

Metagenomic and Metatranscriptomic Analysis of the C, N, and S Cycles in Qinghai Lake, China

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Saline lakes on the Tibetan Plateau are sensitive indicators to environmental change and the microbial response can either amplify or negate further change by altering the carbon, nitrogen, and sulfur cycles. To predict changes in these cycles, baseline information is needed on the pathways and the potential to withstand stress associated with environmental change. Therefore, an Illumina metagenomic and metatranscriptomic dataset was created from water collected at two sites (B and E) in the high elevation (3196 m), saline (12.5 g L⁻¹) Qinghai Lake. Autotrophic *Cyanobacteria* dominated the DNA samples, while heterotrophic *Proteobacteria* dominated the cDNA samples from both sites. Photosystem II was the most active at site B and was associated with photoprotection and osmotic stress genes. Oxidative phosphorylation was most active at site E consistent with the dissolved oxygen in the lake water (8.9 ppm) and was associated with oxidative stress genes. The N cycle was dominated by assimilatory pathways for both sites. N₂-fixation was likely inhibited by the presence of both nitrate and nitrite (0.39 and 0.13 mg L⁻¹, respectively). The production of sulfate through either the SOX system or sulfite dehydrogenase were the most active pathways. These data show that the microbial communities in Qinghai Lake are involved in the C, N, and S cycle, and provide baseline information on the microbial response to environmental change.