

Chromosome-level genome of *Poropuntius huangchuchieni* provides a diploid progenitor-like reference genome for the allotetraploid *Cyprinus carpio*

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Abstract

The diploid *Poropuntius huangchuchieni* in the cyprinid family, which is widely distributed in the Mekong and Red River basins, is one of the most closely related diploid progenitor-like species of allotetraploid common carp, which was generated by merging of two diploid genomes during evolution. Therefore, the *P. huangchuchieni* genome is essential for polyploidy evolution studies in Cyprinidae. Here, we report a high-quality chromosome-level genome assembly of *P. huangchuchieni* by integrating Oxford Nanopore and Hi-C technology. The assembled genome size was 1021.38 Mb, 895.66 Mb of which was anchored onto 25 chromosomes with a N50 of 32.93 Mb. The genome contained 486.28 Mb repetitive elements and 24,099 protein-coding genes. Approximately 95.9% of the complete BUSCOs were detected, suggesting a high completeness of the genome. Evolutionary analysis revealed that *P. huangchuchieni* diverged from *Cyprinus carpio* at approximately 12 Mya. Genome comparison between *P. huangchuchieni* and the B subgenome of *C. carpio* provided insights into chromosomal rearrangements during the allotetraploid speciation. With the complete gene set, 17,474 orthologous genes were identified between *P. huangchuchieni* and *C. carpio*, providing a broad view of the gene component in the allotetraploid genome, which is critical for future genetic analyses. The high-quality genomic dataset created for *P. huangchuchieni* provides a diploid progenitor-like reference for the evolution and adaptation of allotetraploid carps.

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