CITRUS ADVANCED TECHNOLOGY PROGRAM

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

SELECT PERIOD March 2016

(●) *Quarterly Report* ( ) *Final*

Proposal Title

Determining the role of a novel virus in Citrus Blight

Today's Date	Sponsoring Organization (drop-down)	Category (drop down)
3/31/16	Citrus Research and Development Foundation	Pathogen/Disease Detection

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

Citrus blight continues to be a major economic problem in citrus groves in Florida. Thousands of trees each year succumb to citrus blight, with estimated losses at over $60 million per year. The disease can occur on all common citrus cultivars, and Carrizo citrange are especially susceptible. Early symptoms are zinc deficiency in the leaves which may disappear, zinc accumulation in the phloem and eventually high zinc levels in the xylem. Blockage of xylem tissues with amorphous plugs follows with reduced water uptake. The causal agent of citrus blight is unknown. However, symptoms and all of the characteristics associated with citrus blight can be reproduced by root graft inoculations. Therefore in a project previously funded by CRDF we used NGS RNA sequencing protocols to look for novel viruses in roots of sweet orange with blight, but not present in roots of healthy trees, or trees affected by HLB. We identified several related endogenous pararetroviruses related to Petunia Vein Clearing Virus (PVCV) using a collection of 10 RNA libraries prepared from 10 different root samples collected from healthy trees or those with blight or HLB.

In the quarter just ending we have focused our efforts on the remaining objectives: generating complete genome sequences for any and all active blight associated pararetroviruses and developing a active virus specific assay comprehensive enough to detect all blight associated pararetroviruses. Progress towards the generation of a complete genome sequence for the blight associated pararetroviruses was stymied by the discovery of a variable region in the genome. As of the last quarter we were reporting 90% complete genome sequence. This quarter we are pleased to announce complete genome sequence. It should be noted that the complete sequence generated represents a single isolate from an individual tree, and pararetroviruses are known to exhibit considerable genetic diversity. Therefore the complete genome sequence of a single isolate was used to further generate primers to sequence the pararetroviruses from additional infected trees, which is necessary to develop a diagnostic assay capable of detecting all active pararetroviruses. Regardless, we moved ahead with developing assay for the detection of active pararetroviruses, and began screening multiple assays on the 50 tree sample set that was collected in the first year of the project. Of the eight assays developed, two show siginficant promise for being both comprehensively inclusive and highly senstive for detecting the active blight associated pararetrovirus.

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Organization USDA-ARS FDWSRU

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

CITRUS RESEARCH AND DEVELOPMENT FOUNDATION, INC.