

Molecular evolution and biogeography of the New World *Eptesicus* bats.

Date	16th Sep 2022
Time	16:00
Venue	6N11 & Zoom



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Biodiversity is the key to evolution and conservation yet is underestimated in many taxa, and the mechanisms generating biodiversity are often unclear. Bats (Order Chiroptera) are the second largest mammalian Order (>1,400 species) but remain under-studied. Here we used the cosmopolitan bat genus *Eptesicus* as a model system to study the evolution, and biogeography of widespread taxa. Our results indicated a trans-Atlantic colonization of *Eptesicus* from north Africa to the northern Neotropics and high cryptic diversity in the Neotropics. The widespread Nearctic species, *E. fuscus*, showed complex genetic patterns shaped by both gene flow and repeated isolation during the Pleistocene.

Additionally, we showed that population genetic structure illustrated by the Principal Component Analysis can be misinterpreted when using mean-imputed nonrandom missing data. Our integrative analyses across spatial-temporal scales showcase how the studies of non-model systems can shed new light on the understanding of evolution and biodiversity.



About speaker:

Xueling (Ling) Yi joined the Merilä Lab at HKU as a postdoctoral fellow in August 2022. Xueling obtained her doctoral degree in May 2022 at the University of Wisconsin-Milwaukee in the United States. Her PhD research focused on the molecular evolution, biogeography, and population genetics of the New World *Eptesicus* bats. Xueling's research interest includes evolution, biogeography, phylogeny, and population genomics especially in non-model systems. Xueling is going to focus on the genetic diversity and evolution of the nine-spined sticklebacks during her research at HKU.