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CONFERENCE PROCEEDINGS

Student Abstracts

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Student Abstracts 2017 Poster winners



First Place

Toward a better understanding of Asian Citrus Psyllids (Hemiptera: Liviidae) host selection behavior

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Factors controlling the Asian citrus psyllid (ACP), *Diaphorina citri*, host finding and selection are poorly understood. Implementation of an effective ACP control requires an understanding of its host selection process. ACP preferentially selects young expanding flush shoots for feeding and its reproduction solely occurs on these juvenile shoots. Previous research has shown that young shoots are softer with light green color; had higher volatile organic compounds and contained more free amino acids indicating a nutritionally richer diet relative to mature flush shoots. To better understand the host selection behavior of ACP, young shoots of six known Rutaceae host plants were tested in a multiple choice assay. Flush shoots were inserted in an aquatube containing a hydroponic solution to maintain their turgidity, and disposed equidistantly on a circular tray for selection by ACP over a 48 h-period. A combination of visual and olfactory cues showed that ACP adults had a preference for grapefruit relative to three other citrus species namely sweet orange, lemon and lime, and two non-citrus Rutaceae (curry leaf and orange jasmine). In a second trial, ACP adults were released in the desiccator containing four flush shoots of yellow sapote, a non-psyllid host. After a 24 h-period, similar numbers of grapefruit flush shoots were introduced in the arena. A high proportion of ACP adults (ca. 70%) moved from the non-host to suitable host flush shoots. In contrast, when flush shoots of a suitable host plant were introduced and flush shoots of another suitable host were added, settled ACP adults on first host plant rarely move. Taken together, the data provided valuable insight in ACP behavior while searching for a suitable host.



Second Place

Diversity of *Brevipalpus* mites in South Texas from different citrus host plants

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Mites belonging to the genus *Brevipalpus* (Tenuipalpidae: Acari) are considered of economic importance to U.S. agriculture. Besides causing direct feeding damages, *Brevipalpus* species have been associated with the transmission of plant viral diseases, including the Citrus Leprosis Virus (CiLV). Citrus leprosis is caused by CiLV and is among the most serious diseases of citrus in the world because it can ultimately kill citrus trees. Even though leprosis has not been reported to be present in the United States, the potential vectors of this disease, are already established in Texas citrus. The diversity of *Brevipalpus* mites in South Texas citrus orchards was previously studied using morphology and molecular data. However, some of the species in this genus have been recently re-described. In this study, *Brevipalpus* mites were collected from different locations in South Texas from four different citrus host plants, and identified using cytochrome oxidase I sequencing. A total of 216 sequences were obtained. The phylogenetic analysis confirmed the presence of four *Brevipalpus* species in South Texas, including, *B. californicus*, and *B. yothersi*. The haplotype network analysis revealed the existence of 23 different haplotypes. For *B. yothersi*, 11 haplotypes were recovered, and for *B. californicus* 9. The most common haplotype was HAP03, which was included in the *B. californicus* haplotype group, and was found in 66.20% samples from this study. The second most common haplotype was HAP02, which was identified as *B. yothersi*, and was found in 13.43% samples. Both species were recovered from the four different citrus host plants, suggesting that there is no host association of *Brevipalpus* mites with citrus species.



Third Place

Amplification of acaricide target site genes in *Rhipicephalus (Boophilus) annulatus*

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Pesticide resistance is a growing problem around the world with reports of cockroaches, mosquitoes, and ticks. The cattle fever tick, *Rhipicephalus (Boophilus) annulatus* is a tick of veterinary importance being a vector for *Babesia bovis*, *B. bigemina*, and *Anaplasma marginale* (Rodriguez-Vivas et al., 2014). *R. microplus*, a closely related species to *R. annulatus*, has shown resistance to multiple acaricides that target different neurotransmitters namely, voltage-gated sodium channels, gamma-aminobutyric acid receptors (GABA), and octopamine receptors. Single point mutations have been found in these genes that correlate to acaricide resistance. In this study, we are the first to sequence the target site regions of these genes in *R. annulatus*. We designed primers to amplify the acaricide target site region of the different genes in 10 adult *R. annulatus* ticks and sent them in for sequencing. We present the results of our research here.

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- 2. Cattle fever tick, *Rhipicephalus (Boophilus) microplus* (Acari: Ixodidae) potential control on pastures by application of urea fertilizer**, B. Leal, D. B. Thomas, R. Dearth
- 3. Araneae as a potential bio control against the *Rhipicephalus (Boophilus) microplus* (cattle fever tick)**, Bethany Olivarez
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- 6. GPS collar performance on ocelot and bobcat in South Texas**, T.R. Shirley, M.E. Tewes, J.V. Lombardi, J.P. Leonard, A. Ortega-Sanchez, J.P. Wied, T.A. Campbell
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- 11. Change and fragmentation of woody cover in the Lower Rio Grande Valley from 1984-2016.**, J.V. Lombardi, M.E. Tewes, H.L. Perotto, Tyler A. Campbell
- 12. Mexican Fruit Fly (*Anastrepha ludens*) (Loew) Diet Development, Acid Comparison Bioassay**, A.R. Arellano, H.E. Conway, E.J. Salinas, C. Vitek
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- 14. Mexican Fruit Fly (*Anastrepha ludens*) 2016 Trap and Lure Validation, McPhail Trap with Torula Yeast Borax Comparison versus 2-Component Cone Trap Study**, K. Piña, H. Conway, E.J. Salinas, C. Vitek
- 15. Second Year Bait Station Validation Test 2016**, E. Shah, H. Conway, E.J. Salinas, C. Vitek
- 16. Diagnostic Capacity of SNP Markers to Differentiate Sterile and Wild Mediterranean Fruit Flies**, V.L. Ortega , T.N. Todd , R.A. Ruiz
- 17. Examining the utility of two diagnostic methods for revealing the introduction pathway of oriental fruit flies (*Bactrocera dorsalis*) collected in California**, T.N. Terrance and N. Barr
- 18. Invasive Occurrence of the Zoophytophagous *Nesidiocoris tenuis* (Heteroptera: Miridae) in the Lower Rio Grande Valley**, Gabriela Esparza-Díaz, Thiago Marconi, Raúl T. Villanueva, Carlos A. Avila³
- 19. Evaluating the Sensitivity of Real-Time Diagnostic Assays for the Detection of the Old World Bollworm**, L. Ledezma and R. Farris
- 20. Biocontrol of the Asian Citrus Psyllid: *Tamarixia* Wasp**, L.E. Torres, J. Dale, T. Feria Arroyo
- 21. Toward a better understanding of Asian Citrus Psyllids (Hemiptera: Liviidae) host selection behavior**, G. Sanchez, R.R. Saldana, J.M. Hearn, Mamoudou Setamou
- 22. Parasitism rates of *Tamarixia radiata* (Hymenoptera: Eulophidae) to densities of its host, *Diaphorina citri* (Hemiptera: Psylloidea)**, H. Hernandez, D. Flores, C. Vitek
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Biological control of cattle fever ticks

J. Goolsby^{1*}, F. Guerrero², J. Kashefi³, L. Smith³, A. Racelis⁴, D. Amalin⁵, M.J. Flores⁵, N. Abes⁵; K. Verly⁵; N. Singh⁶; P. Azhahianambi⁷, A. Jesudasan⁸, P. DeBarro⁹, A. Sheppard⁹, K. Wyckuys¹⁰, J. Liu¹¹, A. Schwartz¹², H. Hasel¹³, K. Varner¹³, D. Ellis¹⁴, & A. Pérez de León²

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Cattle fever ticks (CFT) *Rhipicephalus microplus* and *Rhipicephalus annulatus* are invasive livestock pests that are endemic to Mexico and invasive along the Texas – Mexico border. Acaricide resistance, alternate wildlife hosts, and pathogenic landscape forming weeds present challenges for sustainable eradication of this pest in the U.S. Classical biological control of CFT is being explored as a strategy to control this pest, especially on alternate hosts such as nilgai antelope and white-tailed deer. Molecular genetic tools were used to compare populations of CFT from the native and introduced ranges to provide insights into optimal search areas for potential biological control agents. Accessions representative of invasive populations of *R. microplus* from subtropical Zapata, Texas, USA and other parts of the invaded range including Brazil and Kenya matched most closely with populations in The Philippines and Cambodia. Similarly, accessions of *R. annulatus* from invaded range in Del Rio, TX matched closely with accessions from the native range in Bulgaria and Romania. These regions should be prioritized for field exploration for biological control agents. Classical biological control using specialist parasitoids, predators and/or nematodes from the native ranges of cattle fever ticks *Rhipicephalus microplus* and *Rhipicephalus annulatus* could complement existing control strategies for this livestock pest in the transboundary region between Mexico and Texas. Methods for field collection of cattle fever tick natural enemies have been developed, including exposure of infested cattle to collect insects that are parasitic on the nymphs and adults, time lapse photography to observe predators of questing larvae, and soil assays to detect entomopathogenic nematodes.

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Cattle fever tick, *Rhipicephalus (Boophilus) microplus* (Acari: Ixodidae) potential control on pastures by application of urea fertilizer

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Cattle fever ticks, *Rhipicephalus (Boophilus) microplus*, spend 3-4 weeks during their on-host stages, but spend up to 80-90% of their entire life cycle questing for a host. Current technology is limited to on-host applications; pasture management control methods during out-break infestations are needed. By using standard pesticide efficacy trials, granular urea was tested in both in vitro and in vivo studies to determine if there was significant impact on both adult reproduction and larval survival. Under the conditions of this present study, there was no detectable effect on either female adults or larval stages.

Araneae as a potential bio control against the *Rhipicephalus (Boophilus) microplus* (cattle fever tick)

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The cattle fever tick *Rhipicephalus (Boophilus) microplus*, is an economically important arthropod because of their ability to vector Babesiosis (cattle fever). Although fever ticks spend up to 80 – 90% of their lives questing for a host, the primary control is via on-host methods. Thus leaving the need for an off-host biocontrol method. Research on the predator-prey relationship between Araneae and ticks is limited, resulting with the experimental idea to test Araneae as a potential predator in a laboratory setting.

Lethal time analysis of acaricides in the Cattle Fever Tick, *Rhipicephalus microplus***D. Sanchez¹, D. Rodriguez¹, J. Tidwell², G. Klafke²**¹University of Texas Rio Grande Valley²USDA-ARS Cattle Fever Tick Research Laboratory

Cattle fever ticks (CFTs), *Rhipicephalus annulatus* and *R. microplus*, are a threat to U.S. cattle industry. Several classes of acaricides are available to combat CFTs and selection caused by acaricide overexposure have led to the resistance of various tick strains. The objective of this study was to determine lethal time of permethrin, amitraz and coumaphos in four different *R. microplus* strains: Deutch (susceptible reference strain), Yucatan, Santa-Luiza and El-Zamora. Acaricide impregnated filter paper packets were used to expose larvae to lethal doses of each compound. Live and dead larvae were counted at different time points and non-linear regression analysis was used to calculate median lethal times (LT50) for each compound and strain. Permethrin and amitraz had the fastest action against Deutch strain (LT50 in minutes, 21.7 and 28.4, respectively). Yucatan, Santa-Luiza and El-Zamora showed low mortality after 24 hours of exposure to permethrin, demonstrating their resistance. Yucatan strain showed to be susceptible to amitraz (99.24% mortality after 24 h). Coumaphos showed to be a slow acting pesticide against ticks. The LT50 for Deutch strain was 143.3 min. Although LT50 values (288.7min for Yucatan, 348.5min for El-Zamora and 678.6min for Santa-Luiza) were higher than Deutch, all the other strains showed to be susceptible to coumaphos after 24 hours of exposure. This study is the first to describe lethal time of acaricides in the CFT. The results of this study help to better understand the toxicology and the physiology of response to acaricides in the CFT and will help improve the existing techniques to detect resistance.

Amplification of acaricide target site genes in *Rhipicephalus (Boophilus) annulatus***H. Moreno¹, J.P. Tidwell², G.M. Klafke², R.J. Miller², A.A. Perez de Leon³**¹University of Texas Rio Grande Valley, Edinburg, TX²USDA-ARS Cattle Fever Tick Research Laboratory, Edinburg, TX – USA³USDA-ARS Knipling-Bushland U.S. Livestock Insects Research Laboratory; Veterinary Pest Genomics Center, Kerrville, TX

Pesticide resistance is a growing problem around the world with reports of cockroaches, mosquitoes, and ticks. The cattle fever tick, *Rhipicephalus (Boophilus) annulatus* is a tick of veterinary importance being a vector for *Babesia bovis*, *B. bigemina*, and *Anaplasma marginale* (Rodriguez-Vivas et al., 2014). *R. microplus*, a closely related species to *R. annulatus*, has shown resistance to multiple acaricides that target different neurotransmitters namely, voltage-gated sodium channels, gamma-aminobutyric acid receptors (GABA), and octopamine receptors. Single point mutations have been found in these genes that correlate to acaricide resistance. In this study, we are the first to sequence the target site regions of these genes in *R. annulatus*. We designed primers to amplify the acaricide target site region of the different genes in 10 adult *R. annulatus* ticks and sent them in for sequencing. We present the results of our research here.

GPS collar performance on ocelot and bobcat in South Texas

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Global positioning system (GPS) telemetry is a widely used research technique to understand the spatial, behavioral, and population ecology of carnivores. Reliability of GPS collars in a variety of cover types is key to conducting statistical analyses and making informed conclusions regarding an animal's behavior. The ocelot (*Leopardus pardalis*) is a medium-sized neotropical felid that is a habitat specialist using dense woody cover in Texas. The bobcat (*Lynx rufus*) is a medium-sized felid and habitat generalist that co-occurs with ocelots in extreme southern Texas. From 2013-2016, we collared 6 ocelots and 3 bobcats on the East Foundation's El Sauz Ranch in Willacy County, TX with Lotek Minitrack GPS collars to track daily movements and fine scale activity patterns. The purpose of this study is to determine the percentage of successful GPS fixes for each species and explore if extrinsic factors (e.g., vegetation, animal behavior, gender, time of day, number of satellites) influence GPS collar performance. Preliminary data for ocelots (n=1) and bobcat (n=1) indicated the female ocelot had a 79.4% success rate, whereas the male bobcat had a 94.6% success rate. Data from this research is essential for understanding ocelot and bobcat ecology and making informed decisions about study designs involving ocelots recovery in South Texas.

Evaluation of non-invasive fecal sampling for monitoring bobcats and ocelots in South Texas

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Field research methods to monitor endangered ocelots (*Leopardus pardalis*) in South Texas include live-trapping and camera detection stations. However, months of trapping effort often result in the capture of only a few individuals, and camera detection stations cannot gather genetic information for population monitoring. Bobcats (*Lynx rufus*) and other carnivores are known to defecate along roads and trails within their home ranges. Thus, it may be possible to incorporate non-invasive scat sampling as an additional monitoring tool for ocelots, with added benefits such as DNA acquisition. We evaluated the feasibility and sampling effort needed to detect ocelots and bobcats from scat in areas where the species co-occur. We collected carnivore scats along ranch roads within and adjacent to known ocelot habitat in South Texas. We extracted DNA from each sample and confirmed species of origin through mitochondrial DNA sequencing. We identified species for 82 of 92 samples collected (89%), including 33 bobcat and 0 ocelot scats. A grid of 26 camera stations within the same study area collected 17 bobcat and 2 ocelot images during a similar 2-week period. Scat sampling is an efficient method to acquire genetic material from bobcats. However, our lack of ocelot detections suggests that ocelots do not prefer to use roads for moving and scat marking as other carnivores do, or that the event is rare and did not occur during our surveys. Sampling will continue in 2017, and we will identify individuals and estimate abundance via microsatellite DNA genotypes.

Effects of rainfall and coyote abundance on spatial distribution of bobcat and ocelot.

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The large mesocarnivore guild in southern Texas includes bobcats (*Lynx rufus*), coyotes (*Canis latrans*), and ocelots (*Leopardus pardalis*) in certain areas of Willacy and Cameron counties. These three species live in close proximity together and have been reported to share similar resources in other parts of their geographic range. Furthermore, coyotes are known to kill and prey upon bobcats, however their effect on ocelot populations is unknown. Frequent droughts in South Texas can affect rodent and mesocarnivore populations. Since 2011, we have conducted long-term remote camera monitoring on the East Foundation's El Sauz Ranch in Willacy County, TX. The objective is to determine the impact of rainfall of coyote abundance and the spatial distribution of bobcats and ocelots. We will use occupancy analyses to examine remote camera data collected between August and November 2012 (drought year) and 2015 (non-drought year). Coyote abundance did not influence ocelot occupancy in drought and non-drought years. We hypothesize that coyotes will have a greater effect on other mesocarnivore species during drought years than during non-drought years. This research is valuable for ocelot recovery in southern Texas and will evaluate the impacts of coyotes on other mesocarnivores in relation to drought.

Analysis of Activity Patterns of Sympatric Ocelot (*Leopardus pardalis*) and Bobcat (*Lynx rufus*) in South Texas Using Cameras

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Ocelots and bobcats are two felids with a geographic range in the United States that overlaps in South Texas. Ocelots and bobcats have similar dietary requirements. Ocelots occur in areas with dense vegetation and bobcats are also known to occur in these areas. The two felids are nocturnal with crepuscular peaks of activity. We established a camera-trap array on the East Foundation's El Sauz Ranch, Port Mansfield, Texas in autumn 2011. We monitored the remote cameras continuously and selected the photographs of ocelots and bobcats to capture times of activity. Circular statistics are useful to analyze cyclical data. We fit kernel density functions to these observed times to estimate the coefficient of overlap (Δ) between the two species. Confidence intervals were estimated with a smoothed bootstrap. The overlap in the time niche is useful to understand along which niche axes the two species are most competitive. This can lead to management practices best suited to protect the endangered ocelot.

Abundance, activity patterns and interactions among ocelots, cattle, nilgai, feral hogs and javelinas

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In southern Texas, ocelots (*Leopardus pardalis albescens*) are located in two small sub-populations on private and public lands in Willacy and Cameron counties. The East Foundation's El Sauz Ranch (EESR) in Willacy County has the largest known population of ocelots in the United States. Research on ocelot interactions with other carnivores and prey species have been previously studied across their geographic range, however interactions with cattle (*Bos taurus*) and other large game species on private lands has not been examined. Since 2011, we have conducted a remote camera survey on the EESR. The objective of this study is to analyze camera data to examine differences in abundance, activity patterns and determine interactions among ocelots, cattle, nilgai (*Boselaphus tragocamelus*), feral hogs (*Sus scrofa*), and javelina (*Pecari tajacu*) on trails and within dense thornshrub. We hypothesize that there will be more interactions on trails compared to dense thornshrub, and ocelots will have more interactions with cattle and nilgai than smaller game species. The information derived from this study will assist management of cattle, large game and ocelots. Furthermore, this will also benefit future ocelot recovery and conservation on private lands in southern Texas.

Change and fragmentation of woody cover in the Lower Rio Grande Valley from 1984-2016.

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The Lower Rio Grande Valley is one of the fastest urbanizing areas in the United States. In addition, cropland and rangeland conversion has led to loss and degradation of woody cover types across the region. The endangered ocelot which is native to southern Texas has seen its geographic range diminished due to loss of dense thornshrub. In the mid-1980's, researchers suggested only 5% of the woody cover in the region remained based on data available at the time. However, the advent of advanced satellite imagery allows quantification of wood cover over the past 32 years. We classified LANDSAT 5 and 8 imagery data every 8 years from 1984-2016 to estimate the rate of land cover change and fragmentation. Over the past 32 years, the amount of woody cover increased from 13.7 to 15.9%, however mean patch area, edge density, patch density and Euclidean distance to nearest patch increased indicating severe fragmentation. Rangeland and intensive cropland conversion were the leading causes of change in woody cover, which can be attributed to rapidly expanding urban areas. These data provides important information for predicting future woody cover fragmentation, focus restoration efforts for ocelot recovery, and development of effective conservation strategies.

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Mexican Fruit Fly (*Anastrepha ludens*) (Loew) Diet Development, Acid Comparison Bioassay

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Bioassay tests were conducted for the Mexican Fruit Fly (MFF) (*Anastrepha ludens*) larvae comparing three different acid types used in the artificial diet prepared at the Center for Plant Health Science and Technology (CPHST) Containment Facility and the Mexican Fruit Fly Mass Rearing Facility. The three acids used were the current acid for production 1) muratic acid (hydrochloric acid, HCL), 2) citric acid and 3) an alternative organic chemical for muratic acid. The muratic acid is typically used to obtain a pH level suitable for rearing MFF (3.75 ± 0.2). These tests were designed to determine if an alternative acid could be found as a potential substitute to improve employee safety and reduce environmental hazards potentially caused by the current delivery system deterioration. In addition, the bioassay test validated the efficacy of the acids for MFF production and indicated if there were any negative effects that might present themselves during the fruit fly rearing process. The alternative organic chemical produced only half as much pupae and converted from egg to pupae 13% and 21% fewer pupae compared to citric and muratic acid, respectively. Egg production and final egg hatch of MFF were compared by treatment type. Results indicated higher egg fecundity rates when using muratic acid compared to citric acid or alternative organic chemical replacement in the first generation. Over the next three generations of egg fecundity there were no significant differences between muratic acid and citric acid. Bioassays are an excellent way of evaluating new diet ingredients and formulations to determine the effect on MFF production and validate quality control parameter differences between treatments.

Comparison of nitrogen sources to improve mass rearing of the arundo scale; a biological control agent of *Arundo donax*

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Arundo donax, known as giant reed, carrizo cane, and arundo is an exotic and invasive weed of riparian habitats in the southwestern U.S. and northern Mexico. Biological control using insect agents from the native range of *A. donax* in Europe may be the best option for long-term and widespread management. The arundo scale, *Rhizaspidiotus donacis*, is one of the key biological control agents. The scale has a six month life cycle, and females produce crawlers which settle and develop on young rhizome tissue, the base of young side-shoots, or on the leaf blade adjacent to the ligule. To determine whether added nitrogen would affect survival or fecundity of *R. donacis*, we released crawlers on microplants of *A. donax* that were treated with one of 4 forms of nitrogen or on controls. Nitrogen applications were continued at biweekly intervals for 21 weeks before refrigerating the plants. Then, all arundo scale on each plant was counted and the developmental stage noted. Individual adult female scale were put in gelatin capsules. Crawlers that emerged in the gel caps were counted to assess fecundity. None of the treatments affected survival to maturity of males or females. Fecundity was similar with control and urea treatments but lower in the other nitrogen sources.

Mexican Fruit Fly (*Anastrepha ludens*) 2016 Trap and Lure Validation, McPhail Trap with Torula Yeast Borax Comparison versus 2-Component Cone Trap Study

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The Mexican fruit fly (*Anastrepha ludens*) is an invasive insect pest that infests citrus groves in Central and South America and a recurring pest in the lower Rio Grande Valley region of south Texas. To prevent *A.ludens* from causing serious damage to citrus, the USDA APHIS PPQ along with Texas Department of Agriculture established a suppression and control program for mass rearing, irradiating, and aerial releasing sterile *A.ludens* using Sterile Insect Technique (SIT). Critical components are the trapping segment and surveillance program (5 per square mile) using the effective lure/trap combination. Bioassays were used to compare *A.ludens* capture results between treatments: 1) 2-component cones (Scentry Biologicals, Inc.), 2) torula yeast borax (ERA International Limited) and 3) 10% propylene glycol capture solution. For each testing period, two-piece multi-lure traps with 300 mL of a 10% propylene glycol capture solution was used for all traps with an addition of three torula yeast tablets in each yeast trap. A Latin Square design was used for initial trap placement using ten traps of each treatment in the orchard. Results of bioassay indicated that 2-component cones, with ammonia acetate and putrescence, captured significantly more sterile *A.ludens* than the capture fluid control throughout the entire testing period. Capture comparisons indicated that at 24 hours, week 1 and week 2 the 2-component cones significantly captured more sterile *A.ludens* than the torula yeast borax pellets. There was no significant difference between the 2-component cone and torula yeast pellets during week 6 and week 8. Validation testing ensure that tested lures meet the USDA requirements for use in fruit fly trapping and surveillance programs.

Second Year Bait Station Validation Test 2016

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The Mexican fruit fly (*Anastrepha ludens*) is considered an invasive agricultural pest in the Lower Rio Grande Valley. Female flies lay their eggs into valuable citrus fruits and the resulting larvae tunnel within the fruit rendering it unmarketable. This consequence has the potential to affect the citrus growers and fruit agribusinesses in the Lower Rio Grande Valley. In combination with Sterile Insect Technique, one method for mitigating the threat imposed by the Mexican fruit fly is using bait stations. Bait stations with protective hats serve as kill stations by utilizing 2-component patch attractants (putrescine and ammonium acetate) in conjunction with a waxy coating infused with the insecticide, Spinosad. Phagostimulants embedded in the waxy surface of the bait stations promote the ingestion of the insecticide by the Mexican fruit flies. The bait stations were employed in the field for up to 52 weeks. Samples were collected, by length of time in the field, and placed into observation cages to determine the longevity and efficiency of the bait stations through percent mortality at 72 hours post placement. After two months in the field, fly mortality from the bait stations placed into observation cages was relatively high at 90% mortality. The effectiveness of the bait stations gradually drops across time, but bait stations that had been left in the field for five months still killed 60% of the flies. Bait stations are another valuable tool for use in an Integrated Pest Management program for fruit fly control.

Diagnostic Capacity of SNP Markers to Differentiate Sterile and Wild Mediterranean Fruit Flies

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Ceratitidis capitata, or the Mediterranean fruit fly (Medfly), is a highly invasive species that can infest a wide variety of agricultural crops. This pest has become established in Sub-Saharan Africa, Mediterranean, Eastern Australia, South America, Central America and Hawaii. Occasional infestations have occurred in Florida and California. Establishment of this pest in the continental United States can lead to major economic hardships for the agricultural industry. The sterile insect technique (SIT) is an effective biological control method used to suppress populations of Medfly worldwide. Sterile male flies are released in overwhelming numbers near an infestation. In such overwhelming numbers wild females are more likely to mate with sterile males and produce inviable eggs thereby eradicating the population. However, an effective method for differentiating between SIT flies and wild flies are necessary in order to determine when to lift a quarantine. An assay consisting of two informative SNP loci was developed to differentiate between SIT and wild flies. Using Medflies collected worldwide and from various SIT facilities, we evaluate the performance of the SNP assay. The SNP assay was tested on 201 wild flies and 113 SIT flies to provide a baseline of expected alleles. Subsequently, flies captured from a recent detection in California were compared to this baseline to estimate ancestry. A decision tree was then used in the interpretation of these data. We show the final outcome for these analyses.

Examining the utility of two diagnostic methods for revealing the introduction pathway of oriental fruit flies (*Bactrocera dorsalis*) collected in California

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The oriental fruit fly (*Bactrocera dorsalis*) is a highly invasive, polyphagous pest of commercial fruits and vegetables. It is native to Asia but is capable of establishing in many tropical and subtropical regions of the world. This pest has already become established in many locations in Africa and the Pacific including Hawaii. The oriental fruit fly is frequently trapped and eradicated in California. To exclude the pest from continental United States of America it is important to identify high risk introduction pathways into California. Movement of infested fruits from Hawaii to California could be a significant pathway. This can be tested by comparing the genetics of flies in Hawaii to flies in California. Prior studies characterized these fly populations using mitochondrial DNA (mtDNA). However, mtDNA is only inherited from a single parent and does not allow for recombination which can restrict population genetic inference. Analysis of Simple Sequence Repeats (SSR) provides another measure of genetic diversity but by using the nuclear genome which is inherited from both parents of a fly. In addition to mtDNA sequencing, we used nine Simple Sequence Repeats (SSR) to characterize the population structure of *Bactrocera dorsalis* in Hawaii and compare this to genetic profiles of flies captured in California. We then compare the results from each method separately for determining if a Hawaiian source of California flies is possible. Our results show that both methods are useful in determining origin and provide identical results for nearly 90% of the captured flies.

Invasive Occurrence of the Zoophytophagous *Nesidiocoris tenuis* (Heteroptera: Miridae) in the Lower Rio Grande Valley

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The Lower Rio Grande Valley (LRGV) located in the southernmost part of Texas is one of the most productive vegetable areas in the State. However, due to its subtropical weather and geographical localization, it is under high pressure of new pests and diseases. Recently, we detected the presence of a new exotic insect species, the tomato bug *Nesidiocoris tenuis* Reuter (Hemiptera: Miridae: Bryocorinae). *Nesidiocoris tenuis* is characterized by its zoophytophagous feeding habit. When abundant prey is present, it acts as predator feeding on small arthropods including crop pests. However, in the absence of an insect prey, it also feeds on its host plants. We monitored *N. tenuis* population in commercial and research crop fields for three years. *Nesidiocoris tenuis* populations raise every year during Fall when optimal developmental temperatures were present (~20 °C), and populations drop when minimum temperatures were lower than ~5°C. Recurrent population pattern indicates, *N. tenuis* is established in the area. In addition, we found *N. tenuis* population densities were higher on tomato fields as compared to adjacent pepper, okra, and squash fields indicating its host preferences. Moreover, insect populations densities were affected by tomato cultivar selection and plastic mulch color. The presence of *N. tenuis* at the LRGV will establish a new trophic insect relationship for growing vegetables. It is unknown if the presence of *N. tenuis* may help to control pests of economic importance, or due to its phytophagous feeding habit, it will also be considered as a new pest in the region.

Evaluating the Sensitivity of Real-Time Diagnostic Assays for the Detection of the Old World Bollworm

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The Old World Bollworm, *Helicoverpa armigera* is a pest species that has a broad host range consisting of approximately 180 cultivated plants. This pest is found in Europe, Asia, Africa and South America. In 2014, this species was detected in Puerto Rico, however it has not been detected in the United States mainland. Entry and establishment of this pest into the U.S. would be devastating to U.S. agriculture because of its wide host range and its resistance to many insecticides. *H. armigera* is closely related to the native *Helicoverpa zea* (corn earworm), and they are very difficult to morphologically differentiate from each other. Two previously published real time identification methods, one based on melting curve analysis and one based on sequence specific probe detection, have been validated by the Department of Agriculture, Center for Plant Health Science and Technology, Mission Laboratory in Edinburg, Texas as a way of identifying and distinguishing between *H. zea* and *H. armigera*. In this study, we evaluated the sensitivity of these real time diagnostic assays for detecting *H. armigera*. This was done by testing various DNA extraction methods and testing various concentrations of extracted DNA. We also evaluated the methods on extractions based on a single moth and on batches of moths. Batch extractions were performed in ratios of 1:1 to 1:24, where a single *H. armigera* was in a pool of *H. zea*. The results show that DNA concentrations of .0005ng/μl can be successfully detected in both real time assays, and the real-time PCR assay using melting curve analysis was more successful at detecting *H. armigera* in batches of *H. zea* at a ratio of 1:24.

Biocontrol of the Asian Citrus Psyllid: *Tamarixia* Wasp**L.E. Torres^{1*}, J. Dale², T. Feria Arroyo³**¹ South Texas College.²Texas Citrus Pest & Disease Management Corporation³University of Texas-Rio Grande Valley

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The Asian Citrus Psyllid (ACP) is associated with the spread of *Huanglongbing* (HLB) also known as Citrus Greening Disease (CGD), being a major threat to the US Citrus production. Incidence of HLB has been on the rise in the Lower Rio Grande Valley (LRGV), representing a major threat for the citrus industry in this region. Biocontrol efforts are crucial to control the population of ACP. Production of the natural predator of ACP, *Tamarixia radiata* (*T. radiata*) is one of the main goals of the Texas citrus industry. Production of *T. radiata* is conducted in the green-house and *Orange Jasmine* is vital as an ACP host plant. The *T. radiata* eggs are laid by the female wasp and undergo four stages before they emerge from an ACP nymph which takes up to 12 days until the cycle restarts. If left unchecked, HLB spread will ultimately diminish the Texas citrus industry's \$200 million contribution to the state's economy. The long-term effects associated with this disease are fruit drop and tree death. Increasing *T. radiata* production is currently the only strategy that the industry has for controlling ACP in residential areas. Preliminary results show that production rates could be associated with temperature fluctuations. Future research could include the use of data loggers to monitor changes in greenhouse temperature that could influence the increase or decrease in production of *T. radiata*.

Toward a better understanding of Asian Citrus Psyllids (Hemiptera: Liviidae) host selection behavior

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Factors controlling the Asian citrus psyllid (ACP), *Diaphorina citri*, host finding and selection are poorly understood. Implementation of an effective ACP control requires an understanding of its host selection process. ACP preferentially selects young expanding flush shoots for feeding and its reproduction solely occurs on these juvenile shoots. Previous research has shown that young shoots are softer with light green color; had higher volatile organic compounds and contained more free amino acids indicating a nutritionally richer diet relative to mature flush shoots. To better understand the host selection behavior of ACP, young shoots of six known Rutaceae host plants were tested in a multiple choice assay. Flush shoots were inserted in an aquatube containing a hydroponic solution to maintain their turgidity, and disposed equidistantly on a circular tray for selection by ACP over a 48 h-period. A combination of visual and olfactory cues showed that ACP adults had a preference for grapefruit relative to three other citrus species namely sweet orange, lemon and lime, and two non-citrus Rutaceae (curry leaf and orange jasmine). In a second trial, ACP adults were released in the desiccator containing four flush shoots of yellow sapote, a non-psyllid host. After a 24 h-period, similar numbers of grapefruit flush shoots were introduced in the arena. A high proportion of ACP adults (ca. 70%) moved from the non-host to suitable host flush shoots. In contrast, when flush shoots of a suitable host plant were introduced and flush shoots of another suitable host were added, settled ACP adults on first host plant rarely move. Taken together, the data provided valuable insight in ACP behavior while searching for a suitable host.

Parasitism rates of *Tamarixia radiata* (Hymenoptera: Eulophidae) to densities of its host, *Diaphorina citri* (Hemiptera: Psylloidea)

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The Asian citrus psyllid (ACP), *Diaphorina citri*, is an efficient vector of the bacterium *Candidatus liberibacter asiaticus*, associated with the deadly citrus disease Huanglongbing (HLB), or citrus greening disease. HLB spreads rapidly and is expanding its geographical range, threatening citrus industries in new areas. A Pakistani strain of *Tamarixia radiata* is successfully being used as a biological control agent for *D. citri* in the Rio Grande Valley, Texas. The USDA-APHIS Mission Laboratory is mass rearing the parasitoid and shipping large numbers to be released in urban environments for the biological control of ACP. Optimal biological control of ACP requires the ability to develop and enhance rearing methodologies in order to effectively and efficiently mass produce *T. radiata* release. In this study, we examined the impact of parasitism rate based on overall densities of *D. citri* and the influence of number of each instars on parasitism. Parasitism rate showed to increase up to an average of 88.8% as densities of *D. citri* were increased. In addition, when instars were manipulated for parasitism rate in overall number of instars, the 4rd stage displayed the highest level of parasitism. These results will help improve mass rearing strategies and success to aid in the biological control program in citrus producing regions.

Texas Psyllid Survey – Zebra Chip Monitoring Program: Comparison of the last two consecutive and contrasting years

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Zebra chip (ZC), an economically important disease of potato (*Solanum tuberosum*), has been recorded to occur in commercial potato fields in the United States, Mexico, Central America, and New Zealand. In the United States, ZC disease was first recorded in the Lower Rio Grande Valley during the early 2000's. Since 2004, Texas potato growers suffered serious economic losses because a high number of tubers were rejected by processors causing entire fields to be abandoned. The putative causal agent, "*Candidatus Liberibacter solanacearum*" has been later found to be transmitted from plant-to-plant by the potato psyllid, *Bactericera cockerelli*. Currently, vector and pathogen control relies extensively on the use of insecticides and monitoring for potato psyllids is an essential part of a successful integrated pest management program. Thus, a Texas Psyllid Survey – Zebra Chip Monitoring Program was initiated in 2009 to better understand insect population trends and movement as well as to make more informed and timely pest management decisions. The purpose of this program is to provide fast and reliable information about insect activity to both farmers and pest managers within their crops and fields. The Texas Psyllid Survey – Zebra Chip Monitoring Program provides this information for the entire potato growing season and throughout the state of Texas at a weekly basis so that cost effective and environmentally sound pest management decisions can be made. Adult psyllids are monitored using yellow sticky traps while eggs and nymphs are monitored by visual inspection of potato leaflets. Here we are presenting and comparing the population densities and reproduction level of potato psyllids for the consecutive, contrasting years of 2015 and 2016. The Monitoring Program for 2017 is currently ongoing.

Diversity of *Brevipalpus* mites in South Texas from different citrus host plants

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Mites belonging to the genus *Brevipalpus* (Tenuipalpidae: Acari) are considered of economic importance to U.S. agriculture. Besides causing direct feeding damages, *Brevipalpus* species have been associated with the transmission of plant viral diseases, including the Citrus Leprosis Virus (CiLV). Citrus leprosis is caused by CiLV and is among the most serious diseases of citrus in the world because it can ultimately kill citrus trees. Even though leprosis has not been reported to be present in the United States, the potential vectors of this disease, are already established in Texas citrus. The diversity of *Brevipalpus* mites in South Texas citrus orchards was previously studied using morphology and molecular data. However, some of the species in this genus have been recently re-described. In this study, *Brevipalpus* mites were collected from different locations in South Texas from four different citrus host plants, and identified using cytochrome oxidase I sequencing. A total of 216 sequences were obtained. The phylogenetic analysis confirmed the presence of four *Brevipalpus* species in South Texas, including, *B. californicus*, and *B. yothersi*. The haplotype network analysis revealed the existence of 23 different haplotypes. For *B. yothersi*, 11 haplotypes were recovered, and for *B. californicus* 9. The most common haplotype was HAP03, which was included in the *B. californicus* haplotype group, and was found in 66.20% samples from this study. The second most common haplotype was HAP02, which was identified as *B. yothersi*, and was found in 13.43% samples. Both species were recovered from the four different citrus host plants, suggesting that there is no host association of *Brevipalpus* mites with citrus species.

Potential phoretic association of *Brevipalpus* Mites with *Anastrepha ludens* (MFF)**K. Zarzosa¹, A. Fuentes^{1,2}, E. Braswell²**¹Department of Biology, University of Texas Rio Grande Valley, Edinburg, TX.²USDA APHIS HST Mission Lab, Edinburg, TX.

The genus *Brevipalpus* includes more than 300 species, are distributed worldwide, and have been reported to infest more than 1,000 different plant species. Besides causing feeding damage, *Brevipalpus* mites have been associated with the transmission of numerous viral plant diseases. The most important viruses spread by these mites cause Citrus leprosis, a potentially fatal disease of citrus plants. While there is no record of Citrus leprosis viruses in the US, they have steadily spread from South America to Central Mexico. As these viruses cannot move without their vectoring mites, it is paramount to understand methods of dispersal for *Brevipalpus* mites. Mites generally dispersal passively through wind driven movement or actively through phoresy, where they attach themselves to another organism for a period of time. Preliminary data shows that phonetic dispersal is possible for *Brevipalpus* mites. Here we evaluate the conditions which drive dispersal.

**Mitochondrial DNA variation within the ND2-COI tRNA region for the members of the
Anastrepha fraterculus group**

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Fruit flies belonging to the genus *Anastrepha* are notorious for their impact, as pests, on subtropical agriculture. The interspecific and intraspecific relationship for some species within the *fraterculus* group of *Anastrepha* is poorly understood due to overlapping geographical distribution and probable hybridization. Commonly utilized molecular markers have proved to distinguish the relationship among other Tephritids. However, these same markers have shown limited resolution for some *Anastrepha* species. This research examines the utility of the ND2/COI tRNA mitochondrial DNA region for distinguishing members in the *fraterculus* group, as well as other *Anastrepha* species. Preliminary results suggest this mitochondrial marker may be effective for differentiating closely related species and could have the capacity for shedding light on the unresolved species boundaries for some members from the *fraterculus* group as well as for examining intraspecific variation.

Rhizobacterial diversity of transgenic cotton plants with respect to conventional plants

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We used Next Generation Sequencing (NGS) pyrosequencing-based analysis of the V3 16S rRNA gene region to identify the structure and diversity of bacterial communities in rhizosphere derived from transgenic and conventional cotton plants. The main objective was to explore whether the genetically modified cotton could affect the complex and delicate interactions within the microbial soil communities at rhizosphere level. Structure and diversity of bacterial communities were assessed using the 16S rRNA gene, based on the Ion Torrent sequencer. We identified the structure of rhizobacterial communities by using QIIME (Quantitative Insights Into Microbial Ecology) platform. Rhizosphere samples collected at vegetative stage showed a similar structure of bacterial communities based in their relative abundance across two years of cultivation period (2015-2016) at phylum level in all genotype cotton plant. The taxonomic analysis indicated that Proteobacteria, Acidobacteria and Actinobacteria were the main members of the phyla in transgenic and conventional cotton collected at vegetative growth stage in both years. The relative abundance of bacterial communities at phylum level were similar when these groups were compared between the conventional and transgenic cottons. However, we found some variations in the transgenic cotton plants with respect conventional plants when rhizobacterial communities were analyzed at family level. Alpha diversity contained within an individual community was similar between conventional and transgenic cotton. Furthermore, Beta diversity revealed that it is possible that they share some bacterial groups between both cotton genotypes. The results obtained were consistent, indicating that variations detected in the rhizobacterial community structure could be possibly due to climatic factors rather than genetic modification derived from transgenic cotton plants.

Effect of Land Use Change on South Texas Chiropterans

Katharine Jones

Bats provide a tremendous ecosystem services, as both pollinators and for pest control. It is estimated that bats are worth more than \$3 billion to the United States alone, due to their consumption of crop pests, such as the corn ear. In Deep South Texas, a significant agricultural area in the southern US that is rapidly urbanizing, there are 14 different species of bats, representing more than a 1/3rd of all species in the state. Most of the species are insectivorous and permanent residents, and undoubtedly have significant impacts on pest populations in the local agricultural and urban landscape that has yet to be recognized. This research, will report on the diversity and abundance of bats, and give us a baseline information to examine the impact that land use change has on these important organisms. Using acoustic monitoring, preliminary research revealed that urban neighborhoods may support 30% of the insectivorous bats in the region. A total of 12 locations will be monitored across a gradient of landscapes, including urban, agricultural areas, and reserves. Ultimately, this data can serve as baseline for the conservation of bats and the ecosystem services they provide.

Associated metabolites to *Brachiaria decumbens* for chemical reclaim coal mining soils applying Biochar-Amendment

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Introduction: Coal mining causes drastic disturbances to the soil profile and its rehabilitation considers the dynamics of the soil-vegetation system. The interactions associated with the rhizosphere play an important role in the uptake and availability of nutrients, pollutant removal, plant growth and microbial colonization, promoted by metabolites involved in biogeochemical processes and other cellular functions in plants. Objective: To identify the metabolites at the rhizosphere using *B. decumbens* as a plant model and biochar-amendment during the process of reclamation of coal mining soils. Methodology: Crude extracts were obtained from 0.5 g of *B. decumbens* roots from treatments with blended edaphic materials, with and non biochar-amendment. Crude extracts were analyzed by high performance liquid chromatography-ultraviolet detector (HPLC-UV); and subsequently, by ultra high performance liquid chromatography coupled to high resolution mass spectrometry (UHPLC-Q-Orbitrap). Results: An initial screening of the metabolites of crude extracts from the plant was obtained by HPLC-UV, and differences in the intensity of the chromatographic profiles for the different treatments were observed. UHPLC-Q-Orbitrap analysis allowed the identification of discriminant metabolites (ESI + / ESI-), using multivariate statistical analysis. Data obtained from Q-Orbitrap were transformed from .RAW to .mzXML format using Proteowizard software (Holman, et al. 2014). Subsequently, pre-processed in the XCMS software (Tautenhahn, et al. 2008) and statistically analyzed by main components (PCA) and discriminant analysis (PLS-DA). The metabolites selected will allow us follow the process through time in a quantitative way over the different treatments by using liquid chromatography coupled to tandem mass spectrometry (UPLC-MS / MS). Conclusion: Differences between treatments according to the microbial communities and the biochar content were observed.

Seedling regeneration, growth, and development on site 55

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A randomized complete block experiment was conducted on Site 55, an abandoned 56 ha upland woodland. The site is surrounded by farm lands on three sides and Baffin Bay on one side and so represents the only permanently wooded habitat available for wildlife. Being the only permanently forested parcel of land in the area, it is subject to a large population of wildlife, over grazing and vegetation trampling. For this reason, research study of species diversity, and their growth and development to decipher the impact of wildlife foraging in the area is critical to understand landscape recovery after agriculture. The experiment was replicated four times with a 10 X 10 meter fencing to exclude grazing animals in the study areas. The same plot dimensions were measured adjacent to each fenced area as control. The Spring 2016 results indicate that species diversity was higher in fenced areas than the control. Also, height measurements of the following species *Southern Zexmenia*, *Drummond Phlox*, *Descurainia pinnata*, *Rudbeckia triloba*, *Dracopis amplexicaulis*, *Verbesina Enceliodes*, *Monarda punctata*, *Gaillardia pulchella*, *Onopordum acanthium L.* indicate that relative height growth was significantly higher in the fenced areas than the control areas.

Physiological analysis of *Sphingobium yanoikuyae* S72: degrading-hydrocarbons bacteria

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Background: Recently studies on members of genus *Sphingobium* have received much attention due to their unique abilities to degrade various pollutants, such as anthracene, biphenyl, toluene, naphthalene, *m*- and *p*-xylene. Here we evaluated the tolerance of *Sphingobium yanoikuyae* S72 at different hydrocarbons and to determine the degradation of naphthalene toluene and biphenyl by this bacteria *in vitro* conditions. **Methodology:** Sterile glass flasks containing 40 ml of Bushnell Haas, were added with 100 µg/ml of the tested hydrocarbons, then were inoculated with 1 ml of bacterial culture and incubated at 30 °C for 25 days under constant stirring at 180 rpm. Bacterial growth was estimated by optical density at 600 nm. For the quantification of percentage of degradation a gas chromatograph Agilent Technologies, 6890N model(GC-MS) was used **Results:** The results of this study indicate that *S. yanoikuyae* S72 has the ability to grow in liquid medium supplemented with naphthalene, phenanthrene, toluene, xylene and biphenyl respectively, as sole carbon source at a concentration of 100 µg/ml. Moreover S72 is capable of degrading biphenyl near of 61% and naphthalene near of 63% in culture medium with these hydrocarbons as the sole source of carbon. **Significance of the study:** The data presented here, suggested that *S. yanoikuyae* S72 strain could be a potential tool for the enhanced degradation of petroleum and hydrocarbons. Furthermore this strain allows to generate greater interest in an in-depth analysis of the metabolic pathways involved in these processes.

Isolation and identification of *Aeromonas* spp. from clinical and environmental samples in Reynosa, Tamaulipas

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Aeromonas are a group of ubiquitous bacteria, Gram-negatives, non sporing rod and facultatively anaerobic. The genus *Aeromonas* is considered an etiologic agent responsible for a variety of infectious complications in humans (Janda y Abbott, 2010). They have been isolated in aquatic environment and soil, also in drinking water and food as beef, poultry, seafood and vegetables (Pérez-Valdespino et al., 2009; Tomás, 2012). Human infections by *Aeromonas* spp had been associated with gastroenteritis caused by water and food contaminated. Some strains of these bacteria have also been associated with pathologies such as diarrhea, sepsis, endocarditis, meningitis and pneumonia (Nam and Joh, 2007). Clinical and biochemical methods for the identification of *Aeromonas* sp are not always specific; nevertheless, molecular methods such as PCR followed by sequencing, using specific genes, as *gyrB*, are useful for the identification of genus and specie. The objective of this work was to identify *Aeromonas* genus, of clinical and environmental isolates, by PCR and sequencing using *gyrB* gene, for implementing a rapid and specific method, which contributes to pathogen identification.

Avian Communities in an Urbanizing Region: Abundance Patterns and Effects of Local Habitat Features

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The Lower Rio Grande Valley of Texas has experienced rapid population growth and increase in urban area since the mid-20th century, which has tremendous implications on biodiversity and the ecological processes that support our subtropical environment. The goals of this study were to: (1) explore abundance patterns of avian communities in suburban and remnant urban woodlands, with a particular interest in native forest species, (2) assess the effects of local habitat variables on avian communities in residential habitats, and (3) provide recommendations to enhance conservation and ecosystem services associated with bird diversity. Data from 55 census points was used to compare avian communities in residential neighborhoods and remnant urban woodlands in McAllen, TX and Edinburg, TX. Results indicated that remnant urban woodlands provided habitat for a few regionally common native forest bird species that otherwise avoided urban environments. Other native forest species remained abundant across a gradient of less to more vegetative cover in residential neighborhoods. Increased tree cover had positive effects on bird diversity and native forest bird species richness, while increased impervious cover and grass cover decreased bird diversity. Omnivores and granivores were 5.1 and 3.0 times more abundant across census points than insectivores. Despite a paucity of native trees in residential neighborhoods, they had a significant positive correlation with overall bird diversity and native forest bird species richness, whereas increasing numbers of the popularly planted Live Oak (*Quercus virginiana*) did not. Recommendations to enhance native bird diversity include conserving remnant urban woodlands and increasing tree cover (with special consideration for native trees) in residential neighborhoods.

Response in varieties of *Bacillus safensis* cane, in greenhouse conditions**J.G. García Olivares², J. Reyes Hernández¹, A. Sánchez Varela², J.D.C. Quiroz Velásquez²**¹Universidad Autónoma de Tamaulipas-Unidad Académica Multidisciplinaria Mante²Centro de Biotecnología Genómica del Instituto Politécnico Nacional Campus Reynosa, Tam.

The study was carried out in the facilities of the faculty of Mante Tamaulipas, five varieties of cane were used 1.- Cp 722086, 2.- Atemex9640, 3.- XMex91917, 4.- InMEX9525, and 5.- SP 724928. Which were inoculated with the bacteria isolated from sugarcane rhizosphere from cultivated lots of the Mante Tamaulipas region. The strain BIOEXPM2-03 was provided by CEBIOGEM-IPN, which was isolated from cane rhizosphere of the Mante Tamaulipas region, which was characterized molecularly using 16S of RNAr and sequencing, in addition the NifH genes, which are associated with nitrogen fixation. Physiological parameters (plant height, biomass weight and stem diameter) were evaluated, with and without treatment (bacterial), chlorophyll and Brix grades (30, 60, 90, and 120 days)) In the seedlings. An ANOVA statistical analysis was performed using a completely randomized block design with 10 replicates and means comparison, Tukey test $P = 0.5$. Response was found in physiological and productive parameters showing these results with the potential to use this bacterium as biofertilizer for cane cultivation for the Mante Tamaulipas region.

A Vision of the *Phaseolus* seed system in Oaxaca

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The management and conservation of landraces for *Phaseolus vulgaris* have influence in the diversity levels reported in previous studies. Oaxaca is located in the Cancer tropic at the South of Mexico, due to the accidental geography of his landscapes, her climatic composition is influenciaded by the Gulf of Mexico and Pacific Ocean. At the present Oaxaca is divided in eight etno-cultural regions (INEGI, 2009) clearly differentiated by the presence of etno linguistic groups and a wide variety of landscapes, weather, wildlife and vegetation. The main linguistics families located in Oaxaca are Zapotecos, Mixteco, Chinanteco, Mixe, Triqui, Mazateco in summarize sixteen different groups, wach one is divided in dialectal variations, which intensify go from little troubles of communication to the mutual unintelligibility (Ordoñez, 2000). Agriculture is the leading activity of these groups, they maintain landraces that have been heirloom (Espinoza-Perez et al., 2014) by his ancestors and all the involved knowledge for the conservation and agronomic management. In this work, we explored the seed systems of the farmers from Oaxaca by surveys, a simple tool that allows the direct contact with the farmer in this frame work we ask the following questions. What are the traits for the differentiate the landraces? What are the differences in the management of these landraces? Which is the gain obtained? What is the consumer preference? Exist landraces lots in threatened?

Establishing a screening methodology to evaluate genotypes of sugar and energy cane for drought tolerance

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Sugarcane production can be affected by extreme environmental conditions, such as drought stress. The aim of this study focused on establishing a screening method to evaluate and select drought tolerant germplasm of *Saccharum* spp. A randomized block design experiment was conducted under greenhouse conditions with 2-months seedlings of five genotypes of *S. spontaneum* (IRAN 28, TUS12-72, TUS12-23, X08-0299, and JW43) and one cultivar (*Saccharum* spp. CP72-1210), under well-irrigated and water stress conditions, at the Texas A&M AgriLife research and Extension Center, Weslaco, Texas. Three irrigation treatments were established with irrigation intervals (3, 6, and 9) days respectively, with four replicates per each genotype in each treatment. Evapotranspiration, stomatal conductance, total biomass, leaf death rate, number of shoots and shoot growth were evaluated during the experiment. JW43 and CP72-1210 presented the highest stomatal conductance when plants were irrigated every 3 days and were not under drought stress, but were significantly lower in plants under more prolonged watering intervals. Accumulated water use by all the genotypes was significantly different among the three treatments. JW43 presented the highest amount of water use, with water requirements that ranged from 207ml/day in well-watered to 104 ml/day in water-stressed treatments, followed by IRAN28, CP72-1210, TUS12-72, X08-0299, and TUS12-23. Significant differences were found in the final biomass among all the treatments. Results indicated that X080-300 and JW43 had the largest reduction (46 and 49%, respectively) of total biomass and a reduction in the number of tillers in the water-stressed treatment compared to the well-watered one. Genotypes CP72-1210 and JW43 presented significant higher percentage of leaf death in the less irrigated treatment.

Using leaf turgor pressure sensors as an indicator to monitor water stress under deficit irrigation strategies in Citrus trees

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The improvement of irrigation water management in South Texas is urgently needed due to frequent and critical drought periods. Deficit irrigation has been investigated widely as a valuable strategy for dry regions where water is the limiting factor for crop production. However, continuous water stress monitoring under deficit irrigation strategies is difficult, and there is a need for a good indicator to signal when irrigation is required. Leaf turgor pressure sensors or known commercially by ZIM sensors have shown a great potential as a novel and non-destructive method for monitoring water stress and scheduling irrigation in fruit trees. The main objective of the current study was to evaluate the performance of ZIM-sensors for monitoring water stress in citrus trees. A greenhouse experiment was conducted in 2-years citrus trees at the Texas A&M University – Kingsville, Citrus Center. Five treatments with eight replicates per each were established, in which we had; full irrigation and sustained and regulated deficit irrigation treatments with 50 and 20% of the required irrigation needs. Two ZIM-sensors per treatment were installed at the beginning of the experiment to monitor water stress and schedule irrigation. The results showed that ZIM-Technology could be a powerful tool for growers to adjust irrigation doses and frequency easily. In addition to its easy installation and maintenance, the data interpretation is quite user-friendly, which based on the visualization of the daily curves of turgor pressure (P_p). Three standard P_p curves identified as states 1, 2, and 3, were used to determine water stress levels among low, moderate, to severe water stress.

Next-Generation Crop Improvement Using Integrative Genomics and Bioinformatics Technologies

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Recent advances in omics-based technologies revolutionized agricultural research by providing new tools such as transcriptomics, genomics, metabolomics, metagenomics and phenomics (omics) tools. These tools offer new avenues to generate improved cultivars with superior traits, which could help meet the rising global demands for food and fuel. In our lab, we are utilizing the latest omics technologies to combat multiple abiotic and biotic stresses affecting productivity of crops cultivated in Texas and beyond. For instance, we are pursuing comparative genomics, transcriptomics and splicing analyses in potato and tomato to identify Zebra Chip disease resistance genes and markers; drought-tolerance pathways in potato; cold, salinity and disease resistance genes and markers in *Citrus*, sugarcane and energycane. In addition to gene discovery and molecular marker development, we are developing new phenotyping tools, databases, and software to aid data mining, and to integrate various omics-resources with existing genetic, biotechnology and breeding resources.

Development of recombinase technology to produce consumer friendly transgenic plants

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Citrus is one of the world's major fruit crops with global availability and popularity. Citrus production has been affected by disease such as Huanglongbing (HLB), Citrus Canker and Phytophthora, causing economic hardship for growers. Therefore, the best solution for the citrus industry is to develop a technology, faster than traditionally breeding, that will develop genetically modified citrus varieties capable of expressing gene for disease resistance. Genetic transformation is a powerful tool to make small changes to one variety without disturbing its general genetic makeup, however, the acceptance of genetic modified plants has public concerns. One of the issues is that during the genetic transformation procedure, marker genes are also introduced in the transgenic plants. These genetic markers make the plant resistant to antibiotic or to herbicides. A precision genetic engineering process called Recombinase mediated cassette exchange (RMCE) has the ability to remove any unrelated sequence in a transgenic plant. RMCE has been used in apple and pears but has never been attempted in citrus. To establish RMCE in citrus a plasmid containing all recombinase cassette for marker removed was constructed and a marker gene called M. cherry, that makes the plant glow under fluorescence was also added. Promoter was split by the recombinase cassette so that only marker free can glow. *Agrobacterium tumefaciens* genetic mediated transformation was performed using hypocotyl segments of Carrizo citrange and Pineapple sweet orange. To optimize the removed of markers, transformed explants were expose to concentration of 0, 10, 25 and 50 μ M of DEX, incubated for 8, 16, and 24 hours at 7, 10, and 14 days post co-cultivation.

Climatic, geographic and physiographic factors that contribute to the distribution of oregano (*Lippia* spp.) in Mexico

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The presence of *Lippia graveolens* is widely distributed in different sites in some cases confirming an association between the presence of the species and climate, soil and geographical factors. In the state of Tamaulipas, humidity and temperatura determine the distribution; in Durango the soil characteristics play that role. In Yucatan, bioclimatic factors have no influence on the distribution of the species, but have an effect on the chemotypes. In the states of Zacatecas, Coahuila and Chihuahua, where more than 80% of oregano is collected, there is no data available on the condition and diversity of this species. Using the Maxent version 3.3.3k program an analysis of information was carried out to estimate the potential distribution of three species of oregano, two of which are considered synonymous: *Lippia graveolens* and *L. berlandieri*.

Use of Seaweed to Stimulate Plant Growth

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Sargassum sp. is a seaweed 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. The project will involve a plant growth study based upon a completed pilot study. Processed seaweed would be a viable option as a fertilizer that is organic, local, has minimal environmental impacts, and low cost compared to other fertilizer. The study will have 6 treatments; powdered seaweed, whole seaweed and compost with seaweed, and compost without seaweed. The control was local Edinburg soil which will also be the base to all the treatments. These treatments were used to grow corn in the pilot and radishes in the following trial. After recording moisture content and water retention in the soil, treatments were compared to find *Sargassum sp.* compost to have significant effects in retention of water and have higher moisture content as a soil treatment.

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Screening for *Phytophthora nicotianae* resistance of different citrus rootstocks and hybrids

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Commercial production of citrus in Texas is located in the Lower Rio Grande Valley (LRGV) and occupies over 27,000 acres. Damage caused by *P. nicotianae* result in significant economic losses to the citrus production in this area. To sustain commercial citrus production, there is an urgent need for a resistant rootstock to *P. nicotianae*. This study aimed to address the problem by challenging Sour Orange, C22 (*C. sunki* x *Poncirus trifoliata*), Sarawak pummelo x Rio Red grapefruit, Sarawak pummelo x Bower mandarin seeds and Sarawak pummelo x Bower mandarin seedlings to high amounts of *P. nicotianae* artificial inoculation. After one year post- inoculation, Sour Orange showed the greatest percentage of plant survival followed by Sarawak x Bower, and C22. The presence of *P. nicotianae* in the plants was confirmed by PCR and the density and viability was confirmed by propagule counts from soil samples. Propagule counts above 20 are considered to be potentially damaging. Propagule counts from the *Phytophthora*-inoculated soil ranged from 400-1300 which are significantly above the average found in field conditions. The study continued with the remaining plants and after six months only one sour orange rootstock plant survived. This plant showed no signs of *P. nicotianae* symptoms indicating potential resistance.

Development of a synthetic lure for monitoring Asian citrus psyllid, *Diaphorina citri* (Hemiptera: Liviidae) populations.

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USDA AFRI National Institute of Food and Agriculture Program: Training the next generation of agricultural scientists: coping with food security and climatic change challenges

The invasive Asian citrus psyllid (ACP) is the vector of the deadly citrus greening disease. ACP was first reported in Texas 2001, but has spread and colonized all groves and residential citrus trees in South Texas. ACP control is recommended as an important strategy to mitigate the spread of citrus greening. Effective control requires the development of sensitive ACP monitoring tools. Currently, ACP populations are monitored using visual observations, tap sampling and unbaited sticky traps. Unbaited yellow or lime-green traps are the most effective methods, but these traps are not potent when ACP populations are low. Thus, there is a need to improve the attraction of these traps by baiting them with ACP lures. As ACP is attracted to young flush shoots of its host plants, we tested synthetic blends formulated from volatile organic compounds (VOC) detected in flush shoots after Gas Chromatography-Mass Spectrometry analysis. Three blends made of VOCs present in flush shoots common to all ACP host plants were formulated and labelled 'MS3', 'MS7' and 'MS8'. The attractiveness of these blends to adult ACP was tested in a controlled environment using baited and non-baited white and lime-green sticky cards in a desiccator. A four-way choice test was also conducted to simultaneously test these three blends versus the control. In single choice tests, MS3 attracted 56.5% more ACP relative to the control. In contrast MS7 and MS8 did not exhibit any preferential attraction relative to the control. In multiple choice tests, MS3 marginally attracted more ACP than MS7 and MS8 and the control. MS3 is composed of three terpenes β -phellandrene, β -caryophyllene and α -phellandrene, and shows promises for ACP attraction. Studies are underway to refine MS3 and determine its effectiveness in groves.

Bioassays of entomopathogenic fungi against *Melanaphis sacchari***Karla Cruz-Aldaco, Student****Antonio Narro Agrarian Autonomous University, Calzada Antonio Narro 1923,
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Six species of entomopathogenic fungi from *Beauveria*, *Metarhizium*, and *Isaria* genera were evaluated against sugarcane aphid *Melanaphis sacchari* (Hemiptera: Aphididae) in laboratory bioassays, and three of them strains were tested under the greenhouse conditions. In both studies, we applied a fungal suspension 1×10^8 conidia/ml with 0.02% nonionic surfactant. The controls were an aqueous solution of nonionic surfactant, and an absolute control (water). In the laboratory, the fungal suspension was applied on a leaf disk of grain sorghum, and followed ten *M. sacchari* adults were placed on the leaf. The mortality was evaluated at 24, 48, and 72 h. Under greenhouse conditions, we tested fungal suspensions on plants with known population of *M. sacchari*. Aphid population counts were conducted at 4, 7, 11 and 14 d after fungal application. Under laboratory, the significant highest percentages of *M. sacchari* mortality at 72 h ($F_{7, 126} = 12.96$; $p < .0001$) were obtained with *B. bassiana*-2879 (90%), *B. bassiana*-2336 (87.5%), and *M. brunneum*-3738 (82%), compared with the three strains of genus *Isaria*, nonionic surfactant solution, and water. Under greenhouse conditions *M. brunneum*-3738 had the significant lowest *M. sacchari* population of 12.2 aphid/plant ($F_{3,122} = 6.13$; $p = .0006$). *Metarhizium brunneum*-3738 and two stain of *B. bassiana* (2879, 2336) were virulent strains that could have the potential to control *M. sacchari*. The pathogenic could present after 72 hours under laboratory, however under greenhouse these effects may take 7-14 days.