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)

genome sequence of Xanthomonas citri & related species

Proposal Title

Identification and characterization of critical virulence and copper resistance genes of Xanthomonas axonopodis pv. citri & related species

Today's Date	Sponsoring Organization (drop-down)	Category (drop down)
10/6/11	Citrus Research and Development Foundation	Unclassified

REPORT UPDATE (500 words; summarize your accomplishments)

Xacm strain
Xanthomonas axonopodis pv. citrumelo (Xacm) is a citrus pathogen causing citrus bacterial spot disease that is geographically restricted within the state of Florida. Illumina, 454 sequencing and optical mapping were used to obtain a complete genome sequence of Xacm strain F1, 4.9Mb in size. The strain lacks plasmids. Phylogenetic analysis revealed that this pathogen is very close to the tomato bacterial spot pathogen Xcv 85-10 with a completely different host range. We also compared Xacm to the genome of citrus canker pathogen Xac 306. Comparative genomic analysis showed differences in several gene clusters like Type 3 effectors, Type 4 secretion system, lipopolysaccharide synthesis and others. In addition to pthA, effectors such as xopE3, xopAI and hrpW were absent in Xacm while present in Xac. These effectors might be responsible for survival and reduced virulence of this pathogen on citrus compared to Xac. We also identified unique effectors in Xacm that may be related to the different host range as compared to Xac. Xacm F1 was shown to be pectate lyase deficient in Hildebrand's medium which is consistent with the sequence analysis. Comparison of the complete genome sequence of Xacm to Xac and Xcv provides valuable insights into the mechanism of bacterial virulence and host-specificity. The complete genome of Xanthomonas axonopodis pv. citrumelo has been deposited at EMBL/DDBJ/GenBank under the accession number NC_016010.

The manuscript entitled "Comparative genomic analysis of Xanthomonas axonopodis pv. citrumelo F1, which causes citrus bacterial spot disease and related strains provides insights into virulence and host-specificity." has been accepted by Journal of Bacteriology.

Xac Aw strain
Whole genome sequencing of Xanthomonas axonopodis pv. citri strain Aw was completed. The doubtful regions were checked and have been confirmed by PCR and sequencing. The annotation curation is done. Plasmid data for the strain was not obtained with high confidence level from initial sequencing. Hence, plasmids were purified from the genome and sequenced separately using 1/8th plate of 454 titanium sequencing. The preliminary sequences for the 2 plasmids have been generated using CLCbio Genomics Workbench. Gap closure was done by PCR and sequencing.
Initial analysis of T3SE revealed presence of XopF1 and avrGf1 gene and absence of HpaA as different from Xac A 306. Genetic analysis of those genes are underway.

Xac A44 (Cu resistant), Xac A*270 and Xacm 1381 (Cu resistant) strain: The chromosomes were completed while the plasmids were still not complete and gap closing is underway for those three strains.

The genome sequencing has provided valuable information regarding the virulence mechanism and copper resistance of citrus canker pathogen and related species.

PI First Name Nian
PI Last Name Wang
Email nianwang@ufl.edu
Phone 863-956-1151 extension 1430
Organization Citrus Research and Education Center

Contract Number 233
Project Duration (years) 3 *Year of Project* 3
Total Funds (current year) $107,054.00

SUBMIT REPORT

CITRUS RESEARCH AND DEVELOPMENT FOUNDATION, INC.