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Genetic Diversity of Decapoda in the Indo-Pacific Region: A Literature Review

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Abstract

The Indo-Pacific region is the global center of marine biodiversity, home to more than 30% of the world's marine species. The order Decapoda, which comprises more than 17,000 species, plays significant ecological and economic roles in this region. This literature review aims to synthesize current knowledge on the genetic diversity and population structure of Decapoda in the Indo-Pacific and to identify the factors influencing these patterns. Molecular studies employing genetic markers such as mitochondrial DNA (mtDNA), microsatellites, and genomic sequencing indicate that Indo-Pacific Decapoda populations generally exhibit high haplotype diversity with relatively low nucleotide differentiation. Several factors, including larval dispersal capability, the duration of the planktonic phase, geographic and oceanographic barriers, and local adaptation to environmental conditions, shape population structure. Anthropogenic activities, particularly overexploitation, have led to declines in effective population size and genetic erosion in several commercially important species, such as Penaeus monodon and Scylla serrata. This review highlights the importance of integrating genetic data into sustainable fisheries management, including ecosystem-based stock assessment, periodic genetic monitoring, and the incorporation of genetic considerations in aquaculture and restocking programs to ensure the long-term sustainability of Decapoda populations in the Indo-Pacific region.

1. INTRODUCTION

The Indo-Pacific region extends from the eastern coast of Africa to the central Pacific Ocean and represents the largest and most diverse marine region in the world. This region serves as the global centre of marine biodiversity, harbouring more than 30% of the world's marine species. The rich biodiversity of the Indo-Pacific highlights the need for effective conservation strategies. Marine protected areas play a crucial role in preserving genetic, species, and phylogenetic diversity, with the Central Indo-Pacific identified as a priority region for conservation efforts (Fan et al., 2023). According to Evans et al. (2016), the complex geological and oceanographic conditions of the Indo-Pacific region have created unique habitats that support evolutionary processes and speciation across various marine taxa. One marine taxonomic group that exhibits high diversity and adaptation in this region is the order Decapoda.

The order Decapoda comprises more than 17,000 species, with a high rate of new species discovery, indicating that many species remain undescribed (De Grave et al., 2023). Members of this order are distributed across marine, freshwater, and terrestrial habitats. Decapods occur in a wide range of environments, from shallow coastal waters to the deep sea, and from tropical to polar regions. This broad distribution reflects their high adaptive capacity and ecological flexibility (Manfrin, 2023). In the Indo-Pacific region, decapods are particularly abundant and diverse, occupying ecological niches such as coral reefs, wetlands, mangrove forests, and deep-sea habitats. The diversity of habitats occupied by these organisms directly reflects the important ecological roles decapods play in maintaining the balance of marine ecosystems.

Decapods function as key predators in many ecosystems, helping regulate populations of other marine organisms. In addition, they also act as detritivores by consuming dead organic material and contributing to nutrient cycling. By breaking down organic matter, decapods help maintain ecosystem health, particularly in mangrove and wetland environments (Briones-Fourzán & Hendrickx, 2022). At the same time, decapods represent a major component of global fisheries, with species such as shrimp and crabs having high economic value. The fisheries industry relies heavily on decapods for both local consumption and international trade (De Grave et al., 2023). Given their significant ecological and economic importance, understanding the population dynamics and genetic diversity of decapods is essential for sustainable management and conservation efforts.

Studies on the genetic diversity and population structure of decapods in the Indo-Pacific region have advanced rapidly over the past two decades alongside the development of molecular technologies. Genetic markers such as mitochondrial DNA (mtDNA), microsatellites, and genomic sequencing have provided deeper insights into population dynamics, connectivity, and the evolutionary history of decapods. This understanding is increasingly important in light of growing anthropogenic pressures on marine ecosystems and the urgent need for science-based conservation strategies.

Reviewing existing research findings is an important step in identifying general patterns and knowledge gaps. Therefore, this article aims to synthesize current knowledge on the genetic diversity of decapods in the Indo-Pacific region and to identify patterns of population structure and the factors influencing them.

2. RESEARCH METHODS

This review analysed scientific publications, research reports, government documents, and other reliable sources on the genetic diversity of Decapoda in the Indo-Pacific region. Literature searches were conducted across national and international journal databases, university repositories, and publications from relevant research institutions.

3. RESULTS AND DISCUSSION

Genetic Diversity of Decapoda in the Indo-Pacific Region

Studies on *Penaeus monodon* and other species reveal high haplotype diversity, with most individuals possessing unique haplotypes. These findings indicate a large effective population size and a single reproductive unit, supporting the assumption of a relatively stable population history (Alam et al., 2016). Phylogenetic analyses of several species within the family Penaeidae using mitochondrial DNA markers such as COI and 16S rRNA also revealed distinct lineages and high genetic differentiation among populations, further supporting the indication of large effective population sizes and historical stability (Alam et al., 2017). This general pattern of high genetic diversity is also reflected in various species of the order Decapoda in the western Indo-Pacific region, including Indonesian waters.

A case study on the moon crab *Matuta victor* from Java Island provides a concrete example of the high genetic diversity of decapods in Indonesian waters. From 91 sequences analyzed across 10 sampling locations on Java Island, 38 haplotypes and 60 polymorphic sites were identified. The overall haplotype diversity reached 0.92088, indicating very high genetic diversity, although nucleotide diversity remained relatively low ($\pi = 0.01845$). This finding is consistent with patterns observed in other brachyuran crabs in the Indo-Pacific region, where high haplotype diversity is accompanied by low nucleotide differentiation, suggesting either a relatively recent population expansion or high levels of gene flow (Syuhada, 2024).

Similar patterns have also been reported in other decapod species across the Indo-Pacific, indicating that this phenomenon is widespread and not restricted to a single taxon or location. A study by Ma et al. (2011) showed that populations of *Scylla paramamosain* on Hainan Island exhibited moderate to high haplotype diversity (0.625–0.914) but low nucleotide diversity (0.001–0.003). A total of 32 haplotypes were identified from 92 individuals, with one dominant haplotype distributed across all sampling locations. This condition reflects a pattern of expansion after a bottleneck event, in which the population experienced rapid growth while the accumulation of new mutations remained limited. The low level of population differentiation suggests high gene flow among locations, likely driven by the planktonic larval phase that allows wide dispersal.

In addition to demographic history, life-history strategies and dispersal ability also play important roles in shaping patterns of genetic diversity in crustaceans. Mattos et al. (2019) compared two crustacean species with different life-history strategies and found contrasting patterns of genetic diversity. The ghost crab *Ocypode quadrata* showed low genetic structure and widely distributed haplotypes along approximately 7,000 km of coastline, reflecting a panmictic population with high dispersal capacity. In contrast, the isopod *Excirolana braziliensis* exhibited strong genetic structure with four distinct lineages and evidence of cryptic species. This fundamental difference is largely due to differences in dispersal ability: crab larvae can disperse over long distances, whereas isopods have limited mobility, leading to genetic isolation among populations. High genetic diversity in crabs may also be facilitated by high population migration rates, which increase the likelihood of encounters and interbreeding among individuals from different regions, thereby enriching genetic variation within populations (Baksir et al., 2022).

Population Structure of Decapoda

The population structure of Decapoda in the Indo-Pacific region is influenced by several factors, including larval dispersal capacity, the duration of the planktonic phase, and the presence of geographic and oceanographic barriers (Hunter et al., 2011). These factors contribute to genetic differentiation among populations, ranging from panmictic conditions to highly fragmented population structures. Larval dispersal potential, which is often assumed to be high due to the planktonic nature of many decapod larvae, is now understood as a more complex process in which oceanographic dynamics and larval behaviour also play important roles in limiting dispersal (Teske et al., 2016). This complexity is further reinforced by geographic barriers that can reduce gene flow and promote genetic differentiation (Johannesson et al., 2018).

Larval dispersal ability represents a key factor in determining the population structure of decapods. For example, the banded coral shrimp *Stenopus hispidus* has a long planktonic larval phase and a high dispersal potential, yet still shows significant genetic differentiation between Atlantic and Indo-Pacific populations, indicating restricted gene flow across ocean basins (Dudoit et al., 2018). Similarly, the amphidromous freshwater prawn Macrobrachium lar exhibits genetic isolation at the edges of its distribution range despite theoretically possessing broad dispersal capability, suggesting that larval dispersal does not occur uniformly across habitats (Castelin et al., 2013). Oceanographic factors, such as ocean currents and tidal dynamics, also play an important role. The crab *Macrophthalmus japonicus*, despite having high dispersal potential, shows genetic isolation in northern Japan due to ocean currents that limit the inflow of larvae from other regions (Kobayashi et al., 2023). These findings emphasise that population structure results from complex interactions between species' biological characteristics and environmental conditions.

According to Syuhada (2024), species with long planktonic larval phases generally exhibit weak or undetectable population structure at the regional scale, reflecting high levels of genetic connectivity through larval dispersal. In contrast, species with short larval phases or direct development tend to exhibit strong population structure even at relatively small geographic scales. Analysis of Molecular Variance (AMOVA) conducted on various shrimp and crab species indicates that approximately 5–40% of total genetic variation is distributed among populations, depending on the life-history characteristics of each species.

An example is the moon crab *Matuta victor* from Java Island, which exhibits a relatively weak population structure, with an FST value of 0.26611. In this case, 73.39% of the genetic variation is within populations, while 26.61% is among populations. This pattern indicates a high level of connectivity among locations along Java Island, likely facilitated by effective larval dispersal and the absence of significant geographic barriers in the coastal waters of Java. Pairwise FST analysis also revealed a wide range of values (−0.32331 to 0.77348), with negative values observed in several location pairs, indicating extremely high genetic homogeneity or even excess gene flow among populations.

Factors Influencing Genetic Diversity and Population Structure

Local adaptation in populations of Decapoda in the Indo-Pacific region has increasingly been understood through comparative genomic studies and genome scans aimed at detecting signals of selection (Veldsman et al., 2021). These approaches reveal that environmental factors, such as temperature, salinity, food availability, and predation pressure, can exert distinct selective pressures across locations, thereby promoting local adaptation even when gene flow among populations persists. This phenomenon is supported by numerous studies on marine species, which show that local environmental conditions can produce genetic differentiation and adaptive signals detectable at the genomic level. Therefore, natural environmental variation represents one of the major drivers of genetic diversity and population structure formation in Decapoda populations across the Indo-Pacific region.

Human activities, particularly overexploitation, have significantly affected the genetic diversity and population structure of decapod species such as the giant tiger prawn *Penaeus monodon* and the mud crab *Scylla serrata* in the Indo-Pacific region. These activities have led to reductions in effective population size and genetic erosion in several locations. Genetic diversity and population structure are crucial for the long-term survival and adaptive capacity of these species; therefore, understanding these dynamics is essential for conservation and management efforts. Populations of *Scylla serrata* in the Western Indian Ocean (WIO) show evidence of recent population bottlenecks, likely due to overexploitation. This condition has led to the formation of a unique metapopulation structure within the WIO, with distinct genetic stocks across the Indo-Pacific (Fratini et al., 2010).

Genetic diversity in *Penaeus monodon* varies across regions, with Southeast Asian populations showing the highest diversity and Western Indian Ocean populations the lowest. This variation is important for understanding the species' adaptive capacity and resilience to environmental change (Vu et al., 2021). Populations of *Penaeus monodon* also exhibit significant genetic structuring, with distinct clusters corresponding to geographic regions. Such structuring has been observed in both wild and domesticated populations, where domestication processes may lead to genetic divergence due to artificial selection (Wong et al., 2020).

Sustainable Fisheries Management

Sustainable fisheries management for economically important species in the order Decapoda requires an ecosystem-based approach that integrates genetic data into stock assessment processes. Information on population genetic structure enables the identification of biologically distinct stock units, allowing fisheries management to be implemented more effectively by establishing catch quotas for each stock while reducing the risk of overexploitation of local populations. In addition, periodic genetic monitoring can detect changes in genetic diversity and trends in effective population size as early indicators of stock degradation (Verry et al., 2020; Jeena et al., 2016).

Genetic diversity is an essential component in maintaining population sustainability. High levels of genetic diversity help preserve the adaptive potential of populations, enabling them to respond to environmental changes and increasing resilience to diseases (Teles & Mantelatto, 2024). Studies on several aquatic organisms indicate that aquaculture stocks can maintain genetic diversity comparable to that of wild populations. However, processes such as domestication, stock mixing, and the potential occurrence of outbreeding depression remain important considerations in the management of genetic resources (de Oliveira et al., 2018).

Restocking or stock enhancement programs require careful consideration of genetic aspects. Programs that focus solely on increasing population size may lead to long-term genetic consequences, such as shifts in adaptive allele frequencies or reductions in natural genetic diversity. Therefore, genetic monitoring is recommended as an integral component of management strategies to minimize negative impacts on the genetic structure of natural populations (Monteiro et al., 2022). The integration of genetic information into fisheries management, aquaculture practices, and restocking programs is expected to support the long-term sustainability of decapod resources and maintain the stability of aquatic ecosystems

4. CONCLUSIONS

This literature review highlights the complexity of genetic diversity within the order Decapoda in the Indo-Pacific region. Decapod populations generally exhibit high haplotype diversity but low nucleotide differentiation, reflecting large effective population sizes, historical stability, and high connectivity among habitats. Population structure ranges from panmictic to highly structured patterns and is influenced by larval dispersal capacity, the duration of the planktonic phase, oceanographic processes, and geographic barriers. A study of the moon crab *Matuta victor* on Java Island demonstrates high connectivity, with 73.39% of genetic variation occurring within populations. AMOVA analyses across several decapod species indicate that approximately 5–40% of total genetic variation is distributed among populations, suggesting the existence of distinct management units. Local adaptation to environmental conditions also contributes to adaptive genetic differentiation despite gene flow among populations. However, overexploitation of commercially important species such as the giant tiger prawn, *Penaeus monodon*, and the mud crab, *Scylla serrata*, has led to population bottlenecks and genetic erosion in several regions, with a diversity gradient observed from Southeast Asia to the Western Indian Ocean. Sustainable management, therefore, requires integrating genetic data into fisheries management, including stock identification, catch quota allocation, and periodic genetic monitoring. Aquaculture and restocking programs should also consider population genetic structure to maintain essential genetic diversity. In addition, climate change further increases the urgency of conserving genetic diversity as the foundation for evolutionary adaptation. Consequently, further research using advanced genomic technologies is needed to support effective conservation and management strategies for Indo-Pacific decapod populations.

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