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Authors

Fisher, T.
He, R.
Nelson, W.
et al.

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A Comparative Transcriptomic Approach to Elucidate Psyllid-*Ca. Liberibacter* Interactions

Fisher, T., He, R., Nelson, W., Vyas, M., Willer, M., Soderlund, C., Gang, D., and Brown, J.K.

School of Plant Sciences, The University of Arizona, Tucson, AZ 85721 USA

Citrus greening is the most destructive disease of citrus crops worldwide. The introduced Asian citrus psyllid (ACP) *Diaphorina citri* Kuwayama transmits the (putative) causal bacterium, *Candidatus Liberibacter asiaticus*. A close relative, *Ca. L. solanacearum*, is the pathogen associated with Zebra chip disease of potato and vein-greening disease of tomato. It is both transmitted by and propagative in the endemic (western U.S) potato psyllid (PoP) *Bactericera cockerelli* Sulc. The PoP occurs widely in the western U.S. and so has been used as a parallel study system for the quarantined ACP-greening complex. To identify proteins involved in global psyllid-*Ca. Liberibacter* interactions, the ACP and PoP transcriptomes were sequenced, yielding a total of 45,976 and 82,224 Illumina unique ACP and PoP transcripts, respectively. Cluster analysis revealed a high degree of sequence and transcript conservation suggestive of roles in core growth and developmental processes, providing the first molecular snapshot of the specific psyllid genes responsive to parasite invasion and circulation in the host. Evidence of inter-psyllid molecular conservation substantiates the suitability of PoP as a study system for ACP-*Ca. L. asiaticus*. Comparative *in silico* expression analysis within and between psyllid species revealed predicted functions involved in *Ca. Liberibacter* parasitism that were both unique and shared in common among adult and nymphal instars. In addition, functional characterization based on Gene Ontology analysis has revealed a number of genes associated with host-parasite interactions that could mediate *Ca. Liberibacter* infection, propagation, and circulation in the psyllid, as well as transmission processes.