

**Speaker:**

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**Date:** Monday, Nov. 09, 2020  
**Time:** 4:00 pm - 4:50 pm  
**Zoom:** 952-3324-4564  
**Passcode:** 835322

**Title:**

“Slicing the Gordian knot: A phylogenetic analysis of the subfamilial relationships of Aphelinidae (Hymenoptera: Chalcidoidea)”

**Abstract:**

Aphelinidae (Hymenoptera: Chalcidoidea) are a diverse group (1,385 species, 40 genera) of parasitoid wasps that exploit whiteflies, scale insects and aphids. They are among the most important taxa used in biological control and are the cornerstone of over 90 successful biocontrol programs. Resolving the phylogeny of Aphelinidae has proved to be a veritable Gordian knot: an intractable problem that morphological and traditional molecular approaches are unable to solve. Next-generation molecular analyses have shown promise for recovering phylogenetic hypotheses for challenging taxa. Here we use an expansive Anchored Hybrid Enrichment (AHE) dataset (1,013 loci, 447,698 bp) to recover a phylogenetic hypothesis for Aphelinidae, explore the influence of exonic and intronic regions on the resulting topology, suggest a revised tribal classification, and develop a hypothesis for the ancestral host and host shifts in Aphelinidae. The conclusions drawn from our investigation will enable biocontrol specialists to evaluate species of Aphelinidae within a phylogenetic context, and to predict and evaluate traits that may influence the success of biological control programs. It will also provide a framework for future work into the phylogenetics of economically important parasitoids in Aphelinidae including the genus *Encarsia* Förster.