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Unravelling the New Insights of Artificial Intelligence Tools in Agriculture

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Introduction

Biogeography—the study of the distribution of organisms across space and time—has traditionally focused on macroorganisms such as plants and animals. However, recent advances in molecular biology and sequencing technologies have revealed that microorganisms, including prokaryotes (bacteria and archaea) and unicellular eukaryotes (protists and fungi), also exhibit distinct biogeographic patterns. This article explores the similarities and differences in the global distribution of prokaryotic and eukaryotic organisms, highlighting the environmental, evolutionary, and ecological factors that shape their biogeography..

Historically, microbial biogeography was overshadowed by the assumption that microbes are cosmopolitan due to their small size and high dispersal potential. The Baas-Becking hypothesis—“everything is everywhere, but the environment selects”—suggested that microbial distribution is primarily governed by environmental conditions rather than geographic barriers.

However, accumulating evidence contradicts this notion. Studies show that microbial communities vary significantly across biomes, latitudes, and even microhabitats3. For example, cobamide-producing prokaryotes exhibit latitudinal gradients similar to those observed in macroorganisms.

Macroorganisms have long been known to follow predictable biogeographic patterns. Latitudinal diversity gradients (LDGs), island biogeography, and species-area relationships are foundational concepts in macroecology. These patterns are shaped by historical events (e.g., continental drift), climate, habitat heterogeneity, and evolutionary processes.

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