4.7 Genome Analysis of *Candidatus* Liberibacter asiaticus Reveals Unique Features for Designing HLB Control Strategies


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Citrus Huanglongbing (HLB) is the most destructive and devastating disease of citrus in the world. Since the initial report of the disease in Florida in August of 2005, HLB has spread throughout 32 of the citrus-producing counties. The causal agent of this disease is believed to be three species of alpha-Proteobacteria, *Candidatus* Liberibacter asiaticus (Las), *Ca. L. africanus* and *Ca. L. americanus*. Las is the most widely-distributed species and the only species that has been detected in Florida to date. Due to its fastidious nature, the bacterium has not been cultured *in vitro*. We obtained and annotated a draft genome of *Ca. L. asiaticus* by using multiple displacement amplification and 454 pyrosequencing from Las-infected Asian citrus psyllids (*Diaphorina citri*). The draft genome contained at least 1,216,073 base pairs with ca. 17X redundancy and an average GC content of 37.4% in 36 contigs, ranging from 1.0 kb to 186 kb. The annotated draft genome contained two rRNA operons and 41 tRNA genes. Approximately 60.4 % of the 1123 predicted coding sequences (CDS) have homologues with known or putative function and 61(5.4%) are pseudogenes, whereas the remaining 34.5 % represent hypothetical-conserved open reading frames (ORFs). It is worthwhile to note that the draft genome shared similar numbers of flagella-related ORFs as *Sinorhizobium meliloti* 1021 and *Agrobacterium tumefaciens* str. C58 even though the Las genome is much smaller than the other two. Putative “toxin” proteins and their type I secretion system were also identified from the draft genome. The metabolite pathways and genome evolution of this unique α-Proteobacterium, which is both an intercellular plant pathogen and insect parasite/symbiont, were also examined.