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Comparative Genomics of Aquatic Organisms: Insights into Biodiversity Origins

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Abstract This study explored the origin of aquatic biodiversity through comparative genomics, and the researchers gained an in-depth understanding of the adaptive evolutionary mechanisms of species in different aquatic environments. They used genomic data to reveal the radiation adaptation of coral reef fish, the metabolic adaptability of deep-sea species, and the genomic diversity in polar ecosystems, thus providing new insights into the conservation of aquatic biodiversity. Comparative genomics can not only help understand the origin of aquatic species diversity, but also provide a scientific basis for the protection and management of fragile aquatic ecosystems, and provide a foundation for further development of genomic research on aquatic organisms, especially in understudied species and extreme environments.

Keywords Aquatic biodiversity; Comparative genomics; Adaptive radiation; Metabolic adaptation; Conservation genomics

1 Introduction

Aquatic ecosystems, encompassing marine, freshwater, and transitional environments, are home to a vast array of species that contribute significantly to global biodiversity. Marine habitats, which cover approximately 70% of the Earth's surface, host a diverse range of organisms adapted to various ecological niches (Kelley et al., 2016). Freshwater ecosystems, although occupying a mere 2% of the Earth's surface, exhibit high species richness and exceptional phylogenetic diversity (Román-Palacios et al., 2022). The unique properties of water, such as its physical and chemical characteristics, play a crucial role in shaping the genetic diversity and population connectivity of aquatic species (Grummer et al., 2019).

Comparative genomics has emerged as a powerful tool for unraveling the evolutionary processes that drive biodiversity in aquatic environments. By comparing the genomes of different species, researchers can gain insights into the physiological and morphological adaptations that have enabled organisms to thrive in diverse habitats (Ovchinnikova and Shi, 2023). Population genomics, in particular, has provided unprecedented resolution for understanding population structuring, speciation, and adaptation in marine environments, which often have low dispersal costs and few physical barriers to gene flow (Kelley et al., 2016). Additionally, genomic and transcriptomic studies have facilitated the discovery of novel bioactive macromolecules and have advanced our understanding of the molecular mechanisms underlying survival, growth, reproduction, and homeostasis in aquatic organisms.

This study provides a comprehensive overview of the role of comparative genomics in elucidating the origins of biodiversity in aquatic ecosystems, attempting to emphasize the evolutionary transitions between marine, freshwater, and terrestrial environments that shape contemporary biodiversity. We will explore the application of genomic tools in conservation, particularly in assessing the impact of environmental stressors such as climate change and human activities on aquatic species. In addition, the potential of next-generation sequencing technology and environmental DNA (eDNA) meta barcoding in advancing ecological research and biodiversity monitoring will be discussed, with the aim of emphasizing the importance of integrating genomic data and deepening our understanding of the complex adaptive processes that control aquatic biodiversity.

2 Comparative Genomics of Coral Reef Fish

2.1 Coral reef fish as models for adaptive radiation

Coral reef fish, such as clownfish and grunts, serve as excellent models for studying adaptive radiation due to their diverse ecological niches and rapid diversification. For instance, clownfish have evolved a mutualistic relationship with sea anemones, which has driven their rapid diversification. Genomic studies reveal that clownfish genomes exhibit bursts of transposable elements, accelerated coding evolution, and hybridization events, all of which have facilitated their adaptive radiation (Xu, 2024). Positive selection in genes related to social behavior and ecological divergence further underscores the role of genomic changes in their diversification (Marcionetti and Salamin, 2022). Similarly, comparative transcriptomics of sympatric species of the genus *Haemulon* (grunts) show positive selection in genes associated with immune response and morphological traits, indicating adaptive divergence despite overlapping habitats (Figure 1) (Bernal et al., 2019).

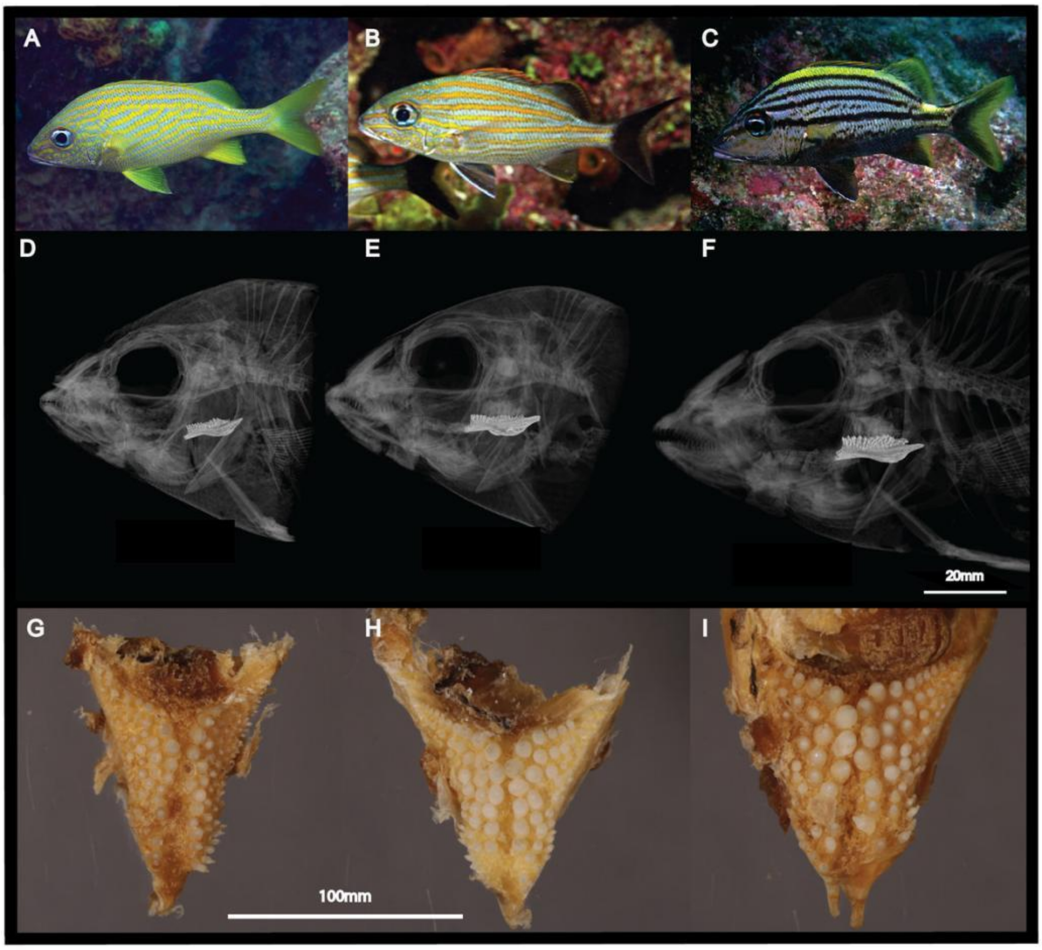

Figure 1 Morphological differences between the three sympatric species of *Haemulon* (Adopted from Bernal et al., 2019)

2.2 Environmental pressures driving coral reef fish diversity

Environmental pressures such as climate change and habitat variability significantly influence the diversity of coral reef fish. Coral reefs are experiencing rapid deterioration due to climate change, which imposes selective pressures on resident species. For example, seascape genomics studies on *Acropora digitifera* have identified genomic regions associated with heat stress resistance, highlighting the role of environmental pressures in shaping genetic diversity (Selmoni et al., 2020). Additionally, *reefscape* genomics leverages advances in 3D imaging to assess fine-scale patterns of genomic variation, enabling the study of spatio-temporal drivers of genetic structuring and adaptive potential in coral reef ecosystems (Bongaerts et al., 2021). These environmental pressures drive the evolution of traits that enhance survival and reproduction in changing conditions, contributing to the overall biodiversity of coral reef fish.

2.3 Application of genomic data to coral reef conservation

Genomic data is increasingly being applied to coral reef conservation efforts to better understand and mitigate the impacts of environmental changes. For instance, population genomics provides insights into the genetic structuring and adaptive potential of coral reef taxa, which is crucial for developing effective conservation strategies (Pinsky et al., 2023). The integration of genomic data with environmental and phenotypic information, as demonstrated in *reefscape* genomics, allows for the identification of key areas for conservation prioritization (Bongaerts et al., 2021). Moreover, the genomic characterization of coral species and their microbial symbionts reveals critical interactions that support coral health, informing strategies to enhance reef resilience (Robbins et al., 2019). These applications underscore the importance of genomics in guiding conservation efforts to preserve the biodiversity and ecological functions of coral reef ecosystems.

3 Comparative Genomics of Deep-Sea Adaptation

3.1 Genetic adaptations to extreme pressure and darkness

Deep-sea organisms have evolved unique genetic adaptations to survive under extreme pressure and darkness. For instance, the Yap hadal snailfish (*YHS*) exhibits high levels of trimethylamine N-oxide (TMAO), a potent protein stabilizer, which is crucial for maintaining protein integrity under high hydrostatic pressure. This adaptation is supported by the presence of multiple copies of the TMAO-generating enzyme flavin-containing *monooxygenase-3* gene (*fmo3*) in the *YHS* genome (Mu et al., 2021). Similarly, deep-sea Actinobacteriota have evolved higher GC content and longer intergenic spaces in their genomes, which may contribute to their survival in high-pressure environments (Roda-García et al., 2023). These genetic modifications are essential for maintaining cellular functions and structural integrity in the deep sea.

3.2 Evolutionary mechanisms underpinning metabolic adaptations

Metabolic adaptations are critical for deep-sea organisms to thrive in environments with limited food supply and low temperatures. The deep-sea fish *Coryphaenoides rupestris* shows genotypic segregation by depth, with distinct genotypes at functional loci that may be linked to different metabolic requirements at varying depths (Gaither et al., 2018). Additionally, Arctic Charr (*Salvelinus alpinus*) morphs adapted to deep-water habitats exhibit genomic divergence in genes associated with cardiac function, membrane transport, and DNA repair, which are vital for coping with the metabolic demands of deep-water environments (Kess et al., 2021). These evolutionary mechanisms highlight the importance of metabolic flexibility in deep-sea adaptation.

3.3 Genomic data in deep-sea conservation efforts

Genomic data play a crucial role in the conservation of deep-sea species by providing insights into their evolutionary history and adaptive mechanisms. For example, the annotated genome assembly of the deep-sea fish *Coryphaenoides rupestris* can inform conservation strategies by identifying loci under disruptive selection that are crucial for survival at different depths (Kelley et al., 2016). Furthermore, the genomic analysis of marine vertebrates, including deep-sea species, can help assess the impact of fisheries and climate change on their populations, thereby guiding conservation efforts (Yuan et al., 2021). Understanding the genetic basis of adaptation in deep-sea organisms is essential for developing effective conservation strategies to protect these unique and vulnerable ecosystems.

4 Technological Advances in Comparative Genomics

4.1 Next-generation sequencing for case studies

4.1.1 Sequencing coral reef fish genomes

Next-generation sequencing (NGS) has revolutionized the study of coral reef fish genomes, enabling researchers to uncover the genetic diversity and evolutionary history of these species. For instance, the development of universal PCR primers for metabarcoding environmental DNA (eDNA) from fishes has allowed for the detection of over 230 subtropical marine species (Figure 2), demonstrating the efficiency and sensitivity of NGS in biodiversity monitoring (Miya et al., 2015). Additionally, genome-wide sequencing approaches have provided new opportunities to understand both neutral and adaptive contributions to the genetic diversity of coral reef organisms, despite the challenges associated with aquatic environments (Bongaerts et al., 2021).

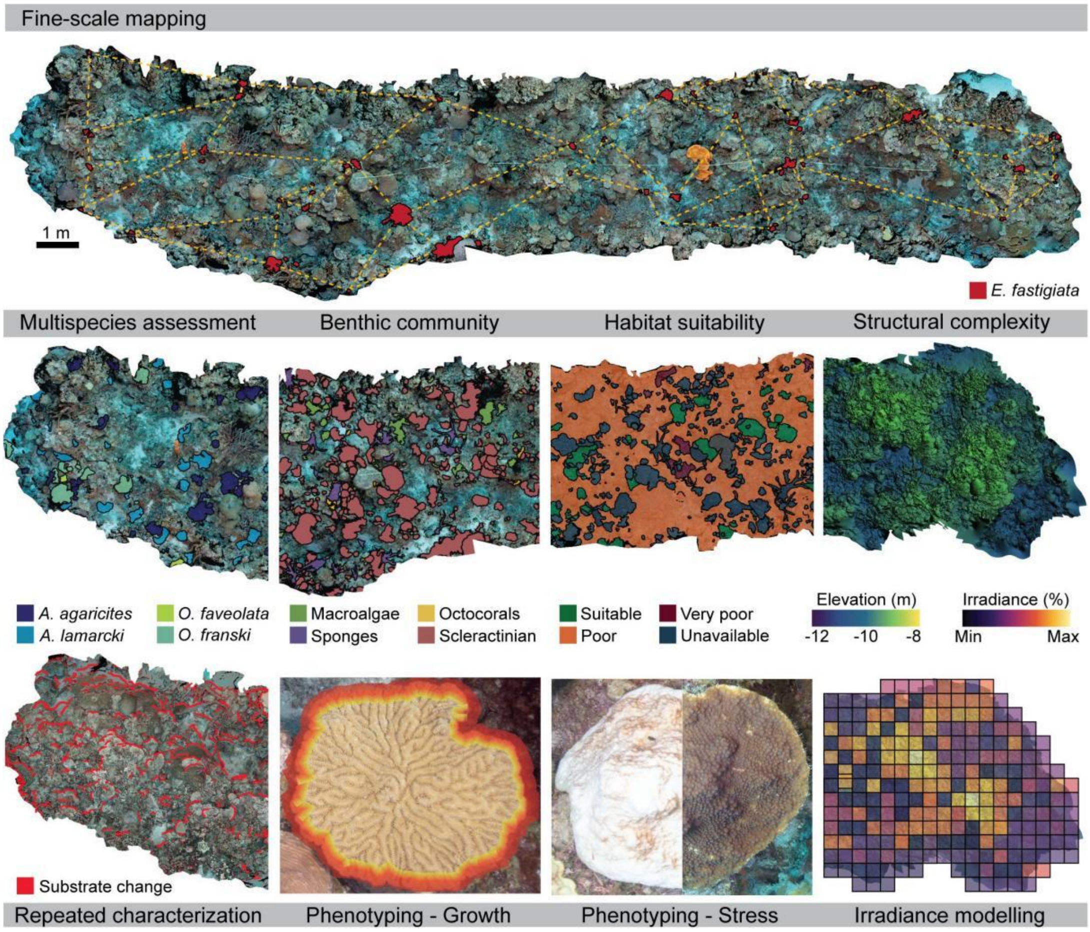

Figure 2 Coral community under gene sequencing research (Adopted from Bongaerts et al., 2021)

4.1.2 Sequencing deep-sea species genomes

The application of NGS to deep-sea species has similarly advanced our understanding of these unique organisms. Large-scale projects such as the Fish10K and Fish-T1K have significantly contributed to the genomic and transcriptomic data available for deep-sea species, facilitating studies on their evolutionary biology and molecular adaptations (Ovchinnikova and Shi, 2023). These projects have highlighted the importance of integrating genomics and transcriptomics to discover novel bioactive macromolecules and understand the molecular mechanisms underlying the survival and adaptation of deep-sea species.

4.2 Bioinformatics tools for comparative analysis

4.2.1 Analyzing large-scale genomic data from coral reefs

Bioinformatics tools are essential for managing and analyzing the vast amounts of genomic data generated from coral reef studies. Tools such as the Bioinformatics tools for Marine and Freshwater Genomics (BiMFG) provide comprehensive databases and techniques for comparative analyses among marine species. These tools facilitate the retrieval and alignment of remote sequences, even when sequence similarities are low, thereby enhancing biodiversity analysis and verification in marine biology (Shih et al., 2010). Additionally, the integration of 3D imaging with genomic data, known as “reefscape genomics,” allows for fine-scale spatial mapping and phenotyping of coral reef organisms, further advancing our understanding of their genetic diversity and adaptive potential (Yu et al., 2017).

4.2.2 Identifying evolutionary patterns in deep-sea genomes

Bioinformatics tools also play a crucial role in identifying evolutionary patterns in deep-sea genomes. The use of metagenomics and other computational techniques has enabled researchers to analyze DNA from microbial communities in environmental samples, providing insights into the evolutionary history and molecular adaptations of deep-sea species (Oulas et al., 2015). Furthermore, the application of bioinformatics in molecular evolution studies has highlighted the potential of these tools to address questions related to the conservation of aquatic biodiversity, particularly in the face of environmental and anthropogenic stressors (Tan et al., 2019).

5 Genomic Studies in Polar Ecosystems

5.1 Genomic diversity of antarctic fish

Antarctic notothenioid fishes are a prime example of vertebrate adaptive radiation in a marine environment. These fishes have diversified from a single common ancestor approximately 25 million years ago to over 140 species today, representing about 90% of fish biomass on the Antarctic continental shelf. Genomic studies have revealed numerous unique traits in notothenioids, such as osteopenia, anemia, cardiomegaly, dyslipidemia, and aglomerular kidneys, which are beneficial or tolerated in their extreme environment but are pathological in humans. Since 2014, 16 notothenioid genomes have been published, enabling comprehensive analyses of their radiation and the genetic underpinnings of their novel traits (Daane and Detrich, 2021). These studies provide insights into the physiological and biochemical adaptations necessary for survival in the cold Southern Ocean and offer models for understanding genetic mechanisms of human diseases (Zhou, 2024).

5.2 Comparative genomics of arctic marine organisms

The Arctic ecosystem, despite its logistical challenges, is crucial for understanding global biodiversity changes. Genomic approaches in the Arctic have provided transformative insights into biotic responses to environmental changes, although their application has been limited due to various constraints. The development of biorepositories from high latitudes is essential for improving conservation, monitoring, and management of Arctic ecosystems through genomic approaches (Colella et al., 2019). Additionally, studies comparing the genomes of marine bacteria from both the Arctic and Antarctic have shown that while some bacterial operational taxonomic units (OTUs) are common to both poles, their genomes are not identical, suggesting significant genomic divergence influenced by geographical isolation and divergence times (Qin et al., 2021).

5.3 Conservation genomics in polar marine species

Conservation genomics aims to preserve the viability of populations and biodiversity. In polar regions, genomic tools are increasingly applied to assess the impact of environmental changes and human activities on marine species. For instance, conservation genomics practices in marine invertebrates have highlighted the discovery of novel genes and genomic innovations that are crucial for adaptation (Lopez et al., 2019). Comparative genomic approaches are also being used to inform the characterization of conservation units, studies of hybridization, and understanding the drivers of divergence, which are essential for preserving molecular biodiversity (Grueber, 2015). Furthermore, the integration of genomics and transcriptomics in large-scale projects has significantly advanced our knowledge of evolutionary biology and the adaptive mechanisms of aquatic organisms (Ovchinnikova and Shi, 2023).

6 Future Directions in Comparative Genomics of Aquatic Organisms

6.1 Integrating multi-omics data for comprehensive genomic insights

The integration of multi-omics data, including genomics, transcriptomics, proteomics, and metabolomics, is essential for a comprehensive understanding of the molecular mechanisms underlying the adaptation and evolution of aquatic organisms. Recent advances in next-generation sequencing and mass spectrometry have enabled the systematic exploration of transcripts, proteins, and metabolites, providing deeper insights into the functional roles of various macromolecules in aquatic species (Klein et al., 2019). For instance, the integration of genomics and transcriptomics has been pivotal in discovering novel bioactive macromolecules from natural resources, which can be developed into marine drugs. Additionally, post-genomic approaches such as metabolomics and metatranscriptomics are expanding our understanding of microbial contributions to ecosystem functions, highlighting the need for a holistic systems biology approach (Reid and Bergsveinson, 2021).

6.2 Expanding genomic research to understudied aquatic species

While significant progress has been made in the genomic study of model organisms, there is a pressing need to expand research to understudied aquatic species. Many aquatic species, particularly those inhabiting brackish water or seawater, remain underrepresented in genomic databases (Rhee and Lee, 2014). Expanding genomic research to these species will provide valuable insights into their unique adaptations and evolutionary histories. For example, the self-fertilizing *killifish Kryptolebias marmoratus* has unique characteristics that make it a potential model species for various research areas, yet genomic information about this species is still scarce. Similarly, freshwater eDNA research has revealed taxonomic biases, with certain species such as fishes being overrepresented, while others like freshwater arthropods are underrepresented (Belle et al., 2019).

6.3 Opportunities for conservation genomics in aquatic ecosystems

Conservation genomics offers significant opportunities to address the challenges faced by aquatic ecosystems, such as habitat loss, climate change, and overfishing. Genomic tools can provide unprecedented resolution for understanding population structuring, speciation, and adaptation in marine environments, which is crucial for assessing the impact of fisheries and climate change on marine species. Additionally, landscape genomics can help researchers assess genetic diversity, population connectivity, and signals of natural selection in freshwater systems, providing a roadmap for conservation efforts (Yuan et al., 2021). The application of eDNA techniques in freshwater conservation can also benefit from the development of general standards and guidelines to harmonize methods and increase international cooperation.

7 Concluding Remarks

Comparative genomics has significantly advanced our understanding of the evolutionary processes and adaptations of aquatic organisms. Studies have shown that genomic tools can elucidate physiological and morphological adaptations to diverse marine habitats, providing insights into population structuring, speciation, and adaptation. The integration of genomics and transcriptomics has revealed the molecular mechanisms underlying survival, growth, reproduction, and homeostasis in aquatic species, highlighting the importance of ancient components of innate immunity systems. Additionally, comparative genomics has been instrumental in identifying the genetic basis of adaptive traits in non-model marine species, even within homogeneous environments. The use of environmental DNA (eDNA) has also emerged as a powerful tool for assessing aquatic biodiversity, offering a more sensitive and comprehensive approach compared to traditional methods.

The application of comparative genomics in conservation biology holds great promise for biodiversity protection. Genomic data can inform the characterization of conservation units, studies of hybridization, and the identification of drivers of divergence, which are crucial for the management of threatened species. The use of eDNA metabarcoding has proven to be an effective method for monitoring aquatic biodiversity, enabling the detection of rare and secretive species with higher accuracy than traditional surveys. This approach can provide essential data for conservation management, particularly in urban and impacted environments where rapid biodiversity assessment is needed. Furthermore, understanding the genomic adaptations of marine mammals to aquatic life can inform conservation strategies aimed at mitigating the impacts of climate change and human activities on these species.

Future research in aquatic comparative genomics should focus on expanding the scope of genomic studies to include a broader range of species and environments. There is a need for more comprehensive genomic datasets that encompass neutral, adaptive, and sex-linked variations to accurately infer eco-evolutionary processes. Additionally, the development of more holistic approaches to gene homology and the integration of phylogenetic analyses with genomic data will enhance our understanding of genome function and evolutionary relationships. Advances in environmental paleomicrobiology, particularly the study of ancient DNA preserved in sediments, can provide valuable insights into the historical responses of aquatic ecosystems to environmental changes, aiding in the prediction of future biodiversity patterns. Finally, continued innovation in sequencing technologies and bioinformatics will be essential for overcoming current challenges and fully realizing the potential of comparative genomics in aquatic research.

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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

Belle C.C., Stoeckle B.C., and Geist J., 2019, Taxonomic and geographical representation of freshwater environmental DNA research in aquatic conservation, Aquatic Conservation: Marine and Freshwater Ecosystems, 29(11): 1996-2009.
https://doi.org/10.1002/aqc.3208

Bernal M., Dixon G., Matz M., and Rocha L., 2019, Comparative transcriptomics of sympatric species of coral reef fishes (genus: *Haemulon*), PeerJ, 7: e6541.
https://doi.org/10.7717/peerj.6541

Bongaerts P., Dubé C.E., Prata K.E., Gijsbers J.C., Achlatis M., and Hernandez-Agreda A., 2021, Reefscape genomics: leveraging advances in 3D imaging to assess fine-scale patterns of genomic variation on coral reefs, Frontiers in Marine Science, 8: 638979.
https://doi.org/10.3389/fmars.2021.638979

Colella J.P., Talbot S.L., Brochmann C., Taylor E.P., Hoberg E., and Cook J., 2019, Conservation genomics in a changing arctic, Trends in Ecology and Evolution, 35(2): 149-162.
https://doi.org/10.1016/j.tree.2019.09.008

Daane J.M., and Detrich H.W., 2021, Adaptations and diversity of antarctic fishes: a genomic perspective, Annual Review of Animal Biosciences, 10(1): 39-62.
https://doi.org/10.1146/annurev-animal-081221-064325

Gaither M., Gaither M., Gkafas G., Gkafas G., Jong M., Sarigol F., Sarigol F., Neat F., Rgnier T., Moore D., Grcke D., Hall N., Hall N., Liu X., Kenny J., Lucaci A., Hughes M., Haldenby S., and Hoelzel A., 2018, Genomics of habitat choice and adaptive evolution in a deep-sea fish, Nature Ecology and Evolution, 2: 680-687.
https://doi.org/10.1038/s41559-018-0482-x

Grueber C., 2015, Comparative genomics for biodiversity conservation, Computational and Structural Biotechnology Journal, 13: 370-375.
https://doi.org/10.1016/j.csbj.2015.05.003

Grummer J.A., Beheregaray L.B., Bernatchez L., Hand B.K., Luikart G., Narum S.R., and Taylor E., 2019, Aquatic landscape genomics and environmental effects on genetic variation, Trends in Ecology and Evolution, 34(7): 641-654.
https://doi.org/10.1016/j.tree.2019.02.013

Kelley J., Brown A., Therkildsen N., and Foote A., 2016, The life aquatic: advances in marine vertebrate genomics, Nature Reviews Genetics, 17: 523-534.
https://doi.org/10.1038/nrg.2016.66

Kess T., Dempson J., Lehnert S., Layton K., Einfeldt A., Bentzen P., Salisbury S., Messmer A., Duffy S., Ruzzante D., Nugent C., Ferguson M., Leong J., Koop B., O'Connell M., and Bradbury I., 2021, Genomic basis of deep-water adaptation in arctic charr (*Salvelinus alpinus*) morphs, Molecular Ecology, 30: 4415-4432.
https://doi.org/10.1111/mec.16033

Klein A.H., Ballard K.R., Storey K.B., Motti C.A., Zhao M., and Cummins S.F., 2019, Multi-omics investigations within the phylum mollusca class gastropoda: from ecological application to breakthrough phylogenomic studies, Briefings in Functional Genomics, 18(6): 377-394.
https://doi.org/10.1093/bfgp/elz017

Lopez J., Kamel B., Medina M., Collins T., and Baums I., 2019, Multiple facets of marine invertebrate conservation genomics, Annual Review of Animal Biosciences, 7: 473-497.
https://doi.org/10.1146/annurev-animal-020518-115034

Marcionetti A., and Salamin N., 2022, Insights into the genomics of clownfish adaptive radiation: the genomic substrate of the diversification, Genome Biology and Evolution, 15(7): evad088.
https://doi.org/10.1093/gbe/evad088

Miya M., Sato Y., Fukunaga T., Sado T., Poulsen J., Sato K., Minamoto T., Yamamoto S., Yamanaka H., Araki H., Kondoh M., and Iwasaki W., 2015, MiFish a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species, Royal Society Open Science, 2(7): 150088.
https://doi.org/10.1098/rsos.150088

Mu Y.N., Bian C., Liu R.U., Wang Y.G., Shao G.G., Li J., Qiu Y., He T.L., Li W.R., Ao J.Q., Shi Q., and Chen X.H., 2021, Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea, PLoS Genetics, 17(5): e1009530.
https://doi.org/10.1371/journal.pgen.1009530

Oulas A., Pavloudi C., Polymenakou P., Pavlopoulos G., Papanikolaou N., Kotoulas G., Arvanitidis C., and Iliopoulos I., 2015, Metagenomics: tools and insights for analyzing next-generation sequencing data derived from biodiversity studies, Bioinformatics and Biology Insights, 9: 75-88.
https://doi.org/10.4137/BBI.S12462

Ovchinnikova T., and Shi Q., 2023, Editorial: aquatic genomics and transcriptomics for evolutionary biology, Frontiers in Genetics, 14: 1183637.
https://doi.org/10.3389/fgene.2023.1183637

Pinsky M.L., Clark R.D., and Bos J.T., 2023, Coral reef population genomics in an age of global change, Annual Review of Genetics, 57(1): 87-115.
https://doi.org/10.1146/annurev-genet-022123-102748

Qin Q.L., Wang Z.B., Cha Q.Q., Liu S.S., Ren X.B., Fu H.H., Sun M.L., Zhao D.L., McMinn A.M., Chen Y., Chen X., Zhang Y., and Li P., 2021, Biogeography of culturable marine bacteria from both poles reveals that 'everything is not everywhere' at the genomic level, Environmental Microbiology, 24(1): 98-109.
https://doi.org/10.1111/1462-2920.15870

Reid T., and Bergsveinson J., 2021, How do the players play a post-genomic analysis paradigm to understand aquatic ecosystem processes, Frontiers in Molecular Biosciences, 8: 662888.
https://doi.org/10.3389/fmolb.2021.662888

Rhee J., and Lee J., 2014, Whole genome data for omics-based research on the self-fertilizing fish *Kryptolebias marmoratus*, Marine Pollution Bulletin, 85(2): 532-541.
https://doi.org/10.1016/j.marpolbul.2014.04.005

Robbins S., Singleton C., Chan C., Messer L., Geers A., Ying H., Baker A., Bell S., Morrow K., Ragan M., Miller D., Forêt S., Hoegh- E., Ball E., Beeden R., Berumen M., Aranda M., Ravasi T., Bongaerts P., Hoegh-Guldberg O., Cooke I., Leggat B., Sprungala S., Fitzgerald A., Shang C., Lundgren P., Fyffe T., Rubino F., Oppen M., Weynberg K., Chan C., Forêt S., Voolstra C., Tyson G., Bourne D., and Tyson G., 2019, A genomic view of the reef-building coral Porites lutea and its microbial symbionts, Nature Microbiology, 4: 2090-2100.
https://doi.org/10.1038/s41564-019-0532-4

Roda-García J.J., Haro-Moreno J.M., and López-Pérez M., 2023, Evolutionary pathways for deep-sea adaptation in marine planktonic actinobacteriota, Frontiers in Microbiology, 14: 1159270.
https://doi.org/10.3389/fmicb.2023.1159270

Román-Palacios C., Moraga-López D., and Wiens J., 2022, The origins of global biodiversity on land sea and freshwater, Ecology Letters, 25(6): 1376-1386.
https://doi.org/10.1111/ele.13999

Selmoni O., Rochat E., Lecellier G., Berteaux-Lecellier V., and Joost S., 2020, Seascape genomics as a new tool to empower coral reef conservation strategies: An example on north-western Pacific *Acropora digitifera*, Evolutionary Applications, 13: 1923-1938.
https://doi.org/10.1111/eva.12944

Shih T.H., Chen C.M., Wang H.W., Pai T.W., and Chang H.T., 2010, BiMFG: bioinformatics tools for marine and freshwater species, Journal of Bioinformatics and Computational Biology, 8(supp01): 17-32.
https://doi.org/10.1142/S0219720010005105

Tan M.P., Wong L.L., Razali S.A., Afiqah-Aleng N., Nor S., Sung Y., Peer Y.Y., Sorgeloos P., and Danish-Daniel M., 2019, Applications of next-generation sequencing technologies and computational tools in molecular evolution and aquatic animals conservation studies: a short review, Evolutionary Bioinformatics Online, 15: 1176934319892284.
https://doi.org/10.1177/1176934319892284

Xu X.Y., 2024, Investigating the impact of embryonic gene editing on the growth rate and fat content of crucian carp, Animal Molecular Breeding, 14(1): 1-9.
https://doi.org/10.5376/amb.2024.14.0001

Yu J., Yu J., Blom J., Glaeser S.P., Jaenicke S., Juhre T., Rupp O., Schwengers O., Spänig S., and Goesmann A., 2017, A review of bioinformatics platforms for comparative genomics, Recent developments of the EDGAR 2.0 platform and its utility for taxonomic and phylogenetic studies, Journal of Biotechnology, 261: 2-9.
https://doi.org/10.1016/j.jbiotec.2017.07.010

Yuan Y., Zhang Y.L., Zhang P.J., Liu C., Wang J.H., Gao H.Y., Hoelzel A., Seim I., Lv M., Lin M.L., Dong L.J., Gao H., Yang Z., Caruso F., Lin W.Z., Fonseca R.R., Wang D., Wang X.Y., Rasmussen M., Liu M.M., Zheng J.S., Zhao L.Y., Campos P.F., Kang H., Iversen M., Song Y., Guo X.Y., Guo J., Qin Y., Pan S., Xu Q., Meng L., A Y., Liu S., Lee S.L., Liu X., Xu X., Yang H.M., Fan G.Y., Wang K., and Li S.H., 2021, Comparative genomics provides insights into the aquatic adaptations of mammals, Proceedings of the National Academy of Sciences of the United States of America, 118(37): e2106080118.
https://doi.org/10.1073/pnas.2106080118

Zhou Y., 2024, Adaptation or extinction: survival strategies of marine organisms under the pressure of climate change, International Journal of Marine Science, 14(2): 57-65.
https://doi.org/10.5376/ijms.2024.14.0008