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Terrestrial Biodiversity and Ecosystems

Examining Evolution from Macro- to Micro-scale: Systematics and Population Genetics in the Fern-spore Feeding Micromoths, Cuprininae (Lepidoptera, Stathmopodidae)

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Interdisciplinary Research Building
跨領域科技研究大樓1樓演講廳
Host: Dr. Jen-Pan Huang 黃仁磐副研究員

[Doctoral Dissertation Defense Presentation]

Abstract

Evolution serves as the foundation of biology, and the timeline of life's evolutionary history reflecthe current scientific theory on the major events that have shaped the development of life on Earths. However, evolution is not confined to large timescales; it is a continuous process, occurring at every moment in our daily lives. Interestingly, when different scales are applied to examine evolution, it is common to observe different results. In other words, different scales offer us the opportunity to explore the effects of evolution even within similar groups of life.

A fascinating example is Cuprininae Sinev, 2015, a group of micro-moths with unique feeding habits and wide distribution despite their small size. These moths specialize in fern-spore feeding (FSF), a rare trait in Lepidoptera. This makes them ideal system for studying FSF evolution through phylogenetic reconstruction and examining speciation, extinction, and transition rates. Our analysis suggests FSF evolved once in the family, with FSF species in Stathmopodinae Meyrick, 1913 likely stemming from taxonomic issues. Surprisingly, FSF species' speciation and extinction rates were similar to non-FSF species, indicating FSF may not be as rare among herbivorous insects as previously thought. We also observed increased transition rate from generalist to specialist over time, echoing the trends of evolution of the host specificity in macro Lepidoptera.

To investigate the intraspecific genetic diversity of these wind-dispersed micro-moths, we conducted a population genomics study focusing on two co-distributed species, *Calicotis routundinidus* (CR) and *Thylacosceles citrinacma* (TC). Both species inhabit low to intermediate altitudes in Taiwan, sharing host plants but differing in geographic range—CR extends to the Ryukyu Islands, while TC ranges into Vietnam and exhibits a broader host range. Despite their phylogenetic close related and overlapping distributions, our results indicate distinct geographic affinities and varying patterns of intraspecific genetic diversity between the two species. We hypothesize the seasonal moonson, combined with the central moutain range may be the reason which shape the different intraspecific genetic diversity and subdivision.

Finally, our study expanded the known diversity of Cuprininae in Taiwan, increasing recorded species from 2 to 20 across 7 genera. We documented the life histories of all species, revealing that most feed on Polypodiales, a fern order that diversified during the Early Cretaceous alongside angiosperms. The prevalence of Polypodiales feeding and the relatively young evolutionary history of Cuprininae suggest that fern spore feeding did not earlier than the evolution of angiosperm feeding within this family.