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Metatranscriptomic reveals protistan and viral metabolic activity on sinking particles
メタトランスクリプトミクス解析による沈降粒子上の原生生物およびウイルスの代謝活性の解明

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研究成果概要

The purpose of using the supercomputer during this period is to perform metatranscriptomic data from the protists and their viral samples (sinking and suspended particle samples) collected from the Oyashio water.

In this study, we showed that taxon-specific metabolic variation between particle types. Sinking particles were enriched in upregulated transcripts from ciliates, dinoflagellates, and viruses, whereas suspended particles showed higher activity of haptophytes and chlorophytes. Diatoms displayed species-specific patterns: *Minidiscus variabilis* was more active in suspended particles, while the chain-forming *Thalassiosira rotula* was enriched in sinking particles. Co-expression network analysis revealed that modules dominated by chain-forming diatoms (*Thalassiosira*, *Chaetoceros*) were positively correlated with POC and PON fluxes, whereas modules enriched in small phytoplankton were negatively correlated. A sinking-associated module dominated by ciliates, dinoflagellates, and viruses was also negatively correlated with fluxes, highlighting lineage-specific roles in particle aggregation and degradation.

発表論文(謝辞あり)

Yang, Qingwei, et al. "Metabolic reprogramming of protists within the microbiome of sinking particles." *bioRxiv* (2025): 2025-05. (under review)