

Large Yellow croaker

Sheima Humod Alali

Intro.To Genomics 485

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outline

- General information
- Genome paper
- General genome inform
- Sequencing strategy
- Sequencing methods
- Genome assembly
- Genome outcome

General information

- Common name: Large Yellow Croaker.
- Scientific Name: *Larimichthys Crocea*.
- Order: Perciformes.
- The L.Croaker, is an economically important marine fish species in China that is largely endemic to coastal waters of the eastern and southern parts of the country. Males can reach 80 cm, but a common size is 60cm.

General inform

- Is a useful species for understanding the evolution of immune systems and the genetic bases of sensory adaptations of Sciaenidae.
- *L. crocea* is an important enough commercial species to have its genome mapped On 2015 it became the 200th organism to have its genome annotated by the NCBI Eukaryotic Genome Annotation Pipeline. Genus *Larimichthys* . We estimate the genome size to be 728 Mb with 19,362 protein-coding genes.

Genome paper



ARTICLE

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OPEN

The draft genome of the large yellow croaker reveals well-developed innate immunity

Changwen Wu^{1,*}, Di Zhang^{2,*}, Mengyuan Kan^{3,*}, Zhengmin Lv^{1,*}, Aiyi Zhu^{1,*}, Yongquan Su^{4,*}, Daizhan Zhou², Jianshe Zhang¹, Zhou Zhang², Meiyong Xu¹, Lihua Jiang¹, Baoying Guo¹, Ting Wang³, Changfeng Chi¹, Yong Mao⁴, Jiajian Zhou¹, Xinxiu Yu¹, Hailing Wang¹, Xiaoling Weng⁵, Jason Gang Jin⁶, Junyi Ye⁵, Lin He² & Yun Liu⁵

The large yellow croaker, *Larimichthys crocea*, is one of the most economically important marine fish species endemic to China. Its wild stocks have severely suffered from overfishing, and the aquacultured species are vulnerable to various marine pathogens. Here we report the creation of a draft genome of a wild large yellow croaker using a whole-genome sequencing strategy. We estimate the genome size to be 728 Mb with 19,362 protein-coding genes. Phylogenetic analysis shows that the stickleback is most closely related to the large yellow croaker. Rapidly evolving genes under positive selection are significantly enriched in pathways related to innate immunity. We also confirm the existence of several genes and identify the expansion of gene families that are important for innate immunity. Our results may reflect a well-developed innate immune system in the large yellow croaker, which could aid in the development of wild resource preservation and mariculture strategies.

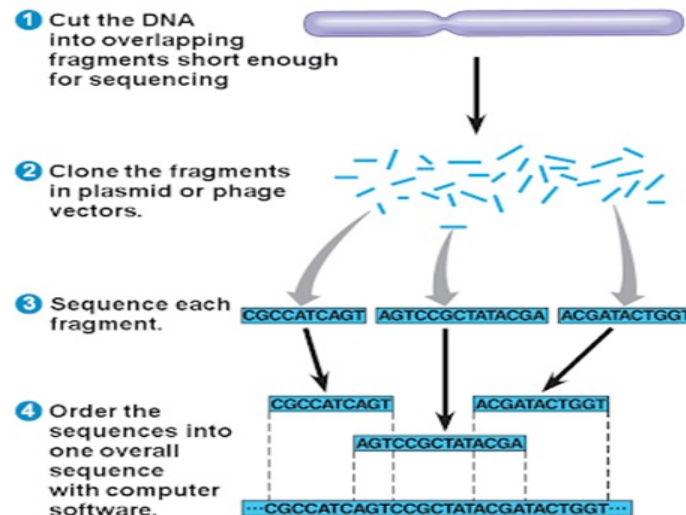
General Genome inform

- **DNA Sources:** wild-caught female croaker from the abdominal muscle
- **Genome Size:** The 25-mer counts were chosen using Jellyfish46, and the estimated croaker genome size is 728 Mb.
- **Number of Gene:** 19,033.

Sequencing strategy

- Whole genome Shotgun Sequencing strategy was used.

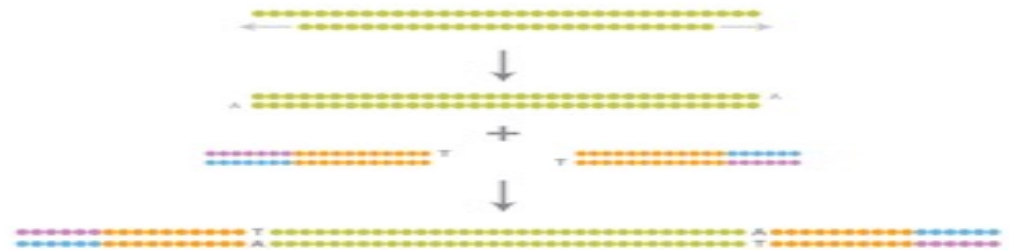
Whole-Genome Shotgun Sequencing overview, steps and achievements



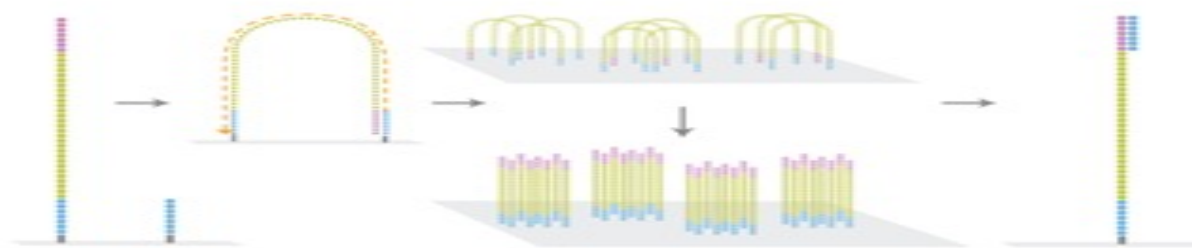
Sequencing methods

- Illumina Sequencing method was used.

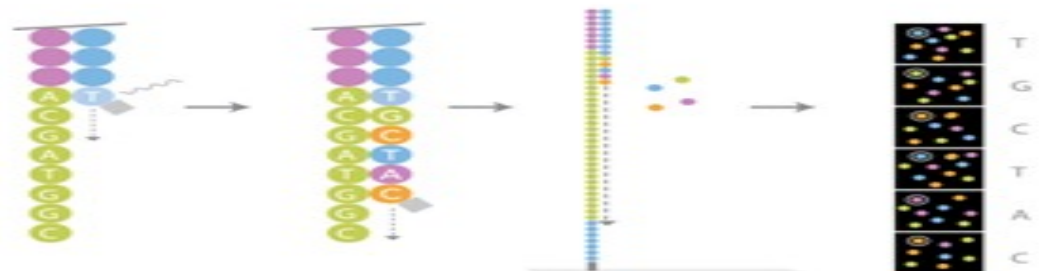
Library Preparation



Cluster Generation



Sequencing



Genome Assembly

- They were de novo assembled.
- 52x Coverage.
- 6,934 contigs N50.
- 350 scaffolds N50.
- 75 heterozygous SNP in croaker.

Genome Assembly

- We performed functional annotation for protein-coding genes in the croaker genome.
- DNA elements are most abundant in the croaker genome 2.96%.

Genome Outcome

- The phylogenetic tree revealed that stickleback (order Gasterosteiformes) was most closely related to croaker (order Perciformes).
- Results revealed a well-established innate immune system and a partially established adaptive immune system in croaker.
- presence of innate immunity-relevant genes encoding TLRs, ILs and TNFs in the croaker genome, which is consistent with previous studies.
- Meanwhile, TNF superfamilies of ligands and receptors showed expansion in croaker, suggesting that innate immunity is strengthened by extra copies of TNF-related genes.

Question

- What is the Sequencing strategy was used?
- How much the genome size?