

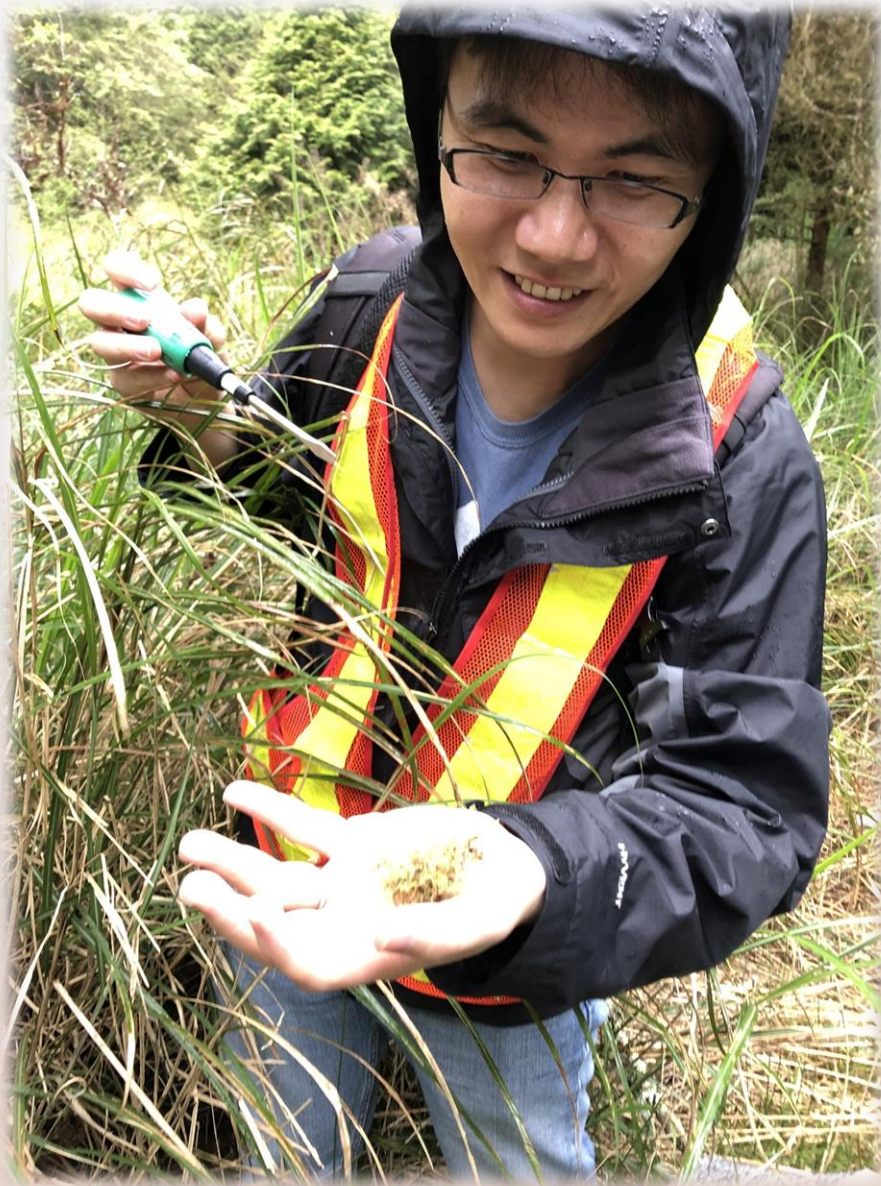


中央研究院生物多樣性研究中心

Biodiversity Research Center, Academia Sinica

biodiv@gate.sinica.edu.tw  
02-2789-9621

# Speciation and Species Delimitation: Making Sense of the Heterogeneous Biodiversity Pattern Across Time and Space



Dr. Jen-Pan Huang  
黃仁磐助研究員

本中心助研究員

Assistant Research Fellow

Biodiversity Research Center, Academia Sinica

Time: 2023. 05. 19 Fri. 10:00

Venue: Auditorium, 1<sup>st</sup> Floor

Interdisciplinary Research Building

跨領域科技研究大樓1樓演講廳

Host: Sheng-Feng Shen 沈聖峰研究員





## Abstract

The processes that underlie the origin and maintenance of biodiversity, as well as how to objectively quantify biodiversity, have long fascinated and puzzled evolutionary biologists. In my research group, we are particularly interested in the mechanisms that give rise to new biological forms, and how understanding the histories of speciation can help with delineating biologically and evolutionarily significant units, thereby informing effective conservation strategies. Many previous studies on species delimitation have focused on determining whether the diverging evolutionary units qualify as "species" or not. However, in this talk I argue that an equally important, but less explored, aspect is understanding what kinds of evolutionary entities have been taxonomically treated as "species." Furthermore, can the new data types, e.g., genomic data, and analytical methods help us incorporate biological and evolutionary significance into species delimitation? My recent findings indicate that evolutionary divergences at different stages along a speciation continuum in *Dynastes* beetles (e.g., from allopatric populations to morphologically distinct taxa that can coexist in sympatry) could be classified as "species" when different data types and models were applied. Additionally, my research group has shown that the island of Taiwan is home to locally endemic sky island species, which are evolutionarily independent lineages resulting from geographical and environmental isolation. The evolutionary status of many divergent taxonomic pairs can be classified as being at the incipient stage of speciation. As a result, the differentiation between two sky island populations of *L. miwai*, for example, can be categorized as allopatric populations, morphological subspecies, or even evolutionarily independent species, depending on the species concept employed. These systems are great candidates for future speciation and species delimitation studies. Finally, our research indicates that distinct horn developmental phenotypes in adult male *Xylotrupes* beetles can evolve quickly, even within a species. Moreover, while it has been suggested that character displacement may have led to closely related rhinoceros beetles with distinct male morphologies coexisting in sympatry, we cannot dismiss the possibility that stochastic character evolution in the *Xylotrupes* system may also produce the same pattern. I will finalize my talk by introducing my future research directions – systematic, speciation, and conservation genomics using beetle systems.