



The University of Hong Kong
School of Biological Sciences

**Public
Seminar**

A metagenomic and metabolomic approach in unraveling the reactivity of modeled multi-species freshwater biofilms exposed to emerging pollutants

Date: 10 August 2021

Time: 9:30-10:30

Venue: 6N-11, KBSB



About the speaker:

Pu Yang comes from Yangzhou, Jiangsu. His PhD study mainly focuses on freshwater biofilms and their reactivity exposed to various stresses supervised by Dr. Olivier Habimana



Abstract:

Freshwater biofilms are exposed to emerging pollutants, and there exist considerable knowledge gaps in freshwater biofilms' reactivity to these compounds. The thesis was first brought to study the level of pollutants in freshwater biofilms sampled from streams in Hong Kong, which was necessary to understand the ecological significance of freshwater biofilms and their roles in response to emerging pollutants. Biofilm samples were found to have a higher accumulation of specific compounds than their corresponding bulk water. And the study also revealed different microbial profiles and structural morphologies based on the extent of pollution exposures and absorption. Erythromycin was selected as a chemical pollutant model as it is a widely used antibiotic in the agriculture industry. In this study, a distinct phenotypic change was observed in biofilms exposed to erythromycin, as characterized by the specific presence of elongated cells, which was justified by increased levels of cell wall biogenesis. Nevertheless, the study identified Verrucomicrobia, Bacteroidetes, and Betaproteobacteri as potential biomarkers to be determined following erythromycin exposure, as revealed by their gene abundance shifts and corresponding metabolism pathways. An untargeted metabolomics study demonstrated that lipid metabolism was critical upon exposure. Silver nanoparticles (AgNP) were selected as model physical emerging pollutants due to their wide applications and increasing freshwater environments. Similar to findings under erythromycin exposure, no considerable diversity differences were observed when freshwater biofilms are exposed to AgNPs. However, Armatimonadota, Bacteroidota, Planctomycetota and Verrucomicrobiota showed significant gene abundance shifts, which implied their roles in response to AgNP exposure. Untargeted metabolomics revealed that Glycerophospholipids metabolism was the key pathways.