The University of Hong Kong
School of Biological Sciences

Harnessing genetic tools for monitoring, understanding and conserving seagrasses in highly urbanized coastal areas.

Date: 15th June 2022

Time: 3:00 PM

Venue: 3N01 & Zoom

About the speaker:

Jaimie Dwi Wai Shan is a MPhil student in the Integrated Biology & Evolutionary Ecology Research (iBEER) group supervised by Dr. Juan Diego Gaitan-Espitia. Her research focuses on developing genetic tools that help to assess, monitor and conserve seagrass populations in Hong Kong.

Abstract:

Seagrasses are important marine primary producers that provide fundamental ecosystem services for human well-being. Despite their key ecological roles, seagrass ecosystems are rapidly declining globally, including populations distributed in the South China coast and Hong Kong. The magnitude and pace of coastal habitat disturbances (e.g., land reclamation, pollution) are major drivers of the rapid decline and deterioration of seagrass populations in this region. In Hong Kong, five seagrass species are currently reported, including one listed as vulnerable in the IUCN red list. These species are highly seasonal with marked changes in abundance and distribution mainly driven by the influence of environmental parameters such as temperature and salinity. The rapid decline of these species is a major concern for conservation managers and stakeholders in Hong Kong. Before planning any conservation interventions aimed to mitigate the extinction risk of local seagrass species, it is essential to understand first their ecological dynamics and genetic diversity. However, traditional approaches for assessing such attributes in seagrasses across time and space are logistically and technically challenging, constraining our capacity to plan effective conservation management. Environmental DNA (eDNA) offers an alternative approach to these methods, mitigating the challenges while enhancing temporal and spatial resolution of ecological surveys. My MPhil study aims to understand the capacity and efficiency of eDNA approaches to monitor and understand seagrass population dynamics (availability, distribution, and abundance) in Hong Kong. I hypothesize that eDNA can reflect changes in seagrass occurrence and abundance across spatial-temporal scales in Hong Kong, but these characteristics would differ when comparing seawater and sediment sources due to the influence of seed banks. Ultimately, this study will provide genetic tools that promote and support long-term ecological and genetic monitoring programs for seagrasses in Hong Kong.