4.14 Characterization of “Candidatus Phytoplasma asteri” citrus Huanglongbing strain in Guangdong, China.

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Huanglongbing (HLB) or yellow shoot disease is a highly destructive disease of citrus. In addition to the citrus growing regions in Asia and Africa, HLB has recently been found in both South and North America. Understanding the etiology of HLB is critical for disease research and management. Despite efforts of over half a century, identification of the HLB causal agent remains highly challenging. Most available data show that HLB is associated with infection by “Candidatus Liberibacter spp.” which are vectored through psyllids. However, Koch’s postulates have not been fulfilled. There have been speculations that other microorganisms may also be involved in HLB. The latter is substantiated by two recent research findings: A phytoplasma closely related to the pigeon pea witches’-broom phytoplasma (16Sr IX) was reported to be associated with citrus HLB in the state of Sã o Paulo, Brazil; And in a survey performed in Guangdong Province, P. R. China in 2006 and 2007, 110 out of 141 citrus samples showing typical symptoms of HLB from 11 different cities were detected positive with the presence of a strain of “Candidatus Phytoplasma asteri”. Many of the samples were mix-infected with “Ca. Liberibacter asiaticus”. To further characterize the HLB phytoplasma from Guangdong, three DNA sequences upstream and downstream of the \textit{rrn} operon (\textit{rrn-up1}, \textit{rrn-down1} and \textit{rrn-down2}) were obtained and used as queries to perform BLAST analyses against the GenBank database. Like the 16S rRNA gene locus, all three sequences identified “Ca. Phytoplasma asteri” strain OY-M, causing onion yellow disease in Japan, as the most similar. However, nucleotide identities varied with \textit{rrn-up1} at 99%, \textit{rrn-down1} at 96% and \textit{rrn-down2} at 98%, contrasting the 99-100% nucleotide identity at the 16S rRNA gene locus. Nucleotide deletions, rather than nucleotide polymorphisms (transversions\transitions) as in the case of 16S rRNA gene sequence analysis, were the main contributors to the sequence variations. More genome-wide sequence characterizations are currently underway.