Jasmonate signaling in rice defense against brown planthopper: mechanisms and applications

Ran Li[1*], Gaochen Jin[1], Huijing Li[1], Siwen Wu[1], Junli Xiao[1], Yumeng Chen[1]

[1] *Institute of Insect Sciences, Zhejiang University, Hangzhou, 310058*

*Correspondence: rli05@zju.edu.cn

Abstract: The phytohormone jasmonate (JA) plays a pivotal role in plant defense against herbivores by modulating the biosynthesis of defensive compounds. The brown planthopper (BPH), a highly destructive piercing-sucking pest in paddy fields, inflicts substantial damage through feeding, oviposition, and the transmission of plant viruses. Our earlier research has shown that BPH infestation activates the JA signaling pathway, and JA positively enhances rice resistance to BPH. Through multi-omics analysis, we identified MYC2 as a key regulator in JA-mediated herbivore resistance, orchestrating the transcriptional regulation of other signaling components. For example, the MYC2-JAMYB transcriptional cascade is involved in rice's chemical defense against BPH, while the MYC2-MAPKKK55/62/70-MKK3-MPK7/14 cascade governs rice's physical defense mechanisms. However, the activation of JA-mediated defense is accompanied by suppressed rice growth. This inherent growth–defense trade-off limits the practical application of JA-based plant defense inducers for enhancing endogenous pest resistance. We identified an easily synthesized methyl ester of the JA receptor agonist 1-oxoindanoyl isoleucine (In-Ile) that selectively enhances rice resistance to BPH without compromising growth or yield. Mechanistically, this agonist activates the OsMYB55-mediated lignin biosynthesis defense receptor module [OsCOI1a/2-OsJAZs (3,4,6,7,12)] without activating the growth-suppression receptor module (OsCOI1b- OsJAZs). These findings demonstrate that synthetic JA agonists can provide nuanced manipulations of endogenous plant defenses without yield penalties—a promising biorational strategy for pest control in rice.

Keywords: rice; brown planthopper; jasmonate signaling pathway; growth-defense tradeoff; jasmonate agonist

Mechanisms of insect oral secretions in modulating plant defense

Yingbo Mao

CAS Center forExcellence in Molecular Plant Sciences

Horizontal Gene Transfer Contributes to Efficient Nitrogen Economy in *Bemisia tabaci*

Zezhong Yang

Tianjin Academy of Agricultural Sciences

Abstract: Nitrogen is an essential element for all life on earth. Nitrogen metabolism, including excretion, isessential for growth, development, and survival of plants and animals alike. Several nitrogenmetabolic processes have been described, but the underlying molecular mechanisms are unclear.Here, we reveal a unique process of nitrogen metabolism in the whitefly Bemisia tabaci, a globalpest. We show that it has acquired two bacterial uricolytic enzyme genes, B. tabaci urea carboxylase (BtUCA) and B. tabaci allophanate hydrolase (BtAtzF), through horizontal gene transfer. These genes operate in conjunction to not only coordinate an efficient way of metabolizing nitrogenous waste but also control B. tabaci's exceptionally flexible nitrogen recycling capacity. Its efficient nitrogen processing explains how this important pest can feed on a vast spectrum of plants. This finding provides insight into how the hijacking of microbial genes has allowed whiteflies to develop a highly economic and stable nitrogen metabolism network and offers clues for pest management strategies.

Molecular Mechanisms of GSS1 in Modulating *Plutella xylostella*-Host Plant Interactions

Wei Chen
GanNan Normal University

Abstract: The glucosinolate sulfatase GSS1 is the predominant secreted effector in *Plutella xylostella* (diamondback moth, DBM), produced in salivary glands and the regurgitant gut. This multifunctional protein plays dual roles in insect-plant interactions: 1) as a pre-detoxification agent that hydrolyzes host plant glucosinolates to facilitate herbivory, and 2) as a source of proteolytic peptides that act as defense elicitors, triggering plant immunity via upregulation of ABA and JA phytohormones. Notably, ABA synergizes with JA to enhance plant resistance against DBM. Intriguingly, GSS1 targets plasmid-localized ABA1 protein, while its proteolytic fragment GSS1-P1 localizes to the nucleus, suggesting a potential retrograde signaling pathway influencing plant defense responses. These findings uncover a complex inter play between insect adaptation and plant counter-defense, offering new insights into co-evolutionary mechanisms.

Keywords: Diamondback moth; Glucosinolate Sulfatases; Oral secretion;Plant hormones;ABA

Population Dynamics and Infestation Patterns of Drosophila suzukii on Raspberry Cultivars in Northwestern Morocco: Toward Sustainable IPM Strategies

Khalid Khfif[1*], Hasnae Ennouinou[1,2,3], Lhoussaine El Rhaffari[4], Fouad Mokrini[5], Rachid Lahlali[2]
1. Plant Protection,Laboratory of Entomology, Research Unit on Nuclear Techniques, Environment, and Quality, National Institute for Agricultural Research (INRA),Tangier,Tangier,Morocco
2. Plant Protection,National School of Agriculture of Meknes,Meknes,Meknes,Morocco
3. Plant Protection,Hassan II Agronomic and Veterinary Institute,Rabat,Rabat,Morocco
4. Faculty of Sciences,Moulay Ismail University of Meknes,Meknes,Meknes,Morocco
5. Plant Protection,Biotechnology Unit, National Institute for Agricultural Research (INRA),Rabat,Rabat,Morocco
* khalid.khfif@inra.ma

Abstract: Raspberry (Rubus idaeus) cultivation represents a key horticultural sector in northwestern Morocco, particularly in the Larache region. However, the invasive spotted-wing drosophila (Drosophila suzukii) poses a serious threat to both yield and export quality. Current management relies heavily on chemical pesticides, raising concerns over resistance, environmental impact, and non-target effects, highlighting the urgent need for sustainable, integrated pest management (IPM) solutions. To support this shift, we investigated the population dynamics and eco-ethology of D. suzukii under Moroccan field conditions from 2022 to 2025 in commercial fields of two raspberry cultivars: R. idaeus 'Yazmin' and 'Maravilla', using traps baited with mashed ripe banana and yeast. Peak adult captures occurred in late April 2022 (14 flies/trap), mid-March 2023 (20), mid-April 2024 (28), and late April 2025 (31) in Yazmin' cultivar, indicating potential seasonal and interannual variability influenced by local climatic factors. Infestation assessments in 2025 revealed a higher adult emergence from 'Yazmin' fruits (55 flies / 20 fruits) compared to 'Maravilla' (32 flies), suggesting cultivar susceptibility differences. These findings provide the first multi-year baseline of D. suzukii dynamics in Morocco and underscore the importance of climate-informed pest forecasting. Ongoing work is focused on modeling degree-day-based phenology and evaluating biological control options to inform a robust and environmentally sound IPM framework adapted to Moroccan agroecosystems.

Keywords: Drosophila suzukii;Population Dynamics;Infestation;IPM

Effect of Rice Varieties on the Preference of Nilaparvata lugens to Rice Plants Infested by Chilo suppressalis

Yubiao Cai[1], Pinjun Wan[1]*, Qiang Fu[1]*
1. China National Rice Research Institute,Chinese Academy and Agricultural Sciences,HANGZHOU,ZHEJIANG,China
* wanpinjun@caas.cn,fuqiang@caas.cn

Abstract: Abstract:【Objective】It has been reported that *Nilaparvata lugens* (brown planthopper, BPH) exhibits a preference of endangering rice plants infested by *Chilo suppressalis* (striped stem borer, SSB). However, it remains unclear whether this phenomenon is influenced by the developmental stage of *N. lugens* and the rice variety. This study aims to investigate the effects of rice varieties and developmental stages of *N. lugens* on the preference for *C. suppressalis*-infested rice plants, as well as how volatiles mediate this behavior, so as to provide a scientific basis for formulating green pest control strategies.【Method】Through indoor choice experiments, the attraction of different developmental stages of *N. lugens* (including 3rd-4th instar nymphs, newly emerged females, gravid females) to nine rice varieties, including Zhongzheyou 8, both damaged and undamaged by *C. suppressalis*, was observed. Based on these observations, representative varieties showing significant differences in attraction were selected for further analysis. RT-qPCR was used to detect changes in the expression of volatile synthesis-related genes in three rice varieties (Zhongzheyou 8, 9311, and Minghui 63) following pest infested.【Result】Among the nine rice varieties, different developmental stages of *N. lugens* consistently showed a preference for rice plants infested by *C. suppressalis*, although this preference varied among rice varieties. For instance, newly emerged female *N. lugens* exhibited a significantly higher preference for Minghui 63 compared to Yongyou 538. Gene expression analysis revealed a significant increase in the expression levels of volatile synthesis-related genes *OsCAS*, *OsLIS*, *OsHPL3*, and *OsRCI-1* in response to *C. suppressalis* infestation. However, when different developmental stages of *N. lugens* were co-infested with *C. suppressalis*, the expression levels of these genes could either increase or decrease compared to plants infested only by *C. suppressalis*, with specific effects depending on the developmental stage of *N. lugens*.【Conclusion】The preference of *N. lugens* for rice plants infested by *C. suppressalis* was commonly observed across the nine tested rice varieties. However, significant differences in the degree of preference were noted among different developmental stages of *N. lugens* across these varieties. Notably, variations in preference among developmental stages of *N. lugens* were primarily observed in the selection of rice varieties Yongyou 538, Zhongzheyou 8, and Minghui 63 by newly emerged female. Infestation only by *C. suppressalis* or in conjunction with *N. lugens* resulted in increased expression levels of the genes *OsCAS*, *OsLIS*, *OsHPL3*, and *OsRCI-1*, indicating that pest infestation in rice plants can regulate the synthesis of rice volatiles, thereby influencing the host selection behavior of *N. lugens*.

Keywords: rice variety;Nilaparvata lugens;Chilo suppressalis;host preference;volatile

Unraveling a Defense Regulatory Pathway in Rice: lncRNA-Mediated Modulation of LRR Proteins in Response to Brown Planthopper Infestation

Yaxuan Wang[1], Pinjun Wan[1]*
1. China National Rice Research Institute,Chinese Academy and Agricultural Sciences,Hangzhou,Zhejiang,China
* wanpinjun@caas.cn

Abstract: The brown planthopper (BPH) poses a severe threat to global rice production through direct feeding damage and transmission of viral diseases. While leucine-rich repeat (LRR) proteins are recognized as key immune receptors in plants, the regulation of their interaction with BPH-secreted effectors via long non-coding RNAs (lncRNAs) remains unexplored. This study employed an integrated approach to uncover this defense regulatory pathway in rice. Transcriptome analysis of rice following BPH feeding identified 60 significantly differentially expressed lncRNAs and 376 significantly differentially expressed *LRR* genes ($|\log_2FC| > 1$). Target prediction analysis to investigate potential regulatory relationships between these lncRNAs and *LRR* genes screened *LRR3* as a candidate gene potentially involved in rice resistance to BPH. Further characterization revealed sequence variation in *LRR3* between resistant and susceptible rice varieties. A 1-bp deletion in the resistant variety causes premature termination of translation, resulting in the loss of the LRR domain. Yeast two-hybrid screening for BPH proteins interacting with LRR3 identified 32 candidate interactors. Among these, a transcript encoding vitellogenin was found to be highly expressed in the BPH salivary gland transcriptome. Based on these findings, we propose a defense pathway model wherein lncRNAs regulate the interaction between LRR proteins and BPH-secreted effectors. Future work will focus on validating protein interactions, elucidating the adaptive mechanisms between rice and BPH, and identifying actionable targets for BPH control and the development of BPH-resistant rice varieties.

Keywords: Brown planthopper and rice interaction; Long non-coding RNAs; LRR; Effectors

Identification and expression of detoxification genes provide insights into host adaptation of the walnut pest Atrijuglans aristata

Dan dan Feng[1], **Lu Zhang**[1]
1. College of Life Sciences,Capital Normal University,Beijing,Beijing,China

Abstract: The rapid development of sequencing technologies has made high-quality reference genomes a prerequisite for studying insect host adaptation. However, previous research has primarily focused on broad-diet insects that cause significant agricultural damage, while systematic studies on specialist species, which exhibit stronger host dependency and greater sensitivity to climate change, have been lacking. The Atrijuglans aristata is a specialist insect that primarily feeds on the green husk of walnuts (Juglans regia) and has adapted to toxic secondary metabolites, such as juglone, which are abundant in the husk. At present, it remains unclear whether detoxification genes play a crucial role in the metabolic resistance of A. aristata to its host plant, which significantly hinders the development of pest control strategies for walnut pests. To elucidate the response mechanism of A. aristata to its host plant, we constructed a chromosome-level genome of A. aristata by integrating PacBio, Nanopore, as well as Illumina sequencing technologies, and systematically identified and classified detoxification-related gene families. Additionally, through comparative transcriptome analysis combined with homology modeling and molecular docking technologies, we further explored the binding affinity between the proteins encoded by candidate genes and the ligand juglone. The results showed that the genome size of A. aristata is 480.99 Mb, comprising 31 pseudo-chromosomes (including Z and partial W chromosome), with a contig N50 and scaffold N50 of 2.68 Mb and 16.01 Mb, respectively. The BUSCO completeness assessment was 95.6%, and a total of 22,542 protein-coding genes were annotated. Within this genome, 84 P450 (cytochrome P450), 48 COE (carboxylesterase), 34 GST (glutathione S-transferase), 26 UDP-glycosyltransferase (UGT), and 57 ABC (ATP-binding cassette) transporter genes were identified. Phylogenetic analysis further classified the P450 genes of the A. aristata into four clans: clan2, clan3, clan4, and clanMITO. Comparative transcriptomics revealed that 383 genes were significantly down-regulated in the larval gut after starvation treatment, and these genes were significantly enriched in pathways related to P450 detoxification metabolic. Moreover, homology modeling and molecular docking analysis of the 12 significantly down-regulated P450 genes indicated that the protein products encoded by these genes exhibit strong binding affinity to the ligand juglone. This study not only enhances our understanding of plant-insect interactions but also offers crucial theoretical evidence for walnut pest control.

Keywords: Atrijuglans aristata;specialist;genome;detoxification metabolism;P450 family;molecular docking

Serotonin-mediated wing dimorphism in Nilaparvata lugens: A survival strategy triggered by host plant senescence

Yutao Hu[1], Wenqing Zhang[1]*

1. State Key Laboratory of Biocontrol and School of Life Sciences,Sun Yat-sen University,Guangzhou,Guangdong,China

* lsszwq@mail.sysu.edu.cn

Abstract: The molecular mechanisms by which insects perceive and behaviorally adapt to host plant nutritional variation constitute a fundamental question in insect-plant coevolution. The brown planthopper (*Nilaparvata lugens*, BPH), a monophagous pest of rice (*Oryza sativa*), exhibits striking wing dimorphism that directly governs its outbreak patterns: long-winged morphs (LW) initiate migration to escape low-quality hosts, while short-winged morphs (SW) drive local population explosions, thriving in high-quality hosts. However, the mechanism underlying this migration-residence behavior in response to host plant senescence remains unclear. Here, we identified early 4th and early 5th instars as sensitive stages in response to the yellow-ripe rice, a phenological stage marking the onset of host plant senescence that must be promptly avoided. High performance liquid chromatography (HPLC) revealed that serotonin (5-HT) levels were significantly increased during the sensitive stages. Exogenous administration of 5-HT and its precursor 5-hydroxytryptophan (5-HTP) significantly promoted long-wing morph development, whereas pharmacological inhibition with α-methyltryptophan (AMTP, a serotonin synthesis inhibitor) attenuated the wing dimorphism response to yellow-ripe rice. Identification and functional analysis of 5-HT synthesis pathway enzymes demonstrated that tryptophan hydroxylase (*Nl*TRH) and aromatic L-amino acid decarboxylase (*Nl*AADC) mediated the release of insulin-like peptide 3 (*NlIlp3*), subsequently regulating the expression of insulin receptors 1 and 2 (*NlInR1*, *NlInR2*), which control wing dimorphism. In contrast, phenylalanine hydroxylase (*Nl*PAH) showed no involvement. This study highlights the vital role of serotonin in wing dimorphism of BPH in response to host plant senescence and offers new targets for sustainable control of the pest.

Keywords: Nilaparvata lugens;wing dimorphism;serotonin (5-HT);tryptophan hydroxylase

Subverting Rice Resistance: How the Brown Planthopper Effector NlSP1 Targets Host Proteins

Hou-Hong Yang[1], Pin-Jun Wan[1]*, Qiang Fu[1]*

1. The National Key Laboratory of Rice Biological Breeding,China National Rice Research Institute,Hangzhou,ZheJiang,China

* wanpinjun@caas.cn,fuqiang@caas.cn

Abstract: Rice (*Oryza sativa* L.), a staple crop feeding over half the world’ s population, faces severe threats from the brown planthopper (BPH, *Nilaparvata lugens*). During feeding, BPH injects salivary effectors that manipulate host processes to enable phloem ingestion and suppress immunity. Critically, rapidly evolving effectors drive "biotype" shifts, allowing BPH to overcome resistant rice varieties. However, how salivary effectors interact with rice proteins to confer virulence remains unclear. Here, we identify NlSP1 as a key BPH salivary effector linked to virulence. It exhibits significantly higher expression in salivary glands and midguts of virulent IR56-BPH populations versus avirulent TN1-BPH and is secreted into rice during feeding. Using yeast systems, we demonstrate NlSP1 specifically interacts with two rice defense proteins: OsPR8 (callose-associated) and OsChia4a (chitinase). Collectively, our work reveals: 1)NlVRSP1 as a critical modulator of BPH virulence. 2) A novel mechanism by which it targets rice defense proteins (OsPR8/OsChia4a) to subvert resistance. This study provides new molecular targets for developing BPH-resistant rice.

Keywords: Brown Planthopper;Herbivore virulence;Salivary protein;rice

Microbial legacies of non-native weeds attenuate herbivore defense by maize

Xueyao Cao[1], Xiao Sun[1]*
1. School of life science,Henan University,Kaifeng,Henan,China
* sunxiao@henu.edu.cn

Abstract: The defenses of crops against insect pests can be enhanced or suppressed by soil microbes and weeds can have strong effect on soil microbial communities. We used eight dominant non-native weed species and eight native weed species to establish soil microbial legacies, and compared non-native vs. native soil legacies on the resistance of maize to herbivores. We then investigated the root metabolomes and microbiomes of non-native and native weeds to elucidate mechanisms. We found that microbial legacies associated with weeds inhibited the resistance of maize to herbivores, with legacies of non-native weeds exhibiting a stronger inhibitory effect. Fungi—particularly Eurotiomycetes—appeared to play a crucial role in these feedback effects of soil microbes on maize. Non-native weeds released fewer phenylpropanoids from their roots, leading to an increase in Eurotiomycetes in the soil, which subsequently decreased the resistance of maize to herbivores. These results provide new insight into how non-native plants can adversely affect native crops and offer guidance for improving management strategies to mitigate the impact of weeds on agricultural lands.

Keywords: invasive plant; field weed; legacy effects; root metabolites; soil microbes; plant defense; herbivore

RNAi-based functional analysis reveals key roles of NlUGT4 and NlUGT7 in the adaption of brown planthopper to rice plant

Yimeng Li, Qiuyu Tian, Qingsong Liu*,Yunhe Li*
State Key Laboratory of Cotton Bio-breeding and Integrated Utilization,School of Life Sciences, Henan University, Kaifeng, 475004, China
*Correspondence：qingsongliu@henu.edu.cn; yunheli@henu.edu.cn

Abstract： The brown planthopper (BPH), *Nilaparvata lugens*(Stal), a major pest of rice that inflicts damage through both direct feeding and the indirect transmission of plant viruses, thereby posing a serious threat to global food production and security. UDP-glycosyltransferases (UGTs) are key Phase II detoxification enzymes in insects and play vital roles in xenobiotic metabolism and detoxification. However, their functional roles in mediating the interaction between BPH and rice remain largely unexplored. Here, based on preliminary transcriptome sequencing, the full-length sequences of two candidate genes including *NlUGT4* and *NlUGT7* were obtained through PCR. Phylogenetic analysis indicated that the two UGTs are closely related to UGTs from small brown planthopper *Laodelphax striatellus*. Quantitative real-time PCR experiments showed that *NlUGT4* was mainly expressed in adult males, while *NlUGT7* exhibited high expression in both fifth-instar nymphs and adult males. Tissue-specific expression analysis revealed that both *NlUGT4* and *NlUGT7* were predominantly expressed in the midgut, indicating possible roles in digestion and detoxification. To investigate their biological functions, double-stranded RNAs (dsRNAs) targeting *NlUGT4* and *NlUGT7* were synthesized and injected into insects via RNA interference. Knockdown of either *NlUGT4* or *NlUGT7* in BPH nymphs significantly reduced their transcript levels and led to a marked decrease in the survival on host plants, respectively. Collectively, these results demonstrate that *NlUGT4* and *NlUGT7* contribute to the adaption of BPH adaptation to rice plants, and highlight their potential as molecular targets for the development of RNAi-based pest control strategies.

Keywords: *Nilaparvata lugens*, Rice, UDP-glycosyltransferases, RNA interference, host adaption