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Editorial

Genetic and Molecular Approaches for Breeding Improvement in Aquaculture

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1. Introduction

Aquaculture has become an increasingly vital sector for global food security, contributing significantly to the supply of high-quality, sustainable animal protein. As the industry intensifies and diversifies, there is growing demand for breeding strategies that are not only efficient and precise, but also adaptable to environmental and production challenges [1,2]. In response, genetic, transcriptomic, and molecular approaches have emerged as transformative tools, enabling the dissection of complex traits and accelerating stock improvement beyond the limits of traditional selective breeding alone [3–5].

This Special Issue, "Genetics and Breeding in Aquaculture," brings together ten original research articles that highlight recent advances in the application of molecular biology, functional genomics, and omics-based technologies in aquaculture breeding. These studies span a wide range of cultured species and address traits such as growth, sex differentiation, pigmentation, disease resistance, and environmental stress response. The contributions can be thematically grouped into four major categories: (1) sex determination and endocrine regulation, (2) growth-trait genetics and breeding technologies, (3) phenotypic regulation and transcriptomic networks, and (4) immune response and environmental adaptation.

2. Synopsis of Special Issue

2.1. Sex Determination and Endocrine Regulation

Sex determination and differentiation are critical biological processes with substantial implications for aquaculture productivity, especially for species exhibiting sexual dimorphism in growth or reproduction [6,7]. Understanding the genetic and hormonal underpinnings of sex control can enable the development of all-male or all-female stocks with improved yield and management characteristics [8,9]. In the zig-zag eel (*Mastacembelus armatus*), Cui et al. [10] conducted a comparative gonadal transcriptomic analysis of males and females across both undifferentiated and differentiated developmental stages. They identified sex-biased differentially expressed genes (DEGs), including male-biased genes such as *sox9*, *gsdf*, and *dmrt2b*, as well as female-biased genes such as *foxl2*, *rspo1*, *gdf9*, *bmp15*, and *wnt4*. Several key signaling pathways were enriched, including the MAPK, Wnt, and TGF-β pathways. These findings provide valuable insights into the molecular basis of sex differentiation in this economically important species and highlight candidate targets for sex-control breeding strategies. Notably, further investigation into the potential crosstalk between these signaling pathways, particularly the interaction between the Wnt and TGF-β pathways during ovarian development, may yield novel insights into the evolutionary diversity of sex determination

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mechanisms in teleosts [11,12]. Zhang et al. [13] identified and analyzed three insulin-like growth factor (IGF) genes, *CmIGF1-1*, *CmIGF1-2*, and *CmIGF2*, in blotched snakehead (*Channa maculata*), showing that their expression was primarily liver-specific, higher in males, developmentally regulated, and significantly influenced by sex steroid hormones (17α-ethynylestradiol (EE_2) and 17α-methyltestosterone (MT)), suggesting a key role in sex-specific growth patterns. These findings not only clarify the molecular basis of sex-differentiated growth in blotched snakehead but also offer valuable genetic targets for hormone-regulated selective breeding strategies aimed at enhancing aquaculture productivity. Liu et al. [14] conducted a comparative analysis of liver enzyme activities and gene expression in yellowfin tuna (*Thunnus albacares*), revealing that females exhibited higher digestive and lipid metabolism capacities, while males showed enhanced sugar metabolism, antioxidant defenses, and elevated expression of growth hormone-related genes. Understanding the distinct metabolic and transcriptional profiles between male and female fish offers valuable insights for precision aquaculture, potentially enabling targeted nutritional and breeding strategies tailored to sex-specific physiological needs [15].

2.2. Growth-Trait Genetics and Breeding Tools

Growth performance constitutes a primary target trait in the genetic improvement of virtually all aquaculture species. Contemporary breeding programs increasingly integrate genomic tools, targeted mutagenesis, and quantitative genetic approaches to enhance growth efficiency while preserving genetic diversity and adaptive potential [16]. Wang et al. [17] developed an integrative growth model combining phenotypic measurements and genome-wide SNP genotyping in a hybrid pufferfish (*Takifugu obscurus* ♀× *Takifugu rubripes* ♂). They identified 13 candidate genes associated with growth traits and confirmed the hybrid's superior growth performance, underscoring its genetic potential for genome-assisted selection. By elucidating the genetic basis underlying heterosis, this study demonstrates the utility of interspecific hybridization as a strategy to combine favorable traits from both parental lines for improved aquaculture productivity. Jiang et al. [18] demonstrated that atmospheric-pressure room-temperature plasma (ARTP) mutagenesis effectively induced genetic variation in Songpu mirror carp, enhanced their growth potential and antioxidant capacity, and showed promise as a tool for selective fish breeding. The implementation of ARTP mutagenesis in Songpu mirror carp represents an innovative application of plasma-based techniques in aquaculture, providing a controllable and efficient method to enhance genetic diversity for selective breeding programs [19]. Xu et al. [20] investigated the genetic parameters of growth and developmental traits in American bullfrog (*Rana catesbeiana*) tadpoles and found that body weight at later developmental stages exhibited moderate heritability and a positive genetic correlation with metamorphosis rate. These findings suggest that late-stage body weight could serve as a reliable selection criterion for breeding high-performance bullfrog lines. By linking growth traits to metamorphic success, this study offers a practical framework for trait-based selection, supporting more targeted and efficient genetic improvement in bullfrog aquaculture.

2.3. Phenotypic Regulation and Transcriptomic Networks

Understanding how gene regulatory networks influence visible traits such as color and size is essential for both breeding and consumer preference-driven markets [21,22]. Wu et al. [23] identified and characterized microRNAs involved in the morphological color change in Midas cichlids (*Amphilophus citrinellus*), suggesting that miR-133-x and miR-183-x may regulate key pigmentation genes during the transition from black to gold coloration. This finding highlights the potential of miRNA-mediated regulatory networks as crucial molecular mechanisms driving pigment cell differentiation and color pattern evolution in vertebrates. Tönißen et al. [24] found that early growth variation in pikeperch (*Sander* *lucioperca*) larvae is not directly linked to size-dependent gene expression, but rather to developmental stage-specific differences in genes related to muscle formation and energy metabolism, highlighting complex regulatory factors that may inform strategies to reduce size-related mortality in aquaculture.

2.4. Immune Response and Environmental Adaptation

With intensifying aquaculture systems and increasing environmental stressors, understanding host–pathogen interactions and pollutant responses at the molecular level has become a research priority [25,26]. Zhang et al. [27] cloned and characterized the *CiSRB1* gene in grass carp (*Ctenopharyngodon idellus*) and demonstrated that its age-dependent expression may modulate susceptibility to grass carp reovirus (GCRV) infection. Their findings offer valuable insights into the molecular basis of age-related antiviral resistance in grass carp and identify *CiSRB1* as a promising target for genetic improvement and disease management in aquaculture. Li et al. [28] assessed the effects of nonylphenol (NP), a pervasive endocrine-disrupting compound (EDC), on BMP2 and BMP4 expression in red crucian carp (*Carassius auratus* red var.) and found that NP exposure downregulated these genes via the BMP-Smad pathway, impairing bone morphogenesis and highlighting the importance of incorporating environmental toxicology into breeding and risk assessment.

3. Conclusions

This Special Issue highlights the diverse and advancing landscape of genetic and breeding research in aquaculture, spanning fundamental investigations into sex differentiation mechanisms to applied approaches for growth-trait enhancement through mutagenesis and genomic selection. Collectively, the ten featured studies provide not only robust empirical evidence and methodological advancements, but also practical insights with direct implications for selective breeding strategies and aquaculture production. Looking forward, the integration of multi-omics technologies, computational biology, and functional validation is expected to significantly accelerate genetic improvement and adaptive capacity across cultured species. As the aquaculture sector navigates the dual imperatives of enhancing productivity and ensuring sustainability, the research presented herein will be instrumental in informing and shaping the development of next-generation, science-driven breeding programs.

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References

1. Sae-Lim, P.; Kause, A.; Mulder, H.A.; Olesen, I. Breeding and genetics symposium: Climate change and selective breeding in aquaculture. *J. Anim. Sci.* **2017**, *95*, 1801–1812. [CrossRef] [PubMed]
2. Yanez, J.M.; Barria, A.; Lopez, M.E.; Moen, T.; Garcia, B.F.; Yoshida, G.M.; Xu, P. Genome-wide association and genomic selection in aquaculture. *Rev. Aquac.* **2023**, *15*, 645–675. [CrossRef]
3. Yáñez, J.M.; Newman, S.; Houston, R.D. Genomics in aquaculture to better understand species biology and accelerate genetic progress. *Front. Genet.* **2015**, *6*, 128. [CrossRef] [PubMed]
4. Chandhini, S.; Rejish Kumar, V.J. Transcriptomics in aquaculture: Current status and applications. *Rev. Aquacult.* **2019**, *11*, 1379–1397. [CrossRef]

5. Wang, J.; Cheng, Y.; Su, B.; Dunham, R.A. Genome manipulation advances in selected aquaculture organisms. *Rev. Aquac.* **2025**, *17*, e12988. [CrossRef]
6. Toyota, K.; Miyakawa, H.; Hiruta, C.; Sato, T.; Katayama, H.; Ohira, T.; Iguchi, T. Sex determination and differentiation in decapod and cladoceran crustaceans: An overview of endocrine regulation. *Genes* **2021**, *12*, 305. [CrossRef]
7. Wang, T.; Yu, Y.; Li, S.; Li, F. Molecular mechanisms of sex determination and differentiation in decapod crustaceans for potential aquaculture applications: An overview. *Rev. Aquac.* **2024**, *16*, 1819–1839. [CrossRef]
8. Martínez, P.; Viñas, A.M.; Sánchez, L.; Díaz, N.; Ribas, L.; Piferrer, F. Genetic architecture of sex determination in fish: Applications to sex ratio control in aquaculture. *Front. Genet.* **2014**, *5*, 340. [CrossRef]
9. Chen, J.; Zhu, Z.; Hu, W. Progress in research on fish sex determining genes. *Water Biol. Secur.* **2022**, *1*, 100008. [CrossRef]
10. Cui, F.; Wang, Y.; Liang, H.; Yang, Y.; Jiang, Z.; Song, J.; Liu, C.; Wu, Y.; Mu, X.; Liu, Y. Comparative transcriptomic analysis of male and female gonads in the zig-zag eel (*Mastacembelus armatus*). *Fishes* **2025**, *10*, 117. [CrossRef]
11. Wu, L.; Wu, F.; Xie, L.; Wang, D.; Zhou, L. Synergistic role of β-catenin1 and 2 in ovarian differentiation and maintenance of female pathway in Nile tilapia. *Mol. Cell. Endocrinol.* **2016**, *427*, 33–44. [CrossRef]
12. Yu, H.; Du, X.; Chen, X.; Liu, L.; Wang, X. Transforming growth factor-β (TGF-β): A master signal pathway in teleost sex determination. *Gen. Comp. Endocrinol.* **2024**, *355*, 114561. [CrossRef] [PubMed]
13. Zhang, X.; Wu, Y.; Zhang, Y.; Zhang, J.; Chen, K.; Liu, H.; Luo, Q.; Fei, S.; Zhao, J.; Ou, M. Molecular characteristics, expression patterns, and response of insulin-like growth factors gene induced by sex steroid hormones in blotched snakehead (*Channa maculata*). *Fishes* **2024**, *9*, 120. [CrossRef]
14. Liu, D.; Yang, H.; Li, S.; Huang, H.; Li, G.; Chen, H. Comparative analysis of enzymatic activities and transcriptional profiles of various hepatic enzymes between male and female yellowfin tuna (*Thunnus albacares*). *Fishes* **2024**, *9*, 184. [CrossRef]
15. Cai, C.; Yang, P.; Shi, Y.; Wang, X.; Chen, G.; Zhang, Q.; Cheng, G.; Kong, W.; Xu, Z. Transcriptomic and metabolomic analysis revealed potential mechanisms of growth and disease resistance dimorphism in male and female common carp (*Cyprinus carpio*). *Fish Shellfish Immunol.* **2025**, *158*, 110150. [CrossRef]
16. D'Agaro, E.; Favaro, A.; Matiussi, S.; Gibertoni, P.P.; Esposito, S. Genomic selection in salmonids: New discoveries and future perspectives. *Aquac. Int.* **2021**, *29*, 2259–2289. [CrossRef]
17. Wang, C.; Shi, Y.; Gao, Y.; Shi, S.; Wang, M.; Yao, Y.; Sun, Z.; Wang, Y.; Zhao, Z. Construction of a growth model and screening of growth-related genes for a hybrid puffer (*Takifugu obscurus*♀ × *Takifugu rubripes*♂). *Fishes* **2024**, *9*, 404. [CrossRef]
18. Jiang, X.; Li, C.; Shang, M.; Hu, X.; Ge, Y.; Jia, Z. A new mutagenesis tool for Songpu mirror carp (*Cyprinus carpio* L.) for selective breeding: Atmospheric-pressure room-temperature plasma mutagenesis technology. *Fishes* **2024**, *9*, 448. [CrossRef]
19. Su, X.L.; Zhao, S.S.; Xu, W.J.; Shuang, L.; Zheng, G.D.; Zou, S.M. Efficiently whole-genomic mutagenesis approach by ARTP in blunt snout bream (*Megalobrama amblycephala*). *Aquaculture* **2022**, *555*, 738241. [CrossRef]
20. Xu, W.; Wang, Y.; Wang, G.; Zhang, L.; Zhang, G.; Huo, Z.; Ge, H. Heritability estimates for growth traits and correlation analysis between weight and metamorphosis rate in the bullfrog *Rana* (*Aquarana*) *catesbeiana*. *Fishes* **2024**, *9*, 105. [CrossRef]
21. Wu, L.; Yang, Y.; Wang, X.; Weng, Z.; Hua, S.; Li, D.; Xia, J.; Liu, X.; Meng, Z. Genome-wide QTL mapping and RNA-seq reveal the genetic variation influencing growth traits in giant grouper (*Epinephelus lanceolatus*). *Aquaculture* **2023**, *563*, 738944. [CrossRef]
22. Liu, J.; Yin, M.; Ye, Z.; Hu, J.; Bao, Z. Harnessing hue: Advances and applications of fish skin pigmentation genetics in aquaculture. *Fishes* **2024**, *9*, 220. [CrossRef]
23. Wu, G.; Mu, X.; Liu, Y.; Liu, C.; Wang, X.; Yang, Y.; Song, H. Identification and characterization of microRNAs in morphological color change of polychromatic Midas cichlids (*Amphilophus citrinellus*). *Fishes* **2024**, *9*, 194. [CrossRef]
24. Tönißen, K.; Franz, G.P.; Rebl, A.; Lutze, P.; Grunow, B. Does size matter? Small and large larvae of pikeperch (*Sander lucioperca*) in a comparative gene expression analysis. *Fishes* **2024**, *9*, 33. [CrossRef]
25. Molbert, N.; Agostini, S.; Alliot, F.; Angelier, F.; Biard, C.; Decencière, B.; Leroux-Coyau, M.; Millot, A.; Ribout, C.; Goutte, A. Parasitism reduces oxidative stress of fish host experimentally exposed to PAHs. *Ecotoxicol. Environ. Saf.* **2021**, *219*, 112322. [CrossRef]
26. Zhang, M.; Shan, C.; Tan, F.; Limbu, S.M.; Chen, L.; Du, Z.Y. Gnotobiotic models: Powerful tools for deeply understanding intestinal microbiota-host interactions in aquaculture. *Aquaculture* **2020**, *517*, 734800. [CrossRef]
27. Zhang, Y.; Shi, J.; Lu, Y.; Luo, Q.; Chu, P.; Huang, R.; Chen, K.; Zhao, J.; Wang, Y.; Ou, M. Molecular cloning and characterization of scavenger receptor Class B Type 1 in grass carp (*Ctenopharyngodon idellus*) and its expression profile following grass carp reovirus challenge. *Fishes* **2024**, *9*, 276. [CrossRef]
28. Li, D.; Cui, X.; Chen, S.; Xu, J.; Li, Y.; Zhang, Q.; Sun, Y. Mechanistic insights into nonylphenol stress on BMP2 and BMP4 gene expression in red crucian carp (*Carassius auratus* red var.). *Fishes* **2024**, *9*, 159. [CrossRef]