

Speaker:

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Date: Monday, Oct. 25, 2021**Time:** 4:00 pm - 4:50 pm**Zoom:** 948 0131 1028**Passcode:** 347039**Title:**

“Comparative Genomics Reveals that Metabolism Underlies Evolution of Entomopathogenicity in Bee-loving *Ascosphaera* spp. Fungi”

Abstract:

Ascosphaera (Eurotiomycetes: Onygenales) is a diverse genus of fungi that is exclusively found in association with bee nests and comprises both saprophytic and entomopathogenic species. To date, most genomic analyses have been focused on the honeybee pathogen *A. apis*, and we lack a genomic understanding of how pathogenesis evolved more broadly in the genus. To address this gap we sequenced the genomes of the leaf-cutting bee pathogen *A. aggregata* as well as three commensal species: *A. pollenicola*, *A. atra* and *A. acerosa*. We carried out de novo annotation and comparison of the assembled genomes, including the previously published genome of *A. apis*. To identify candidate virulence genes in the pathogenic species, we performed secondary metabolite-oriented analyses and clustering of biosynthetic gene clusters (BGCs). Additionally, we captured single copy orthologs to infer the phylogeny and created codon-aware alignments to determine orthologs under selective pressure in our pathogenic species. Our results show several shared BGCs between *A. apis*, *A. aggregata* and *A. pollenicola*, with virulence and antifungal resistance related genes present in the bee pathogens and commensals. Genes involved in metabolism and protein processing exhibit signatures of positive selection in the pathogens under a fitted branch-site model. Metabolism and protein processing genes are important in other fungal pathogens, suggesting a common route to evolution of pathogenicity. We also identified known virulence genes in *A. pollenicola*, *A. acerosa* and *A. atra* supporting previous proposals that these commensals may be opportunistic pathogens.