



The University of Hong Kong
School of Biological Sciences

**Qualifying
Seminar**

Genetic consequences of natural and human assisted invasions - a study of Hong Kong birds

Date: 28th March (Fri)

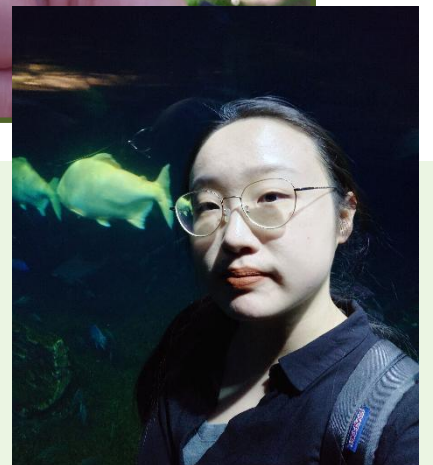
Time: 9:00 - 10:00 am

Venue: KBSB 6N-11 & Zoom



About the speaker:

Zhenyue Wang is a PhD student supervised by Prof. Juha Merilä and Dr. Kerry Reid. Her research focuses on better understanding the genomics behind multiple successful avian invasions in the HKSAR.



Abstract:

Biological invasions, which refer to the introduction, establishment and spread of non-native species to new areas, can be classified into human-mediated introductions (HMIs) and natural range-expanding colonisations (NRECs). These biological invasions can pose threats to biodiversity, the larger ecosystem and agriculture. Therefore, understanding the key features enabling invasive species to establish successfully in a new territory is crucial. While the negative ecological consequences of invasions are well-studied, the genetic consequences of invasions are less clear. Invasive populations are often expected to experience founder effects from small starting populations, which in turn should lead to inbreeding depression, reduced genetic diversity and thus overall limit invasion success. Yet, failures are not always seen – a phenomenon termed ‘the paradox of invasion biology’. The possible resolution to this paradox is that the expected loss of diversity is counteracted by admixture from different source populations, though several alternative reasons may also exist. To date most of our knowledge on the paradox comes from single-species case studies which can be limited or biased species-specific biological or invasion factors, while a comprehensive study comparing genetic diversity, admixture, life-history traits and demographic history in multiple invasive species over similar time frames is still needed to more robustly understand the genetic consequences of biological invasions and how failures are being avoided. This project aims to investigate the genomic consequences of several successful avian invasions originating from NRECs and HMIs from 1936 onward in the Hong Kong SAR (HKSAR) to improve our knowledge on how invasive species overcome the paradox of invasion biology and to hopefully direct conservation and invasive species management.