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Differentiation of “Candidatus Liberibacter asiaticus” isolates from Brazil, China, and the United States

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“Candidatus Liberibacter asiaticus” is associated with citrus Huanglongbing (HLB, yellow shoot disease), a highly destructive disease currently threatening world citrus production. HLB has a long history in China and was found in Brazil in 2004 and U.S.A. in 2005. There is an urgent need to differentiate isolates of “Ca. L. asiaticus” from different geographical regions for effective control of HLB. In this study, isolates of “Ca. L. asiaticus” collected from Brazil, China and the United States were evaluated based on two previously characterized genomic loci, one locus (trn1) with variable tandem repeat numbers (TRNs), and the other locus (snp1) is characteristic in single nucleotide polymorphisms (SNPs). A total of 299 strains (84 Brazil, 132 China and 83 U.S.) were analyzed. At the trn1 locus, “Ca. L. asiaticus” strains were divided into TRN-A and TRN-B groups. TRN-A isolates dominated the China and U.S. populations but were not detected in the Brazil isolates. In contrast, TRN-B dominated the Brazil isolates but occurred at low frequencies in China (3%) and U.S. (6%). SNP Analyses at the snp1 locus established Term-A and Term-G groups. Term-A group included all Brazil and China isolates, along with 6% U.S. isolates which were also TRN-B isolates. The remaining (94%) U.S. isolates were in Term-G group. By combining data from the analyses of the two genomic loci, it is shown that the TRN-A:Term-A genotype was unique to China, TRN-A:Term-G genotype was unique to U.S., and the TRN-B:Term-A genotype dominated the Brazil isolates. No TRN-B:Term-B isolates were found.