

## Identification of single pollen grains found in a glacier using a whole genome amplification method

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Pollen taxon in sediment samples can be identified by analyzing pollen morphology. Identification of related species based on pollen morphology is difficult and is limited primarily to genus or family. Because many pollen grains in glaciers contain protoplasm, genetic information of pollen grains should enable identification of plant taxa below the genus level. The present study attempted to analyze the DNA of *Pinus* pollen grains collected from subsurface snow layers on the Belukha Glacier in the Altai Mountains of Russia in the summer of 2003 in order to identify them. *Pinus* is a taxon with approximately 111 recognized species in two subgenera, four sections and 11 subsections. Each *Pinus* pollen grain was amplified using a whole genome amplification method, and some regions of chloroplast genome were sequenced. As a result, each pollen grain was identified at subsection level and was narrowed down to around 10 species.

Keywords: glacier, ice core, pollen analysis, *Pinus*, DNA, WGA