Geophysical Research Abstracts
Vol. 14, EGU2012-13852-1, 2012
EGU General Assembly 2012

Shift in prokaryotic diversity in Arctic sediment along a continuum Glacier -River - Fjord using massive 16S rRNA gene tag sequencing

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In Arctic environment, one of indirect consequences of the global climate warming is the significant amplification of the amount of inland water during the spring thaw resulting from the snow cover and permafrost melting. These freshwater transfers to the coast cause sedimentary transfers. The Arctic fjords that represent deep glacial valleys of the sea are particularly vulnerable systems. Although the previous studies have highlighted potentially the high bacterial diversity in Arctic environment by the pyrosequencing, a new-generation sequencing and high throughput method, does not escape the same bias as the one of classical molecular biology techniques involved at different stages of the analysis. In this context, our objective was to characterize the prokaryotic diversity associated to the sediment transfer along a gradient from the head of the glacier to mud patch sediment in the Goule river streaming in Kongsfjorden (Svalbard) during an active thaw. The prokaryotic diversity in sediment was characterized by combining a massive of 16S rRNA gene tag sequencing with a specific and original approach in order to overcome the bias associated to the sampling and extraction. The sediment was extracted by three different methods. One method was done in duplicate. Negative controls performed at extraction and PCR stages were also sequenced. The phylogenetic analysis of the environmental samples below phylum level revealed significantly changes in the diversity and the function of the prokaryotic community along the gradient. The subglacial Goule river sediment is characterized by bacteria with specific functions methylotroph bacteria, aerobic chemoautolithotrophic bacteria (Alphaproteobacteria with Methylobacteriaceae) whereas the mouth of the river Goule and the freshwater part of the Goule River was dominated by sulphate-reducing-bacteria, anaerobic chemooorganotroph (Deltaprotobacteria with the Desulfobulbaceae and Desulfuromonadaceae) and by chemoheteroorganotrophic aerobic bacteria (Bacteroidetes with the Flavobactericeae and Verrucomicrobia with Verrucomicrobiaceae). It is interesting to note that the Cyanobacteria, phototroph organisms, most of which are specialized in the nitrogen fixation (Nostocaceae), are mainly present in the Goule river sediment. The study of the prokaryotic diversity with our approach was very relevant and important in the context of the representativeness of diversity explored in cold sediment. It allowed to reveal rigorously changes in prokaryotic diversity and specific functions associated to sediment transfer along the Goule River.