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Functional profiling of bacterial communities in Lake Tuz using 16S rRNA gene sequences

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Abstract

The 16S rRNA amplicon sequencing technique is a key aspect of studies of microbial communities but does not provide direct evidence of a community's functional capabilities. This work aimed to assess the structure of the uncultured bacterial communities from two locations in Lake Tuz in Turkey to provide information on their roles in the lake ecosystem. The most abundant phyla in the lake water were Firmicutes (84%) for lake sample site 1 (TG1), 70% for lake sample site 2 (TG2), Fusobacteria (9% for TG1, 22% for TG2) and Proteobacteria (6% for TG1, 7% for TG2). The most abundant genera were Romboutsia (45% for TG1, 35% for TG2), Clostridium sensu stricto 1 (8% for TG1, 8% for TG2), Cetobacterium (9% for TG1, 22% for TG2) and Photobacterium (2% for TG1, 3% for TG2). PICRUSt constitutes a novel bioinformatics tool to establish profiles for bacterial protein functions based on metagenomic 16S rRNA data for a community of unculturable bacteria. PICRUSt also provides information on whole-community metabolic functions related to adaptation, bioremediation potential and the ability of various groups of microorganisms to survive in highly saline water. The overall results provide an effective strategy for assessing the metabolic capacities of microbes in situ in a high-salt aquatic environment such as Lake Tuz and the potential of these microbes to serve as bioremediation agents. This approach provides useful insights into predictive metagenomics of an unculturable microbial community for which only marker-gene surveys are currently available. © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

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