

ACC021-P07

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## DNA analysis of a single *Pinus* pollen grain in a glacier used for pollen analysis at species level (Part 2)

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Pollen is a regular component in mid- and low- latitude glaciers since most of them are located within a few tens km from vegetation. Protoplasm of the most pollen grains can be well-preserved, and such pollen grains are difficult to obtain from sediment cores of lakes, peat, and so on. Modern pollen analysis is used to identify pollen taxon from pollen morphology. Thus, the identification 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 new pollen analysis that can identify down to species level. The plant species belonging to the same genus are often distributed in different vegetation zones, identification down to the species therefore is extremely useful for reconstructions of past vegetation, climate and environment in ice core study. However no studies have ever tried to obtain DNA sequence from pollen in glaciers. This study attempted to analyze DNA of a single *Pinus* pollen grain extracted from sub-surface snow taken in Belukha Glacier of Russia's Altai Mountains in July 2003. The chloroplast genome in *Pinus* pollen were amplified by the polymerase chain reaction (PCR) and sequenced. So far, sequence data have been obtained at success rate of around 50%.