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

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ABSTRACT

The humpback puffer, *Tetraodon palembangensis*, also known as *Pao palembangensis*, is a species of poisonous freshwater pufferfish mainly distributed in Southeast Asia (Thailand, Laos, Malaysia and Indonesia). Despite interesting biological features, such as its very inactive nature, *tetrodotoxin production* and body expansion mechanisms, molecular research on the humpback puffer is still rare because of the lack of a high-quality reference genome. Here, we reported a first chromosome-level genome assembly of an adult humpback puffer, of which the genome size is 362 Mb with ~1.78 Mb contig N50 and ~15.8 Mb scaffold N50s. Based on the genome, ~61.5 Mb (18.11%) repeat sequences were also identified, and totally 19,925 genes were annotated, 99.20% of which could be predicted with function using protein-coding function databases. Finally, a phylogenetic tree was constructed with single-copy gene families from ten teleost fishes. The humpback puffer genome will be a valuable genomic resource to illustrate possible mechanisms of tetrodotoxin synthesis and tolerance, providing clues for future detailed studies of biological toxins.

DOI

dx.doi.org/10.17504/protocols.io.bkczksx6

COLLECTION CITATION

Rui Zhang, Chang Li, Mengjun Yu, Xiaoyun Huang, Mengqi Zhang, Shanshan Liu, Shanshan Pan, Weizhen Xue, Congyan Wang, Chunyan Mao, He Zhang, Guangyi Fan 2020. Protocols for "Chromosome-level genome assembly of the humpback puffer, Tetraodon palembangensis". protocols.io

https://dx.doi.org/10.17504/protocols.io.bkczksx6

KEYWORDS

humpback puffer, *Tetraodon palembangensis*

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 CREATED

Aug 27, 2020

LAST MODIFIED

Aug 27, 2020

COLLECTION INTEGER ID

41081

ABSTRACT

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The humpback puffer, *Tetraodon palembangensis*, also known as *Pao palembangensis*, is a species of poisonous freshwater pufferfish mainly distributed in Southeast Asia (Thailand, Laos, Malaysia and Indonesia). Despite interesting biological features, such as its very inactive nature, tetrodotoxin production and body expansion mechanisms, molecular research on the humpback puffer is still rare because of the lack of a high-quality reference genome. Here, we reported a first chromosome-level genome assembly of an adult humpback puffer, of which the genome size is 362 Mb with ~1.78 Mb contig N50 and ~15.8 Mb scaffold N50s. Based on the genome, ~61.5Mb (18.11%) repeat sequences were also identified, and totally 19,925 genes were annotated, 99.20% of which could be predicted with function using protein-coding function databases. Finally, a phylogenetic tree was constructed with single-copy gene families from ten teleost fishes. The humpback puffer genome will be a valuable genomic resource to illustrate possible mechanisms of tetrodotoxin synthesis and tolerance, providing clues for future detailed studies of biological toxins.

**FILES**

- Hi-C library preparation for the *Lateolabrax maculatus* genome
  - **Version 1**
  - by Chang Li

- BGISEQ-500 WGS library construction
  - **Version 1**
  - by Xinming Liang, Beijing Genomics Institute

- The pipeline of Hi-C assembly
  - **Version 1**
  - by Kailong Ma

**Citation:** Rui Zhang, Chang Li, Mengjun Yu, Xiaoyun Huang, Mengqi Zhang, Shanshan Liu, Shanshan Pan, Weizhen Xue, Congyan Wang, Chunyan Mao, He Zhang, Guangyi Fan (08/27/2020). Protocols for "Chromosome-level genome assembly of the humpback puffer, *Tetraodon palembangensis*."  
[https://dx.doi.org/10.17504/protocols.io.bkc2ksx6](https://dx.doi.org/10.17504/protocols.io.bkc2ksx6)

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