Advances in the Study of Genetic Diversity of Important Marine Animals in China by Using Computer Aided Systems

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Abstract. The study of genetic diversity of Marine animals can not only reveal the origin and evolution history of species, but also provide theoretical basis for the conservation of genetic resources, breeding and genetic improvement of mariculture animals, as well as the restoration and stability of the entire Marine ecosystem. In this paper, the genetic diversity of important Marine animals (mainly including fishes, shrimps, crabs and shellfish) in China in the past ten years is reviewed. Their application in germplasm identification, system evolution, population genetic structure analysis, improvement of plant species, and other aspects this paper expounds the further promote Marine animals, genetic diversity research, speed up the cultivation of excellent germplasm resources, and promote the healthy development of Marine aquaculture, realize the reasonable development and sustainable utilization of Marine biological resources.

Keywords: Marine Animals, Computer Aided System, Genetic Diversity, Molecular Markers

1. Introduction
Since the 21st century, three major problems of population, resources, and environment have become increasingly prominent. The development of modern marine agriculture has become a major strategic and competitive focus of the world's major marine countries. China has abundant marine animal resources and the largest mariculture industry in the world. The exploration and sustainable utilization of marine animal resources have become a meaningful way to address the protein demand and food safety problems of China's 1.6 billion population in the future, and also an inevitable choice for China's modern agricultural development strategy. Therefore, the protection and sustainable utilization of marine animal diversity will play an essential role in improving human dietary structure, increasing the nutrition level, and promoting the rapid and healthy development of the national economy and society. In general, biodiversity includes genetic diversity, species diversity, and ecosystem diversity. Genetic diversity is not only the basis of species diversity and ecosystem diversity, but also the basis of life evolution and species differentiation, and also an important foundation for evaluating natural biological resources. As the disappearance of a species is first presented in the decrease of genetic diversity, the prosperity of a species or population is often accompanied by the increase and stability of genetic diversity, and the rise and fall of a species often determine the succession behavior.
of the whole community or ecosystem. Hence, studies on the genetic diversity of marine animals have essential theoretical and practical significance. They can not only reveal the origin and evolutionary history of species, provide useful information for the classification and evolution of marine animals, but also provide a theoretical basis for the conservation of genetic resources, the breeding and genetic improvement of mariculture animals, and the restoration of the whole marine ecosystem[5-6].

The study of genetic diversity will help us understand the current situation of biological resources more clearly, to provide correct theoretical guidance for adopting more appropriate strategies to protect and use existing resources rationally. For important marine economic animals, the studies of genetic diversity can monitor the change of genetic structure and the influence of fishery practice on population and population genetic structure. They can also reveal the changes in gene frequency caused by mutation, natural and artificial selection, migration, mixing, etc., leading to the inherent nature of evolution. Hence, the detection of genetic diversity can not only be used in the study of Marine Animal Germplasm resources but also in the study of system evolution, genetic breeding, and many other aspects. This paper focuses on reviewing the research progress of marine economic animal genetic diversity in recent years in China to promote the development of marine animal genetic diversity.

2. Marine Fish
The study of fish genetic diversity was initially based on isozyme markers. However, the number of isozyme markers is limited, the detection efficiency is low, and it can only reflect the expression information of the coding region of the genome. Hence, with the rapid development of molecular marker technology, the isozyme is gradually replaced by various DNA molecular markers. The molecular markers can provide technical support for the study of fish genetic diversity which are widely used in fish germplasm resources, interspecific and interspecific hybridization, chromosome manipulation and genetic linkage map construction.

The difference in the genetic variation level between cultured population and wild population is a common concern in fish industry as most of the fry of cultured fish are produced by limited breeding population, which leads to bottleneck effect, genetic drift and inbreeding decline of population genetic diversity. This inevitably results in the loss of some specific alleles in the gene pool of cultured population. As a result, its diversity in genetic inheritance was lower than that of wild population. The results suggested that the level of genetic diversity of cultured population decreased in different degrees. Similar results have been reported in other cultivars. However, it has also been reported that there is no significant difference between them in the number of effective alleles, suggesting that the natural population is experiencing the crisis of loss of some alleles, especially some rare alleles. The genetic diversity of some newly cultured marine fishes, such as halibut plaice, has not declined significantly. However, the genetic management of their parents should be enhanced in the future. The proper size of their parents should be maintained, their parents should be changed regularly to avoid generations of breeding, and scientific genetic management such as necessary purification and rejuvenation should be performed to ensure their healthy and sustainable development.

3. Marine Crustaceans
In recent years, with the promotion of artificial propagation technology, small population propagation, excessive fishing, and pollution of water environment, marine crustaceans, especially shrimp and crab resources in China have been severely degraded. Hence, the study of their genetic diversity is of considerable significance to protect the germplasm resources of shrimp and crab and ensure the healthy development of aquaculture. Currently, various genetic markers have been rapidly applied to the research of marine crustacean genetic diversity, and have been widely used in germplasm resources, population differentiation, system evolution and molecular breeding.

Based on the theory of establishing a shared platform for the development of marine organisms:

\[ P(C) = M - C^{-e} + \varepsilon, \] which is evaluated as follows:  
\[ E[P(C)] = M - C^{-e} \]  
(1)
The dominant genetic diversity of marine animals is evaluated as follows:

\[ \pi_g = MR_g \left( M - C^{-g} \right) + Cr_g, 0 \leq r_g \leq 1 \] (2)

The genetic diversity of other marine animals is assessed as:

\[ \pi_i = MR_i \left( M - C^{-i} \right) - Cr_i, \text{ where } 0 \leq r_i \leq 1, i = 1, 2, \ldots, n \] (3)

The overall assessment of critical marine animal diversity is:

\[ \pi = \left( MR_g + \sum_{i=1}^{n} MR_i \right) \left( M - C^{-e} \right) - C, r_g + \sum_{i=1}^{n} r_i = 1 \] (4)

Currently, there are no studies on the cultivation of new crabs abroad. During the 11th five-year plan period, BLUP breeding program was applied to obtain new crab varieties and new strains with independent intellectual property rights in China's marine aquaculture breeding, including new strains of Portunus trituberculatus, which were respectively bred by Institute of Oceanography, Chinese Academy of Sciences and Institute of yellow sea aquaculture, and new strains of blue crab, which were bred by Xiamen University. At the same time, many functional genes and genomic genetic information of crab were improved and stored. A high-throughput genetic marker system was developed for species identification, genetic diversity detection and family identification, which provided markers for candidate genes related to economic traits, laying a solid foundation for the subsequent application of molecular marker technology to directional breeding of new varieties. The genome of prawn is enormous, and the number of haploid chromosomes is about 43-44. Hence, massive genetic markers are required to construct the genetic linkage map of prawn. In China, due to the breakthrough of parent culture technology of Penaeus chinensis and Penaeus vannamei, the breeding work of Penaeus chinensis has been carried out earlier and progressed smoothly, and massive molecular data have been accumulated at the same time. The genetic linkage map of Penaeus vannamei was first reported. The genetic linkage map of male and female of Penaeus vannamei was established based on the AFLP molecular markers and the strategy of “quasi test crossing” with single pair hybrid parents and F1 generation as a mapping population.

4. Marine Shellfish

As an important mariculture object in China, shellfish play a leading role in the mariculture industry for a long time. The increasing cultivation of economic shellfish makes it a pillar industry in the marine renewable resources industry. The international research on the genetic diversity of marine shellfish began in the 1970s, mainly based on the variation of external morphology and isoenzyme to evaluate the level of genetic diversity. In recent years, with the continuous development of molecular biology techniques, the studies on the genetic diversity of marine economic shellfish in China have gradually deepened, and the results obtained provide relevant references for marine biological classification, shellfish system evolution, and germplasm identification, population genetic variation, and differentiation, genetic diversity protection, marker-assisted breeding of excellent varieties.

K dominance curve is used to show the “internal diversity” of Macrobenthos Community and describe the ecological characteristics of the community. Figure 1 shows that the diversity of Macrobenthos in the open sea area is higher than that in the offshore and the transitional regions in spring and summer. Taking the whole investigation area as the research object, the diversity in spring is higher than that in summer, as shown in Figure 2.
Figure 1. K dominance curve of macrobenthos between three regions in two seasons

Figure 2. K dominance curve of amphibian between seasons based on integrated data

Pearl oyster falls in Mollusca, cladochrcania, pterygoid subclass, perliera, and Pearl mollusc. It is the main shellfish that produces sea water pearls with high economic value. Pinctada martensii, P. maxima, and Pteria penguin are among the most crucial pearl shells developed in China and the world. Among them, “Nanzhu” produced by Pinctada martensii is famous for a long time. However, since the 1970s, overfishing and environmental degradation have led to the depletion of natural resources of the species. The long-term artificial inbreeding and arbitrary diffusion of shellfish for production in the past 30 years have led to serious degradation of germplasm and destruction of genetic structure. Therefore, domestic scholars have carried out the research on the genetic diversity of Pinctada martensii, to further understand the genetic characteristics of the species, cultivate excellent species, and promote the pearl industry. In this section, the research progress in the genetic diversity of Pinctada martensii in the last ten years is summarized.

5. Conclusions
In the last ten years, the rapid development of molecular biotechnology has driven the study of marine animal genetic diversity to a new stage. As a series of molecular genetic markers are identified, it is
possible to obtain more direct and accurate genetic information at the DNA level. However, as all the current molecular markers have defects in their usage or background due to various reasons, it is necessary to explore co-dominant markers with higher polymorphism, stability, applicability, easier operation, and lower cost. For now, genetic diversity studies are still based on the comprehensive analysis of multiple genetic markers. Marine animal genes will be identified in batches. More and more genes and their regulatory networks will be analyzed. Through the screening, identification and functional analysis of critical dominant genes and the linkage analysis of their economic properties, more molecular markers will be obtained and located. Hence, the molecular marker-assisted breeding technology can be established to accelerate the creation and cultivation of excellent germplasm, promote the healthy development of marine aquaculture, and achieve the protection, rational development and sustainable utilization of marine biological resources.

References
[1] Chen, Y. , Huang, L. , Wu, W. , Ruan, Y. , Wu, Z. , & Xue, Z. , et al. (2014). Speciation analysis of lead in marine animals by using capillary electrophoresis couple online with inductively coupled plasma mass spectrometry. Electrophoresis, 35(9), 1346-1352.
[2] Ketchum, R. N. , Dieng, M. M. , Vaughan, G. O. , Burt, J. A. , & Idaghdour, Y. . (2016). Levels of genetic diversity and taxonomic status of epinephelus species in united arab emirates fish markets. Marine pollution bulletin, 105(2), 540-545.
[3] Cassidy C. D’ Aloia, Boganowicz, S. M. , Harrison, R. G. , & Buston, P. M. . (2016). Cryptic genetic diversity and spatial patterns of admixture within belizean marine reserves. Conservation Genetics, 1-13.
[4] Andrew Zaffos, Seth Finnegan, & Shanan E. Peters. (2017). Plate tectonic regulation of global marine animal diversity. Proceedings of the National Academy of Sciences of the United States of America, 114(22), 201702297.
[5] Pál Schmitt, Culloch, R. , Lieber, L. , Molander, S. , & Kregting, L. . (2017). A tool for simulating collision probabilities of animals with marine renewable energy devices. PLoS ONE, 12(11), 1-11.
[6] Jinik Hwang, So Yun Park, Mirye Park, Sukchan Lee, & Taek-Kyun Lee. (2017). Seasonal dynamics and metagenomic characterization of marine viruses in goseong bay, korea. Plos One, 12(1), e0169841.