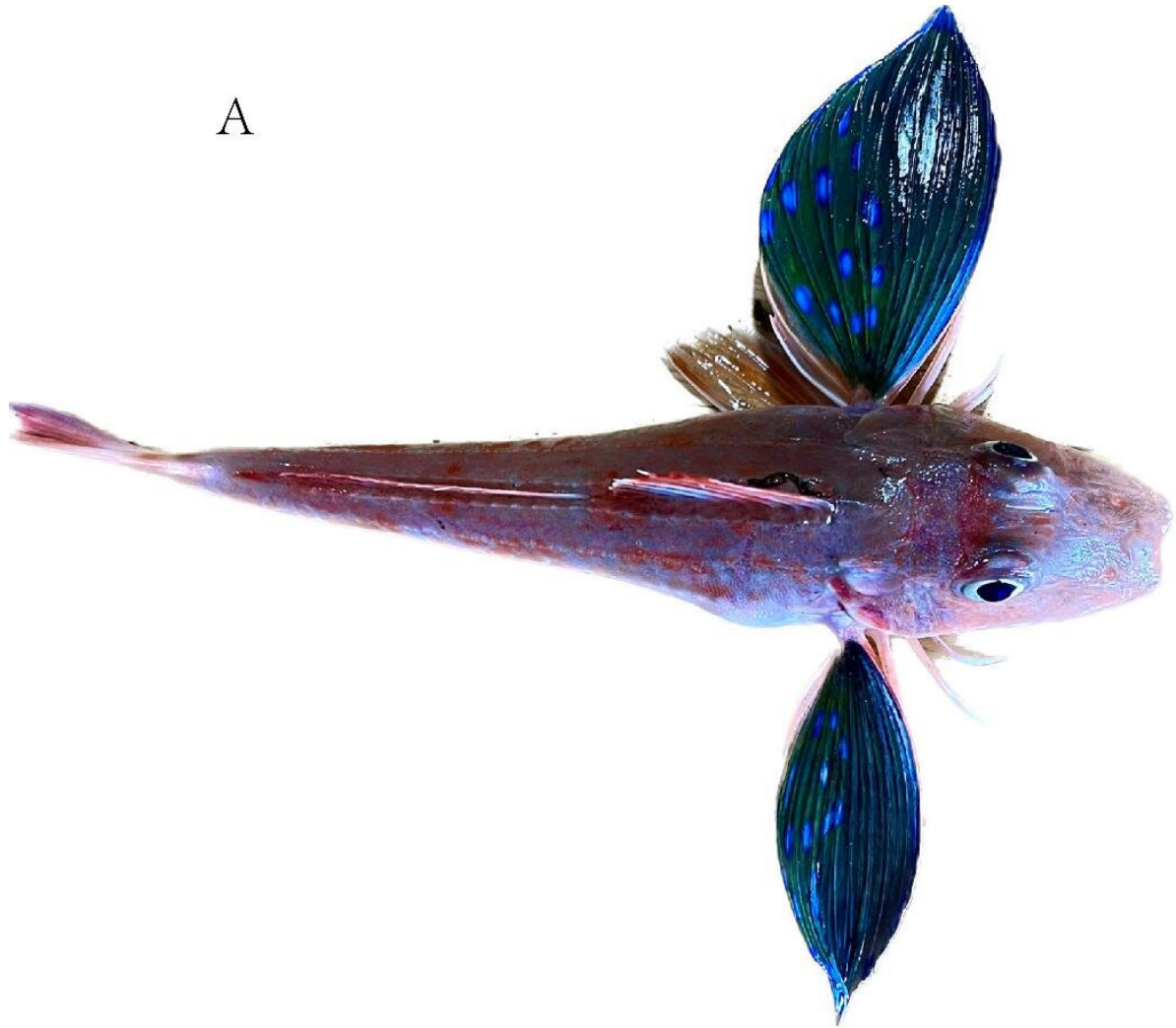


Scientists create high-quality chromosome-level reference genome of *Chelidonichthys spinosus*

July 18 2023, by Li Yuan

A



B



Total length: 14.80 cm
Total weight: 31.2 g
Sex: immaturation (juvenile)

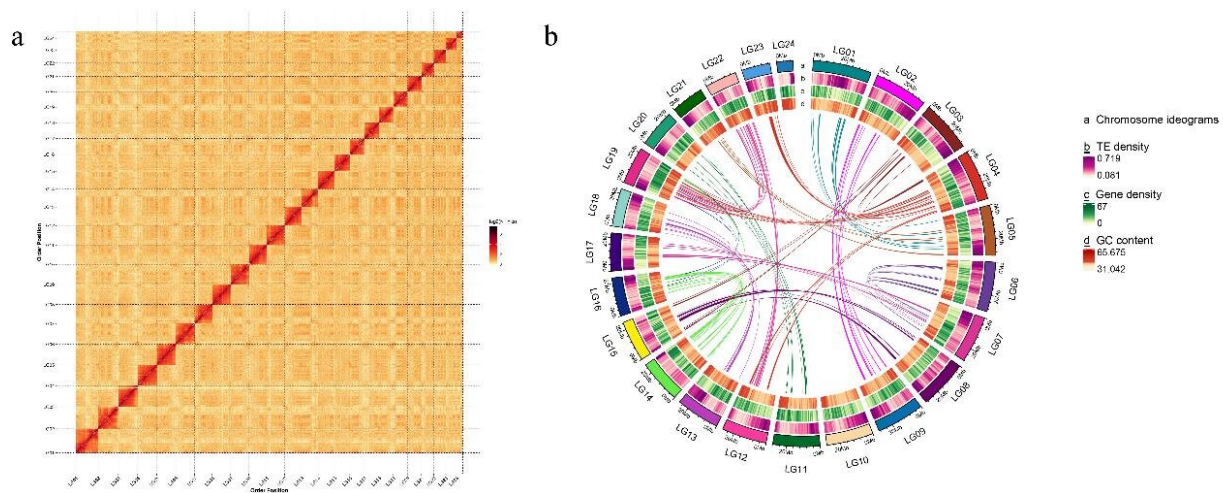
Photography of *Chelidonichthys spinosus* specimen. Credit: IOCAS

Chelidonichthys spinosus, commonly known as the spiny red gurnard in the order Scorpaeniformes, is a typical migratory fish that undertakes offshore overwintering migrations in late autumn and early winter, and returns to nearshore areas for spawning in the spring.

It has a snow-white belly, reddish-brown body, and underneath its gills, it possesses a pair of colorful, shimmering green fluorescent "butterfly wings." Below these wings, there are three pairs of appendages resembling ballet dancers feet. In reality, these are six separate pectoral fins that are highly flexible and contain taste buds that aid in foraging.

In order to investigate the evolutionary mechanisms behind the unique morphological features and ecological adaptations of *C. spinosus*, a research team led by Prof. Zhang Hui from the Institute of Oceanology of the Chinese Academy of Sciences (IOCAS) has conducted deep sequencing of its genome using Illumina short-read, PacBio long-read, and Hi-C techniques. They obtained high-quality chromosome-level reference genome of *C. spinosus* in the Yangtze River Estuary. The results were published in *Scientific Data* on July 12.

The results showed that the genome size of *C. spinosus* is approximately 624.7Mb, with a contig N50 length of about 13.77Mb and a scaffold N50 length of about 28.11Mb. A substantial 99.29% of the initially assembled sequences were successfully anchored to 24 chromosomes, and the genome contained 35.96% repeat sequences and 8,235 non-coding RNAs.



Characteristics of the *C. sinosus* genome. (a) Hi-C intra-chromosomal contact map of the *C. sinosus* genome assembly. (b) Circos plot of the *C. sinosus* genome assembly. Credit: IOCAS

A total of 25,358 [protein-coding genes](#) were predicted, of which 24,072 genes (94.93%) were functionally annotated. Co-linearity analysis showed a significant co-linearity between *C. sinosus* and *Cyclopterus lumpus*, suggesting a potentially close phylogenetic relationship between the two species.

"The assembled [genome](#) sequences can provide valuable information for elucidating the genetic adaptation and potential molecular basis of *C. sinosus*, which can be used to establish more effective management and conservation strategies for this species," said Wang Yibang, first author of the study.

"These [genomic data](#) can also be used for future comparative genomics and [phylogenetic studies](#), which may shed light on the genomic evolution and phylogeny of Scorpaeniformes and other teleost fish and

vertebrates," added Prof. Zhang.

More information: Yibang Wang et al, Chromosome genome assembly and annotation of the spiny red gurnard (*Chelidonichthys spinosus*), *Scientific Data* (2023). [DOI: 10.1038/s41597-023-02357-y](https://doi.org/10.1038/s41597-023-02357-y)

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