



## The major histocompatibility complex, feather microbiome, and body odor in Rosy-faced lovebirds *Agapornis roseicollis*

**Date: 13<sup>th</sup> Dec 2023**

**Time: 16:00**

**Venue: 6N-11**



### About the speaker:

Derek obtained his B.Sc. (Hons) in CUHK, majoring in Cell and Molecular Biology with a minor of Biology. He joined The Sin Lab (Dr. Simon Sin) to pursue his Ph.D. study in HKU. His PhD research focuses on the intricate aspects of animal communication, mate choice, and microbiome in birds using multidisciplinary approach.

### Abstract:

Emerging evidence highlights the pivotal role of olfaction in avian communication. Particularly, a few bird species have been shown to utilize odour cues to discriminate the major histocompatibility complex (MHC) genotypes of potential mates. Evidence of MHC-based mate choice has been found in diverse bird species. However, how MHC genes affect phenotypical variations in the context of mate choice is poorly understood. The microflora hypothesis proposes that the body odour, shaped by feather microbes, contains information of MHC genes. Yet, the existing evidence supporting this hypothesis is controversial. This doctoral thesis aimed to investigate the potential effects of MHC genes on body odour by examining the relationships between MHC genes, feather microbiome, and feather odour in captive rosy-face lovebirds (*Agapornis roseicollis*), a small monogamous parrot that is easily to be kept in captivity.

First, a panel of microsatellite markers were developed for rosy-faced and other lovebirds (*Agapornis spp.*) using whole-genome re-sequencing data to determine the relatedness between studied birds. Next, the diversity and evolution of the MHC genes were investigated at the genus level. The results revealed a moderate level of polymorphisms at both MHC class I and II genes in *Agapornis*. Such polymorphism was generally attributed to balancing selection, while mate choice might also play a role.

Combining the bacterial 16S rRNA amplicon sequencing, whole-genome sequencing, and gas-chromatography mass-spectrometry data, this thesis, for the first time, demonstrated the co-variation between MHC genes, feather microbiome, and feather odour in *A. roseicollis*. Particularly, the results showed that individuals with a similar MHC class II genotype shared a similar feather microbiome and odour chemical profiles, while individuals with a similar MHC class I genotype only shared a similar feather odour chemical profile. The correlation between microbiome and feather odour was robustly supported in both alpha- and beta-diversity analysis. These findings suggest for the potential existence of multiple MHC-signaling routes and provide support for the role of feather microbes in mediating the production of MHC-signaling odorants. The complex pattern underlying the relationship between MHC genes, feather microbiome, and feather odour chemical profile were also unrevealed in the thesis, offering further mechanistical insights on how MHC genes influences body odour.

Finally, the body odour could also be affected by diseases. There is a globally widespread and highly lethal virus in parrots - Psittacine beak and feather disease virus. This thesis also developed a qPCR assay to characterize the viral load in *A. roseicollis*. All the birds studied were asymptomatic and behaved healthily. The temporal data revealed that the viral load was extremely low in the studied birds. Combining the feather microbiome and chemical data, the results further showed that the effects of the virus on the body odour was likely minimal.

Overall, the thesis deepens our understanding of MHC evolution, MHC-based mate choice and avian social communication. It also provides novel insights into the ongoing and vigorous debate on the mechanisms by which MHC genes affect phenotypic traits, opening numerous exciting avenues for future studies.