

Reconstructing Ecological Responses to Last Global Warming Recorded in Japan Sea Sediment through Ancient DNA Analysis

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The advancements of scientific ocean drilling towards climate and ocean changes through sedimentological, paleontological and biogeochemical approaches and biosphere frontiers through next-generation sequencing of genomic DNA from the deep biosphere lead to an emerging field of ancient DNA genomics. In semi-closed ocean basins, climate-driven changes in marine ecosystem are pronounced because of the channel closure and physicochemical stratification based on salinity and temperature. The lack of O₂ to benthic organisms results in the formation of undisturbed sediment with laminated layers, each of which tends to record the past ocean change at high temporal resolution. As pilot studies demonstrated that DNA and other biomolecules are well preserved at geological time scale under O₂-deprived conditions, ancient DNA genomics is becoming a new powerful tool to decode the past ecological change. We investigated ancient DNA obtained from thinly laminated layers deposited in the Japan Sea across the most recent global warming event rapidly occurred after Younger Dryas. Metabarcoding of 18S rRNA gene sequences clarified that across the transition from oxygenated to anoxic bottom water conditions, dominant protist populations were shifted from radiolarians (Acantharia) to diatoms (Thalassiosirales) and unclassified Stramenopiles. These results suggest that the inflow of Tsushima Current with nutrient-rich, warm seawater and rapid global warming triggered the complex anoxia-ecology interactions. It is also suggested that the long-term ecological change reconstructed in this study provides realistic information to predict ecosystem perturbation caused by current global warming.

Keywords: Japan sea, Ancient DNA, Last Global Warming, anoxic bottom water