

## アイスコア試料や絶滅生物標本からの古代 DNA 解析

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### Ancient DNA analysis of extinct animal and ice core samples

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Ancient DNA has been obtained from many kinds of substrates. Ice cores, permafrost, as well as subfossil and recent skeletal remains stored in museums are potentially accessible for DNA analysis. Ancient DNA analyses are helpful in clarifying the phylogenetic relationships among organisms with branching dates (time-tree). Analyses of extinct animals and ice cores have often been used in reconstructing the past environments. However, the DNA in these samples is often highly degraded and fragmented, and therefore in order to analyze the small amount of DNA preserved in these samples, an effective technique to extract total DNA, shotgun sequencing from ancient DNA extracts, and bioinformatics and molecular evolution analysis from large-scale sequence data set are required.

Ice cores drilled from glaciers can provide a means of direct analysis of microbes in the past. The species composition of microorganisms in the ice core could reflect the environmental condition at that time. Despite the crucial role of cyanobacteria in various ecosystems, little is known about their evolutionary histories, especially microevolutionary dynamics, because of the lack of knowledge regarding their mutation rates. Here, we reconstruct the microorganisms by molecular DNA analysis collected from Kyrgyzstan that dates back to approximately 12,500 cal years before present. We successfully sequenced the 16S rRNA and 16S–23S internal transcribed spacer (ITS) region. We detected two cyanobacterial operational taxonomic units (OTUs) from the ancient ice core samples, and these are shared with those from the modern glacier surface. In addition, we were successful in estimating the mutation rate by comparing the ancient and modern populations. We also demonstrated that the ancient sequences from the ice sample were not contaminated from modern samples by a model selection framework. The cyanobacteria detected from the ice core have been revealed to be distributed on glaciers all over Asia and in polar regions, and they also show regional adaptations shaped by dispersal limitations.

Ancient DNA analyses have been started to reveal the origin and the evolution of extinct animals. We show DNA analysis from extinct elephant birds of Madagascar, and obtain several new findings on the evolution of these birds and their relatives (Palaeognathae; ratites and tinamous). Palaeognathae is believed to have originated in the Southern Hemisphere. Here we recovered genome fragments from extinct elephant birds, and reconstructed a robust phylogenomic time-tree for the Palaeognathae. Molecular and morphological evidence strongly suggested the Northern Hemispheric origin of Palaeognathae. Ancestors were probably volant (flying) birds, and migrated to the Southern Hemisphere (notopaleognaths) and explosively speciated around the Cretaceous-Paleogene boundary. Although Gondwana had already broken into smaller landmasses in this time, Antarctica, South America, and Australia were still connected. The ancestral notopaleognaths could expand their distribution into the whole of Antarctica, South America, and Australia, and then occasionally migrated to Madagascar and New Zealand centering from Antarctica. Gigantism subsequently occurred independently on each landmass. Our results implied that DNA analyses from ancient samples could lead reconstructions of past fauna and flora, and show a clear picture of the evolution.