Microdiversity and phylogeography of lake bacteria

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Video Byte

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Abstract

Microbial phylogeography is the study of diversification and distribution of microorganisms across space and time, offering unique insights into eco-evolutionary processes that influence the ubiquity and diversity of microbial populations in the environment. However, our understanding of microbes lags far behind that of macroorganisms, primarily because many dominant microorganisms are difficult to culture. A recent study evaluated the microbial phylogeography of one tiny inhabitant of freshwater ecosystems. Bacterioplankton are common to many freshwater ecosystems despite the fact that these habitats are geographically disconnected, and better understanding their microdiversity is key to uncovering the eco-evolutionary processes behind their dominance. Using long-read amplicon sequencing, researchers evaluated pelagic bacterioplankton assemblages in 11 deep freshwater lakes in Japan and Europe. Their method uncovered 7-101 amplicon sequence variants for each of the 11 predominant bacterial lineages, identifying microdiversity that could not be resolved using conventional approaches. Although further improvements in the throughput of this sequencing technology are needed to better detect rare variants. The results suggest that long-read sequencing is an ideal complement to short-read amplicon sequencing and metagenome assembly-based approaches, helping to uncover the complex ecological processes underlying the ubiquity of freshwater bacterioplankton.