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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, [tetradotoxin 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 tetradotoxin synthesis and tolerance, providing clues for future detailed studies of biological toxins.

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The pipeline of Hi-C assembly
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