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What does a metagenomics approach tell us about the “everything is everywhere” hypothesis?

The “everything microbial is everywhere” hypothesis proposed in the 20th century by Baas-Becking has received considerable attention in the decade following the publication of Findlay, et al. in 1996 (Global diversity and body size. *Nature* 383:132-133). We generated eukaryotic and prokaryotic SSU rDNA libraries from three lakes: oligotrophic Toolik Lake in Alaska, USA and two temperate reservoirs (mesotrophic Lake Townsend and eutrophic City Lake in North Carolina). We sequenced a sample of clones from the libraries and aligned them with each other and with GenBank entries. Real-time PCR (Q-PCR) was used to test whether the clones found in one of the libraries could be detected in other lake samples. In most cases, the abundance of target taxa was one to several orders of magnitude lower than in the source lake. Nevertheless, the target microbial taxa were detected by Q-PCR, suggesting that the growth potential of individual populations is dictated by local environmental conditions. The endemic presence of many microbial taxa in widely dispersed freshwater samples has implications for ecosystem assessment as well as ecosystem resistance and resilience.

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