

プランクトン群集へのDNAメタバーコーディングを用いた古環境復元：穴道湖における研究例

Reconstruction of paleo-environment using DNA metabarcoding on the plankton community: a case study in Lake Shinji, Japan

*仲村 康秀¹、瀬戸 浩二¹、香月 興太¹、齋藤 文紀¹、山岸 聖¹、高原 輝彦¹、安藤 卓人²、小木曾 映里³
*Yasuhide Nakamura¹, Koji Seto¹, Kota Katsuki¹, Yoshiki Saito¹, Satoshi Yamagishi¹, Teruhiko Takahara¹, Takuto Ando², Eri Ogiso-Tanaka³

1. 島根大学、2. 秋田大学、3. 国立科学博物館

1. Shimane University, 2. Akita University, 3. National Museum of Nature and Science

The DNA metabarcoding (DNA-MB) is a promising method to elucidate the composition of organisms contained in environmental samples. This approach is widely used in earth science studies. The DNA-MB focused on the plankton community could be effective to clarify the paleo-environment because plankton contain the primary producers. Moreover, they possess large biomass and respond sensitively to environmental changes. Such analysis, however, demands wide knowledge on diverse taxa. We conducted a sedimentary study targeted on plankton community in Lake Shinji, Japan. The salinity of the lake is relatively low (the PSU is ca. 1–5), but it was a semi-closed bay filled with sea water before 2000 years ago. Previous studies reported that the concentration of sulfur, which indicates the inflow of sea water, decreased in a certain period during the past 2000 years, and therefore, it is hypothesized that in this period, the semi-closed bay became an almost freshwater lake. This hypothesis was, however, not supposed by enough biological evidences.

Given this situation, a sediment core of ca. 4 m was sampled in July 2021 from the lake. Quantitative PCRs targeted on two aquatic plants (*Potamogeton panormitanus* and *Stuckenia pectinata*) were conducted for the sediment samples taken from every 6 cm, in order to clarify the fluctuation of DNA quantity of these species. The DNA-MB focused on plankton was also performed for the same samples. To obtain the reference data for the identification of plankton, water and surface sediments were sampled from May 2020 to March 2021 at 6 stations located in the lake and its adjacent aquatic areas, and the DNA-MB was conducted for these samples.

The quantitative PCRs on two aquatic plants showed a clear tendency that the two species were detected chiefly in the samples lower than ca. 2.5 m in core depth. By the DNA-MB, marine plankton were mainly detected in the same samples, and the plankton composition was largely different among the samples upper and lower than ca. 2.5 m. This core depth corresponded to the timing of the sulfur decrease, and the age was estimated at 1250–1290 CE. These results suggest that the desalinization of the lake and the drastic change of ecosystem started around 1250–1290 CE. Although some issues remain in reconstructing the paleo-ecosystem, our results show that DNA-MB of the whole plankton community is effective in reconstructing paleo-environments.

キーワード：環境DNA、堆積物古代DNA、原生生物、堆積物コア、人新世、定量PCR

Keywords: environmental DNA, sedaDNA, protist, sedimentary core, Anthropocene, quantitative PCR