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# Editorial: Mining, development, and utilization of genetic resources related to economic traits of aquatic animals based on omics technology

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Editorial on the Research Topic
Mining, development and utilization of genetic resources related to economic traits of aquatic animals based on omics technology

The research on genetic resources of aquatic animals has made significant progress in the past few decades, especially in the mining of functional genes and regulatory networks related to economic traits, which was strongly supported by the mature commercialization of high-throughput sequencing technology, also known as omics technology (Munang'andu et al., 2018; Martyniuk et al., 2020; Davey et al., 2021). It is efficient to reveal the signal pathways closely related to the development, growth, sexual maturity, neuroendocrine, and nutritional metabolism of aquatic animals using omics technology. We anticipate that in the coming years, many novel and disruptive technologies will apply in the aquaculture industry and facilitate the blooming of research on the genetic resources of aquatic animals.

It is our pleasure to present this Research Topic, "*Mining, Development, and Utilization of Genetic Resources Related to Economic Traits of Aquatic Animals Based on Omics Technology*", to the broad readership of Frontiers in Marine Science. We have selected four original research papers on different economic aquaculture animals, including the giant freshwater prawn (*Macrobrachium rosenbergii*), the Pacific white shrimp (*Litopenaeus vannamei*), the sea cucumber (*Apostichopus japonicas*), and the scallop (*Patinopecten yessoensis*) (Figure 1). Scientists used omics technologies such as RNA-seq and WGBS to find out the potential connections between genes and economic traits, which shed light on the mining of the genetic resources of aquatic animals, especially invertebrates. Here, we briefly highlight the key points of each paper in this Research Topic so as to facilitate readers quick and convenient grasping of the core principles of various research projects and comfortable exploration of key points of interest.

Wei et al. obtained and confirmed the function of several germ cell-related genes, including RAD51, SPDS, and Fem-1C, in germ cells of *M. rosenbergii*, using transcriptome

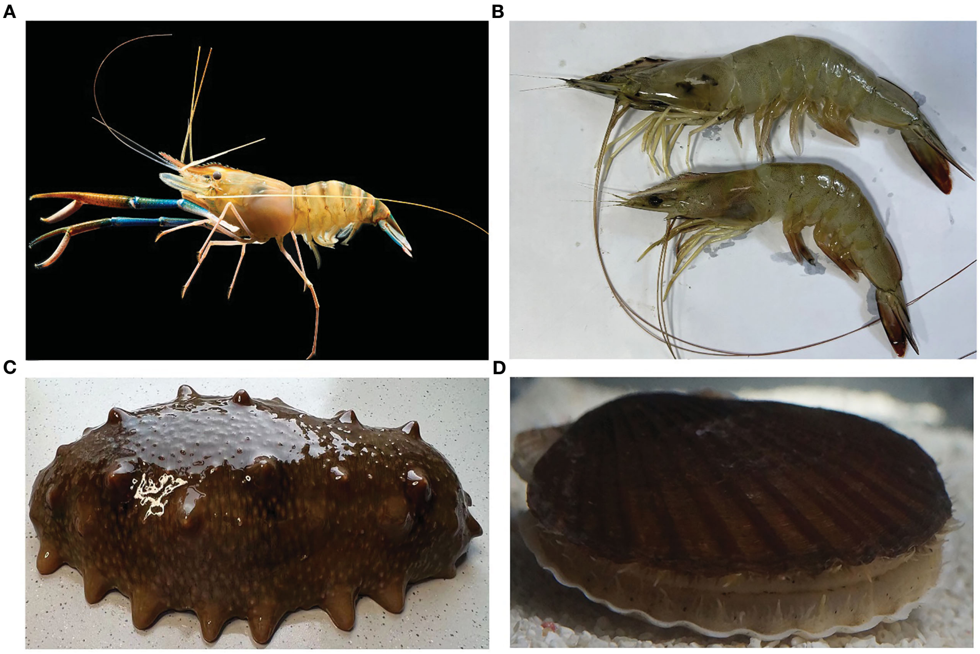

FIGURE 1
Photos of aquatic animal involved in this Research Topic **(A)**. *Macrobrachium rosenbergii*. **(B)** *Litopenaeus vannamei*. B. **(C)**. *Apostichopus japonicas*. **(D)** *Patinopecten yessoensis*.

technology. This discovery will provide a theoretical basis for molecular mechanism research on the regulation of gonadal development and molecular breeding to overcome the precocious puberty issue in giant freshwater prawns. Si et al. identified and analyzed the Ras superfamily genes in the Pacific white shrimp, *L. vannamei*, based on genome and transcriptome data, which made the research of this gene family a step forward in crustaceans. The authors found 108 Ras superfamily genes and provided clues for the structure, classification, evolution, and function of these genes in shrimp, which is of great significance to understanding the growth, development, and immunity mechanisms of shrimp or other crustaceans. Chang et al.made the first attempt to investigate the differentially expressed genes (DEGs) and differentially methylated genes (DMGs) in the body wall tissue of sea cucumbers in response to heat stress. Significant changes in overall DNA methylation levels and gene transcription patterns have been found under heat stress, enriched in energy metabolism and immune regulation-related pathways. This study provided important targets for further revealing the response or adaptation mechanism of sea cucumbers to heat stress and understanding the epigenetic regulatory mechanism in this species. Developing carotenoid-enriched varieties is one of the focuses of marine animal breeding. In order to understand the molecular mechanism of carotenoid deposition in marine animals, Li et al.identified the key module and hub genes involved in carotenoid accumulation regulation in scallops through comparative transcriptome analysis and weighted gene co-expression network analysis (WGCNA). 683 DEGs have been found between normal Yesso scallops with white muscle and Haida golden scallops with carotenoid-enriched orange muscle, among which PyBCO-like 1, WDR3, RPP29, TBL3, RIOK2, and NOB1, HSP70s, HSP702Bs, and ACOX1 were identified as hub genes. The results will provide new insights into the regulation of carotenoid accumulation and a feasible solution for carotenoid content improvement in scallops.

We are happy that many young scientists contributed innovative work to this Research Topic. As guest editors of this Research Topic, we are very grateful to all the authors for their efforts and contributions. We also thank all reviewers for their careful evaluation and valuable suggestions of the articles assigned to them, which made great improvements to these articles. Finally, we are glad to acknowledge Frontiers in Marine Science for always supporting this Research Topic.

## Author contributions

BZ wrote the draft of the manuscript. All the guest editors reviewed and revised the manuscript. All authors contributed to the article and approved the submitted version.

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## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## Publisher's note

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