Variation of bacterial communities in Muztagh ice core from 1869 to 2000

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Many studies focusing on the physical and chemical indicators of the ice core reflected the climate changes. However, only few biological indicators indicated the past climate changes which are mainly focused in biomass rather than diversity. How the biodiversity response to the climate change during the past hundred years is still unknow. Glaciers in Mt. Muztagh Ata region are influenced by the year-round westerly circulation. We firstly disclosed annual variations of bacterial community compositions in ice core over the past 130 years from Muztagh Glacier, the western Tibetan Plateau. Temporal variation in bacterial abundance was strongly controlled by DOC, TN, δ^{18}O, Ca^{2+}, SO_4^{2-}, NH_4^+ and NO_3^-. Proteobacteria, Actinobacteria and Firmicutes were the three most abundant bacterial phyla, accounting for 49.3%, 21.3% and 11.0% of the total community, respectively. The abundances of Firmicutes and Bacteroidetes pronouncedly increased over time throughout the entire ice core. UPGMA cluster analysis of the bacterial community composition separated the all ice core samples into two main clusters along the temporal variation. The first cluster consisted of samples from 1951 to 2000 and the second cluster contained main samples during the period of 1869-1950. The stage 1 and stage 2 bacterial community dissimilarities increased linearly with time on the basis of the Bray-Curtis distance, indicating a similar temporal–decay relationship between the stage 1 and stage 2 bacterial communities. Of all the environmental variables examined, only DOC and NH_4^+ exhibited very strong negative correlations with bacterial Chao1-richness. ^{18}O was another important variable in shaping the ice core bacterial community composition and contributed 1.6% of the total variation. Moreover, DistLM analysis indicated that the environmental variables explained more variation in the stage 1 community (20.1%) than that of the stage 2 community (19.9%).