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### Title

Sequencing and annotation of the Wolbachia endosymbiont of Diaphorina citri by the CG-HLB Genome Resources group reveals candidate sources of interaction with the insect host

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### **Sequencing and annotation of the Wolbachia endosymbiont of *Diaphorina citri* by the CG-HLB Genome Resources group reveals candidate sources of interaction with the insect host**

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The Citrus Greening – Huanglongbing (CG-HLB) Genome Resources group serves as a bioinformatics resource for diverse projects related to the biology of CG-HLB. A major recent project concerns the generation and annotation of a draft genome sequence for the Wolbachia endosymbiont (wDi) of the Asian citrus psyllid, of particular interest given the potential for control of psyllid behavior through manipulation of its bacterial endosymbionts. The Wolbachia draft genome was assembled and contigs aligned using the wPip strain from mosquito, its closest relative among completed Wolbachia genome sequences. OrthoMCL analysis of the annotated draft genome sequence confirmed the presence of 670 genes common to all sequenced Wolbachia genomes. Candidate host interaction factors include 54 predicted ankyrin proteins hypothesized to play a role in host reproductive manipulation, a Type IV secretion system linked to ankyrin protein export, and a bacterioferritin linked to host iron homeostasis. Several metabolic capabilities were identified in wDi that are absent from Liberibacter. FtsZ and Wsp phylogenies indicate that the Wolbachia strain in the Florida *D. citri* isolate falls into a sub-clade of supergroup B, distinct from Wolbachia present in Chinese *D. citri* isolates, supporting the hypothesis that the *D. citri* introduced into Florida did not originate from China. The Wolbachia sequence and annotation can be viewed on the CG-HLB Genome Resources Website (<http://citrusgreening.org/>), together with the sequences of publically available Liberibacter genomes sequenced to date. Future plans involve development of a searchable Liberibacter diagnostic sequence database using the over 1700 publically available *Ca. Liberibacter* gene sequences.