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)

Metabolic pathways analyzed, possible virulence factors found

Proposal Title

Insight into the causative agent of citrus greening disease (HLB) using computational structure/function analysis of genome encoded proteins.

Today's Date	Sponsoring Organization (drop-down)	Category (drop down)
5/28/11	Citrus Research and Development Foundation	Unclassified

REPORT UPDATE (500 words; summarize your accomplishments)

During the third period, we continued manual analyses of protein sequences, structures and functions with the emphasis on the data integration over Candidatus Liberibacter asiaticus (C. L. asiaticus) proteome. Based on these analyses, we started to construct a list of potential virulence factor and initiated building a model of the metabolic network of C. L. asiaticus (in collaboration with Dr. Andrei Osterman).

For each protein in C. L. asiaticus proteome, we selected the closest homologous structure as the template for structure modeling, analyzed the domain architecture of the protein and collected evidence to support function prediction by the consensus of all information, including homology, structure models, the context of the sequence in the genome, and the integrity of metabolic and signaling pathways. For about 80% of all proteins, we generated confident structure prediction based on homology modeling. For around 60% of all proteins, we obtained specific function predictions and for 20% only general function predictions could be achieved. Remaining 20% are currently unassigned.

Based on the function prediction and manual analyses, we classified proteins into different categories as described in details at: http://prodata.swmed.edu/congqian/category.html. One important category is potential virulence factors. Based on the local sequence properties (virulence factors are likely to be secreted or exposed on the surface of the bacterium), evolutionary history and predicted functions, we assembled a list of potential effectors, which may help us to understand the mechanism of C. L. asiaticus infection. Another important category is the proteins in metabolic pathways, for which we built the metabolic network model of this bacterium in collaboration with Dr. Andrei Osterman. This model not only offered insights into metabolic properties of the bacterium, but also provided further validation of the functions of these proteins. Presently, we are still optimizing the metabolic model and predicting proteins essential for the survival of C. L. asiaticus. Among them we will determine potential drug target if certain essential proteins lack orthologs in the plant or their sequence and structure properties are different enough to allow specific interaction between a drug and a bacterial protein.

In the next period, we will incorporate manually verified structure and function predictions into a public website. We will work on further identification of potential virulence factors or proteins that are relevant to important processes during infection by two approaches: (1) comparative analysis between C. L. asiaticus and the closely related proteome, Candidatus Liberibacter solanacearum, (2) homology relationship between C. L. asiaticus proteins with known virulence factors. We hope that our hypotheses about the virulence factors can lead to advances in understanding and controlling of citrus greening.

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SUBMIT REPORT

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