Protocols for chromosome-level genome assembly of the spotted sea bass, Lateolabrax maculatus

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Abstract

Background: The spotted sea bass (*Lateolabrax maculatus*) is a valuable commercial fish that is widely cultured in China. While analyses using molecular markers and population genetics have been conducted, genomic resources are lacking.

Finding: Here, we report a chromosome-scale assembly of the spotted sea bass genome by high-depth genome sequencing, assembly and annotation. The genome scale was 0.62 Gb with contig and scaffold N50 length to be 31 Kb and 1,040 Kb, respectively. Hi-C scaffolding of the genome resulted in 24 pseudochromosomes containing 77.68% of the total assembled sequences. A total of 132.38Mb repeat sequences were detected, accounting for 20.73% of the assemble genome. 22,015 protein-coding genes were predicted, of which 96.52% were homologous to proteins in various databases. In addition, we constructed a phylogenetic tree using 1,586 single-copy gene families and identified 125 unique gene families in the spotted sea bass genome.

Conclusions: We assembled a spotted sea bass genome, which will be a valuable genomic resource to understand the biology of the spotted sea bass, and will also lead to the development of molecular breeding techniques to generate spotted sea bass with better economical traits.

Collection

PROTOCOLS

1. [DNA extraction for vertebrate tissues using Phenol:Chloroform:Isoamylol](#)

CONTACT: [Chang Li](#)

2. [Short insert size WGS libraries preparation for assembly of the Lateolabrax maculatus genome](#)

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3. **Mate-pair large libraries preparation for assembly of the Lateolabrax maculatus genome**

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4. **Fish genome assembly and annotation pipeline**

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5. **Hi-C library preparation for the Lateolabrax maculatus genome**

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6. **The pipeline of Hi-C assembly**

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