

Provisional assembly and analysis of two *Candidatus Liberibacter solanacearum* genomes derived from independent new zealand sources

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The unculturable α -proteobacterium *Candidatus Liberibacter solanacearum* (CLso) is associated with Zebra Chip, an important emerging disease of potato (*Solanum tuberosum*). This phloem-limited bacterium, transmitted by the tomato-potato psyllid *Bactericera cockerelli*, was first identified in 2008 and is related to the *Ca. Liberibacter* species implicated in Huanglongbing (citrus greening), currently considered the most serious and destructive disease of citrus in the world. Two New Zealand CLso genomes have been provisionally assembled against the 1.26 Mbp genome of a USA isolate of CLso obtained from psyllids infesting potatoes (CLso-ZC1). The two independent New Zealand sources were a single psyllid from a colony which originated from insects collected from tamarillo (NZCLso-TPP), and a CLso infected tomato plant (NZCLso-Tom). Preliminary analysis of the genome alignments revealed that, despite being sourced from two different host organisms, the two NZ genomes are much more similar to each other than to the single USA genome. The first genome drafts identified 227 regions missing from the alignments. Many of these missing regions are intergenic. There are also four coding regions, containing 24 putative genes (approximately 2% of the putative coding sequences) which are currently missing. It is uncertain if these regions are missing from the NZ CLso genomes, or are not visible due to either genomic rearrangements or a high level of polymorphism. We have not been able to manually sequence these regions to date. One major inversion of 55 kB has been located in the NZCLso-Tom genome compared to CLso-ZC1, and both NZ CLso genomes contain two large putative prophage regions similar to the US CLso-ZC1 genome. The draft assemblies for the putative prophage regions confirm the similarity of the NZ genomes and the difference between the NZ genomes and the US genome. These findings suggest that there is significant genotypic variance in CLso.

Notes