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🌐 Protocols for "Chromosome-level genome assembly of the humpback puffer, *Tetraodon palembangensis*"

Rui Zhang¹, Chang Li¹, Mengjun Yu¹, Xiaoyun Huang¹, Mengqi Zhang¹, Shanshan Liu¹, Shanshan Pan¹, Weizhen Xue¹, Congyan Wang¹, Chunyan Mao¹, He Zhang², Guangyi Fan¹

¹BGI-Qingdao, BGI-Shenzhen, Qingdao 266555, China;

²BGI-Qingdao, BGI-Shenzhen, Qingdao 266555, China. Department of Biology, Hong Kong Baptist University, Hong Kong, China

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ABSTRACT

In this study we assembled the first chromosome-level genome assembly of the humpback puffer (*Tetraodon palembangensis*), a species of poisonous freshwater pufferfish mainly distributed in Southeast Asia. This utilized Oxford Nanopore and BGISEQ-500 sequencing, stLFR libraries and Hi-C assembly, and the protocols for nucleic acid extraction, library construction and sequencing are all made available here. The resulting genome size was 362 Mb with a ~1.78 Mb contig N50 and ~15.8 Mb scaffold N50. Based on the assembled genome, ~61.5Mb (18.11%) repeat sequences were identified, 19,925 genes were annotated, and 90.01% of these genes could be predicted with function. Finally, a phylogenetic tree of ten teleost fish species was successfully constructed using this and public data. These protocols are made available for others carrying vertebrate genome assembly, and the open data and published study for comparative genome studies.

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FILES

Protocol

NAME

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

VERSION 1

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Chang Li

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Protocol

NAME

RNA isolation with TRIzol

VERSION 1

CREATED BY

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Protocol

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BGISEQ-500 WGS library construction

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The pipeline of Hi-C assembly

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stLFR library construction

VERSION 1

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Protocol

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RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing

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BGISEQ-500 Sequencing

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