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The Asian Citrus Psyllid Genome (*Diaphorina citri*, Hemiptera)

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The Asian citrus psyllid, *Diaphorina citri* (Hemiptera), is an important pest of citrus because it vectors bacteria responsible for huanglongbing, which is one of the most serious diseases of citrus worldwide. The first genome draft of *D. citri* (DIACI_1.0) was completed in 2011 (ARS, Ft. Pierce, FL), however, gaps in the assembly prompted additional sequencing using the long run PacBio system at the Los Alamos National Lab, NM. The revised draft genome (DIACI_1.1) was assembled using the new software PB-Jelly, with an improved N50 of 38 kb (up from 25 kb) and an increase by over 10 million in the number of resolved bases. The genome and transcriptome have been submitted into the public domain at the National Center for Biotechnology Information, NCBI, and the genome is currently being submitted to be processed and made available for access by the larger research community [http://www.ncbi.nlm.nih.gov/genome?LinkName=bioproject_genome&from_uid=29447]. The psyllid transcriptome identified over 25,600 predicted genes, and is supported by an additional 19,598 previous EST's. Life-stage specific transcripts were identified for adults, nymphs and eggs. BlastX analyses showed that the psyllid genome has the most similarity to the Pea Aphid, *Acyrtosiphon pisum*, another hemipteran. The transcriptome data was provided to the Innocentive® Challenge Program in 2011 to advance efforts for RNAi development against psyllids. Other researchers are also using these data to develop strategies to suppress psyllid populations. Efforts are now focused on annotation of the psyllid genome which will provide more information on the genetic basis of psyllid biology. Free Downloads of the most recent datasets can be found at: <http://www.psyllid.org/node/10> which includes the transcriptome and predicted protein files in FASTA format, and the gene locations on the DIACI_1.1 Genome assembly (GFF3 format).