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Microbial Diversity and Bioinformatics

Population Genomics of Natural *Saccharomyces* Yeast in Taiwan

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Time: 2022. 04. 29 Fri. 10:00
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 蔡怡陞副研究員

Doctoral Dissertation Defense Presentation

~Attendee must wear mask~
～與會者請配戴口罩～

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Abstract

Population genetics is the study of genetic variations within and between groups of individuals. With a long history of domestication, the budding yeast *Saccharomyces cerevisiae* is a great model for population, ecology and evolutionary studies, given that more than a thousand isolates have been collected from a wide range including both artificial and natural niches. Previous studies pointed to East Asia as the geographical origin of the species, where highly genetically diverse wild populations were discovered. Among them, three isolates from Taiwan revealed unprecedented divergence to populations from the rest of the world. However, a lack of systemic survey and isolation in Taiwan limits our knowledge of the species' distribution and diversity in nature. Here I describe the fundamental ideas behind population genetic approach, strategies to sample broadly, and findings from the 121 isolates collected in Taiwan. Overall, *S. cerevisiae* is prevalent in diverse habitats in low abundance, contrary to their dominance in domesticated environments. Multiple coexisting and admixing natural lineages elevated the total genetic diversity within limited geographical range, comparable to that of continent level. These distinct lineages diverged from Chinese counterparts during a common period when land bridges connected both regions. Polymorphism pattern within each lineage indicated that the diversity was shaped by differences in life history and selective pressure. Combining extensive sampling, metabarcoding, isolate collection and whole-genome resequencing, we illuminate the pre-domestication phase of *S. cerevisiae* at an unprecedented resolution. These findings establish that *S. cerevisiae* harbors rich natural diversity, making it a powerful model system in microbial ecology.