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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 (*trn*1) with variable tandem repeat numbers (TRNs), and the other locus (*snp*1) is characteristic in single nucleotide polymorphisms (SNPs). A total of 299 strains (84 Brazil, 132 China and 83 U.S.) were analyzed. At the *trn*1 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 *snp*1 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.