



Unusual bacterioplankton community structure in ultra-oligotrophic Crater Lake

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ABSTRACT: The bacterioplankton assemblage in Crater Lake, Oregon (U.S.A.), is different from communities found in other oxygenated lakes, as demonstrated by four small subunit ribosomal ribonucleic acid (SSU rRNA) gene clone libraries and oligonucleotide probe hybridization to RNA from lake water. Populations in the euphotic zone of this deep (589 m), oligotrophic caldera lake are dominated by two phylogenetic clusters of currently uncultivated bacteria: CL120-10, a newly identified cluster in the verrucomicrobiales, and ACK4 actinomycetes, known as a minor constituent of bacterioplankton in other lakes. Deep-water populations at 300 and 500 m are dominated by a different pair of uncultivated taxa: CL500-11, a novel cluster in the green nonsulfur bacteria, and group I marine crenarchaeota. β -Proteobacteria, dominant in most other freshwater environments, are relatively rare in Crater Lake ($\leq 16\%$ of nonchloroplast bacterial rRNA at all depths). Other taxa identified in Crater Lake libraries include a newly identified candidate bacterial division, ABY1, and a newly identified subcluster, CLO-1, within candidate division OP10. Probe analyses confirmed vertical stratification of several microbial groups, similar to patterns observed in open-ocean systems. Additional similarities between Crater Lake and ocean microbial populations include aphotic zone dominance of group I marine crenarchaeota and green nonsulfur bacteria. Comparison of Crater Lake to other lakes studied by rRNA methods suggests that selective factors structuring Crater Lake bacterioplankton populations may include low concentrations of available trace metals and dissolved organic matter, chemistry of infiltrating hydrothermal waters, and irradiation by high levels of ultraviolet light.

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