

## **Microbial diversity, composition, and function in anoxic meromictic marine lakes of Palau: Oxygen minimum zones in miniature?**

MICHAEL BEMAN\*, MATTHEW MEYERHOF,  
JESSE WILSON, KELLY HENRY AND MICHAEL DAWSON<sup>1</sup>

<sup>1</sup>Life and Environmental Sciences and Environmental Systems,  
University of California – Merced, Merced, CA, 94353  
USA (\*correspondence: mbeman@ucmerced.edu)

Steep chemical gradients occur in aquatic ecosystems when oxygen is depleted through microbial activity, such as in oceanic oxygen minimum zones (OMZs). Human-driven expansion of OMZs and other low-oxygen aquatic ecosystems compresses habitat for aerobic macroorganisms and alters microbial ecology and biogeochemistry, yet our understanding of these changes is limited by a lack of systematic analyses of low-oxygen ecosystems. Marine lakes are an ideal comparative system, as they span a deoxygenation gradient from well-mixed holomictic lakes, to stratified, anoxic, meromictic lakes that vary in their extent of anoxia. We analyzed 7 marine lakes in the Republic of Palau using next-generation sequencing of 16S rRNA genes and quantitative PCR for nitrogen- and sulfur-cycling functional genes. Microbial diversity typically increased with depth or was minimal at mid-depth in meromictic lakes, while community similarity declined sharply with increasing depth. Community similarities ranged from 9% to 86% across samples, reflecting the dominance of typical marine *Cyanobacteria*, SAR11, and SAR86 bacteria in the epilimnion of most lakes, and markedly different community composition in the anoxic hypolimnion. Hypolimnion bacteria included anoxygenic phototrophs, sulfate-reducing bacteria, and SAR406—all of which are known to participate in the biogeochemical cycling of carbon, nitrogen, and sulfur in other anoxic aquatic habitats. Quantitative PCR showed that ammonia-oxidizers were limited to discrete depths, whereas nitrite oxidizers were present over a wide range of conditions, including anoxic and sulfidic conditions. Denitrifier nitrite reductase (*nirS*) genes were also detected in the sulfidic hypolimnion of all meromictic lakes, whereas anammox *nirS* and 16S rRNA genes were not. Collectively these data provide new insight into open ocean OMZs and provide a new model system for microbial ecology and biogeochemistry within low-oxygen marine ecosystems.