

Genetic Diversity and Fingerprinting of HLB Bacteria

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This is the first year report of the two-year project on the genetic diversity and fingerprinting of Huanglongbing-associated bacteria. The project involves three objectives: 1). Analyses of historically and currently available literature data on HLB and identify important issues to address; 2). Study what microorganisms are involved in HLB in addition to what we currently know; and, 3). Use genomic information to study the variation of HLB-associated bacteria and their source of origins.

While the current descriptions of HLB are mainly yellowing and mottling of citrus leaves, literature research showed that symptoms of HLB are complex, including: yellow shoots from the green canopy, yellowing or mottling of the entire leaf, premature defoliation, dieback of twigs, decay of feeder rootlets and lateral roots, decline in vigor, stunted growth, bearing multiple off-season flowers, producing small, irregularly-shaped fruit that remains green at the bottom, fruit tastes bitter, and ultimately and finally the death of the entire plant.

Furthermore, HLB diagnosis should involve a continuous observation of symptom development. Literature study also indicated that the true etiology of HLB is awaited for more research. “*Ca. Liberibacter* spp.” are bacteria associated with HLB. Pathogenicity test on these bacteria has never been performed. As we further examine the microflora of citrus, we identified a known plant pathogen, phytoplasma, associated with HLB in China in addition to the currently known “*Ca. L. asiaticus*”. A manuscript describing our discovery has been published in *Phytopathology*.

Using the currently available information, the geographical distribution of HLB associated bacteria have been summarized. Among the several HLB associated bacteria, only *Ca. L. asiaticus* has been detected in Florida. “*Ca. L. asiaticus*” and “*Ca. Phytoplasma asteri*” are found in China. In Brazil, “*Ca. L. asiaticus*”, “*Ca. L. americanus*” and a peageon pea phytoplasma are detected. “*Ca. L. asiaticus*” and “*Ca. L. africanus*” are present in Africa.

Current research focuses in the direction of characterization of “*Ca. Liberibacter asiaticus*” and HLB phytoplasma at the genomic sequence levels. This will further reveal the diversity of HLB associated bacteria at a higher resolution, which in turn will help to the creation of an improved system to assist identification, differentiation and fingerprinting of HLB associate bacteria.

Although HLB has not been found in California, the destructiveness of the disease and its presence in Florida, plus the recent recognition of Asian citrus psyllid in southern California is alarming to the citrus industry. A comprehensive understanding of HLB is critical for the disease control and prevention. The preventive efforts currently implemented in California need to exclude all forms of HLB, including the potential pathogen of phytoplasma we recently identified. The association of different types of HLB-associated bacteria to different continents could also help us to track source of HLB infection.

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