Marine Biodiversity and Ecosystems

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Using Metatranscriptomics in Estimating Metazoan Diversity: From Genes to Communities

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Venue: Auditorium, 1st Floor,
Interdisciplinary Research Building
跨領域科技研究大樓1樓演講廳
Host: Dr. Ryuji Machida 町田龍二副研究員

Doctoral Dissertation Defense Presentation

~Attendee must wear mask~
~與會者請配戴口罩~

Abstract

Metatranscriptomics is a high-throughput sequencing method that allows direct access to community transcriptomic information through random sequencing of RNA (messenger RNA [mRNA] and ribosome RNA [rRNA]) transcripts from samples in specific environmental conditions (Chapter 1). Using metatranscriptomics in studying metazoan communities, like zooplankton research, has been uncommon and not rigorously validated. To address this, we first provide a theoretical framework to validate the allometric scaling of RNA abundance (mRNA and rRNA) according to the assumptions of the metabolic theory of ecology and growth rate hypothesis. Considering physiological factors affecting RNA production in molecular tools being used to characterize community diversity, such as RNA transcript reads from metatranscriptomics, could provide a theoretical baseline to model metabolic rate, energy flux, and turnover of phosphorus-rich RNA through next-generation sequencing technology (Chapter 2). Then, we tested and compared metatranscriptomics with PCR-based methods using genomic (gDNA) and complementary DNA (cDNA) amplicons, and morphology-based data for characterizing mock communities. Metatranscriptomics provided better species richness and composition estimates that resembled those derived from morphological data (Chapter 3). Metatranscriptomics was further tested using field-collected samples (Fei Tsui reservoir), with the results showing consistent species diversity estimates among biological and technical replicates. Metatranscriptomics allowed the detection of less dominant taxa while addressing issues on laborious work and lack of taxonomic expertise needed in morphological analysis (Chapter 4). Moreover, the integration of allometric scaling helped improve the correlation between transcript reads and species biomass both in mock communities and field-collected samples. Overall, this study offers a theoretical framework for using metatranscriptomics in community ecology studies while demonstrating its advantages as an effective tool for monitoring the diversity of complex zooplankton communities (Chapter 5).