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## Onshore Contribution to the Microbial Communities in the Lakes on the Qing-Tibetan Plateau

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The inland lakes on the Tibetan Plateau are inhabited by diverse microbial communities, which play a significant role in biogeochemical cycles of biogenic elements (e.g. carbon, nitrogen). Onshore inputs provide essential nutrient sources as well as microbiota to the lakes. However, little is known about which microbes from onshore could survive inside nearby lakes and how such survival varies in response to salinity change. In order to fill the knowledge gap, soils were collected from the shores of Erhai Lake (salinity 0.1%), Gahai Lake (salinity 7.0%), Xiaochaidan Lake (salinity 7.2%), and Lake Chaka (salinity 24.1%) on the Qing-Tibetan Plateau and 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 onshore soils were filled into each microbial cage. The microbial cages made of the soils from the shore of each lake were dropped into itself. The dialysis bag-caged soils were incubated in situ for 50 days. The microbial communities of the original soil (as a control), caged soil, and lake water and sediment at the sites where the microbial cages were located were studied by using illumine sequencing. Duplicates were performed for the sample sets from each lake. The results showed that the onshore contribution of microbial communities in lakes varied with salinity: in the freshwater Erhai Lake, Proteobacteria and Bacteoidetes were the dominant

contributors to the lake microbial community; in the mid-salinity Tuosu Lake and Xiaochaidan Lake, major contributing bacteria were Proteobacteria, Bacteoidetes and Firmicutes; in the hypersaline Lake Chaka, Proteobacteria, Bacteoidetes, Firmicutes and unclassified bacteria.

**Key words:** Onshore contribution, microbial community, lakes, Qing-Tibetan Plateau

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