

## Genomic and Developmental Mechanisms Underlying Growth and Environmental Adaptation in Largemouth Bass (*Micropterus salmoides*)

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**Abstract** Algal Largemouth bass (*Micropterus salmoides*) is an important fish in aquaculture and fisheries management, and its growth and environmental adaptability are crucial for the economy and ecosystems. This study analyzed the genome structure of largemouth bass and identified key genes related to growth and environmental adaptation. It further analyzed the roles of these genes in regulating growth and adapting to environmental changes, and explored the growth regulation pathways, hormonal control, and cellular and molecular processes of largemouth bass to understand its developmental mechanisms. Advances in genome sequencing technologies, transcriptomics, proteomics, and the application of bioinformatics tools help to more accurately analyze the genome and developmental data of largemouth bass. This research aims to reveal the genomic and developmental mechanisms of largemouth bass, deepen the understanding of its molecular basis for growth regulation and environmental adaptation, and hopes to further promote the research and development of largemouth bass, contributing new knowledge and strategies for aquaculture and ecological protection.

**Keywords** *Micropterus salmoides*; Genome structure; Developmental mechanisms; Environmental adaptation; Inheritance

### 1 Introduction

Largemouth bass (*Micropterus salmoides*) is a prominent freshwater fish species widely distributed across North America. Known for its significant role in recreational fishing and aquaculture, the largemouth bass has been extensively studied for its ecological and economic importance. This species exhibits remarkable adaptability to various environmental conditions, making it an ideal model for studying the genomic and developmental mechanisms underlying growth and environmental adaptation (Chen et al., 2022; Cui et al., 2023).

Understanding the growth and environmental adaptation mechanisms in largemouth bass is crucial for several reasons. Firstly, environmental changes, such as hypoxic stress, can significantly impact the physiological and molecular responses in largemouth bass, affecting their survival and growth rates. For instance, research has shown that hypoxic conditions lead to differential expression of microRNAs in the liver, which in turn regulate key signaling pathways involved in stress responses (Sun et al., 2020). Additionally, environmental chemicals can disrupt endocrine functions, influencing reproductive development and overall fitness. Studies have identified specific gene clusters affected during ovarian development, highlighting the impact of environmental disruptors on gene expression and physiological endpoints (Basili et al., 2018). These insights are vital for developing strategies to mitigate the adverse effects of environmental stressors on largemouth bass populations.

This study provides a comprehensive overview of the genomic and developmental mechanisms underlying the growth and environmental adaptation of largemouth bass. By elucidating the molecular and genetic basis of growth regulation in largemouth bass, it explores physiological and genomic responses to environmental stressors such as hypoxia and endocrine disruptors. It identifies potential pathways and gene networks involved in the adaptation process, thereby contributing to the formulation of effective conservation and management strategies for largemouth bass populations. By integrating recent research findings, this study will offer valuable insights into the complex interactions between genetic, developmental, and environmental factors in largemouth bass, ultimately enhancing our understanding of their adaptive capacity and providing references for future research directions.

## 2 Genomic Insights into Largemouth Bass

### 2.1 Genome structure and organization

The genomic structure and organization of largemouth bass (*Micropterus salmoides*) have been explored to understand the genetic basis of various physiological traits. The *Dmrt1* gene, which plays a crucial role in sex determination and differentiation, has been identified and characterized in largemouth bass. The *Dmrt1* gene consists of five exons and four introns, and its expression is highly conserved and exhibits significant gender dimorphism, being highly expressed in the testis of mature fish but only weakly expressed in other tissues (Yan et al., 2019). This gene's structure and expression patterns provide insights into the genetic mechanisms underlying sex differentiation in largemouth bass.

### 2.2 Key genes involved in growth

Several studies have identified key genes involved in the growth of largemouth bass. For instance, the metabolic adaptation to high-starch diets involves the up-regulation of genes related to fatty acid and TAG synthesis and the down-regulation of genes related to TAG hydrolysis and  $\beta$ -oxidation. This indicates that largemouth bass can adapt to dietary changes by modulating the expression of genes involved in metabolism (Chen et al., 2022). Additionally, nutritional programming at early developmental stages can significantly impact growth and dietary plant protein utilization, with specific programming windows leading to improved growth and protein utilization (Schwepe et al., 2022). These findings highlight the importance of specific genes and developmental stages in the growth regulation of largemouth bass.

### 2.3 Genes related to environmental adaptation

Largemouth bass exhibit remarkable adaptability to various environmental stressors, which is mediated by specific genes. For example, exposure to high environmental ammonia (HEA) triggers the up-regulation of Rhesus (Rh) glycoproteins, which play a role in ammonia excretion, and the activation of ion-regulatory and metabolic pathways to mitigate ammonia toxicity (Egnew et al., 2019). Similarly, intermittent hypoxic exposure promotes liver vascular remodeling through the regulation of angiogenesis-related genes, such as Jagged, PI3K, and MAPK, enhancing hypoxia tolerance (Yan et al., 2023). Additionally, microRNA regulation under hypoxic conditions involves the differential expression of miRNAs and their target genes, which are enriched in pathways like VEGF and MAPK signaling, contributing to the hypoxic stress response (Sun et al., 2020). These studies underscore the genetic basis of environmental adaptation in largemouth bass, involving a complex interplay of various genes and regulatory mechanisms.

## 3 Developmental Mechanisms

### 3.1 Growth regulation pathways

Growth in largemouth bass (*Micropterus salmoides*) is regulated by a complex interplay of genetic and molecular pathways. Key pathways include the growth hormone–insulin-like growth factor 1 (GH-IGF1) axis, glycolysis, and the myostatin/transforming growth factor beta (TGF- $\beta$ ) signaling pathways. These pathways are crucial for muscle growth and overall development. For instance, RNA sequencing has identified several genes involved in these pathways, such as phosphoenolpyruvate carboxykinase 1, *FOXO3b*, and heat shock protein beta-1, which are associated with growth traits in largemouth bass (Li et al., 2017). Additionally, selective breeding and domestication have led to the identification of candidate genes like *psst1* and *grb10*, which are linked to growth and early development (Sun et al., 2023).

### 3.2 Hormonal control of development

Hormonal regulation plays a pivotal role in the development of largemouth bass. Hormones such as estradiol (E2) and vitellogenin (VTG) are critical for ovarian development and overall reproductive health. Studies have shown that environmental chemicals can disrupt these hormonal pathways, leading to altered gene expression and physiological endpoints. For example, quercetin and tretinoin have been identified as potential endocrine disruptors that significantly alter the expression of reproductive-associated genes in largemouth bass (Basili et al., 2018). Furthermore, the GH-IGF1 axis is also influenced by hormonal signals, which regulate growth and metabolic processes (Li et al., 2017).

### 3.3 Cellular and molecular processes

At the cellular and molecular levels, largemouth bass exhibit various adaptive mechanisms to environmental stressors. For instance, miRNAs play a significant role in regulating gene expression related to hypoxic stress. Differential expression of miRNAs in the liver under hypoxic conditions has been linked to the VEGF, MAPK, and phosphatidylinositol signaling pathways, which are crucial for cellular responses to low oxygen levels (Sun et al., 2020). Additionally, metabolic adaptation to dietary changes, such as high-starch diets, involves the upregulation of genes related to bile acid synthesis, inflammation, and energy metabolism, indicating a state of 'self-repair' in largemouth bass (Chen et al., 2022). These cellular and molecular processes are essential for maintaining homeostasis and promoting growth and development in varying environmental conditions.

## 4 Environmental Adaptation Mechanisms

### 4.1 Physiological adaptations

Largemouth bass (*Micropterus salmoides*) exhibit several physiological adaptations that enable them to thrive in diverse environmental conditions. One significant adaptation is their ability to regulate ionic balance in varying salinity levels. The expansion of the *claudin* gene family, which is crucial for cell tight junctions and osmotic homeostasis, plays a vital role in this process. This gene family has 27 members and 68 copies in largemouth bass, facilitating their adaptation to both fresh and brackish water environments (Sun et al., 2020). Additionally, largemouth bass can adapt to high environmental ammonia (HEA) by modulating their ammonia excretion rates and upregulating specific mRNA expressions, such as Rhesus glycoproteins, which aid in ammonia excretion. Furthermore, they exhibit metabolic adaptations to dietary changes, such as high-starch diets, by restoring metabolic functions through inflammation, bile acid synthesis, and energy metabolism (Chen et al., 2022).

### 4.2 Behavioral adaptations

Behavioral adaptations in largemouth bass are less documented compared to physiological and genetic adaptations. However, their ability to modify feeding habits in response to environmental changes is notable. For instance, largemouth bass have shown adaptability to formulated feeds instead of traditional forage fish diets, which is crucial for aquaculture sustainability. This dietary transition is supported by genetic markers associated with food habit domestication traits (Cui et al., 2023). Additionally, largemouth bass exhibit changes in activity levels and metabolic rates in response to hypoxic conditions, which helps them conserve energy and survive in low-oxygen environments (Yang et al., 2019).

### 4.3 Genetic basis of adaptation

The genetic basis of adaptation in largemouth bass is underpinned by several genomic and transcriptomic modifications. Whole-genome resequencing has revealed selective sweep regions and candidate genes associated with growth, early development, and immune traits, which are crucial for their adaptation to various environmental pressures (Sun et al., 2023). The identification of sex-specific markers and the XX/XY sex determination system also highlights the genetic mechanisms underlying sex dimorphism and potential for selective breeding (Du et al., 2021). Moreover, the response to environmental contaminants, such as endocrine disruptors, involves specific gene expression changes that can be used as biomarkers for environmental stress (Sanchez et al., 2009; Basili et al., 2018). These genetic insights provide a comprehensive understanding of the adaptive mechanisms in largemouth bass, facilitating their conservation and breeding programs.

## 5 Integration of Genomic and Developmental Data

### 5.1 Combined genomic and developmental studies

The integration of genomic and developmental data in largemouth bass (*Micropterus salmoides*) has provided significant insights into their adaptive mechanisms to environmental stressors. For instance, studies have shown that exposure to high environmental ammonia (HEA) triggers a series of physiological and molecular responses. These responses include changes in oxygen consumption, ion regulation, and the expression of specific genes such as Rhesus glycoproteins, which play a crucial role in ammonia excretion (Egnew et al., 2019). Similarly, the liver proteome response to various environmental contaminants has been analyzed to identify potential biomarkers, revealing alterations in proteins associated with cellular ion homeostasis, oxidative stress, and energy production

(Sanchez et al., 2009). These findings underscore the importance of combining genomic and developmental data to understand the complex adaptive mechanisms in largemouth bass.

## 5.2 Insights from integrated approaches

Integrated approaches combining genomic and developmental data have yielded valuable insights into the metabolic adaptations of largemouth bass. For example, a study investigating the effects of high-starch (HS) diets on largemouth bass revealed that while short-term exposure to HS diets induced metabolic disorders, long-term exposure led to metabolic adaptation. This adaptation was associated with the up-regulation of genes related to bile acid synthesis, inflammation, and energy metabolism, indicating a self-repair response (Chen et al., 2022). These integrated studies highlight the dynamic nature of metabolic regulation and the ability of largemouth bass to adapt to dietary changes through coordinated genomic and developmental responses.

## 5.3 Case studies

A study on the metabolic adaptation of largemouth bass to a high-starch (HS) diet conducted short-term (2 weeks) and long-term (8 weeks) feeding trials to explore the effects of low-starch (LS) and high-starch (HS) diets on the growth performance, metabolism, and liver health of largemouth bass. The results indicated that although short-term exposure leads to metabolic disturbances, long-term exposure results in the recovery of metabolic functions (Figure 1) (Chen et al., 2022).

Chen et al. (2022) presented three typical liver tissue pathological phenotypes: no obvious abnormalities, nuclear crowding, and liver fibrosis. They summarized different liver phenotypes and glycogen accumulation conditions. The metabolic adaptation of largemouth bass liver to a high-starch diet is characterized by an increase in liver glycogen content, accompanied by enhanced inflammatory and apoptotic responses. The study indicates that largemouth bass experience metabolic disturbances when initially exposed to a high-starch diet, but can recover metabolic function through mechanisms such as upregulation of bile acid synthesis, inflammation, and energy metabolism genes over prolonged exposure. This suggests that the species has the ability to adapt to dietary changes through comprehensive genomic and developmental mechanisms, providing important insights into the metabolic adaptation of fish to dietary changes.

Another comprehensive study on the effects of high environmental ammonia (HEA) on largemouth bass demonstrated the species' ability to adapt to sub-lethal ammonia concentrations over time. The study found that ammonia excretion rates were initially inhibited but later restored, accompanied by the up-regulation of Rhcg mRNA expression. Additionally, physiological parameters such as plasma ion concentrations and muscle water content were disrupted and subsequently recovered, indicating a complex interplay between genomic and physiological responses to environmental stress (Egnew et al., 2019).

## 6 Technological Advances and Methodologies

### 6.1 Genomic sequencing technologies

Genomic sequencing technologies have revolutionized the study of largemouth bass (*Micropterus salmoides*) by providing comprehensive insights into their genetic makeup. High-throughput sequencing platforms, such as Illumina and PacBio, have enabled the generation of large-scale genomic data, facilitating the identification of genetic variations and adaptive traits. These technologies have been instrumental in understanding the genetic basis of growth, environmental adaptation, and resistance to pollutants in largemouth bass. For instance, the study on ammonia toxicity in largemouth bass utilized genomic tools to assess the expression of Rhesus glycoproteins, which play a crucial role in ammonia excretion and adaptation to high environmental ammonia (Egnew et al., 2019).

### 6.2 Transcriptomic and proteomic approaches

Transcriptomic and proteomic approaches have provided valuable insights into the molecular responses of largemouth bass to environmental stressors. Transcriptomics, which involves the study of RNA transcripts, has been used to investigate the gene expression profiles under various conditions. For example, the study on

ammonia toxicity employed transcriptomic analysis to evaluate the expression of genes involved in ion regulation and metabolic pathways, revealing adaptive mechanisms at the molecular level (Egnew et al., 2019).

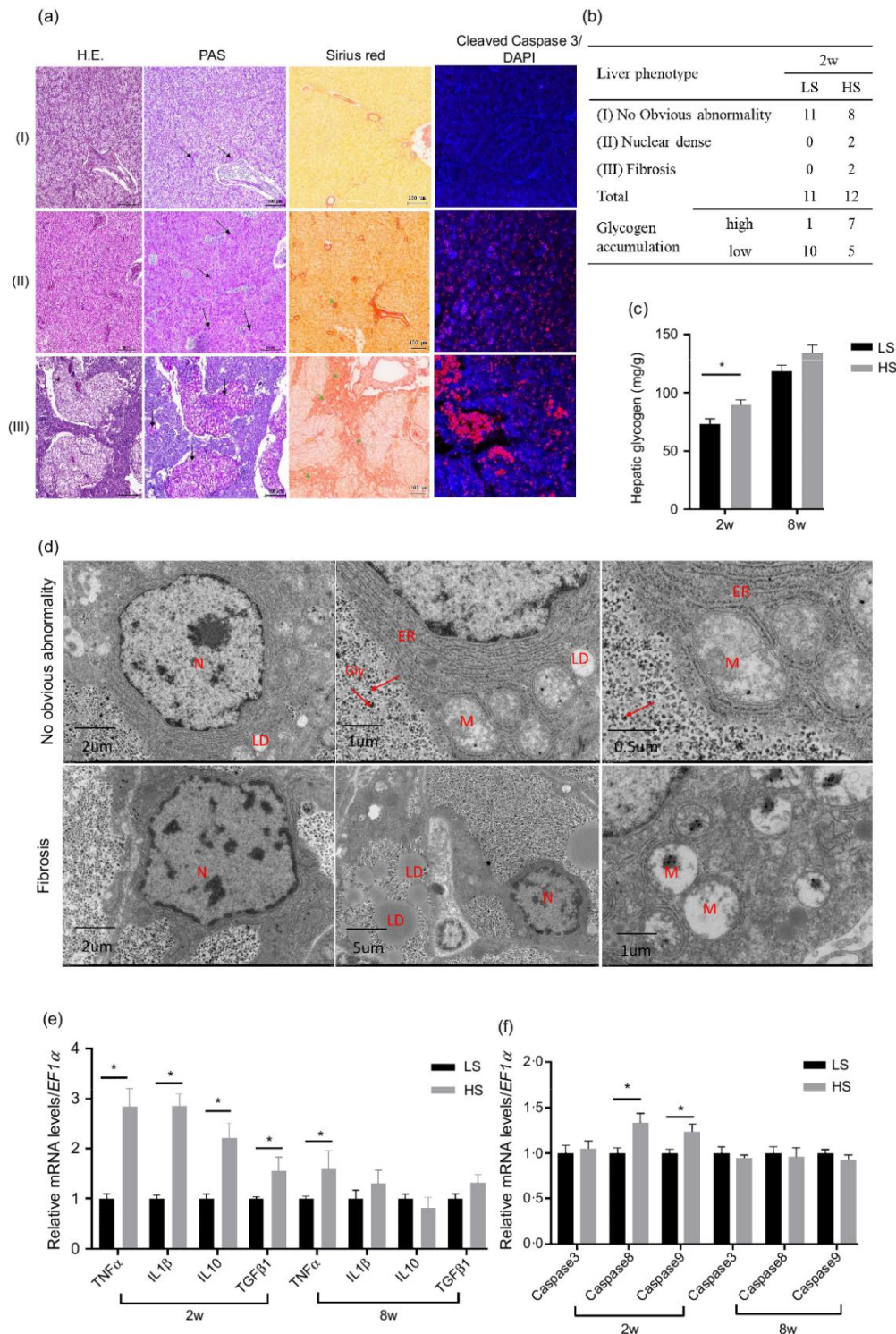


Figure 1 Effects of HS diet on hepatic histopathological, inflammatory and apoptosis responses of largemouth bass at 2w and 8w (Adopted from Chen et al., 2022)

Image caption: (a) Three phenotypes of hepatic histopathological examination with symptoms from light to heavy by HE staining. (b) Statistical results of liver phenotypes and glycogen accumulation. (c) Hepatic glycogen content. (d) Liver ultrastructure. Note the part of mitochondria (M), nucleus (N), endoplasmic reticulum (ER), glycogen granules (Gly) (red arrows showed) and lipid drop (LD). (e) Effects of HS diet on the transcriptional levels of hepatic pro- and anti-inflammation-related genes. (f) Effects of HS diet on the transcriptional levels of hepatic apoptosis-related genes (Adapted from Chen et al., 2022)

Proteomics, the large-scale study of proteins, has also been pivotal in identifying biomarkers of environmental exposure. The liver proteome response of largemouth bass exposed to different contaminants was analyzed using two-dimensional gel electrophoresis and mass spectrometry. This approach identified differentially expressed proteins associated with oxidative stress, energy production, and cellular ion homeostasis, providing potential biomarkers for monitoring environmental contamination (Sanchez et al., 2009). These proteomic studies are essential for understanding the physiological impacts of pollutants and developing strategies for environmental management.

### 6.3 Bioinformatics tools and analysis

The integration of bioinformatics tools and analysis has been crucial in managing and interpreting the vast amounts of data generated from genomic, transcriptomic, and proteomic studies. Bioinformatics platforms facilitate the annotation of genes, identification of genetic variants, and functional analysis of proteins. In the context of largemouth bass research, bioinformatics tools have been used to analyze gene expression data, identify key regulatory pathways, and predict the functional impacts of genetic variations.

For instance, the study on liver proteome response utilized bioinformatics to identify and categorize differentially expressed proteins, linking them to specific biological processes and pathways affected by environmental contaminants (Sanchez et al., 2009). Similarly, the transcriptomic analysis in the ammonia toxicity study employed bioinformatics to interpret the expression patterns of genes involved in ammonia excretion and ion regulation, providing insights into the adaptive mechanisms of largemouth bass (Egnew et al., 2019).

In summary, the advancements in genomic sequencing technologies, transcriptomic and proteomic approaches, and bioinformatics tools have significantly enhanced our understanding of the genomic and developmental mechanisms underlying growth and environmental adaptation in largemouth bass. These methodologies continue to provide critical insights that inform conservation and management strategies for this important species.

## 7 Applications and Implications

### 7.1 Aquaculture and fisheries management

Research on the genomic and developmental mechanisms underlying growth and environmental adaptation in largemouth bass (*Micropterus salmoides*) provides significant benefits for aquaculture practices and fisheries management. These studies offer a theoretical foundation for optimizing farming practices and improving fisheries management. Utilizing genomic data and marker-assisted selection techniques can develop largemouth bass strains with superior growth and disease resistance traits. For example, identifying genes associated with growth and immunity can enable selective breeding to enhance growth rates and disease resistance (Sun et al., 2023). Understanding the mechanisms of largemouth bass adaptation to different environmental conditions can inform more scientific management strategies, such as regulating water salinity and temperature to optimize growth and health (Yi et al., 2021).

### 7.2 Conservation strategies

Genomic research is also critical for conservation strategies, especially in maintaining genetic diversity and enhancing population adaptability. Genomic analysis can identify and preserve critical genetic diversity in wild populations, ensuring sufficient adaptability to environmental changes (Du et al., 2022). Genomic data can help determine which habitats are most crucial for the survival and reproduction of largemouth bass, leading to more effective habitat protection strategies (Sun et al., 2020).

### 7.3 Future prospects in largemouth bass research

The future of largemouth bass research is promising, with significant potential for advancements in several areas. Techniques like CRISPR can be used to improve the genetic traits of largemouth bass, enhancing growth rates and environmental adaptability (Figure 2) (Du et al., 2021). Researching the epigenetic changes in largemouth bass under different environmental conditions can reveal adaptation mechanisms, providing new ideas for optimizing farming and management (Sun et al., 2020). Studying the physiological and metabolic responses of largemouth

bass in the context of climate change can help develop strategies to mitigate the impacts of global warming on fisheries and aquaculture (White and Wahl, 2020).

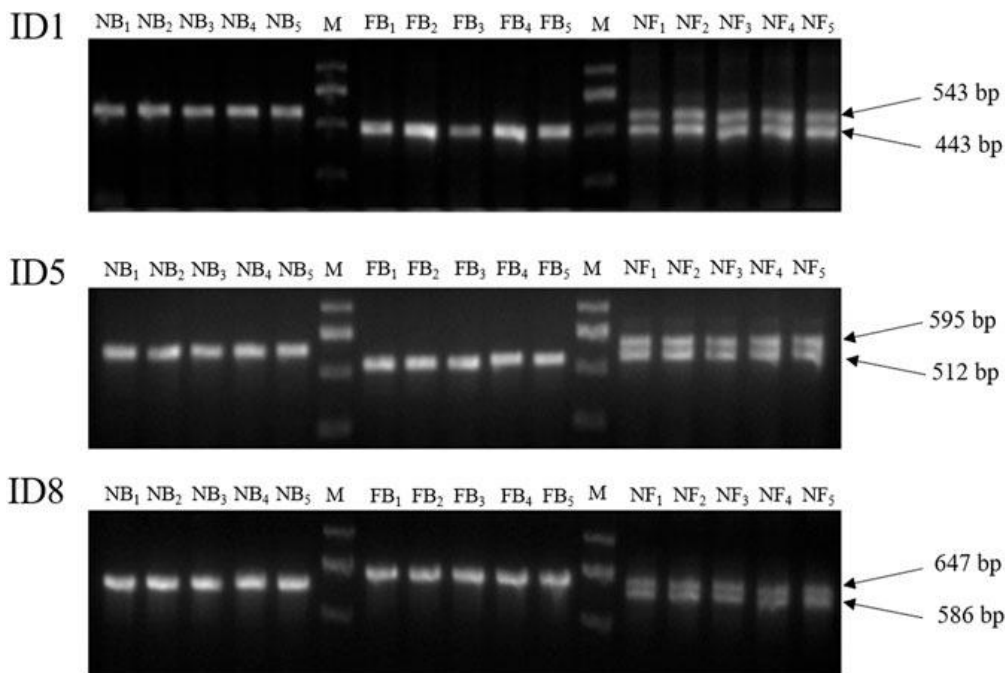


Figure 2 PCR amplification results of ID1, ID5, and ID8 in 5 NB, five FB, and five NF individuals, respectively (Adopted from Du et al., 2021)

Image caption: M: DNA Marker DL 2 000; NB: *Northern largemouth bass*; FB: *Florida largemouth bass*; NF: the F1 hybrid of the *Northern largemouth bass* ♀ × *Florida largemouth bass* ♂ (Adopted from Du et al., 2021)

The PCR amplification results of ID1, ID5, and ID8 revealed genotypic differences among various largemouth bass individuals. By analyzing these genotypes, key genes related to growth rate can be identified. CRISPR technology can precisely target and edit these growth-related genes. For example, by deleting or knocking out genes that negatively regulate growth, or by inserting and activating gene fragments that promote growth, the growth and development of largemouth bass can be accelerated. Combined with the PCR amplification results, we can determine which genes exhibit significant differences among different individuals, thus serving as targets for CRISPR editing. Precise editing of these target genes can not only enhance the growth rate of largemouth bass but also improve their adaptability to the environment, ultimately achieving more efficient and sustainable aquaculture.

## 8 Challenges and Future Directions

### 8.1 Technical and methodological challenges

One of the primary technical challenges in studying the genomic and developmental mechanisms underlying growth and environmental adaptation in largemouth bass (*Micropterus salmoides*) is the complexity of their physiological responses to environmental stressors. For instance, the study on ammonia toxicity revealed that largemouth bass exhibit a range of physiological and molecular responses to high environmental ammonia (HEA), including changes in oxygen consumption, ion regulation, and gene expression (Egnew et al., 2019). This complexity necessitates advanced and precise methodologies to accurately measure and interpret these responses.

Another challenge is the need for comprehensive and integrative approaches to study metabolic adaptations. The research on high-starch diets demonstrated that largemouth bass undergo significant metabolic changes, including alterations in glycolysis, gluconeogenesis, and lipid metabolism, which require sophisticated analytical techniques to monitor and understand (Chen et al., 2022). Additionally, the identification of biomarkers for environmental contaminants involves intricate proteomic analyses, as seen in the study where various proteins were differentially expressed in response to different contaminants (Sanchez et al., 2009).

## 8.2 Research gaps and opportunities

Despite significant advancements, several research gaps remain. One notable gap is the limited understanding of the long-term effects of environmental stressors on largemouth bass. While short-term studies provide valuable insights, long-term studies are essential to fully comprehend the adaptive mechanisms and potential cumulative impacts of stressors such as ammonia and high-starch diets (Egnew et al., 2019; Chen et al., 2022).

Moreover, there is a need for more research on the molecular mechanisms underlying endocrine disruption in largemouth bass. The study utilizing *in silico* computational transcriptomics identified potential endocrine disruptors and their effects on gene expression, but further validation and exploration of these findings are necessary to develop effective mitigation strategies (Basili et al., 2018). Opportunities also exist in the field of nutritional programming. The research on plant protein utilization highlighted the potential of early-life nutritional interventions to improve growth and dietary adaptation in largemouth bass (Schwepe et al., 2022). Expanding this research could lead to more efficient and sustainable aquaculture practices.

## 8.3 Emerging trends and innovations

Emerging trends in this field include the use of omics technologies and computational models to study the complex interactions between environmental factors and fish physiology. The application of proteomics, as demonstrated in the study on environmental contaminants, allows for the identification of novel biomarkers and a deeper understanding of the physiological responses to pollutants (Sanchez et al., 2009). Similarly, the use of transcriptomics and dynamic modeling to study endocrine disruptors represents a significant innovation in understanding the molecular basis of environmental adaptation (Basili et al., 2018).

Another promising trend is the focus on metabolic and nutritional adaptations. The research on high-starch diets and nutritional programming underscores the importance of diet in modulating physiological responses and growth in largemouth bass (Chen et al., 2022; Schwepe et al., 2022). These studies pave the way for developing tailored dietary strategies to enhance fish health and productivity.

In conclusion, addressing the technical and methodological challenges, filling the research gaps, and leveraging emerging trends and innovations will be crucial for advancing our understanding of the genomic and developmental mechanisms underlying growth and environmental adaptation in largemouth bass.

## 9 Concluding Remarks

The research on largemouth bass (*Micropterus salmoides*) has provided significant insights into the genomic and developmental mechanisms underlying their growth and environmental adaptation. Largemouth bass exhibit various physiological and molecular responses to high environmental ammonia (HEA). These responses include changes in oxygen consumption, ion regulation, and the expression of ammonia excreting genes, which help the fish adapt to long-term sub-lethal ammonia concentrations. Computational transcriptomics has identified novel endocrine disruptors, such as quercetin and tretinoin, which affect ovarian development by altering gene expression patterns linked to reproductive endpoints. Largemouth bass can adapt to high-starch diets through metabolic adjustments. Short-term exposure to high-starch diets induces metabolic disorders, but long-term exposure leads to metabolic adaptation via improved inflammatory responses, bile acid synthesis, and energy metabolism. The *Dmrt1* gene plays a crucial role in sex determination and differentiation in largemouth bass, exhibiting sexually dimorphic expression patterns in gonads. MicroRNAs (miRNAs) play a significant role in regulating gene expression in response to hypoxic stress. Specific miRNAs and their target genes are involved in pathways that help largemouth bass cope with low oxygen levels.

Genomic and developmental studies are crucial for understanding the complex mechanisms that enable largemouth bass to adapt to various environmental stressors. These studies provide valuable information on. Understanding how largemouth bass respond to environmental challenges, such as ammonia toxicity and hypoxia, can inform strategies to improve aquaculture practices and enhance fish survival and growth. Identifying endocrine disruptors and their effects on gene expression during ovarian development can help mitigate the impact of environmental chemicals on fish populations. Insights into how largemouth bass metabolically adapt to



different diets can guide the formulation of feeds that promote optimal growth and health. Knowledge of the genetic basis of sex determination and differentiation can aid in the development of breeding programs aimed at producing desired sex ratios for aquaculture.

The research on largemouth bass has significantly advanced our understanding of their genomic and developmental responses to environmental and dietary challenges. Future research should focus on: investigating the long-term effects of environmental pollutants and stressors on largemouth bass at the genomic and physiological levels to develop sustainable aquaculture practices; further elucidating the molecular pathways involved in stress responses and adaptation to improve the resilience of largemouth bass to changing environmental conditions; utilizing genomic information to enhance selective breeding programs aimed at improving growth rates, stress tolerance, and reproductive success in largemouth bass; combining omics technologies with traditional physiological and ecological studies to gain a comprehensive understanding of the factors influencing largemouth bass health and performance. By continuing to explore these areas, we can better support the sustainable management and conservation of largemouth bass populations, ensuring their viability for both aquaculture and sport fisheries.

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### Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

### Reference

- Basili D., Zhang J., Herbert J., Kroll K., Denslow N., Martyniuk C., Falciani F., and Antczak P., 2018, In silico computational transcriptomics reveals novel endocrine disruptors in largemouth bass (*Micropterus salmoides*), *Environmental Science and Technology*, 52(13): 7553-7565.  
<https://doi.org/10.1021/acs.est.8b02805>.
- Chen P., Zhu Y., Wu X., Gu X., Xue M., and Liang X., 2022, Metabolic adaptation to high-starch diet in largemouth bass (*Micropterus salmoides*) was associated with the restoration of metabolic functions via inflammation, bile acid synthesis and energy metabolism, *British Journal of Nutrition*, 129: 381-394.  
<https://doi.org/10.1017/S0007114522001180>.
- Cui J., Jiang Z., Wang Z., Shao J., Dong C., Wang L., Li X., Du J., Li S., Qiao Z., and Zhang M., 2023, Eight single nucleotide polymorphisms and their association with food habit domestication traits and growth traits in largemouth bass fry (*Micropterus salmoides*) based on PCR-RFLP method, *PeerJ*, 11: e14588.  
<https://doi.org/10.7717/peerj.14588>.
- Du J., Li S., Shao J., Song H., Jiang P., Lei C., Bai J., and Han L., 2022, Genetic diversity analysis and development of molecular markers for the identification of largemouth bass (*Micropterus salmoides* L.) based on whole-genome re-sequencing, *Frontiers in Genetics*, 13: 936610.  
<https://doi.org/10.3389/fgene.2022.936610>.
- Du J., Zhou J., Li S., Shao J., Peng J., Dong C., and Bai J., 2021, A PCR-based method for genetic sex identification and evidence of the XX/XY sex determination system in largemouth bass (*Micropterus salmoides* L.), *Aquaculture*, 545: 737220.  
<https://doi.org/10.1016/J.AQUACULTURE.2021.737220>.
- Egnew N., Renukdas N., Ramena Y., Yadav A., Kelly A., Lochmann R., and Sinha A., 2019, Physiological insights into largemouth bass (*Micropterus salmoides*) survival during long-term exposure to high environmental ammonia, *Aquatic Toxicology*, 207: 72-82.  
<https://doi.org/10.1016/j.aquatox.2018.11.027>.
- Li S., Liu H., Bai J., and Zhu X., 2017, Transcriptome assembly and identification of genes and SNPs associated with growth traits in largemouth bass (*Micropterus salmoides*), *Genetica*, 145: 175-187.  
<https://doi.org/10.1007/s10709-017-9956-z>.
- Sanchez B., Ralston-Hooper K., Kowalski K., Inerowicz H., Adamec J., and Sepúlveda M., 2009, Liver proteome response of largemouth bass (*Micropterus salmoides*) exposed to several environmental contaminants: potential insights into biomarker development, *Aquatic toxicology*, 95(1): 52-59.  
<https://doi.org/10.1016/j.aquatox.2009.08.002>.
- Schwepe C., Wojno M., Molinari G., and Kwasek K., 2022, Effects of applying nutritional programming at different early stages of Largemouth bass (*Micropterus salmoides*, Lacepède) development on growth and dietary plant protein utilization, *Journal of Animal Physiology And Animal Nutrition*, 106(6): 1431-1443.  
<https://doi.org/10.1111/jpn.13770>.

- Sun C., Li J., Dong J., Niu Y., Hu J., Lian J., Li W., Li J., Tian Y., Shi Q., and Ye X., 2020, Chromosome-level genome assembly for the largemouth bass *Micropterus salmoides* provides insights into adaptation to fresh and brackish water, *Molecular Ecology Resources*, 21: 301-315.  
<https://doi.org/10.1111/1755-0998.13256>.
- Sun C., Zhang X., Dong J., You X., Tian Y., Gao F., Zhang H., Shi Q., and Ye X., 2023, Whole-genome resequencing reveals recent signatures of selection in five populations of largemouth bass (*Micropterus salmoides*), *Zoological Research*, 44: 78-89.  
<https://doi.org/10.24272/j.issn.2095-8137.2022.274>.
- White D., and Wahl D., 2020, Growth and physiological responses in largemouth bass populations to environmental warming: Effects of inhabiting chronically heated environments.. *Journal of thermal biology*, 88: 102467.  
<https://doi.org/10.1016/j.jtherbio.2019.102467>.
- Yan H., Zhao L., He Q., Hu Y., Li Q., He K., Zhang D., Liu Q., Luo J., Luo W., Chen S., Li L., and Yang S., 2023, Exposure to intermittent environmental hypoxia promotes vascular remodeling through angiogenesis in the liver of largemouth bass (*Micropterus salmoides*), *Environmental Science and Technology*, 57(46): 17796-17807.  
<https://doi.org/10.1021/acs.est.2c07329>.
- Yan N., Hu J., Li J., Dong J., Sun C., and Ye X., 2019, Genomic organization and sexually dimorphic expression of the *Dmrt1* gene in largemouth bass (*Micropterus salmoides*), *Comparative biochemistry and physiology, Part B, Biochemistry and Molecular Biology*, 234: 68-77.  
<https://doi.org/10.1016/j.cbpb.2019.05.005>.
- Yang S., Wu H., He K., Yan T., Zhou J., Zhao L., Sun J., Lian W., Zhang D., Du Z., Luo W., He Z., Ye X., and Li S., 2019, Response of AMP-activated protein kinase and lactate metabolism of largemouth bass (*Micropterus salmoides*) under acute hypoxic stress, *The Science of the Total Environment*, 666: 1071-1079.  
<https://doi.org/10.1016/J.SCITOTENV.2019.02.236>.
- Yi H., Chen X., Liu S., Han L., Jianhui L., Su Y., Bi S., Liu X., Zhang Y., Zhao X., and Li G., 2021, Growth, osmoregulatory and hypothalamic–pituitary–somatotrophic (HPS) axis response of the juvenile largemouth bass (*Micropterus salmoides*), reared under different salinities, *Aquaculture Reports*, 20: 100727.  
<https://doi.org/10.1016/j.aqrep.2021.100727>.



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