



RESEARCH PAPER

Latitudinal–environmental variations driving the local adaptation of *Pampus argenteus* stocks along the Chinese coast

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Abstract

The distribution of *Pampus argenteus* (Euphrasen, 1788) spans a pronounced latitudinal–environmental gradient from the subtropical to the subpolar zones. The species is reported to have multiple stocks along coastal China, exhibiting different spawning behaviors and habitat preferences. Such ecological variations might imply potential genetic divergence and local adaptation. We resequenced 117 genomes from six coastal stocks of *P. argenteus* in China. Although no hierarchical genetic structure was identified, over 50% of the single-nucleotide polymorphisms (SNPs) indicated moderate to strong divergence in at least two stocks. The Mantel test identified 21 100-kb sliding windows with significant isolation by distance and environment, while a majority did not. Given the lack of genome-wide isolation by distance, the 21 windows may be under selection pressure from the latitudinal–environmental variations. Among the 21 windows, certain genes were linked to circadian clock regulation and thermal stress response, suggesting sea surface temperature and sunshine duration as selective forces. A total of 17 genes regulated neuron activity; variations near these genes might subsequently shape the different spawning and migratory behaviors among the stocks. Additionally, 1204 SNPs were mapped to non-coding regions; 14 transcriptional and translational factors were identified in the 21 windows. These findings imply that alterations in gene expression might contribute to the local adaptation of the *P. argenteus* stocks.

Keywords *Pampus argenteus* · Whole-genome resequencing · Population structure · Sunshine duration · Sea surface temperature · Local adaptation

Special Topic: Ecology & Environmental Biology.

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Introduction

Variations in habitat environments can influence the fitness of marine organisms, leading to spatially divergent selection and local geographic adaptations among populations (Kenchington et al. 2015; Leggett et al. 1984). The correlations among phenotypic, environmental, and genetic variations help identify loci undergoing local adaptation and natural selection. Numerous genes associated with growth

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