

# Chromosome-level genome assembly of *Acanthogobius ommaturus* provides insights into evolution and lipid metabolism

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## Abstract

*Acanthogobius ommaturus* is a large, economically important annual fish widely distributed in coastal and estuarine areas. The adults will die after breeding, and its life cycle is only one year. The first chromosome-level genome assembly of *A. ommaturus* was obtained by PacBio and Hi-C sequencing in this study. The final genome assembly after Hi-C correction was 921.49 Mb, with contig N50 and scaffold N50 values of 15.70 Mb and 40.99 Mb, respectively. The assembled sequences were anchored to 22 chromosomes by using Hi-C data. A total of 18,752 protein-coding genes were predicted, 97.90% of which were successfully annotated. *A. ommaturus* is phylogenetically closely related to *Periophthalmodon magnuspinnatus*, *Boleophthalmus pectinirostris*, diverging approximately 31.9 million years ago with the two goby species. The *A. ommaturus* genome displayed 597 expanded and 3,094 contracted gene families compared with the common ancestor. A total of 1155 positive selected genes (PSGs) ( $p < 0.05$ ) were identified. Based on comparative genomic analyses, we obtained several expanded genes such as ACSBG2, LRP1, LRP6 and ZNF638 involved in lipid metabolism. Totally twenty candidate genes were identified under positive selection, which associated with lifespan including ERCC6, IGF1, POLG, and TERT. Interspecific collinearity analysis showed a high genomic synteny between *A. ommaturus* and *Periophthalmodon magnuspinnatus*. The effective population size of *A. ommaturus* decreased drastically during 200-100Ka because of Guxiang ice age, then increased gradually following warm periods. This study provides pivotal genetic resources for in-depth biological and evolutionary studies, and underlies the molecular basis for lipid metabolism.

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