International Journal of Molecular Ecology and Conservation, 2025, Vol.15, No.2, 54-62
http://ecoevopublisher.com/index.php/ijmec

Research Insight Open Access

Phylogenetic Reconstruction and Genomic Adaptive Evolution in *Siniperca* spp.

Chengmin Sun [1], Rudi Mai [2]
1 Center for Tropical Marine Fisheries Research, Hainan Institute of Tropical Agricultural Resouces, Sanya, 572025, Hainan, China
2 Tropical Biological Resources Research Center, Hainan Institute of Tropical Agricultural Resources, Sanya, 572025, Hainan, China
Corresponding author: rudi.mai@hitar.org

International Journal of Molecular Ecology and Conservation, 2025, Vol.15, No.2 doi: 10.5376/ijmec.2025.15.0006
Received: 18 Jan., 2025
Accepted: 24 Feb., 2025
Published: 06 Mar., 2025

Preferred citation for this article:
Sun C.M., and Mai R.D., 2025, Phylogenetic reconstruction and genomic adaptive evolution in *Siniperca* spp., International Journal of Molecular Ecology and Conservation, 15(2): 54-62 (doi: 10.5376/ijmec.2025.15.0006)

Abstract *Siniperca* or Chinese perch is a freshwater fish family indigenous to East Asia, of great economic value and ecological particularity. Though of great significance in aquaculture, the phylogenetic histories of the *Siniperca* genus are unclear due to morphological convergence and a dearth of molecular data. We rebuilt the genome-wide single-copy orthologous genes-based phylogenetic framework of *Siniperca* and inferred divergence times between species using a molecular clock model in this study. We further performed comparative genomics to identify expansions of gene families, positive selection signals, and adaptive evolutionary trajectories linked with ecological specialization. Several genetic candidates for environmental tolerance, immune response, and sensory systems were detected, suggesting lineage-specific adaptation to various freshwater environments. This study not only illuminates the phylogenetic history of *Siniperca*, but also reveals the genetic mechanism of its adaptive divergence, providing theoretical evidence for species conservation, utilization of resources, and molecular breeding in aquaculture.

Keywords *Siniperca*; Phylogenetic reconstruction; Comparative genomics; Adaptive evolution; Freshwater fish

1 Introduction

The *Siniperca* genus is a family of freshwater fish endemic to East Asia in the *Sinipercidae* family. It contains some of its species such as *S. chuatsi*, *S. scherzeri*, *S. kneri*, and *S. undulata*, which are found mainly in the Yangtze, Pearl, and Amur river basins. They are carnivorous species, solitary, and prefer clean, slow-moving freshwater environments. Despite their ecological divergence, their phylogenetic relationships and placements within the genus are controversial due to convergent morphological features coupled with limited molecular markers (Liang et al., 2019; Zhang et al., 2023). Advances in genome sequencing coupled with phylogenomic methods in the past few years have paved new ways in resolving these taxonomic ambiguities as well as their evolution.

Siniperca chuatsi (mandarin fish) and *S. scherzeri* are two of the most valuable Chinese freshwater aquaculture species, with high consumer demand and excellent meat quality, and they grow rapidly. The production of *S. chuatsi* has been more than 300,000 tons each year, becoming China's pillar of carnivorous fish production (Zhao et al., 2017; Chen et al., 2020). However, high-level production has brought with it new issues, including more frequent outbreak of disease, reduced genetic variation, and depression in inbreeding. They have generated growing interest in using molecular technologies like whole-genome selection, marker-assisted breeding, and genome-wide association studies to improve desirable traits including disease resistance, growth rate, and feed efficiency (Chen et al., 2020). A good understanding of the evolutionary and genetic basis of these traits is required to guide upcoming breeding programmes.

Phylogenetic analysis forms the foundation of understanding speciation, the evolution of traits, and the conservation of biodiversity. In this genomics era, having the capability to combine high-throughput sequencing with phylogenomics enables scientists to have the ability to uncover ancient evolutionary relationships and identify genomic regions under selection. In *Siniperca* spp., where there has been ecological divergence and niche specialization, the integration of phylogenetic reconstruction and adaptive evolution analysis encapsulates how these fishes evolve to respond to environmental stresses such as temperature, turbidity, and prey availability. In addition, investigations of positively selected genes and fast-evolving gene families can reveal genetic mechanisms of carnivory, metabolic thrift, and immunity. These findings not only enhance evolutionary biology but also have applied relevance to genetic improvement and conservation strategies.

2 Genetic Basis and Evolutionary Characteristics of *Siniperca* Species

2.1 Species composition and current research on phylogenetic relationships

Siniperca is comprised of a series of freshwater species that are spread across East Asia, mainly China, with two dominant genera, *Siniperca* and *Coreoperca*. Interspecific relationships, *Sinipercidae* monophyly, and species boundaries have been explained through recent phylogenetic analysis using thousands of nuclear coding sequences and next-generation sequencing methods. For example, *S. scherzeri* has been determined to be the most basal taxon of *Siniperca*, and species delimitation analyses confirmed the singularity of *S. chuatsi* and *S. kneri*, within closely related species pairs. Estimates of divergence times suggest that *Sinipercidae*'s ancestor evolved in southern China over 50 million years ago and was shaped by the subsequent historical climatic and geological events (Zhao et al., 2017).

2.2 Genetic diversity and phenotypic differentiation of germplasm resources

Genetic diversity in F1 and F2 generations of interspecific hybrids between *S. chuatsi* and *S. scherzeri* is extensive, as shown by hybrids and natural populations analyses. F1 and F2 generations from the hybridization between *S. chuatsi* and *S. scherzeri* possess greater genetic diversity and extensive morphological differentiation, especially for F1 hybrids. Microsatellite and SNP analyses indicate that hybrid and backcross populations maintain intermediate or higher levels of heterozygosity than parental species, indicative of their vigorous breeding power. There are particular molecular markers used in identifying hybrids and genetic breeding schemes. Population analysis of *S. scherzeri* within the Pearl River drainage also identified particular genetic lineages due to vicariance and demographic history, highlighting the genetic intricacy of the genus (Zhang et al., 2022; Chen et al., 2024) (Figure 1).

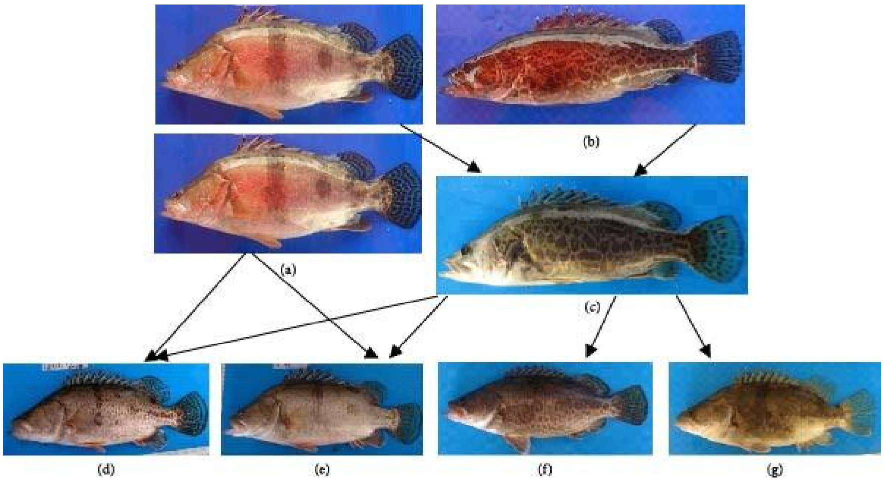

Figure 1 Morphology of the *S. chuatsi* ♀ × *S. scherzeri* ♂, F1, F2, and backcross hybrids (Adopted from Chen et al., 2024)
Image caption: a: *S. chuatsi*, b: *S. scherzeri*, c: F1 (CS), d: CS-C (81%), e: C-CS (19%), f: F2 large size (97%), g: F2 small size (3%) (Adopted from Chen et al., 2024)

2.3 Potential adaptive traits and mechanisms of ecological divergence

Comparative and genomic studies have revealed adaptive characters and molecular routes of ecological divergence in *Siniperca*. Differentially expressed genes for metabolism, pigmentation, and the immune system are triggered by structural variants impacting cis-regulatory elements leading to phenotypic diversity among closely related species, e.g., *S. chuatsi* and *S. scherzeri*. Gene family expansion and positive selection are linked to features like predatory feeding, growth, and habitat tolerance. For instance, adaptive gene evolution for feeding and aggression-related genes occurs quickly, while gene family diversity for growth, immunity, and mobility explains niche preference between species like *S. undulata* and *S. obscura*. Such findings emphasize the role of genomic structure and evolution in ecological adaptation control among *Siniperca* species (Chen et al., 2020; Zhang et al., 2022; Jiang et al., 2023).

3 Phylogenetic Reconstruction and Analytical Methods

3.1 Sample collection and genome data construction strategies

Phylogenetic reconstruction must be done with cautious broad sampling, in which all aspects of taxonomic and geographic diversity of *Siniperca* species are covered. Multiple samples have been enabled to generate genome-scale data through next-generation sequencing and significantly improved the resolution and power of phylogenetic inference. Approaches entail whole-genome sequencing, enrichment of targeted nuclear coding regions, and strict sequencing quality control of the data to limit errors and achieve maximum coverage (Young and Gillung, 2019; Dissanayake, 2020).

3.2 Identification and alignment of single-copy orthologous genes

A critical part of phylogenomics is the identification of single-copy orthologous genes, excellent markers for making inferences about evolution. The process is eased by bioinformatic pipelines that clip gene families so that only those that occur as single copies in every sampled taxon remain. High-quality multiple sequence alignments are then generated within these genes, as the quality of the alignments directly impacts the validity of resulting phylogenetic analysis (Young and Gillung, 2019; Dissanayake, 2020).

3.3 Phylogenetic tree construction and divergence time estimation

Phylogenetic trees are also constructed using a number of methods, including maximum likelihood, Bayesian inference, and distance-based approaches. Maximum likelihood and Bayesian methods are applied as they are more precise, especially with genome-scale data, though it is computationally costly. RAxML and IQ-TREE are some of the programs used in tree estimation. Divergence time estimation applies molecular clock models and fossil calibrations to infer divergence timing, putting observed patterns into a background of evolution (Horiike, 2016; Kendall et al., 2018; Young and Gillung, 2019).

3.4 Topological interpretation and taxonomic implications of phylogenetic results

Phylogenetic tree topology analysis is the driving force to the realization of evolutionary relationships and to taxonomic recast direction. Well-supported phylogenomic frameworks will resolve past evolutionary disputes, define species limits, and reveal diversification patterns. Phylogenetic results combined with morphological and ecological information enable improved species delimitation and can uncover new taxa or recast those previously recorded. Methodological integrity, including artefact detection and control and model violation, is crucial for ensuring reliability in taxonomic conclusions (Young and Gillung, 2019; Struck et al., 2023).

4 Comparative Genomics and Detection of Adaptive Evolution Signals

4.1 Gene family expansion/contraction analysis and functional enrichment

In *Siniperca* species, comparative genomics has been used successfully to interpret gene family expansions and contractions—those significant signatures of adaptive evolution. Scientists have found extensive expansions of gene families involved in immune response, sensory perception (e.g., vision and smell), and energy metabolism. These tendencies are most probably adaptations to the predatory life style, environmental heterogeneity, and enhanced prey detection ability in a range of aquatic habitats. Functional enrichment analyses have revealed that the gene families are overrepresented in biological processes such as immune defense, nutrient acquisition, and responding to environmental stimuli, suggesting that gene family evolution is closely linked with ecological specialization and evolutionary innovation (Steffansson et al., 2004; Regev et al., 2015; Csilléry et al., 2018).

4.2 Screening of positively selected genes and identification of rapidly evolving regions

Since *Siniperca* differentiated into various species, certain genes have undergone strong positive selection in adapting to the evolutional environment. Identification of such genes is typically achieved by estimating the nonsynonymous to synonymous substitution ratio (dN/dS) and site-specific evolutionary models. Advances such as Bayesian inference and machine learning techniques such as convolution neural networks and transfer learning have improved the identification of rapidly evolving genomic regions. These approaches are especially powerful in *Siniperca* to detect candidate genes for the polygenic traits of feeding behavior, aggressiveness, and temperature tolerance where scientists can detect recent positive selection even in polygenic trait scenarios (Csilléry et al., 2018; Lartillot et al., 2020; DeGiorgio et al., 2025).

4.3 Candidate genes related to environmental adaptation and their biological functions

Most of the candidate genes uncovered by positive selection analysis or gene family evolution analysis in *Siniperca* are involved in key functions of environmental adaptation, including immune regulation, sensory perception (especially olfaction and vision), reproduction, and stress response. These functions are critical for *Siniperca* species to adapt to freshwater systems with fluctuating thermal, oxygen, and feeding regimes. Functional enrichment and annotation analysis also connect these genes to important adaptive characters such as disease resistance, prey specialization, and environmental stress tolerance and shed light on their ecological functions in evolutionary divergence (Ellegren, 2008; Csilléry et al., 2018; Salazar-Tortosa et al., 2023).

4.4 Convergent evolution at the genomic level and inter-species ecological comparisons

Comparative genomic analysis between *Siniperca* and other freshwater fish have found examples of convergent evolution—where unrelated lineages develop the same characters or gene changes independently under the same environmental pressures. For example, conserved signatures of selection have been detected across species in genes that are associated with visual receptors, mucosal immunity, and metabolism. Comparisons of gene regulatory networks and adaptive loci among taxa may uncover convergent adaptive strategies and the level of regulatory and functional convergence (Figure 2). Such studies improve our understanding of *Siniperca* species and other species adapting to similar hydrology and temperature environments, and reveals the genomic foundation of convergent phenotypes (Regev et al., 2015; Csilléry et al., 2018).

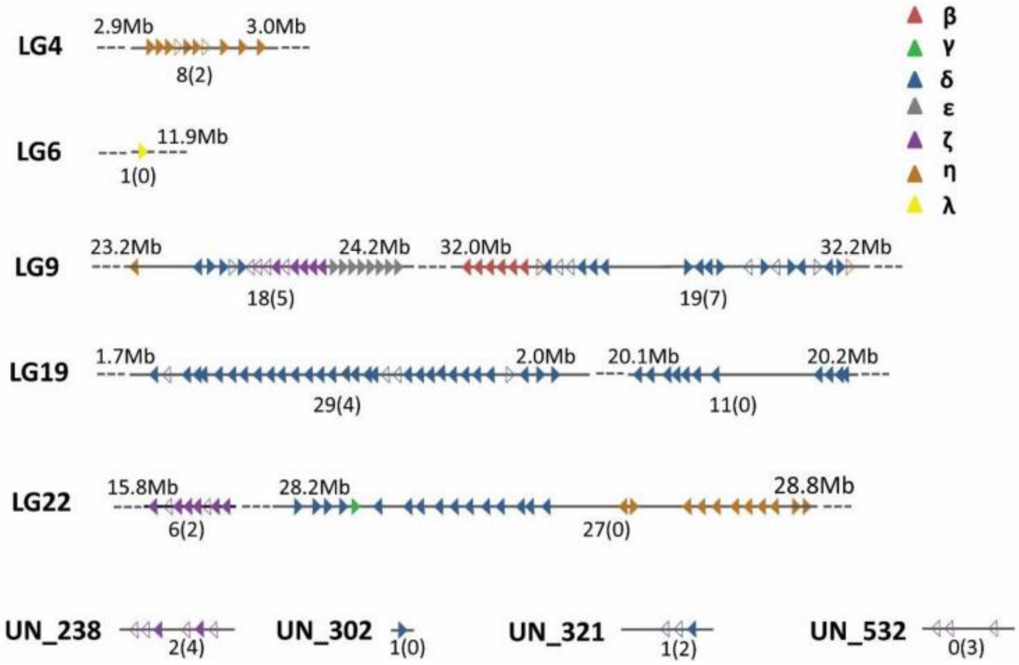

Figure 2 Genomic structure and sequence information of the *Siniperca* genus (Adopted from Liang et al., 2019)

5 Analysis of Adaptive Evolutionary Mechanisms at the Genomic Level

5.1 Selective pressures from ecological factors such as temperature, water environment, and diet

Siniperca members are dispersed in diverse freshwater ecosystems throughout China and possess impressive ecological adaptations to temperature, water quality, and diet. *Siniperca* members vary from subtropical low-oxygen water to cold oxygen-rich rivers in northern China and possess physiological and metabolic distinctions. Genomic analysis indicates that metabolic genes underwent rapid evolutionary rates, allegedly an adaptation to their carnivorous diet as well as environmental sensitivity (Han, 2024). Ecological stresses such as temperature fluctuations, fluctuating dissolved oxygen, and nutrient differences apparently have exerted positive pressure on energy metabolism genes, oxidative stress response genes, and nutrient uptake genes (Huang, 2020; Bafna et al., 2021). Aside from that, adaptive evolution can also be facilitated through events of gene loss to prefer against duplicative functions in new habitats, a process that occurs within aquatic and flying mammals but which also might be promoted to *Siniperca* species (Langer et al., 2018).

5.2 Adaptive evolutionary pathways of systems involving metabolism, immunity, and sensory functions

At the advanced freshwater ecosystem level, *Siniperca* species have signatures of adaptive evolution in immunity and metabolism genes. Regions of positive selection are generally enriched in pathogen recognition, mucosal immunity, and antimicrobial peptide production genes, suggesting that such systems are largely the primary targets of long-term selective pressure. *Siniperca* spp. are predatory fish. also exhibit adaptive evolution of metabolic enzymes for detoxification and energy use (Huang, 2020; Slodkowicz and Goldman, 2020). Genes that regulate sensory function-especially those that deal with smell and sight-exhibit species-specific divergences as well as rapid evolution. This is likely because of adaptation to different water turbidity and prey detection processes.

5.3 Association analysis between phenotypic variation and gene function variation

Siniperca species exhibit intense phenotypic variability in body size, head morphology, coloration, and aggression. How the genetic basis for such traits is established is a cornerstone question in evolutionary genomics. Recent advancements in statistical models such as the phenotype-genotype branch-site model (PG-BSM) and evolution-guided regression models have enabled correlation of some genetic change with phenotypic evolution (Wang and Chen, 2024). In *Siniperca*, these approaches allow one to identify codon replacements or gene loss events for traits such as pyloric caeca formation and feeding behavior, giving strong evidence on how genetic divergence is involved in ecological specialization (Youssef et al., 2019; Huang, 2020).

5.4 Integration of molecular mechanisms with morphological and ecological adaptation

Integrating phylogenetic histories with protein structure information and ecological data throws additional light on *Siniperca* species adaptive evolution. Positively selected sites are clustered in functionally key regions of proteins—catalytic domains and signal interfaces, for example—indicates their involvement in trait development. These molecular adaptations must be accompanied by morphological traits such as jaw morphology, dentition, and feeding mode. Synthesis studies that integrate genomic data, behavioral ecology, physiological performance, and environmental characteristics reveals how *Siniperca* species achieve ecological success and drive lineage diversification through molecular innovation (Slodkowicz and Goldman, 2020; Tong et al., 2023).

6 Scientific Significance and Application Prospects of the Research

6.1 Contributions to fish phylogeny and evolutionary biology

This research contributes to fish phylogeny knowledge by applying genomic and phylogenetic methods to explain *Siniperca* evolutionary relationships. Based on high-throughput sequencing and comparative genomics, the study provides insight into *Siniperca* adaptive evolution, speciation, and diversification and contributes to overall evolutionary biology by providing an account of mechanisms of ecological adaptation and lineage divergence in freshwater fishes. The integration of genomic data into evolutionary research is an indication of the increasing scientific trend in utilizing the ability of new technology to explore complex biological questions better, hence accelerating the advancement of science and widening the boundaries of evolutionary science (Konieczny, 2023).

6.2 Providing a genomic basis for conservation and precision breeding of *Siniperca* species

Evolutionary information and genomic data generated by this study form a sound foundation for conservation of *Siniperca* species. Genetic diversity, population genetic structure, and detection of adaptive loci in the study enable the development of site-based conservation practices for maintaining genetic integrity and potential adaptation in nature populations. Besides, identification of key genes and markers for desirable traits enables precision breeding to be possible through broodstock selection for optimal growth, disease resistance, and environmental adaptability. The uses are consistent with current and future trajectories of genetic DNA testing and genomic assessment in resource management and sustainable aquaculture (Shi, 2024).

6.3 Application potential of genomic information in trait improvement and environmental adaptation assessment

Genomic information gained from this research have great potential for *Siniperca* aquaculture enhancement in traits. With the linkage of genetic markers with desirable economic traits, i.e., growth rate, feed conversion, and resistance to stress, marker-assisted selection can be utilized by breeders to speed up genetic progress. Besides, the ability to assess and estimate adaptive genetic variation improves the possibility of predicting and estimating the environmental fitness of culture stocks, promoting the development of resilient aquaculture systems in the shadows of a changing environment. The use of genomic information within these fields mirrors larger trends in science research, where new technologies and new modes of analysis are propelling limits of innovation and utilitarian applications in industry and conservation alike (Konieczny, 2023; Shi, 2024).

7 Challenges and Strategic Recommendations

7.1 Limitations in genome data coverage and representativeness

Current studies of *Siniperca* spp. are severely handicapped by inadequate coverage and representativeness of genome data. Most genomic studies sample only a small number of species or populations, whose scope in attempting to cover the complete scope of genetic diversity and adaptive variation necessary in order to make robust evolutionary and functional inference is limited. This lack of whole-genome resources also restrains finding key genes for important traits and adaptation and thereby reduces breeding and conservation program efficiency (Guo et al., 2018; Xiao et al., 2020; Zhong et al., 2022; Bao et al., 2024; Shao et al., 2025).

7.2 Constraints in phylogenetic and functional analysis models

Phylogenetic and functional analysis platforms of *Siniperca* tend to be limited by reliance on a small number of genetic markers or a single-omics that are unable to produce good resolution to distinguish between genetically close species or to uncover complex evolutionary relationships. In addition, the incomplete reference databases and restricted experimental verification reduce gene function annotation and adaptive mechanisms understanding precision (Guo et al., 2018; Xiao et al., 2020; Zhong et al., 2022; Bao et al., 2024).

7.3 Necessity of multi-omics integration and fine-scale functional validation

One of the emerging requirements is to utilize multi-omics approaches including genomics, transcriptomics, proteomics, and metabolomics to respond to *Siniperca* biology in an integrated manner. Multi-omics can be used in combination to reveal the molecular basis of attributes like growth, immunity, and environment adaptation at different levels of biology. However, sophisticated high-resolution functional verification such as gene editing and physiological assays is underdeveloped, while uses of omics information are limited to aquaculture and conservation (Guo et al., 2018; Xiao et al., 2020; Zhong et al., 2022; Bao et al., 2024; Shao et al., 2025).

7.4 Future research suggestions: integration of functional experiments, physiological validation, and ecological simulation

Future research should expand the number of genome sequencing study objects to more *Siniperca* species and populations, thus ensuring broader data representativeness and coverage. Evolution and use of advanced phylogenetic and functional analysis models, supported by improved reference databases, will help in more accurate evolutionary and functional inference. Incorporation of multi-omics data with functional assays, physiological validation, and ecological modeling will provide an integrated picture of trait development and environmental acclimatization, eventually leading to precision breeding, sustainable aquaculture, and effective conservation planning for *Siniperca* spp. (Guo et al., 2018; Xiao et al., 2020; Bao et al., 2024; Zhong et al., 2022; Shao et al., 2025).

8 Concluding Remarks

Recent advances in large-scale genomic sequencing and phylogenetic analysis have enabled *Siniperca* phylogeny to be reconstructed more confidently. High-throughput sequencing of thousands of nuclear coding sequences and comprehensive analyses have confirmed the monophyly of *Sinipercidae*, supporting classification into two genera, *Siniperca* and *Coreoperca*. Notably, *Siniperca* scherzeri was identified as the most basal taxon, and well-defined *Siniperca* clades were delineated, providing unequivocal support to the validity of several contentious species and clarifying relationships that had hitherto remained ambiguous due to limited morphological differentiation.

Genomic analysis has revealed widespread signals of adaptive evolution in *Siniperca*, particularly in genes associated with predatory feeding, growth, and environmental adaptation. Positive selection scans revealed sudden evolution in feeding behavior, aggressiveness, and physiological traits such as euryhalinity and pyloric caeca formation. Genome-wide association analysis also detected SNPs and candidate genes for economically important traits such as growth, muscle, and bone development, thus leaving a molecular legacy of adaptation and trait evolution in *Siniperca*.

Together with high-quality genome assemblies, phylogenetic analysis, and functional genomics, they provide new insights into *Siniperca* breeding and conservation. Genomic resources facilitate accurate species identification, genetic diversity inference, and marker-assisted selection breeding in aquaculture. Population history and adaptive evolution guide conservation management, and adaptive evolution genes involved in growth and adaptation aid precision breeding and environmental adaptability. These improvements collectively enhance the *Siniperca* species' ecological adaptation and sustainable use research.

Acknowledgments

Thanks to the animal research team for their support and help in data collection and data collection.

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.

References

Bafna V., Zhou D., Stobdan T., Iranmehr A., Kryazhimskiy S., Haddad G., and Zhao H., 2021, Multiple mechanisms drive genomic adaptation to extreme O_2 levels in *Drosophila melanogaster*, Nature Communications, 12: 997.
https://doi.org/10.1038/s41467-021-21281-6

Bao L., Peng J., Tuo Y., Fang H., and Chu W., 2024, Research progress on nutritional requirements and formulated feeds for *Siniperca*: a comprehensive review, Fishes, 9(12): 487.
https://doi.org/10.3390/fishes9120487

Chen J., Lin L., Han L., Li G., Liu X., Huang C., Zhang Z., Bi S., Liang J., Li H., Zhang Y., Liu S., Yi H., Sun J., Wei X., and Chen Q., 2024, Morphological characteristics, genetic diversity, and microsatellite analysis of the progenies (F1, F2, and backcross descendant) of *Siniperca chuatsi* and *Siniperca scherzeri*, Aquaculture Research, 2024(1): 6672569.
https://doi.org/10.1155/2024/6672569

Chen X., Zhang Z., Yin Z., Li J., He S., Tang S., Xu J., Lv L., Dou Y., Li L., Liang X., Cai W., Zhang Y., Kuhl H., Wuertz S., and Tao Y., 2020, Mandarin fish (Sinipercidae) genomes provide insights into innate predatory feeding, Communications Biology, 3: 361.
https://doi.org/10.1038/s42003-020-1094-y

Csilléry K., Rodríguez-Verdugo A., Guillaume F., and Rellstab C., 2018, Detecting the genomic signal of polygenic adaptation and the role of epistasis in evolution, Molecular Ecology, 27: 606-612.
https://doi.org/10.1111/mec.14499

DeGiorgio M., Santos A., Arnab S., and Fumagalli M., 2025, Efficient detection and characterization of targets of natural selection using transfer learning, Molecular Biology and Evolution, 42(5): msaf094.
https://doi.org/10.1093/molbev/msaf094

Dissanayake A., 2020, Applied aspects of methods to infer phylogenetic relationships amongst fungi, Mycosphere, 11: 2652-2676.
https://doi.org/10.5943/mycosphere/11/1/18

Ellegren H., 2008, Comparative genomics and the study of evolution by natural selection, Molecular Ecology, 17(21): 4586-4596.
https://doi.org/10.1111/j.1365-294X.2008.03954.x

Guo C., Zhang T., Li Z., Beauchamp D., Li W., Hicks B., Liu J., and Lin M., 2018, Impacts of hatchery-reared mandarin fish *Siniperca chuatsi* stocking on wild fish community and water quality in a shallow Yangtze lake, Scientific Reports, 8: 11481.
https://doi.org/10.1038/s41598-018-29758-z

Han Y.P., 2024, Population genomics of primates: diversity, structure, and evolutionary dynamics, International Journal of Molecular Evolution and Biodiversity, 14(3): 108-119.
https://doi.org/10.5376/ijmeb.2024.14.0014

Horiike T., 2016, An introduction to molecular phylogenetic analysis, Robotics and Autonomous Systems, 4: 36-45.
https://doi.org/10.7831/RAS.4.36-45

Huang Y., 2020, Dissecting genomic determinants of positive selection with an evolution-guided regression model, Molecular Biology and Evolution, 39(1): msab291.
https://doi.org/10.1093/molbev/msab291

Jiang J., Zhao J., Lu L., and Li C., 2023, Comparative genomics revealed drastic gene difference in two small Chinese perches, *Siniperca undulata* and *S.* obscura, G3: Genes|Genomes|Genetics, 13(7): jkad101.
https://doi.org/10.1093/g3journal/jkad101

Kendall M., Bentley S., Parkhill J., Lees J., Colijn C., and Harris S., 2018, Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study, Wellcome Open Research, 3: 33.
https://doi.org/10.12688/wellcomeopenres.14265.2

Konieczny M., 2023, The importance of scientific research and new trends and directions of their development, Catholic Pedagogy, 33: 267-274.
https://doi.org/10.62266/pk.1898-3685.2023.33.20

Langer B., Roscito J., Foerster L., Hiller M., Hecker N., and Sharma V., 2018, A genomics approach reveals insights into the importance of gene losses for mammalian adaptations, Nature Communications, 9: 1215.
https://doi.org/10.1038/s41467-018-03667-1

Lartillot N., Rodrigue N., and Latrille T., 2020, A Bayesian mutation–selection framework for detecting site-specific adaptive evolution in protein-coding genes, Molecular Biology and Evolution, 38: 1199-1208.
https://doi.org/10.1093/molbev/msaa265

Liang X., He S., and Lv L., 2019, Genome-wide identification and characterization of olfactory receptor genes in Chinese perch, *Siniperca chuatsi*, Genes, 10(2): 178.
https://doi.org/10.3390/genes10020178

Regev A., Thompson D., and Roy S., 2015, Comparative analysis of gene regulatory networks: from network reconstruction to evolution, Annual Review of Cell and Developmental Biology, 31: 399-428.
https://doi.org/10.1146/annurev-cellbio-100913-012908

Salazar-Tortosa D., Enard D., and Huang Y., 2023, Assessing the presence of recent adaptation in the human genome with mixture density regression, Genome Biology and Evolution, 15(10): evad170.
https://doi.org/10.1093/gbe/evad170

Shao J., Wu L., Lai M., Wang H., Zhang D., Qin Z., Wang Y., Lin J., and Liang P., 2025, Integrative unveiling of optimum dietary protein requirement for *Siniperca scherzeri*: growth performance, feed utilization, serum biochemical and immune parameters and hepatic health maintenance, Aquaculture.
https://doi.org/10.1016/j.aquaculture.2024.742004

Shi C., 2024, Genetic DNA testing: current applications and future prospects, Frontiers in Business, Economics and Management, 598: 742004.
https://doi.org/10.54097/tc834k28

Slodkowicz G., and Goldman N., 2020, Integrated structural and evolutionary analysis reveals common mechanisms underlying adaptive evolution in mammals, Proceedings of the National Academy of Sciences, 117: 5977-5986.
https://doi.org/10.1073/pnas.1916786117

Steffansson P., Liberles D., Betts M., Roth C., and Sælensminde G., 2004, The adaptive evolution database (TAED): a phylogeny based tool for comparative genomics, Nucleic Acids Research, 33: D495-D497.
https://doi.org/10.1093/nar/gki090

Struck T., Valero-Gracia A., and Fleming J., 2023, Identifying and addressing methodological incongruence in phylogenomics: a review, Evolutionary Applications, 16: 1087-1104.
https://doi.org/10.1111/eva.13565

Tong Z., Shi S., Wei F., Hu Y., Shi P., Huang S., Tian R., Xu S., Yang H., Xu Y., Wang X., Yang G., Yu L., and Guo Y., 2023, Molecular mechanisms of adaptive evolution in wild animals and plants, Science China Life Sciences, 66: 453-495.
https://doi.org/10.1007/s11427-022-2233-x

Wang Y.L., and Chen J., 2024, Genetic adaptation in avian species to rapid environmental changes, International Journal of Molecular Evolution and Biodiversity, 14(4): 197-207.
https://doi.org/10.5376/ijmeb.2024.14.0021

Xiao M., Bao F., Qian K., and Wang Y., 2020, GC-MS metabolomics reveals metabolic differences of the farmed mandarin fish *Siniperca chuatsi* in recirculating ponds aquaculture system and pond, Scientific Reports, 10: 6090.
https://doi.org/10.1038/s41598-020-63252-9

Young A., and Gillung J., 2019, Phylogenomics—principles, opportunities and pitfalls of big-data phylogenetics, Systematic Entomology, 45(2): 225-247.
https://doi.org/10.1111/syen.12406

Youssef N., Bielawski J., Jones C., and Susko E., 2019, A phenotype-genotype codon model for detecting adaptive evolution, Systematic Biology, 69(4): 722-738.
https://doi.org/10.1093/sysbio/syz075

Zhang Q., Lin M., Liang X., Kuang Y., Dou Y., and Gao J., 2022, Phylogeographic structure and population demography of the leopard mandarin fish (*Siniperca scherzeri*) in the Pearl River drainage, Environmental Biology of Fishes, 105: 477-486.
https://doi.org/10.1007/s10641-022-01247-3

Zhang X., Chen Q., Weng S., Wang M., Lai C., Lv Y., Zhang L., Jiang R., Tu G., Yan Z., He J., and Zhang L., 2022, Long-read genome assemblies reveal a cis-regulatory landscape associated with phenotypic divergence in two sister *Siniperca* fish species, Zoological Research, 44: 287-302.
https://doi.org/10.1101/2022.11.09.515789

Zhang Y., Li M., Liu S., Li G., Han C., Li S., Huang J., Yang J., and Lin H., 2023, Genome-wide identification, evolution and expression of TGF-β signaling pathway members in mandarin fish (*Siniperca chuatsi*), International Journal of Biological Macromolecules, 253: 126949.
https://doi.org/10.1016/j.ijbiomac.2023.126949

Zhao J., Song S., and Li C., 2017, Species delimitation and phylogenetic reconstruction of the sinipercids (Perciformes: Sinipercidae) based on target enrichment of thousands of nuclear coding sequences, Molecular Phylogenetics and Evolution, 111: 44-55.
https://doi.org/10.1016/j.ympev.2017.03.014

Zhong J., Liu X., Xu Z., Wei Y., Huang Z., Zhu Y., and Zhang X., 2022, Recovery of *Siniperca chuatsi* rhabdovirus from cloned cDNA, Journal of Fish Diseases, 46(2): 127-135.
https://doi.org/10.1111/jfd.13726