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Deciphering Structure and Microbial Interactions in Intestinal Microbiome of Grey Mullet (*Mugil cephalus* L.)



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Interdisciplinary Research Building

跨領域科技研究大樓1樓C102交誼室

Host: Dr. Daryi Wang 王達益副研究員

Doctoral Dissertation Defense Presentation



Abstract

The fish intestinal tract fosters a vast and complex population of microbes known as gut microbiota, which play crucial roles in host health and development. Taking advantage of next generation sequencing (NGS) technologies, much attention has focused on bacterial symbiosis in the fish gut to elucidate host-microbe interactions and how the interactions respond to environmental change. However, the dynamics of gut microbiota in fishes moving across habitats are poorly understood, particularly for migratory fish. Using the grey mullet (*Mugil cephalus*) as a model organism, we conducted a comprehensive study to: 1. investigate structure and membership of gut microbiota in *M. cephalus* species complex exhibiting different migration routes; 2. examine the impact of changes in salinity on the dynamics of the grey mullet gut microbial community, understand the microbial interactions using generalized Lotka-Volterra models, and identify keystone taxa from the model; and 3. validate model interactions of keystone species with other microbial members through feeding trials that compare responses of hosts administered with and without keystone species. Our “observation–modelling–validation” framework extends methods investigating gut microbiota dynamics as a tool not only useful in predicting the stability and reactivity of microbial population to environmental disturbance, but also in identifying key microbial interactions that have the potential to be manipulated for a wide range of aquaculture applications.