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Marine Biogeography of Prokaryotic and Eukaryotic Plankton: Patterns and Processes

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Abstract

Marine plankton—microscopic organisms drifting in the ocean—form the foundation of aquatic food webs and drive global biogeochemical cycles. These communities include both prokaryotic plankton (bacteria and archaea) and eukaryotic plankton (protists, microalgae, and small metazoans). Despite their microscopic size, plankton exhibit distinct biogeographic patterns shaped by environmental gradients, ocean currents, and evolutionary history. Understanding these patterns is essential for predicting ecosystem responses to climate change, nutrient shifts, and anthropogenic pressures.

Keywords: Medicinal plants; Marine Biogeography

Introduction

This article explores the biogeography of marine plankton, comparing the distributional trends and ecological drivers of prokaryotic and eukaryotic communities across oceanic realms. These organisms are not randomly distributed. Instead, their diversity and abundance vary with latitude, depth, temperature, nutrient availability, and hydrodynamic features such as gyres and upwelling zones[1].

Plankton communities follow latitudinal diversity gradients, with higher species richness in tropical and subtropical regions. However, this pattern is more pronounced in eukaryotic plankton than in prokaryotes. Vertical zonation also plays a role. The epipelagic zone (0–200 m) supports photosynthetic plankton, while deeper zones (mesopelagic to bathypelagic) host heterotrophic

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and chemoautotrophic microbes adapted to low light and high pressure [2].

These drivers interact to produce complex spatial patterns, including distance-decay relationships and latitudinal asymmetries. Prokaryotic plankton often exhibit cosmopolitan distributions, with similar taxa found across vast oceanic regions. However, finer-scale analyses reveal biogeographic structuring based on functional traits and ecological niches [3].

Eukaryotic plankton, by contrast, display stronger biogeographic boundaries due to larger genome sizes, slower reproduction, and greater sensitivity to environmental change. Metazoan mesoplankton (e.g., copepods, mollusks) show clear latitudinal and seasonal patterns. Association networks reveal ecological linkages among bacteria, archaea, and protists, suggesting co-evolution and functional interdependence [4].

Biogeographic studies rely on molecular tools such as 16S and 18S rRNA gene sequencing, metagenomics, and single-cell genomics. Marine plankton exhibit rich and dynamic biogeographic patterns shaped by environmental gradients, ecological processes, and evolutionary history. While prokaryotic plankton often show broad distributions, eukaryotic communities are more constrained by geography and environmental variability[5].

Conclusion

Monitoring plankton biogeography provides early indicators of ecosystem change and helps refine climate models. Understanding their biogeography informs conservation, fisheries management, and biogeochemical modeling. Integrating molecular tools, ecological theory, and oceanographic data is essential for mapping these patterns and predicting future changes. As climate and human pressures intensify, plankton biogeography will remain a vital frontier in marine science.

References

1. Kent AG, Dupont CL, Yooseph S, Martiny AC. Global biogeography of Prochlorococcus genome diversity in the surface ocean. The ISME journal. 2016;10(8):1856-65.
2. Rossello-Mora R, Lucio M, Pena A, et al., Metabolic evidence for biogeographic isolation of the extremophilic bacterium Salinibacter ruber. The ISME journal. 2008;2(3):242-53.
3. Pagaling E, Wang H, Venables M, et al., Microbial biogeography of six salt lakes in Inner Mongolia, China, and a salt lake in Argentina. Applied and environmental microbiology. 2009;75(18):5750-60.
4. Coleman-Derr D, Desgarennes D, Fonseca-Garcia C, et al., Plant compartment and biogeography affect microbiome composition in cultivated and native Agave species. New Phytologist. 2016 ;209(2):798-811.
5. Cohan FM, Koeppel AF. The origins of ecological diversity in prokaryotes. Current Biology. 2008;18(21):R1024-34.

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