Posters & Abstracts:

2011 Annual Conference of the Subtropical Plant Science Society; Wednesday February 9, 2011

001: Transplanted watermelon plants by chisel, strip-tillage and bedding methods result in similar yield and quality; by D. J. Makus, *USDA-ARS, Weslaco, TX 78596.*

Abstract. Watermelon plants grown in semi-arid, subtropical south Texas (Lat. 26° N) are subject to wind and high solar loads. In an effort to provide an environment that would reduce wind-related sand blasting, early transplant desiccation, and vine damage and reduce soil temperatures, watermelon seedlings were transplanted into chisel- and strip-tilled high surface residue (14 t/ha) Raymondville silt-loam soil and compared to the standard method of plowing and bedding. A diploid, ‘Jamboree’, and a triploid ‘Tri-X 313’ watermelon were used as sub-plots in a transplant establishment (main-plots) experiment with four replications. Maintaining high soil residue reduced average daily soil temperatures in the chisel and strip-tilled establishment plots at 5 (P=0.03), 10 (P=0.20), and 30 cm (P=0.01) depths compared to bedded melons. Daily maximum surface temperatures (unreplicated), measured by IR thermometry, were lowest in the bedded plots, suggesting that soil cooling by water loss might be the reason for the lower temperatures. However, seasonal moisture at 30 cm was influenced only by date and not by transplant method. Rainfall for the experimental period was unseasonably high (52% of ET). Plant establishment method did not influence average fruit weight, marketable fruit weight, or marketable fruit number, but planting into high residue soil increased both marketable yield (%) and marketable fruit (%) with ‘Jamboree’ showing the greatest response to a high residue environment. Fruit quality attributes (objective color and firmness) were not affected by plant establishment method, but ‘Tri-X 313’ soluble solids (%) was higher than that of ‘Jamboree’ (12.0 vs. 11.5 %). Cultivars did differ in fruit weight, marketable fruit, and marketable yield (%), and marketable fruit number (%).

002: SPATIAL AND TEMPORAL DISTRIBUTION OF PHYSICO-CHEMICAL PROPIERTIES OF WATER FROM SUB-SALINE LAKE ALCHICHICA, PUEBLA , MEXICO., *Almora-Hinojosa Manlio A.1 ; Valdés María1; Mendoza Alberto, Escuela Nacional de Ciencias Biológicas1 y Centro de Biotecnología Genómica2, IPN. Prol. De Carpio y Plan de Ayala s/n. 11340. D.F. México.

003: Host Plants of Psyllidae in South Texas. Donald B. Thomas, ***USDA-ARS Kika de la Garza, Subtropical Agriculture Research Center***

Abstract: Diaphorina citri breeds on Rutaceae, especially orange jasmine and *Citrus* where it is the vector of HLB. Adults but not nymphs are regularly found on non-rutaceous trees in the dooryard setting. The only report of *D. citri* breeding on a non-Rutaceae was a record on Jackfruit, family Moraceae. The validity of that report has been questioned as the result of greenhouse experiments. However, in 2010 we found *D. citri* breeding on fig trees, also family Moraceae. Recently Chinese scientists have reported *D. citri* not only breeding on *Pithecellobium lucidum*, a Legume, but that the trees were infected with HLB. *Pithecellobium flexicaule*, is a common tree in south Texas and has species of psyllids that also visit citrus trees raising the possibility of a non-citrus reservoir for the HLB bacteria if (when) it reaches Texas. Hackberry trees (Celtis spp.) support a guild of psyllids, one of which, Tetragonocephala, is the vector of hackberry decline. Adults of another psyllid, *Leuronota maculata*, is as abundant on citrus trees as it is on hackberry. A related species, *L. fagarae*, breeds on prickly-ash, *Zanthoxylum fagara*, a native Rutaceae.

004: Effect of extended chilling on flight ability of irradiated mass reared Mexican fruit flies. Hugh E. Conway. ***USDA APHIS PPQ CPHST Mission Laboratory.***

Abstract: The Mexican fruit fly, *Anastrepha ludens* (Loew), (MFF) is a serious pest of commercial fruit and a recurrent pest of citrus in south Texas. The ongoing MFF eradication program in south Texas uses sterile insect technique (SIT) with aerial release. The newly developed cost effective double box aerial release machine extends the length of MFF chilling for up to 4 ½ hours from fly knockdown to final release. Tests with 20 replications were conducted to evaluate the effect of extended chilling on MFF flight ability and establish a baseline for comparison to aerial release tests. Sets of 100 MFF were collected after knock-down and hourly across a seven hour period from the MFF mass rearing chill room (8.6 ± 1.1°C) and placed into flight ability tubes located in observation cages. After 24 hours, the tubes were removed and flight ability recorded. Data indicate a slight reduction in flight ability based on days spent in eclosion towers. At knock-down, there was a 6% difference in flight ability with 75.4 ± 1.6 % (SE) and 68.7 ± 3.8% in 4/5 compared to 6/7 day flies, respectively. Across the first five hours, there was a gradual decrease in flight ability of 10% and 13% in the 4/5 and 6/7 day flies, respectively. During the last two hours, there was an additional drop in flight ability by 15% in the 4/5 day flies (49.3 ± 2.7%) and 10% in the 6/7 day flies (45.8 ± 5.8%). Chilling MFF for extended periods negatively affects flight ability, especially beyond five hours. The chilled effect baselines will assist in validating the effectiveness of MFF aerial release machines.

005: STANDARDIZATION OF LABORATORY AND FIELD METHODS FOR EVALUATING EFFICACY OF TRANSGENIC TECHNOLOGIES.

S. M. Greenberg[1, 3], J. J. Adamczyk[1], J. J. Alejandro[1], J. Holloway[2] ***[1]USDA ARS Beneficial Insects Research Unit, Kika de la Garza Subtropical Agricultural Research Center, 2413 East Hwy. 83, Weslaco, TX 78596 [2]Bayer CropScience, Lubbock, TX***

Abstract: Assessing the efficacy of transgenic plants under new environmental and management regimes is of prime importance to the Companies which produce new or improve existing transgenic products; breeders, which create different varieties stacked with Bt endotoxins; and growers, which use them for production. Laboratory and field performance of cotton containing endotoxins should be standardized. Only this can provide accurate and stabilize data for insect control with different transgenic technology. In this presentation, we will also discuss approaches and criteria for mass rearing standardized laboratory colonies of beet armyworm (BAW), *Spodoptera exigua* (Hübner); fall armyworm (FAW), *Spodoptera frugiperda* (J. E. Smith); and bollworm (BW), *Helicoverpa zea* (Boddie) for laboratory and field evaluation methods for efficacy of Bt cottons.

006: USING a SIMULATION MODEL to EVALUATE VOLUNTEER COTTON- WEEVIL ECOLOGY

William G. Meikle[1], Randy Coleman and John J. Adamczyk ***USDA ARS Beneficial Insects and Honey Bee Research Units, Kika de la Garza Subtropical Agricultural Research Center, 2413 E. Highway 83, Weslaco TX 78596***

Abstract: The Lower Rio Grande Valley is one of the few places in the continental U.S. where cotton grows year round, and one of the few places where boll weevils have yet to be eradicated. Volunteer cotton is often suspected as being the source for boll weevil infestations in commercial fields. Presently, in LRGV commercial cotton fields, there is a mandated non-hostable period from September 1 to March 1. For all noncommercial cotton, except for cotton grown under permit issued by the Texas Dept. of Agriculture, the non-hostable period is year round. In commercial fields, tillage and herbiciding effectively destroy volunteer and regrowth cotton.

Presently, a coordinated program for detecting, destroying, and assessing destruction of volunteer cotton in non-cropping habitat has not been implemented. However, the need for a highly coordinated effort has not been demonstrated and data for many parameters to support it are lacking. The assumption is that volunteer cotton represents a potential refuge for boll weevil and a source of weevils that threaten commercial cotton. However, only one study, (Jones et al. 1989. J. Econ. Entomol. 82: 1626-1632), conducted in bay shoreline habitat of central Tamaulipas, Mexico, has adequately examined aspects of

phenology and ecology of wild cotton and the boll weevil. Although volunteer cotton establishes to some extent yearly in the LRGV, what role it may play relative to boll weevil reproductive success and survival and its impact on the eradication program is largely unknown. We are improving our ability to identify situations and areas where suspected stands of cotton may occur, and simulation modeling may be an ideal companion tool to study the interaction between volunteer cotton and boll weevil.

007: Testing the efficacy of an “Attract and Kill” strategy for the control of Citrus Leafminer in Texas

Nagarjuna P. Peddabhoini*[1], Mamoudou Setamou[1], Robert Saldaña[1] & Shad D. Nelson[2] *[1] Texas A&M University – Kingsville.*

ABSTRACT: The production of enough and affordable food to meet demands of an increasing world population will likely require an increase in agrochemical and pesticide use. However, there are growing concerns over environmental impacts and non-target impacts of these chemicals. Thus, to meet demand of higher food output while protecting our environment, innovative ways of pest management need to be developed. In the present work, we are developing an ‘attract and kill’ strategy to control the citrus leafminer in Texas citrus. This approach utilizes the mate finding behavior of adult citrus leafminer to reduced amount of chemical insecticides to control this pest. Citrus leafminer (CLM), *Phyllocnistis citrella* Staiton, is an invasive species that has emerged as an economically important pest in Texas citrus in the last two decades. CLM larvae feed on young flush shoots of citrus by creating shallow tunnels, usually referred as mines, causing leaf curling and distortion. This feeding damage results in reduced photosynthesis of leaves and can potentially reduce growth of young plants. Openings created by these mines are also used as entry sites by the bacterial pathogen of citrus canker (*Xanthomonas axonopodis*). We compared the whole grove treatment with imidacloprid (Provado), to ‘attract and kill’ treatments in which mixtures of CLM pheromone and imidacloprid were applied to 1,000 citrus leaves per acre. Results on CLM counts and damage showed that treatment with the highest rate of CLM pheromone (MalEx 14%) was equally affective as the whole grove treatment with imidacloprid, thus presentation a viable option for CLM control with little or no footprint left on the environment.

008: Artificial MicroRNA-mediated silencing of stearoyl-acyl carrier protein-desaturase genes in *Nicotiana benthamiana*.

Jiantao Zhang[1], Hernan Garcia-Raiz[2], Xiaofeng Wang[1] *1. Texas AgriLife Research Center and Department of Plant Pathology & Microbiology, Texas A&M University System, Weslaco, TX 78596.*

Abstract: All positive-strand RNA viruses replicate their RNA genomes in association with host intracellular membranes. As the building materials of membranes, lipids play essential roles in viral replication. In yeast, synthesis of unsaturated fatty acids is required for replication of *Brome mosaic virus* (BMV), a well-established model virus. We set to test whether UFAs are required for BMV replication in plants. Converting saturated to unsaturated fatty acids is controlled by stearoyl-acyl carrier protein-desaturase (SACPD) family in plants. Three cDNAs encoding SACPD were cloned from *Nicotiana benthamiana*. *NbSACPD-A* and *-B* share >90% identity and both are ~80% identical to *NbSACPD-C*. In this study, artificial microRNA (amiRNA) approach was employed to knock down the *SACPDs* expression in *N. benthamiana*. Three sets of amiRNAs, each set included three amiRNAs, were designed to specifically target *NbSACPD-C* only, both *NbSACPD-A* and *-B*, or all three genes, respectively. The efficiency of amiRNA knocking down expression of their target genes was analyzed by a transient expression assay. The most efficient amiRNAs were individually introduced into *N. benthamiana* genome by *Agrobacterium tumefaciens*-mediated transformation. Transgenic plants were selected by PCR, and presence of amiRNAs was detected by Northern blotting using amiRNA-specific probes. Accumulation of *NbSACPD-A/B* or *NbSACPD-C* mRNA was substantially decreased in plants expressing amiRNA targeting *NbSACPD-A/B* or *NbSACPD-C* respectively, whereas expression of only *NbSACPD-A/B* but not *NbSACPD-C* was reduced in all tested 26 transgenic plants expressing the amiRNA targeting *NbSACPD-A/B/C*. Preliminary data indicated that BMV replication was reduced in all transgenic plant. Further work is underway to analyze the fatty acid composition and at what specific steps BMV replication was affected.

009: Effects of Soil and Foliar Calcium Sources on the Survival of Asian Citrus Psyllid.

Marisol Esparza*, Juan Raygoza, Shad D. Nelson, and Mamoudou Setamou. ***Texas A&M University-Kingsville (Citrus Center), Dept. of Agronomy & Resource Sciences MSC 228, 700 Univ. Blvd, Kingsville, TX 78363***

Abstract: Asian citrus psyllid (ACP), *Diaphorina citri Kuwayana (Fig. 1a),* is one of many pests impacting citrus trees and citrus related plants in the Rio Grande Valley of Texas. These pests damage citrus by infesting young flush shoot (Fig.1b,c) and disrupting the normal growth stages of the citrus plant by twisting the plant's foliage and decreasing photosynthesis. Psyllids are small insects, 3 to 4 mm (1/8 to 1/6 inch) in length with a simple life cycle that progresses from egg through 5 instars to the adult stage (fig. 1d). Despite the direct feeding damage caused by ACP on citrus foliage, the pest is economically important because of its ability to vector the bacterial pathogen of the deadly citrus greening disease. There is no known cure for 'citrus greening disease' and vector control is one of the recommended options for the disease management. ACP is readily killed by many chemical insecticides; however its control remains a challenge in organic production. We investigated the effects of difficult composts and bio-pesticides for nutrient uptake and physical control in the field. As a follow-up study, a laboratory study was done to determine if applications of macronutrients such as Calcium, Potassium and Manganese-Zinc to citrus has an effect on ACP survival and population. Current results for applying Calcium to the foliage to citrus trees showed a decrease in ACP survival.

010: Screening of Phenolic Secondary Metabolites in Citrus Leaves by High Performance Liquid Chromatography for Possible Psyllid Management Jose Luis Perez, Nasir Malik* *USDA-ARS Weslaco, Texas 78596*

Abstract: In this study, we investigated the chemical composition of leaves that are prone to psyllid feeding and those that are less susceptible. Furthermore, plants were subjected to insect and water stress in order to evaluate the chemical reaction of the plants. Studies were initiated to investigate any links between metabolic profiles of the citrus leaves and the extent of ACP infestation. Initially profile of polyphenols in young (more susceptible) leaves versus mature (less susceptible leaves showed that with the age of grapefruit ('Rio Red') leaves there occurs a drastic decline in flavonoids. For example, the levels of the flavonoid naringin declined by 90%, while there substantial losses in apigenin 7-*O*-glucoside and flavonoid 1 (identity yet to be determined), when young leaves matured. In addition, we compared the changes in leaf polyphenols resulting from psyllids infestation (psyllids stress) to changes resulting from water stress. These studies provide interesting insight to metabolic changes in satsuma leaves in response to different stresses. For example, two flavonoids appear only in leaves infected with ACP; i.e. they are absent in normal and water stressed leaves. In addition, caffeic acid levels increased nearly 100% in water stressed leaves but declined nearly 80% in leaves infested with psyllids.

011: Sweet Orange Scab (SOS) in the US: Discovery, Characterization, Economic Impact and Current Status <u>Aditi Satpute</u>, Madhurababu Kunta, John da Graca and Mani Skaria Texas A&M University-Kingsville, Citrus Center, 312 N. International Blvd, Weslaco, TX 78596 .

Abstract: Sweet orange scab (SOS) caused by Elsinoe australis has not previously been reported in the USA, and is thus an actionable disease. In 2010, a lemon sample with scab symptoms collected in Spring, TX during the Citrus Commodity Survey conducted by the Texas A & M University-Kingsville Citrus Center gave a positive polymerase chain reaction (PCR) result for E. australis. An additional find came from a tangerine orchard in Orange, TX. Samples were then collected by USDA-APHIS-CPHST staff and sent to their laboratory in Beltsville, MD, which confirmed the PCR result and cultured the fungus.

USDA-APHIS-PPQ then collected samples from numerous counties which were visually screened at the Citrus Center, with suspect ones being forwarded to Beltsville. SOS was detected by PCR from fruit collected from several counties including Hidalgo, Cameron and Willacy. USDA-APHIS-PPQ also confirmed its presence in Louisiana and Mississippi. Since the disease had not been reported in California, Texas citrus growers voluntarily stopped shipments of fruit to that state until the publication of the USDA-APHIS risk assessment which concluded that packinghouse-treated citrus does not pose a threat to other citrus producing areas. There remain several unanswered questions, including why PCR positive results are obtained from fruit with atypical symptoms which appear to be affected by late season wind scar, why not all such affected fruit is PCR positive (only 43% of 'wind scar' affected fruit tested positive in an initial study), and what symptoms the cultured fungus produces. Koch's postulates have not yet been performed, and in order to do this, the Citrus Center has been attempting to culture the fungus.

012: POTENTIAL ROUTES OF DISPERSAL *OF CACTOBLASTIS CACTORUM* IN TEXAS AND MEXICO DUE TO CLIMATE CHANGE Brenda M. Garcia[1], Simon del Alto[1], Teresa P. Feria[1], Angel Felicísimo[2], Jordan Goulovob[3], Christopher P. Brooks[4], and Gary N. Ervin[4] *[1] University of Texas–Pan American, 1201 W University Drive, Edinburg, TX, 78541;*

Abstract: The arrival of *Cactoblastis cactorum* on the southeastern coast of the United States, its steady spread to neighboring states, and the relatively close distance to Texas has raised concerns over the potential damage it may inflict on native *Opuntia* if it were to reach Texas and Mexico. *Opuntia* crops are prominent in these areas, both in terms of human consumption (medicine and beverages) and forage for livestock. *Cactoblastis cactorum*'s range extension in these geographic areas would lead to devastating problems by undermining native ecological communities and leaving land susceptible to erosion. Consequently, there will also be an economic effect that would significantly impact Texas. With an increase in climate change, there is a high potential for the rapid spread of *C. cactorum* to lands in which *Opuntia* thrives. We predicted the potential distribution of *C. cactorum* and determined the factors that facilitate its spread by using bioclimatic mapping through MaxEnt, coupled Atmospheric-Oceanic General Circulatory Models, climate change scenarios and Geographic Information Systems. Our results show the potential routes of expansion that *C. cactorum* is most likely to follow in the near future (forty years from present). Our findings will serve as information to be used in developing efforts to successfully prevent large scale damage to *Opuntia* in Texas and Mexico.

015: Phylogeographic and Population Genetic Studies Uncover Two Founding Events in Asian Citrus Psyllid Populations Collected in the Americas. de León, J.H.[1,*], Sétamou, M.[2], Gastaminza, G.A[3], Buenahora, J[4], Cáceres, S.[5], Yamamoto, P.T.[6], Logarzo, G.A.[7], Stañgret, C.R.W.[8] *[1]USDA, ARS Weslaco, TX USA*

Abstract: A phylogeographic analysis inferred from the partial mitochondrial cytochrome oxidase subunit I gene (433 bp) was performed with 22 populations (n=132) of *Diaphorina citri* collected in the Americas and one in the Pacific. Eight populations (n=46) from four countries in South America, 14 (n=76) from four countries in North America, and one from Hawaii (n=10) were analyzed. Twenty-three haplotypes (hp) were identified that fell into two groups, hp1-8 were identified in South America (Group 1) and hp9-23 were identified in North America and Hawaii (Group 2). Hp1 and 9 were present in the highest frequencies within each population and within their group, 81-85%. Sharing of haplotypes was not observed between the two groups. An analysis of molecular variance uncovered significant genetic structure (Φ_{CT}=0.733; P<0.001) between the two groups in the Americas. A neighbor-joining phylogram and two haplotype networks (ParsimonySplits and Statistical Parsimony) discriminated the two groups, while both networks identified hp1 and 9 as the ancestral or founding haplotypes within their respective group. Significantly negative neutrality tests (Tajima's *D* and Fu's *Fs*), non-significant mismatch distribution parameters (SSD and HRI), and low genetic diversity levels provided evidence of demographic expansion within each group in the Americas. The data suggest that two founding events of

D. citri occurred in the Americas, one in South America and one in North America. Furthermore, North America and Hawaii appear to share a similar source of invasion. These data are important to the development of biological control programs against *D. citri* in the Americas.