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Review Article

Molecular Insights into the Genetic Diversity of Marine Zooplankton

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ABSTRACT

Zooplankton are fundamental components of marine trophic networks and served as bioindicators of environmental changes. Assessing their genetic diversity is essential for biodiversity assessment, ecosystem monitoring, and evidence-based conservation strategies. The conventional morphological identification methods are limited in detecting cryptic species and lack phylogenetic resolution, necessitating the use of molecular approaches. Hence, this review synthesises the recent advancements in genomic tools for investigating marine zooplankton genetic variability, encompassing techniques such as DNA barcoding and metabarcoding, complete mitochondrial genome analysis, as well as environmental DNA profiling. We systematically evaluated the advantages of each method, the application of genetic markers, and their effectiveness in species identification, population genetics, and evolutionary studies. The genetic methods have greatly improved taxonomic resolution, revealed hidden biodiversity, and offered deeper insights into the population structure and community dynamics of marine zooplankton in response to human-induced pressures. Despite these achievements, several challenges persist, including incomplete genetic reference databases, sequencing errors, and the lack of standardised protocols. Accordingly, future research should prioritise the expansion of comprehensive genetic libraries, the refinement of bioinformatics pipelines, and the integration of multi-marker approaches to deepen our understanding of marine zooplankton genetic variation and ecological interactions. Continued improvement in these molecular methodologies will be important for the effective conservation of marine biodiversity, the mitigation of environmental fluctuation impacts, and the promotion of sustainable fisheries management.

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INTRODUCTION

The oceans and seas encompass over 70 % of the Earth's surface and harbour exceptionally high levels of biodiversity, with zooplankton representing a dominant component of pelagic ecosystems in terms of both abundance and biomass (Azam et al. 1983; Steinberg et al. 2008). Notably, the extensive swarms of Antarctic krill (*Euphausia superba*) in the Southern Ocean sustain complex marine food webs by supporting ecologically and economically important species, including baleen whales, penguins, and seals, thereby highlighting the vital ecological role of zooplankton on a global scale (Atkinson et al. 2004). Zooplankton comprise a taxonomically diverse assemblage, ranging from microscopic copepods to larger taxa, such as euphausiids, decapod larvae, and ichthyoplankton (Ward et al. 2012). As primary consumers, zooplankton mediate the transfer of energy from autotrophic phytoplankton to higher trophic levels, including fish, marine mammals, and seabirds (Putra et al. 2025) (Figure 1). Furthermore, zooplankton contribute significantly to biogeochemical cycling, particularly of carbon and nutrients through the biological pump mechanism. By producing and exporting organic particulate matter, zooplankton facilitate the sequestration of carbon into the deep ocean, thereby, playing a pivotal role in regulating global climate dynamics (Lindeque et al. 2013).

The genetic diversity within marine zooplankton populations is a critical factor in their ability to adapt and survive under environmental pressures (Möllmann et al. 2008). The genetic variation in DNA sequences also enables zooplankton's adaptive responses to ecological fluctuations, incorporating changes in sea temperature, salinity, food availability, as well as exposure to pathogens and pollutants (Bucklin et al. 2021a). The populations with low genetic diversity are more susceptible to extreme habitat dynamics, potentially destabilizing marine ecosystems as a whole (Lindeque et al. 2013). Therefore, understanding zooplankton genetic variability is integral not only for uncovering their evolutionary patterns but also for informing conservation efforts and the sustainable management of marine resources.

However, our understanding of zooplankton genetic variation remains limited, especially in terms of population differentiation across diverse geographical regions and habitats (McGinty & Irwin 2025). The global warming, microplastic pollution, various pollutants (heavy metals, pesticides, and other toxic chemicals), as well as overexploitation further exacerbate pressures on zooplankton populations, leading to significant shifts in community structure (Möllmann et al. 2008). As a result, more precise methods are needed to monitor and to analyse their genetic dynamics (Lenz et al. 2021). In this context, the molecular investigations, using techniques such as DNA barcoding and metabarcoding have become invaluable tools for species identification and the analysis of genetic variation among individuals, revealing details that are usually inaccessible through traditional morphological methods (Lindeque et al. 2013). These approaches also offer deeper elucidation of phylogenetic relationships, geographical distribution, as well as potential adaptation and speciation processes in marine zooplankton (Filatov et al. 2021; Filatov 2023).

With advancements in molecular technologies, our interpretation of zooplankton genetic diversity can be significantly enhanced, enabling crucial insights into the impacts of anthropogenic activities on marine ecosystems. Thus, this scientific article aims to present a inclusive review of the application of molecular methods in marine zooplankton genetic variability studies. It focuses on the latest molecular techniques for identifying and analysing genetic variation, as well as their implications for the management of marine fisheries resources. In addition, this review highlights key challenges in marine zooplankton genetic research and proposes recommendations for future investigations. By advancing our knowledge of genetic diversity through genomic approaches, more effective and sustainable conservation strategies and marine ecosystem management practices can be developed and implemented.

Figure 1. The Census of Marine Zooplankton hosts an online gallery showcasing visuals of various zooplankton species (available at http://www.cmarz.org/galleries.html). The photographic records were contributed by R.R. Hopcroft and C. Clarke (University of Alaska Fairbanks) and L.P. Madin (Woods Hole Oceanographic Institution). These illustrations were subsequently compiled and visually integrated into a representative figure by the first author (A.P.).

MOLECULAR MARKERS AND DNA-BASED APPROACHES IN MARINE ZOOPLANKTON RESEARCH

Molecular markers

The molecular markers have become indispensable tools in marine zooplankton genetic research, enabling accurate species identification and providing perspectives into phylogenetic relationships, population connectivity, and evolutionary dynamics (González et al. 2020). Derived primarily from DNA sequences, commonly used markers include mitochondrial genes (e.g., COI), nuclear ribosomal genes (e.g., 18S, 28S rRNA), internal transcribed spacers (ITS), and non-coding regions such as microsatellites (Parent et al. 2012; Bucklin et al. 2016). Notably, the COI region is widely applied in DNA barcoding due to its high interspecific variability and low intraspecific variation, facilitating discrimination of morphologically similar taxa (Hebert et al. 2003). Its integration into global databases like BOLD and GenBank enhances cross-taxon comparisons and facilitates the detection of cryptic species (Blanco-Bercial et al. 2011a; Cornils et al. 2017; Porter & Hajibabaei 2018). Although nuclear genes evolve more slowly than mitochondrial genes, they provide a more reliable signal for reconstructing deeper phylogenetic relationships among marine zooplankton clades (Bucklin et al. 2003; Di Capua et al. 2017). Conversely, microsatellites, characterized by high allelic diversity and codominant inheritance, are particularly suited for fine-scale genetic analyses and enable evaluations of gene flow, mating systems, heterozygosity, and demographic structure (Weydmann et al. 2014; Goetze et al. 2015).

Genomic strategies in marine zooplankton investigation

The molecular techniques offer substantial advantages over conventional morphology-based methods in marine zooplankton genetic diversity and ecological studies, primarily by providing enhanced taxonomic resolution and reliable species identification, including for cryptic taxa (Bucklin et al. 2022). These DNA-based approaches reduce subjective biases inherent in morphological identifications and facilitate detection of rare or minute species often overlooked by traditional methods. Among these, the DNA barcoding utilises standardised short genetic markers, typically mitochondrial COI, to identify individual species, whereas DNA metabarcoding analyses mixed DNA from bulk organism samples to characterise entire community compositions. The environmental DNA (eDNA) metabarcoding extends this capability by extracting DNA directly from biospheric matrices such as seawater, empowering non-invasive detection of elusive species without physical specimen collection (Djurhuus et al. 2018; Carroll et al. 2019) (Figure 2).

The application of molecular tools in marine zooplankton research has revealed extensive phylogenetic, taxonomic, and functional diversity, encompassing at least 15 phyla and 41 functional groups, including both holoplankton and meroplankton (Bucklin et al. 2021b). The significant efforts to barcode key taxa such as Copepoda have yielded extensive COI sequence libraries, although geographic and taxonomic gaps remain (Weydmann et al. 2017; Figure 3). Beyond Copepoda, the DNA barcoding has been successfully applied to other major marine zooplankton taxa, including Cnidaria, Ctenophora, Amphipoda, Euphausiacea, Gastropoda, Chaetognatha, and pelagic Tunicata (O'Brien et al. 2024). The representative case studies illustrated the effectiveness of these molecular methods across diverse marine regions with DNA barcoding characterised zooplankton diversity in the Gulf of Alaska (Questel et al. 2025), eDNA metabarcoding elucidated community composition in the Ulleung Basin (Choi et al. 2024), and DNA metabarcoding demonstrated complex assemblages along the South African coast (Singh et al. 2021; Huggett et al. 2022).

At the population genetic level, the molecular markers such as microsatellites and single nucleotide polymorphisms (SNPs) provide insights into genetic structure, gene flow, and microevolutionary dynamics (e.g., genetic drift, natural selection, and local adaptation) within the marine zooplankton species (Bucklin et al. 2018). High-throughput sequencing techniques such as RNA-Seq, have produced extensive SNP datasets with over 110,000 SNPs have been identified and validated in *Calanus sinicus*, enabling more precise population genetic analyses (Yang et al. 2014). Furthermore, the SNP-based investigations have also resolved previous uncertainties from microsatellite-based hybridisation studies among *Calanus* species, confirming the genetic distinctness of *C. finmarchicus* and *C. glacialis* and highlighting the limitations of microsatellite markers (Choquet et al. 2023). Despite their utility, the molecular methods face challenges, including PCR and primer biases that can skew community composition estimates by preferentially amplifying certain taxa (Elbrecht & Leese 2015; Goldberg et al. 2015), as well as issues of DNA degradation and potential false positives in eDNA samples (Takahashi et al. 2023; Wang et al. 2023). The taxonomic resolution is further constrained by incomplete reference databases, especially in underexplored marine regions (Weigand et al. 2019). The complementary quantitative approaches such as qPCR and digital droplet PCR (ddPCR) also offer high-precision detection and quantification, valuable for monitoring invasive species and environmental changes (Wood et al. 2019).

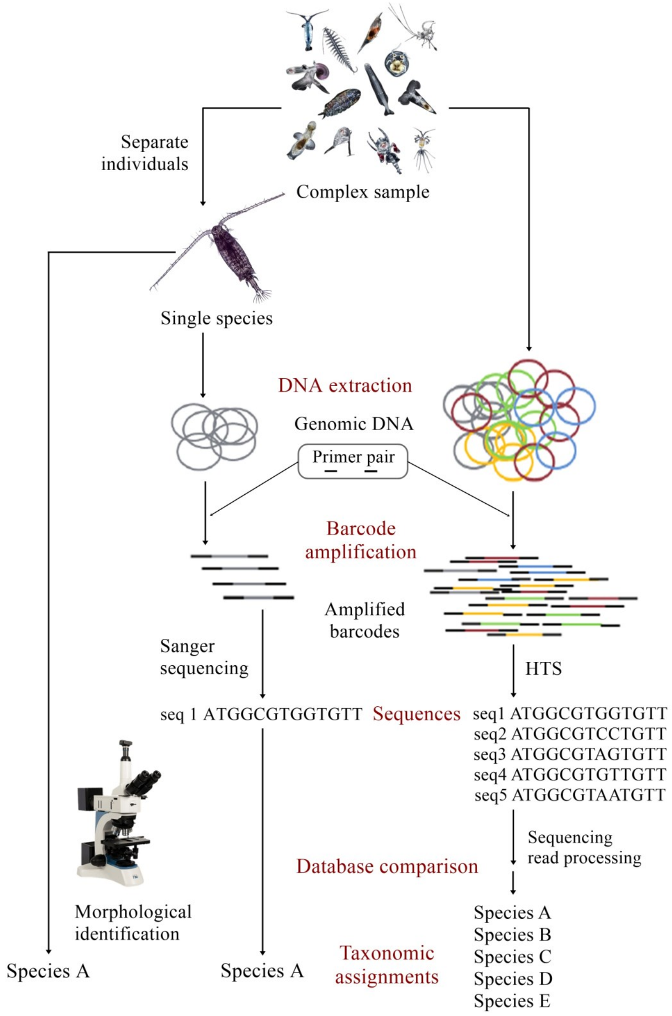

Figure 2. The schematic representation of marine zooplankton sample taxonomy analysis using morphological identification (left arrow), barcoding (middle arrow), or metabarcoding (right arrow). The colored circles represent extracted genomic DNA, consisting of identical copies of the genome (barcoding) or multiple copies of genomes from the species present in the sample (metabarcoding). The amplified products are identical in barcoding, while metabarcoding produces a mixture of amplified products from different genomes. After sequencing the amplification products, taxonomic assignment is made by comparing the obtained sequences with reference databases. The figure was modified by the first author (A.P.) based on studies by Corell and Rodríguez-Ezpeleta (2014) and Bucklin et al. (2016). The complex sample image was sourced from Peijnenburg and Goetze (2013), and the Copepoda image was obtained from micromagus.net.

PATTERNS OF GENETIC DIVERSITY AND PHYLOGEOGRAPHY IN MARINE ZOOPLANKTON

The genetic diversity serves as the foundation for evolutionary potential, ecological adaptability, and long-term population viability in marine zooplankton. This diversity is expressed at multiple hierarchical levels, most notably within species (intraspecific variation) and across geographic ranges (phylogeographic structure). Both are shaped by a combination of environmental pressures and intrinsic biological traits. Notably, the intraspecific genetic variation denotes the extent of genetic differentiation among individuals or subpopulations within a species, primarily driven by mutation, gene flow, and genetic drift (Agashe 2009; Peijnenburg & Goetze 2013). Such variation is crucial for maintaining population resilience and adaptive capacity under fluctuating environmental conditions. It enables species to occupy diverse ecological niches and to maintain ecological functions under stress (de Bruin et al. 2024). Specifically, the copepod populations from distinct habitats, such

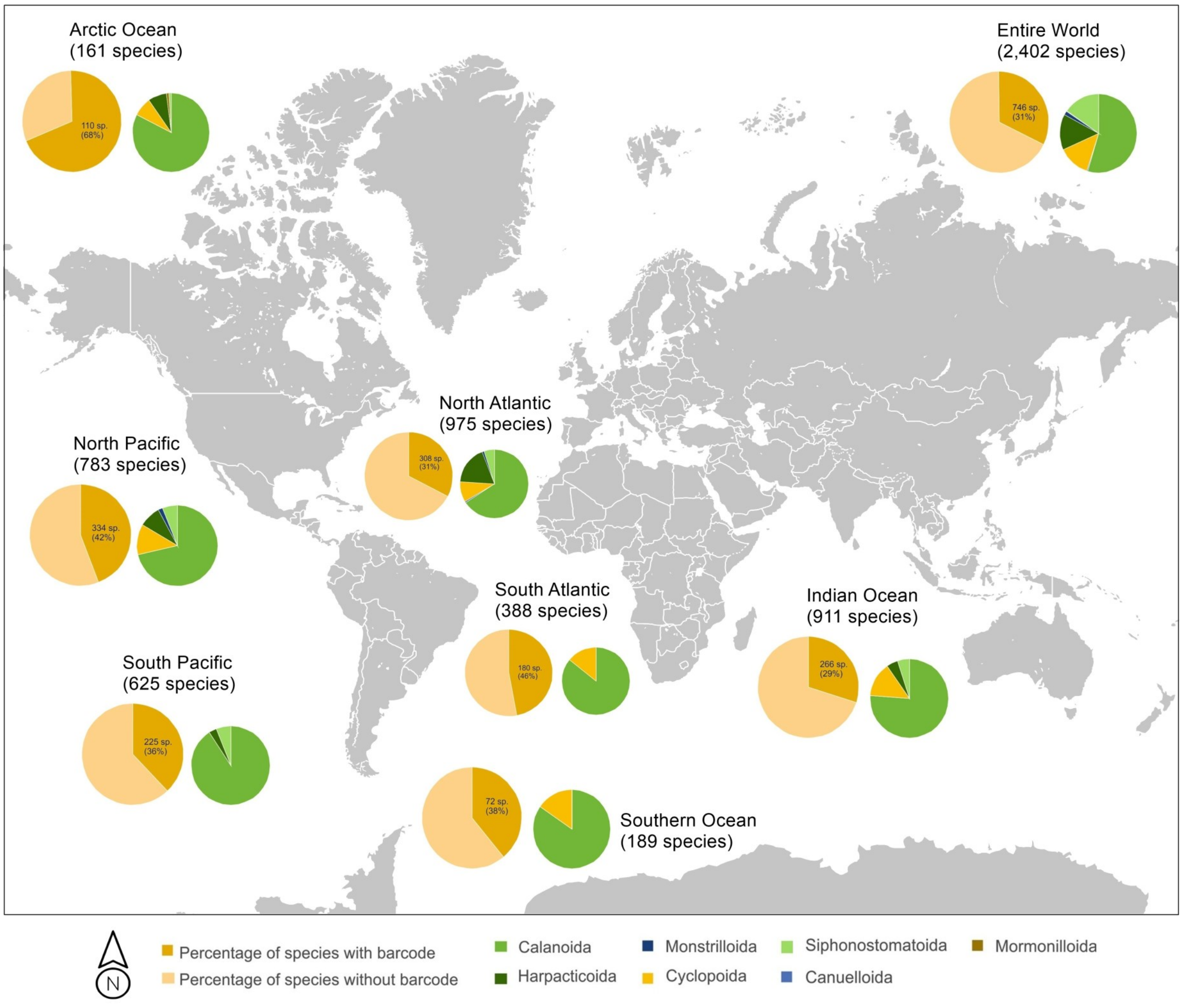

Figure 3. The global distribution of Copepoda with and without COI barcode across various oceanic regions. The recent data indicates that there are currently 12,155 sequences for 752 copepod species, representing approximately 31 % of the total 2402 valid species. The highest number of species is found in the North Atlantic (975 species), Indian Ocean (911 species), and the North and South Pacific (783 and 625 species, respectively), while fewer species are recorded in the South Atlantic (388 species), Southern Ocean (189 species), and Arctic (161 species). The figure was modified by the first author (A.P.) based on Bucklin et al. (2021b).

as estuarine, neritic, and oceanic zones often exhibit localized genetic structuring in response to environmental gradients (Unal & Bucklin 2010; Bashevkin et al. 2020). These patterns suggest that microevolutionary processes contribute significantly to population differentiation, even in highly dispersive marine taxa.

Extending beyond local variation, the phylogeographic structure reflects genetic divergence among marine zooplankton populations separated by geographical or oceanographic barriers. The physical discontinuities, such as current systems, thermal fronts, or bathymetric features can restrict dispersal and limit gene flow, leading to population subdivision over evolutionary timescales (Blanco-Bercial & Bucklin 2016; Bucklin et al. 2021a). The regional adaptation further reinforces this divergence, as populations become genetically fine-tuned to distinct environmental regimes (Gluchowska et al. 2017). Insights from phylogeographic studies have elucidated historical dispersal routes and delineated biogeographic boundaries among marine zooplankton populations. Moreover, these studies have contributed to the development of predictive frameworks for assessing species responses to large-scale environmental perturbations, such as ocean warming, deoxygenation, and acidification (Putra et al. 2025). Building upon these findings, the spatial and temporal dynamics of marine zooplankton genetic diversity are further shaped by a complex interplay of abiotic and biotic determinants (Botterell et al. 2023). Among abiotic factors, temperature and salinity are particularly influential, as they regulate key physiological processes, including metabolism, fecundity, and larval development (Dam 2013; McGinty et al. 2021; Putra 2025). The thermal gradients can impose intense selective pressures, fostering local adaptation in some populations while contributing to genetic erosion in others (Gluchowska et al. 2017). Similarly, the salinity fluctuations in transitional environments such as estuaries frequently promote genomic divergence between marine and brackish-adapted lineages. In parallel, the life-history of marine zooplankton traits play a pivotal role in modulating the rate and extent of genetic differentiation. The species characterised by rapid generation turnover and high fecundity generally maintains greater levels of genetic variability, enhancing their evolutionary potential. Conversely, the taxa with longer generation times or low reproductive output may be more vulnerable to stochastic genetic drift and demographic bottlenecks, particularly in fragmented or stressed habitats (Spitze 1995; Litchman et al. 2013; Chust et al. 2016). Collectively, these interacting factors influence the persistence, structure, and evolutionary trajectory of genetic diversity across marine zooplankton assemblages.

MOLECULAR PERSPECTIVES ON MARINE ZOOPLANKTON EVOLUTION

While the preceding section examined spatial patterns and ecological drivers of genetic diversity, the molecular approaches provide essential insights into the evolutionary history and adaptive potential of marine zooplankton (Bucklin et al. 2021a). Advances in molecular systematics and population genomics have facilitated precise reconstructions of lineage divergence, post-glacial recolonisation pathways, and microevolutionary responses to environmental pressures. These molecular data have revolutionised understanding of marine zooplankton evolution by enabling fine-scale resolution of phylogenetic relationships and historical population dynamics (Bucklin et al. 2018). Notably, the phylogeographic analyses utilising mitochondrial and nuclear DNA sequences have revealed significant genetic discontinuities across geographic regions, reflecting historical isolation, dispersal barriers, and climate-driven range shifts (Caudill & Bucklin 2004; Bucklin et al. 2022). Such studies have clarified post-glacial colonisation routes, vicariance patterns, and cryptic speciation within morphologically indistinct taxa (Millette et al. 2011; Stepien et al. 2024).

The molecular markers, particularly the mitochondrial COI gene, have been instrumental in delineating evolutionary lineages and resolving taxonomic uncertainties among diverse marine zooplankton taxa (Machida et al. 2021). Moreover, the multilocus sequence data and emerging phylogenomic methods provide comprehensive frameworks for interpreting diversification tempo and mode in the context of paleoceanographic fluctuations. These molecular reconstructions enable mapping of evolutionary trajectories and assessment of past environmental impacts on current genetic structure (Blanco-Bercial et al. 2011b; El-Khodary et al. 2020). Beyond historical reassessments, the genetic tools illuminate mechanisms of adaptive evolution in marine zooplankton. These include selective pressures, such as thermal stress, salinity variation, and trophic shifts drive genomic changes (Dam 2013). The recent high-resolution genomic studies employing SNP markers and transcriptomic analyses have identified loci linked to physiological tolerance and ecological performance (Bucklin et al. 2018; Trubovitz et al. 2020). These findings demonstrate rapid adaptive shifts mediated by selection on genes associated with stress response, reproduction, and metabolic regulation (Johnston et al. 2022; Zhao et al. 2023). Remarkably, populations in high-salinity or thermally variable environments often exhibit unique allelic variants or differential gene expression that enhance fitness under extreme conditions. This molecular evidence underscores the critical role of microevolutionary processes in sustaining population viability amid accelerating climate change. Hence, integrating genetics and environmental genomics provides a robust framework for evaluating marine zooplankton resilience, elucidating the molecular basis of adaptation and the adaptive potential of populations facing unprecedented environmental changes.

GENETIC CONNECTIVITY AND DISPERSAL DYNAMICS IN MARINE ZOOPLANKTON

Gene flow and dispersal mechanisms

The genetic connectivity is fundamental to the population dynamics and evolutionary processes of marine zooplankton (Cowen et al. 2007). Dispersal, largely driven by ocean currents and modulated by species-specific biological traits, shapes gene flow and population structure (Treml et al. 2008). The molecular evidence shows that allele distributions align closely with oceanographic variables, such as current patterns, temperature, and salinity, which can restrict gene flow and promote local adaptation and population differentiation (Filatov 2023; Peluso et al. 2024). The speciation in marine zooplankton often occurs sympatrically, driven by ecological niche specialization rather than geographic isolation, as demonstrated by integrative genomic and evolutionary analyses (Norris & Hull 2012; Filatov et al. 2021). Moreover, zooplankton dispersal is strongly influenced by life history characteristics, particularly during vulnerable larval stages (Chust et al. 2016; de Bruin et al. 2024). The ontogenetic vertical migration, where different life stages occupy distinct depth layers modulates interaction with stratified ocean currents, affecting dispersal trajectories and connectivity (Kobari & Ikeda 2001; Bandara et al. 2021). The daily vertical migration also impacts spatial distribution and genetic exchange by shifting populations between surface and deeper waters to balance feeding and predator avoidance (Bandara et al. 2021). The larval duration correlates positively with dispersal potential, as species exhibiting extended larval phases tend to possess more genetically homogeneous populations owing to broader gene flow, whereas shorter larval stages result in more localised genetic structuring (Modica et al. 2017; Bashevkin et al. 2020). The reproductive strategies further influence connectivity, with broadcast spawners facilitating extensive gene flow through planktonic gamete dispersal, while the brooding species typically show reduced connectivity and greater population differentiation (Riginos et al. 2014). The recent advances in high-throughput genomic sequencing and eDNA analyses have enhanced resolution in detecting these connectivity patterns and dispersal dynamics over large spatial scales (Yan et al. 2023; Rawoot et al. 2024).

Mitochondrial genome contributions to connectivity and dispersal in marine zooplankton

The mitogenome is extensively used to assess zooplankton connectivity due to its maternal inheritance, lack of recombination, and relative stability, making it a robust marker for population structure and dispersal analyses (Avise 1989; Havird et al. 2016; Fields et al. 2018). The next-generation sequencing (NGS) technologies have improved mitogenome resolution, allowing detailed reconstructions of zooplankton population history and migration patterns beyond classic mitochondrial markers (Cowen & Sponaugle 2009; Bucklin et al. 2018). The animal mitogenomes typically comprise 37 genes, including ribosomal RNAs, transfer RNAs, and protein-coding genes, with marine zooplankton exhibiting considerable intra- and interspecific variability within their mitogenomes (Boore 1999). Despite the ecological significance of many marine zooplankton species, the comprehensive mitogenome assemblies remain limited, with several notable taxa sequenced and additional data pending characterization (Genome 10K Community of Scientists 2009; GIGA Community of Scientists 2014). The relatively slower accumulation of mitogenomic data in marine zooplankton compared to vertebrates highlights the need for expanded sequencing efforts (Table 1).

Table 1. Mitochondrial genomes of marine zooplankton species and their corresponding lengths.

Taxon and species	Length (bp)	Reference
Copepoda		
Calanus finmarchicus	>29,462	Weydmann et al. 2017
Calanus glacialis	>27,342	Weydmann et al. 2017
Calanus hyperboreus	17,910	Kim et al. 2013
Calanus sinicus	>20,460	Minxiao et al. 2011
Paracyclopina nana	15,981	Ki et al. 2009
Tigriopus californicus	14,600	Burton et al. 2007
Tigriopus japonicus	14,628	Machida et al. 2002
Tigriopus sp.	14,301	Jung et al. 2006
Euphausiacea		
Euphausia pacifica	16,898	Shen et al. 2011
Euphausia superba	>15,498	Shen et al. 2010
Ostracoda		
Vargula hilgendorfii	15,923	Ogoh & Ohmiya 2004
Amphipoda		
Onisimus nanseni	14,734	Ki et al. 2010
Decapoda		
Acetes chinensis	15,740	Kim et al. 2012
Cnidaria		
Aurelia aurita	16,937	Shao et al. 2006
Cassiopea frondosa	15,949	Kayal et al. 2011
Chrysaora quinquecirrha	16,775	Hwang et al. 2014
Ctenophora		
Mnemiopsis leidyi	10,000	Pett et al. 2011
Pleurobrachia bachei	11,016	Kohn et al. 2012
Chaetognatha		
Sagitta decipiens	11,121	Miyamoto et al. 2010
Sagitta enflata	12,631	Miyamoto et al. 2010
Sagitta ferox	12,153	Li et al. 2016
Sagitta nagae	11,459	Miyamoto et al. 2010
Paraspadella gotoi	11,423	Helfenbein et al. 2004
Pterosagitta draco	10,426	Wei et al. 2016
Spadella cephaloptera	11,905	Papillon et al. 2004

Role of metagenomics in understanding zooplankton diversity

The metagenomics, involving the direct sequencing of genetic material from environmental samples, has become a powerful method to characterise marine zooplankton diversity without isolating individual organisms (Monchamp et al. 2022). Unlike PCR-based metabarcoding, which targets specific genetic markers (e.g., mitochondrial COI, nuclear 18S rRNA) through amplification, the metagenomics employs untargeted shotgun sequencing, capturing the entire genomic content and thus avoiding primer bias and amplification errors (Tringe & Rubin 2005; Singer et al. 2020). Initially developed for microbial community analysis in aquatic ecosystems, the metagenomics is increasingly applied to eukaryotes, including zooplankton (Grossart et al. 2020). This approach enables comprehensive taxonomic and functional profiling, improving detection of rare, cryptic, and novel taxa beyond the capabilities of metabarcoding (Tang et al. 2015). From a population connectivity perspective, the metagenomics provides high-resolution insights into gene flow and genetic structure within zooplankton communities (Song et al. 2021). When combined with oceanographic models and eDNA analyses, it facilitates the elucidation of dispersal patterns and real-time monitoring of community genetic dynamics (Monchamp et al. 2022). Thus, the metagenomics represents a transformative tool for assessing marine biodiversity and sustainably managing its ecosystems (Di Capua et al. 2024).

ANTHROPOGENIC IMPACT ON MARINE ZOOPLANKTON GENETIC DIVERSITY

The anthropogenic activities, primarily fossil fuel combustion and deforestation, are the main drivers of current climate change, exceeding the influence of natural factors (National Academy of Sciences 2020). Rising sea temperatures caused by global warming affect zooplankton distribution, population dynamics, and genetic connectivity (Viitasalo & Bonsdorff 2022; Ratnarajah et al. 2023). Elevated temperatures accelerate metabolism, alter life history traits, and shift spawning phenology, thereby modifying genetic structures over time (Bashevkin et al. 2020). Concurrent ocean acidification, resulting from increased atmospheric CO_2, impairs larval survival, particularly in calcifying taxa such as pteropods, reducing genetic diversity by increasing mortality and selection pressure (Putra et al. 2025). Additionally, altered ocean circulation and enhanced stratification fragment populations, limiting gene flow and promoting genetic isolation (Treml et al. 2008). Collectively, these factors could disrupt evolutionary trajectories and constrain the adaptive capacity of marine zooplankton (Johnson et al. 2022) (Figure 4).

Furthermore, the marine pollution from industrial, agricultural, and domestic sources significantly threatens zooplankton genetic diversity (Botterell et al. 2023). The microplastics, prevalent throughout oceans, are ingested by zooplankton, imposing selective pressures that can alter gene expression and diminish genetic variability (Cole et al. 2013). Notably, metagenomic and eDNA-based approaches have revealed shifts in zooplankton community composition and function linked to microplastic exposure, suggesting ecosystem-level genetic restructuring (Ali et al. 2025). The chemical contaminants, such as heavy metals, pesticides, and persistent organic pollutants bioaccumulate in marine zooplankton, causing DNA damage and mutagenesis, which reduce genetic diversity through strong environmental selection (van Straalen & Timmermans 2002; Goswami et al. 2014). This genetic erosion undermines population resilience and adaptability, threatening marine ecosystem stability (Belfiore & Anderson 2002). Additionally, overfishing disrupts trophic interactions by depleting predator populations, which can lead to marine zooplankton population outbreaks and decreased genetic diversity due to dominance by fewer species (Möllmann et al. 2008; Vereshchaka 2024). Human-induced habitat degradation, including coastal reclamation, eutrophication, coral reef destruction, and seagrass loss reduces spawning and nursery grounds critical for zooplankton reproduction and development (Song et al. 2021). Such habitat loss induces genetic bottlenecks and fragmentation, restricting gene flow and increasing population isolation (Li & Roossinck 2004; Botterell et al. 2023). Consequently, reduced genetic connectivity impairs adaptive capacity, escalating vulnerability to environmental changes and destabilizing marine ecosystems (Ezard & Travis 2006) (Figure 4).

CHALLENGES AND RESEARCH OUTLOOK

The molecular analyses have provided valuable insights into the marine zooplankton genetic diversity, yet several technical and logistical challenges continue to affect data quality and reliability. Importantly, sampling in dynamic ocean environments requires meticulous planning to capture spatial and temporal variability, as zooplankton communities fluctuate across depths and seasons, complicating representative sampling. The morphological similarity among co-occurring species hinders individual separation for sequencing, alt-

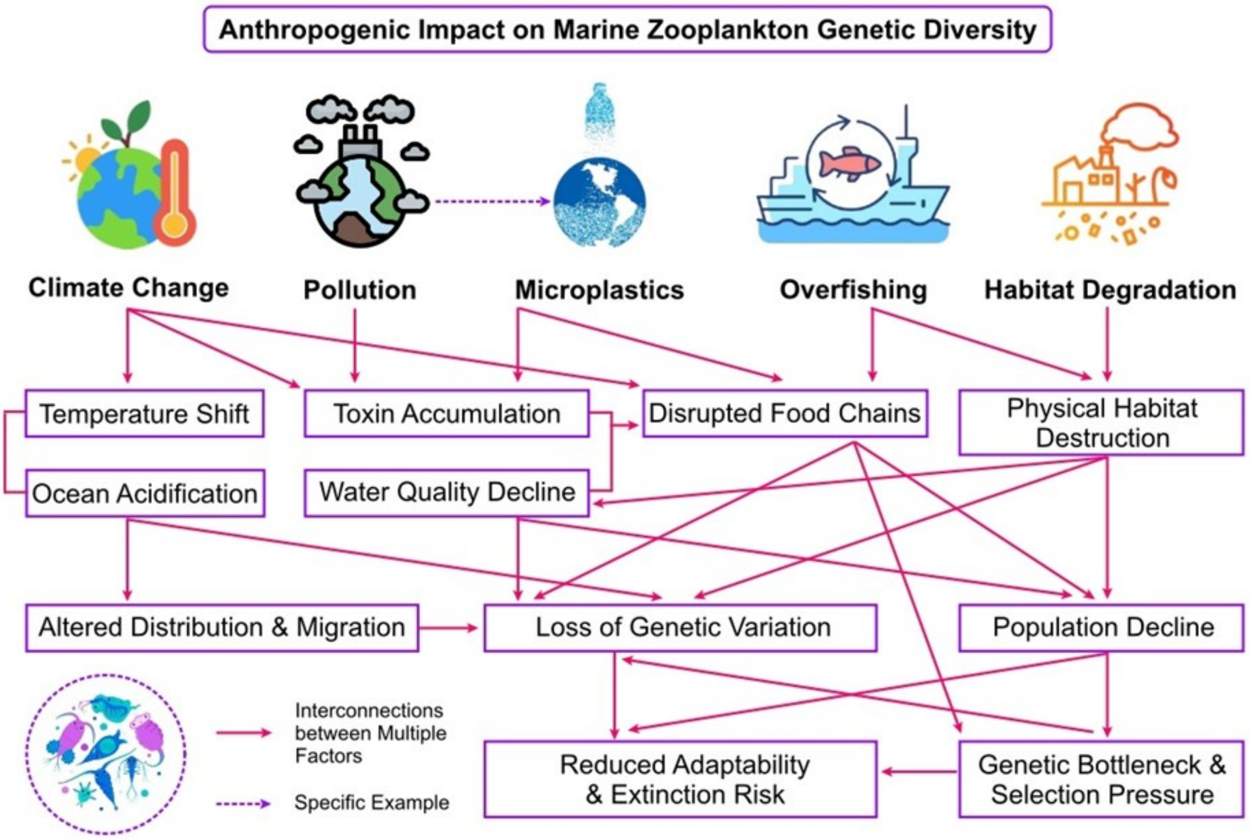

Figure 4. This diagram illustrates the interconnected relationships between various factors influencing the genetic diversity of marine zooplankton. The environmental changes driven by anthropogenic activities, such as climate change, pollution, overfishing, and habitat degradation, can result in significant ecological disturbances. The disruptions in the food chain, increased selective pressures, and declining zooplankton populations can reduce genetic variation, heighten extinction risks, and diminish the adaptive capacity of marine ecosystems to global changes. The illustration was constructed by the first author (A.P.).

hough metabarcoding and metagenomics offer promising alternatives constrained by incomplete reference databases, particularly in understudied regions like the Southern Hemisphere. Risks of contamination from microorganisms and phytoplankton further complicate molecular analyses, necessitating rigorous sample preparation and sequence quality control. Moreover, the high costs and infrastructure demands of NGS restrict accessibility, especially in resource-limited settings. The standardisation of bioinformatics workflows remains critical to ensure reproducibility and integration of data across studies and laboratories. Despite advances in monitoring marine ecosystem responses, zooplankton molecular data have yet to be fully integrated into conservation policies, highlighting the need for effective zooplankton indicators to support biodiversity goals and adaptive management.

Looking forward, the future research must address these challenges by expanding global reference libraries such as comprehensive COI databases, supported by sustainable taxonomic verification and voucher specimen management. Integrating genetic data with ecological and functional traits will deepen understanding of zooplankton population structure, connectivity, and adaptation to environmental drivers like temperature and salinity. Advances in metagenomics, mitogenomics, and affordable NGS technologies promise broader and more detailed analyses, especially in developing countries. Field-deployable tools for real-time genetic monitoring will enhance responsiveness to climatic shifts and biodiversity changes. The multidisciplinary collaboration across genetics, ecology, oceanography, and bioinformatics, combined with artificial intelligence applications, will improve data accuracy, reduce analytical bias, and refine models of marine zooplankton distribution and adaptation. This integrated approach will be pivotal for effective marine ecosystem monitoring and sustainable fisheries management.

CONCLUSION

The genomic tools have substantially advanced the study of marine zooplankton by enabling accurate species identification, uncovering cryptic diversity, and providing high-resolution insights into biodiversity patterns, population connectivity, and genetic responses to environmental change. These molecular approaches also support long-term monitoring of zooplankton populations and enhance understanding of their ecological and biogeographic dynamics. Integrating genetic data is essential for evidence-based ocean management, facilitating biodiversity assessment, ecosystem response prediction, and conservation consistent with sustainable resource use. The genetic information is particularly valuable for anticipating the impacts of climate change and environmental degradation on marine ecosystems. Despite these advances, key challenges persist, including limited sampling representativeness, incomplete reference databases, and the lack of standardized, reproducible bioinformatics pipelines. Open-access repositories such as BOLD and GenBank serve as key infrastructures, with continuous expansion and curation being crucial for the progress of molecular biodiversity research. Nevertheless, the ecological relevance of genetic variation in marine zooplankton remains poorly resolved. Thus, a multidisciplinary framework integrating genetic, ecological, and evolutionary perspectives is therefore required to elucidate zooplankton functional roles in ocean ecosystems. Emerging technologies, including mitogenomics, metagenomics, and artificial intelligence, hold promise for revealing the functional diversity and adaptive mechanisms that underpin marine zooplankton responses to environmental change.

AUTHORS CONTRIBUTION

A.P. and S.A.: Conceptualisation, methodology, resources, investigation, data curation, formal analysis, validation, visualisation, writing – original draft, review & editing. I.N.S.: Methodology, validation, supervision, writing – review & editing. Ilham, F.H., and M.H.R.A.: Methodology, resources, data curation, formal analysis. A.L., H.T., Rina, M.Mulyono, T.Y., M.Maulita, Y.N., I.J.P.D., S.R., and S.P.S.: Resources, investigation, data curation, validation. Hamdani, M.Ariana, T.H.R., L.A.J.Q., A.R.A., C.M., and M.A.H.J.: Resources, investigation, funding acquisition. M.Azril, Hawati, and M.M.M.: Resources, investigation, validation. The authors have read and approved the final version of the manuscript for publication.

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CONFLICT OF INTEREST

The authors declare that there are no financial or non-financial conflicts of interest that could have influenced the results of this study.

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