The University of Hong Kong
School of Biological Sciences

Public Seminar

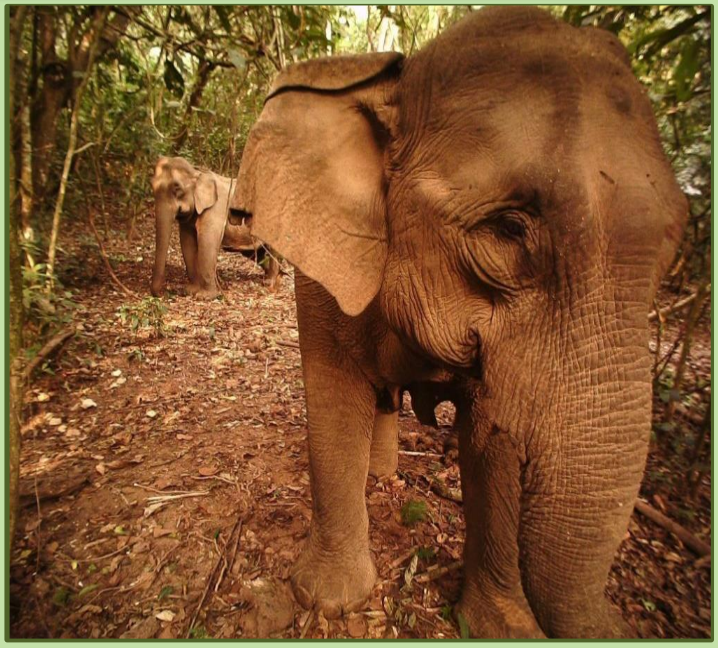
Population genetics and habitat evaluation to inform conservation of Asian elephants in China

Date: 11 May 2022 (Wed.)

Time: 14:30

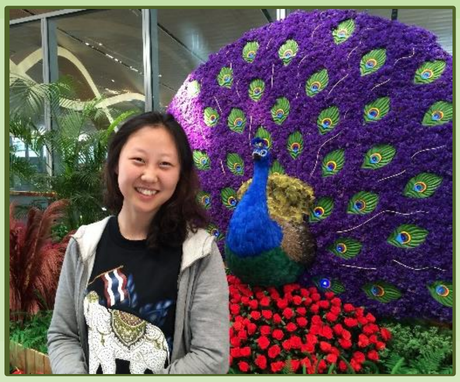
Venue: Room 3N -01, KBSB

& Zoom



About the speaker:

Ying Chen is a PhD student supervised by Prof. David Dudgeon & Dr. Hannah Mumby. She is passionate about conservation and management of endangered species using interdisciplinary approaches.



Abstract:

Ensuring the long-term viability of fragmented populations is a matter of great conservation concern, requiring information on population genetics and habitat suitability. Asian elephants (*Elephas maximus*) were formerly widespread in China, extending northward to the Yellow River 4,000 years ago. However, they have been persecuted, hunted and domesticated, disappearing from much of their historical range. Remnant wild individuals are represented by fragmented populations in Yunnan Province, where the landscape has become increasing fragmented due by cropland and plantations, plus the rapid development of transport infrastructure and expansion of urban areas. Effective legal enforcement of laws against harming elephants in China has allowed the population to double in size to around 300 individuals since the 1970s, and they have begun to expand their range within Yunnan. While this increase provides some reason for optimism over the future of elephants in the country, it is not known whether the historical shrinkage in range and abundance in China has been associated with any genetic bottlenecks or loss of variability in the remaining populations, whether there is genetic exchange between them, nor whether they have sufficient adaptive potential to support further population growth. It is also not known why elephants are confined to southwestern Yunnan, the role played by environmental and anthropogenic variables in determining their habitat suitability, nor whether there is sufficient suitable habitat to support further population growth and range expansion. In this talk, I will describe research that attempts to answer these questions, using combination of molecular- and landscape-scale approaches. My findings have implications for planning, management and conservation of a globally endangered, iconic megafaunal species.