CITRUS ADVANCED TECHNOLOGY PROGRAM

QUARTERLY & FINAL REPORTS: Control of Citrus Greening, Canker & Emerging Diseases of Citrus

▶ INSTRUCTIONS

(●) *Quarterly Report* ( ) *Annual Report* ( ) *Final*

Required: What is the "headline" for this report (e.g. a one-sentence "newspaper headline" describing what you accomplished)

Partial ACP transcriptomes annotated, deposited in GenBank

Proposal Title

The citrus psyllid transcriptome and time course differential gene expression in Ca. Liberibacter-infected/free whole psyllids and organs

Today's Date	Sponsoring Organization (drop-down)	Category (drop down)
4/25/12	Citrus Research and Development Foundation	Infection Responses

REPORT UPDATE (500 words; summarize your accomplishments)

For the Asian citrus psyllid (ACP), we constructed and sequenced two Illumina Paired-end libraries for ACP uninfected/infected salivary glands (SGs) and generated 818 M reads, totaling 83 Gb raw data. We are presently combining the ACP SG with the alimentary canal (guts) data generated previously to make the assembly DcGs. In addition, combining the data that we generated from two 454 Titanium libraries and six Illumina Paired-end libraries of Asian citrus psyllid (ACP) and the Sanger sequence data from Genbank for this species, we have made a hybrid assembly "ACPisp" to yield 98,265 Unitrans from 140 M Illumina reads, 664 K 454 reads and 19 K Sanger reads, respectively. Of the 98,265 total unitrans, 22,543 unitrans (23%) were annotated with an average unitrans length of 1,848 bp. This dataset will provide deeper insights into the whole trancriptome of ACP.
To translate peptide sequences from transcript (coding) sequences: (1) the ESTScan program was installed, (2) the hemiptera sequences were downloaded from Genbank, (3) these were used to train the ESTScan matrix, and (4) ESTScan was used with the hemiptera matrix to extract the peptide sequences from the ACPisp transcript sequences. An additional matrix was created using all the Genbank insecta sequences, and a second set of peptides were generated using the insecta sequences. The hemiptera matrix performed better than the insecta matrix, creating slightly more and longer sequences. ESTScan was also used to extract peptides from our WFB assembly using the same matrix. The two peptide files were used as input into orthoMCL, and the resulting clusters were used as input into cmpPAVE in order to investigate functionally similar transcripts between these two genomes.

Secondly, we have made an extensive comparative transcriptome analysis of ACP and whitefly (also important agricultural sucking pest and invasive species), the potato psyllid, and pea aphid. Results indicated the presence of a suite of immunity and stress-related genes.

Thirdly, for potato psyllid, we constructed and sequenced a suite of Illumina RNA-seq libraries to investigate infected and uninfected potato psyllid gene expression changes reared at different temperatures. We have identified a branch of genes that were differentially expressed under different temperatures in the Ca. Liberibacter-infected and uninfected potato psyllid. This work also will provide a good reference for the study of temperature affects for ACP in the future.

We continue work on several manuscripts that are expected to be submitted during May-July.

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Contract Number 21

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Total Funds (current year) $164,999.00

SUBMIT REPORT

CITRUS RESEARCH AND DEVELOPMENT FOUNDATION, INC.