

trapping program, visual surveys, psyllid collections and chemical treatments within a 400m radius of all psyllid finds. Psyllids collected in these surveys were tested for HLB. Despite the surveys and suppression efforts within two years the psyllid had spread throughout five Southern California counties, principally in Los Angeles County, but not to the Central Valley where the majority of commercial citrus is located. In March 2012 a psyllid collected from a grafted pummelo (of unknown origin) during a visual survey in Los Angeles County tested positive for HLB, the first such find in California. Plant material collected from the tree (exhibiting classic HLB leaf symptoms) confirmed that the tree was positive for HLB. A trace forward and trace back of the HLB positive tree was initiated to determine the original source of the budwood of the HLB positive tree (as yet unsuccessfully). Eradication of the tree ensued paralleled by the CDFA developed HLB-positive protocol previously established. All citrus and citrus relatives, ACP nymphs and adults within a 800m radius were collected and tested. With the positive HLB find the Citrus Pest Disease Prevention committee, working with CDFA, has provided the funding for HLB testing of all host plants and ACP (adults and nymphs) in the first 500 m around the find every two months for a year and the testing of ACPs in the next 500m around the find and the host plants that show symptoms. To date no other HLB-positive psyllids or trees have been detected.

S12011

Comparative study of different host range strains of *Xanthomonas citri* subsp. *citri*: Chemotaxis and biofilm formation.

Sena M.¹, Ferragud E.¹, Redondo C.¹, Johnson E.G.², Graham J.H.², Girón J.A.³, and Cubero J.¹

¹Instituto Nacional de Investigaciones Agrarias y Agroalimentarias (INIA), Plant Protection, Spain; ²University of Florida (UF-CREC), Citrus Research and Education Centre, USA; and ³University of Florida (UF-EPI), Emerging Pathogen Institute, USA. sena.marta@inia.es

Xanthomonas citri subsp. *citri* strain A (*Xcc* A) is one of the causal agents of Citrus Bacterial Canker (CBC). Bacterial strains within this species are classified according to differences in host range as well as phenotypic and genotypic characteristics. *Xcc* A has a broad host range within the genus *Citrus* and close relatives, whereas *Xcc* A* and *Xcc* A^W strains are limited to Key Lime (*Citrus aurantifolia*). The aim of this study was to compare the chemotactic profile and biofilm formation of *Xcc* A, A* and A^W strain types compared to *Xanthomonas alfalfae* subsp. *citrumelonis*, causal agent of Citrus Bacterial Spot, and *Xanthomonas campestris*, causal agent of Black Rot in crucifers. Our results suggest differences in the chemotactic profile between broad and limited host range *Xcc* strains and xanthomonads from other hosts. Differences in biofilm formation were found among the strains and the inoculated host. At the early stages of biofilm formation, *Xcc* A produced an interwoven fibrillar structure while *Xcc* A^W fibres had a linear structure. TEM revealed that surface motility structures on cells varied; *Xcc* A formed lateral appendages at the edge of the bacterial colony while *Xcc* A^W possessed a single polar flagellum. Purification and sequencing of *Xcc* surface proteins revealed the presence of type IV pilus associated with biofilm and twitching motility in other bacterial species. Current studies are focused on the role of this protein in biofilm formation and the possible differences among the *Xanthomonas* strains.

S12012

A new minisatellite-based scheme for the global surveillance of *Xanthomonas citri* pv. *citri*, the causal agent of Asiatic Citrus Canker.

Magne M.¹, Leduc C.¹, Vernière C.¹, Vital K.¹, Gordon J.², Escalon A.¹, Guérin F.², Gagnevin L.¹, and Pruvost O.¹

¹CIRAD (CIRAD), UMR PVBMT, Réunion, France; and ²Université de la Réunion, UMR PVBMT, Réunion, France. olivier.pruvost@cirad.fr

Xanthomonas citri pv. *citri* (*Xcc*), the causal agent of Asiatic Citrus Canker, is an internationally major bacterial pathogen currently not reported from countries in the Mediterranean basin, including the EU. Some pathological diversity among strains was reported, leading to the description in *Xcc* of pathotypes differing in host range and aggressiveness. *Xcc* is recognized as a monomorphic pathogen and the very low intra-pathovar diversity at housekeeping genes precludes the use of the increasingly popular MLST (MultiLocus Sequence Typing) for the global molecular surveillance of *Xcc*.

We developed a new MLVA (MultiLocus Variable number of tandem repeats Analysis) scheme. It targeted 51 minisatellite loci dispersed over the *Xcc* genome with tandem repeat size ranging from 10 to 217-bp, thus allowing the use of standard agarose gel electrophoresis in laboratories that are not equipped with a genotyper. Among these loci, 34 were found to be polymorphic within a strain collection composed of strains from all continents where *Xcc* has been recorded, including recent outbreaks in Africa where the bacterium is reemerging. This typing scheme displayed a maximal typeability and repeatability. The produced data support the usefulness of this new MLVA scheme for global surveillance of *Xcc*.

S12013

Analysis of microRNAome of Chinese citron 'C-05' resistant to Citrus Canker disease.

Dai S.M., Chen Y.M., Li D.Z., Li F., Yan J.W., and Deng Z.N.

Hunan agricultural university, China. dsm531@126.com

MicroRNAs (miRNAs) are small RNAs (sRNAs) 20-24 nucleotides in length, and commonly exist in organism. During the last 20 years, research on isolation and function identification of miRNAs made the people understand regulation of gene expression more deeply. Some research showed miRNAs played important role in resistant response of plant to pathogenic bacteria. Citrus Canker is a quarantine bacterial disease, which seriously affect the development of citrus industry. By field trials for many years, we obtained a special material ('Chinese Citron' C-05) resistant to citrus canker which would provide a good base to carry on the research about resistance of citrus to this disease. In this research, Illumina/Solexa deep sequencing technology was applied to analyze microRNAome of Chinese Citron C-05 and susceptible Bingtangcheng (as control). Comparing with Bingtangcheng, miRNAs profile of Chinese Citron C-05 had 69 miRNAs only expressed before inoculation of pathogen bacteria, 64 miRNAs after inoculation and before appearance of hypersensitive necrosis reaction, 74 miRNAs after appearance of reaction. Moreover, through prediction and function analysis of target genes, results showed 69 metabolic pathways were regulated by these differentially expressed miRNAs only in Chinese Citron C-05. Among these pathways, we were interested in 3 pathways related to plant resistance which were helpful to reveal molecular mechanism of 'Chinese Citron' C-05 resistant to citrus canker. Now, we were verifying miRNAs regulated these 3 pathways and expression of target genes.

S12014

The role of auxin in the citrus defense to early infection by *Xylella fastidiosa*.

Rodrigues CM, Souza AA, Takita MA, and Machado MA.

Centro de Citricultura Sylvio Moreira, IAC, Laboratory of Biotechnology, Brazil. marcos@centrodecitricultura.br

Many studies have shown the involvement of plant hormones in plant responses to biotic and abiotic stresses. Recent studies indicate that auxin has an important role in stress responses. Previous results from our group showed induction of some genes involved in auxin pathway in Ponkan mandarin (*Citrus reticulata* Blanco), tolerant to citrus variegated chlorosis, one day after challenge with *X. fastidiosa*, the causal agent of this disease. Thus, the study aimed to evaluate the differential expression of some genes involved in this pathway in mandarin and the susceptible sweet orange (*Citrus sinensis* L. Osb) in early stage of infection. The genes evaluated were: *IAA9* (*Aux/IAA*), *ARF6*, *TIR1*, *UBA1*, *UBC2*, *E3*, *SKP*, and *BIG*. The RNAs from mandarin and orange infected or not (control) with the bacteria were extracted. RT-qPCR analyses were carried and as a result, all genes were significantly induced in mandarin. However, in sweet orange it was observed significant induction just for *UBC2* and *UBA1* genes. Because there was also a repression in expression of *E3*, *SKP*, and *ARF6*, ubiquitination may be involved in other pathways. It was evident in this work the importance of differential expression of genes involved in auxin metabolism in resistance and susceptibility to *X. fastidiosa* of mandarin and orange, respectively. In addition, the results indicate that this pathway plays an important role in the defense response of mandarin in the initial stage of infection by *X. fastidiosa*.

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