

Editorial

Genetics and Biotechnology—The Section Editor-in-Chief's View

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Genetics and biotechnology make increasingly important contributions to fishery science, fishery management, aquaculture, and related fields. It is fitting that *Fishes* has a dedicated Section on Genetics and Biotechnology, which was set up in 2021. Just two years later—with the help of journal staff, 24 Editorial Board members, peer reviewers, and of course the authors themselves—we have a corpus of work that shows the ongoing development of our discipline. This Editorial will highlight a selection of the interesting results published in this Section of *Fishes*.

Understanding the genetic structuring within a species is critical for effective fishery or conservation management. Campbell et al. [1] showed very high levels of genetic differentiation among populations of Shoshone sculpin *Cottus greeniei* in the Hagerman Valley of Idaho in the western United States; hence, preserving the genetic diversity of this species will require the protection and preservation of multiple isolated populations. Ollé-Vilanova et al. [2] showed significant genetic differentiation between an Iberian Peninsula–Strait of Gibraltar stock and North African stocks of bullet tuna *Auxis rochei*, and suggested that distinct management regimes should be implemented for these two genetic stocks. Nguyen et al. [3] found that populations of giant mottled eels *A. marmorata* in central Vietnam were genetically similar to eels found in North Pacific populations, while those from farther south resembled South Pacific populations, highlighting a combination of differentiated stocks and thus informing fishery management. An analysis of variations in mitochondrial *COI* sequences by Zuo et al. [4] revealed Colombia as the most likely origin of the invasive mussel *Mytella strigata* in China.

The past decade has seen the development and use of environmental DNA (eDNA) assays to document the occurrence of species in ecosystems of interest. Demonstrating the sensitivity of eDNA techniques, Przybyla-Kelly et al. [5] directly observed the invasive round goby *Neogobius melanostomus* in 23% of trawl samples and detected its eDNA in 74% and 66% of samples assayed using digital droplet PCR and quantitative PCR, respectively, mostly in samples collected at <30 m depths and in the fall in lakes Huron and Michigan in North America. Although snorkel surveys remain the most efficient sampling method when water clarity is high, Westhoff et al. [6] applied eDNA assays to sample for longnose darter *Percina nasuta*, a small-bodied cryptic fish, detecting the species 27 km upstream of their known range. Harris et al. [7] showed that under-ice eDNA sampling correctly identified overwintering grounds for striped bass *Morone saxatilis* in a complex river system, allowing for comparisons of population size and location between years, with the potential of being used more easily in river systems than traditional acoustic tagging surveys. Kagayama et al. [8] designed a loop-mediated isothermal amplification (LAMP) eDNA assay to detect invasive carps, silver carp *Hypophthalmichthys molitrix*, bighead carp *H. nobilis*, black carp *Mylopharyngodon piceus*, and grass carp *Ctenopharyngodon idella*, showing that despite having limitations, the LAMP assay can rapidly analyze eDNA samples and is robust to inhibition.

Molecular markers are immensely useful for reconstructing the evolution of life. Molecular markers are immensely useful for reconstructing the evolution of life. Li et al. [9]



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sequenced the complete mitochondrial DNA (mtDNA) molecule of giant honeycomb oyster *Hyotissa hyotis*, the first such sequence for the family Gryphaeidae, and compared it with those of other members of the superfamily Ostroidea. The gene order for *H. hyotis* proved quite different from those of other ostreids, indicating extensive mitochondrial rearrangements and providing insight into the mitochondrial evolution of oysters. Mukherjee et al. [10] reported the molecular evolution of parvalbumin genes in bony fishes based on 19 whole genomes and 70 transcriptomes, finding unexpectedly high parvalbumin diversity in teleosts; the authors also characterized parvalbumin gene expression in 17 tissues of common carp *Cyprinus carpio*, a species with 21 parvalbumin genes in its genome.

The advent of cost-effective large-scale DNA sequencing has driven a deeper understanding of the genomic responses of aquatic organisms to their environment. Among the many thought-provoking papers published in *Fishes* in this area, Hu et al. [11] analyzed the transcriptomes and metabolomes of hepatopancreas to determine the response of the prawn *Palaemon carinicauda* to early-stage infection by the microsporidian *Enterocytozoon hepatopenae*; the results showed 730 differentially expressed genes that were involved in the metabolic, detoxification, and antioxidant pathways, advancing the understanding of mechanisms underlying the stunted growth of shrimps after infection. Ji et al. [12] characterized the physiological and transcriptomic responses of the Asiatic hard clam *Meretrix meretrix* to the alga *Heterosigma akashiwo*, which is responsible for harmful algal blooms; the results showed 544 unigenes that were differentially expressed between the control and exposed clams, with significant up-regulation of lysosome-related genes and transport proteins, suggesting that clam metabolism was remodeled, possibly for the digestion of *H. akashiwo*. Yang et al. [13] analyzed the physiological changes and immune responses in hepatopancreas and other tissues of pearl oyster *Pinctada fucata* to different temperatures and salinities; the expression levels of antioxidant genes varied between tissues, providing insight into molecular mechanisms of stress response and reference values that can be used to establish a model for choosing shellfish aquaculture sites. Zhang et al. [14] identified divergent patterns at the genomic, transcriptomic, and epigenomic levels between two groups of common carp; after enrichment analysis, a series of pathways associated with amino acid metabolism, including growth regulation, lipid metabolism, and the citrate cycle, were revealed.

The application of genetics has driven useful advances in the development of sustainable aquaculture production. Nile tilapia *Oreochromis niloticus* is often produced under unfavorably high temperatures. Zhou et al. [15] exposed six-week-old juveniles to water temperatures of 28, 32, and 36 °C for 15 weeks, observing that high temperatures affected tilapia gill morphology, reduced hypoxia tolerance, and inhibited aerobic metabolism, ultimately threatening viability and survival, with transcriptional data showing the metabolic pathways that mediate these outcomes. A limited supply of fish meal has driven development of feeds using soybean meal, which is not well utilized by some cultured species. Seibel et al. [16] evaluated a diverse range of stress markers to assess the effects of soybean meal on the welfare of rainbow trout *Oncorhynchus mykiss*. The transcription level of certain genes emerged as potentially useful indicators of inadequate nutrition, providing a basis for improved and minimally invasive monitoring of feeding regimen effects for trout farming. Dinh et al. [17] estimated genetic parameters for growth traits and designed an optimum breeding program for olive flounder *Paralichthys olivaceus*, an important aquaculture species in East Asia. The heritability levels of all growth traits were moderate, indicating that single-trait selection based on individual body weight may be effective. Chen et al. [18] screened the genome of Yellow River common carp (*Cyprinus carpio haematopterus*) for quantitative trait loci (QTLs) and genes related to growth, identifying 47 QTLs for four growth traits and three consensus QTLs, knowledge of which can be used in molecular-marker-assisted selective breeding.

The application of biotechnology methods drives both ongoing and future developments in aquaculture and conservation. Zhuo et al. [19] explored the mechanisms by which triploid loaches *Misgurnus anguillicaudatus* are rendered sterile through transcriptome analy-

ses of triploid offspring and diploid controls at four periods, demonstrating the importance of the estrogen signaling and steroid biosynthesis pathways. Yan et al. [20] performed a transcription knock-down of the anti-Müllerian hormone gene in male Nile tilapia *Oreochromis niloticus* using antisense RNA technology, with fish in treatment groups exhibiting an increased weight and significant decrease in the gonadosomatic index, demonstrating that antisense RNA technology has strong prospects for practical application. Vibriosis of large yellow croaker *Larimichthys crocea* has resulted in large economic losses in relation to aquaculture production, and the many serotypes of lineages within the genus *Vibrio* have inhibited the development of vaccines. Li et al. [21] prepared a recombinant *Vibrio* rDLD protein and investigated its potential as a candidate subunit vaccine, showing the increased survival rate of large yellow croakers against *Vibrio alginolyticus* and *V. parahaemolyticus*, facilitating the development of a potential subunit vaccine. Natural populations of the freshwater bivalve *Anodonta woodiana* have dramatically declined recently, and Chen et al. [22] evaluated several fish species as potential host fishes for captive propagation; they found that yellow catfish *Pelteobagrus fulvidraco* was the most suitable host, informing future conservation propagation programs.

I hope you have found the collection of articles as interesting and stimulating as I have. I invite your continued interest in, and contributions to, the Genetics and Biotechnology section of *Fishes*.

Conflicts of Interest: The author declares no conflict of interest.

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