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Genetic and Ecological Factors Contributing to the Endangerment of Rare Aquatic Species

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Abstract This study reviews the genetic and ecological drivers of endangered rare aquatic species, as well as corresponding conservation strategies and future directions. Rare aquatic species play an important role in maintaining the health and stability of ecosystems, but their populations have dropped sharply due to habitat destruction, pollution, overfishing and the effects of invasive species. This study analyzes the impact of genetic diversity, population structure and environmental changes on the distribution and survival of rare aquatic species, explores the effectiveness of existing protection strategies and puts forward suggestions for improvement; explores in detail the application of environmental DNA (eDNA) technology in monitoring and protection, as well as the potential of genetic interventions such as gene rescue and assisted gene flow. Meanwhile, case studies show that ecological connectivity and adaptive management are crucial to enhancing the resilience of these species. Through integrated genetic and ecological data, it emphasizes the need for conservation planning to coordinate between biodiversity and ecological balance, provides a systematic perspective for the conservation of aquatic ecosystems, and calls for strengthening international cooperation to address multiple threats to endangered aquatic species.

Keywords: Rare aquatic species; Genetic diversity; Habitat conservation; Environmental DNA (eDNA); International cooperation

1 Introduction

Rare aquatic species, including amphibians, corals, fish and aquatic plants, play a vital role in maintaining the health and stability of aquatic ecosystems. These species often serve as indicators of environmental quality and help support ecosystem resilience and function (Makuch et al., 2023; Yi et al., 2023). The genetic diversity of rare aquatic plant populations like *Luronium natans* is crucial for their survival and adaptation to changing environments. The presence of rare species can enhance ecosystem services such as water purification and nutrient circulation, which are critical to both human and ecological health (Belle et al., 2019).

Despite their ecological importance, many rare aquatic species are facing significant threats, leading to alarming rates of endangerment and extinction. Anthropogenic activities such as habitat destruction, pollution, overfishing and introduction of invasive species have severely affected aquatic biodiversity (McKnight et al., 2017). Climate change further aggravates these threats by changing water temperature, flow states, and habitat availability, making these species increasingly difficult to survive (Grummer et al., 2019). Recent research highlights the critical role of genetic factors in the conservation of these species, highlighting the need for comprehensive genetic data to inform conservation strategies. The spread of this antibiotic-resistant gene in aquatic environment poses a new threat to both aquatic species and human health (Hooban et al., 2020).

This study aims to fully understand and protect rare aquatic species by summarizing the latest research on population genetics, environmental DNA (eDNA) methods and environmental changes, including the analysis of genetic diversity and population structure, the role of eDNA in monitoring and protection, and the impact of environmental factors on the survival and distribution of rare aquatic species. Through these analyses, to protect and preserve the biodiversity of aquatic ecosystems.

2 Genetic Factors Contributing to Endangerment

2.1 Loss of genetic diversity and its implications

Loss of genetic diversity is one of the key factors that lead to the endangerment of rare aquatic species. Genetic diversity provides populations with the adaptation basis needed to respond to environmental changes, disease threats, and long-term survival. However, in the case of small populations or broken geographical distribution, the impact of genetic drift will appear rapidly, leading to a decrease in genetic diversity, further limiting the adaptability and ecological elasticity of the population. For example, Macquaria australasica has been reduced to the minimum threshold required for difficult maintenance of genetic diversity and adaptation to evolution due to severe habitat fragmentation.

Similarly, the critically endangered Gavialis gangeticus also exhibits a worrying genetic condition. The latest study conducted a genetic diversity analysis of mitochondrial DNA in 103 individuals in 14 breeding sites in India, and found that there were only 5 haplotypes in this species, with the overall haplotype diversity (hd) being only 0.462 ± 0.048, and the nucleotide diversity (Pi) being as low as 0.00029 ± 0.00004, reflecting an extremely low level of genetic variation (Sharma et al., 2020). This highly homogeneous genetic structure, especially the singularity observed for the first time on the ultra-variable control zone of 520 bp, suggests that the population has experienced significant genetic bottlenecks, which may be related to the sharp decline in historical populations and human assisted introduction. The current lack of obvious genetic structure also suggests that this group may be expanded from a few founding individuals. This study reveals the genetic status of wild Ganges crocodile populations for the first time based on mitochondrial DNA. The results highlight the vulnerability faced by the species in the natural environment, and emphasizes the urgent need to conduct systematic genetic assessments of other Ganges crocodile populations, thereby formulating targeted protection strategies to enhance genetic connectivity between different populations and laying the foundation for the long-term survival of Ganges crocodile.

2.2 Inbreeding depression in small populations

Inbreeding depression is another important genetic factor affecting small populations. Incombination increases homozygousness of individuals and increases the frequency of recessive harmful alleles, resulting in decreased adaptability, worsening individual health and ultimately increasing the risk of population extinction (Coleman et al., 2018). Studies have shown that the Australian sea lion (*Neophoca cinerea*) has experienced a significant historic genetic bottleneck event, resulting in its current small effective population size, thereby aggravating the potential risk of inbreeding and weakening its evolutionary adaptation potential (Bilgmann et al., 2021). Based on the analysis of genome-wide neutral SNP data from 2238 loci on 72 individuals on the coast of South Australia (SA) and Western Australia (WA) and found that both populations had traces of genetic bottlenecks. Estimated by linkage imbalance method, the current effective population sizes of the SA and WA populations were 424 (CI = 397-458) and 160 (CI = 146-178), respectively. The model prediction results also show that inbreedings such as disease epidemics will significantly increase the population's inbreeding levels and genetic risks in the future than other threats such as fishery-related deaths.

Inbreeding inhibition was also observed in the marmoratus (*Gadopsis marmoratus*). An investigation found that artificially set water barriers in habitats resulted in population separation, with obvious incomparable phenomena and evidence of recent bottleneck events in isolated populations above the obstacles, further revealing the negative effects of isolation and population shrinkage on the genetic health of freshwater fish (Liddell et al., 2021). These cases show that for endangered species, maintaining appropriate effective population sizes, reducing isolation and promoting genetic communication are key measures to avoid inbreeding depression and maintain genetic diversity and adaptability.

2.3 Genetic drift and population bottlenecks

Genetic drift and population bottlenecks play a crucial role in the endangerment of rare aquatic species. Genetic drift leads to random changes in allelic frequency, which may lead to the loss of genetic variation, especially in small populations (Sharma et al., 2020). Population bottleneck, i.e., a significant reduction in population size, exacerbates the impact of genetic drift and further reduces genetic diversity. *Pristis pectinata* has experienced severe population collapse, but it still maintains a high degree of genetic diversity, which may be due to the drift of life history traits that mitigate genetic effects (Chapman et al., 2011). In contrast, the Australian sea lions have low effective population sizes, insufficient genetic variation, and inability to maintain long-term viability, highlighting the impact bottleneck of genetic effects (Bilgmann et al., 2021).

3 Ecological Factors Contributing to Endangerment

3.1 Habitat loss and degradation (e.g., pollution, urbanization)

Habitat loss and degradation remain one of the main factors threatening aquatic biodiversity, with its root causes often lie in anthropogenic interference such as pollution, urbanization expansion and agricultural activities. Although the freshwater ecosystem covers only less than 0.01% of the earth's surface area, it carries disproportionate biodiversity and is therefore extremely sensitive to external disturbances. As land use changes continue to intensify, freshwater habitats face increasingly serious fragmentation problems. This not only destroys important migration channels, but also interferes with the natural hydrological processes of water bodies, negatively affecting fish populations and other organisms that depend on water (Corrales et al., 2019).

In this context, invasive Alien Species (IAS) have become another key driver of aquatic ecosystem changes. In recent years, with the rapid development of modeling methods, scientists have continuously tried to evaluate the distribution, ecological impact and management strategies of invasive species. A systematic review study shows that the current modeling methods used in aquatic ecosystems are mostly based on multi-species or ecosystem models, especially dynamic and non-spatial models (Reid et al., 2018). Most models also comprehensively consider other stressors when analyzing the impact of IAS, such as fishing, climate change and nutrient input. At the species and population level, studies have generally found that IAS has negative effects, mainly manifested in increased predation pressure, increased competition and interference to ecosystem function. At the multi-species or ecosystem level, the model shows the coexistence of positive and negative effects. The study also points out that the current modeling framework still has limited capabilities in predicting future impacts of IAS, especially in evaluating the pathways for introduction, establishment and diffusion of IAS. To achieve more comprehensive management and early warning, it is necessary to further develop a converged space-time modeling approach and incorporate emerging technologies to improve predictive capabilities of IAS's future nutritional behavior and spatial distribution (Reid et al., 2018).

3.2 Climate change and its effects on aquatic ecosystems

Climate change is having a profound impact on aquatic ecosystems through various mechanisms, especially the rise in water temperatures, changes in hydrological conditions and the increase in the frequency of extreme weather events, which together threaten the living environment of aquatic organisms. These changes may not only lead to habitat loss, but also trigger displacement of species distribution ranges and make aquatic species more susceptible to composite effects from other stressors such as pollution, overfishing, and habitat fragmentation. According to multiple studies, if the current warming trend continues to develop, some aquatic species, especially some fish, are most likely to face extinction risk due to multiple stresses (Telat and Irfan, 2018).

Migratory fish are more susceptible to climate change due to their high sensitivity to changes in the hydrologic environment. For example, heating may interfere with its original seasonal migration behavior, change the timing and location of breeding, and the habitat damage and barrier construction caused by human activities will further limit its survival and reproduction space (Tamario et al., 2019). Human factors such as global transportation, trade and alien invasion are also aggravating the instability of ecosystems, further affecting the diversity and ecological function of local species (Telat and Irfan, 2018).

3.3 Overexploitation and unsustainable fishing practices

Overfishing and illegal fishing methods (such as electric fishing and explosive fishing) have become important reasons for the endangerment of aquatic species around the world, especially posing a serious threat to migratory fish, which not only reduces population size, but also destroys the stability of the ecosystem (Yi et al., 2023). Traditional survey methods are difficult to fully grasp the population dynamics of aquatic organisms, so the role of molecular marking technology in the protection of aquatic organisms is becoming increasingly prominent. In recent years, with the development of sequencing technology, molecular tools such as SNP, SSR and mitochondrial genes have been widely used to evaluate the genetic diversity and population structure of aquatic species (Chapman et al., 2011; Yi et al., 2019). Huo et al.'s study on fine-scale plateau loach revealed significant genetic differentiation among its populations and proposed specific protection strategies for the study of tooth bass. In addition, research on species such as coral and rainbow trout has also strengthened the understanding of their evolutionary and conservation needs. These research results provide a solid foundation for the formulation of scientific aquatic biological conservation and fishery management policies.

3.4 Invasive species and their impact on native populations

Invasive species are the main driver of biodiversity loss in aquatic ecosystems. These species often outperform native species in resources, alter habitat structures, and introduce new diseases. For example, invading large plants can significantly reduce fish populations by changing habitats and increasing eutrophication. In the Guadiana River Basin, the abundance of invasive species was found to be the best predictor of the decline in native fish populations, highlighting the serious threat they pose to local communities (Lu, 2024). The introduction of invasive species, coupled with habitat degradation, creates a challenging environment for the conservation of local aquatic species.

4 Interactions Between Genetic and Ecological Factors

4.1 Feedback loops between reduced genetic diversity and ecological resilience

Reduced genetic diversity in small and isolated populations leads to a decrease in adaptive potential and adaptability, which in turn affects ecological resilience. *Macquarie australasica* populations have shown that low genetic diversity and smaller effective population sizes lead to increased inbreeding inhibition and reduced adaptation potential, making these populations more susceptible to environmental changes and habitat fragmentation (Pavlova et al., 2017). Similarly, Rio Grande silver minnow (*Hybognathus amarus*) shows that maintaining high allelic diversity in immune genes is critical to resist parasites and the environment despite its endangered extinction (Osborne et al., 2017). These examples highlight the critical feedback loop, that the reduction in genetic diversity reduces ecological resilience and further exacerbates the vulnerability of species extinction.

4.2 Synergistic effects of habitat fragmentation and genetic isolation

The interaction between habitat fragmentation and genetic isolation often exacerbates the declining process of rare aquatic species. The broken environment weakens gene flow between populations, forming small populations isolated from each other, and thus triggering a decline in genetic diversity. For example, Macquarie bass, under the combined influence of natural and anthropogenic barriers, exhibits significant genetic differentiation, which limits the population’s ability to spread and weakens its genetic basis (Ackiss et al., 2021). Similarly, isolated populations of cutthroat trout (*Oncorhynchus clarkii*) still generally exhibit sustained loss of genetic diversity under different habitat conditions, indicating that the negative effects of isolation are long-term (Carim et al., 2016). Research on the lake-type *Coregonus artedi* population located at the edge of the distribution also revealed similar problems. Although there is a high degree of uncertainty in the response of these populations under environmental stress, the study found that their genetic differentiation levels are high, and that neutral and non-neutral genetic diversity is closely related to lake area, while harmful mutation frequency and inbred coefficient are significantly correlated with latitude (Ackiss et al., 2021). Although the estimated hypoxia-cold water habitat conditions vary between lakes, they do not leave a significant signal in the population's genome.

4.3 Case studies highlighting the interplay of genetic and ecological factors

Several case studies reveal the complex interactions of genetic and ecological factors in the protection of endangered aquatic species. Due to habitat fragmentation and loss, Macquarie perch has a problem of decreasing genetic diversity and shrinking effective population size. It is necessary to intervene through auxiliary gene flow and other measures to alleviate the adaptability and reduce the risk of inbreeding. In the study of Cisco fish (*Coregonus artedi*), individuals with populations at the edge of geographical distribution exhibit a high degree of genetic differentiation, which is closely related to the environmental characteristics of local lakes (Yi et al., 2023). Although these southern lake areas generally live in marginal environments with double oxygen and heat restriction, studies have shown that neutral and non-neutral genetic diversity is more related to lake area than directly driven by latitude or oxygen and heat conditions in water. In individual lakes, haplotype diversity in major histocompatibility complex (MHC) regions provides clues to explore the adaptation mechanisms of individuals to stress and immune responses, further supporting the role of genetic factors in ecological adaptability (Table 1) (Ackiss et al., 2021). Although increased frequencies of harmful mutations and increased inbred coefficients were observed in some populations, such genomic data did not form a consistent pattern of ecological genetic responses across all lakes. These findings once again emphasize that when formulating protection strategies, differences in genetic characteristics in the environment cannot be ignored. Instead, more accurate and adaptable protection measures should be formulated by integrating ecological and genetic data to improve the resistance of endangered aquatic species to future environmental changes.

Table 1 Analysis of molecular variance (AMOVA) with Rapture loci in 29 inland lake cisco populations (Adopted from Ackiss et al., 2021)

Source of variation	% variance	*F* statistic	*p*-Values
Within individuals	0.4860	F_{IT}	-
Among individuals in lakes	0.1223	F_{IS}	<0.001
Among lakes in lineages	0.2557	F_{SC}	<0.001
Among lineages	0.1358	F_{CT}	<0.001

5 Conservation Genetics and Its Role in Mitigating Endangerment

5.1 Use of molecular markers in monitoring genetic diversity

Molecular markers are of great value in conservation genetic research and can help researchers analyze the genetic structure and diversity of endangered species. Among many molecular tools, single nucleotide polymorphism (SNP) has been widely used in genetic research of aquatic animal populations due to its advantages such as high throughput, strong stability and suitable for large sample analysis (Yi et al., 2023; Wenne, 2023). Through SNP technology, researchers can not only identify species and their hybrids in the natural environment, but also evaluate the potential impact of proliferation and release and farming escape on wild populations, thus providing a basis for the protection and management of aquatic biological resources. SNP markers have also been used to explore genomic regions associated with phenotypic variation, revealing the mechanisms of species adaptation to environmental changes (Wenne, 2023). In some experimental studies, the phenomenon of simulated selective fishing leading to hereditary changes in the life cycle of fish has also been confirmed, further suggesting that natural populations may have an evolutionary response to human activities. These research results not only expand people's understanding of the genetic diversity of aquatic species, but also provide important reference for the formulation of scientific conservation strategies (Amoutchi et al., 2023).

5.2 Genetic rescue: techniques and challenges

Gene rescue, as a means of recovery of genetic diversity, has shown potential in a variety of endangered species by introducing new genetic material into target populations to alleviate the adverse effects of inbreeding and enhance their adaptability. Research on Macquarie perch shows that despite the small scale of translocation, regular genetic introduction can still effectively improve the genetic health status of the population, alleviate inbreeding depression and improve viability (Pavlova et al., 2017). Gene rescue still faces many obstacles in practice, including the lack of systematic assessment of the impact of inbreeding and the lack of data on health monitoring. Similar issues are also particularly prominent in captivity breeding plans. The only remaining wild population of the European sturgeon (*Acipenser sturio*) is located in the estuary of the Gironde River in France. The long-term population decline has made it extremely lack of genetic diversity. To avoid further aggravation of genetic erosion during release, the species' recovery plan emphasizes the importance of maintaining genetic diversity and controlling inbred risks. Studies have shown that despite the obvious genetic bottlenecks in the original population, most of the original genetic diversity is preserved in recaptured individuals through carefully managed multi-year release measures (Roques et al., 2018). The study found that the kinship between parents does not significantly affect the probability of offspring being re-enacted, but kinship should still be paid attention to inbred management to avoid inbred accumulation. These findings emphasize that successful population recovery depends not only on quantitative supplementation, but also on long-term planning and dynamic management strategies based on genetic data.

5.3 Assisted gene flow and its applications in aquatic conservation

Assisted gene flow is a protective strategy that enhances genetic connections between populations by intentionally migrating individuals or gametes, especially for species genetically isolated due to habitat fragmentation or climate change. This method helps enhance the adaptability and viability of endangered populations. Introducing auxiliary gene flow in the management of Macquarie bass can simulate its historical gene communication pattern, thereby improving its population maintenance capabilities (Zhou and Mai, 2024). Similarly, in the study of African snakehead fish, genetic monitoring showed that in order to avoid the mixing of population genes in different adaptation contexts, it is necessary to identify local adaptive genetic variants before gene transfer to protect their unique adaptive characteristics. Flanagan et al. (2017) further pointed out that before implementing strategies such as auxiliary gene flow, rigorous research and planning must be carried out through genomic tools in order to maximize the protection role and avoid potential risks. They proposed an adaptive management framework to help conservation biologists determine under what circumstances genomic tools are most effective, how to design local adaptive assessment and monitoring programs, and clarify the pathways to the application of results in actual conservation actions. This framework not only applies to assisted gene flow, but also helps identify protection units and decide whether other methods (such as public park experiments) should be used to replace expensive genomic studies, thereby improving resource use efficiency.

6 Ecological Restoration Strategies for Rare Aquatic Species

6.1 Habitat restoration and management practices

Habitat restoration and management strategies play a central role in the protection of rare aquatic species, and to achieve long-term and effective recovery, it is crucial to understand the genetic structure and population dynamics among populations. Taking the Mediterranean red coral (*Corallium rubrum*) as an example, Gazulla et al. (2021) revealed that genetic diversity and structure can remain relatively stable even after experiencing significant population declines in protected areas. This "demo-genetic" approach can identify key population connection units and diffusion mechanisms during recovery, providing data support for conservation planning. The study also found that there are obvious spatial genetic structural differences between individuals at different developmental stages, suggesting the important role of local larval diffusion restriction and early mortality on genetic structural formation. By identifying key populations with significant connectivity, refined recommendations are provided for the management of the Réserve Naturelle de Scandola Marine Reserve. As Mijangos et al. (2015) highlighted, integrating genetic data into habitat recovery strategies helps to select recovery areas with good connectivity and ecological potential, thereby increasing the survival rate of transplanted populations and the possibility of long-term population maintenance.

6.2 Establishing and managing marine protected areas (MPAs)

Marine protected areas (MPAs) are core tools for maintaining marine biodiversity and supporting the recovery of endangered species populations. Their effectiveness depends on the protection of ecological function restoration and genetic connectivity. On the coast of Scotland, the *Modiolus modiolus* coral reef, as a key marine habitat with high biodiversity, is incorporated into multiple MPAs for conservation. Genetic studies have shown that medium to high levels of genetic connectivity are prevalent among populations within and outside the protected areas, and that allelic richness remains at a high level between reefs (Mackenzie et al., 2022). Although most populations do not show significant spatial genetic structures, some reefs still show potential genetic isolation, suggesting that different regional populations should not be considered completely independent units in management. This finding emphasizes that even populations within non-designated protected areas may play a key role in the overall genetic network. Therefore, protection measures within the MPA should be coordinated with the management of surrounding unprotected areas, thereby supporting population stability and adaptability on a larger spatial scale. Cheng et al. (2019) pointed out that MPA also plays an important role in restoring ecosystem functions such as predation, which is indispensable for maintaining overall ecological balance. Further, Laikre et al. (2016) stressed that by strengthening connectivity between MPAs and strictly enforcing protection norms, its effectiveness in improving genetic diversity and enhancing ecological resilience can be maximized.

6.3 Enhancing ecosystem connectivity for species migration

Improving spatial connectivity in ecosystems is considered one of the key measures to enhance the genetic diversity and resilience of rare aquatic species. Especially for species that exhibit low diffusion ability and slow growth in life history characteristics, their population maintenance in marine protected areas (MPAs) is crucial for the long-term survival of the species. Cossu et al. (2017) found that although their populations are sparse, they still maintain high genetic diversity and effective population size in two MPAs in northern Sardinia, through microsatellite genetic analysis of the endemic endemic species, the giant Mediterranean cape (*Patella ferruginea*). This discovery challenges the previous view that there are only two endangered residual populations in the species. The study further revealed that although the population size is still sustainable, there are differences in the spatial genetic structure of the populations in the two protected areas, which may be limited by the combined effects of the life history characteristics of the species, local topography and marine current fields. Marshall et al. (2019) pointed out that ensuring ecological connectivity between protected areas can promote larval diffusion and population replenishment, thereby enhancing the stability and adaptability of the overall population. The study emphasized that in marine conservation practice, we should not only focus on the establishment of protected areas themselves, but also comprehensively consider the biological characteristics of the species and its microhabitat structure to improve conservation effectiveness.

6.4 Climate adaptation strategies for aquatic ecosystems

Faced with the challenges brought by climate change, formulating a scientific climate adaptation strategy is particularly important for maintaining the stability and biodiversity of aquatic ecosystems. Marine protected areas (MPAs) play a central role in enhancing ecosystem resilience to climate disturbances by maintaining critical habitats and promoting genetic diversity (Sala and Giakoumi, 2018). However, successful adaptive management also needs to be based on an in-depth understanding of the genetic landscape of natural populations, and then guide specific measures such as species restoration and habitat reconstruction. Research shows that selecting individuals with higher genetic diversity to participate in recovery programs can help improve population adaptability and long-term survival (Yi et al., 2023).

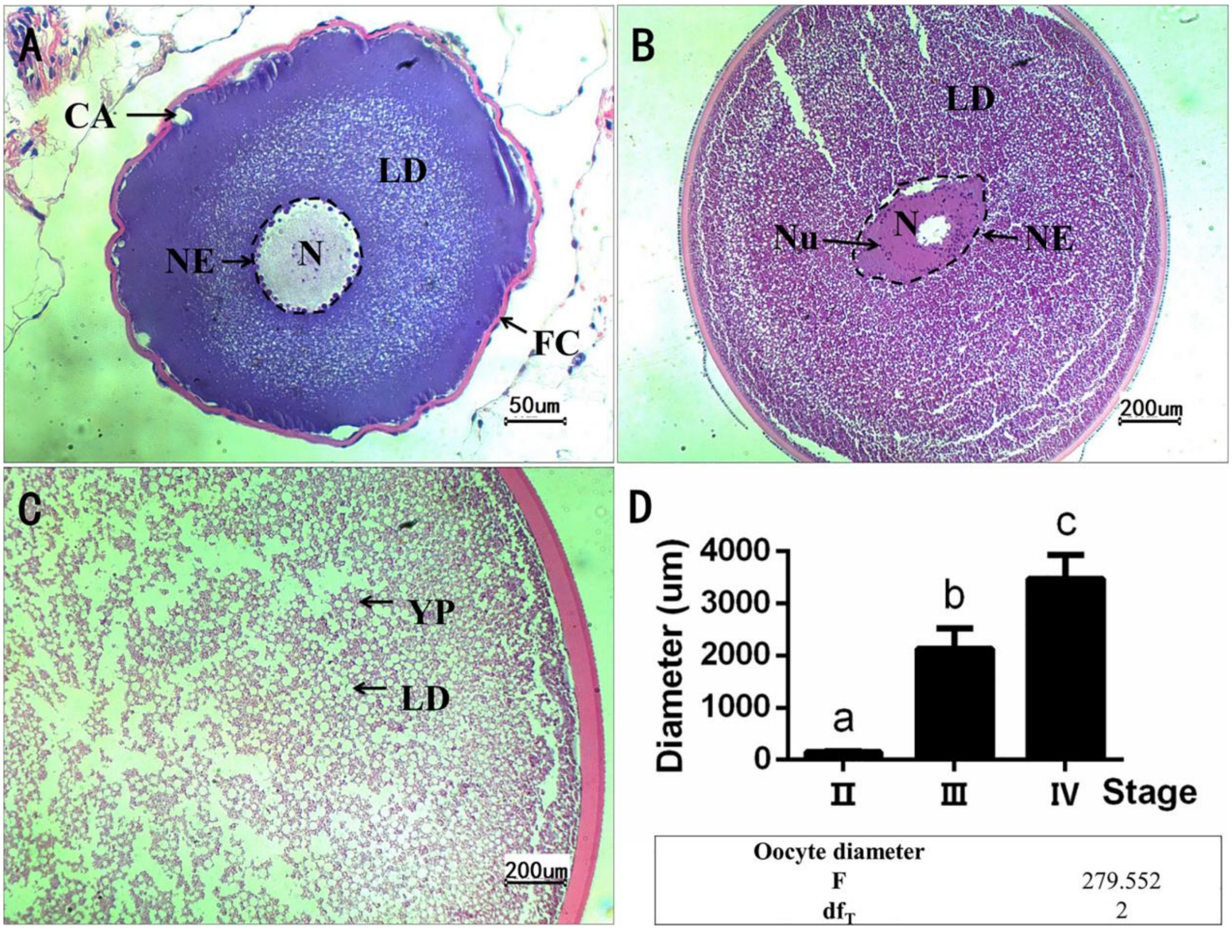
In recent years, with the rapid development of sequencing technology, population genetic research based on molecular markers has become a powerful tool for formulating climate adaptation strategies. Among several key aquatic species, microsatellite markers, mitochondrial DNA, and single nucleotide polymorphisms (SNPs) have been widely used to reveal their genetic structure, population history and geographical pattern (Chapman et al., 2011; Yi et al., 2019). Researchers used GBS technology to analyze *Triplophysa tenuis*, a endemic fish in the Tarim River Basin in Xinjiang, and found that it has a high genetic differentiation among multiple populations, which provides a reference for the division of regional protection priorities (Ferreira et al., 2021).

7 Case Studies of Rare Aquatic Species Conservation

7.1 Conservation of the Chinese sturgeon (*Acipenser sinensis*)

As a critically endangered species endemic to China, the Chinese sturgeon (*Acipenser sinensis*) has significantly reduced its natural reproductive ability due to human activities and water conservancy projects. Although the population still maintains a high genetic diversity and provides certain recovery potential for its long-term survival (Shen et al., 2020), projects such as the Three Gorges Dam have changed the water temperature and flow rate in the middle and lower reaches of the Yangtze River, causing serious interference to the Chinese sturgeon spawning habitat, and especially affecting the structural characteristics of oocytes in key development stages, such as yolk accumulation (YP), lipid droplet distribution (LD) and follicle cell (FC) integrity (Wang et al., 2017). Unstable water temperature often leads to insufficient yolk formation and abnormal lipid droplets, which has become one of the main factors affecting the success rate of artificial reproduction (Zhu et al., 2020).

To cope with this challenge, research has begun to focus on the exploration of energy metabolism mechanisms during the development of ovarians of artificial reproduction. Under artificial feeding conditions, the transition process of the ovaries of Chinese sturgeon female parent fish from stage II to stage IV is a bottleneck for artificial reproduction. Related studies show that with the development of the ovaries, the volume of oocytes increases significantly, while the lipid reserves in the fish muscles decrease significantly, reflecting that individual energy is allocated to ovarian development. The expression levels of genes associated with lipid and amino acid metabolism in the stage II and III ovaries are significantly higher than those in stage IV, suggesting that this stage is the peak period of energy demand. The differential metabolites levels in various metabolic pathways such as arginine, cystine, methionine, and purine in phase III serum peaked, while the IV stage showed an increase in alanine, histidine, taurine and lipid oxides, revealing their potential key role in late ovarian development (Figure 1) (Zhu et al., 2020). Therefore, revealing the energy regulation mechanism of ovarian development from molecular and metabolic levels is of great significance to improving the success rate of artificial reproduction in Chinese sturgeons. At the same time, strengthening water environment management to stabilize water temperature and flow rate and providing a support for the normal development of oocytes is still an indispensable part of restoring the natural reproductive potential of the species. Combining genetic, ecological and physiological multidimensional information will help optimize existing conservation and fishery enhancement strategies (Jiang et al., 2020).



Oocyte diameter	
F	279.552
df_T	2

Figure 1 Representative micrograph of HE stained ovarian slices (Adopted from Zhu et al., 2020)

7.2 Efforts to protect the vaquita (*Phocoena sinus*)

Phocoena sinus is one of the most endangered marine mammals in the world, with less than 30 in the wild. The conservation of this species is mainly focused on reducing bycatch deaths caused by illegal gillnet fisheries, which is the main reason for the rapid decline in its population. To alleviate this problem, a variety of management measures, including a comprehensive gillnet ban and the promotion of alternative fishing gear, have been adopted, while emphasizing enhanced enforcement of regulations and international cooperation to protect its main habitat, the Gulf of California (Yao et al., 2021). As a national first-class protected aquatic animals in China, the Chinese sturgeon (*Acipenser sinensis*) also faces problems such as habitat destruction and restricted reproduction. Under artificially controlled reproductive conditions, its ovarian development was found to be responsive to lipid levels in the feed. Yao et al. (2021) studied six key genes related to yolk product deposition and hydrolysis (vtgr, atp6v1c1, atp6v1h, ctsb, ctsd, ctsl), and analyzed their tissue-specific expression, transcription patterns at different ovarian development stages, and their response to lipid levels. The results showed that vtgr was the highest in ovarian stage II, ctsl reached its peak in stage IV, and the remaining four genes were the strongest in stage III. Studies have shown that high-fat feed can promote ovarian development and upregulate the expression of multiple key genes, providing new insights into the molecular regulatory mechanisms of Chinese sturgeon deposition and hydrolysis, and also has reference value for subsequent artificial reproduction and population recovery (Yao et al., 2021).

7.3 Lessons from the recovery of the green sea turtle (*Chelonia mydas*)

Thanks to the continuous advancement of multi-faceted conservation efforts, Green Sea Turtle (*Chelonia mydas*) has shown a significant trend in population recovery in recent years. The core of the protection strategy lies in strict protection of nesting beaches and the effective reduction of accidental fishing incidents through fishery regulatory measures. International agreements established by transnational cooperation have strengthened the protection of its migration channels and further reduced the damage to its life cycle by artificial interference. At the same time, habitat restoration projects and the demarcation of marine reserves also provide a safer and more stable living environment for green sea turtles. Public education and community participation also play an important role, not only strengthening the protection awareness of local residents, but also encouraging more people to participate in sustainable use and conservation practices. The effectiveness of this series of comprehensive measures shows that organic combination of habitat protection, policy supervision and social participation is an effective path to promote the recovery of endangered species.

8 Challenges in Conservation Efforts

8.1 Limited resources and funding for rare species conservation

In the context of scarce resources and limited funds, how to efficiently allocate investments to support aquatic biodiversity conservation is one of the core challenges facing conservation biology at present. Especially in freshwater ecosystems, the world's most threatened ecosystem, rare local fish are becoming increasingly vulnerable due to habitat fragmentation, climate change and hydrological disturbances. Roy et al. (2021) pointed out that using tools such as Species Distribution Modelling (SDM) to evaluate habitat suitability and predict spatial distribution of rare fish is an important means to optimize protection decisions and improve the efficiency of fund use. *Amblypharyngodon mola* is a native freshwater fish with important ecological and economic value in tropical wetland ecosystems in India and Bangladesh, but the lack of systematic research on key ecological indicators has limited the development of conservation measures for the species. Recent modeling studies have shown that the main environmental factors affecting the distribution of *A. mola* include annual runoff precipitation, soil pH and topographic altitude, clearly pointing out the role of hydrological climate, soil and landform conditions in their habitat selection (Roy et al., 2021). Although similar studies provide scientific basis for precise protection in areas with limited resources, as emphasized by Belle et al. (2019), habitat modeling and integrated monitoring of genetic tools including environmental DNA (eDNA) also rely on large amounts of capital investment. Therefore, future conservation strategies should not only focus on species ecological needs, but also weigh the efficiency of resource allocation and technical feasibility to maximize the protection of freshwater biodiversity under realistic constraints.

8.2 Integrating genetic and ecological research for conservation planning

In the protection of aquatic mammals, the integration of genetics and ecological data is becoming increasingly critical. Genetic research provides us with important information on population structure, gene flow and genetic diversity, which helps to evaluate species' adaptability and resilience in the face of environmental changes and human interference. In recent years, with the development of molecular marker and high-throughput sequencing technologies, these tools have become increasingly widely used in actual protection. For example, genetic research has provided scientific basis for conservation strategies for multiple aquatic mammals by defining the management units and clarifying classification disputes (Loizaga et al., 2023). Loizaga et al. reviewed the relevant research on more than 40 aquatic mammals conducted in Latin America between 2011 and 2022, and found that most of the work focused on population structure, systematic geography, gene flow and diffusion patterns, while genetic applications in law enforcement and evidence collection and illegal trade control are still relatively weak. Against the backdrop of increasing climate change and human pressures, the potential of next-generation sequencing technologies in predicting changes in genetic diversity has not been fully utilized. The study calls for priority to pay attention to species and regions with high endangerment and large research gaps in the future, promote the establishment of regional conservation genetics cooperation networks, and jointly respond to cross-border ecological problems.

8.3 Balancing human activities and biodiversity preservation

Against the backdrop of increasing frequent human activities, how to achieve the protection of aquatic ecosystems while meeting the needs of social development has become a major challenge in the current protection work. Artificial environmental disturbances, such as habitat fragmentation, pollution and over-exploitation, have posed a serious threat to a variety of aquatic species. Especially in marine ecosystems, more than 60% of commercial fish populations fall into recession or collapse due to overfishing, while bycatch problems lead to non-target deaths in 300,000 to 600,000 marine mammals each year (Dyke and Lamb, 2020). Freshwater systems are also facing compound threats such as climate change, water conservancy development and alien invasion, which seriously weakens the living environment and ecological functions of local species (Reid et al., 2018). In this context, it is particularly critical to develop scientific and effective protection strategies. Measures such as the establishment of marine fishing ban areas, limited-time fishing, reduced fishing intensity and improved fishing gear can not only significantly reduce bycatch mortality, but also help maintain the sustainable use of target populations. In freshwater systems, dam removal is a means of ecological restoration that has gradually become popular in recent years, helping to restore the natural hydrological processes of rivers and enhance ecological connectivity. Therefore, the protection of aquatic biodiversity requires not only a scientific basis of multidisciplinary collaboration, but also a dynamic and flexible balance mechanism between ecological protection and human activities.

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Conflict of Interest Disclosure

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Reference

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