# 70th ANNUAL MEETING

# Subtropical Agriculture and Environments Society

(*Formerly*: Subtropical Plant Science Society &

Rio Grande Valley Horticultural Society)

## CONFERENCE PROCEEDINGS

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## 67-2016

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Texas A&M University – Kingsville - Citrus Center

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# Poster Abstracts

## 1. Animal Science

### Retention of native forest birds in urban habitats of the Lower Rio Grande Valley

**John Brush, Alexis Racelis, and Timothy Brush**

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Abstract

An estimated 95% of native habitat in the Lower Rio Grande Valley of Texas has been cleared for agriculture and development, threatening a subset of tropical bird species at their northern range limits. Understanding the effects of increasing amounts of urbanization on these native forest birds is important to inform conservation efforts in this biologically diverse region. We evaluated the retention of native forest species in response to local and landscape habitat variables (percent tree cover, amount of dense habitat remaining, and proximity to water). 55 point-count stations were established in residential habitats and remnant urban woodlands, with each point surveyed three times between April and June in 2015. 19 bird species were chosen to represent native forest birds, with presence/absence used to calculate species retention at study points. Local tree cover and amount of dense habitat remaining both had significant positive effects on number of forest birds retained. These results corroborate findings in similar studies, indicating that preservation of remnant urban woodlands is important on a landscape scale to support native forest bird species, and that increased tree cover on a local scale (such as yards and neighborhood) is a viable method to increase habitat for such species.

# Poster Abstracts

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### A mutation in the para-sodium gene is associated with pyrethroid resistance in the brown dog tick, *Rhipicephalus sanguineus*

**Jason Tidwell[1], Rafael Barreto[2], Felix Guerrero[3], Phil Kaufman[4], Adalberto Pérez de León[3], and Robert Miller[1]**

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*3 USDA-ARS, Knipling-Bushland U.S. Livestock Insects Research Laboratory*

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Abstract

Pyrethroids are acaricides used to control tick infestations on domestic animals as well as livestock. High resistance to pyrethroids has been reported in samples of the brown dog tick, *Rhipicephalus sanguineus*, from Florida and Texas. The resistance levels were characteristic of knockdown resistance (kdr) mutations in the voltage-gated sodium channel. These mutations have been identified in the second and third domains of the sodium channel gene. We amplified segment 5 and segment 6 of domains II and III, respectively, from cDNA. A single nucleotide point mutation (SNP) was identified in a highly conserved region of domain III S6 resulting in an amino acid change from phenylalanine to leucine. This is the first reported *kdr* mutation in *Rhipicephalus sanguineus*.

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## Edaphic factors as a measurement of spatial division between ocelot (*Leopardus pardalis*) and bobcat (*Lynx rufus*) habitat in South Texas

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**Jon S. Horne**, *Feline Research Program, Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, USA*
**Michael E. Tewes**, *Feline Research Program, Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, Kingsville, TX, USA*

### Abstract

Precipitation patterns, disturbance regimes, and soil characteristics are major influences in the type of habitat that occurs on a site. The endangered ocelot (*Leopardus pardalis*) shares habitat with the bobcat (*Lynx rufus*) in South Texas. Two known ocelot populations live in Willacy and Cameron counties of South Texas. In 1997, collared ocelots and bobcats were radio tracked at Laguna Atascosa National Wildlife Refuge. Once the cats left an occupied location, soil samples were taken and sent for chemical and physical analysis. We compare soil pH, salinity, texture, and fertility with ocelot and bobcat use. Ocelots and bobcats were both found on sites with loamy soils. Ocelots preferred sites with higher clay levels, while bobcats preferred sites with sandier soils. In addition, ocelots were tracked on slightly more acidic soils with lower salinity. We will juxtapose vegetation and prey species associated with each site through ongoing research. This information can be used to identify sites with ideal soils to reestablish habitat and corridors best suited for ocelot use.

## Entomology

### 2015 Bait Station Validation Test

**Kari Piña[1], Dr. Hugh Conway[1], Dr. Christopher Vitek[2]**

[1]*United State Department of Agriculture, Animal and Plant Health Inspection Services, Plant Protection and Quarantine, Mission Laboratory, Edinburg, TX*

[2]*Department of Biology, University of Texas-Rio Grande Valley, Edinburg, TX*

Abstract

The Mexican fruit fly (*Anastrepha ludens*) is an invasive pest that infests citrus groves in Central and South America and is a reoccurring pest in the Lower Rio Grande Valley region of South Texas. One solution to prevent Mexican fruit flies from causing serious damage to citrus are bait stations that act as kill stations with 2-componet patch attractants (putrescene and ammonia acetate) that attracts the flies. Phagostimulants on the surface of the bait station cause the flies to feed on the insecticide, Spinosad, imbedded in the waxy outer covering. Bait stations with and without a protective hat have been weathered in the field for four to 52 weeks. The protective hat on a bait station serves to protect the bait station from any weather damage it may sustain and to prolong the potency of the insectcide. The bait stations were collected and placed into observation cages to determine percent mortality. Results from the first year of laboratory tests with observation cages indicates significantly higher mortality from bait stations with hats taken from the field over both control and bait stations without hats.

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## FUNCTIONAL ANALYSES OF BTB-FAMILY PROTEINS DURING PLANT-INSECT INTERACTIONS IN TOMATO

**Carol Vargas-Bautista[1] Sonia C. Irigoyen[1], Ashley M. Jacques[1], Carlos A. Avila[1,3] and Kranthi K. Mandadi**

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Abstract

In Texas and world-wide, pathogens, insects and abiotic stresses cause major losses in yield, quality and productivity of food and bioenergy crops. We have recently shown that members of a BTB-domain protein family (AtBT1-5) in *Arabidopsis thaliana*, a model plant, mediate responses to diverse biotic and abiotic stresses, nutrient, environmental and defense hormone signals. In this study, our goal was to identify and characterize similar central stress regulatory genes and networks in agronomic crops such as tomato and potato. Using bioinformatics tools, we have identified six BT-like proteins in tomato. Multiple sequence alignment and maximum-likelihood analyses showed that the six BT-like proteins are phylogenetically closer to the *Arabidopsis* orthologs. Transcriptome profiling and expression analysis indicated that the six *BT* genes are differentially expressed in various tissues. For instance, expression of a *BT* gene (Solyc06g071830) was more abundant in flowers (99-fold) and leaves (14-fold), when compared to roots. Interestingly, expression of Solyc06g071830 was up-regulated (3-fold) when tomato leaves were subjected to herbivory stress caused by beet armyworm (*Spodoptera exigua*). Further characterization of Solyc06g071830 genetic analysis (loss-of-function and gain-of-function), sub-cellular localization and biochemical interactions will provide a better understanding of its mechanism of action during tomato-insect interactions and defense. This knowledge will help design novel strategies for tomato crop protection against insect stresses.

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### Ducting Test Using Worley Emergence Towers

**Eric Shah[2], Dr. Hugh Conway[1], Dr. Christopher Vitek[2], Tim Roland[1], Joe Hinojosa[1], John Gottfried[1]**

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The Mexican fruit fly (*Anastrepha ludens*) is considered an invasive agricultural pest in the Lower Rio Grande Valley. This organism lays its eggs into valuable citrus fruits and renders it unmarketable, potentially affecting the major Rio Grande Valley citrus agribusiness. The goal of suppression and eradication of the natural population of Mexican fruit flies is gradually being accomplished through Sterile Insect Techniques (SIT). This method involves the mass rearing and release of sterile flies with the prospect of them mating with wild flies and thus reducing the fertile population. In the Edinburg mass rearing facility, the adult flies eclose in Worley towers. These towers depend on a ducting system in order to expel heat and waste gasses that will ultimately cause mortality. A prototype ducting system set at various cubic feet per minute (CFM) were tested against the current DC fans in order to determine the optimal setting. The test concluded that the 90 CFM ducting was better for quality control while being more cost effective than the current DC fans.

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## Mitochondrial DNA divergence within the ND2-COI tRNA region of the *fraterculus* Group (Anastrepha)

**Robert Mier[1], Raul Ruiz-Arce[2], W. Evan Braswell[2], Alexis Racelis[1]**

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Abstract

*Anastrepha* fruit flies are among the most diverse Tephritids in the neotropical region. Within the Anastrepha fruit flies lies the fraterculus species complex, which include the notorious polyphagous species *A. fraterculus* and *A. obliqua*. The relationship between *A. fraterculus* and *A. obliqua* is poorly understood due to their overlapping geographical distribution and probable hybridization. Commonly utilized molecular markers have proved to distinguish the relationship of other Tephritids. However, the same markers have provided limited resolution between the two *Anastrepha* species. This research examines variation of a mitochondrial gene, ND2/COI tRNA region, among *A. fraterculus*, *A. obliqua* and other members of the *fraterculus* species group for its capacity to resolve differences.

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## Molecular identification of *Anastrepha suspensa* (Loew), the Caribbean Fruit Fly and other tropical and subtropical species

**Oscar Obregón[1], Raul Ruiz[1], Donald Thomas[2], and Norman Barr[1]***
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*Abstract*

Accurate identification of tropical and subtropical fruit fly pests is important to confirm the presence or spread of an invasive species and respond to pest detections. Expert identification that relies on morphology alone can be difficult to perform when flies are collected as eggs, larvae, and pupae. This is because many species lack diagnostic characters at these life stages. The Caribbean fruit fly, *Anastrepha suspensa* (Loew), is a pest that can be confused with other exotic pests in the genus *Anastrepha* based on morphology and mitochondrial DNA. New methods that target informative DNAs are needed to support its accurate identification. To address this problem, we generated DNA sequences of the internal transcribed spacer region 2 (ITS2) from *A. suspensa* and related species to determine if this nuclear DNA region can be useful in pest diagnosis. Our reference dataset includes 206 sequences from seven economically important taxa. Our analysis detected two unique character states in the ITS2 fragment that are useful for diagnosis of *A. suspensa*. These diagnostic characters occurred as one insertion event and one base substitution in the ITS2 alignment.

## Validation of real-time PCR diagnostics for the identification of *Helicoverpa armigera* and *Helicoverpa zea*

**Daniel Garza[1], Roxanne E. Farris[2*], Lisa A. Ledezma[2], and Norman B. Barr[2]**
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### Abstract

The Old World Bollworm, *Helicoverpa armigera*, is among the most destructive of insect pests. It has a broad host range, feeding on approximately 180 cultivated plants, many of which happen to be crops of high value and importance. This pest is found in Asia, Europe, Africa, and South America. It has not yet been introduced to the mainland of the United States, however, in September 2014; this species was detected in Puerto Rico, placing the United States at risk. A closely related species, *H. zea*, is native to the U.S. and morphologically similar to *H. armigera*. This similarity makes it very difficult to accurately identify these two species. Recently published studies have reported the use of real time PCR methods for identifying and distinguishing *H. zea* and *H. armigera*; these methods include the use of sequence specific probes and non-specific intercalating dyes. In the present study, we evaluate these methods to determine whether results are consistent with published findings and reproducible using the instrumentation housed the USDA APHIS Mission Laboratory

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### Effect of Betadine panel wash on Mexfly production

**Amber R. Arellano[2], Dr. Hugh Conway[1], Dr. Christopher Vitek[2], Sandra Leal[3], Donald B. Thomas[4]**

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#### Abstract

The Mexican fruit fly (*Anastrepha ludens*) is an invasive species that is an agricultural pest in south Texas. Citrus and other host fruits are damaged by the Mexican fruit fly larvae by feeding on them, rendering the fruit inedible and unmarketable. The Mexican Fruit Fly Suppression and Eradication Program have established control methods using the Sterile Insect Technique (SIT) by irradiating and releasing sterile flies. The Mass Rearing Facility that produces these flies have experienced bacterial contamination of their egg laying panels which resulted in occurrences of *Morganella* spp., *Providencia* spp. and nematodes which increased mortality in the flies. Betadine (Povidone-iodine, 10%, Topical solution) is a germicide that acts to oxidize and halogenize against a wide variety of pathogenic bacteria, protozoa, viruses, parasites, and nematodes. Betadine is proven to effectively surface sterilize and provide microbial protection to fish eggs. In this experiment Mexican fruit fly egg laying panels were treated using a 100 ppm Betadine solution to determine if it would affect the quality and quantity of Mexican fruit fly production. Results show that this methodology of spraying the egg laying panels with 100 ppm Betadine solution provides microbial protection and is recommended for the Moore Air Base Mass Rearing Facility.

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## Novel hosts of *Brevipalpus* spp., vector of the citrus leprosis virus, in the Lower Rio Grande Valley

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### Abstract

The Tenuipalpidae are commonly referred as false spider mites or flat mites and are considered the most important plant feeding mites in the world, especially those included in the *Brevipalpus* genus. *Brevipalpus* mites have gained special attention because of their ability to transmit numerous plant viruses, including Citrus Leprosis Virus (CiLV). Citrus leprosis is among the most serious diseases of citrus in the world because it can ultimately kill citrus trees. Although not in the US, the disease is moving north through Mexico, and the potential vectors of this disease, *Brevipalpus* mites, are widespread and common in Texas citrus. However, its distribution and specific host range in the LRGV is still unknown. Understanding the host range of these mites in the LRGV is significantly important because host plants may represent cryptic asymptomatic reservoirs of CiLV and other *Brevipalpus* transmitted viruses. In this study *Brevipalpus* mites were collected from different host plants throughout the LRGV. The analysis included ten cities: Alamo, Brownsville, Edinburg, La Feria, McAllen, Mission, Pharr, Rio Hondo, San Benito and Weslaco. A total of 280 leaf samples from 93 different plant species were collected. *Brevipalpus* mites were recovered in 48 of the 93 plant species sampled. Fourteen of these plant species were identified as new hosts for *Brevipalpus* mites, ten of which are native to Texas.

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## Diagnosis of *Lobesia botrana* using Multiplex Real Time PCR

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### *Abstract*

The European grapevine moth, *Lobesia botrana,* is an economic pest of grapes. It is widely distributed across Europe, southern Russia, the Middle East, and northern Africa and has been introduced into eastern Africa, Chile, and Argentina. It was first detected in California in 2009. In 2010 an eradication program implemented by the USDA, drastically reduced the number of *Lobesia botrana* in California. Identification of this pest is problematic because of similarities to species in the genus *Paralobesia* which are also found in California. Immature stages of many *Lobesia* and *Paralobesia* cannot be identified to species using morphology. To address this problem we developed a real time multiplex PCR assay to diagnose the pest in California. The real time assay includes a nucleic acid probe that targets a segment of DNA in the internal transcribed spacer region 2 (ITS2) of *L. botrana.* Based on our results the probe does not target the ITS2 DNA of other moths in California.

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## Boll Weevil Resistance to Malathion

**Jason Carlson[1], David Bartels[1], Cynthia Garcia[1], Charles Suh[2], Larry Smith[3]**
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### Abstract

Around 1892 the boll weevil (*Anthonomus grandis*) migrated north from Mexico into the U.S. and spread throughout the Cotton Belt. Since then, it has cost America's cotton producers more than $15 billion in lost production and control costs. In 1971-1973 a pilot boll weevil eradication experiment was conducted in southern Mississippi and parts of Louisiana and Alabama by the Animal Plant Health Inspection Service and Agriculture Research Service of the USDA. In 1978, USDA's Animal and Plant Health Inspection Service launched the National Boll Weevil Eradication Program, with the goal of eradicating boll weevil from the U.S. Currently, Malathion is the only insecticide utilized to treat boll weevil populations, as it is inexpensive, has low mammalian toxicity, and is extremely effective against boll weevils. Cotton farmers have reduced their use of pesticides to be between 40 to 100%, and increase yields by at least 10%, since the program's inception in the 1970s. All of the 15 million acres of U.S. cotton are involved in the program, and the weevil has been eradicated in 98% of that production area. However, eradication efforts are still underway on less than one million acres of cotton in south Texas, as boll weevils can still be found in some areas. Since south Texas is still under active eradication treatments, there were concerns within the Boll Weevil Eradication Program that weevils were developing resistance to Malathion. With assistance from the Boll Weevil Eradication Foundation, we conducted a study using three different concentrations of Malathion to determine if insecticide resistance was present in the population. The results of our study indicate that no weevil resistance to Malathion was detected.

# Poster Abstracts

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## Silver Plastic Mulch as a Method for Whitefly Control in Tomato Plants

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### Abstract

The Lower Rio Grande Valley (LRGV) in Texas once was an extremely productive area for wintertomatoes. At its peak, the LRGV maintained 40,000 acres of tomato production. Over the pastseveral decades, an invasion of devastating diseases, most notably the Tomato Yellow Leaf Curl Virus (TYLCV) has practically wiped out the tomato growing industry and is still a limiting factor for farmers interested in planting this high---value crop. In an effort to resurrect the tomato industry based on interest from local organic farmers in the LRGV, we experimented with two mulches, silver reflective plastic and hay. Bare soil was the control. With the presence of the TYLCV's main vector, the whitefly (Bemesia tabacii), we tested the tomato variety, Tycoon F1, which has notable resistance to TYLCV. Nine sticky traps were collected each week for four weeks and counted for number of whiteflies. A total of four harvests were collected and measured for average fruit weight and total marketable fruit. A one---way ANOVA showed a significant difference in the average marketable fruit weight between the silver plastic mulch and hay, however the silver plastic compared bare soil was not significant. Whiteflies were trapped and counted across each over the mulch and followed a similar trend as marketable fruit. Silver plastic had the best overall performance but the difference was not statistically significant. Corresponding author: Lindsey Richards, lindsey.richards01@utrgv.edu

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## Agroecological methods to manage brassica pests on organic farms

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Abstract

Push-pull agriculture utilizes plants that possess natural attractant and repellant volatiles in order to drive the activity of a pest away from a cash crop. This is accomplished by intercropping repellant “push” plants and attractant “pull” plants alongside a target cash crop. The combined effects of the push and pull species form a trap in which a pest is exposed to a predator and/or presented with a more desirable food source. The end result of push-pull technology increases biodiversity and decreases the need for synthetic pesticides. This push-pull technology will be used in an attempt to reduce the prevalence of cabbage loopers (*Trichoplusia ni*), green peach aphids (*Myzus persicae*), and beet armyworms (*Spodoptera exigua*) on organically grown kale. A section of farm land has been designated for the growth of kale intercropped with the pull plants alyssum, fennel, and dill and the push plants cilantro and onion in order to assess insect pervasiveness associated with a specific intercropped plant. A previous study revealed higher prevalence of pests on kale plants near fennel and high prevalence of the predatory convergent ladybug (*Hippodamia convergens*) on kale surrounded by dill. Combined with alyssum’s ability to attract beneficial insects, these three plants have been chosen to create a dead-end trap for these dominant brassica pests. In addition to field testing, insect movement in response to plant volatiles will be analyzed using an olfactometer by tracking insect movement toward or away from the push-pull plant species. This serves to generate data in regards to which plants possess the most potent attractant and repellant volatiles. The plant volatiles responsible for the push-pull mechanism will then be identified through gas chromatography

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## What is the Economic Impact of the Sugarcane Aphid Outbreak in South Texas?

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### Abstract

The sugarcane aphid (SCA) has become the most important pest in sorghum since its detection in 2013. Due to its rapid population growth, great dispersion capacity, and reduced availability of effective insecticides, this insect has caused significant economic losses to sorghum growers and local economies. Little work has been conducted to assess and better understand the economic implications of the SCA outbreak. The objective of this study was to estimate the overall economic impact of SCA in the Lower Rio Grande Valley (LRGV), Texas, where 11.5% of the state production is located. Forty-one local producers were surveyed resulting in a representative sample of 46,578 acres in 2014 and 49,761 acres in 2015. The questionnaire gathered detailed information about yearly crop yields, crop acreage, insecticide application decisions, and management and production practices. Collected data were used to estimate the reduction in growers' profit associated to the SCA infestation. Aggregated farm-level economic loss estimates were then used to assess the total economic impact of the SCA outbreak in the LRGV. Empirical results indicate that SCA reduced profit by $64.29/acre in 2014 and by $36.17/acre in 2015. At the aggregate level, SCA caused a total economic loss to farmers in the LRGV of about $20.39M and $11.21M in 2014 and 2015, respectively. In terms of total regional economic impacts, the burden was greater in 2014 with losses of $8.4M in output, $4.4M in value-added, $1.9M in labor income, and 50 jobs. In 2015, economy-wide losses totaled $6.8M in output, $3.7M in value-added, $1.9M in labor income, and 59 jobs. This study provides insights of the economic repercussions of the SCA at both the farm and regional levels.

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## Environmental Science

### Potential trade offs of regulating and cultural ecosystem services in urban areas of the Lower Rio Grande Valley, Texas

**Katharine Jones and Alexis Racelis**

*Katharine Jones is an undergraduate student that is working in Dr. Racelis urban ecology lab at the University of Texas Rio Grande Valley.*

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Abstract

Urban environments present a unique set of challenges to the maintenance or restoration of ecosystem services, where there are often tradeoffs between certain regulating ecosystem services that typically operate at a relatively large scale (such as storm water retention, carbon sequestration, and energy savings) with cultural ecosystem services (such as aesthetics and other values) that often drive urban landscapes, especially at the urban/suburban household unit. This is especially apparent in the fastest urbanizing area in the state, the Lower Rio Grande Valley, which has grown nearly 45% in population each decade for the past 20 years, and where only 5% of natural areas remain. In this area, we compare remotely sensed tree cover data with average home values estimated using a hedonic pricing method to test our hypothesis of a positive association between urban tree cover (as a proxy for regulating services in urban areas) and home value (as a proxy for aesthetics). We also examine whether urban tree cover can predict other associated cultural services, such as early elementary school performance. Understanding this dynamic between urban ecosystem services is paramount to helping city managers best encourage homeowners to manage urban landscapes that best maximize the conservation of services that are most salient to these areas.

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# Molecular detection of environmental isolates of *Cryptococcus neoformans* from pigeon excreta in Northeast Tamaulipas

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## Abstract

The genus *Cryptococcus* comprises more than 38 species, two of which are the main agents of systemic human cryptococcosis*. Cryptococcus neoformans* and *C. gattii* are a significant cause of morbidity and mortality. This disease can be acquired from the environment exposure via fungal cell inhalation. Both *C. neoformans* and *C. gattii* have been isolated from a variety of environmental sources. *C. neoformans* is commonly isolated from dried pigeon excreta and *C. gattii* from decaying wood in living trees. The present study aimed to evaluate the environmental distribution the *C. neoformans* in 57 samples of pigeon guano from public places from Northeast Tamaulipas (Reynosa, Rio Bravo and Matamoros). Samples were processed and inoculated on Niger seed agar (NSA) and we selected characteristic colonies for molecular confirmation. Polymerase chain reaction specific for *C. neoformans* (Luo & Mitchell, 2002) was applied for *C. neoformans* molecular identification. *C. neoformans* associated to pigeon excreta was isolated from one of the 57 (1.75%) sample from Reynosa, Tamaulipas. These results indicate a low prevalence of *C. neoformans*, from environmental samples.

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## Plant Science

### Impact of Citrus Management Strategies and nutrient application effects on plant physiology, fruit quality and yield

Julian Gonzales III, Shad D. Nelson, Mamoudou Sétamou, Catherine R. Simpson

Abstract

The Citrus Greening Disease otherwise known as Huanglongbing (HLB) has devastated the Florida citrus industry and has emerged as a threat to citrus groves in the Lower Rio Grande Valley (LRGV). The Asian citrus psyllid (*Diaphorina citri Kuwayama*) is believed to be the main insect vector of citrus greening disease, which was first discovered in Florida in 1998 and was discovered in southern Texas in 2012. In response to this threat, growers and researchers have developed management programs to control the vector in order to control the spread of the disease. While this program has been highly successful, we must still prepare to manage trees infected with HLB. There is evidence that nutritional programs and management strategies are able to maintain tree health and keep infected citrus fields in production. The development of plant diseases and pest infestations can directly be linked to the nutrients that are important for plant growth. Recent field and laboratory experiments conducted at Texas A&M University Kingsville Citrus Center have shown that applications of different nutrients applied at different rates on citrus trees have the potential to reduce psyllid populations and limit their development. Our current research project is being conducted using applications of recommended rates and high rates of calcium and potassium silicate foliar nutrient sprays. Our objectives for this concurrent field and greenhouse trial is to determine the impact of multiple nutrients and variable rates on psyllid development and reproduction. We hypothesize that higher rates and combinations of calcium and potassium silicate will increase the leaf hardness and therefore limit the ability of psyllids to feed and reproduce.

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## Genome sequence of *Sphingobium yanoikuyae* S72, a polycyclic aromatic Hydrocarbon-degrading Strain.

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### Abstract

The genus *sphingomonas* was proposed by Yabuuchi *et al*. in 1990. Their outer membrane have been described to contain glycosphingolipds instead of lipopolysaccharide. By 2001, sphingomonas genus has been subdivided into four genera: Sphingomonas, Sphingobium, Novosphingobium, and Sphingopyxis. Recently, studies on members of these genera have received much attention due to their unique capabilities to degrade various pollutants, such as anthracene, biphenyl, toluene, naphthalene, *m*- and *p*-xylene. Here, we described the draft genome sequence of *Sphingobium yanoikuyae* S72 strain with a view to provide important information on the endogenous and exogenous genes needed to establish pathways for degradation of polycyclic aromatic hydrocarbons (PAHs). **Methodology/principal findings:** *S. yanoikuyae* S72, was isolated in Rio Bravo Tamaulipas, Mexico. The genomic DNA was extracted using Promega® Wizard Genomic DNA purification kit according to manufacturer's instructions. The whole genome of this strain was sequenced using an Illumina Hiseq™ 2000 sequencing system. The reads were assembled and annotated using the CLCbio assembler, versión 4.0 and RAST annotation server (http://rast.nmpdr.org/) respectively. The draft genome was 5, 531, 313 bp in length with GC content of 64.1 %. A total of 5014 coding sequences (CDS) and 52 structural RNAs were predicted. **Conclusions/ significance:** As expected, *S. yanoikuyae* S72 genes encode diverse arrays of proteins with putative functions in metabolism of aromatic compounds. Sixty-two (62) CDS were putatively annotated to be responsible for metabolism of aromatic compounds. At least 41 genes were associated with metabolism of central aromatic intermediates while 16 genes were involved in peripheral catabolic pathway for aromatic compound. Furthermore a depth analysis of the genome (core-genome, pan-genome, pathways, phylogeny etc.) can provide insights into the mechanisms of polycyclic aromatic hydrocarbon degradation and potential in applications bioremediation.

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# The effects on bacterial diversity associated with the rhizosphere of transgenic cotton plants with respect to conventional plants

**Lourdes Vital L.*** **and Alberto Mendoza H.**

Abstract

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Cotton plant (*Gossypium hirsutum*) is an important crop because plays an important role in the economic development, socio-economic, commerce, food, medical and textile industry in México and other countries. However, biotic and abiotic factors such as pests, temperature, drought and diseases reduced crop production. For this reason, genetically modified plants were generated to improve agronomic traits such as insect resistance and/or herbicide tolerance mainly. Some researchers argue that environmental safety must be demonstrated before using GMOs because this plants are capable of releasing proteins derived from modified genes at their roots exudates thus, could generate conditions that affect the complex and delicate interactions within the microbial soil communites. The goal of this study was to study, by a metagenomic analysis of rhizosphere derived from transgenic and conventional cotton plants. In this study we evaluated different growth-stage (before sowing, vegetative, flowering and harvest) of bacterial community structure at the rhizosphere of cotton using the next generation sequencing technique. Our results revealed that at the rhizosphere of transgenic and conventional cotton were colonized by five main members of the phyla Proteobacteria, Firmicutes, Acidobacteria, Actinobacteria, Gemmatimonadetes and Bacteroidetes. Dominant Families were Bacillaceae, Rhodospirillaceae, Chitinophagaceae, Rubrobacteraceae, unclassified (derived from Solibacterales), Bradyrhizobiaceae and Paenibacellaceae. The relative abundance of bacterial communities at phylum and family level were similar when these groups were compared between the conventional and transgenic cottons. We identified by using MG-RAST and Quantitative Insights Into Microbial Ecology pipelines many differences in the structure of bacterial communities depending of growth stages more than genetic modifications. We concluded that transgenic cotton plants did not affect the rhizobacterial communities found in the rhizosphere, when comparing them to conventional plants.

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## Ecosystem Impacts of Guineagrass; An Invasive Weed of South Texas

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### Abstract

Megathrysus infestus, Guineagrass is an exotic weed from East Africa, which is especially invasive in South Texas and Northeastern Mexico. Guineagrass has many ecosystem impacts including dominance of natural environments, loss of biodiversity, reduced quail populations, changes in fire ecology, weediness in agriculture, urban areas, and appears to create a pathogenic landscape for livestock disease vectors including cattle fever ticks. Field studies are underway to document the impact of Guineagrass on the ecosystem in Cameron County, TX. This area is repeatedly re-invaded by cattle fever ticks which may be due the pathogenic landscape created by Guineagrass. The change in plant diversity from native riparian vegetation to a Guineagrass dominated landscape, may be changing the diversity and abundance of ground-dwelling tick predators. Fewer tick predators such as ground beetles and ants may be influencing cattle fever tick populations. Changes in ecosystem services due to Guineagrass invasion appears to be having profound effects on the ecology of South Texas and Northeastern Mexico. One solution could be to develop host specific biological control agents for M. infestus. A candidate agent from the native range of M. infestus in Kenya, Africa will be imported for preliminary host range testing.

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# Use of Seaweed to Stimulate Plant Growth

**Vanessa Thomas, Dr. Michael Persans, Dr. Hudson DeYoe**

## Abstract

*Sargassum fluitans* is a seaweed that is commonly found in large quantities at certain times of the year on the beach at South Padre Island, Texas. The purpose of this study was to determine if this seaweed stimulates plant growth as a locally available organic soil conditioner. A previous study found that *S. fluitans* can increase soil nutrients meaning that *Sargassum* might be an environmentally friendly and effective fertilizer. *Sargassum* was collected and cleaned manually by soaking in fresh water for several hours. It was then refrigerated, dried and tested for salinity. Half of the seaweed was powdered and the other half was used whole. Four treatments (control, powdered seaweed, whole seaweed, commercial organic fertilizer) were applied to Golden Bantam Sweet Corn seeds grown in Sunshine Mix 0 soil. There were eight replicates of each treatment. The corn grew for 28 days, the stalk height and number of leaves was measured, and then the soil was carefully removed from the roots. Wet weight was recorded for each plant which was then dried at 75C for 7 days. The dry weight was measured and plant water content was calculated. Water percentage in all 4 treatments was close to 90%. Nutrients were then analyzed by weight of Nitrogen and Carbon. The percent of Nitrogen in all the samples was under 2% with Carbon found to vary from 28.85% to 39.65%. Further study will begin spring 2016, with additional testing of the seaweed as a compost and as a soil conditioner.

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# Inter-annual measurements of evapotranspiration of *Arundo donax* along the Rio Grande River

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## ABSTRACT

Giant reed (*Arundo donax* L.), a woody grass native to the Mediterranean, is one of the worst weeds in the arid southwest, including Texas and Mexico where it has negatively impacted riparian ecosystems and displaced native flora and fauna. Additionally, neglecting the growth of giant reed would allow a hospitable habitat for the transition of Cattle Fever Tick, and cause a concern for national and water security along the Rio Grande River with its dense and tall vegetation. The USDA-ARS have released biological control agents to reduce its growth rate, distribution along waterways and its tremendous rate of vegetative reproduction. This study used a three-dimensional eddy covariance system to measure evapotranspiration (ET) fluxes throughout the growing season for giant reed, and to determine the reduction of water use with the introduction of a biological control regime. Results show an average reduction of total monthly ET of 42 mm when compared between peak growing seasons of giant reed in 2014 and 2015. Future research will be conducted to determine the significance of current results using remote sensing before the release of *Tetramesa romana*. In essence, our data suggest that any efforts to reduce the water-using potential of giant reed would be extremely timely, given the growing scarcity of water in agriculturally important areas of the southwestern US.

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### Reproducible DNA Preparation from Monocots and Dicots for Genomic Applications

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Abstract

High-throughput genomic procedures depend on the quality of the DNA used. Co-purification of molecules can negatively impact the functionality of plant DNA preparations employed in these procedures. We present a simplified, rapid and scalable SDS/chloroform-based method that provides the high-quantity and -quality DNA required by the newly emerging biotechnology and molecular breeding applications. The method is applied to isolating DNA from tissues of the major monocot crop plants, sugarcane and rice, and dicot crop plants, citrus, potatoes, and tomatoes, which provide a challenge due to the presence of fiber, polysaccharides, or secondary metabolites. The DNA isolated by this method is suitable for several downstream applications including Southern blot hybridizations, marker-assisted selection, and genotyping. This method has been used in a diverse range of experiments ranging from screening plant lines overexpressing reporter genes to analyzing plant responses to abiotic stress.

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## Mapping the Spatial Distribution of Tanglehead (*Heteropogon contortus*) on South Texas Rangelands

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### Abstract:

Tanglehead (Heteropogon contortus [L.] P. Beauv. ex Roem. & Schult.) is a grass native to Southwestern US rangelands; however, its prevalence as an invasive on South Texas rangelands has grown. In the last decade, large areas of monotypic tanglehead stands have emerged, simplifying native vegetative communities in Jim Hogg, Brooks and Kleberg counties. Unfortunately, little is known regarding the spatial extent of this invasion and its impact. The goal of this project is to determine this extent and spatial distribution of tanglehead in critical areas of South Texas. To address this goal, specific tanglehead dominated areas have been identified using high-resolution aerial photography, field verification, ranch information, and data collected from previous research. This information was used to conduct an unsupervised classification using NAIP (National Agriculture Imagery Program) color infrared aerial photography into four classes: woody vegetation, tanglehead, non-tanglehead herbaceous, and bare ground. Overall accuracy for two images averaged 85.75%. With this level of accuracy, it is possible to classify tanglehead and quantify its spatial distribution.

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## Assessment and Influence of Citrus Flush Shoot Nutrient Quality on Asian Citrus Psyllid Population Densities

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### Abstract

Asian Citrus Psyllid *Diaphornia citri* Kuwayama, 1908 (Hemiptera: Liviidae) is a phytophagous pest on citrus and other rutaceae host plants. Psyllids feed on the phloem sap extracted from the flush shoots of citrus and reproduce exclusively on younger flush stages. This feeding habit causes direct leaf damage known as epinapsis, but also causes indirect damage by transmitting the phloem inhibiting bacterium *Candidatus Liberibacter asiaticus*, putative causal pathogen of the deadly citrus greening disease or Huanglongbing (HLB). Asian citrus psyllids are the only known vector for the bacterium, so vector control plays a very important role in disease control. In order to control psyllid populations it is very important to understand the biology and nutritional ecology of the psyllids. As psyllids are a phloem feeding insect, studying the composition of phloem sap important at each flush stage. Phloem sap was extracted from all five flush stages and the total free amino acids and total essential amino acids were recorded. The flush shoots from which the phloem sap was extracted were analyzed for their nutritional composition. These results were correlated with the population densities of Asian citrus psyllid on different flush stages. The population densities were higher at younger stages and tend to decrease as the flush matured. The total free amino acids and essential amino acids also followed this pattern, with higher quantities in younger flush stages which decreased as the leaf matured. This suggests that the nutritional quality phloem sap composition of younger flush shoots might be adequate to promote the growth and reproduction of Asian Citrus Psyllids.

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## Multifunctionality of Cover Crops in South Texas: Looking at multiple benefits of cover cropping on small farms in a subtropical climate

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### Abstract

Situated in deep South Texas, the Lower Rio Grande Valley (LRGV) is considered one the most productive agricultural regions in the southern US. With the highest concentration of organic farms in the state (Hidalgo county), the LRGV has a strong potential to be leaders in sustainable agriculture. Finding management practices that comply with organic certification and increase the health of the agroecosytem and the farmers working the land is increasingly pertinent. Cover cropping, or the intentional planting of non-cash crop vegetation, can serve multiple functions in an agroecosystem by decreasing environmental pollutants that originate from the agroecosystem, reducing inputs needed for crop production, and potentially decreasing on-farm costs for farmers—overall increasing the sustainability of the farm. Use of cover crops on otherwise fallow lands have shown to enhance ecosystem services such as: attracting native beneficial insects (pollinators), increase nutrient availability in topsoil, prevent nutrient leaching, increase soil organic matter, and reduces soil erosion. In this study, four cover crops (Lab lab, Sudan Grass, Sunn Hemp, and Pearl Millet) were analyzed in the subtropical region of south Texas to see how their multiple functions enhance ecosystem services. The four cover crops were assessed to see their potential to harbor native insects, their potential to increase soil nitrogen, to increase soil organic matter, and to suppress weeds. The preliminary results suggest that these subtropical varieties of cover crops have potential to enhance ecosystem services on agricultural land in the RGV by increasing soil organic matter (in all varieties), increasing nitrogen in topsoil (Lab lab, Sunn Hemp), and reducing weeds (Sudan Grass).

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## Pathology

# Expression of *pr1* gen isoforms in *Metarhizium anisopliae* during pathogenic process in *Diaphorina citri*

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Abstract

The entomopathogenic fungus *Metarhizium anisopliae* (Metschnikoff) Sorokin (Hypocreales: Clavicipitaceae) produces several subtilisin-like proteases that are involved in the pathogenic process. The identification, characterization and evaluation of the expression of these proteases can give an approach of fungal adaptability to different substrates and how pathogenic process may initiate. In this study, End-Point RT-PCR was used for assessing expression of the *pr1* gene isoforms in two strains of *M. anisopliae* with different pathogenic activities toward the Asian citrus psyllid, *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae). Selected strains Ma57 (more pathogenic) and Ma62 (less pathogenic) were tested for *pr1* gene isoforms expression at 0h, 6h, 12h, 24h, 48h, 72h, 96h, 120h, 144h, 168h after conidia inoculation. Results revealed that only six isoforms, D, F, G, H, J and K were expressed in both strains. A, B, C, E and I isoforms were not expressed in any of the two strains at all times. D and J isoforms exhibited a different and irregular expression pattern in Ma57 and Ma62 strains. F and G isoforms were expressed from 0h to 168h, while H isoform was expressed from 6h to 168h in both strains. K isoform was expressed during the all times tested in Ma57 strain and only showed an irregular expression pattern in Ma62 strain. Although both strains harbour the eleven isoforms in their genome, the expression patterns during the infection process toward *D. citri* is different, so more studies are needed to understand the role of these proteases in the patogenic process.

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# Correlation of Viability of *Candidatus* Liberibacter asiaticus With Symptom Development and Age of Leaf Tissues

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**Project funded in part by USDA-NIFA HSI Collaborative Grant Award No. 2011-38422-30826**

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### Abstract

Citrus Huanglongbing (HLB) is one of the most serious diseases of citrus worldwide. The disease is caused by several species of phloem-limited Gram negative bacteria belonging to the genus *Candidatus* Liberibacter. Quantitative real-time PCR (qPCR) targeting the amplification of the 16S rRNA region of the DNA is one of the widely used techniques to detect the pathogen. Although qPCR can detect the presence of the bacterium, it cannot quantify live and dead bacteria separately. This is overcome by the use of Propidium monoazide (PMA), a DNA intercalating dye that binds to DNA of bacteria with "compromised" cell walls or dead cells. It also acts as a PCR inhibitor, therefore only allowing amplification of DNA from live cells. PMA treated samples were used to quantify live and dead cells in leaf samples differing in age and severity of the symptoms by TaqMan and SYBR real-time PCR assays. The results from this research will be highly useful in developing novel HLB disease management strategies.

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### Mycorrhizal Fungi: Potential Roles In Weeds And Nematode Suppression

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Abstract

Mycorrhizal fungi are widely known to have beneficial effects on the host plants. They play an important role in nutrient cycling and also protect the host plant from biotic and abiotic stresses. In this research we will investigate the effect of mycorrhizal fungi on the growth of weeds and plant parasitic nematodes in an organic farm. On-farm field research trials will be conducted to analyze the potential for mycorrhizal fungi to suppress weeds and pests and increase yield in carrots and beans. This study will be done at a certified organic farm, Terra Preta, located in Edinburg, Texas. We will grow carrots and bush beans plants inoculated with commercial mycorrhizal fungi simultaneously with non-inoculated plants. To estimate the potential for weed suppression, weed growth in each plots will be monitored and the total weed biomass for each plots will be calculated at the end of the experiment. Nematode suppression potential will be assessed by extracting and estimating nematodes from the rhizosphere soil from each treatment. We will also analyze the response of nematodes to mycorrhizal fungi in the lab using a nematode olfactometer. Results from this study will help the organic farmers in the Lower Rio Grande Valley to make a choice on whether or not to invest on mycorrhizal inoculum for their farms.

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# BIOINFORMATIC ANALYSIS OF *TRICHODERMA* GENES INVOLVED IN THE TRYPTOPHAN-INDEPENDENT INDOLE ACETIC ACID BIOSYNTHESIS PATHWAY

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Abstract

*Trichoderma* species have been widely used in the world as growth promoters. Growth promotion is due to the production of auxins, being Indole Acetic Acid (IAA) the most important one. IAA can be synthetized by *Trichoderma* via a Tryptophan-Dependent pathway, however a Tryptophan-Independent pathway has been described in other species. In order to investigate if a Tryptophan-Independent pathway is present in *Trichoderma* spp, a bioinformatic analysis using Hidden Markov Models profiles of proteins was performed across seven different *Trichoderma* species. The complete pathway was found to operate with a set of 7 proteins; in *Trichoderma* four out of seven species, *T harzianum, T asperellum, T virens* and *T atroviride*, were positive for all the proteins in the analysis, Indoleamine-2,3-dioxygenase, Kynureninase, Anthranilate phosphoribosyltransferase, Phosphoribosylanthranilate isomerase, Indole-3-glycerol phosphate synthase, Indole Synthase and Kynurenine Formamidase; *T citrino, T reesei* and *T longibrachiatum* were negative for the protein Kynurenine Formamidase. The results indicate that, in all seven species of *Trichoderma,* a Tryptophan-Independent pathway could be synthetizing Indole Acetic Acid.

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## Evaluation of root tissue as a source material for Huanglongbing (HLB) diagnosis in Citrus

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### Abstract

Huanglongbing (HLB) is a destructive disease in citrus whose causal agents are unculturable, phloem-limited Gram-negative Alpha-proteobacteria that belongs to the genus '*Candidatus* Liberibacter'. So far, three species of *Candidatus* Liberibacter, CL asiaticus (CLas), americanus (CLam) and africanus (CLaf), are known to be causing HLB. Unlike CLaf and CLam, each of which is limited to Africa and America, respectively, CLas is the most wide spread and destructive strain of liberibacter causing huge economical loss in citrus industry around the world. These HLB causing bacteria are transmitted by citrus psyllids, *Diaphorina citri* in Asia and America and *Trioza erytreae* in Africa. Since there are no known resistant commercial citrus cultivars available, the early HLB detection is critical to devise an efficient disease control strategy that is now heavily dependent on the chemical method against the population of citrus psyllids. Currently, symptomatic citrus leaves, sometimes similar to symptoms induced by other biotic/abiotic stresses, are source materials for the detection of HLB-causing bacteria in citrus by qPCR. However, the uneven distribution of HLB-causing bacteria in the aerial part of a plant can lead to a misdiagnosis. Previous work conducted in our lab indicated that HLB-positive plant exhibits more uniform CLas distribution in the root system suggesting that the root tissue can be an alternative source material for more reliable HLB diagnosis in citrus. We surveyed one hundred young grapefruit trees for HLB by qPCR once a month for three months period using leaf and root samples. The results showed that HLB diagnosis using root tissue is as sensitive as the one obtained with leaf samples. This indicates that root tissue is another good source material for HLB diagnosis especially when no visible symptoms are present on the leaf tissue.

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# First report in Mexico on two *Bdellovibrio* strains isolated from soil using the culture-dependent technique.

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### Abstract

*Bdellovibrio* spp. are small, uniflagellated motile Gram negative bacteria that prey upon other Gram negative bacteria to derive nutrient for growth and reproduction. They are ubiquitous in nature and their potential applications in agriculture, animal husbandry, aquaculture, food industry and medicine have been reported. In the present study, two strains of *Bdellovibrio* were isolated from soil samples using the culture-dependent technique with two members of the family *Enterobacteriaceae* (*Klebsiella* sp. and *Salmonella* sp.) as host. We identified and confirmed the *Bdellovibrio* strains using microscopy, PCR amplification and sequencing of the 16S rRNA gene. Host range analysis was carried out using double-layer agar plating technique. The *Bdellovibrio* strains were bacteriolytic, plaque-forming and highly motile Gram negative bacteria. They were observed to be different strains based on *hit* locus, restriction enzyme cleavage pattern of amplified 16S rRNA gene and host range analyses. Here, the first report on *Bdellovibrio* strains isolated from soil in Mexico corroborates earlier report indicating that populations of *Bdellovibrio* found in soil are heterogenous thereby the need to identify the various strains. Furthermore, this work is expected to pave way for basic line of research in BALOs with ultimate goal of utilizing them for biotechnological applications.

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## Evaluation of soil adjuvant OR-079 with Metalaxyl for *Phytophthora* root rot control in citrus

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### Abstract

Foot rot, caused by *Phytophthora nicotianae*, is a very important disease affecting citrus production in South Texas. *P. nicotianae* infects feeder roots and the trunk of citrus trees causing poor water and nutrient uptake leading to yield loss, fruit size reduction, tree decline and eventually tree death. Effective treatments for *Phytophthora* diseases are limited; therefore optimization of available products is of great importance. We hypothesize that the effectiveness of Metalaxyl in reducing *P. nicotianae* soil propagules can be increased when applied together with the soil conditioner OR-079. To test our hypothesis we applied metalaxyl, OR-079, and metalaxyl plus OR-079 to mature grapefruit trees with *Phytophthora* infection. *Phytophthora* propagule counts present in the soil were assessed at 4, 8 and 12 weeks post treatment using standardized methods and compared to an untreated control. Results show that all treatments had significantly reduced *Phytophthora* counts in the soil at 4 and 8 weeks post application than that of untreated control, but were not statistically different to the control by 12 weeks. In addition, OR-079 did not increase metalaxyl effectiveness in reducing Phytophthora propagules in the soil but it reduced its activity when mixed. Moreover, leaf nutrient analysis indicates that neither OR-079 nor metalaxyl have an effect on nutrient leaf content. These results indicate that metalaxyl as well as OR-079 are effective at reducing *Phytophthora* propagules in the soil when used separately. These products should not be mixed as their activity is reduced when combined and reapplication is recommended after 3 months since both chemicals lose their activity by 12 weeks post application.

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## Study of Haplotype complex of the Potato Psyllid and *Candidatus* Liberibacter solanacearum on the Sierra Madre Oriental, México

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Abstract

*Bactericera cockerelli* is a vector of the bacterium *Candidatus* Liberibacter solanacearum (CaLsol), the causal agent of Zebra chip disease (ZCD). *Bactericera cockerelli* (common name: potato psyllid) was an insect endemic to the mountains of Mexico; however, this insect and its associated disease soon underwent a rapid geographic expansion. Our objectives in this study were to evaluate the incidence of *B. cockerelli* and ZCD in the fields of Perote, Veracruz; to determine *B. cockerelli* and *Ca*Lsol haplotypes in different hosts native to the Sierra Madre Oriental; and to evaluate the proportion of *B. cockerelli* that carries *Ca*Lsol. On location in Perote, we found *B. cockerelli* in 13 of the 24 fields examined, and we confirmed that 16 of 18 fields had > 45% of tubers with ZCD symptoms. For this study, we collected 1085 *B. cockerelli* specimens. A representative subsample of 226 specimens taken from all of the examined sites and host plants were tested for the presence of *Ca*Lsol in *B. cockerelli*. Additional tests were run on these samples to identify the haplotypes of the psyllid and the bacterium. This study provides the first confirmation of the presence of the Southwestern US *B. cockerelli* haplotype in Perote. We found the highest percentage of *B. cockerelli* carrying the *Ca*Lsol bacterium in tomato fields – areas which also featured a higher proportion of the *Ca*Lsol haplotype B than did fields planted with potato, pepper or tomatillo. This finding suggests that tomato fields play an important role in the yearly manifestations of *B. cockerelli* in Mexico and are a common cause of local Zebra chip disease infections.