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Comparative genomics analysis of *Liberibacter* species to elucidate pathogenesis and culturability

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Liberibacter crescens BT-1, a gram negative, rod-shaped bacterial isolate, was previously recovered from mountain papaya and sequenced. As L. crescens is culturable and is not a pathogen of citrus, comparative genomics of this strain with other uncultured, pathogenic *Liberibacter* should suggest genes involved in both phenotypes. Genomic comparison to *Liberibacter* sp. revealed differences in metabolic pathways and virulence genes. Specific differences in metabolism include the inability of *L. asiaticus* and *L. solanacearum* to synthesize histidine, tryptophan, and thiamine, as well as a reduced ability to produce other amino acids. *L. asiaticus* and *L. solanacearum* possess a thiamine ABC transporter not found in *L. crescens*, which may compensate for the inability to synthesize thiamine. Diversity in the flp pilus operon and metal ABC transporters were observed that may contribute to the pathogenesis of the uncultured species. These differences may contribute to variation in virulence and culturability among species. Finally, two putative prophage regions were found in *L. crescens* that share moderate functional similarity to the phage regions of *L. asiaticus*, but sequence similarity is not conserved. Additional genomic comparisons will expand our understanding of virulence and vector-interactions of the described *Liberibacter* sp.