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Translating Anatomical Structures and Functional Genomics of *Candidatus Liberibacter asiaticus* and *solanacearum* Into Circulative, Propagative Vector-Mediated Transmission Processes

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Ca. Liberibacter asiaticus is the putative fastidious bacterial causal agent of citrus greening disease, also known as Huanglongbing (HLB), translated from Chinese as yellow dragon disease. The HLB bacterial pathogen is indigenous to Asia but has been introduced and dispersed to citrus throughout the Americas. A related bacterium that is indigenous to the Americas causes damage to potato (zebra chip) and tomato (vein-greening) and other solanaceous hosts. The causal agents are propagative and circulative in the psyllid vector, *Diaphorina citri* (Kuwayama) and *Bactericera cockerelli* (Sulc.), the Asian citrus and potato (or tomato) psyllid, respectively. The specific psyllid proteins that are indirectly or directly involved in the circulative, propagative transmission pathway are not known. However, if proteins were known that function at key points in the pathway e.g. post-ingestion, infection, biofilm formation, nutrition, circulation, and/or acquisition were known, such knowledge could be exploited to knock out their expression and abate pathogen transmission. To this end a combined approach involving functional genomics and anatomical localization of the bacterium is being implemented. Results indicate that *Ca. Liberibacter* establishes biofilms on the outer surfaces of the alimentary canal and salivary glands of the Asian citrus psyllid (ACP) *Diaphorina citri* Kuwayama and the potato psyllid (PP) *Bactericera cockerelli* Sulc. *In silico* transcript profiling of infected and uninfected ACP and PP identified a number of mis-expressed, unique transcripts (unitrans). Functional predictions (gene ontology associations) implicate certain of these unitrans in *Ca. Liberibacter* infection of the psyllid host and/or in psyllid-mediated *Ca. Liberibacter* transmission processes.