

**Soil and Water Sciences Department  
Graduate Student Exit Seminar****Speaker:** **Ryan Blaustein**  
**Ph.D. Degree Candidate****Advisor:** Dr. Max Teplitski**Title:** **Defining the Interactions within the Citrus  
Microbiome during Huanglongbing Disease  
Progression and in Response to Phytopathogen  
Removal****Date:** Monday, September 18, 2017**Time:** 3:00 pm – 4:00 pm**Location:** McCarty Hall A, Room G186

Huanglongbing (HLB; “citrus greening”) is a major threat to global citrus production. Any successful effort to manage the disease will almost certainly require an integrated strategy where manipulation of the citrus microbiome may be an important component. This work utilized 16S rRNA gene sequencing to investigate (1) the interactions and associations between native microbiota and *Liberibacter* (i.e., the HLB pathogen) and (2) the effects of novel antimicrobials on the citrus microbiome. First, the core citrus leaf and root microbiota were defined across several variables, including HLB symptom severity, location, cultivar, and season/time. The relative abundance of *Liberibacter* among leaf microbiota negatively correlated with alpha diversity and positively correlated with HLB symptom progression, suggesting community diversity decreases as symptoms progress. Network analysis identified mutually exclusive relationships between *Liberibacter* and *Burkholderiaceae*, *Micromonosporaceae*, and *Xanthomonadaceae*, which may mediate the inverse association between the phytopathogen and the stable microbiota. Next, while the antimicrobials tested did not impact the relative abundance of the *Liberibacter* in leaves, they significantly suppressed its proliferation in roots and induced its removal in many cases. The compounds did not grossly disrupt microbiota structure, suggesting target-specificity against the phytopathogen. Moreover, the metagenomic functions of the microbiota in both studies, as predicted from 16S taxonomic assignments, were compared. Metagenomes contained enrichments in a variety of key functions based on host health-state. Interestingly, the functional profiles of root microbiota of asymptomatic trees were more similar those of HLB-diseased trees that had received treatment than untreated controls, suggesting that the antimicrobials caused the microbiome to shift towards a “healthier” functional state. Overall, our findings advance the understanding of microbiota-pathogen-host relationships, which not only have applications for biocontrol of HLB, but also broader plant disease management.

For our off-campus students, off-campus faculty, and on-campus students who cannot attend, this seminar can be viewed via live or watched at a later date via this link: [Ryan Blaustein](#). In addition, all seminars are archived for viewing on our [SWSD Seminar Page](#).