



The University of Hong Kong
School of Biological Sciences

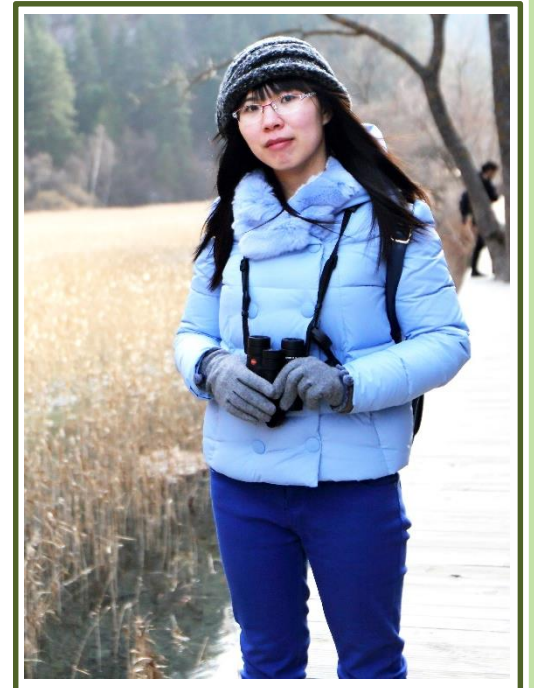
**Public
Seminar**

CONSERVATION GENOMICS AND THE EVOLUTION OF THE WIDESPREAD ENDANGERED BUNTING SPECIES

Date: December 9th, 2024

Time: 10:00 AM

Venue: 6N11 + Zoom



About the speaker:

Guoling obtained her Bachelor's degree from South China Normal University and her Master's degree from Sun Yat-Sen University. In 2020, she joined The Sin Lab to pursue her PhD at HKU. Her research interests encompass the conservation genomics of endangered species, as well as adaptation evolution, natural selection, and speciation.

Abstract:

Population declines can reduce genetic diversity and lead to increased inbreeding and inbreeding depression due to deleterious mutations. These genetic features are influenced by demographic history, bottlenecks, and natural selection. Understanding the interaction of different processes is crucial for effective conservation management of endangered species. Small populations often receive more conservation attention due to genetic vulnerability. However, large populations are often overlooked and can also be at risk of extinction.

In this thesis, I investigated the effects of these processes on the genetic features of three widespread bunting species - the Critically Endangered yellow-breasted bunting, the Vulnerable rustic bunting, and the Least Concern little bunting - with similar distribution ranges, using whole-genome resequencing data. In the first part of my study, I aim to address the population structure of yellow-breasted bunting, the genetic threats faced by this species, and its evolutionary potential. Subsequently, I used empirical data from the three bunting species alongside simulations to explore the genetic consequences of demographic history, bottlenecks, and natural selection. Lastly, I investigated genetic differentiation using the bunting system to understand how various evolutionary forces had shaped the genomic landscape within and between species.

In summary, this study advances our comprehension of the interplay of various evolutionary processes and their impacts on genetic diversity, inbreeding, and deleterious mutations. These findings are pivotal for effectively conserving endangered species, particularly those with large populations that have suffered from rapid declines in recent years.

--- ALL ARE WELCOME ---