

## Potential of paleogenomics on plant species by using pollen in ice cores

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Many pollen grains in glaciers contain protoplasm, genetic information of pollen grains should enable identification of plant taxa at the species level and estimation of plant genetic diversity. It therefore may allow reconstructions of past vegetation and forestry ecosystem in association with climate and environment in ice core study. This study attempted to obtain genetic information from a single *Pinus* pollen grain by whole genome amplification method. Pollen grains used in this study were *Pinus* extracted from a pit and an ice core obtained from the Belukha glacier in the summer of 2003. The pollen grains were collected from the layers of 1.8-1.9 m depth, 45.3-45.9 m depth and 101.5-101.7 m depth, and these grains seemed to have deposited on the glacier in 2002, 1923 and the 1600s, respectively. The results in this study showed the success rates in obtaining the sequence data were 23.8% (n=21) for the pollen in the year 2002, 13% (n=68) for the pollen in 1923 and 26% (n=19) for the pollen in the 1600s.

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