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メタオミクスを利用した海洋プランクトン動態に関する研究
Study on the dynamics of marine plankton using meta-omics data

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研究成果概要

Increasing anthropogenic CO₂ emissions and the resulting climate change have become one of the most serious global crises. The ocean is estimated to absorb about 25% of anthropogenic CO₂ and therefore plays a critical role in the global carbon cycle. The marine biological pump is one of the most important mechanisms of carbon sequestration in the ocean. However, the efficiency of biological pump, i.e., whether the carbon fixed by phytoplankton photosynthesis can be exported to the deep ocean or remineralized to CO₂ in the surface layer largely depends on the surface planktonic communities. In my current study, I introduced a comprehensive dataset consisting of both the oceanic CO₂ absorption measurements and eukaryotic 18S rRNA gene composition across the surface North Pacific. The qiime2 software installed on the SuperComputer System was applied to analyze the 18S rRNA gene amplicon sequencing data. Through this analysis, the composition of microeukaryotic communities in 519 surface seawater samples were generated, which allows us to draw a linkage between oceanic CO₂ absorption with the surface microeukaryotic communities. As the result, fourteen co-occurrence modules having distinct microeukaryotic composition and ecological roles were detected. Three key modules that were mainly composed of phytoplankton, radiolarian, and dinoflagellate taxa, respectively, exhibited contrasting effects on air-sea CO₂ flux. This study demonstrates that microeukaryotic communities can either enhance oceanic CO₂ absorption or release depending on their ecological configuration, highlighting the surface microeukaryotic community dynamics as a fundamental mechanism regulating air-sea CO₂ flux in the North Pacific.