

# Pleistocene isolation caused by sea-level fluctuations shaped genetic characterization of *Pampus minor* over a large-scale geographical distribution

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## Abstract

The southern lesser pomfret (*Pampus minor*) is an economically important fish, and its numbers are declining because of overfishing and environmental pollution. In addition, owing to the similarities of its external morphological characteristics to other species in the genus *Pampus*, it is often mistaken for grey pomfret (*P. cinereus*) or silver pomfret (*P. argenteus*) juveniles. In this study, the genetic diversity and structure of 264 *P. minor* individuals from 11 populations in China and Malaysia coastal waters were evaluated for the first time, to the best of our knowledge, using mitochondrial cytochrome b fragments. The results showed that *P. minor* had moderate haplotype diversity and low nucleotide diversity. Furthermore, two divergent lineages were detected within the populations, but the phylogenetic structure corresponded imperfectly with geographical location; thus, the populations may have diverged in different glacial refugia during the Pleistocene low sea levels. Analysis of molecular variation (AMOVA) showed that genetic variation originated primarily from individuals within the population. Pairwise  $F_{ST}$  results showed significant differentiation between the Chinese and Malaysian populations. Except for the Xiamen population, which was classified as a marginal population, the genetic differentiation among the other Chinese populations was not significant. During the Late Pleistocene, *P. minor* experienced a population expansion event starting from the South China Sea refugium that expanded outward, and derivative populations quickly occupied and adapted to the new habitat. The results of this study will provide genetic information for the scientific conservation and management of *P. minor* resources.