

**Speaker:**

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Date: Monday, Feb. 22, 2021**Time:** 4:00 pm - 4:50 pm**Zoom:** 952-3324-4564**Passcode:** 835322**Title:**"The Dynamics of the Psyllid Microbiome and the *Candidatus* Liberibacter Host-Interface"**Abstract:**

Symbiotic associations between insects and microbes are ubiquitous. In the Hemiptera, sap-feeding insects associate with endosymbionts that are both obligate and facultative for insect survival. The roles of facultative endosymbionts for their insect host, if any, are generally unknown. Nevertheless, some facultative endosymbionts are known to influence insect phenotype and fitness by conferring resistance to natural enemies and pesticides and manipulating insect development and reproduction. In the superfamily Psylloidea, less is known about the diversity and prevalence of their facultative symbionts compared to other sap-feeding pests such as aphids (Aphididae). Here, using 16S rRNA gene amplicon sequencing we identify facultative symbionts across divergent psyllid host lineages. Taking advantage of a new comprehensive phylogenomic analyses of Psylloidea, we included psyllid samples from 45 species of 35 genera of 7 families, collected from 11 international geographical regions for this study. Psyllid DNAs were extracted following a nondestructive DNA extraction protocol in order to correctly identify psyllid species with high confidence using both a molecular and morphological diagnostic approach. Across psyllid lineages, psyllid species harbored relatively few facultative endosymbionts with an average of three symbionts, ranging from one to seven. The identity of facultative endosymbionts was predominantly in the family Enterobacteriaceae (56.4 %) and Anaplasmataceae (19.7 %). In this process, putative novel *Candidatus* (Ca.) Liberibacter species, that are potential threats to our global agricultural industry, are also detected from three psyllid species. To obtain more genomic information and the evolutionary relationships of these Ca. Liberibacter species, I also conducted a high throughput metagenomic sequencing approach on Ca. Liberibacter infected psyllid DNAs. The phylogenetic analyses reveal that the two Ca. Liberibacter species detected from 16s rRNA amplicon sequencing are closely related to Ca. L. americanus and Ca. L. psyllauros. However, one appears to be distinct species from Ca. L. americanus, and the other is a haplotype of Ca. L. psyllauros. Taken together, our results demonstrate that the superfamily Psylloidea has prevalent but relatively few facultative symbiont taxa including Ca. Liberibacter species that are present throughout the psyllid tree of life.