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Microbial Diversity and Bioinformatics

# Comparative Genomics of Free-Living Nematodes

## Ms. YiChien Lee
## 李宜謙小姐

### Ph.D. Candidate

[1.] TIGP Biodiversity Program, Academia Sinica
[2.] Biodiversity Research Center, Academia Sinica
[3.] Department of Life Science, National Taiwan Normal University

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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. Isheng Jason Tsai 蔡怡陞研究員

[Doctoral Dissertation Defense Presentation]

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## Abstract

Over 70% of nematode species are free-living. They are found in a wide variety of habitats and are essential for maintaining microenvironments. However, studies on nematodes have mainly focused on parasites and terrestrial free-living. Free-living nematodes in aquatic ecosystems represent 50% of all nematode species but are poorly understood. Recently, studies of marine free-living nematodes have focused on their potential to address nematode phylogeny questions and explore the evolution of nematode parasitism and adaptation to extreme environments. My Ph.D. aims to sequence the genome of a marine free-living nematode to reconstruct nematode phylogeny and compare it with published nematode genomes to investigate nematode genome diversity. During the sampling process, we analyzed the nematode community around the northern coast of Taiwan. It is important to note that marine nematode species are not amenable to axenic culture under laboratory conditions. To alleviate this issue, we utilized multiple displacement amplification (MDA) and Smartseq2 to amplify nanograms of genomic DNA and mRNA from one individual, respectively. We evaluated the bias of this protocol using *Caenorhabditis elegans*. While reduced genome coverage was detected in repetitive regions, we generated assemblies that covered 98% of the reference genome using long-read sequences produced with Oxford Nanopore Technologies (ONT). Annotation of the sequenced transcriptome and available assemblies showed that gene predictions were more precise, comprehensive, and contained fewer false positives than de novo transcriptome assembly methods. Our results demonstrate the robustness of MDA in combination with ONT, paving the way for the study of genome diversity in the phylum Nematoda and beyond.