Agricultural Biological Invasions between U.S. & China - lessons learned & developing preventive strategies for the future

Yulu Xia

NSF Center for Integrated Pest Management at NCSU

Abstract: United States and China share similar climates, flora, and fauna. Invasive pests have been a major threat to each other's agricultural production and ecosystem. The issue becomes even more severe in recent decades as increasing in trade volume and human traffic. This presentation illustrates a few examples of economically and/or ecologically significant invasions between the two countries, discussing the pathway and lessons learned from these invasions, proposing practical strategies in combating the issue.

Keywords: Invasive species; pests; biological invasions; climate; early detection and response

The Role of Oxygen Concentration in Phytosanitary Irradiation: Mechanisms, Thresholds, and Applications

Guoping Zhan, Qing Ying, Ju Peng, Chen Ma, Yunlong Ma

Chinese Academy of Inspection and Quarantine Center for Biosecurity Sanya

Abstract: Oxygen concentration is a key factor influencing the efficacy of phytosanitary irradiation, affecting the biological response of insect pests during treatment. This report explores two primary mechanisms by which oxygen modulates irradiation effects: the radioprotective effect under hypoxia and the stimulatory effect under elevated oxygen conditions. Under hypoxic environments (typically & lt; 4% O_2), reduced levels of reactive oxygen species (ROS) generation lead to decreased biological damage and higher survival rates in insect pests. Experimental studies have demonstrated that radiotolerance significantly increases at oxygen concentrations below a critical threshold of approximately 3–4% O_2. For example, late third-instar of *Bactrocera dorsalis* irradiated under 0–2% O_2, and *Zeugodacus cucurbitae* irradiated at 0, 1, 2, and 3% showed elevated adult emergence and required higher doses to achieve the same level of control. Such findings have crucial implications for the development and validation of PI protocols involving modified atmosphere packaging (MAP) or storage. Conversely, oxygen-rich environments enhance the formation of ROS and have been shown to increase treatment efficacy by inducing greater biological damage. Studies on *Brevipalpus yothersi* irradiated in 100% O_2 confirm that enriched oxygen conditions can improve outcomes by reducing fecundity and hatch rates compared to ambient air. These opposing effects underscore the necessity of establishing oxygen thresholds and incorporating species-specific responses into treatment modeling. A meta-analysis of documented insect responses highlights key variability across taxa and developmental stages. This report concludes with a discussion of the regulatory implications of oxygen levels in PI treatments and suggests potential strategies for integrating oxygen monitoring and control into routine phytosanitary protocols. As global trade in fresh produce continues to rise, a more nuanced understanding of atmospheric influences on irradiation efficacy is essential for safeguarding biosecurity and enhancing treatment reliability.

Keywords: Irradiation; oxygen level; radioprotective effects; fruit flies

Molecular regulator of the post-mating oviposition in the oriental fruit fly

Yuanyuan Peng[1,2], Xinyu Lan[1,2], Jinjin Wang[1,2], Hongbo Jiang [1,2]

1. Key Laboratory of Entomology and Pest Control Engineering, College of Plant Protection, Southwest University, Chongqing 400715, China; 2. Key Laboratory of Agricultural Biosafety and Green Production of Upper Yangtze River (Ministry of Education), Southwest University, Chongqing 400715, China

Abstract: This study aimed to identify key small-molecule effectors in the male accessory gland (MAG) secretion that trigger oviposition in females and elucidate the molecular mechanism by which these compounds are perceived by the female reproductive system to induce egg-laying. Using the globally invasive pest *Bactrocera dorsalis* (oriental fruit fly) as a model, we employed behavioral assays, metabolomics, RNA interference, ultra-high-performance liquid chromatography, calcium imaging, in situ hybridization, transcriptome sequencing, and gene editing coupled with behavioral analyses. These approaches were used to (1) identify small-molecule compounds transferred from the male MAG during mating that stimulate oviposition and (2) dissect their mechanistic action in females. We identified N-AP, a small molecule in the male MAG secretion, as the key bioactive compound triggering oviposition. Quantitative analysis revealed the dynamic transfer of N-AP from the MAG to the female reproductive tract during mating. RNAi knockdown confirmed that N-AP synthesis in males regulates female egg-laying. Furthermore, we demonstrated that N-AP binds to the ionotropic receptor complex BdIR25a+BdIR85a in the female reproductive tract to activate oviposition. This study unveils a novel “N-AP–IR” signaling system governing post-mating oviposition in *B. dorsalis*: N-AP, secreted by the male MAG, is transferred to the female reproductive tract during copulation and is specifically detected by the BdIR25a+BdIR85a receptor complex expressed in signum-surrounding cells, thereby inducing egg-laying.

Keywords: *Bactrocera dorsalis*; N-AP; egg-laying; ionotropic receptor

Microbiota enables cross-species adaptation in an invasive polyphagous fruit fly

Zhonggeng Liu, Zhenyu Zhang, Hongyu Zhang, Xiaoxue Li

Huazhong Agricultural University

Abstract: Polyphagous insects, which exploit a diverse array of host plants, frequently become global pests with significant economic repercussions. Despite their impact, the mechanisms enabling these insects to thrive across a wide variety of resources remain poorly understood. In this study, we examine the invasive polyphagous fruit fly, *Bactrocera dorsalis* (Tephritidae), and uncover the critical role of microbiota in facilitating its adaptability. Our findings reveal that microbiota is essential not only for normal larval development on the fruit fly’s primary host plant but also for enabling rapid adaptation to a range of alternative host plants. A stable microbiota community within the fruit fly requires bacterial contributions from both eggs and host plants. While the composition of the microbiota varies across generations and is influenced by the host plant, the benefits provided by these microbial communities extend beyond any single host. Remarkably, the microbiota confers fitness advantages that support larval survival even on suboptimal or non-host plants, underscoring their role in the fly’s broad host adaptability. This microbial adaptability likely contributes to the host range expansion and invasive potential of *B. dorsalis*. Our results suggest that polyphagous insects may rely on gut microbiota-mediated nutrient acquisition as a versatile strategy for adapting to new host plants and invading new environments. Understanding these microbiota-host interactions could be key to developing novel management strategies for controlling invasive species that pose economic threats on a global scale.

Keywords: *Bactrocera dorsalis*; polyphagous; invasive species; microbiota; host use

Myrmeleon fuscus is a promising predator of the red imported fire ant, Solenopsis invicta Buren：from laboratory to field trials

Jianjun Mao, Lisheng Zhang

Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, PR China

Abstract: The red imported fire ant *Solenopsis invicta* (Hymenoptera: Formicidae) is an aggressive social insect pest native to South America and now present in many countries. Chemical control is the main strategy for managing this pest; however, it leads to environmental pollution and harmful effects on non-target arthropods. Although phorid flies have been shown as parasitoids against *S. invicta*, predators of *S. invicta* have rarely been reported. In this study, a natural predator, *Myrmeleon fuscus* (Neuroptera: Myrmeleontidae) against *S. invicta* was assessed. The 1st, 2nd, and 3rd instar larvae of *M. fuscus* preyed on both small and large *S. invicta* workers. The ratio of *S. invicta* workers consumed by *M. fuscus* was dependent on prey density, suggesting a type II functional response of *M. fuscus* to *S. invicta*. The maximum daily predation amounts of the 3rd instar *M. fuscus* larvae on small and large *S. invicta* workers were 47.17 and 13.19, respectively. The searching effects of *M. fuscus* on *S. invicta* were negatively correlated with prey density. As the predation efficiency of M. fuscus was influenced by predator density, *M. fuscus* had an intraspecific interference response to *S. invicta*. The foraging *S. invicta* workers were reduced by 24.43% due to predation of the 3rd instar *M. fuscus* larvae on the 30th day after predator release. Nest migration was not observed outside the mesocosm area during the experimental period. We demonstrated that *M. fuscus* is an excellent predator of *S. invicta* and has promising potential for the management of this invasive ant.

Keywords: Antlion; *Solenopsis invicta* workers; predation efficiency; functional response; colonization

Identification of *Cydia pomonella* nucleopolyhedrovirus, virulence and environmental stability analysis

Yuting Li

Shenyang Agricultural University

Abstract: The codling moth, *Cydia pomonella* (Lepidoptera: Tortricidae), is a globally notorious pest with a wide distribution range. *Cydia pomonella* nucleopolyhedrovirus (CypoNPV) was isolated from an infected laboratory-reared colony and investigated for its biology, genome, virulence, and environmental stability. CypoNPV was characterized by electron microscopy of occlusion bodies (OBs), genomic sequencing, bioassays, and heat and UV treatment. CypoNPV OBs exhibited an irregular polyhedral shape, varying in size from 0.99 to 3.99 μm. The complete genome of the virus was sequenced, assembled, and analyzed. The genome was 112909 bp in length, with 34.44% GC content, and encoded 124 putative ORFs, including 38 baculovirus core genes. Phylogenetic and Kimura-2 parameter analyses revealed that CypoNPV is a novel species closest to CrpeNPV and EpgrNPV. Bioassays revealed that CypoNPV was virulent and effective in controlling *C. pomonella*. Environmental stability analysis indicated that CypoNPV has certain tolerance to high temperatures but is relatively sensitive to UV radiation. This work first reported the whole genome of CypoNPV as well as its biological characteristics for the possibility of developing this virus as a bio-pesticide in the future.

Keywords: *Cydia pomonella*; nucleopolyhedrovirus; genome analysis; bioassay; field control; stability

Olfactory molecular mechanism of host volatiles regulating sex-specific behavior in *Bactrocera dorsalis*

Xiaofeng Chen

Yunan Agricutural University

Abstract: *Bactrocera dorsalis*, a globally invasive pest devastating fruits and vegetables, exhibits sex-specific behavioral responses to host volatiles: males are strongly attracted to methyl eugenol (ME), while females specifically respond to oviposition attractants such as γ-octalactone. This study integrated behavioral assays, molecular biology, and structural biology to elucidate the pivotal role of odorant binding proteins (OBPs) in these processes. We identified key OBPs involved in ME perception of male and γ-octalactone perception of female. CRISPR-mediated knockout of these OBPs severely impaired olfactory responses to ME and γ-octalactone in this fly. Furthermore, we took OBP83g-2 which is a critical OBP for γ-octalactone perception as a model, revealing the transcriptional regulatory mechanisms of OBP83g-2 induced by γ-octalactone. These findings establish a theoretical foundation for developing behavior-based pest management strategies and provide novel molecular targets for precision control of agricultural pests.

Keywords: *Bactrocera dorsalis*; sex-specific behavioral responses; odorant binding proteins; transcriptional regulation

Progress in IAS Risks: from prospective mapping to intelligent monitoring network

Haoxiang Zhao, Xiaoqing Xian, Wanxue Liu

State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China

Abstract: We focused on advancing risk management of invasive alien species from prospective mapping to intelligent monitoring networks. It developed China's Public Service Platform for IAS Prevention and Control, integrating big data, 3S, AI, and spatiotemporal visualization to support data sharing, monitoring-early warning, and decision-making through modules like species info and spatiotemporal distribution. Risk assessment models were established for prioritizing potential IAS, quantifying management priorities, and multi-node risk assessment under collaborative invasion, evaluating introduction pressure, establishment risks, and spread dynamics. Intelligent monitoring technologies include data collection systems, image recognition, and real-time monitoring devices integrated with platforms, enhancing efficiency and early warning. The project provides data and technical support for national IAS management, aiding policy formulation, censuses, and routine monitoring.

Keywords: Invasive alien species; risk management; public service platform; risk assessment model; intelligent monitoring

Rickettsia impacts the reproduction of *Bemisia tabaci* through nutritional and hormonal signaling pathways

Xiyu Bao, Junbo Luan*

College of Plant Protection, Shenyang Agriculture University, Shenyang, Liaoning, China

Abstract: Interactions between symbionts in multi-partner mutualistic associations in insects have substantial effects on host fitness. However, the emergence, mechanism, and consequences of microbial coexistences remain largely elusive. There are generally only low levels of EAAs in the phloem of various plant species posing a nutritional challenge for phloem-feeding insects. We found symbionts *Portiera*, *Hamiltonella* and *Rickettsia* possess most genes involved in lysine synthesis in the whitefly *Bemisia tabaci* MEAM1 although their genomes are reduced. *Hamiltonella* maintains a nearly complete lysine synthesis pathway. In contrast, *Portiera* and *Rickettsia* require the complementation of whitefly horizontal transferred genes for lysine synthesis and have lysine exporter lysE. Trough *Hamiltonella* elimination, homologous *E. coli* gene knockout, and RNA interference, we demonstrate that whitefly can cooperate with *Portiera* and *Rickettsia* for lysine synthesis, that impacts both whitefly reproduction and symbiont fitness. We further found that *Rickettsia* infection promotes fecundity, female bias and development of the whitefly *Bemisia tabaci* MED. We demonstrate that *Rickettsia* have been horizontally acquired by *B. tabaci* MED from *B. tabaci* MEAM1 during periods of coexistence. *Rickettsia* is transmitted maternally and horizontally from female *B. tabaci* MED individuals. Our findings reveal that *Rickettsia* infection stimulates juvenile hormone synthesis, in turn enhancing fecundity, copulation events, and the female ratio of the offspring. We also certified that *Rickettsia* was integrated into metabolic cooperation between whitefly and obligate symbiont *Portiera* for branched-chain amino acid synthesis, which regulated the target of rapamycin signaling pathway, thereby facilitating host reproduction and development.

Keywords: amino acids; hormone; HTGs; reproduction; *Rickettsia*; TOR

RNA Interference in Tuta absoluta: Advances and Sustainable Management Approaches

Xiaodi Wang, Fanghao Wan, Zhichuang Lü* and Wanxue Liu*

State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, PR China

Abstract: Tomato leaf miner (*Tuta absoluta*) is a quarantined pest that damages Solanaceae crops worldwide. The overuse of traditional pesticides negatively affects both human health and the environment. RNA interference (RNAi), based on double-stranded RNA (dsRNA) induction, offers a promising alternative for *T. absoluta* control, though its efficacy depends on target gene selection and overcoming dsRNA instability/delivery challenges. Using RNAi and CRISPR/Cas9 screening in *T. absoluta*, we identified key target genes across vital processes: growth/development (*Krüppel-homologue 1*, *ecdysone receptor*), lethality (*DNA methyltransferase 1*, *chitin synthase*, *β-1,3-glucanase*), oviposition (chromatin remodeling factors *ISWI*, *BRM*), sex ratio/genitalia (*doublesex*, *Masculinizer*), and host selection (*Opsin*). To overcome dsRNA instability and low delivery efficiency, we developed an RNAi system based on dsRNA/nanoparticle complexes targeting *T. absoluta* genes. We determined the optimal fusion ratio of nanoparticles to dsRNA and demonstrated that nanoparticle encapsulation enhances the stability of dsRNA. Nanoparticles also reduced the size of dsRNA particles, thereby improving the absorption efficiency of dsRNA by plant leaves. This nano-delivery system significantly enhanced the RNAi-based control efficacy against *T. absoluta*. Safety assessment confirmed the absence of sequence homology between the target genes and humans or key natural enemies (e.g., *Nesidiocoris tenuis*) within the ecological niche, indicating minimal risk to these non-target organisms. This study demonstrates the successful application of nanocarrier-delivered RNAi for controlling *T. absoluta*, a non-model pest, providing a foundation for developing green, safe, efficient, and sustainable control strategies against *T. absoluta* and other pests.

Keywords: *Tuta absoluta;* RNA interference; nanoparticles; pest control

Modeling control of invasive fire ants by gene drive

Yiran Liu, Samuel E. Champer, Benjamin C. Haller, Jackson Champer

Peking University

Abstract: *Solenopsis invicta*, commonly known as the fire ant, is characterized by aggressive behavior and exceptional invasive capabilities, rendering conventional control methods largely ineffective. Here, we explore the implementation of homing suppression gene drive in fire ants by developing a spatially explicit model that incorporates both monogyne and polygyne colony structures, enabling comprehensive evaluation of genetic control strategies. Ants may present unique challenges for gene drive due to their colony structure and haplodiploidy. Our results reveal that after an extended time, gene drive effectively eliminates polygyne colonies, but monogyne populations often persist at low level. Though standard suppression drives in haplodiploids have reduced power, new dominant-sterile resistance or two-target strategies, as well as drives that affect the colony structure, can restore high suppressive capability. Interspecific competition can also exert a positive effect on gene drive-mediated population suppression dynamics. In particular, a gene drive release during the invasion phase significantly enhances population suppression, enabling native ants to successfully recolonize their original habitats. Overall, we conclude that while gene drive in fire ants may take place over extended time scales, its long-term results, even with imperfect efficiency, are quite promising.

Keywords: Invasive fire ant; suppression gene drive; computational modeling

Genomes of *Bactrocera correcta* (Diptera: Tephritidae) reveal regional invasion patterns and thermal adaptation

Weisong Li, Yuan Zhang, Zuxing Liao, Neng Zhang, Yujia Qin, Zhihong Li*

China Agricultural University

Abstract: The guava fruit fly (*Bactrocera correcta*) is a highly invasive agricultural pest, yet the genomic mechanisms underlying its thermal adaptation and rapid range expansion remain largely unexplored. Here, we present a chromosome-level genome assembly of *B. correcta* and perform comprehensive comparative genomic analyses, revealing a notable expansion of the HSP70 gene family. Transcriptomic profiling under heat stress conditions (35°C and 38°C) consistently showed upregulation of HSP70 genes, underscoring their pivotal role in thermotolerance. Population genomic analysis of 249 individuals sampled across the species' distribution range uncovered two major invasion routes: one originating in Sri Lanka and spreading through India and Myanmar into western Yunnan, China; and another, also originating in Sri Lanka, dispersing across Southeast Asia into eastern Yunnan and eventually reaching Hainan Province, China. To trace invasion origins, we developed a machine learning-based random forest model that demonstrated high classification accuracy, with predictions validated using independent populations from Laos. Furthermore, environmental association analyses using LFMM and redundancy analysis (RDA) identified candidate adaptive SNPs associated with local environmental variables and potential genomic offsets, highlighting signatures of local adaptation during range expansion. Species distribution modeling with the Biomod2 package projected an increase in climatically suitable habitats under future climate scenarios, indicating elevated risks of further invasion. Collectively, our findings provide new insights into the genomic drivers of *B. correcta*'s invasion success and offer predictive tools for risk assessment and management of this economically important pest.

Keywords: *Bactrocera correcta*; genome; invasion history; thermal adaptation

Development of molecular detection for key fruit and maize pests using environmental DNA (eDNA)

Dingzhou Cai, Anjuan Li, Yuxi Mo, Lijun Liu, Zhihong Li*

China Agricultural University

Abstract: This study developed an optimized eDNA metabarcoding protocol for non-invasive surveillance of key fruit (*Grapholitha molesta*, *Carposina sasakii*) and maize pests. Forkey fruit pests, the results demonstrated that eDNA with the highest concentration and quality was obtained through a filtration process combining a 10 μm mixed cellulose ester (MCE) membrane and a 0.45 μm cellulose acetate (CA) membrane, after soaking the victim pulp for 15 min. The primers developed for these two species of fruit moths exhibited high sensitivity, with minimum detection limits of 0.1 and 0.01 ng/μL, respectively. For the key maize pests, we briefly introduce the preliminary eDNA research on moth and storage pests. This study provided a critical theoretical foundation for the development of non destructive pest testing technology, and also offered valuable references for eDNA research on other species, which will be vital to the field monitoring of pests.

Keywords: Environmental DNA; fruit-boring moths; maize moth pests; storage pests

Reunification of an invasive plant with its specialist herbivore selects for rapid adaptive changes in defensive volatiles

Xincong Zhai, Xiao Sun*
Henan University

Abstract: Reassociation of invasive plants with specialist herbivores can select for the restoration of relaxed defense syndromes, however, we know little about how volatiles in plant defenses respond to such reunions. We studied populations of invasive *Ambrosia artemisiifolia* with varying reassociation histories (0, 12, 16, and 20 years) with the specialist *Ophraella communa* and found that longer reassociations correlated with higher abundances and diversities of generalist herbivores in a common-garden. Plants with longer reassociation histories were less attractive to *Ophraella*, and this correlated with reduced emissions of limonene and α-pinene, in turn correlating with increased defense against *Ophraella*. In contrast, longer reassociated plants were more attractive to the generalist Spodoptera littoralis and the reduced limonene emission correlated with weaker defense against *Spodoptera*. Our results imply that a specialist may drive rapid evolution of volatile-related defenses, enhancing plant resistance to this specialist but at the cost of weaker defense against a generalist.

Keywords: Plant volatiles; invasive plant; defense; evolution; tradeoff; generalist herbivore; specialist herbivore; reassociation; *Ambrosia artemisiifolia*

OBP7-mediated undecanal regulating of the heap-corpse behavior in red imported fire ants

Fenghao Liu

Fujian Agriculture And Forestry University

Abstract: The red imported fire ant (*Solenopsis invicta*) is a highly invasive social pest with significant harmful impacts. Its unique heap-corpse behavior effectively prevents the spread of pathogens within the nest, maintaining cleanliness and thereby facilitating its rapid invasion. This study focuses on the key chemical signals regulating this behavior and the molecular mechanisms of odorant-binding proteins, employing multidisciplinary approaches to reveal the role of undecanal and its specific binding protein SiOBP7.The main findings are as follows:(1)GC-MS analysis of corpse volatiles, combined with electroantennography (EAG) and behavioral assays, identified Undecanalas the key compound triggering heap-corpse behavior, with an optimal concentration of10 μg/μL. (2)Transcriptome analysisrevealedSiOBP7, an odorant-binding protein specifically responsive to undecanal. It encodes133 amino acids and contains PBP and GOBP domains, with phylogenetic analysis indicating Hymenoptera-specific conservation. (3) Spatial and temporal expression profiling demonstrated that SiOBP7is predominantly expressed in adult workers, particularly within the antennae and head. In situ hybridization and scanning electron microscopy localized its expression to the tenth antennal segment, which is rich in sensilla.(4)Functional validation through recombinant protein expression and fluorescence competitive binding assays revealed a strong binding affinity between SiOBP7 and Undecanal, with a dissociation constant (Ki) of 9.42 ± 1.92 μmol/L.(5)RNA interference (RNAi) targeting SiOBP7significantly reduced the ants' EAG response to Undecanal and weakened their heap-corpse behavior, also inducing escape responses. The above results indicate that SiOBP7 plays an important role in the recognition of Undecanal and the mediation of Heap-Corpse behavior in *S. invicta*. This study elucidates for the first time the molecular mechanism by which the Undecanal-SiOBP7 pathway regulates heap-corpse behavior behavior in red imported fire ants. The findings provide novel insights into behavioral regulation in social insects and establish atheoretical foundation for developing chemoattractant-based control strategies.

Keywords: Red imported fire ant; undecanal; odorant-binding protein; heap-corpse behavior; olfactory recognition

Workers modulate stridulation signals to target queens for cannibalism in fire ants

Wennan Dai

Lanzhou University

Abstract: Ants employ a wide range of communication systems to coordinate colony activities, with chemical signals being the most extensively studied. While studying mechanisms of social regulation in the invasive fire ant *Solenopsis invicta*, we discovered a surprising behavior: workers sometimes cannibalize a high proportion of virgin queens. Our experiments revealed that this queen cannibalism is triggered by food deprivation. Under such stressful conditions, workers produce a distinct vibrational signal directed specifically at young queens. Although chemical analyses showed no significant differences in cuticular hydrocarbons between targeted and non-targeted queens, playback experiments demonstrated that different vibrational signals elicited distinct behavioral responses. These findings uncover a novel role for stridulation in regulating social behavior and challenge the long-standing view that ant communication is dominated solely by chemical cues.

Keywords: Cannibalism; stridulation; *Solenopsis invicta*; eusociality; food scarcity; invasive species