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### Authors

Zhang, M.  
Powell, Charles A.  
Chuan, Yu  
et al.

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**Characterization of the microbial community structure in ‘*Candidatus Liberibacter asiaticus*’-infected citrus plants treated with antibiotics**

Zhang, M.<sup>1,2,3</sup>, Powell, C.A.<sup>1</sup>, Chuan, Y.<sup>1</sup>, and Duan, Y.<sup>2</sup>

<sup>1</sup>Indian River Research and Education Center, IFAS-UF, Fort Pierce, FL34945, USA

<sup>2</sup>USDA-ARS, US Horticultural Lab, Fort Pierce, FL34945, USA

<sup>3</sup>State Key Lab for Conservation and Utilization of Subtropical Agro-bioresources, Guangxi Univ., Nanning, Guangxi, CHINA 530004

The updated PhyloChip™ G3 were used to explore the differences in the relative abundance and phylogenetic diversity of the bacterial communities associated with HLB-affected citrus plants in the field over a growing season and those treated with antibiotic combinations of AG (Ampicillin at 1000 mg/L and Gentamicin at 100 mg/L) and PS (Penicillin at 1000 mg/L and Streptomycin at 100 mg/L). Both antibiotic treatments resulted in significantly lower Las bacterial titers ( $P < 0.05$ ) and their hybridization scores. Of the 50,000+ available operational taxonomic units (OTUs) on PhyloChip™ G3, 7,028 known OTUs in 58 phyla were detected from the field plants, and 7,407 OTUs in 53 phyla from the inoculated potted plants. Proteobacteria was the constantly dominant phylum of bacteria (38.7%~44.1%) vying for prevalence based on the season, followed by Firmicutes (23.5%~29.0%), Actinobacteria (12.4%~16.1%), Bacteroidetes (6.2%~6.6%) and Cyanobacteria (2.3%~3.2%). Circular tree comparing the Las-free and the Las-infected samples indicated that only 17 families present in the Las-free plants, such as *Cyanobacteriaceae*; but more than 137 families detected in the Las-infected plants, such as *Staphylococcaceae* and *Pseudonocardiaceae*. *Cyanobacteria* are believed to be responsible for introducing oxygen into the atmosphere and fixing nitrogen and phosphorus assimilation for plant growth. Both *Staphylococcaceae* and *Pseudonocardiaceae* were recognized as an emerging opportunistic pathogen of plant and animals. When compared to the bacterial populations in the leaves of citrus trees receiving the water control treatment, the *Bacteroidete* population decreased ( $P < 0.05$ ) by 59.6% and 51.8% in the plants receiving AG and PS treatments, respectively. The overall diversity of bacteria also decreased with the antibiotic treatments. Bacterial cells in close proximity may be able to modify their microenvironment; thus, making the composition of the microbial community an important factor in the ability of Las to cause HLB progression. A low Las level was seen as a both a seasonal fluctuation, part of the bacterial population dynamics, and as a response to the antibiotic treatments.