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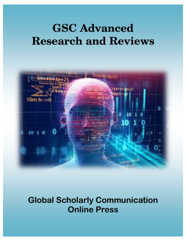

(REVIEW ARTICLE)

Population genetic structure of macrozoobenthic invertebrates: Its implications for coastal resource management

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Abstract

Population genetics is not only a mere tool in determining the evolutionary aspect of an organism, nevertheless, also as a tool that implicates macrozoobenthic invertebrate population at the risk of over-exploitation, extinction, declining in number, and sustainable in status. These implications make the population genetically useful that unravel mysterious propound doubts beneath the vast seas and oceans. Macroozoobenthos species such as snails, clams, mussels, lobsters, crabs, shrimps, abalones, oysters, and corals are meroplankton that once in their life cycle they spent as plankton. They float in the water column and have transported hundreds to thousands of nautical miles depending on the water current before settling down and resume benthic mode of life. Their creeping and sedentary lifestyles are prone to easy collecting and gleaning, resulting in over-exploitation and over-harvesting in different regions. Thus, this review aims to consolidate several findings on the population genetic structure of macrozoobenthic species, which has implications for coastal resource management. Collectively, studies revealed that population genetic structures of macrozoobenthic invertebrates such as fine-scale, mesoscale and panmictic population that has genetic diversity, genetic differences, genetic homogeneity, and low genetic variability governed by the demographic barrier, salinity, water temperature, current, distance, and many others. Thus, population genetics is a vital tool in drafting, formulating, and conceptualizing conservation and protection measures of macrozoobenthic species with regards to coastal resource management.

Keywords: Fishery management; Panmictic; Genetic diversity; Sedentary; Mesoscale.

1. Introduction

The population genetics in many types of research has used to examine the organism's adaptation to different environmental conditions as part of their evolution. The speciation of the different organisms in its localities or regions that are exotic or endemic could be determined using population genetics. The population structure and their distribution, both geographically and spatially, could be resolved using population genetics. Application of population genetics is not only limited to evolutionary biology but instead reflected population identity and their status in the wild in the past, real-time, and possible future trends. However, inferences of population genetics toward fishery management, conservation, and protection strategy is not yet compiled to date. Thus, the review aims to consolidate researches that examined macrozoobenthos species and their implication for management and conservation measures. There are several ecological studies undertaken previously that used population genetics data as a guiding principle in the conservation and management of different macrobenthic invertebrates [1-11]. The data in the genetic

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differentiation of several macroinvertebrates used to formulate a management scheme in determining the appropriate spatial scale in restocking or stock enhancement program [2,12]. The benthic invertebrates vary from a fine to mesoscale spatial genetic diversity indicating limited larval dispersal, to a vast panmictic population, indicating high levels of gene flow and long larval period [13, 3, 14, 15, 16]. With these, management could be evaluated whether inter-regional or interstate in order to protect the particular species. The findings in genetic variability within the small proximity lead to the notion that species should protect within the local rather than the big scale [17, 12, 19]. The findings in the genetic variability of the two interconnected stock will give the idea that a particular species have their adaptable characteristic restricted formed [19, 20]. The report on the genetic differences among benthic invertebrates made by different environmental gradients such as water temperature, salinity, pressure, and others led to the formulation of protecting the species exclusively on their endemic habitat [21]. The high genetic diversity data could use to predict benthic invertebrate if it is still capable to replenish their natural stock [8, 22]. High genetic diversity gives a hint of whether the organism lives in higher density or not [20]. It also provides information if the organism can expand its territorial domain. With the result in higher genetic diversity managers' in fisheries management can suggest for the establishment of a no-take zone marine protected areas so that there would be a continuous healthy stocking into the ecosystem. The Higher genetic diversity of the species will also reflect the importance of the site as the center of genetic diversity in the region, and the need to protect this site should well-emphasize [23].

The low genetic diversity of the benthic population gives us a warning on the over-exploitation as it is the sign at the brink of extinction [10]. Low genetic diversity could also mean that the organism is no longer capable of reproduction, and the ability to survive to the different environment parameters is no longer possible [24, 10]. The low genetic diversity also manifests that certain macrobenthic invertebrates are under fishery pressure, and there is a need for an immediate regulation on the utilization of the species [25, 11, 9]. There is a concern of introducing species used for aquaculture and other purposes that later exhibit genetic diversity deterioration due to founder effect, which happens when a particular species was isolated from its natural and larger population [26]. If the organism has shallow genetic differentiation, this gives an idea that the organism is a homogenous and well-mixed population [8, 27]. Moreover, the need for single management should call into the attention of several stakeholders [8, 5]. As it requires a vast management scale, whether at the national level, interstate, or multi-state efforts [7, 6, 4]. This single, panmictic, and well-mixed population disclosed the genetic connectivity of the benthic species even at a broader geographical scale. The knowledge of genetic connectivity among stocks is critical in determining the appropriate geographic units for fisheries management, including quotas, design of marine protected areas, and international relations related to the source of recruitment for fishery stocks in a complex geopolitical environment [4].

2. The implications of the genetic differentiation for coastal resource management

In some instances, a barrier (hydrographical or landlock) for marine benthic invertebrates may create genetic differences. The hydrographic features of the northern North Sea constitute a barrier between Norway and the North Atlantic that give a clear genetic differentiation between Norwegian and Atlantic great scallop *Pecten maximus*. Besides, the Norwegian Trench also adds to the genetic differentiation of these two stocks by possibly reducing the connectivity between the population from the western and eastern North Sea [1]. These hydrographic and oceanographic features are important factors shaping the genetic differentiation structure of giant clams. All three species of endangered giant clam (*Tridacna crocea, Tridacna maxima and Tridacna squamosa*) showed limited gene flow and a highly significant genetic population structure. Based on a hierarchical they could be divided into three to six groups from west to east: (1) Western Indian Ocean (*T. maxima and T. squamosa*), (2) Red Sea (*T. maxima and T. squamosa*), (3) Eastern Indian Ocean (including Java Sea in *T. maxima*), (4) central Indo-Malay Archipelago, (5) Western Pacific and (6) Central Pacific (*T. maxima*) [3]. Strong genetic differentiation made by hydro-geographical distribution also reported in the Indo-West Pacific populations of sea star *Linckia laevigata* that can group into four biogeographic regions: (1) Western Indian Ocean (2) Eastern Indian Ocean (3) Indo-Malay-Philippines Archipelago and (4) Western Pacific. One of the reasons for the differentiation of the sea star could attribute to the bifurcation of the South Equatorial Current, forming the north-flowing East African Coast Current and the south-flowing Mozambique Current [14]. Great geographical population structure differences were also evident in soft-shell clam *Mya arenaria*. Bayesian cluster analysis identified four groups of soft-shell clam located in the Mediterranean, Celtic Sea, along the continental coast of the North Sea and in Scotland. Deep genetic divergence between the Mediterranean and the Atlantic soft-shell clam is a common pattern in native European marine invertebrates, which typically results from a combination of historical vicariance and the cessation of contemporary gene flow due to the presence of the Almería-Oran oceanographic front [28]. A distinct population genetic differences between the Atlantic and the eastern Mediterranean population was also reported in Norway lobster

Nephrops norvegicus [29]. Jenkins et al. [30] reported that European lobster *Homarus gammarus* has a pronounced phylogeographic break between the Atlantic and Mediterranean basins, while structure within the Mediterranean was also apparent, partitioned between lobster from the central Mediterranean and the Aegean Sea. The partition on the lobster population ascribes to restricted gene flow between the Atlantic and Mediterranean basins, most frequently due to isolation by distance and an oceanographic barrier to connectivity. Genetic discrimination was also reported between the north and south regional populations in a highly dispersive marine invertebrates *Parastichopus californicus.* Local oceanography and directional processes of ocean currents played an important role in shaping the genetic structure of giant California sea cucumber *P. californicus* [31]. The hydrological barrier exists, due to prevailing surface currents was one of the identified causes that resulted to four population subdivisions in blacklip rock oyster, and these are; 1. the Noumea (New Caledonia); 2. the Bowen (North Queensland, Australia); 3. west Wessel Island and 4. east Wessel Island [32]. The influence of ocean circulation pattern, latitude, sea surface temperature, and ocean turbidity produce the three putative subspecies of spiny lobster *Panulirus homarus*. These are *P. homarus rubellus* from the southwest Indian Ocean, *P. homarus megasculptus* from the northwest Indian Ocean, and *P. homarus homarus* from the tropical region in-between. In the southwest Indian Ocean, the dispersion of larval *P. homarus* over a 4-month period was observed at the Delagoa Bight, which separates *P. homarus rubellus* and *P. homarus homarus*. On the South of the contact zone, larvae were advected southwestwards by prevailing boundary current or were retained in nearshore eddies close to release locations. Some larvae released in southeast Madagascar dispersed across the Mozambique Channel and reached the African shelf. In the northwest Indian Ocean, larvae were retained within the Arabian Sea. Larval retention and self-recruitment in the Arabian Sea could explain the recent genetic divergence between *P. homarus megasculptus* and *P. homarus homarus* [33]. The influence of the restricted water movement yields significant genetic variation in antipatharian black coral *Antipathes fiordensis* among sites, suggesting larval dispersal is restricted even at distances of 10 to 15 km. Most genetic differentiation occurred between sites within fjords rather than among fjords [15]. Despite relative proximity, oceanographic characteristic of the region tends to develop genetic differences within species. The genetic difference happens to the population of lollyfish *Holothuria atra* in Fiji, where the Vanua Balavu and Taveuni populations were genetically divergent from those in Vanua Levu, despite their close relative proximity. This genetic variation may be due to Somosomo Strait, the narrow channel that passes between the islands of Taveuni and Vanua Levu. With this scenario, there was unexpectedly high genetic differentiation, inferring low connectivity between the two populations (Taveuni and Vanua Levu) that were spatial nearest to each other. With this situation, part of the management plan should maintain viable breeding populations on each island to safeguard the genetic biodiversity of sea cucumber stocks within the fishery [12]. Another factor that creates genetic differences among macrozoobenthic invertebrates is the geographical barrier observed in inter-population differentiation between natural abalone *Haliotis asinina* from the Gulf of Thailand and that from the Andaman Sea. As a result, *H. asinina* in coastal waters of Thailand can be differentiated from the Andaman Sea stocks [19]. Restricted gene flow between locations also reported in green abalone *Haliotis fulgen,* which resulted in significant genetic differentiation among locations off Baja California, Mexico. The significant difference was caused by Isla Guadalupe, which indicates restricted gene flow between this and the other locations [20].

A sedentary invertebrate with limited larval dispersal tends to create a genetic differentiation at a fine-scale population structure. This fine spatial scale is common among abalone species, like the case of greenlip abalone *Haliotis laevigata* from southeast Australia. The highly genetic differences in greenlip abalone were found among large biogeographic regions (Great Australian Bight, Spencer Gulf, Bonnie Upwelling, Port Phillip Bay, northeast Tasmania) as well as significant genetic differentiation on a scale of ten of kilometers within regions. Unlike the closely related blacklip abalone, which shows minimal scale patterns of differentiation (hundreds of meters) [2]. A significant genetic difference across hundreds of meters also reported in the population of blacklip abalone *Haliotis rubra* from Tasmania, Australia. This genetic difference also indicates that larval dispersal restricted on a fine spatial scale. With the limited distance of larval dispersal, abalone populations across Tasmania are largely self-recruiting. Low levels of larval exchange appear to occur at the mesoscale (7–20 km), but age estimates based on shell size indicated that successful migration of larvae between any two sites might take only once every few years [13]. Another species with a limited larval dispersal was evident in sea cucumber *Cucumaria pseudocurata*. Despite the general trend of strong geographic structuring of populations, there is evidence of significant gene flow between adjacent sites separated by as little as four kilometers of the ocean or as much as one hundred kilometers along the coast. The most significant genetic disjunction observed separated Alaskan and Queen Charlotte Island (Haida Gwaii) samples from Vancouver Island and all sample sites further south. The northern population samples found to contain equal or more significant variability than many southern sites [16].

There are some species that, despite their potential for long-distance dispersal, populations are maintained through self-seeding and may have undergone selective adaptation in response to environmental conditions. This phenomenon leads to the difference in the genetic composition of coral reefs *Montastraea cavernosa* by having the presence of private sequence types that limited to a single location, suggesting selection to local environmental conditions. The majority of variation existed within location rather than among them. These further suggest that moderate to high gene flow occurs within and among populations of *M. cavernosa* in the Western Atlantic. These findings benefit conservation efforts in coastal resource management, and successful management should address local populations independently, as the degree of self-seeding may vary among locations [17]. An indication of population subdivision and genetic differentiation through local adaptation also reported in species with substantial larval dispersal variation, such as spiny lobster *Panulirus argus*. Very high geographic specificity of *P. argus* haplotypes was noticeable among sampling groups in the Caribbean and Brazilian coast. An indication of population subdivision and genetic differentiation in the spiny lobster *P. argus* evidenced by the magnitude of its control region sequence variation [18].

Environmental gradients tend to create genetic differentiation among macrozoobenthic invertebrates. In most cases, salinity creates a different population as it restricted gene flow between bodies of water. A typical example of salinity gradient is the significant genetic differentiation in rare brackish-water crab *Ptychognathus ishii* which detected among many local populations, with the most remarkable difference between populations on the Japanese mainland and those on smaller islands, such as Tsushima Island, Kakeroma Island, and Okinawa Island. Additionally, genetic differentiation found between some local populations on the mainland [21]. Another water gradient that is known to cause genetic differentiation is the water temperature. This is in the case of blood clams *Tegillarca granosa* in China, particularly Guangxi and Shandong population is bigger than between the Shandong and Zhejiang population. Because Shandong population located in a temperate climate zone, where blood clams cease to grow in the winter season while the Guangxi population inhabits a subtropical area and can grow all year long [34].

3. The implications of the higher genetic diversity for coastal resource management

The higher genetic diversity of macrozoobenthic invertebrates connotes its sufficient large population size that can sustain a natural population in a given location. The manager could use this adequate large size for their establishment of the catch quota of a certain valued species. The findings on higher genetic diversity in western rock lobster *Panulirus cygnus* of Western Australia, suggest the effective population sizes were sufficiently large to ensure genetic drift was negligible. This genetic diversity could also contribute to population expansion if suitable environmental factors exist [8]. It also appears that the effective population size of green abalone *Haliotis fulgens* off Baja California, Mexico remains sufficient to maintain the high genetic diversity. Therefore, it suggested that there are still genetic resources available that can lead to the recovery of wild populations so long as adequate management strategies are designed and complemented by both government and fishers [20]. The high genetic diversity was also manifested in the current picture of northern abalone *Haliotis kamtschatkana* of British Columbia, as a collection of spawning aggregates connected by gene flow, indicates that population abundance levels have not been low for sufficiently long periods to result in the loss of genetic diversity within aggregates or to cause random genetic differentiation among aggregates. This shows that northern abalone aggregates are not genetically depauperate or heavily inbred, and have the genetic capacity for population expansion when favorable environmental conditions prevail [22]. High haplotype diversity but low nucleotide diversity was previously reported in Asian green mussel *Perna viridis* population in Sabah. The low nucleotide diversity but high haplotype diversity could be an indication of a genetic bottleneck. This scenario can be observed in a population experiencing rapid expansion from a low effective population size, assuming there is sufficient time for haplotype to increase through mutation but insufficient time for accumulation of large sequence differences. This scenario has been reported in other marine organism that have undergone a severe demographic reduction, suggesting that although green mussel in Sabah has gone through severe mortality but because high genetic diversity, evidence for genetic bottleneck was not detected [35]. On the contrary, low nucleotide diversity and high haplotype diversity was detected in all populations of hard clam *Meretrix petechialis* in selected coastal areas in China. Species population growth, environmental heterogeneity, and living habits are the basis for maintaining high haplotype diversity in natural populations. High haplotype diversity in hard clam could mean a population expansion event [36]. In other instances, high genetic diversity could be derived from an ancient origin, allowing for the mutation to accumulate over time, like in the case of three species of squat lobster *Munida* sp. [37]. However, in the case of swimming crab *Portunus trituberculatus*, large population size may contribute to preserving high levels of genetic diversity. High population genetic diversity was observed in all populations of swimming crabs collected along the China seas and Japan [38]. High genetic diversity was also reported in a subdivided population of tropical blacklip rock oyster *Saccostrea* *echinata* in northern Australia. The long-distance dispersal potential of larval recruits and high tolerance to fluctuating environmental conditions are attributable characteristics in blacklip rock oysters. The study confirmed that despite the potential for high levels of gene flow, *S. echinata* do not belong to a single panmictic unit. Hence, the development of management policy for culture practices and translocation of farmed oyster will become increasingly crucial as hatchery production develops and aquaculture operations expand [32].

The genetic diversity of a particular species will not only reflect on its population size but also gives a hint of its habitat. This habitat might be a sink of genetic diversity coming from other sources, which could use as a reference point in protecting and conserving the ecosystem. Because of this, Hawai'i and Kingman reef are important centers of the genetic diversity in the region rather than an evolutionary dead-end for migrants from the Indo-Pacific. This was reported that sea cucumber *Holothuria atra*, which is one of the most common and widest-ranging tropical, coral reef sea cucumber in the world, happened to be genetically diverse, suggesting that Hawai'i and Kingman reef are important sites [23].

In some instances, a depleted population might show higher diversity than in a healthy population, which happens in blacklip abalone *Haliotis rubra* of southeastern Tasmanian. In a deplete stock where the number of adults diminished, the local reproductive output will be low, and concurrently, local recruitment will also reduce. Under these circumstances, the migrant larvae will represent a higher proportion of total larval recruitment. Given that the source of these migrants is likely to be varied both in space and through time, the end result may be a local population with a more diverse genetic composition than those populations that are self-recruiting [13]. Hence, identifying the source of larval origin should be considered in drafting the conservation and protection policy of a particular species.

4. The implications of the low genetic diversity for coastal resource management

The low genetic diversity in macrozoobenthic invertebrates appeared after experiencing a reduction in density. Many populations of benthic and broadcast spawning marine invertebrates have struggled to recover or have collapsed. The genetic technique and data derived from it may help to distinguish populations that are self-sustaining from those at risk of further decline. These circumstances had already happened in many macrozoobenthic invertebrates. One of these factors that contribute to low genetic diversity is the over-collection of the species from the wild. Like in many other benthic species, it was shown that the potential effect from its fishery is the low genetic diversity in sea cucumber *Parastichopus regalis* as observed in the location that has fishery pressure in the Western Mediterranean sea. Thus, as suggested, there is a need for appropriate management of this species, such as a establishing a close fishery season, establishing protected areas (i.e., no-take zone) to conserve a healthy population, and favor recruitment in the nearby area [25]. Another concern species that is on the brink of low genetic diversity is the population of pink abalone *Haliotis corrugata* at the Point Loma kelp forest near San Diego, California, USA. Collectively, the findings suggest that restoration effort will need to achieve a greater density (0.18 m^{-2}) to improve local recruitment. This further suggests that the Point Loma kelp forest population of pink abalone is the insufficient density for long-term viability, may be reliant upon immigration, and cannot be defined as an independent local population unit [24]. This case most likely happens to all invertebrates that have an economic important like the blue kingcrab *Paralithodes platypus* in Alaska. This species has decreased substantially since the mid-1980, and despite fishery closures, abundance has not rebounded to previous levels. One of the findings of this study was comparison suggested that genetic diversity within each location had changed over time. This low genetic diversity was attributed to the smaller population size of blue king crab [11].

An introduced species for aquaculture and other purposes might result in low genetic diversity caused by the founder effect. One type of this, is the introduction of Manila clam in North America, Polynesia, the US Virgin Islands, and the Atlantic and Mediterranean coasts of Europe. The levels of genetic diversity within introduced populations were comparable to those described from native regions, suggesting that multiple introduction events and mixed source populations can counterbalance the loss of genetic diversity caused by the founder effect [26]. It clearly stated that over-exploitation of the macrozoobenthic might result in low genetic diversity. The effect of over-exploitation and low level of genetic diversity was observed in the surf clam *Paphia undulata* in Thailand waters. The findings suggest that over-exploitation and low levels of genetic variation of the surf clam population may be responsible for the low productivity. Besides, it also found out that the relatively low amount of genetic diversity of the Gulf of Thailand and the Andaman Sea stocks may reduce their ability to survive in a changing environment. Therefore, it suggested that there should be an immediate reduction of fishing efforts and initiation of restocking programs and aquaculture development of this species. These suggested conservation fishery measures should be considered in order to maintain the sustainability of the surf clam fishery [10]. The same experience was also happening in spiny lobster *Panulirus homarus* in the Indo-West

Pacific. This species supports a valuable capture fishery that resulted in a significant decline in many countries over recent times. Low levels of the genetic structure of *P. homarus* were observed within the Southeast Asian Archipelago, suggesting that this species is under intense fishing pressure and there is a declining annual catch. Thus, there is a need for several management units over the species distribution necessary to have better control for stocks of this species [9].

5. The implications of the single or panmictic population for coastal resource management

The panmictic population of most invertebrates indicates genetic homogeneity over a wide geographical range due to an extended pelagic larval stage in the water column for a long period of time. This observed in western rock lobster *Panulirus cygnus* in Western Australia, where a single population thrived in the whole western region. Since the species occupied a wide geographical range, an effort to conserve this species requires an interconnected effort of different regions. The conservation areas should be more prominent as it requires protecting the spawning ground and settlement to ensure higher survival [8]. It suggested that all management and conservation efforts on panmictic shovel-nosed lobster *Thenus unimaculatus* population in Indian waters must coordinate at the national level for the panmictic stock. This may be due to the planktonic phyllosoma larval phase that extends for >1 month in the wild and their transport and dispersal by monsoon currents of the northern Indian Ocean [7]. The panmictic population requires an interstate management strategy for the conservation measure. This was in the case of a genetically homogenous population of horseshoe crab *Limulus polyphemus*. The genetic data indicate that this species has no signs of inbreeding and substantially similar to other Mid-Atlantic populations [6]. Therefore, it recommended that part of the conservation strategy, multi-state management is needed for the Long Island Sound horseshoe crab population [6].

Another panmictic population observed was the population stock structure pattern of *Panulirus homarus* in southern Sri Lanka and south India that showed no significant genetic variation between these two populations. This species has a high potential for dispersal, suggesting that this species might have very little intra-specific population structuring over large geographic areas. These useful findings can use for management plans to develop sustainable mariculture of this species and conservation from over-exploitation [39]. A high genetic flow among the stock mostly resulted in a single and panmictic population. This is in the case of the sea cucumber *Holothuria parva* in the Persian Gulf, where the enclosed landlocked promotes a panmictic population that only requires a single management unit among regions within the gulf [27]. Long pelagic larval phase and high level of ongoing gene flow are just among attributable characteristics of shallow differentiation of wild population pearl oyster *Pinctada radiata* in Qatari territorial waters. This panmictic population should be considered to constitute a single management unit [5]. Knowledge of genetic connectivity among stocks is critical in determining the appropriate geographic units for fisheries management, including quotas, design of marine protected areas, and international relations related to the source of recruitment for fishery stocks in a complex geopolitical environment such as managing the panmictic population of queen conch in the Caribbean Sea [4]. The existence of connectivity among queen conch *Strombus gigas* populations in Northern Intra-American suggests a metapopulation structure with sources and sinks throughout the region, supported by larval transport via oceanographic features of the Intra-American Sea. A better understanding of the interaction and potential connectivity via larval transport among different populations would contribute to better management of the conch population. Numerous factors can influence the geographic population structure and dynamic, such as transport, settlement, and recruitment processes. Surveys of geographic genetic variation serve as a tool to indirectly assess larval dispersal [40]. Similar species showing a wide panmictic population was observed in the genetic analysis of tropical ornate spiny lobster *Panulirus ornatus* that showed no evidence for genetic differentiation among populations over the broad and oceanographically complex region spanning Australia, Papua New Guinea, Indonesia, and Vietnam. This a consequence of both the high dispersal potential of larvae, whereby they remain in the water column for periods of 4.5 to 7 months coupled with favorable seasonal currents that transport these larvae over long-distance between known adult spawning sites. The panmictic genetic population structure of *P. ornatus* throughout its Indo-Pacific distribution indicates that the species is a single stock requiring a single fishery management plan to ensure sustainable exploitation of this valuable resource. Consequently, multi-jurisdictional fishery policy should be developed by managers from Australia, Papua New Guinea, the Philippines, Vietnam, and Indonesia [9]. A recent study found a global homogeneity of the genetic structure in Pacific cupped oyster *Crassotrea gigas* at both the spatial and temporal scales. Multiple and repeated introduction, as well as individual introductions with extremely high propagule loads, increases the probability to reduce the founder effect. This might be the case for the Pacific oyster for which several repeated introductions from Canada and Japan of adults, but also high quantities of spat, happened by the end of the 1960s in Europe, especially in France and the Netherlands. This phenomenon led to a failure detection of genetic differences between Asian and European populations within the Pacific cupped oyster species [41]. High levels of gene flow were also reported in three squat lobster *Munida* species in the southwest Pacific Ocean, suggesting among population leading to panmixia or recent demographic expansion [37]. A fine-scale population genetic structure also shown by spiny lobster *Panulirus homarus* in the Western Indian Ocean. This is because the larval dispersion of spiny lobster was spent over four months floating in the ocean. Minimum sea surface temperature was correlated with genetic variability, suggesting ambient temperature and larval tolerance of spiny lobster as selective factors in dispersal success [33].

Marine macrozoobenthic invertebrates usually exhibit a fine-scale population structure due to its limited distance of larval dispersal. This is contrary to previous species that requires a wide range of hydro-geographical setting for conservation and protection purposes. The species that manifest the fine-scale population requires only small management areas. This is the case of blacklip abalone population, which shows panmictic across as much as 3-5 km. These findings will have important implications for current management and will inform the development of representative spatial management systems for the fishery [2]. Contrary to homogenization expectation, the pattern of isolation by distance was observed in this coral species, suggesting that dispersal distance of *Plectorhinchus flavomaculatus* is no more than 300 km. [42]. Silliman [43] reported a fine-scale structure of Olympia oyster *Ostrea lurida* from the west coast of North America. Geographical regions of reduced gene flow aligned with known marine biogeographic barriers, such as Cape Mendocino, Montery Bay, and the current around Cape Flattery are among the driving force that shapes the population structure of Olympia oyster in this region.

6. Conclusion

The population genetics examine species evolution through its adaptation, speciation, and population structure that implicates macrozoobenthic invertebrate population at the risk of extinction, endangered, over-exploitation, declining in number, and sustainable in status. These implications help policy makers formulate and conceptualize the conservation and protection platforms of the commercially important macrozoobenthic species that is under anthropogenic fishing pressures. Sampling strategy in revealing population genetics of extinct, endangered, and rare species does not compromise the well-being of each individual as it requires small piece of tissues as a sample. The data that could generate from population genetics gives more information about different aspects of scientific discipline. Different stakeholders (i.e., student, scientist, politician, businessman, professor, and many others) benefits from the small piece of tissue that gives the bulk of information derived from the post-glacial era to possible population expansion that recovered from the past bottleneck experience of a specific macrozoobenthic species.

Compliance with ethical standards

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The author declares no possible conflict of interest from any individual, party, or entity.

References

[1] Romain M, Gregory C, Pierre B, Laurent C, Florian B, Oivind S and Jean L. (2016). Genetic structure of a commercially exploited bivalve, the great scallop (*Pecten maximus*) along the European coasts. Conservation Genetics, 17(1), 57-67.

[2] Mundy C. (2013). Genetic population structure in greenlip abalone from SE Australia: implications for management of an important commercial fishery. Sardi Seminar Series.

[3] Hui M, Kraemer WE, Seidel C, Nuryanto A, Joshi A and Kochzius M. (2016). Comparative genetic population structure of three endangered giant clams (Cardiidae: Tridacna species) throughout the Indo-West Pacific: Implications for divergence, connectivity and conservation. Journal of Molluscan Studies, 82, 403-414.

[4] Banks MA, Minch JD and Stoner AW. (2014). Preliminary report on population genetic structuring among queen conch (*Strombus gigas*) from the Bahamas. Report to Community Conch.

[5] Al-Saadi A. (2013). Population structure and patterns of genetic variation in a pear oyster (*Pinctada radiata*) native to the Arabian Gulf. Queensland University of Technology, Brisbane, Australia.

[6] Kasinak JM, Bartholomew KA, Beekey M and Mattei J. (2010). Movement patterns and population genetic of the American horseshoe crab in relation to Long Island Sound conservation strategies. Biology Faculty Publication. Sacred Heart University, Fairfiled, USA.

[7] Jeena NS, Gopalakrishnan A, Kizhakudan JK, Radhakrishnan EV, Kumar R and Asokan PK. (2015). Population genetic structure of the shovel-nosed lobster (*Thenus unimaculatus*; Decapoda, Scyllaridae) in Indian waters based on RAPD and mitochondrial gene sequences. Hydrobiologia.

[8] Kennington WJ, Berry O, Groth DM, Johnson MS and Melville-Smith R. (2009). Evaluation of population structure in the western rock lobster. University of Western Australia.

[9] Dao HT. (2016). Recruitment and genetic population genetics of spiny lobster (*Panulirus ornatus* and *Panulirus homarus*) in the south-east Asian archipelago. Ph.D. Dissertation, James Cook University, Australia.

[10] Donrung P, Tunkijjanukij S, Jarayabhand P and Poompuang S. (2011). Spatial genetic structure of the surf clam (*Paphia undulata*) in Thailand waters. Zoological Studies, 50(2), 211-219.

[11] Stoutamore JL. (2014). Population genetics and mating structure of blue king crab (*Paralithodes platypus*). A Master of Science Thesis, University of Alaska, Fairbank.

[12] Lopez EH, Eastwood E and Drew J. (2017). Genetic connectivity among populations of lollyfish (*Holothuria atra*). In Mangubhai, S., Lalavanua, W., Purcell, S.W. (eds). Fiji's sea cucumber fishery: Advances in science for improved management. Wildlife Conservation Society. Report No. 01/17, Suva, Fiji, 62-70.

[13] Miller KJ, Maynard BT and Mundy CN. (2008). Genetic diversity and gene flow in collapsed and healthy abalone fisheries. Molecular Ecology.

[14] Otwoma LM and Kochzius M. (2016). Genetic population structure of the coral reef sea star (*Linckia laevigata*) in the Western Indian Ocean and Indo-West Pacific. PLoS ONE, 11(10).

[15] Miller KJ. (1997). Genetic structure of black coral population in New Zealand's fjords. Marine Ecology Progress Series, 161, 123-132.

[16] Arndt AD. (1996). Population diversity and molecular evolution of selected Eastern Pacific sea cucumber (Class: Holothuroidea) based on mitochondrial DNA. Simon Fraser University.

[17] Goodbody-Gringley G, Woollacott RM and Giribet G. (2011). Population structure and connectivity in the Atlantic scleractinian coral (*Montastraea cavernosa* Linnaeus, 1767). Marine Ecology, 1-17.

[18] Diniz FM, Maclean N, Ogawa M, Cintra IH and Bentzen P. (2005). The hypervariable domain of the mitochondrial control region in Atlantic spiny lobster and its potential as a marker for investigating phylogeographic structuring. Marine Biotechnology, 462-473.

[19] Tang S, Tassanakajon A, Klinbunga S, Jarayabhand P and Menesveta P. (2004). Population structure of tropical abalone (*Haliotis asinina*) in coastal waters of Thailand determined using microsatellite markers. Marine Biotechnology, 6, 604-611.

[20] Gutierrez-Gonzalez JL, Cruz P, Rio-Portilla MA and Perez-Enriquez R. (2007). Genetic structure of green abalone (*Haliotis fulgens*) population Off Baja California, Mexico. Journal of Shellfish Research, 26(3), 839-846.

[21] Kawane M and Wada K. (2015). Genetic population of the rare brackish-water crab (*Ptychognathus ishii*; Sakai, 1939) (Varunidae) on the Japanese coast. Japanese Journal of Benthology, 70, 13-20.

[22] Withler RE, Campbell A, Li S, Miller KM, Brouwer D and Lucas BG. (2001). High levels of genetic variation in Northern abalone (*Haliotis kamtschatkana*) of British Columbia. Canadian Science Advisory Secretariat.

[23] Skillings DJ, Bird CE and Toonon RJ. (2011). Gateways to Hawai'i: Genetic population structure of the tropical seacucumber (*Holothuria atra*). Journal of Marine Biology, 1-16.

[24] Coates JH, Hovel KA, Butler JL and Bohonak AJ. (2014). Recruitment and recovery of pink abalone (*Haliotis corrugata*) in a historically over-exploited kelp forest: Are local population self-sustaining? Journal of Experimental Marine Biology and Ecology, 400, 184-192.

[25] Maggi C and Gonzalez-Wanguemert M. (2015). Genetic differentiation among *Parastichopus regalis* population in the Western Mediterranean Sea: Potential effects from its fishery and current connectivity. Mediterranean Marine Science, 16(3), 489-501.

[26] Chiesa S, Lucentini L, Freitas R, Marzano FN, Breda S, Figuera E, Caill-Milly N, Herbert RJ, Soares AM and Argese E. (2016). Mapping the stranger: Genetic diversity of Manila clam in European coastal lagoons. Bulletin Japanese Fisheries Research Education, 42, 55-65.

[27] Ali-Abadi MA, Naysi LA, Zolgharnean H and Zanoosi HP. (2016). The study of population genetics structure of *Holothuria parva* in the Persian Gulf using mtDNA sequences. International Journal of Life Sciences Biotechnology and Pharma Research, 5(1), 14-17.

[28] De Noia M, Telesca L, Vendrami DLJ, Gokalp HK, Charrier G, Harper EM and Hoffman JI. (2020). Population genetic structure is unrelated to shell shape, thickness and organic content in European population of the soft-shell clam (*Mya arenaria*). Genes, 11, 298.

[29] Gallagher J, Finarelli JA, Jonasson JP and Carlsson J. (2018). Mitochondrial d-loop DNA analyses of Norway lobster (*Nephrops norvegicus*) reveals genetic isolation between Atlantic and Mediterranean population.

[30] Jenkins TL, Ellis CD, Triantafyllidis A and Stevens JR. (2019). Single nucleotide polymorphisms reveal a genetic cline across the north-east Atlantic and enable powerful population assignment in the European lobster. Evolutionary Applications, 12, 1881-1899.

[31] Xuereb A, Benestan L, Normandeau E, Daigle RM, Curtis JMR, Bernatchez L and Fortin MJ. (2018). Asymmetric oceanographic processes mediate connectivity and population genetic structure, as revealed by RADseq, in a highly dispersive marine invertebrate (*Parastichopus californicus*). Molecular Ecology, 27, 2347-2364.

[32] Nowland SJ, Silva CNS, Southgate PC and Strugnell JM. (2019). Mitochondrial and nuclear genetic analyses of the tropical black-lip rock oyster (*Saccostrea echinata*) reveals population subdivision and informs sustainable aquaculture development. BMC Genomics, 20, 711.

[33] Singh SP, Groeneveld JC, Hart-Davis MG, Backeberg BC and Willows-Munro S. (2018). Seascape genetics of the spiny lobster (*Panulirus homarus*) in the Western Indian Ocean: Understanding how oceanographic features shape the genetic structure of species with high larval dispersal potential. Ecology and Evolution, 8, 12221-12237.

[34] Wang YJ, Zeng QG and Xu LN. (2013). Population structure of the blood clam (*Tegillarca granosa*) in China based on microsatellite markers. Genetics and Molecular Research, 12(2), 892-900.

[35] Lau JS, Ransangan J and Rodrigues KF. (2018). Genetic diversity and population structure of the Asian green mussel (*Perna viridis*) in the water of Sabah, Malaysia based on mitochondrial DNA d-loop sequence. Turkish Journal of Fisheries and Aquatic Sciences, 18, 109-117.

[36] Zheng JH, Nie HT, Yang F and Yan XW. (2019). Genetic variation and population structure of different geographical populations of *Meretrix petechialis* based on mitochondrial gene COI. Journal of Genetics, 98, 68.

[37] Yan RJ, Schnabel KE, Rowden AA, Guo XZ and Gardner JPA. (2020). Population structure and genetic connectivity of squat lobster (*Munida* Leach, 1820) associated with vulnerable marine ecosystems in the Southwest Pacific Ocean. Frontiers in Marine Science, 6, 791.

[38] Hui M, Shi G, Sha Z, Liu Y and Cui Z. (2019). Genetic population structure in the swimming crab (*Portunus trituberculatus*) and its implications for fishery management. Journal of the Marine Biological Association of the United Kingdom, 99, 891-899.

[39] Senevirathna J and Munasinghe D. (2014). Genetic diversity and population structure of *Panulirus homarus* populations of Southern Sri Lanka and South India revealed by the mitochondrial COI gene region. International Conference on Food, Biological and Medical Sciences. Bangkok, Thailand.

[40] Morales F. (2004). Genetic signals of metapopulation structure of the queen conch (*Strombus gigas*) throughout Northern Intra-American Sea. 60thGulf and Caribbean Fisheries Institute.

[41] Lapégue S, Heurtebise S, Cornette F, Guichoux E and Gagnaire PA. (2020). Genetic characterization of cupped oyster resources in Europe using informative single nucleotide polymorphism (SNP) panels. Genes, 11, 451.

[42] Han ZQ, Li YZ, Chen GB and Gao TX. (2008). Population genetic structure of coral reef species *Plectorhinchus flavomaculatus* in South China Sea. African Journal of Biotechnology, 7(11), 1774-1781.

[43] Silliman K. (2019). Population structure, genetic connectivity, and adaptation in the Olympia oyster (*Ostrea lurida*) along the west coast of North America. Evolutionary Applications, 12, 923-939.

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