CITRUS ADVANCED TECHNOLOGY PROGRAM

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

SELECT PERIOD September 2014

(●) *Quarterly Report* ( ) *Final*

Proposal Title

Molecular basis of Citrus Greening and related diseases gleaned from genome analyses of hosts and pathogens

Today's Date	Sponsoring Organization (drop-down)	Category (drop down)
10/15/14	Citrus Research and Development Foundation	Citrus Genomics

REPORT UPDATE (500 words-It is not necessary in this public report to disclose your institution's proprietary information or intellectual property.)

We continued to computationally analyze genomes with the goal to suggest hypotheses about molecular mechanisms of Liberibacter pathogenicity. We added the genome of Liberibacter solanacearum (CLso-ZC1, 1192 proteins) to the analysis of Liberibacter americanus (Sao Paulo, PW_SP, 983 proteins), Liberibacter asiaticus (gxpsy, psy62, A4,1109 proteins), and Liberibacter crescens: (BT-1, 1378 protiens). Similarly to other Liberibacter, solanacearum genome contains 2 prophages, but they are not arranged in tandem. One of the prophages is highly similar, in agreement with the hypothesis that prophage proteins and their homologs integrated in the Liberibacter genome may be the cause of pathogenicity. Prophages of culturable (and possibly non-pathogenic or less pathogenic) L. crescens are less similar to those of other species. Comparative analysis of the genomes identified about 70 potential pathogenicity genes. 40% of them have homologs in the prophage region. Many contain predicted signal peptides, suggesting that they are exported. Some of these proteins are not of bacterial origin, but are more similar to Eukaryotic proteins, additionally reinforcing the evidence for their hypothesized pathogenicity. Some of the highlights are mentioned here. Hypothetical protein CLIBASIA 3975 is homologous to Protein tyrosine phosphatase (PTPc), which is a Eukaryotic protein not needed in Bacteria that functions in numerous eukaryotic signalling pathways. These phosphates are frequently exploited by pathogenic bacteria for virulence. In addition, CLIBASIA 3975 possesses a signal peptide and is expected to be a secreted protein. Hypothetical protein CLIBASIA 3630 is homologous to Von Willebrand factor type A (vWFA), a mainly extracellular eukaryotic domain that functions in immune defenses. vWFA in the pilus of a Streptococcal pathogen mediates adhesion to host cells, so it is likely that this protein is one of the pathogenicity factors. CLIBASIA 3975 also has a pilus domain TadG. Hypothetical protein CLIBASIA 1935 is similar to OmlA protein from Xanthomonas axonopodis pv. citri. Since X. citri is a citrus canker pathogen and expression of OmlA is enhanced when grown on citrus leaves, this protein may be a potential virulence factor. In addition it has a predicted signal peptide, suggesting that it secreted. More distant homologs of this protein are from the "BLIP" (b-Lactamase Inhibitor) Fold. There is a loop in the protein structure that is known to insert in lactamase active site and inhibit it. Similarly located loop is present in CLIBASIA 1935, suggesting that this protein may be an inhibitor or some enzyme from Citrus.

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Form PR-12 Quarterly Reports **SUBMIT REPORT**

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