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Microbial Diversity and Bioinformatics

Determination of Core Soil Microbial Community from the Offshore Islands of Taiwan

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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

Abstract

The assemblages of microbes in the environment are complex; soil, in particular, is a massive reservoir for microorganisms. The application of microbial land management is beneficial in agricultural settings. Nevertheless, to manage such a vast number of different microbes in the soil remains a challenging task. Core community was shown in the literature to moderate and drive specific functions across different environments. The discovery of the core microbial community provides a stepping stone to dissect the stable component of a microbial network. In this study, bacterial and fungal community from the soil of Taiwan's offshore islands were characterised. Distinct bacterial and fungal phyla profile were found in each island. The number of shared taxa between the islands were higher in bacteria compared to fungi. Construction microbial network and taxa assignment into network modules indicated the microbial community of Green Island is highly connected. Modules of Orchid Island and Dongsha Island are composed mostly of strongly correlated taxa. Defining the core microbial community of each island has revealed that modules between the islands are correlated, suggesting a set of core species is necessary in soil community of the offshore islands despite separated by sea.