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High-quality reference genome of the Siamese fighting fish Betta splendens, a model species for the study of aggression

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Abstract

Siamese fighting fish Betta splendens are notorious for their aggressiveness and accordingly have been widely used to study aggression. However, the lack of a reference genome has so far limited the understanding of the genetic basis of aggression in this species. Here we present the first reference genome assembly of the Siamese fighting fish.
We first sequenced and de novo assembled a 465.24 Mb genome for the B. splendens variety Giant, with a weighted average (N50) scaffold size of 949.03 Kb and an N50 contig size of 19.01 Kb, covering 99.93% of the estimated genome size. To obtain a chromosome-level genome assembly, we constructed one Hi-C library and sequenced 75.24 Gb reads using the BGISEQ-500 platform. We anchored approximately 93% of the scaffold sequences into 21 chromosomes and evaluated the quality of our assembly using the high contact frequency heatmap and BUSCO. We also performed comparative chromosome analyses between Oryzias latipes and B. splendens, revealing a chromosome conservation evolution in B. splendens. We predicted a total of 23,981 genes assisted by RNA-seq data generated from brain, liver, muscle and heart tissues of Giant, and annotated 15% repetitive sequences in the genome. Additionally, we resequenced other five B. splendens varieties and detected ~3.4M single-nucleotide variations (SNVs) and 27,305 indels.
We provide the first chromosome-level genome for the Siamese fighting fish. The genome will lay a valuable foundation for future research on aggression in B. splendens.

Troubleshooting

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The pipeline of Hi-C assembly

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