

**Speaker:**

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Date: Monday, Mar. 08, 2021**Time:** 4:00 pm - 4:50 pm**Zoom:** 952-3324-4564**Passcode:** 835322**Title:**

"Fairyfly fairytale: Unraveling the phylogenetics of Mymaridae (Hymenoptera: Chalcidoidea)"

Abstract:

The superfamily Chalcidoidea (Hymenoptera) is an immensely diverse (24 families, estimated 500,000 species) and economically important group of mostly minute parasitoid wasps often utilized for the biological control of many insect pests. Despite their economic and ecological importance, the systematics surrounding the exploration of individual families is wanting. The Mymaridae (fairyflies) are among the most stunningly minute (smallest measuring 0.139 mm), abundant, morphologically diverse, and economically important families of egg-parasitoid wasps within Chalcidoidea in need of a sound phylogenetic hypothesis. The family is comprised of 116 genera and over 1,400 described species and several genera have been used in place of pesticides for control of insect pests in both agricultural and natural ecosystems. Based on past morphological and molecular analyses, Mymaridae are strongly supported as monophyletic, and sister group to the rest of Chalcidoidea. Little has been done to evaluate any proposed higher-level relationships within the family in a robust evolutionary context. Using a combination of traditional ribosomal genes and next-generation sequencing (Anchored Hybrid Enrichment) my research is unraveling congruent support for 3 new subfamily classifications and 5 tribes within the family. This exciting seminal molecular framework will allow for evaluation of morphological characters to further describe and classify the subfamilies and tribes, timing of diversification rates, and exploration of evolutionary patterns of host associations directed especially at tribes which includes numerous species beneficial to biological control.