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DNA analysis of a single *Pinus* pollen grain in Belukha glacier, Altai Mountains, Russia

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Pollen is a regular component in mid- and low- latitude glaciers since most of them are located within a few ten km from vegetation. In addition, many of the pollen grains contain protoplasm, this suggests that DNA information of the pollen preserved for long periods can be obtained. Modern pollen analysis is used to classify pollen taxon from pollen morphology. Thus, the classification of related species based on the morphology is difficult and limited primarily to plant genus or family. Obtaining DNA information from each single pollen grain in glaciers should allow classification below genus level. It is therefore extremely useful for reconstructions of past vegetation, climate and environment in ice core study. However, no studies have ever tried the detailed classification by obtaining DNA sequence from pollen in glaciers. This study attempted to analyze DNA of a single *Pinus* pollen grain extracted from surface snow taken in Belukha glacier of Russia's Altai Mountains in July 2003. A 149 bp *rpoB* fragment from the chloroplast genome in each *Pinus* pollen grain was amplified using polymerase chain reaction and the DNA products were sequenced in order to classify them at section level. *Pinus* is recognized with approximately 111 species in two subgenera, four sections, and 17 subsections. From the obtained sequences, the pollen grains were classified as sect. *Quinquefoliae* and sect. *Pinus* within four sections namely *Quinquifoliae*, *Parrya*, *Trifoliae* and *Pinus*. *Pinus sibirica* in sect. *Quinquefoliae* and *P. sylvestris* in sect. *Pinus* are currently distributed on the surrounding of the glacier. The consistent results for the section may suggest that the source of the pollen in the glacier is *Pinus* trees found on its surroundings.

Keywords: glacier, pollen analysis, DNA, ice core