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

Terrestrial Biodiversity and Ecosystems

# *De Nematomorpho Investigatio*: Distribution Modeling, Population Genetics and also Epibionts of *Chordodes formosanus* (Phylum Nematomorpha)

**Mr. Mattia De Vivo**
**馬帝亞先生**

**Ph.D. Candidate**

[1] TIGP Biodiversity Program, Academia Sinica
[2] Biodiversity Research Center, Academia Sinica
[3] Department of Life Science, National Taiwan Normal University

**Time:** 2023. 7. 25 Tue. 14:00
**Venue:** Auditorium, 1st Floor,
Interdisciplinary Research Building
跨領域科技研究大樓1樓演講廳
**Host:** Dr. Jen-Pan Huang 黃仁磐助研究員

[Doctoral Dissertation Defense Presentation]

## Abstract

The phylum Nematomorpha (commonly known as “horsehair worms” in English and “鐵線蟲” in Taiwan) is known for being one of the most understudied animal groups, especially from what concerns molecular ecology. This is often justified by the fact they do not infect humans or animals related to anthropic activities, although they became famous from popular science perspective due to the fact they seem to induce their arthropod hosts to jump into freshwater. Given our own low knowledge on them, I decided to apply tools that are usually used to work on non-model organisms for filling some gaps.

More precisely, I focused on *Chordodes formosanus*, which is widely regarded as the most common horsehair worm species in Taiwan. I checked the species’ distribution compared to the ones of its hosts (three Mantodea species) and its population genetics through two different kinds of data (a fragment of the mitochondrial cytochrome c oxidase subunit 1, also known as COXI, and double digest restriction-site associated DNA sequencing, ddRADseq).

For the second part (Chapter 2), my ENMEval models show how hosts and parasite have high distribution overlap, although different metrics can lead to different niche overlap estimation. Furthermore, there are suitable modeled areas for *C. formosanus* in which it has not been reported yet; this raises concerns for possible extirpation or sampling bias.

For what concerns the second part (which is reported in Chapter 3), both my COXI and ddRADseq dataset tends to consider *C. formosanus* as a single species, without any population structure based on geography alone in its known Taiwanese range (and, in the case of COXI, whole known range). This is interesting, because non-flying organisms dependent on freshwater usually have dispersal issues in Taiwan, given the orology of the island. Furthermore, calculations of the effective population size (*Ne*) trends show how the species is decreasing in number of individuals; this is surprising, since it is the most common Nematomorpha taxon in the island, although its numbers are still pretty high. These last results might be congruent with the distribution modeling and may show signs of extirpation in some areas with cultivated land.

Additionally, in Chapter 4 I reported for the first time sac fungi (Division Ascomicota) living on hairworms; more specifically, I collected *Colletotrichum fructicola*, usually a plant pathogen, growing on the cuticle of living *C. formosanus* specimens.

My research increased the knowledge on several aspects about Nematomorpha and also laid the foundation for possible protocols to follow for checking on parasites’ distribution and conservation status, which are needed given the fact parasite conservation is a recent conservation sub-field that still needs to have standardized methods.