* indicated distinct divergence between the island samples of Okinawa Group and the other island groups. On the other hand, the island samples of the Osumi and Tokara Groups showed extremely low genetic diversity suggesting a recent population expansion, and distorted distribution of genetic polymorphism into the southern side of Tokara Gap. The estimated divergence time of *A. pellopleurus* and the congener was 10.75–31.49 MYA.

Morphological investigation revealed that the samples of Okinawa Group and the other island groups are diverged in several characters of scalation and coloration.

The population genetic analysis of SNP dataset showed distinct genetic divergence among four sample groups of northern and southern Okinawajima Island and two peripheral island groups of Okinawa Group.

DISCUSSION

The phylogeny, allele composition and population genetic characteristics based on mtDNA suggested the Northern Ryukyu population was formed by a recent founder event from the island populations of the southern side of Tokara Gap, suggesting that *A. pellopleurus* is historically one of the Central Ryukyu endemics.

The divergence time in Miocene suggests that *A. pellopleurus* has the common historical background with the major Central Ryukyu endemics. Given that the distribution of *A. pellopleurus* and the congener is located in the both sides of East China Sea and is able to be formed by simple allopatric speciation, it is suggested that the major Central Ryukyu endemics including *A. pellopleurus* was founded by the formation of Okinawa Trough.

The distinct genetic divergence suggests that the populations of the Northern Ryukyus to Amami Groups and Okinawa Group belong to different species. Given the two extant syntypes collected from Amami Group, the former species was designated as *A. pellopleurus* sensu stricto by lectotypification. On the other hand, *A. okinavensis* (Thompson, 1912) is resurrected for the latter species. Morphological investigation provided the detail description of *A. pellopleurus* and *A. okinavensis* with renewed diagnoses.

The population genetic structure of *A. okinavensis* demonstrates that the northern and southern populations in Okinawajima Island is genetically different entities reproductively isolated and deserve full species status. In addition, it is suggested that the populations of the two peripheral island groups of Okinawa Group are considered as different species. Therefore, this study revealed that *A. pellopleurus* traditionally treated as a single species consist of five species.