



Pronounced differences in community structure and population dynamics of Polynucleobacter bacteria in three contrasting freshwater habitats located in East Asia and Central Europe

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Seasonal dynamics in community structure of bacterioplankton belonging to the Polynucleobacter cluster (Betaproteobacteria) were investigated in three contrasting freshwater habitats over one year. The investigated habitats were the large shallow eutrophic Taihu Lake (China), the deep oligo-mesotrophic Lake Mondsee (Austria) and an alpine dystrophic pond (Austria). Fluorescent in situ hybridization (FISH) with a set of probes specific for the entire Polynucleobacter cluster and subclusters A (PnecA), B (PnecB), C (PnecC), and D (PnecD) was performed. The entire Polynucleobacter cluster contributed up to 6.9% in Lake Mondsee, 3.5% in Taihu Lake, and 59% in the dystrophic pond to the total number of bacterioplankton. Subclusters PnecC and PnecB were numerically important subclusters, whilst the other two subclusters (PnecA and PnecD) were either not detected or only found with very low cell numbers. PnecC bacteria were the only Polynucleobacter bacteria found in the dystrophic pond, and they were of relative importance from late autumn to midwinter in Taihu Lake. PnecB bacteria, which could be detected by FISH all the year, showed pronounced differences in their seasonal dynamics in Lake Mondsee and Taihu Lake. In Lake Mondsee the PnecB population peaked during the warmer season (water temperature > 10°C) whilst they peaked in Taihu Lake during winter (water temperature < 10°C). Subcluster PnecC contributed up to 59% of total bacterioplankton in the dystrophic pond. Cultivation-independent and cultivation techniques were combined to investigate the microdiversity (intraspecific diversity) of this population. At the date of maximum

PnecC numbers a very low intraspecific diversity consisting of only three 16S-23S-ITS genotypes was observed. The three detected genotypes were not known from other habitats. Our results suggest: (i) a high ecological diversity within the Polynucleobacter cluster, (ii) potential local adaptation of PnecC genotype to different types of freshwater habitats.