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Molecular Mechanisms Underlying the Diversification of Aquatic Life Forms

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Abstract The diversification of aquatic life forms is a significant phenomenon in biological evolution, and understanding the molecular mechanisms behind it is crucial for uncovering the origins of biodiversity and its adaptability. This study explores the key molecular mechanisms driving the diversification of aquatic life forms, including gene duplication, horizontal gene transfer, mutations, and their roles in genetic variability. It also analyzes how gene regulatory networks and epigenetic modifications influence the evolution of developmental pathways, and how environmental factors such as water conditions, predation pressure, and climate change drive molecular diversification. By examining the molecular evolution of key aquatic adaptations such as respiratory systems, sensory systems, and reproductive strategies, the study summarizes the evolutionary strategies of aquatic organisms in various ecological environments. These findings not only deepen the understanding of biodiversity and adaptive evolution in aquatic organisms but also provide a scientific basis for the development of biodiversity conservation strategies and highlight future research directions.

Keywords Diversification; Molecular mechanisms; Aquatic life forms; Gene duplication; Evolutionary strategies

1 Introduction

Aquatic life forms encompass a vast array of organisms that inhabit marine, freshwater, and brackish environments. These organisms have evolved a multitude of adaptations to thrive in their respective habitats, ranging from physiological mechanisms to morphological traits. For instance, water striders have developed superhydrophobic bristles and elongated legs to navigate water surfaces, a transition that occurred approximately 200 million years ago. Similarly, the *Nepomorpha*, or true water bugs, have diversified significantly since the late Permian, adapting to various aquatic environments. The deep-sea fish *Coryphaenoides rupestris* exhibits genotypic segregation by depth, highlighting the role of vertical habitat gradients in promoting intraspecific diversity (Gaither et al., 2018; Ye et al., 2020; Finet et al., 2022).

Understanding the mechanisms underlying the diversification of aquatic life forms is crucial for several reasons. It provides insights into the evolutionary processes that drive speciation and adaptation. For example, the study of carbon concentrating mechanisms (CCMs) in aquatic photosynthetic organisms reveals how these systems contribute to global net primary productivity and marine carbon sequestration (Griffiths et al., 2017; Zhou and Mai, 2024). It helps in predicting how current and future environmental changes, such as global warming and cooling, will impact biodiversity.

Research on the Anomura crustaceans shows that speciation rates are influenced by global temperature changes, with marine clades responding differently to cooling and warming trends (Davis et al., 2016). Understanding diversification aids in conservation efforts by identifying key adaptive traits and environmental pressures that shape biodiversity.

This study leverages current knowledge on the molecular mechanisms driving the diversification of aquatic life forms to analyze the genetic and molecular basis of key adaptive traits in various aquatic organisms. It explores the role of environmental factors, such as climate change and habitat alterations, in shaping diversification patterns and discusses the implications of these findings for biodiversity conservation and management.By integrating the results of multiple studies, this research aims to provide a comprehensive understanding of how molecular mechanisms promote the diversification of aquatic life forms, thereby offering valuable insights for evolutionary biology and conservation science..

2 Genetic Basis of Diversification

2.1 Role of gene duplication

Gene duplication is a fundamental mechanism that contributes to the diversification of aquatic life forms by providing raw genetic material for evolutionary innovation. For instance, the genome of the water strider *Gerris buenoi* reveals numerous local gene duplications and expansions of gene families that are crucial for adaptations to a water surface lifestyle. These duplications affect processes such as growth, vision, desiccation resistance, detoxification, olfaction, and epigenetic regulation, which are essential for the water strider's survival and diversification in aquatic environments (Armisén et al., 2018). Similarly, the duplication of the Na^+/K^+-ATPase gene in clitellate annelids is associated with their transition from marine to freshwater habitats, suggesting that these duplications played a significant role in their diversification (Horn et al., 2019). The dynamic evolution of gene families, including gene duplication and deletion, has been shown to drive phenotypic diversity and adaptation in various aquatic species, such as African cichlid fishes and Hawaiian drosophilids (Harris and Hofmann, 2015).

2.2 Horizontal gene transfer

Horizontal gene transfer (HGT) is another critical mechanism that accelerates microbial evolution and promotes diversification and adaptation in aquatic environments. In marine ecosystems, the cyanobacterium *Prochlorococcus* exhibits a highly streamlined genome with frequent gene exchange, facilitated by mobile genetic elements known as tycheposons. These elements drive genomic plasticity and niche differentiation by carrying genes important for nutrient acquisition and other adaptive traits. The efficient dispersal and transmission of tycheposons through extracellular vesicles and phage particles highlight the significant role of HGT in the diversification of marine microbes (Hackl et al., 2020). Furthermore, the formation of new ecologically distinct populations (ecotypes) in the *Microcystis aeruginosa* complex is driven by mutations in key functional genes and the acquisition of new metabolic pathways through HGT, allowing these populations to exploit new resources and coexist with parental populations (Escalera et al., 2021).

2.3 Mutations and genetic variability

Mutations and genetic variability are essential for the adaptive diversification of aquatic organisms. In the rotifer *Brachionus calyciflorus*, genetic variation and differences in gene expression related to temperature tolerance play a significant role in local adaptation and ecological diversification. The identification of candidate genes associated with metabolism and stress response highlights the importance of genetic variability in adapting to different thermal environments (Paraskevopoulou et al., 2019). The adaptation of fishes to changing salinity involves genetic changes in osmoregulatory systems, with natural selection targeting genes coding for key cellular ion exchange enzymes such as V-type, Ca^{2+}, and Na^+/K^+-ATPases. These genetic changes support the transition across salinity boundaries and contribute to the diversification of fish species (Velotta et al., 2022). The study of diatoms also reveals that habitat transitions, such as from marine to freshwater environments, are influenced by genetic variability and adaptive mutations, which play a crucial role in their diversification (Roberts et al., 2023).

3 Regulatory Networks and Evolution

3.1 Gene regulatory networks

Gene regulatory networks (GRNs) play a crucial role in the diversification of aquatic life forms by orchestrating the expression of genes in response to environmental changes. In marine mammals, for instance, the adaptation to aquatic environments involved significant modifications in GRNs. Comparative genomics has revealed that genes associated with thermoregulation, such as *NFIA* and *SEMA3E*, have undergone convergent evolution to facilitate the transition from land to water. These genes are involved in the formation of blubber and vascular development, respectively, which are essential for maintaining body temperature in aquatic environments (Figure 1) (Triant et al., 2021; Yuan et al., 2021). The loss of the UCP1 locus in many marine mammals indicates a shift in their thermostatic strategy from enhancing heat production to limiting heat loss, further highlighting the role of GRNs in evolutionary adaptation.

The gene plays a crucial role in determining whether adipocytes develop into energy-storing white fat cells or heat-producing brown fat cells by regulating adipocyte differentiation. In brown fat cells, the action of the UCP1 protein can convert stored energy into heat, which is vital for maintaining body temperature in cold aquatic environments. Research has found convergent amino acid substitutions in the *NFIA* gene across multiple marine mammal species, suggesting that these species may promote the formation of adipose tissue through similar mechanisms to adapt to aquatic environments. Additionally, the *SEMA3E* gene plays an important role in vascular development. The vascular structures of marine mammals, such as the complex retia mirabilia, are crucial for thermoregulation, effectively reducing heat loss in water. Studies show that the convergent evolution of the *SEMA3E* gene may help these animals develop their vascular systems more effectively to maintain body temperature in cold environments.

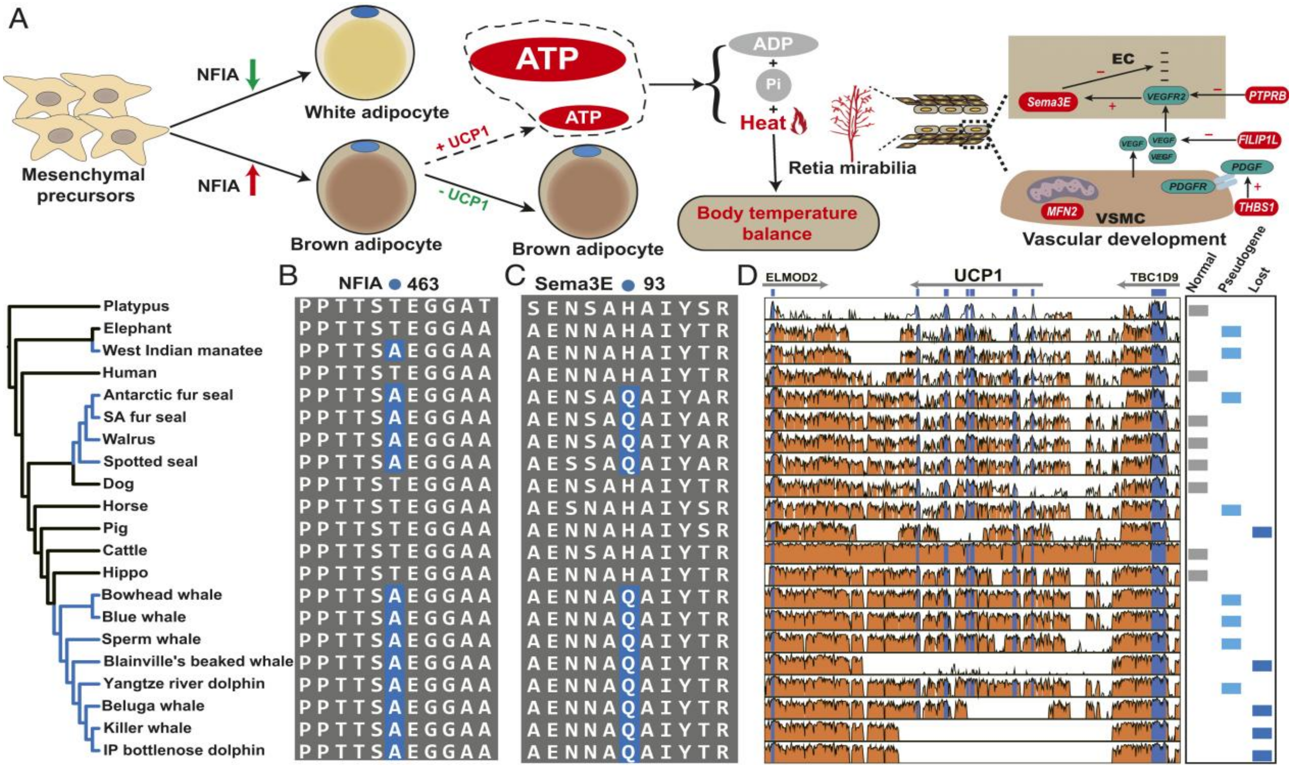

Figure 1 Convergent evolution of thermoregulation in marine mammals (Adopted from Yuan et al., 2021)
Image caption: (A) Schematic diagram of thermoregulation in marine mammals. Up- or down-regulation of nuclear factor I A (*NFIA*) affects the cell fate of mesenchymal precursors, the integrity of *UCP1* gene affects the fate of brown adipocyte, and the well-developed retia mirabilia in marine mammal aids in the heat transfer to maintain body temperature balance. VSMC, vascular smooth muscle cell; EC, endothelial cell. (B) A unique amino acid change in the *NFIA* gene of marine mammals. Shared amino acid change are highlighted in blue, IP, Indo-Pacific. (C) A unique amino acid change in the *SEMA3E* gene of cetaceans and pinnipeds. Blue highlighting indicates the shared amino acid change. (D) VISTA sequence conservation plot of the *UCP1* gene, using goat (ARS1) as a reference (Adopted from Yuan et al., 2021)

3.2 Epigenetic modifications

Epigenetic modifications, including DNA methylation and histone modifications, are pivotal in regulating gene expression without altering the underlying DNA sequence. These modifications can lead to phenotypic changes that are essential for the adaptation to new environments. In the context of aquatic life forms, epigenetic changes may influence the expression of genes involved in critical physiological processes such as thermoregulation, diving, and navigation. For example, the unique changes in genes like *NFIA* and *SEMA3E* in marine mammals suggest that epigenetic mechanisms could be at play in regulating these genes to meet the demands of an aquatic lifestyle (Yuan et al., 2021). Although specific studies on epigenetic modifications in aquatic life forms are limited, the existing evidence underscores their potential role in facilitating rapid and reversible adaptations to environmental changes.

3.3 Evolution of developmental pathways

The evolution of developmental pathways is a key factor in the diversification of aquatic life forms. Developmental pathways are regulated by a complex interplay of transcription factors and gene regulatory networks. In plants, for example, the evolution from unicellular aquatic algae to complex flowering plants involved significant changes in transcription factors and their associated regulatory networks. These changes were driven by alterations in DNA binding specificity, protein-protein interactions, and cis-regulatory elements, which collectively contributed to the functional evolution of transcription factors (Romani and Moreno, 2020). Similarly, in marine mammals, the adaptation to aquatic environments required modifications in developmental pathways to support new physiological and morphological traits. The study of these evolutionary processes in both plants and animals provides valuable insights into the molecular mechanisms underlying the diversification of life forms in aquatic environments.

4 Environmental Factors Driving Molecular Diversification

4.1 Adaptation to different water conditions

Adaptation to varying water conditions is a significant driver of molecular diversification in aquatic life forms. The transition between marine and freshwater environments, characterized by steep salinity gradients, poses a substantial osmotic challenge for many species. For instance, diatoms exhibit molecular acclimation mechanisms to cope with hypo-osmotic stress when transitioning from saline to freshwater environments, highlighting the role of cellular mechanisms in overcoming salinity barriers (Bilcke and Kamakura, 2023). Similarly, the genomic adaptations in marine mammals, such as changes in genes associated with thermoregulation and deep diving, underscore the importance of molecular changes in adapting to aquatic lifestyles. These adaptations are crucial for survival and diversification in different aquatic habitats.

4.2 Pressure of predation and competition

Predation and competition are pivotal biotic factors influencing the diversification of aquatic species. In postglacial freshwater fish species, predation and competition have been implicated in the divergence into multiple ecomorphs within lakes, suggesting that these biotic pressures drive morphological and ecological diversification (Condamine et al., 2019; Tiddy et al., 2023). The unequal body shape diversification in the Gondwanan fish radiation (*Characiformes*) is influenced by competition for niches and habitat variation. Neotropical characiform lineages exhibit greater morphological diversity compared to their African counterparts, likely due to competition with cypriniform fishes in Africa and the availability of diverse habitats in the Neotropics (Burns et al., 2023). These examples illustrate how predation and competition pressures can lead to significant diversification in aquatic life forms.

4.3 Influence of climate change

Climate change is a critical abiotic factor driving molecular diversification in aquatic ecosystems. Global cooling and warming have been shown to influence speciation rates in marine and freshwater clades differently. For example, speciation rates in marine clades of Anomura crustaceans are positively correlated with global cooling, while freshwater clades show increased speciation rates with global warming (Davis et al., 2016). Climate fluctuations have played a significant role in the diversification of true water bugs (*Nepomorpha*) during the Mesozoic, with palaeoecological opportunities promoting lineage diversification (Friedman et al., 2021). The interaction of multiple climate-change drivers, such as ocean warming, acidification, and deoxygenation, also affects aquatic productivity and species responses, highlighting the complex influence of climate change on molecular diversification (Häder and Gao, 2023). Understanding these dynamics is crucial for predicting and mitigating the impacts of ongoing climate change on aquatic biodiversity.

5 Molecular Evolution of Key Aquatic Adaptations

5.1 Evolution of respiratory systems

5.1.1 Gills and lung evolution

The evolution of respiratory systems in aquatic life forms has been a critical adaptation for survival in diverse environments. In vertebrates, the transition from terrestrial to aquatic life necessitated significant modifications in respiratory structures. For instance, cetaceans exhibit a series of evolutionary changes in morphology and physiology, including the development of specialized lungs and the reduction of olfactory structures, which are less useful underwater (Yang et al., 2019). Similarly, the blue-spotted mudskipper, an amphibious fish, has evolved hemoglobin with high oxygen affinity, allowing it to switch between aquatic and aerial respiration effectively (Xu et al., 2018; Storz et al., 2019). In invertebrates, such as the Onchidiidae family, adaptations include the development of gills for underwater respiration and lung sacs for breathing in wetland environments.

5.1.2 Adaptations to hypoxia

Aquatic organisms have developed various strategies to cope with hypoxic conditions. Amazonian fishes, particularly the genus *Astronotus*, exhibit remarkable hypoxia tolerance through metabolic adjustments such as increased glycolytic metabolism and anaerobic respiration (Braz-Mota and Almeida-Val, 2021). These adaptations enable them to survive in environments with fluctuating oxygen levels. Similarly, the blue-spotted mudskipper has evolved hemoglobin with properties that support efficient oxygen transport under hypoxic conditions, facilitating its facultative air-breathing capability (Storz et al., 2019).

5.1.3 Cutaneous respiration

Cutaneous respiration, or breathing through the skin, is another adaptation observed in some aquatic and semi-aquatic species. Anolis lizards, for example, have developed a unique underwater rebreathing mechanism that allows them to respire using air bubbles trapped against their skin, enhancing their ability to remain submerged for extended periods (Boccia et al., 2021). This adaptation is facilitated by their hydrophobic skin, which supports the formation of a thin air layer, or plastron, aiding in gas exchange.

5.2 Development of sensory systems

5.2.1 Evolution of vision in water

The evolution of vision in aquatic environments has involved significant changes in sensory systems. Marine mammals, for instance, have undergone convergent evolution in sensory genes, resulting in adaptations that enhance their ability to navigate and hunt in underwater environments 24. These adaptations include modifications in genes associated with vision, allowing for improved light detection and image processing in the aquatic medium.

5.2.2 Lateral line system

The lateral line system is a mechanosensory system that allows aquatic animals to detect water movements and vibrations. This system is particularly well-developed in fish and some amphibians, providing them with crucial information about their surroundings, such as the presence of predators or prey. The evolution of this system has been a key adaptation for survival in aquatic habitats.

5.2.3 Electroreception

Electroreception is the ability to detect electric fields generated by other organisms. This sensory adaptation is found in various aquatic species, including some fish and amphibians. It allows them to locate prey, navigate, and communicate in environments where visibility is limited. The genetic basis of electroreception involves specific ion channels and receptors that have evolved to detect electric signals in the water (Houssaye and Fish, 2016).

5.3 Diversification of reproductive strategies

5.3.1 Sexual vs. asexual reproduction

Aquatic life forms exhibit a wide range of reproductive strategies, including both sexual and asexual reproduction. Sexual reproduction, which involves the combination of genetic material from two parents, is common in many aquatic species and promotes genetic diversity. Asexual reproduction, on the other hand, allows for rapid population growth and is observed in some invertebrates and plants.

5.3.2 Viviparity and oviparity

Viviparity (live birth) and oviparity (egg laying) are two reproductive strategies that have evolved in aquatic organisms. Marine mammals, such as cetaceans, exhibit viviparity, giving birth to live young that are well-developed and capable of swimming shortly after birth (Yang et al., 2019). In contrast, many fish and amphibians are oviparous, laying eggs that develop and hatch outside the mother's body.

5.3.3 Parental care

Parental care is a significant adaptation that enhances the survival of offspring in aquatic environments. This behavior is observed in various species, including fish, amphibians, and some invertebrates. Parental care strategies range from guarding eggs to providing food and protection for the young (Harrison, 2015). These behaviors increase the chances of offspring survival and contribute to the success of the species.

6 Case Studies in Aquatic Diversification

6.1 Diversification of fish in coral reefs

Coral reefs are hotspots of biodiversity, particularly for fish species. The evolutionary history of reef fishes and corals shows a marked congruence, with both groups exhibiting rapid lineage diversification during the Oligocene and Miocene epochs (34-5.3 million years ago) (Bellwood et al., 2017). This period saw the establishment of modern coral reef ecosystems, characterized by high turnover and fast growth, which facilitated the colonization of new habitats and the appearance of new taxa. Despite the rapid increase in biodiversity, functional changes in fishes and corals over the last 5.3 million years have been limited, suggesting that recent diversification may be driven more by ecological opportunities, such as color variation in fish, rather than by significant functional innovations.

Functional traits, such as diet, body size, and water column use, have played a fundamental role in the evolution and diversification of reef fish lineages. Independent transitions to planktivory across different reef fish families highlight how ecological opportunities for exploiting different resources can drive speciation and adaptation (Floeter et al., 2108). The generalist feeding strategy has been pivotal during the evolutionary history of reef fishes, acting as a reservoir for future diversity (Gajdzik et al., 2019).

6.2 Evolution of marine mammals

Marine mammals have undergone significant evolutionary changes, often driven by climatic factors. For instance, global cooling has been identified as a driver of diversification in marine clades, such as the Anomura crustaceans. Speciation rates in these clades are correlated with cooler global temperatures, suggesting that climate change has historically played a crucial role in shaping marine biodiversity (Davis et al., 2016). This pattern contrasts with freshwater clades, where speciation rates are positively correlated with global warming, indicating that different environmental pressures can lead to diversification in marine and freshwater habitats.

6.3 Speciation in freshwater environments

Transitions between marine and freshwater environments have contributed to diversification. Diatoms, for example, have repeatedly colonized and diversified in freshwater habitats. These transitions often trigger rapid morphological or physiological changes and can lead to increased rates of speciation and extinction over longer timescales (Figure 2) (Roberts et al., 2023). The ability of some taxa to adapt to low salinity environments through specific genetic changes further underscores the role of habitat transitions in driving diversification.

These transformations are crucial factors driving the diversification of diatom species. Particularly in freshwater environments, diatoms have undergone significant diversification, a process that may be driven by multiple genes and evolutionary mechanisms. Research also indicates discrepancies between gene trees and species trees, which may be due to inconsistencies in gene ordering or estimation errors in the gene trees. These findings suggest that diatoms are capable of adapting to different environments through complex evolutionary mechanisms, thereby sustaining their survival and diversification across various habitats. The frequent transitions of diatoms between marine and freshwater environments not only drive their species diversification but also provide important insights into the adaptive evolution of aquatic organisms.

Freshwater environments present unique opportunities and challenges for diversification. The "freshwater fish paradox" describes the high concentration of vertebrate diversity in continental freshwaters, with over 15 000 fish species representing more than 20% of all vertebrate species in a tiny fraction of the Earth's surface area (Val et al., 2022). Landscape evolution, particularly river capture events, has been proposed as a significant driver of this diversity. River captures can accelerate biotic diversification by affecting dispersal, speciation, and extinction rates. Large, lowland river basins in tropical regions, such as South America, Africa, and Southeast Asia, exhibit the highest fish species richness, likely due to their stable tectonic conditions and high habitat volume.

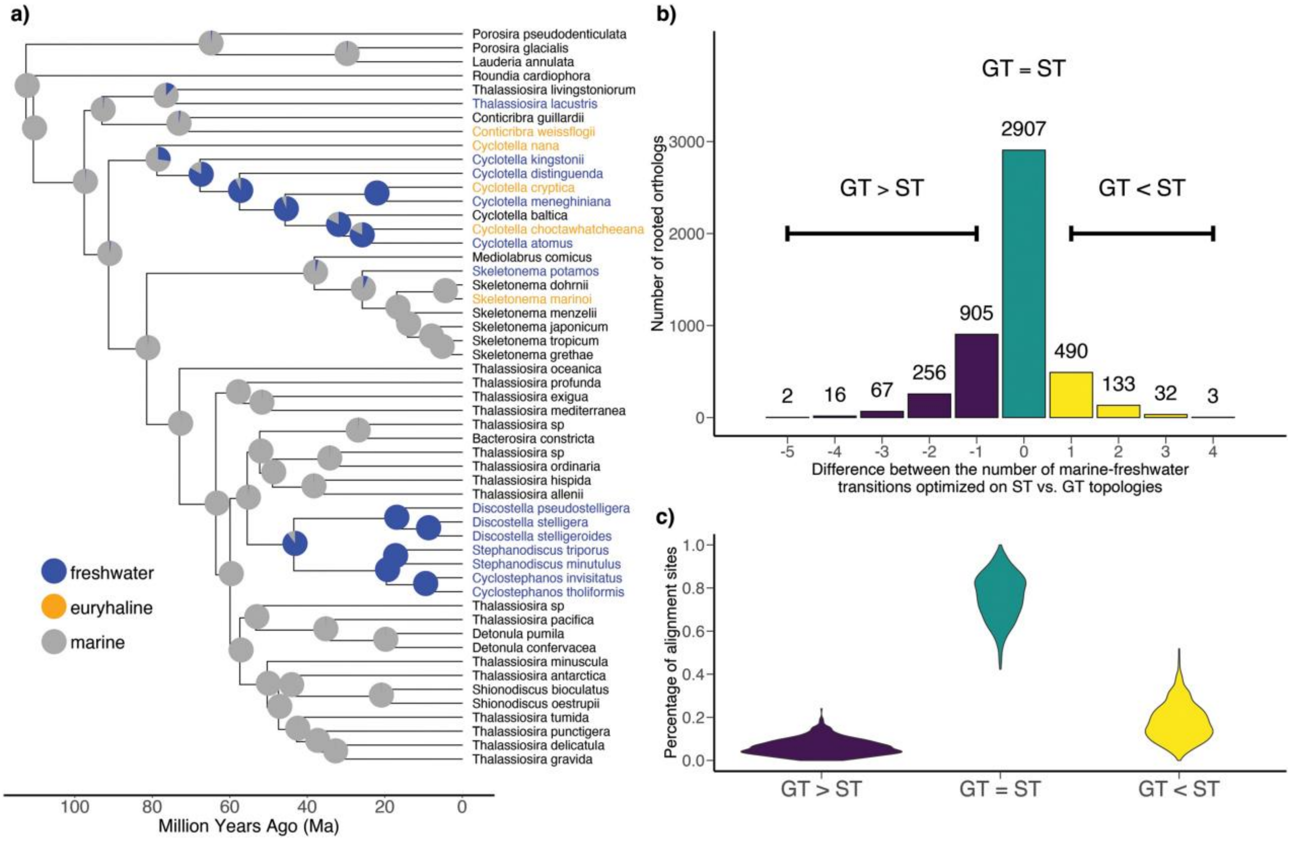

Figure 2 The temporal sequence of marine–freshwater transitions (Adopted from Roberts et al., 2023)

Image caption: (a) Divergence times and ancestral state reconstruction of marine and freshwater habitat in *Thalassiosirales*; (b) Summary of the difference between the number of parsimony optimized marine-freshwater transitions on rooted orthologs with the estimated gene tree topology (GT) versus the topology constrained to match the species tree (ST); (c) Summary of the percentage of aligned amino acid sites that have greater (purple), equal (green), or fewer (yellow) numbers of state transitions on the GT versus ST (Adopted from Roberts et al., 2023)

7 Technological Advances in Studying Molecular Diversification

7.1 Genomics and transcriptomics

Recent advancements in genomics and transcriptomics have significantly enhanced our understanding of molecular diversification in aquatic life forms. The integration of these technologies has allowed researchers to delve into the genetic and transcriptomic underpinnings of species adaptation and diversification. For instance, large-scale projects such as the Marine Mammal Genome Project and the Fish10K have provided extensive genomic data that facilitate the study of evolutionary biology in aquatic organisms (Ovchinnikova and Shi, 2023). These projects have enabled the identification of novel bioactive macromolecules and the exploration of differential gene expression and evolutionary selection mechanisms. Additionally, the genomic analysis of deep-sea fish like *Coryphaenoides rupestris* has revealed how genetic differentiation at functional loci can drive adaptation to different depths, highlighting the role of disruptive selection in promoting intraspecific diversity (Gaither et al., 2018).

7.2 CRISPR and gene editing techniques

CRISPR and other gene editing techniques have revolutionized the study of molecular mechanisms underlying diversification. These tools allow for precise manipulation of genetic material, enabling researchers to investigate the functional roles of specific genes in adaptation and speciation. For example, studies on water striders have identified genes involved in both bristle density and leg length, traits essential for water surface locomotion. The genetic correlation between these traits suggests that pleiotropy might facilitate diversification by simultaneously impacting multiple adaptive traits. Such insights are crucial for understanding how genetic changes contribute to the exploitation of new ecological niches and subsequent species diversification.

7.3 Bioinformatics and phylogenetic analysis

Bioinformatics and phylogenetic analysis are indispensable in studying the evolutionary relationships and diversification patterns of aquatic organisms. The use of multilocus approaches and coalescent-based phylogeography has proven effective in resolving recent diversification events. For instance, the colonization and diversification of aquatic insects in Macaronesia were elucidated using 59 nuclear loci derived from a draft genome, highlighting the value of combining genomics with phylogenetic reconstruction. Similarly, the phylogenomic analysis of diatoms has provided insights into the transitions between marine and freshwater habitats, revealing the role of gene tree discordance and hemiplasy in adaptation 1. These methodologies enable researchers to construct well-resolved phylogenies and understand the complex evolutionary processes driving diversification in aquatic life forms.

8 Concluding Remarks

The diversification of aquatic life forms is driven by a multitude of molecular mechanisms and environmental factors. In deep-sea fish such as *Coryphaenoides rupestris*, genomic differentiation at functional loci is influenced by depth, suggesting disruptive selection and ecotype differentiation linked to distinct phenotypic requirements at different depths. Freshwater eDNA has proven effective in detecting invasive species, assessing community assemblages, and mapping the distribution of rare taxa. However, there is a notable geographical and taxonomic bias in eDNA research, with under-representation in regions like Africa and South America and among certain taxa such as freshwater arthropods. Climate change, particularly global cooling, has been identified as a significant driver of diversification in marine clades, while global warming influences speciation rates in freshwater clades. Cryptic species are more frequently found in freshwater habitats compared to terrestrial or marine environments, likely due to the greater heterogeneity and fragmentation of freshwater habitats. Diatoms exhibit complex molecular acclimation mechanisms to cope with salinity changes, which are crucial for their survival and diversification in varying aquatic environments. The molecular mechanisms underlying biomineralization in marine invertebrates, such as corals and molluscs, are critical for their adaptation to changing environmental conditions, including ocean acidification and temperature changes. CCMs in aquatic photosynthetic organisms play a vital role in global carbon sequestration and primary productivity, with significant implications for understanding their evolutionary origins and future applications. Advances in sequencing technologies and molecular markers have enhanced our understanding of genetic diversity and population structure in aquatic species, which is essential for effective conservation strategies. The evolutionary history and diversification of aquatic bugs (*Nepomorpha*) are influenced by climate fluctuations and tectonic reconfigurations, with significant implications for understanding their adaptation and diversification dynamics. Incorporating biological traits at multiple spatial-temporal scales is crucial for forecasting responses of aquatic ecosystems to environmental changes and developing effective conservation strategies.

The findings from these studies have profound implications for conservation and biodiversity. Understanding the genomic differentiation and cryptic diversity in aquatic species can help in designing targeted conservation efforts that address specific ecological and genetic needs. Harmonizing eDNA methods and increasing international cooperation can improve the monitoring and conservation of freshwater biodiversity, especially in under-represented regions. Insights into how climate change drives diversification can inform conservation planning to mitigate the impacts of global warming and cooling on aquatic species. Knowledge of molecular acclimation mechanisms and biomineralization processes can aid in predicting the resilience of aquatic organisms to environmental stressors and guide conservation strategies. The use of advanced genetic tools and molecular markers can enhance the effectiveness of conservation programs by providing detailed information on population structure and genetic diversity.

Future research should focus on several key areas to further our understanding of the molecular mechanisms underlying the diversification of aquatic life forms. Further studies on the genomic differentiation of deep-sea species across different depths can provide deeper insights into the mechanisms of disruptive selection and ecotype differentiation. Expanding eDNA research to under-represented regions and taxa can improve our understanding of global freshwater biodiversity and inform conservation efforts. Investigating the long-term impacts of climate change on the diversification and speciation of both marine and freshwater species can help predict future biodiversity patterns. Developing more efficient methods for identifying cryptic species in various habitats can enhance biodiversity assessments and conservation strategies. Exploring the molecular mechanisms of salinity tolerance in different aquatic organisms can provide insights into their adaptability and resilience to environmental changes. Further research on the molecular pathways of biomineralization in marine invertebrates can improve our understanding of their responses to ocean acidification and other stressors. Investigating the evolutionary origins and potential applications of CCMs in aquatic photosynthetic organisms can contribute to global carbon sequestration efforts. Integrating genetic data with conservation planning can enhance the effectiveness of conservation strategies and ensure the long-term survival of aquatic species. Developing trait-based conservation approaches that consider multiple biological scales can improve the forecasting and management of aquatic ecosystems under changing environmental conditions.

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Conflict of Interest Disclosure

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

Reference

Armisén D., Rajakumar R., Friedrich M., Benoit J.B., Robertson H.M., Panfilio K.A., Ahn S.J., Poelchau M., Chao H., Dinh H., Doddapaneni H.V., Dugan S., Gibbs R., Hughes D., Han Y., Lee S.L., Murali S., Muzny D., Qu J., Worley K., Torres M.M., Abouheif E., Bonneton F., Chen T., Childers C., Cridge A., Crumière A., Decaras A., Didion E., Duncan E., Elpidina E., Favé M., and Khila A., 2018, The genome of the water strider *Gerris buenoi* reveals expansions of gene repertoires associated with adaptations to life on the water, BMC Genomics, 19: 1-16.
https://doi.org/10.1186/s12864-018-5163-2

Bellwood D., Goatley C.F., and Bellwood O., 2017, The evolution of fishes and corals on reefs: form function and interdependence, Biological Reviews, 62(9): 1645-1654.
https://doi.org/10.1111/brv.12259

Bilcke G., and Kamakura S., 2023, Scaling the invisible wall: molecular acclimation of a salinity-tolerant diatom to freshwater, Molecular Ecology, 32(11): 2692-2694.
https://doi.org/10.1111/mec.16971

Boccia C.K., Swierk L., AYALA-VARELA F.P., Boccia J., Borges I.L., Estupiñán C.A., Martin A.M., Martínez-Grimaldo R., Ovalle S., Senthivasan S., Toyama K., Castañeda M., García A., Glor R., and Mahler D., 2021, Repeated evolution of underwater rebreathing in diving Anolis lizards, Current Biology, 31(13): 2947-2954. e4.
https://doi.org/10.1016/j.cub.2021.04.040

Braz-Mota S., and Almeida-Val V.M.F., 2021, Ecological adaptations of amazonian fishes acquired during evolution under environmental variations in dissolved oxygen: a review of responses to hypoxia in fishes featuring the hypoxia-tolerant *Astronotus* spp., Journal of Experimental Zoology, Part A Ecological and Integrative Physiology, 335(9-10): 771-786.
https://doi.org/10.1002/jez.2531

Burns M.D., Knouft J.H., and Dillman C.D., 2023, The role of abiotic and biotic factors in the unequal body shape diversification of a Gondwanan fish radiation (*Otophysi:Characiformes*), International Journal of Organic Evolution, 78(2): 253-266.
https://doi.org/10.1093/evolut/qpad203

Chikina M., Robinson J., and Clark N., 2016, Hundreds of genes experienced convergent shifts in selective pressure in marine mammals, Molecular Biology and Evolution, 33(9): 2182-92.
https://doi.org/10.1093/molbev/msw112

Condamine F.L., Rolland J., and Morlon H., 2019, Assessing the causes of diversification slowdowns: temperature-dependent and diversity-dependent models receive equivalent support, Ecology Letters, 22(11): 1900-1912.
https://doi.org/10.1111/ele.13382

Davis K.E., Hill J., Astrop T.I., and Wills M.A., 2016, Global cooling as a driver of diversification in a major marine clade, Nature Communications, 7(1): 13003.
https://doi.org/10.1038/ncomms13003

Escalera G., Segura A.M., Kruk C., Ghattas B., Cohan F.M., Iriarte A., and Piccini C., 2021, Genotyping and multivariate regression trees reveal ecological diversification within the *Microcystis aeruginosa* complex along a wide environmental gradient, Applied and Environmental Microbiology, 88(3): e01475-21.
https://doi.org/10.1128/aem.01475-21

Finet C., Decaras A., Rutkowska M., Roux P., Collaudin S., Joncour P., Viala S., and Khila A., 2022, Leg length and bristle density both necessary for water surface locomotion are genetically correlated in water striders, Proceedings of the National Academy of Sciences of the United States of America, 119(9): e2119210119.
https://doi.org/10.1073/pnas.2119210119

Fischer C., Koblmüller S., Börger C., Michelitsch G., Trajanoski S., Schlötterer C., Guelly C., Thallinger G., and Sturmbauer C., 2021, Genome sequences of *Tropheus moorii* and *Petrochromis trewavasae* two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika, Scientific Reports, 11(1): 4309.
https://doi.org/10.1038/s41598-021-81030-z

Floeter S.R., Bender M.G., Siqueira A.C., and Cowman P.F., 2018, Phylogenetic perspectives on reef fish functional traits, Biological Reviews, 93(1): 131-151.
https://doi.org/10.1111/brv.12336

Friedman S.T., Collyer M.L., Price S.A., and Wainwright P., 2021, Divergent processes drive parallel evolution in marine and freshwater fishes, Systematic Biology, 71(6): 1319-1330.
https://doi.org/10.1093/sysbio/syab080

Gaither M., Gaither M., Gkafas G., Gkafas G., Jong M., Sarigol F., Sarigol F., Neat F., Régnier T., Moore D., Gröcke 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

Gajdzik L., Aguilar-Medrano R., and Frédérich B., 2019, Diversification and functional evolution of reef fish feeding guilds, Ecology letters, 22: 4 572-582.
https://doi.org/10.1111/ele.13219

Griffiths H., Meyer M., and Rickaby R., 2017, Overcoming adversity through diversity: aquatic carbon concentrating mechanisms, Journal of Experimental Botany, 68: 3689-3695.
https://doi.org/10.1093/jxb/erx278

Hackl T., Laurenceau R., Ankenbrand M., Bliem C., Cariani Z., Thomas E., Dooley K., Arellano A., Hogle S., Berube P., Leventhal G., Luo E., Eppley J., Zayed A., Beaulaurier J., Stepanauskas R., Sullivan M., Delong E., Biller S., and Chisholm S., 2020, Novel integrative elements and genomic plasticity in ocean ecosystems, Cell, 186: 47-62.e16.
https://doi.org/10.1101/2020.12.28.424599

Häder D.P., and Gao K., 2023, Aquatic productivity under multiple stressors, Water, 15(4): 817.
https://doi.org/10.3390/w15040817

Harris R., and Hofmann H., 2015, Seeing is believing: Dynamic evolution of gene families, Proceedings of the National Academy of Sciences, 112: 1252-1253.
https://doi.org/10.1073/pnas.1423685112

Harrison J.F., 2015, Handling and use of oxygen by pancrustaceans: conserved patterns and the evolution of respiratory structures, Integrative and Comparative Biology, 55(5): 802-815.
https://doi.org/10.1093/icb/icv055

Horn K., Williams B., Erséus C., Halanych K., Santos S., Châtelliers M., and Anderson F., 2019, Na^+/K^+-ATPase gene duplications in clitellate annelids are associated with freshwater colonization, Journal of Evolutionary Biology, 32: 580-591.
https://doi.org/10.1111/jeb.13439

Houssaye A., and Fish F., 2016, Functional (Secondary) Adaptation to an Aquatic Life in Vertebrates: An Introduction to the Symposium., Integrative and Comparative Biology, 56(6): 1266-1270.
https://doi.org/10.1093/ICB/ICW129

Ovchinnikova T.V., 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

Paraskevopoulou S., Dennis A.B., Weithoff G., Hartmann S., and Tiedemann R., 2019, Within species expressed genetic variability and gene expression response to different temperatures in the rotifer *Brachionus calyciflorus* sensu stricto, PLoS ONE, 14(9): e0223134.
https://doi.org/10.1371/journal.pone.0223134

Roberts W.R., Ruck E.C., Downey K.M., Pinseel E., and Alverson A., 2023, Resolving marine-freshwater transitions by diatoms through a fog of gene tree discordance, Systematic Biology, 72(5): 984-997.
https://doi.org/10.1093/sysbio/syad038

Romani F., and Moreno J.F., 2020, Molecular mechanisms involved in functional macroevolution of plant transcription factors, The New Phytologist, 230(4): 1345-1353.
https://doi.org/10.1111/nph.17161

Rutschmann S., Detering H., Simon S., Funk D., Gattolliat J., Hughes S., Raposeiro P., DeSalle R., Sartori M., and Monaghan M., 2017, Colonization and diversification of aquatic insects on three Macaronesian archipelagos using 59 nuclear loci derived from a draft genome, Molecular Phylogenetics and Evolution, 107: 27-38.
https://doi.org/10.1016/j.ympev.2016.10.007

Storz J.F., Natarajan C., Grouleff M.K., Vandewege M., Hoffmann F.G., You X., Venkatesh B., and Fago A., 2019, Oxygenation properties of hemoglobin and the evolutionary origins of isoform multiplicity in an amphibious air-breathing fish the blue-spotted mudskipper (*Boleophthalmus pectinirostris*), Journal of Experimental Biology, 223(2): jeb217307.
https://doi.org/10.1242/jeb.217307

Tiddy I.C., Schneider K., and Elmer K., 2023, Environmental correlates of adaptive diversification in post-glacial freshwater fishes, Journal of Fish Biology, 104(3): 517-535.
https://doi.org/10.1111/jfb.15621

Triant D.E., Nowick K., and Shelest E., 2021, Editorial: gene regulation as a driver of adaptation and speciation, Frontiers in Genetics, 39(11): msac251.
https://doi.org/10.3389/fgene.2021.793933

Val P., Lyons N.J., Gasparini N., Willenbring J.K., and Albert J., 2022, Landscape evolution as a diversification driver in freshwater fishes, Frontiers in Ecology and Evolution, 9: 788328.
https://doi.org/10.3389/fevo.2021.788328

Velotta J.P., McCormick S., Whitehead A., Durso C.S., and Schultz E.T., 2022, Repeated genetic targets of natural selection underlying adaptation of fishes to changing salinity, Integrative and Comparative Biology, 62(2): 357-375.
https://doi.org/10.1093/icb/icac072

Xu G., Yang T., Wang D., Li J., Liu X., Wu X., and Shen H., 2018, A comprehensive comparison of four species of Onchidiidae provides insights on the morphological and molecular adaptations of invertebrates from shallow seas to wetlands, PLoS ONE, 13(4): e0196252.
https://doi.org/10.1371/journal.pone.0196252

Yang G., Tian R., Xu S., and Ren W., 2019, Molecular adaptation mechanism of secondary aquatic life in cetaceans, Scientia Sinica Vitae, 49: 380-391.
https://doi.org/10.1360/N052018-00211

Ye Z., Damgaard J., Yang H., Hebsgaard M., Weir T., and Bu W., 2020, Phylogeny and diversification of the true water bugs (Insecta: Hemiptera: Heteroptera: *Nepomorpha*, Cladistics, 36(1): 72-87.
https://doi.org/10.1111/cla.12383

Yuan Y., Zhang Y.L., Zhang P.J., Liu C., Wang J., Gao H., Hoelzel A., Seim I., Lv M., Lin M., Dong L., Gao H., Yang Z., Caruso F., Lin W., Fonseca R., Wang D., Wang X., Rasmussen M., Liu M., Zheng J., Zhao L., Campos P., Kang H., Iversen M., Song Y., Guo X., Guo J., Qin Y., Pan S., Xu Q., Meng L., A Y., Liu S., Lee S.H., Liu X., Xu X., Yang H., Fan G., Wang K., and Li S., 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., and Mai R.D., 2024 Marine biology under climate change: challenges adaptations and future directions, International Journal of Marine Science, 14(2): 120-129.
https://doi.org/10.5376/ijms.2024.14.0015