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Diversity of the T4-like Myoviruses Community in Response to Salinity in Saline Lakes of the Qinghai-Tibetan Plateau

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1 Introduction

Viruses are the most abundant biological entities on Earth. They can influence the succession of individual microbial populations, biogeochemical cycles of C/N and, ultimately, microbial community structure through killing specific host species and thus releasing cellular nutrients (Suttle 2007; Zhong and Jacquet 2014). Tailed viruses are

capable of attacking and breaking down the cell wall peptidoglycan. As a set of tailed dsDNA viruses, Myoviridae are commonly dominant in aquatic ecosystems. T4-like myoviruses are a major component in Myoviridae and could be classified into five groups (i.e., T-evens, Pseudo T-evens, Schizo T-evens and Thermo T-evens and Exo T-evens) with known cultured representatives (Bellas and Anesio 2013). Previous

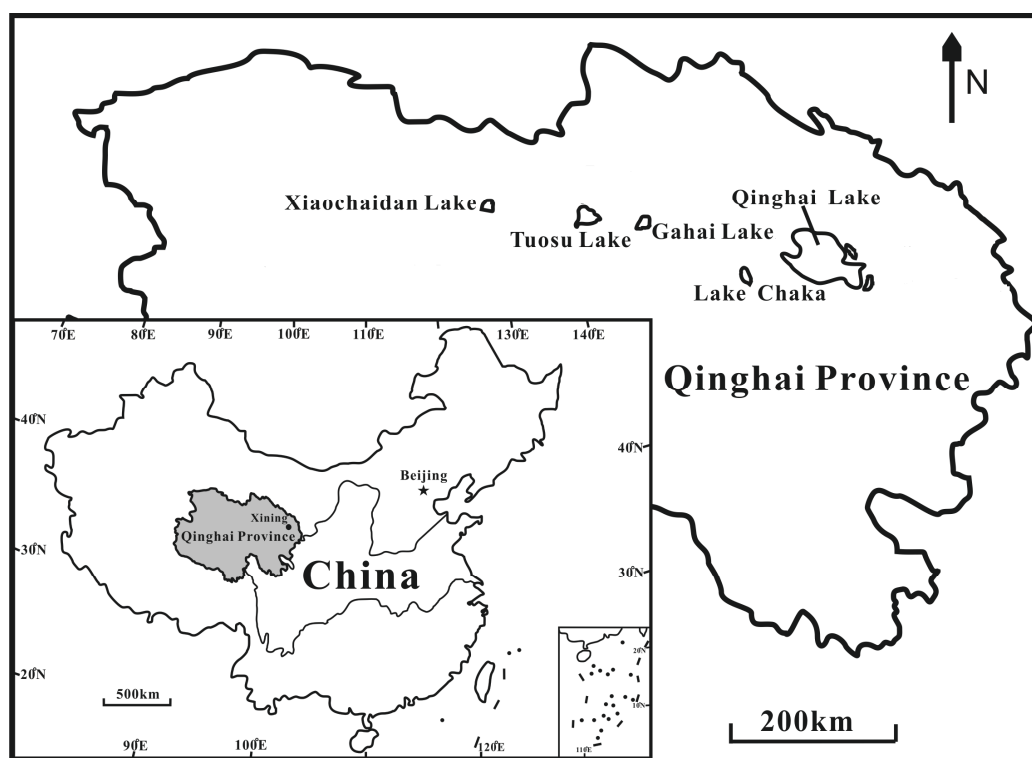


Fig. 1. A geographic map showing the locations of the studied lakes on the Qinghai-Tibet Plateau, China.

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bacteriophage diversity studies were mainly focused in ocean and freshwater, but little is known about the bacteriophage distribution in the saline and hypersaline lakes, which accounted for more than a half of the terrestrial aquatic systems (Wilhelm and Suttle 1999; Wommack and Colwell 2000). In order to investigate how T4-like bacteriophage distribute in response to salinity change in saline and hypersaline lakes, T4-like myovirus diversity was examined in six saline and hypersaline lakes with salinity ranging 10.5~241.2g/L on the Qinghai-Tibetan Plateau, China (Fig. 1) by using major capsid gene (g23)-based phylogenetic analysis (Filée et al. 2005; López-Bueno et al. 2009; Bellas and Anesio 2013).

2 Result and Discussion

A total of 223 g23 gene clones were obtained and were clustered into 53 operational taxonomic units (OTUs) (Fig. 2). Among the identified OTUs, 19 and 32 OTUs were affiliated with to marine- and freshwater-related myoviridae, respectively; and two OTUs were classified into an unknown group. The identified T4-like phage OTUs in the studied saline and hypersaline lakes were unique. The relative abundance of marine-related T4-like phage OTUs in saline lakes showed positive correlation

with salinity of the lake water ($R^2=0.594$). For example, about 40% of T4-like phage OTUs from Chaka Lake (Salinity, 241.2g/L) were affiliated with marine group, and about 75% of T4-like phage OTUs from Qinghai Lake (Salinity, 10.8g/L) were clustered to freshwater group. Together our results suggest that salinity is an important factor influencing diversity and distribution of T4-like bacteriophage community in saline and hypersaline lakes.

Key words: T4-like bacteriophages, major capsid gene (g23), saline lake, Qinghai-Tibet Plateau.

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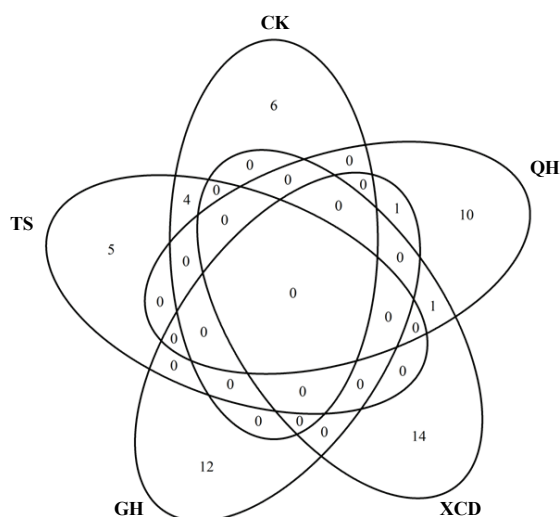


Fig. 2. Venn diagram illustrating the distribution of the OTUs of T4-like bacteriophages in the studied lakes.