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植物プランクトン由来のゲノムよびメタトランスクリプトーム解析
Analyzing phytoplankton metranscriptome and genome

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研究成果概要

　　This study is using the supercomputer of Institute for Chemical Research, Kyoto University, to analyze the metatranscripotme which sampled from the Matsu archipelago, located along the Chinese coast near the mouth of the Minjiang Rive.

　　Diatoms and dinoflagellates were the major communities in this sampling area. Diatoms account for more than 20% of global carbon fixation and nearly 40% of marine primary production. They are also easily consumed by zooplankton. Thus, the abundance of diatoms is important for energy transfer. Dinoflagellates are also one of the major primary producers in marine ecosystems. They can be parasites, symbionts, and grazers. Some dinoflagellate species can produce toxins and are the main source of toxic red tides. Both communities were varied and succeed due to nutrient input. In this study, we focus on how nitrogen and phosphorus affect gene expression in diatoms and dinoflagellates.

　　Phytoplankton samples for RNA analysis were collected by using a 20 μm mesh plankton net and filtered through 1 mm and 200 μm mesh screens to remove copepods and other mesoplankton. After the nutrient manipulations, we acquired original, nitrogen replete, nitrogen free, phosphorus replete and phosphorus free samples for total RNA extraction and RNA-seq sequencing. After sequencing and bioinformatic analyzing, 16,672,517 contigs had been generated by assembly. Future study will mainly focus on the differential gene expression and the functional group enrichment analyze, that may reveal ecological functions of diatoms and dinoflagellates in a coastal ecosystem.