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Microbial Succession in Response to Salinity in the Sediments of Lakes on the Northeastern Qinghai-Tibetan Plateau, China

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Salinity is an important factor controlling the microbial distribution in lakes. However little is known about how microbial communities evolve in response to salinity variation. In this study, we investigated the microbial succession in the field settings of Qinghai-Tibetan lakes, by transplanting freshwater Erhai Lake (salinity 0.1%) sediments to four higher-salinity lakes: Tuosu Lake (salinity 2.3%), Gahai Lake² (salinity 7.0%), Xiaochaidan Lake (salinity 7.2%) and hypersaline Lake Chaka (salinity 24.1%) to mimic salinity increase scenarios and by transplanting hypersaline Lake Chaka sediments to the above four lower-salinity lakes to mimic salinity decrease scenarios. In the meanwhile, in order to study how microbial community responds to salinity in the laboratory, we selected the sediments of Erhai Lake and Xiaochaidan Lake for microcosm experiments. Transplanting experiments were performed according to Reed et al. (2013). Microbial cages were constructed using dialysis tubing (diameter: 64mm) with molecular weight cutoff of 6-8 kD. Around 60 ml lake sediments were filled into each microbial cage. The dialysis bag-caged sediments were incubated in situ or at in situ temperature

in the laboratory for 50 days. We examined the microbial composition of experiment sediments by 16S rRNA gene illumina sequencing. Our results showed that the *Proteobacteria*, *Bacteroidetes*, *Actinobacteria* and *Firmicutes* were dominant groups in our samples. Microbial compositions in the transplanted samples were distinct from their surrounding lake water and sediments. The microbial community structures changed with salinity in both field and lab experiments. The phylogenetic groups respond differently to salinity increase/decrease. For example, *Beta*-, *Delta*- and *Gammaproteobacteria* decreased with salinity increase in the field experiments; while *Gammaproteobacteria* increased with salinity rising in laboratory experiments. Overall, our results gave a systematic investigation of microbial composition variation with salinity change.

Key words: salinity, microbial community, saline lakes.

References

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