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Title: *Microbial succession in freshwater reservoirs on South - West Spitsbergen under accelerated deglaciation*

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Lake and ponds are prominent features of the Arctic landscape. These environments provide diverse aquatic habitats for microbial communities, but often with a simplified food-web structure relative to temperate latitudes. Arctic aquatic environments and their biota are proving to be excellent models for wider understanding in many fields ecology, microbiology, paleobiology etc. Investigations of this reservoirs deliver the information about global changes of climate and their possible effects in different areas of the Earth. Microbial plankton dynamics and physico-chemical parameters of twenty four reservoirs on the forefields of two glaciers Werenskiöld and Torell in the Hornsund catchments of Spitzbergen (Svalbard Archipelago) were investigated during the summer 2010. We analyzed components of microbial loop: bacteria, viruses, heterotrophic nanoflagellates and zooplankton. Bacterial abundance, biomass, cell size and live activity (CTC+, MEM+, 6CFDA+) were analyzed as well. Molecular methods Fluorescence In Situ Hybridization (FISH) and Denaturing Gradient Gel Electrophoresis (DGGE) of 16S rRNA were used to examine bacterial community composition. The FISH and DGGE-patterns of different samples were analyzed in relation to physical, chemical, and biological data. In the samples concentrations of chlorophyll a, dissolved organic carbon (DOC), total phosphorus (TP) and nitrogen (TN) were investigated. Additionally in situ temperature, pH and conductivity were measured. Twenty studied reservoirs can be classified as oligotrophic on the basis of chlorophyll a and inorganic nutrient concentrations, five as a nutrient reache. Chlorophyll a concentrations ranged between 0.0 and 32.08 $\mu\text{g l}^{-1}$, DOC ranged between 0.29 and 11.08 mg l^{-1} . Bacterial concentrations were usually low, but in the nutrient reach reservoirs high and typical for eutrophic waters. Bacterial abundance ranged between 0.83 and 11.6 10^6 ml^{-1} in nutrient reach reservoirs. In this environments algae, heterotrophic bacteria, flagellates, zooplankton and viruses create very effective „microbial loop” dependence on quality and quantity of organic matter and temperature. Spectacular were variable the quantity of easily available organic matter as well as the presence and differentiation of phytoplankton. DGGE and FISH indicated marked differences in the bacterial community structure of studied reservoirs. This is very characteristic that some species were present in almost all



samples, but some species were only occasional or absent. The obtained results permit, that in analysed reservoirs growing up different bacterial groups and the main factor of this is the limnological age of reservoir.