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Advances and Challenges in Wild Fish Species Identification in Hainan Island and the South China Sea

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Abstract This study explores the progress and challenges of species identification of wild fish in Hainan Island and the South China Sea region. Hainan Island and the South China Sea region are rich in Marine and freshwater habitats with a wide variety of fish species. Traditional morphological methods have limitations when distinguishing different fish species. By using technologies such as DNA barcoding, environmental DNA (eDNA), and high-throughput sequencing, the accuracy and efficiency of fish species identification will be enhanced, making it easier to discover hidden new species, monitor new species, and invasive fish communities. New technologies such as vision artificial intelligence image recognition, multi-modal data fusion, and regional fish database construction have developed a more intelligent and standardized species identification system. The combination of technological research and practice has made Hainan Island and the South China Sea region a popular area for the development and application of fish species identification technology.

Keywords Hainan Island and the South China Sea; Fish species identification; DNA barcoding and environmental DNA (eDNA); Image recognition and multi-modal technologies; Biodiversity conservation

1 Introduction

Hainan Island and the South China Sea are the core areas of wild fish diversity in China. A total of 363 species of fish were discovered in the coastal waters of Hainan Island, belonging to 226 genera, 114 families and 24 orders. The finnadiformes were the most common (Xiong et al., 2018; Luo et al., 2023). A total of 188 species of fish were detected in the sea area near Wuzhizhou Island by using environmental DNA technology. There are 41 species around Xidao (Xi et al., 2022; Wang et al., 2024). The freshwater system on the island is equally impressive. A total of 154 species of freshwater fish were recorded in Hainan, among which 31 species were endemic to the local area and held a special position in the national fish diversity (Xiong et al., 2018).

Accurate identification of wild fish, as well as effective resource protection and fishery management, are fundamental tasks. Reliable identification technology can help identify changes in fish diversity and formulate effective countermeasures. DNA barcoding and environmental DNA (eDNA) techniques can distinguish fish with similar appearances and many previously unrecorded species can be discovered (Zhang et al., 2023; Wang et al., 2024). These technologies provide comprehensive and non-invasive monitoring methods to avoid the decline in the number of rare or endemic fish species due to overfishing or habitat destruction, and can achieve sustainable fishery development (Xiong et al., 2018; Zhang et al., 2023)

This study will explore the new progress in the identification of wild fish in Hainan Island and the South China Sea region. Traditional methods and molecular techniques. Through means such as organizational DNA barcoding, environmental DNA testing and ecological investigation, the significance of precise identification in biodiversity assessment, ecological change monitoring and management protection is expounded. This study will also analyze how to solve problems such as incomplete species records and environmental pressure, as well as the challenges encountered, providing a foundation for future research and decision-making.

2 Deficiencies of Traditional Morphological Methods

2.1 It is difficult to accurately distinguish between similar species

In Hainan Island and the South China Sea region, people usually distinguish different fish by observing their shapes, colors and fin features. But when the fish look very similar, this method is prone to mistakes. For instance, although scientists have conducted extensive research on local fish, the known species of fish are still far fewer than the actual existing ones (Zhang et al., 2023). Especially for fish of the same genus or family, the differences in appearance are very small and it is easy to mistake them, which will affect the accuracy of biodiversity research.

The differences in the composition of fish species in different sea areas also reflect the flaws of morphological methods. For instance, five shared species were discovered in the northern and southern waters of Hainan Island, suggesting that subtle differences in appearance might have been overlooked, resulting in incomplete species records (Zhang et al., 2023). This problem is more prominent in sea areas with a wide variety of fish species and rapid changes, which also indicates that traditional methods are difficult to accurately reflect the diversity of fish species.

2.2 Expert participation is required and standards are difficult to unify

The morphological identification of fish mainly relies on the experience of experts. This method is difficult to formulate unified standards and is not suitable for large-scale investigations, especially in areas lacking professionals. For instance, recording 363 species of fish in the coastal waters of Hainan Island requires experts to identify them for a long time (Luo et al., 2023), and the efficiency is very low. Furthermore, the judgments of different experts may vary, thereby affecting the comparability of the research results.

In long-term monitoring and biodiversity assessment, the lack of unified standards is one of the main problems. The fish communities in Hainan Island and the South China Sea change with the seasons and environment, and a unified approach must be adopted to accurately track the changes (Luo et al., 2023). If the identification standards are not unified, effective comparisons cannot be made and effective protection and management measures cannot be formulated.

2.3 Juvenile fish and hidden species are difficult to identify

The physical characteristics of juvenile fish have not yet fully developed, making it difficult to accurately identify them using traditional methods. This will lead to incomplete statistics of species numbers and make it impossible for people to understand the growth patterns of fish schools. For example, investigations in the coastal waters and estuaries of Hainan Island may miss or wrongly discover juvenile fish, thereby affecting the study of the living habits of important species (Luo et al., 2023; Luo et al., 2024).

Covert species refer to fish that look similar but have different genes, and traditional methods cannot distinguish them. The existence of such species implies that the actual biodiversity may be underestimated (Zhang et al., 2023; Wu, 2024). Therefore, many current studies suggest combining genetic testing and morphological observation to improve the accuracy of fish identification.

3 Application of Molecular Technology in Fish Species Identification

3.1 DNA barcoding technology: fast and accurate species identification

DNA barcoding technology (such as COI gene sequencing) has greatly enhanced the identification efficiency and accuracy of fish in Hainan and the South China Sea. Compared with traditional methods, it can easily distinguish fish with similar appearances or at different growth stages (Hubert et al., 2008; Naz et al., 2023) This technology can accurately identify small fish and economic fish species by comparing genetic differences among species (Hubert et al., 2008).

After establishing the DNA barcode database, identification becomes more reliable, and new species or covert species can also be discovered (Kyle et al., 2007; Naz et al., 2023). Furthermore, this technology is applicable to the identification of processed fish products and juvenile fish, making up for the deficiencies in morphology and contributing to fishery management and ecological protection (Naz et al., 2023; Seetapan et al., 2024).

3.2 Environmental DNA (eDNA) technology: efficient and non-destructive monitoring

The combination of environmental DNA (eDNA) and high-throughput sequencing changes the non-invasive monitoring method of wild fish communities, making fish monitoring more convenient. By analyzing the DNA extracted from water samples, various fish species can be detected without the need for fishing or direct observation (Naz et al., 2023; Ferreira et al., 2024) Environmental DNA technology is applicable to biodiversity surveys in complex sea areas such as Hainan Island and the South China Sea.

The use of multi-gene markers (such as COI, 12S rRNA, etc.) can further increase the detection rate and reduce misjudgment (Naz et al., 2023; Ferreira et al., 2024) Integrating eDNA technology into routine monitoring can conduct a more comprehensive assessment of fish resources and provide a scientific basis for conservation policies (Ferreira et al., 2024).

3.3 Genomic and transcriptomic analysis

Genomic and transcriptome techniques can precisely identify molecular differences among closely related species. For example, SNP markers can be used to study fish genetic diversity, population structure and adaptability (Figure 1) (Wenne, 2023). These methods can distinguish covert species from hybrid individuals and make up for the deficiencies of traditional techniques (Hubert et al., 2008; Wenne, 2023).

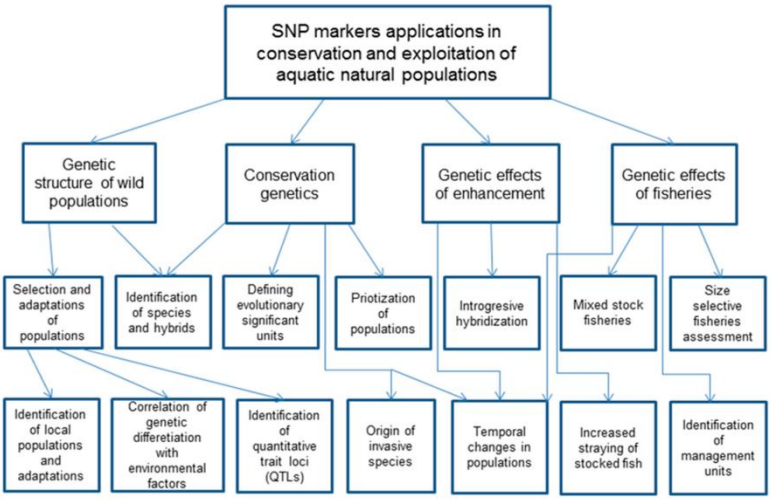

Figure 1 An integrated concept map showing the main fields and directions of SNP applications related to aquatic exploited animal populations (Adopted from Wenne, 2023)

Because genomic and transcriptome analysis, evolutionary relationships among species, as well as environmental changes or human activities (such as restocking and selective fishing) can have genetic impacts (Wenne, 2023). By analyzing microscopic genetic changes and formulating more scientifically based conservation measures, support is provided for the scientific conservation of fish resources in Hainan Island and the South China Sea (Wenne, 2023; Li, 2024).

4 Application of Intelligent and Integrated Technologies in Fish Identification

4.1 AI image recognition technology

Artificial intelligence technology is playing a role in fish monitoring in Hainan Island and the South China Sea. Through deep learning algorithms, computers can automatically identify the types of fish in underwater videos and photos and conduct quantitative statistics (Rauf et al., 2019; Banan et al., 2020; Yang et al., 2020; Malik et al., 2023). This non-contact monitoring method greatly improves work efficiency and is particularly suitable for large-scale ecological surveys.

4.2 Multi-technology fusion recognition

Combining multiple recognition methods can obtain more reliable results. For instance, combining spectral analysis techniques with machine learning can distinguish similar fish species more accurately than a single

method (Ren et al., 2022; Sueker et al., 2023). This comprehensive scheme can not only avoid the subjectivity of traditional morphology, but also reduce the cost of molecular detection. By integrating different data such as images and genes, the system can make up for each other's deficiencies. This multi-technology integration approach is particularly suitable for monitoring the diverse fish communities in the South China Sea region (Ren et al., 2022; Sueker et al., 2023; Xie et al., 2024).

4.3 Standardized database construction

Establishing a unified fish database is very important for both research and management. These databases collect characteristic data of various types of fish, providing references for scientific research and management (Rauf et al., 2019; Yang et al., 2020; Xie et al., 2024). The existing public databases not only support AI training but also facilitate the comparison of different research results (Figure 2) (Rauf et al., 2019; Xie et al., 2024).

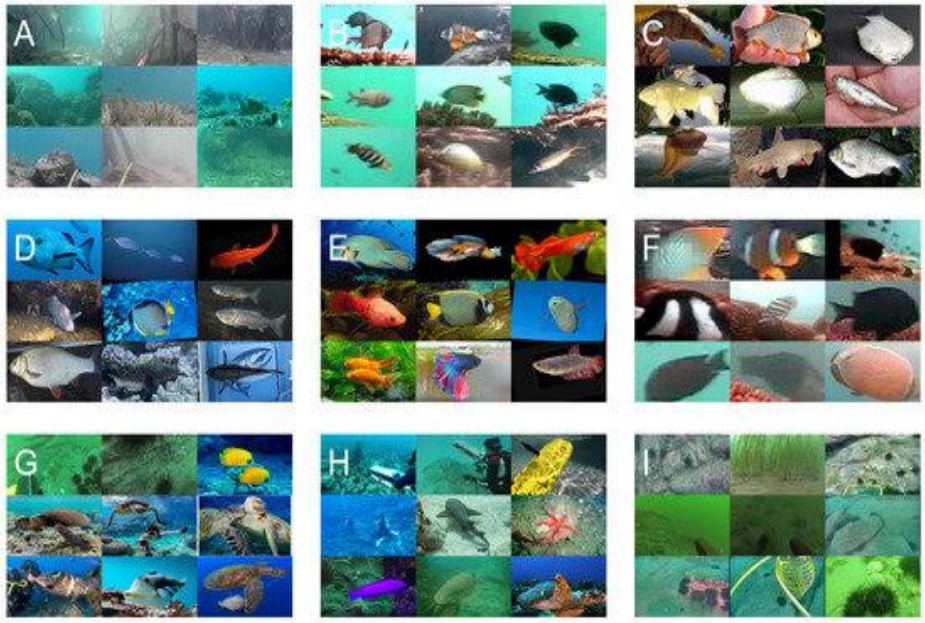

Figure 2 Data set related images (A-I) (Adopted from Xie et al., 2024)

Standardized databases can visually display the distribution of fish, which is helpful for formulating measures for the protection of fish populations and resource management. With the continuous enrichment of data, the accuracy and operability of wild fish species identification in Hainan Island and the South China Sea region can be enhanced (Rauf et al., 2019; Xie et al., 2024).

5 The Main Difficulties Faced by Fish Species Identification in Hainan and the South China Sea

5.1 Genetic data of endemic fish species are lacking

The Hainan Island and the South China Sea region have high biodiversity and rich fish resources. The barcode and molecular data of some endemic wild fish species are seriously insufficient, and the genetic information is still incomplete. DNA barcoding technology has been applied to Marine fish in this area, but the number of species with obtained barcode sequences is still much lower than the actual number of existing species (Xiong et al., 2018; Xu et al., 2021; Zhang et al., 2023). This situation is particularly prominent among deep-sea fish and freshwater fish, making it difficult to accurately identify some endemic and rare fish species, which hinders the accurate identification of species and the assessment of biodiversity.

The insufficiency of genetic data not only affects species identification but also hinders the discovery of new species. This leaves a gap in our understanding of the local fish diversity, and some endangered species in need of protection may thus be overlooked (Xiong et al., 2018; Xu et al., 2021; Zhang et al., 2023). To solve this problem, it is necessary to strengthen the genetic sampling work of endemic fish species.

5.2 The promotion of genetic testing technology is difficult

Although genetic testing technology is very advanced, it faces many obstacles when applied in grassroots units. These technologies require expensive equipment and professional talents, which many local institutions find difficult to afford (Xiong et al., 2018; Xu et al., 2021). Therefore, most conservation projects are still using traditional observation methods, although these methods are not accurate enough.

This technological gap also leads to uneven data quality in different regions, affecting the formulation of unified monitoring standards. To change this situation, it is necessary to reduce technical costs, strengthen personnel training and develop more convenient operation methods (Xiong et al., 2018; Xu et al., 2021).

5.3 The research data are scattered and difficult to integrate

At present, research data on local fish are scattered among various institutions and lack unified management. This situation has led to a lot of repetitive studies and also resulted in differences in species records (Xiong et al., 2018; Xu et al., 2021; Zhang et al., 2023). The absence of a data sharing mechanism is not only detrimental to scientific research cooperation but also affects long-term monitoring work.

It is very important to establish a comprehensive database. This database should contain the morphological characteristics, genetic information and ecological data of fish, facilitating the use of researchers and managers (Xiong et al., 2018; Xu et al., 2021; Zhang et al., 2023). Establishing such a sharing platform is a key issue that needs to be addressed in the future.

6 Future Work Priorities and Improvement suggestions

6.1 Improve species surveys and data collection

Further expand the fish sampling areas in Hainan and the South China Sea region to reveal the biodiversity of wild fish. Due to the limited investigation area and seasonal influence, information on many endemic and rare fish species is still missing (Xiong et al., 2018; Xi et al., 2022; Zhang et al., 2023; Wang et al., 2024). It is suggested to adopt new detection techniques such as eDNA for systematic investigation, which will help establish a more complete list of species and outline the basic data (Xi et al., 2022; Wang et al., 2024).

Meanwhile, attention should be paid to the construction of the localized database. The ideal database should contain comprehensive information such as species classification, genetic characteristics and distribution areas, facilitating researchers' query and use (Xi et al., 2022; Wang et al., 2024). This resource sharing platform will significantly enhance the standardization and convenience of fish research.

6.2 Develop practical detection technologies

It is necessary to focus on developing an economical detection solution suitable for use at the grassroots level. Although genetic testing technology has good effects, its high cost limits its widespread application (Zhang et al., 2023; Wang et al., 2024). It is suggested to develop a detection toolkit that is easy to operate and low-cost, so that more local institutions can participate in species monitoring.

It can be considered to combine new technologies with traditional methods and improve the technical level of grassroots personnel through professional training. This way, not only can the quality of detection be guaranteed, but also the scope of participation can be expanded to achieve more comprehensive biodiversity conservation (Zhang et al., 2023; Wang et al., 2024).

6.3 Establish a multi-party cooperation mechanism

It is suggested to establish a cross-regional collaboration platform to integrate resources from all parties. At present, the research data are scattered among different institutions and lack effective sharing channels (Xiong et al., 2018; Zhang et al., 2023; Wang et al., 2024). By establishing a cooperative network that includes scientific research institutions, government departments and protection organizations, information sharing and method unification can be promoted.

Through this collaborative platform, standardized databases can be established, protection actions can be coordinated, and new challenges brought about by environmental changes can be addressed. Multi-party

cooperation can not only optimize resource allocation and avoid repetitive work, but also improve management efficiency and protect fish resources in Hainan Island and the South China Sea (Xiong et al., 2018; Xi et al., 2022; Wang et al., 2024).

7 Concluding Remarks

Hainan Island and the South China Sea region, as important hotspots for fish diversity in China, hold a special position in the development of species identification technology. This area is rich in Marine and freshwater fish resources. So far, hundreds of fish species distributed in different habitats have been recorded. However, affected by the complexity of the ecosystem, there are still obvious deficiencies in the existing species cognition.

The ecological uniqueness of Hainan Island and the South China Sea region provides a good condition for the innovation of identification technology, but also brings more challenges. Interdisciplinary research cooperation has led to significant progress in fish identification technology. The combination of traditional morphological classification methods and molecular labeling techniques (such as DNA barcoding and environmental DNA) has enhanced the ability to accurately identify species in complex environments. Establishment of Molecular manipulation taxonomic units (MOTUs) and regional gene databases. It can also improve the ability of species identification. The multi-technology integration strategy aims to develop more intelligent technologies to monitor the high diversity and dynamic changes of fish communities more effectively.

The foundation for achieving the sustainable development of fishery resources lies in the close cooperation between research and practical application. Build a standardized biological census network and an efficient data exchange platform to promote rapid detection technologies, and combine these technologies with fishery protection, development, management and policy implementation. By establishing an open data sharing system and through the cooperation of multiple parties such as research institutions and management institutions, research results can be transformed into executable fishery protection strategies. With the continuous development of technology, Hainan Island and the South China Sea region have become internationally leading demonstration areas for fish monitoring technology, providing a direction for global biodiversity conservation.

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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

Banan A., Nasiri A., and Taheri-Garavand A., 2020, Deep learning-based appearance features extraction for automated carp species identification, Aquacultural Engineering, 89: 102053.
https://doi.org/10.1016/j.aquaeng.2020.102053

Ferreira A.O., Azevedo O.M., Barroso C., Duarte S., Egas C., Fontes J., Ré P., Santos A., and Costa F., 2024, Multi-marker DNA metabarcoding for precise species identification in ichthyoplankton samples, Scientific Reports, 14(1): 19772.
https://doi.org/10.1038/s41598-024-69963-7

Hubert N., Hanner R., Holm E., Mandrak N.E., Taylor E., Burridge M., Watkinson D., Dumont P., Curry A., Bentzen P., Zhang J., April J., and Bernatchez L., 2008, Identifying Canadian freshwater fishes through DNA barcodes, PLoS One, 3(6): e2490.
https://doi.org/10.1371/journal.pone.0002490

Kyle C., Wilson C., and Wilson C., 2007, Mitochondrial DNA identification of game and harvested freshwater fish species, Forensic Science International, 166(1): 68-76.
https://doi.org/10.1016/J.FORSCIINT.2006.03.025

Li M.M., 2024, Molecular mechanisms underlying the diversification of aquatic life forms, International Journal of Aquaculture, 14(4): 184-194.
https://doi.org/10.5376/ija.2024.14.0019

Luo Z., Yang C., Wang L., Liu Y., Shan B., Liu M., Chen C., Guo T., and Sun D., 2023, Relationships between fish community structure and environmental factors in the nearshore waters of Hainan Island, South China, Diversity, 15(8): 901.
https://doi.org/10.3390/d15080901

Malik H., Naeem A., Hassan S., Ali F., Naqvi R.A., and Yon D.K., 2023, Multi-classification deep neural networks for identification of fish species using camera captured images, PLoS ONE, 18(4): e0284992.
https://doi.org/10.1371/journal.pone.0284992

Naz S., Chatha A., and Khan R., 2023, Pragmatic applications of DNA barcoding markers in identification of fish species – a review, Annals of Animal Science, 23: 363-389.
https://doi.org/10.2478/aoas-2022-0073

Rauf H.K., Lali M.I.U., Zahoor S.Z.H., Shah S., Rehman A.U., and Bukhari S.A.C., 2019, Visual features based automated identification of fish species using deep convolutional neural networks, Computers and Electronics in Agriculture, 167: 105075.
https://doi.org/10.1016/j.compag.2019.105075

Ren L.R., Tian Y., Yang X.Y., Wang Q., Wang L.S., Geng X., Wang K.Q., Du Z.F., Li Y., and Lin H., 2022, Rapid identification of fish species by laser-induced breakdown spectroscopy and Raman spectroscopy coupled with machine learning methods, Food Chemistry, 400: 134043.
https://doi.org/10.1016/j.foodchem.2022.134043

Sueker M., Daghighi A., Akhbardeh A., Mackinnon N., Bearman G., Baek I., Hwang C., Qin J., Tabb A., Roungchun J., Hellberg R., Vasefi F., Kim M., Tavakolian K., and Zadeh H., 2023, A novel machine-learning framework based on a hierarchy of dispute models for the identification of fish species using multi-mode spectroscopy, Sensors, 23(22): 9062.
https://doi.org/10.3390/s23229062

Wang C.Z., Ma Z.H., Cao K., Wang X., Xi R., Jiang T., Yang R., and Xing Y.C., 2024, Species diversity of fish at the Wuzhizhou Island South China Sea based on environmental DNA, Biodiversity Data Journal, 12: e127120.
https://doi.org/10.3897/BDJ.12.e127120

Wenne R., 2023, Single nucleotide polymorphism markers with applications in conservation and exploitation of aquatic natural populations, Animals, 13(6): 1089.
https://doi.org/10.3390/ani13061089

Wu J.N., 2024, Interpretation of ensemble forecasting study on the response of fish distribution in the Yellow and Bohai Seas of China to climate change, International Journal of Marine Science, 14(1): 1-5.
https://doi.org/10.5376/ijms.2024.14.0001

Xi R., Gao W., Wang X., and Xing Y., 2022, Species diversity of coral reef fishes around the West Island of Sanya City South China Sea based on environmental DNA, Biodiversity Data Journal, 10: e89685.
https://doi.org/10.3897/BDJ.10.e89685

Xie Y.J., Xiang J., Li X.Y., and Yang C., 2024, An intelligent fishery detection method based on cross-domain image feature fusion, Fishes, 9(9): 338.
https://doi.org/10.3390/fishes9090338

Xiong W., Wang Q., Xie D., Fletcher D.H., and He D., 2018, Factors influencing tropical Island freshwater fishes: species status threats and conservation in Hainan Island, Knowledge and Management of Aquatic Ecosystems, 419: 6.
https://doi.org/10.1051/KMAE/2017054

Xu L., Wang X., Damme K., Huang D., Li Y., Wang L., Ning J., and Du F., 2021, Assessment of fish diversity in the South China Sea using DNA taxonomy, Fisheries Research, 233: 105771.
https://doi.org/10.1016/j.fishres.2020.105771

Yang L., Liu Y., Yu H., Fang X., Song L., Li D., and Chen Y., 2020, Computer vision models in intelligent aquaculture with emphasis on fish detection and behavior analysis: a review, Archives of Computational Methods in Engineering, 28: 2785-2816.
https://doi.org/10.1007/s11831-020-09486-2

Zhang J.X., Xu L., Du F.Y., Tang Q.H., Wang L.G., Ning J.J., Huang D., Li Y., Liu S.S., and Wang X.H., 2023, DNA barcoding of marine fish species in the waters surrounding Hainan Island northern South China Sea, Frontiers in Marine Science, 10: 1249073.
https://doi.org/10.3389/fmars.2023.1249073