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Chromosome-level genome assembly of the silver pomfret *Pampus argenteus*

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Pampus argenteus **(Euphrasen, 1788) is one of the major fishery species in coastal China.** ***Pampus argenteus*** **has a highly specialized morphology, and its declining fishery resources have encouraged massive research efforts on its aquacultural biology. In this study, we reported the first high-quality chromosome-level genome of** ***P. argenteus*** **obtained by integrating Illumina, PacBio HiFi, and Hi-C sequencing techniques. The final size of the genome was 518.06 Mb, with contig and scaffold N50 values of 20.47 and 22.86 Mb, respectively. The sequences were anchored and oriented onto 24 pseudochromosomes based on Hi-C data corresponding to the 24-chromatid karyotype of** ***P. argenteus*****. A colinear relationship was observed between the** ***P. argenteus*** **genome and that of a closely related species (*Scomber japonicus*). A total of 24,696 protein-coding genes were identified from the genome, 98.9% of which were complete BUSCOs. This report represents the first case of high-quality chromosome-level genome assembly for** ***P. argenteus*** **and can provide valuable information for future evolutionary, conservation, and aquacultural research.**

Background & Summary

Pampus argenteus (Euphrasen, 1788; Fishbase ID: 491), also known as the silver pomfret, is a commercially important fish in the Northwest Pacific area that is widely distributed throughout the South China Sea to coastal Japan, Korea, and Russia[1,2]. It belongs to the family Stromateidae of the suborder Stromateoidei[3], which was identified in Scombriformes according to a recent phylogenetic study[4]. This species is one of the major fishery species in coastal China, with harvests exceeding three million tons in 2016[5]. Overfishing and environmental changes have resulted in a noticeable decline in *P. argenteus* fishery resources in recent years[6,7]. The aquaculture of *P. argenteus* has made substantial progress, which in some ways compensates for the decline in fishery resources[8,9]. However, the industry is still facing many restrictions and issues owing to the high sensitivity of *P. argenteus* to injury and pathogenic infection during aquaculture and transportation[10]. Due to the medusivorous habit of *P. argenteus*[11], its aquaculture greatly relies on fish bait composed of jellyfish and minced fish meat. Using fish bait leads to higher costs in water quality control and risking outbreaks of harmful pathogens, which have become one of the major bottlenecks in *P. argenteus* aquaculture, necessitating substitution with better formulated feeds[12]. However, the digestive and immune systems of *P. argenteus* are considered specialized for the digestion of jellyfish and tolerance of medusocongestin[13,14]. The inclusion of jellyfish in an artificial diet can significantly improve the growth performance and survival rate of *P. argenteus* larvae and juveniles[15]. The impact of changing fish bait to formulated feed on *P. argenteus* at different growth stages still requires further clarification. Clarifying the genetic basis of the physiological process of *P. argenteus*, particularly those related to the immune response[16], intestinal enzyme activities[14], stress responses[17], etc., is becoming increasingly important for the future prospects of the aquaculture industry. However, the genome of *P. argenteus*, which represents the foundation of physiological responses[18], has not yet been completely sequenced.

In addition to its fishery importance, *P. argenteus* is considered one of the most advanced species within Stromateoidei[19]. The dorsal and anal fin spines of *P. argenteus* are reduced into small blades, with a pelvic fin absent from its abdominal region. Stromateoidei is distinct from other Actinopterygii by having a unique

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