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Species diversity and distribution of genus *Pampus* (Pelagiaria: Stromateidae) based on global mitochondrial data

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Due to the highly similar external morphology of the *Pampus* species, misidentifications frequently occur and hinder the understanding of the taxonomy and species distributions of the genus. In this study, we generated 271 mitochondrial sequences and obtained 1,226 sequences from the public databases to understand the species diversity and distributions of the genus *Pampus*. Most phylogenetic analyses and species delimitations congruently concluded seven valid species within the genus *Pampus* (i.e., *P. argenteus*, *P. candidus*, *P. chinensis*, *P. cinereus*, *P. liuorum*, *P. minor*, and *P. punctatissimus*). Sequences of *P. argenteus* are reported through the northern South China Sea to the Japan Archipelago, which covered the type locality of *P. echinogaster*. Sequences of *P. echinogaster* in the public databases are all identified as *P. argenteus*, suggesting that the species should be synonymized with *P. argenteus*. Furthermore, sequences of *P. griseus* were identical to our *P. cinereus* data and, therefore, should be treated as a synonym of the latter. Inference on divergence time and ancestral distribution implied that the genus *Pampus* originated in the central Indo-Pacific region around 8.35–11.33 million years ago (the late Miocene), associated with the rise of the Indonesian–Australian Archipelago biodiversity hotspot. The divergence between *P. cinereus* and *P. liuorum* dated back to 1.20–1.72 million years ago, which might be related to glacial isolation during the Mid-Pleistocene transition.

KEYWORDS

mitochondrial data, *Pampus*, species distribution, taxonomy, the Indonesian–Australian Archipelago, the middle Miocene transition