2.1 研究生发表的代表性高质量论文清单

序号	研究生	文章标题	期刊名	发表年度	分区	影响因子
1	杨昌利	Induced heat shock protein 70 confers biological tolerance in UV-B stress–adapted *Myzus persicae* (Hemiptera)	International Journal of Biological Macromolecules	2022	一区	8.025
2	周操	Role of insecticide-mediated transcription of the TOR and JH signaling pathway-related genes in the regulation of reproduction in *Sogatella furcifera*	Entomologia Generalis	2022	一区	6.608
3	朱睿	Identification of potential sex determination genes and functional analyses in *Neoseiulus californicus* under prey stress	Pest Management Science	2022	一区	4.462
4	欧后丁	Host deprivation effects on population performance and paralysis rates of *Habrobracon hebetor* (hymenoptera: Braconidae)	Pest Management Science	2021	一区	4.462
5	Muhammad S Waqas	Biology, ecology, and management of cotton mealybug Phenacoccus solenopsis Tinsley (Hemiptera: Pseudococcidae).	Pest Management Science	2021	一区	4.462
6	王骏	Seed priming with calcium chloride enhances wheat resistance against wheat aphid Schizaphis graminum Rondani	Pest Management Science	2021	一区	4.462
7	杨熙彬	Characterization and functional analysis of chitinase family genes involved in nymph–adult transition of Sogatella furcifera	Insect Science	2021	一区	3.605
8	李海银	Smurf participates in *Helicoverpa armigera* diapause by regulating the TGF-β signaling pathway	Insect Science	2021	一区	3.262
9	汪佳佳	Comparative mitogenomes of six species in the subfamily Iassinae (Hemiptera: Cicadellidae) and phylogenetic analysis.	International journal of biological macromolecules	2020	一区	8.025
10	何宝玉	First report of leaf spots on Photinia serrulata caused by Nigrospora oryzae in China. Plant Disease	Plant Disease	2019	一区	3.809
11	吴渊明	Draft genomes of two blister beetles Hycleus cichorii and Hycleus phaleratus.	GigaScience	2018	一区	7.267
12	曹宇	Different population performances of *Frankliniella occidentalis* and *Thrips hawaiiensis* on flowers of two horticultural plants	Journal of Pest Science	2018	一区	5.742
13	张晓娜	Laboratory and Field evaluation of an entomopathogenic fungus, Isaria cateniannulata strain 08XS-1, against Tetranychus urticae (Koch)	Pest Management Science	2016	一区	4.462
14	张涛	Induced resistance fombined with RNA interference attenuates the counteradaptation of the western flower thrips	International Journal of Molecular Sciences	2022	二区	6.208
15	付迪	Three Heat Shock Protein Genes and Antioxidant Enzymes Protect Pardosa pseudoannulata (Araneae: Lycosidae) from High Temperature Stress	International Journal of Molecular Sciences	2022	二区	6.208
16	陈绪美	Isolation of Peptide Inhibiting SGC-7901 Cell Proliferation from Aspongopus chinensis Dallas	International Journal of Molecular Sciences	2022	二区	6.208

17	龚涛	Identification and functional analysis of a defensin CcDef2 from *Coridius chinensis*	International Journal of Molecular Sciences	2022	二区	6.208
18	李佳静	Identification and characterization of a double-stranded RNA degrading nuclease influencing RNAi efficiency in the rice leaf folder *Cnaphalocrocis medinalis*	International Journal of Molecular Sciences	2022	二区	6.208
19	周叶鸣	Estimated divergence times of *Lecanicillium* in the family cordycipitaceae provide insights into the attribution of *Lecanicillium*	Frontiers in Microbiology	2022	二区	6.091
20	张越	Immune function analysis of LsSd, a transcription factor of the Hippo signaling pathway, in the cigarette beetle *Lasioderma serricorne*	Frontiers in Physiology	2022	二区	4.755
21	周文桢	Juvenile Hormone Is an Important Factor in Regulating *Aspongopus chinensis* Dallas Diapause	Frontiers in Physiology	2022	二区	4.566
22	杨熙彬	Identification and profiling of *Sogatella furcifera* microRNAs and their potential roles in regulating the developmental transitions of nymph-adult	Insect Molecular Biology	2022	二区	3.424
23	智妍	Two New Species of Betacixius Matsumura, 1914 (Hemiptera: Fulgoromorpha: Cixiidae) from Southwestern China, with an Updated Checklist and Key to Species.	Insects	2022	二区	3.139
24	张涛	Copper chaperone for superoxide dismutase *FoCCS1 in Frankliniella occidentalis m*ay be associated with feeding adaptation after host shifting	Insects	2022	二区	3.139
25	严斌	Mitogenomic phylogeny of Typhlocybinae (Hemiptera: Cicadellidae) reveals homoplasy in tribal diagnostic morphological traits	Ecology and Evolution	2022	二区	3.167
26	江艳	Comparative Analysis of Mitochondrial Genomes among Twelve Sibling Species of the Genus *Atkinsoniella* Distant, 1908 (Hemiptera: Cicadellidae: Cicadellinae) and Phylogenetic Analysis	Insects	2022	二区	3.139
27	李草	Effects of Nano-Graphene Oxide on the Growth and Reproductive Dynamics of Spodoptera frugiperda Based on an Age-Stage, Two-Sex Life Table	Insects	2022	二区	3.139
28	刘靖	Herbivore-Induced Rice Volatiles Attract and Affect the Predation Ability of the Wolf Spiders, Pirata subpiraticus and Pardosa pseudoannulata	Insects	2022	二区	3.139
29	龚明富	Juvenile Hormone Synthesis Pathway Gene SfIPPI Regulates Sogatella furcifera Reproduction	Insects	2022	二区	3.139
30	曾庆会	*SfDicer2* RNA Interference Inhibits Molting and Wing Expansion in *Sogatella furcifera*	Insects	2022	二区	3.139
31	潘应拿	Assessment of suitable reference genes for qRT-PCR normalization in *Eocanthecona furcellata* (Wolff)	Insects	2022	二区	3.139
32	余春	Fruit Fly in a Challenging Environment: Impact of Short-Term Temperature Stress on the Survival, Development, Reproduction, and Trehalose Metabolism of *Bactrocera dorsalis* (Diptera: Tephritidae)	Insects	2022	二区	3.139

33	姜日新	Discovery of the Genus Anapleus Horn, 1873 from Cretaceous Kachin Amber (Coleoptera: Histeridae)	Insects	2022	二区	3.139
34	杨佳鹏	Biological quality of Anisopteromalus calandrae (Hymenoptera: Pteromalidae) reared with cold-stored larvae of Lasioderma serricorne (Coleoptera: Anobiidae)	Journal of Stored Products Research	2022	二区	2.643
35	张越	Life history traits of the parasitoid *Anisopteromalus calandrae* (Hymenoptera: Pteromalidae) on three beetle hosts	Journal of Stored Products Research	2022	二区	2.643
36	张越	Identification and profiling of Sogatella furcifera microRNAs and their potential roles in regulating the developmental transitions of nymph-adult	Journal of Stored Products Research	2022	二区	2.643
37	龚念	Structural Features and Phylogenetic Implications of Four New Mitogenomes of Caliscelidae (Hemiptera: Fulgoromorpha)	International Journal of Molecular Sciences	2021	二区	6.208
38	何宝玉	Microbiome Structure of the Aphid *Myzus persicae* (Sulzer) Is Shaped by Different Solanaceae Plant Diets	Frontiers in microbiology	2021	二区	5.64
39	许抗抗	Disruption of the Serine/Threonine Kinase Akt Gene Affects Ovarian Development and Fecundity in the *Cigarette Beetle,* Lasioderma serricorne.	Frontiers in Physiology	2021	二区	4.755
40	赵正学	Endemism Patterns of Planthoppers (Fulgoroidea) in China	Frontiers in Ecology and Evolution	2021	二区	4.493
41	吴丽红	Fitness of fall armyworm, *Spodoptera frugiperda* to three solanaceous vegetables	Journal of Integrative Agriculture	2021	二区	4.384
42	严斌	A Chromosome-Level Genome Assembly of *Ephestia elutella* (Hübner, 1796) (Lepidoptera: Pyralidae)	Genome Biology and Evolution	2021	二区	4.065
43	严斌	Chromosome-level genome assembly of *Nephotettix cincticeps* (Uhler, 1896) (Hemiptera: Cicadellidae: Deltocephalinae)	Genome Biology and Evolution	2021	二区	4.065
44	周操	Role of SfJHAMT and SfFAMeT in the reproductive regulation of Sogatella furcifera and its expression under insecticide stress	Pesticide Biochemistry and Physiology	2021	二区	3.963
45	江滔	Chromosomal-level Genome Assembly of a True Bug, *Aspongopus chinensis* Dallas, 1851 (Hemiptera: Dinidoridae)	Genome Biology and Evolution	2021	二区	3.416
46	李琴	Two sexes respond equally to food restriction in a sexually dimorphic but not body mass dimorphic jumping spider	Ecology and Evolution	2021	二区	3.167
47	孙良玉	Cloning and differential expression of three heat shock protein genes associated with thermal stress from the wolf spider Pardosa pseudoannulata (Araneae: Lycosidae)	Ecology and Evolution	2021	二区	3.167
48	王显益	Structural features of the mitogenome of the leafhopper genus Cladolidia (Hemiptera: Cicadellidae: Coelidiinae) and phylogenetic implications in Cicadellidae.	Ecology and Evolution	2021	二区	3.167
49	赵如娜	Different host plants distinctly influence the feeding ability of the brown citrus aphid Toxoptera citricida	Insects	2021	二区	3.139

50	狄雪塬	Does Larval Rearing Diet Lead to Premating Isolation in *Spodoptera litura* Fabricius (Lepidoptera: Noctuidae)?	Insects	2021	二区	3.139
51	江艳	Characterization of Two Complete Mitochondrial Genomes of *Atkinsoniella* (Hemiptera: Cicadellidae: Cicadellinae) and the Phylogenetic Implications	Insects	2021	二区	3.139
52	曾广	Life table and preference choice of *Frankliniella occidentalis* (thysanoptera: thripidae) for kidney bean plants treated by exogenous calcium.	Insects	2021	二区	3.139
53	姜霖	Functional Response and Predation Potential of Carabus elysii Adults against the Terrestrial Slug *Agriolimax agrestis.*	Insects	2021	二区	3.139
54	王秀琴	Artificial diet significantly enhance fitness and be applicable in mass-rearing of *Ephestia elutella* (Hübner) (Lepidoptera: Pyralidae)	Crop Protection	2021	二区	3.036
55	龚念	Comparative analysis of twelve mitogenomes of Caliscelidae (Hemiptera: Fulgoromorpha) and their phylogenetic implications	PeerJ	2021	二区	2.984
56	张越	Stability evaluation of candidate reference genes for RT-qPCR normalization in Lasioderma serricorne (F.)	Journal of Stored Products Research	2021	二区	2.643
57	欧后丁	Host Deprivation Effects on the Functional Response and Parasitism Rate of *Habrobracon hebetor* (Hymenoptera: Braconidae) on *Ephestia elutella* (Lepidoptera: Pyralidae) in the Laboratory	Journal of Economic Entomology	2021	二区	2.447
58	严毅	Two lysozymes are involved in the larva-to-pupa transition and the antibacterial immunity of Lasioderma serricorne (coleoptera: Anobiidae)	Journal of Stored Products Research	2021	二区	2.643
59	周叶鸣	Fast recognition of *Lecanicillium* spp. and its virulence against *Frankliniella occidentalis*	Florentine in Microbiology	2020	二区	6.064
60	毛鑫	Microbiome-Guided Exploration of the Microbial Assemblage of the Exotic Beverage “Insect Tea” Native to Southwestern China	Frontiers in Microbiology	2020	二区	6.064
61	苏丽	Molecular Characterization and Expression of *OfJNK* and *Ofp38* in *Ostrinia furnacalis* (Guenée) Under Different Environmental Stressors	Frontiers in Physiology	2020	二区	4.755
62	吴渊明	Genomic content of chemosensory receptors in two sister blister beetles facilitates characterization of chemosensory evolution.	BMC Genomics	2020	二区	3.594
63	汪佳佳	The Phylogenetic Implications of the Mitochondrial Genomes of Macropsis notata and *Oncopsis nigrofasciata*	Frontiers in Genetics	2020	二区	3.258
64	赵正学	Testing Seven Hypotheses to Determine What Explains the Current Planthopper (Fulgoridae) Geographical and Species Richness Patterns in China	Insects	2020	二区	3.139
65	何佳春	Biological Traits of the Pincer Wasp Gonatopus flavifemur(Esaki&Hashimoto) Associated with Different Stages of Its Host,the Brown Planthopper Nilaparvata lugens(Stål)	Insects	2020	二区	3.139
66	周叶鸣	New potential strains for controlling *Spodoptera frugiperda*	Biocontrol	2020	二区	2.581

		in China: *Cordyceps cateniannulata* and *Metarhizium rileyi*				
67	赵正学	Determinants of Delphacidae richness and endemism in China	Ecological Entomology	2020	二区	2.233
68	汪佳佳	Characterization and phylogenetic implications of the complete mitochondrial genome of Idiocerinae (Hemiptera: Cicadellidae). International journal of biological macromolecules	International journal of biological macromolecules	2018	二区	3.909
69	周操	Protective and detoxifying enzyme activity and ABCG subfamily gene expression in Sogatella furcifera under insecticide stress	Frontiers in Physiology	2018	二区	3.394
70	周叶鸣	*Lecanicillium* cauligalbarum sp. nov.(Cordycipitaceae, Hypocreales), a novel fungus isolated from a stemborer in the Yao Ren National Forest Mountain Park, Guizhou	MycoKeys	2018	二区	3.110
71	武承旭	Delay in Mating Reduces Reproductivity but Increases Life Span in *Tobacco Cutworm, Spodoptera litura Fabricius* (Lepidoptera: Noctuidae)	Journal of Economic Entomology	2018	二区	2.447
72	金剑雪	Expression Differences of Resistance-Related Genes Induced by Cycloxaprid Using qRT-PCR in the Female Adult of Sogatella furcifera (Hemiptera: Delphacidae)	Journal of Economic Entomology	2017	二区	2.447
73	金剑雪	Monitoring Trends in Insecticide Resistance of Field Populations of Sogatella furcifera (Hemiptera: Delphacidae) in Guizhou Province, China, 2012–2015	Journal of Economic Entomology	2017	二区	2.447
74	刘健锋	Effects of Temperature on Development and Survival of *Orthopygia glaucinalis* (Lepidoptera: Pyralidae) Reared on *Platycarya strobilacea*	Journal of Economic Entomology	2015	二区	2.447
75	董文鸽	Fragmented mitochondrial genomes of the rat lice, *Polyplax asiatica* and *Polyplax spinulosa*: intra-genus variation in fragmentation pattern and a possible link between the extent of fragmentation and the length of life cycle	BMC Genomics	2014	二区	4.547
76	董文鸽	Fragmented mitochondrial genomes are present in both major clades of the blood-sucking lice (suborder Anoplura)-evidence from two Hoplopleura rodent lice (family Hoplopleuridae)	BMC Genomics	2014	二区	4.547

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Induced heat shock protein 70 confers biological tolerance in UV-B stress–adapted *Myzus persicae* (Hemiptera)

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ABSTRACT

As an environmental stress factor, ultraviolet-B (UV-B) radiation directly affects insect growth, development, and reproduction. Heat shock protein 70s kDa (Hsp70s) plays an important role in the environmental adaptation of insects. To determine the role of *MpHsp70s* in the UV-B tolerance of *Myzus persicae* (Sulzer), we identified the complete complementary DNA sequences of seven *MpHsp70s*. They were found to be ubiquitously expressed during different developmental stages and were highly expressed in second-instar nymphs and wingless adults. The expression levels of the *MpHsp70s* were significantly upregulated when exposed to different durations of UV-B stress. Nanocarrier-mediated ds*MpHsp70* suppressed the expression of the *MpHsp70s* and reduced the body length, weight, survival rate, and fecundity of *M. persicae* under UV-B exposure. When the combinational RNAi approach was adopted, the effects on the survival rate and fecundity were greater under UV-B stress, except for *MpHsc70-4*. These results suggest that *MpHsp70s* are essential for the resistance of *M. persicae* to UV-B stress.

1. Introduction

As an important environmental stress factor, solar ultraviolet (UV) radiation significantly impacts both biological and non-biological organisms in the ecosystem. According to their wavelengths, UV radiation can be divided into three different types: UV-C, 100–280 nm; UV-B, 280–315 nm, and UV-A, 315–400 nm [1]. Among them, UV-B is the strongest light wave reaching the earth and is effectively absorbed by the ozone layer in the atmosphere; however, approximately 10 % of it can penetrate the ozone layer and reach the earth [2]. In recent years, the emission of hydrochlorofluorocarbons from human activities has damaged the ozone layer in the atmosphere, thus leading to a sharp increase in the UV-B radiation reaching the earth's surface [3,4]. High doses of UV-B radiation are harmful to all organisms [5] as they can induce oxidative stress via the production of reactive oxygen species (ROS), which cause damage to the DNA, membrane lipids, and proteins and severely affect growth, physiology, biochemistry, and population structure [6–8]. Although UV-B is harmful to most organisms, some possess complete anti-stress mechanisms, including antioxidants, cell apoptosis, DNA repair, and molecular chaperones (e.g., heat shock proteins [Hsps]), which protect the body from damage caused by UV-B stress [1,9–12].

Hsps are a class of highly conserved molecular chaperone proteins that are involved in maintaining and regulating the conformation and function of various cellular proteins [13,14]. Hsps can be classified according to their molecular weight, structural characteristics, and functions, namely Hsp100, Hsp90, Hsp70, Hsp60, Hsp40, and small Hsps [13]. Among them, the Hsp70 family is the most common and evolutionarily conserved member and is widely present in prokaryotes and eukaryotes [15–17]. The Hsp70 family is further divided into two subgroups according to its response patterns to various stimuli, namely stress-inducing proteins (Hsp70s) and constitutively expressed proteins (Hsc70s) [18–20]. Several studies have shown that under stress conditions, such as high or low temperatures, hypoxia, and UV exposure, Hsp70s can play multiple roles in protein folding, degradation, and transportation; protein–protein interaction; and prevention and dissolution of protein aggregates [13,21–24].

In nature, insects can adapt to fluctuating and unfavorable environmental conditions because of their environmental adaptability [25,26]. Growth, development, survival, and geographic distribution of insects are influenced by various environmental factors, including UV radiation [27,28]. Previous studies have shown that the transcription

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Article

Role of insecticide-mediated transcription of the TOR and JH signaling pathway-related genes in the regulation of reproduction in *Sogatella furcifera*

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With 5 figures

Abstract: Sublethal concentrations of insecticides can affect the population dynamics of insects by inducing changes in their reproductive traits; however, the underlying molecular mechanisms remain unclear. In previous transcriptomic experiments, triazophos was found to promote *SfTOR* transcription. Therefore, in this study, two representative insecticides, thiamethoxam (inhibiting reproduction) and triazophos (stimulating reproduction), were selected to evaluate the transcription of the key genes involved in the target of rapamycin (TOR) and juvenile hormone (JH) pathways under stress in *Sogatella furcifera*. The results showed that thiamethoxam could significantly inhibit the transcription of *SfRheb, SfTOR, SfS6K*, and *SfHMGR*, whereas triazophos significantly promoted the transcription of *SfRheb, SfTOR, SfS6K, SfHMGR, SfMet*, and *SfKr-h1*. Moreover, RNA interference (RNAi) technology was used to target and silence TOR signaling pathway-related genes. The results showed that RNAi-mediated silencing of *SfRheb, SfTOR*, and *SfS6K* significantly inhibited ovarian development and fecundity. The transcription of JH signaling pathway-related genes (i.e., *SfHMGR, SfFAMeT, SfMet*, and *SfKr-h1*) and *SfVg* was significantly inhibited. However, the effects of *SfRheb* and *SfTOR* silencing on female reproduction were partially mitigated by the JH analog methoprene. These results indicate that the TOR signaling pathway can regulate the JH signaling pathway and *SfVg* transcription. In addition, insecticide stress can influence the transcription of TOR signaling pathway-related genes and transduction of stress signals via the JH signaling pathway, thereby affecting the transcription of *SfVg* and ultimately regulating reproduction in females.

Keywords: *Sogatella furcifera*, insecticides, target of rapamycin, juvenile hormone, reproduction

1 Introduction

As one of the most important pests of rice, white-backed planthopper (*Sogatella furcifera*) nymphs and adults suck phloem sap from the rice plant and act as the vectors of southern rice black-streaked dwarf virus, which seriously affects the yield and quality of rice (Wu et al. 2017). *S. furcifera* is a typical r-strategic migratory pest, which has strong fecundity and is likely to cause outbreaks. Although the application of chemicals remains to be the main strategy for controlling *S. furcifera*, the long-term and large-scale use of insecticides can easily lead to the resurgence of pests by stimulating reproduction and insecticide resistance (Wu et al. 2020).

To date, there has been extensive research on ecological issues related to the sublethal effects of insecticides on *S. furcifera* (Liu et al. 2016, Zhou et al. 2019b). For example, thiamethoxam is a widely used neonicotinoid with excellent insecticidal activity and an ideal substitute for imidacloprid. It can not only directly kill target insects but also significantly inhibit the reproduction of *S. furcifera* at its sublethal concentration (Yang et al. 2017). Triazophos, a broad-spectrum organophosphorus insecticide, has also been widely used to

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Research Article | Full Access

Identification of potential sex determination genes and functional analyses in *Neoseiulus californicus* under prey stress

Rui Zhu, Jianjun Guo, Gang Li, Rundong Liu, Tianci Yi, Daochao Jin

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Abstract

BACKGROUND

Phytoseiid mites are important natural enemies of spider mites. Sex-determination mechanism are important basic scientific issues in the reproduction and evolution of predatory mites. Clarifying sex-determination mechanism may provide reference for exploring genetic approach to have the phytoseiid mites produce more female offspring, which could improve their effectiveness as a biological control agent.

RESULTS

We used transcriptome sequencing to identify and characterize 20 putative sex-determination genes in the phytoseiid mite *Neoseiulus californicus*, a species with uncommon pseudo-arrhenotoky, including *doublesex-like* (*dsx1-like*), *transformer-2* (*tra-2*), *intersex* (*ix*), and *fruitless-like* (*BTB2*). A significant negative correlation was found between prey stress and offspring sex ratio. But the most genes identified showed no difference in expression between the groups with lowest and highest female offspring ratios. The hatching rate and sex ratio of female offspring were reduced when the *ix* gene was silenced, and the oviposition days and fecundity were reduced when the *BTB2* gene was silenced. The fecundity was reduced when the *tra2* gene was silenced and the *snf* gene is essential for oviposition in female. There was no effect on reproduction and female sex determination when silencing the *dsx1-like* and *dsx2-like* gene.

CONCLUSION

The genes *BTB2*, *tra2* and *snf* are involved in oviposition, and *ix* may be involved in female sex determination and egg formation in *Neoseiulus californicus*. The results are conductive to further understanding molecular regulatory mechanism of sex determination in predatory mites and may provide a reference for better use of this predatory by producing more females.

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Research Article | Full Access

Host deprivation effects on population performance and paralysis rates of *Habrobracon hebetor* (hymenoptera: Braconidae)

Hou-Ding Ou, Remzi Atlihan, Xiu-Qin Wang, Hao-Xi Li, Xiao-Fei Yu, Xin Jin, Mao-Fa Yang

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Citations: 4

Abstract

BACKGROUND

Habrobracon hebetor (Hymenoptera: Braconidae) is a gregarious ectoparasitoid that attacks the larvae of several species of pyralid and noctuid moths. The reproduction and population dynamics of parasitoids in general are affected by host deprivation. However, how host deprivation affects *H. hebetor* is unknown. The effect of host deprivation on the parental generation, life table parameters, and the paralysis rate of the F_1 generation of *H. hebetor* were evaluated using the age-stage, two-sex life table under laboratory conditions.

RESULTS

The results indicated that the greatest longevity and the least lifetime fecundity of the F_0 generation occurred after 19 days of host deprivation (PW-20 treatment). The life table parameters (intrinsic rate of increase, r; finite rate of increase, λ; and net reproductive rate, R_0) and the paralysis rate parameters (net paralysis rate, C_0; transformation rate, Q_p; stable paralysis rate, ψ; and finite paralysis rate, ω) of F_1 individuals after PW-20 treatment were significantly higher than those of individuals subjected to the control treatment (no host deprivation). However, no difference was detected between the two host deprivation treatments: host deprivation after 1 day of host contact and immediate host deprivation (PW treatment).

CONCLUSION

Our results demonstrated that the effectiveness of *H. hebetor* did not decrease even during host deprivation for 19 days. Meanwhile, it was observed that mass rearing of the parasitoid could be improved by providing 10 individuals of 5th instar larvae of *Ephestia elutella* (Lepidoptera: Pyralidae) with a 20% honey-water solution.

FULL TEXT LINKS

Review Pest Manag Sci. 2021 Dec;77(12):5321-5333. doi: 10.1002/ps.6565. Epub 2021 Aug 12.

Biology, ecology, and management of cotton mealybug Phenacoccus solenopsis Tinsley (Hemiptera: Pseudococcidae)

Muhammad S Waqas [1], Zuhua Shi [2], Tian-Ci Yi [1], Rong Xiao [1], Ali Az Shoaib [2] [3], Asem Ss Elabasy [2] [3], Dao-Chao Jin [1]

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PMID: 34312983 DOI: 10.1002/ps.6565

Abstract

The cotton mealybug Phenacoccus solenopsis Tinsley (Hemiptera: Pseudococcidae), is a highly invasive and harmful pest. It causes considerable loss of cotton crops in China, India and Pakistan. Little is known about its bionomics since it was first recorded in Pakistan and India in 2005. Rapid spread of this pest worldwide has accelerated research on its biology, ecology and management. The P. solenopsis has a short life cycle, and optimal temperatures lead to an increase in the number of generations per year, which is a serious threat to cotton crop production. Cotton mealybug is native to the USA, although it has now spread to >43 countries. Insecticidal control is the primary and dominant practice for this pest, and its resistance to commonly used insecticides is increasing. Biocontrol agents have strong potential for the management of nymphal instar stages. We read >250 articles related to our review title and finally reviewed recent advances in the understanding of P. solenopsis biology, ecology and control approaches, aiming to highlight integrated and biological management practices of this pest. © 2021 Society of Chemical Industry.

Keywords: Phenacoccus solenopsis; biological characteristics; cotton; integrated management; invasive pest.

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Pest Management Science / Volume 77, Issue 10 / p. 4709-4718

Research Article | Full Access

Seed priming with calcium chloride enhances wheat resistance against wheat aphid *Schizaphis graminum* Rondani

Jun Wang, Jia Song, Xiao-Bao Wu, Qian-Qian Deng, Zhong-Yan Zhu, Ming-Jian Ren, Mao Ye ✉,
Ren-Sen Zeng ✉

First published: 19 June 2021
https://doi.org/10.1002/ps.6513

Abstract

BACKGROUND

Calcium is an essential macronutrient for plant growth. Although it has been shown that exogenous Ca application can increase plant resistance to abiotic stress, little is known about its potential to enhance plant tolerance to biotic stress. Here, we investigated whether pretreatment of wheat (*Triticum aestivum* L.) seeds with calcium chloride ($CaCl_2$) improves plant resistance against wheat aphid (*Schizaphis graminum* Rondani). The developmental time, population size, feeding behavior of aphids on plants grown from $CaCl_2$- and water-pretreated seeds, and plant defense responses to aphid attack were investigated.

RESULTS

Seed pretreatment with $CaCl_2$ extended aphid development time and reduced aphid population size and feeding efficiency. In addition, the pretreatment significantly increased the concentration of Ca^{2+} in wheat leaves, and upregulated expression levels of *TaCaM* genes and callose synthase genes (*TaGSL2*, *TaGSL8*, *TaGSL10*, *TaGSL12*, *TaGSL19*, *TaGSL22* and *TaGSL23*). Callose concentration in the leaves of plants grown from $CaCl_2$-pretreated seeds increased significantly upon aphid attack. Further, callose deposition was observed mainly in the phloem.

CONCLUSION

These results suggest that seed pretreatment with $CaCl_2$ primes the plant response against wheat aphid attack, leading to modulation of callose deposition in the phloem in response to aphid attack. © 2021 Society of Chemical Industry.

1 INTRODUCTION

Insect Science / Volume 28, Issue 4 / p. 901-916

ORIGINAL ARTICLE | Full Access

Characterization and functional analysis of chitinase family genes involved in nymph–adult transition of *Sogatella furcifera*

Xibin Yang, Cao Zhou, Guiyun Long, Hong Yang, Chen Chen, Daochao Jin

First published: 14 June 2020
https://doi.org/10.1111/1744-7917.12839
Citations: 10

Abstract

Chitinase degrades chitin in the old epidermis or peritrophic matrix of insects, which ensures normal development and metamorphosis. In our previous work, we comprehensively studied the function of *SfCht7* in *Sogatella furcifera*. However, the number and function of chitinase genes in *S. furcifera* remain unknown. Here, we identified 12 full-length chitinase transcripts from *S. furcifera*, which included nine chitinase (*Cht*), two imaginal disc growth factor (*IDGF*), and one endo-*β*-N-acetylglucosaminidase (*ENGase*) genes. Expression analysis results revealed that the expression levels of eight genes (*SfCht3*, *SfCht5*, *SfCht6-1*, *SfCht6-2*, *SfCht7*, *SfCht8*, *SfCht10*, and *SfIDGF2*) with similar transcript levels peaked prior to molting of each nymph and were highly expressed in the integument. Based on RNA interference (RNAi), description of the functions of each chitinase gene indicated that the silencing of *SfCht5*, *SfCht10*, and *SfIDGF2* led to molting defects and lethality. RNAi inhibited the expressions of *SfCht5*, *SfCht7*, *SfCht10*, and *SfIDGF2*, which led to downregulated expressions of chitin synthase 1 (*SfCHS1*, *SfCHS1a*, and *SfCHS1b*) and four chitin deacetylase genes (*SfCDA1*, *SfCDA2*, *SfCDA3*, and *SfCDA4*), and caused a change in the expression level of two trehalase genes (*TRE1* and *TRE2*). Furthermore, silencing of *SfCht7* induced a significant decrease in the expression levels of three wing development-related genes (*SfWG*, *SfDpp*, and *SfHh*). In conclusion, *SfCht5*, *SfCht7*, *SfCht10*, and *SfIDGF2* play vital roles in nymph–adult transition and are involved in the regulation of chitin metabolism, and *SfCht7* is also involved in wing development; therefore, these genes are potential targets for control of *S. furcifera*.

Introduction

The white-backed planthopper, *Sogatella furcifera* (Horváth) (Hemiptera: Delphacidae), is one of the most destructive rice pests, which damages rice by sucking plant juices, ovipositing, and transmitting southern rice black-streaked dwarf virus; this causes substantial rice yield loss (Zhou *et al*., 2008). Insecticidal control of *S. furcifera* is a convenient option, but

FULL TEXT LINKS

WILEY Full Text Article

Insect Sci. 2022 Oct;29(5):1251-1261. doi: 10.1111/1744-7917.13007. Epub 2022 Feb 18.

Smurf participates in Helicoverpa armigera diapause by regulating the transforming growth factor-β signaling pathway

Haiyin Li [1], Qin Lu [1], Yan Li [1], Yufang Yan [1], Zhiyong Yin [1], Jianjun Guo [1], Weihua Xu [2]

Affiliations

PMID: 35064956 DOI: 10.1111/1744-7917.13007

Abstract

Diapause, an important strategy used by insects to avoid adverse environments, is regulated by various cell signaling pathways. The results of our previous studies demonstrated that the transforming growth factor-β (TGF-β) signaling pathway regulated pupal diapause in Helicoverpa armigera, which was accompanied by downregulation of proteins in TGF-β signaling. However, to date the mechanism underlying this phenomenon remains unknown. Here, we cloned the E3 ubiquitin ligases gene Smurf. In vitro experiments showed that Smurf directly bound to TGF-β receptor type I (TGFβRI) and Smad2. Overexpressing Smurf promoted ubiquitination of TGFβRI and Smad2, thereby downregulating their protein levels. Conversely, silencing of the Smurf gene suppressed ubiquitination of TGFβRI and Smad2 thereby increasing their protein levels. Results from in vivo co-immunoprecipitation assays revealed that the binding of Smurf to TGFβRI or Smad2 was stronger in diapause pupae than in nondiapause pupae. Injection of Smurf inhibitor A01 into diapause pupae markedly upregulated expression of TGFβRI and Smad2 proteins, leading to resumption of development in diapause pupae. Taken together, these findings suggested that ubiquitin ligase E3 Smurf participated in H. armigera diapause by regulating TGF-β signaling, and thus could be playing a crucial role in insect diapause.

Keywords: Helicoverpa armigera; Smurf; TGF-β signaling; degradation; diapause; ubiquitination.

Related information

MedGen
PubChem Compound (MeSH Keyword)

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International Journal of Biological Macromolecules
Volume 149, 15 April 2020, Pages 1294-1303

Comparative mitogenomes of six species in the subfamily Iassinae (Hemiptera: Cicadellidae) and phylogenetic analysis

Jiajia Wang, Yunfei Wu, Renhuai Dai, Maofa Yang

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https://doi.org/10.1016/j.ijbiomac.2020.01.270

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Abstract

For elucidating phylogenetic relationships among members of the family Cicadellidae, mitogenomes of six members of the subfamily Iassinae, including *Batracomorphus lateprocessus*, *Iassus dorsalis*, *Krisna concava*, *Krisna rufimarginata*, *Gessius rufidorsus*, and *Trocnadella arisana*, were sequenced. The mitogenomes are 14,724–15,356-bp long. Moreover, typical 37 genes in mitogenomes were identified; arrangement of these genes in the studied species was consistent with that in the inferred ancestral insects, except for tRNA genes, with a simple switch between the positions of *trnI* and *trnQ* in *Trocnadella arisana*. Most protein-coding genes in the Iassinae mitogenomes showed typical ATN start codons (ATA/ATT/ATC/ATG) and TAR (TAA/TAG) or an incomplete stop codon T--; ATP8 of all sequenced species showed the start codon TTG. The secondary structures of *16S rRNA* and *12S rRNA* were predicted. *16S rRNA* comprised 6 domains with 43 helices, and *12S rRNA* comprised 3 domains with 25 helices. All subfamilies, except Cicadellinae and Evacanthinae, were recovered as monophyletic. As reported previously, treehoppers originated from paraphyletic Cicadellidae. Iassinae and Coelidiinae, Megophthalminae and treehoppers, and Cicadellinae and Evacanthinae were sister groups with high nodal support.

Previous

Next

Keywords

DISEASE NOTES

OPEN

First Report of Leaf Spots on *Photinia serrulata* Caused by *Nigrospora oryzae* in China

B.-Y. He, T. Cernava, H.-D. He, H.-X. Li, X.-Y.-L. Chen, and H. Yang

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Photinia serrulata (Lindl.) (syn. *Photinia serratifolia*) is a popular evergreen ornamental shrub that is cultivated worldwide for floral and pharmacological properties. Leaf extracts for *P. serrulata* have been reported to contain antioxidant, antibacterial, anthelmintic, and purgative properties (Song et al. 2007). From 2015 to 2018, leaf spots were observed on leaves of *P. serrulata* cultivated on the West Campus of Guizhou University (20°26′26″ N, 106°39′20″ E), Guiyang, Guizhou province, China. The disease incidence increased to 60 to 70% in 2018. In June of 2018, leaf samples with symptomatic black spots were collected from *P. serrulata* grown on the West Campus of Guizhou University. The leaves were surface sterilized with 10% bleach for 30 s and 75% ethanol for 30 s, rinsed three times with sterilized distilled water, air dried, placed on potato dextrose agar, and incubated at 25°C in the dark for 8 days. The colonies of the pathogen cultures were white with a regular round shape at the early stage and became darker gray with fluffy hyphae after 7 days. Conidia were produced from clusters of conidiophores. The single-celled, globose-shaped conidia

GigaScience, 7, 2018, 1–7

doi: 10.1093/gigascience/giy006
Advance Access Publication Date: 10 February 2018
Data Note

DATA NOTE

Draft genomes of two blister beetles Hycleus cichorii and Hycleus phaleratus

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Abstract

Background: Commonly known as blister beetles or Spanish fly, there are more than 1500 species in the Meloidae family (Hexapoda: Coleoptera: Tenebrionoidea) that produce the potent defensive blistering agent cantharidin. Cantharidin and its derivatives have been used to treat cancers such as liver, stomach, lung, and esophageal cancers. *Hycleus cichorii* and *Hycleus phaleratus* are the most commercially important blister beetles in China due to their ability to biosynthesize this potent vesicant. However, there is a lack of genome reference, which has hindered development of studies on the biosynthesis of cantharidin and a better understanding of its biology and pharmacology. **Results:** We report 2 draft genomes and quantified gene sets for the blister beetles *H. cichorii* and *H. phaleratus*, 2 complex genomes with >72% repeats and approximately 1% heterozygosity, using Illumina sequencing data. An integrated assembly pipeline was performed for assembly, and most of the coding regions were obtained. Benchmarking universal single-copy orthologs (BUSCO) assessment showed that our assembly obtained more than 98% of the Endopterygota universal single-copy orthologs. Comparison analysis showed that the completeness of coding genes in our assembly was comparable to other beetle genomes such as *Dendroctonus ponderosae* and *Agrilus planipennis*. Gene annotation yielded 13 813 and 13 725 protein-coding genes in *H. cichorii* and *H. phaleratus*, of which approximately 89% were functionally annotated. BUSCO assessment showed that approximately 86% and 84% of the Endopterygota universal single-copy orthologs were annotated completely in these 2 gene sets, whose completeness is comparable to that of *D. ponderosae* and *A. planipennis*. **Conclusions:** Assembly of both blister beetle genomes provides a valuable resource for future biosynthesis of cantharidin and comparative genomic studies of blister beetles and other beetles.

Keywords: blister beetle *Hycleus cichorii*; blister beetle *Hycleus phaleratus*; genome sequencing; reference gene set; cantharidin

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https://doi.org/10.1007/s10340-017-0887-3

ORIGINAL PAPER

Different population performances of *Frankliniella occidentalis* and *Thrips hawaiiensis* on flowers of two horticultural plants

Yu Cao[1,2] · Junrui Zhi[1] · Runzhi Zhang[1,3] · Can Li[2] · Yan Liu[2] · Zhaoyun Lv[1] ·
Yulin Gao[4]

Received: 1 December 2016 / Revised: 23 May 2017 / Accepted: 25 May 2017 / Published online: 29 August 2017

Abstract *Gardenia jasminoides* and *Rosa chinensis* are economically important horticultural plants in China. *Frankliniella occidentalis* and *Thrips hawaiiensis* are serious coexisting pests that previously demonstrated opposite population trends on *G. jasminoides* and *R. chinensis* flowers. To further study the different performances between *F. occidentalis* and *T. hawaiiensis*, we investigated their population dynamics in the field (for 5 years) and their life history characteristics on the two flowers in the laboratory. In the field, the density of *F. occidentalis* was lower than that of *T. hawaiiensis* on *G. jasminoides* but was higher than that of *T. hawaiiensis* on *R. chinensis*. Under laboratory conditions, *F. occidentalis* showed significantly slower development, and lower survival and fecundity levels than *T. hawaiiensis* on *G. jasminoides*, but the opposite was true on *R. chinensis*. Significant differences in the net reproductive rate (R_0) between *F. occidentalis* and *T. hawaiiensis* were observed, with respective values of 38.66 ± 2.85 and 47.91 ± 2.70 on *G. jasminoides*, and 55.64 ± 2.15 and 32.45 ± 2.16 on *R. chinensis*. The intrinsic rates of increase (r_m) of *F. occidentalis* and *T. hawaiiensis* were 0.156 ± 0.008 and 0.198 ± 0.007, respectively, on *G. jasminoides*, and 0.172 ± 0.003 and 0.165 ± 0.002, respectively, on *R. chinensis*. Thus, the performances of both thrips with respect to population size in the laboratory were in accordance with those in the field, suggesting that the innate capacity for insect population increases may directly impact their population dynamics in fields. Thus, the population performance of different thrips species on flowers is species-dependent, which could be exploited in thrips control programs by breeding pest-resistant cultivars.

Keywords Western flower thrips · Flower-inhabiting thrips · Insect population development · *Gardenia jasminoides* · *Rosa chinensis* · Life history

Key message

- *Frankliniella occidentalis* and *Thrips hawaiiensis* are important pests of *Gardenia jasminoides* and *Rosa chinensis*, which are economically important horticultural plants in China.
- Reasons for the different *F. occidentalis*' and *T. hawaiiensis*' population dynamics associated with flower species are unknown.
- The *F. occidentalis* population developed faster and was larger on *R. chinensis*, while the same was true for *T. hawaiiensis* on *G. jasminoides* in the laboratory.

Communicated by M. Traugott.

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Pest Management Science / Volume 72, Issue 5 / p. 1059-1066

Research Article | Open Access

Laboratory and field evaluation of an entomopathogenic fungus, *Isaria cateniannulata* strain 08XS-1, against *Tetranychus urticae* (Koch)

Xiaona Zhang, Daochao Jin, Xiao Zou, Jianjun Guo

First published: 18 January 2016
https://doi.org/10.1002/ps.4233
Citations: 5

Abstract

BACKGROUND

The two-spotted mite, *Tetranychus urticae* Koch, is one of the most serious mite pests of crops throughout the world. Biocontrol of the mite with fungal agents has long been paid much attention because of the development of insecticide resistance and the severe restriction of chemical pesticides. In this study, the efficacy of submerged conidia of the entomopathogenic fungus *Isaria cateniannulata* strain 08XS-1 against *T. urticae* eggs, larvae and female adults was evaluated at different temperatures and humidity in the laboratory and under field conditions.

RESULTS

The results showed that a suspension of 2×10^7 submerged conidia mL^{-1} caused the highest mortalities of mite eggs, larvae and females (100, 100 and 70% respectively) at 100% relative humidity and 25 °C in the laboratory. In the field experiments against the mites, a suspension of 2×10^8 submerged conidia mL^{-1} achieved significant efficiency – the relative control effects were 88.6, 83.8 and 83%, respectively, in cucumber, eggplant and bean fields after 10 days of treatment.

CONCLUSION

The results suggest that the *I. cateniannulata* strain 08XS-1 is a potential fungal agent, with acceptable production cost of conidia, against *T. urticae* in the field in an area such as southwestern China with higher air humidity.

1 INTRODUCTION

International Journal of
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Article

Induced Resistance Combined with RNA Interference Attenuates the Counteradaptation of the Western Flower Thrips

Tao Zhang, Li Liu, Yulian Jia, Junrui Zhi *, Wenbo Yue, Dingyin Li and Guang Zeng

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Abstract: The western flower thrips, *Frankliniella occidentalis* Pergande, is an invasive pest that damages agricultural and horticultural crops. The induction of plant defenses and RNA interference (RNAi) technology are potent pest control strategies. This study investigated whether the anti-adaptive ability of *F. occidentalis* to jasmonic acid (JA)- and methyl jasmonate (MeJA)-induced defenses in kidney bean plants was attenuated after glutathione S-transferase (GST) gene knockdown. The expression of four GSTs in thrips fed JA- and MeJA-induced leaves was analyzed, and *FoGSTd1* and *FoGSTs1* were upregulated. Exogenous JA- and MeJA-induced defenses led to increases in defensive secondary metabolites (tannins, alkaloids, total phenols, flavonoids, and lignin) in leaves. Metabolome analysis indicated that the JA-induced treatment of leaves led to significant upregulation of defensive metabolites. The activity of GSTs increased in second-instar thrips larvae fed JA- and MeJA-induced leaves. Co-silencing with RNAi simultaneously knocked down *FoGSTd1* and *FoGSTs1* transcripts and GST activity, and the area damaged by second-instar larvae feeding on JA- and MeJA-induced leaves decreased by 62.22% and 55.24%, respectively. The pupation rate of second-instar larvae also decreased by 39.68% and 39.89%, respectively. Thus, RNAi downregulation of *FoGSTd1* and *FoGSTs1* reduced the anti-adaptive ability of *F. occidentalis* to JA- or MeJA-induced defenses in kidney bean plants.

Keywords: *Frankliniella occidentalis*; glutathione S-transferase; induced defense; jasmonic acid; methyl jasmonate; RNA interference; metabolites; counteradaptation

check for updates

Citation: Zhang, T.; Liu, L.; Jia, Y.; Zhi, J.; Yue, W.; Li, D.; Zeng, G. Induced Resistance Combined with RNA Interference Attenuates the Counteradaptation of the Western Flower Thrips. *Int. J. Mol. Sci.* **2022**, *23*, 10886. https://doi.org/10.3390/ijms231810886

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1. Introduction

In the co-evolution of plants and insects, plants developed a series of constitutive and inducible defense mechanisms against insect feeding stress. However, insects also evolved complex anti-defense mechanisms, including behavioral, physiological, and biochemical adaptations, to increase survival and reproduction [1–4]. Important progress has been made in the theory of plant defense [5,6]. In defense against herbivorous insects, plants induce the production of secondary compounds in response to various induction factors, and those compounds cause direct toxicity to insects [7,8]. Phytohormones are important inducing factors that regulate plant defense responses, and predominantly include jasmonic acid (JA), salicylic acid, ethylene, and abscisic acid and its related derivatives [9]. Among the phytohormones, the JA signaling pathway is the most important pathway for regulating plant defenses against insects. Activation of the JA signaling pathway in plants activates corresponding defensive enzymes and proteins and a series of defensive compounds that counteract the harm caused by herbivorous insects [10–12]. To activate the plant JA defense system, the JA signaling pathway is induced by chewing and rasping/sucking by insect mouthparts and also by the exogenous synthesis of JA and methyl jasmonate (MeJA) [6,13]. The activation of the JA signaling defense network by exogenous JA and its derivatives significantly upregulates JA biosynthetic enzymes, such as lipoxygenase (LOX), antioxidant enzymes (such as polyphenol oxidase and peroxidase),

International Journal of
Molecular Sciences

MDPI

Article

Three Heat Shock Protein Genes and Antioxidant Enzymes Protect *Pardosa pseudoannulata* (Araneae: Lycosidae) from High Temperature Stress

Di Fu, Jing Liu, Ying-Na Pan, Jia-Yun Zhu, Feng Xiao, Min Liu and Rong Xiao *

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Abstract: *Pardosa pseudoannulata* (*P. pseudoannulata*) is an essential natural predatory enemy in rice ecosystems. The fluctuating climate may cause them to experience heat stress, whereas heat shock proteins (HSPs) and antioxidant enzymes help resist heat damage. Herein, we cloned and characterized the full-length genes *PpHSP27*, *PpHSP60*, and *PpHSC70* from *P. pseudoannulata*. Changes in gene expression levels and superoxide dismutase (SOD), catalase (CAT), and glutathione transferase (GST) activities in adult male and female *P. pseudoannulata* were measured at different stress exposure times and temperatures. We found that the abovementioned HSP genes belong to the sHSP, HSP60, and HSP70 families. The expression of the three HSP genes and the activities of SOD, CAT, and GST were significantly upregulated with the increasing stress temperature and time. The knockdown of the three HSP genes via RNA interference significantly decreased the survival rate of male and female *P. pseudoannulata* during high temperature stress. Thus, *PpHSP27*, *PpHSP60*, and *PpHSC70* play an important role in the heat tolerance of *P. pseudoannulata*, and SOD, CAT, and GST enable recovery heat stress-induced oxidative damage. Their changes and regulation during high temperature stress can improve spiders' adaptability in the field and enhance the biological control of environmental pests.

Keywords: *Pardosa pseudoannulata*; heat-shock protein (HSP) genes; antioxidant enzymes; heat stress; RNAi; thermotolerance

Citation: Fu, D.; Liu, J.; Pan, Y.-N.; Zhu, J.-Y.; Xiao, F.; Liu, M.; Xiao, R. Three Heat Shock Protein Genes and Antioxidant Enzymes Protect *Pardosa pseudoannulata* (Araneae: Lycosidae) from High Temperature Stress. *Int. J. Mol. Sci.* **2022**, *23*, 12821. https://doi.org/10.3390/ijms232112821

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Accepted: 20 October 2022
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1. Introduction

Arthropods are relatively susceptible to high temperatures because they do not have mechanisms to regulate their body temperature. High temperatures can significantly affect their growth, development, reproduction, survival, and other processes [1,2]. The intensity, frequency, and duration of high temperatures are increasing because of global warming, and these trends are expected to deteriorate with increased global warming [3,4]. During their long evolution, arthropods have evolved various behavioral, morphological, physiological, and molecular strategies to avoid high-temperature damage. The production of heat shock proteins (HSPs) and the enhancement of antioxidant enzymes are considered important strategies for arthropods to cope with heat stress [5–9].

As with adverse environmental factors, such as hypoxia, heavy metal ion pollution, UV stress, and starvation, heat stress causes protein denaturation and loss of function in the organism [5,8,10]. As a chaperone protein, HSP cooperates with auxiliary molecular chaperones and auxiliary proteins to mediate activities such as protein folding, localization, and degradation, and prevents the protein denaturation caused by the abovementioned reasons [11–13]. Based on the relative molecular weight and amino acid (AA) sequence homology, HSPs may be divided into HSP110, HSP90, HSP70, HSP60, small heat shock proteins (sHSPs), and other families [13–15]. Of these, HSP70 is the most

International Journal of
Molecular Sciences

Article

Isolation of Peptide Inhibiting SGC-7901 Cell Proliferation from *Aspongopus chinensis* Dallas

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Abstract: *Aspongopus chinensis* Dallas is used as a traditional Chinese medicine as well as an edible insect. Although its anti-tumor effects have been observed, the anti-tumor active component(s) in the hemolymph of *A. chinensis* remains unknown. In this study, a combination usage of ultrafiltration, gel filtration chromatography, FPLC and RP-HPLC to separate and purify active peptides was performed based on the proliferation of the human gastric cancer SGC-7901 cell line treated with candidates. One peptide (MW = 2853.3 Da) was isolated from the hemolymph of *A. chinensis.* A total of 24 amino acid residues were continuously determined for the active peptide: N′-ECGYCAEKGIRCDDIHCCTGLKKK-C′. In conclusion, a peptide that can inhibit the proliferation of gastric cancer SGC-7901 cells in the hemolymph of *A. chinensis* was purified in this study, which is homologous to members of the spider toxin protein family. These results should facilitate further works for this peptide, such as the cloning of genes, expression in vitro by prokaryotic or eukaryotic systems, more specific tests of anti-tumor activity, and so on.

Keywords: anti-cancer peptide; *Aspongopus chinensis* Dallas; MTT; inhibition; IC_{50}

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Citation: Chen, X.-M.; Zhang, S.-Q.; Cao, M.-L.; Guo, J.-J.; Luo, R. Isolation of Peptide Inhibiting SGC-7901 Cell Proliferation from *Aspongopus chinensis* Dallas. *Int. J. Mol. Sci.* **2022**, *23*, 12535. https://doi.org/10.3390/ijms232012535

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Published: 19 October 2022

1. Introduction

Cancers are a serious threat to human health. There were 19.3 million new cancer cases and 10 million cancer deaths in 2020 [1]. Lung cancer, colorectal cancer, breast cancer, gastric cancer, and liver cancer are the top five cancers with the highest morbidity and mortality worldwide [2]. However, there are no adequate efficacious medicines for cancer treatments. Meanwhile, many disadvantages are associated with current medicines, such as high price, severe adverse reactions, drug resistance, relapse after drug cessation, and so on [3]. Therefore, the development of new anti-cancer drugs is a major issue at present.

Development of anti-cancer chemicals should be based on chemical design and screening according to targets, or based on the screening of natural chemicals. For natural anti-cancer chemical screening, medicinal insects are important resources for active component isolation. It has been proven that cantharidin and its derivatives from meloid insects possess inhibitory effects on various cancer cells, such as laryngeal cancer, gastric cancer, leukemia, esophageal cancer, liver cancer, lung cancer, cervical carcinoma and prostatic cancer [4–9]. Bee venom and propolis (Apidae and Vespidae, Hymenoptera), which are traditionally utilized as medicines, also have inhibitory effects on the proliferation of leukemia, liver cancer, and esophageal carcinoma cells [10,11]. Mastoparan is an α-helical and amphipathic tetradecapeptide obtained from the venom of the wasp *Vespula lewisii* that exhibits tumor cell cytotoxicity [12]. It induced caspase-dependent apoptosis in melanoma cells through the intrinsic mitochondrial pathway, protecting mice against tumor development. In addition, chemicals originating from *Bombyx mori*, *Chrysomya megacephala*, *Musca domestica*, and *Holotrichia diomphalia* larvae also have certain inhibitory effects on various tumor cells [13–16].

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Article

Identification and Functional Analysis of a Defensin CcDef2 from *Coridius chinensis*

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Abstract: *Coridius chinensis* belongs to Dinidoridae, Hemiptera. Previous studies have indicated that *C. chinensis* contains abundant polypeptides with antibacterial and anticancer activities. Antimicrobial peptides (AMPs), as endogenous peptides with immune function, play an indispensable role in the process of biological development and immunity. AMPs have become one of the most potential substitutes for antibiotics due to their small molecular weight and broad-spectrum antimicrobial activity. In this study, a defensin CcDef2 from *C. chinensis* was characterized based on bioinformatics and functional analyses. The mature peptide of CcDef2 is a typical cationic peptide composed of 43 amino acid residues with five cations, and contains three intramolecular disulfide bonds and a typical cysteine-stabilized αβ motif in defensins. Phylogenetic analysis showed that CcDef2 belongs to the insect defensin family. Analysis of gene expression patterns showed that *CcDef2* was expressed throughout developmental stages of *C. chinensis* with high levels at the nymphal stage and in adult tissues tested with the highest level in the fat body. In addition, the *CcDef2* expression was significantly upregulated in adults infected by bacteria. After expressed in *Escherichia coli* BL21(DE3) and renatured, the recombinant CcDef2 showed a significant antibacterial effect on three kinds of Gram-positive bacteria. These results indicate that CcDef2 is an excellent antibacterial peptide and a highly effective immune effector in the innate immunity of *C. chinensis*. This study provides a foundation for further understanding the function of *CcDef2* and developing new antimicrobial drugs.

Keywords: *Coridius chinensis*; antimicrobial peptide; defensin; innate immunity; antibacterial activity

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1. Introduction

Multicellular organisms are constantly infected by pathogens and parasites in the surrounding environment, and the immune system can help them resist the invasion of bacterial pathogens. Insects have no specific immune system similar to vertebrate T-lymphocytes and B-lymphocytes, so innate immunity is the only way for insects to face pathogen infection [1,2]. Insect innate immunity mainly consists of humoral immunity and cellular immunity. Humoral immune responses include the production of antimicrobial peptides (AMPs), reactive intermediates of oxygen or nitrogen, and the complex enzymatic cascades that regulate coagulation or melanization of hemolymph [3–6]. Cellular responses refer to the immune response mediated by blood cells, including phagocytosis, nodulation, and encapsulation [7,8]. As a requisite part of the humoral immune mechanism, AMP is the first barrier of host defense and can kill bacteria, fungi, viruses, and protozoa or slow down their growth [9,10].

AMPs may be classified into four groups based on the differences in amino acid composition and structural characteristics: cecropin, defensin, glycine-rich peptides, and proline-rich peptides [11]. Cecropin was the first insect AMP that was isolated from the hemolymph of the pupae of *Hyalophora cecropia*. [12]. Since then, cecropins have been isolated from *Bombyx mori*, *Antherea pernyi*, Drosophila, and Sarcophagidae. The isolation

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Article

Identification and Characterization of a Double-Stranded RNA Degrading Nuclease Influencing RNAi Efficiency in the Rice Leaf Folder *Cnaphalocrocis medinalis*

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Abstract: Rice leaf folder *Cnaphalocrocis medinalis* is one of the most serious pests of rice in rice-planting regions worldwide. DsRNA-degrading nucleases (dsRNases) are important factors in reducing the efficiency of RNA interference (RNAi) in different insects. In this study, a *dsRNase* gene from *C. medinalis* (*CmdsRNase*) was cloned and characterized. The *CmdsRNase* cDNA was 1395 bp in length, encoding 464 amino acids. The CmdsRNase zymoprotein contains a signal peptide and an endonuclease NS domain that comprises six active sites, three substrate-binding sites, and one Mg^{2+}-binding site. The mature CmdsRNase forms a homodimer with a total of 16 α-helices and 20 β-pleated sheets. Homology and phylogenetic analyses revealed that CmdsRNase is closely related to dsRNase2 in *Ostrinia nubilalis*. Expression pattern analysis by droplet digital PCR indicated that the expression levels of *CmdsRNase* varied throughout the developmental stages of *C. medinalis* and in different adult tissues, with the highest expression levels in the fourth-instar larvae and the hemolymph. CmdsRNase can degrade dsRNA to reduce the efficiency of RNAi in *C. medinalis*. Co-silencing of *CmCHS* (*chitin synthase* from *C. medinalis*) and CmdsRNase affected significantly the growth and development of *C. medinalis* and thus improved RNAi efficacy, which increased by 27.17%. These findings will be helpful for green control of *C. medinalis* and other lepidopteran pests by RNAi.

Keywords: *Cnaphalocrocis medinalis*; RNA interference; RNAi efficiency; dsRNA degrading nuclease; dsRNase

check for updates

Citation: Li, J.; Du, J.; Li, S.; Wang, X. Identification and Characterization of a Double-Stranded RNA Degrading Nuclease Influencing RNAi Efficiency in the Rice Leaf Folder *Cnaphalocrocis medinalis*. *Int. J. Mol. Sci.* **2022**, *23*, 3961. https://doi.org/10.3390/ijms23073961

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1. Introduction

RNA interference (RNAi) is a highly conserved mechanism triggered by double-stranded RNA (dsRNA) in the evolutionary process; therefore, homologous mRNAs are degraded efficiently and specifically. The essence of RNAi is post-transcriptional gene silencing. The transcription of the silenced genes continues to proceed normally, but the transcribed messenger RNA (mRNA) undergoes sequence-specific degradation in the cytoplasm, with the result that these genes cannot be normally expressed as proteins [1]. RNAi exists in most eukaryotes, but the efficiency of RNAi varies greatly among different species [2–5]. RNAi has high efficiency, specificity, and transmissibility, and is widely used as a powerful tool in the exploration of gene function analysis, biomedical research, biological pest control, and other fields. The use of RNAi technology to control pests is currently one of the hotspots in scientific research. The difference in RNAi efficiency among different species of insects limits the use of RNAi technology in basic insect research and pest control; for example, the RNAi efficiency in most coleopteran insects is high and long-lasting [6–9], whereas the RNAi efficiency in most dipteran, hemipteran, and lepidopteran insects is variable and unstable [10–12]. There are many factors that affect the efficiency of RNAi in insects, including delivery methods [13–15], dsRNA transport in cells [16], target

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Estimated Divergence Times of *Lecanicillium* in the Family Cordycipitaceae Provide Insights Into the Attribution of *Lecanicillium*

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Background: The genus *Lecanicillium* W.Gams & Zare is a recognized insect pathogen but members of the genus have been found parasitizing various hosts including arthropods, nematodes, plants, and fungi. The new classification system for fungi proposed to reject *Lecanicillium* and transfer some of the species to the genus *Akanthomyces*. However, the attribution problem of most species in the original genus *Lecanicillium* remains unsolved. The current study aimed to improve understanding of the pivotal internal phylogeny in *Lecanicillium* by estimating the divergence times of *Lecanicillium* to provide additional insights into the status of this genus within the family Cordycipitaceae.

Results: Dating analyses support the supposition that the ancestor of *Lecanicillium* was in the Cretaceous period (84.36 Mya, 95% HPD: 72.12–94.74 Mya). After originating from a common ancestor, eight clades of *Lecanicillium* were derived and evolved independently in parallel with other genera of Cordycipitaceae. Based on the clear divergence age estimates, *Lecanicillium* clade 8 originated earlier as an independent group in the Cretaceous period (75.61 Mya, 95% HPD: 63.31–87.54 Mya), while *Lecanicillium* clades 1–7 originated later as an independent group in the boundary of the Cretaceous and Paleogene periods (64.66 Mya, 95% HPD: 52.75–76.74 Mya). *Lecanicillium huhutii* formed an independent branch in a polytomy together with a clade containing *Lecanicillium tenuipes* (BI posterior probabilities 1, ML bootstrap 100%).

Conclusion: The pivotal internal phylogeny, origin, and evolutionary history of *Lecanicillium* in the family Cordycipitaceae were investigated. Phylogenetic and morphological analyses indicated that there are eight representative clades (four representative branches of evolutionary history), including clade 1 (members have a relatively uniform sporulation structure comprising globose heads with a higher number of conidia), clade 8 (including all members of *Gamszarea*), clades 2–5 (the differences of the divergence time estimations were smaller compared with other clades), and clade 6–7 (members are close to *Gibellula*, *Hevansia*, and *Ascopolyporus*). Based on the above findings, a novel spider-pathogenic fungus, *Lecanicillium huhutii*, is described. All other species in *Lecanicillium* clade 1 (*Lecanicillium araneogemum*, *L. nodulosum*, *L. pissodis*, and *L. uredinophilum*) should be transferred to the genus *Akanthomyces*. Furthermore, the monotypic genus *Parengyodontium* should be merged with the

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Immune function analysis of *LsSd*, a transcription factor of the Hippo signaling pathway, in the cigarette beetle *Lasioderma serricorne*

Yue Zhang[1], Jiapeng Yang[1], Renhuai Dai[1]*, Wenjia Yang[2] and Xiaomin Zhang[3]

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The Scalloped (Sd) is a transcription factor that regulates organ size control in the Hippo-signaling pathway. Recent studies have showed that Hippo signaling also functions in the innate immune response. Although the Sd gene has been reported in many insects, their immune functions remain unexplored. In this study, the *LsSd* gene of *Lasioderma serricorne*, with a complete open reading frame that encodes a protein composed of 402 amino acids was identified. *LsSd* was predominantly expressed in early pupae. Tissue-specific analyses revealed that the highest concentrations of *LsSd* were detected in the midgut and brain. At 1–24 h after *Escherichia coli* infection, *LsSd* expression increased substantially. However, *LsSd* expression was downregulated 3–12 h after *Staphylococcus aureus* infection. RNA interference-mediated silencing of the *LsSd* transcript resulted in deformed, considerably smaller, and degenerated wings. Meanwhile, *LsCycE*, *LsDiap1*, and *LsVg*, which are involved in cell proliferation and wing development, were drastically reduced when *LsSd* was depleted. In a survival assay, the *LsSd* knockdown considerably decreased the susceptibility to *S. aureus*, a gram-positive bacterium. In addition, knockdown of *LsSd* remarkably downregulated the transcription of *LsCact* in response to *S. aureus* stimulation, while upregulating the expression of five immune-related genes. Our results provide conclusive proof for the important roles of *LsSd* in the immune response of *L. serricorne*.

KEYWORDS

***Lasioderma serricorne*, *LsSd* gene, Hippo-signaling pathway, wing development, immune response**

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Juvenile Hormone Is an Important Factor in Regulating *Aspongopus chinensis* Dallas Diapause

Wen-Zhen Zhou, † You-Fang Wu, † Zhi-Yong Yin, Jian-Jun Guo,* and Hai-Yin Li*

Abstract

Aspongopus chinensis is a Chinese traditional edible and medicinal insect, which is in great demand in the society. This insect reproduces once a year which is caused by reproductive diapause resulting in insufficient production in wild resources. However, the mechanism of diapause in *A. chinensis* is still unclear. In this study, we focus on the relationship between juvenile hormones (JHs) and *A. chinensis* diapause. The results showed that JHIII concentration in diapause adult individuals was significantly lower than that in diapause termination adult individuals. When exogenous JHIII was injected into diapause adults, the rate of mating was increased significantly, development of the reproductive systems was accelerated, consumption of fat intensified, the expression of juvenile hormone acid o-methyl-transferase (JHAMT) was upregulated, and juvenile hormone epoxide hydrolase (JHEH) and fatty acid synthase (FAS) gene expressions were downregulated. In addition, RNAi of *JHAMT* decreased JH concentration, delayed the development of reproductive systems, slowed down fat consumption, and delayed the mean mating occurrence time significantly. Conversely, RNAi of *JHEH* resulted in an increased concentration of JH, development of reproductive systems was accelerated, consumption of fat was intensified, and mean mating occurrence time advanced significantly. Taken together, these findings uncovered that JH plays an important role in regulating reproductive diapause in *A. chinensis* and, thus, could provide a theoretical basis for further research on the diapause of *A. chinensis*.

Keywords: *Aspongopus chinensis*, JH, reproduction system, JHEH, JHAMT, diapause

Introduction

Aspongopus chinensis Dallas, 1851, is a Chinese traditional edible and medicinal insect (Guo et al., 2019). The previous studies showed that hemolytic lymph extracted from *A. chinensis* inhibits the activity of cancer cells (Yang et al., 2017; Tan et al., 2019a, Tan et al., 2019b). Therefore, *A. chinensis* is in great demand in the society. However, despite its medicinal value and information about its bioecology being discovered (Wei et al., 2015; Gu et al., 2017)
a diapause for up to 7 months and reproduces once a year (Wei et al., 2015) which resu
insufficient production in the wild resources. To improve the utilization of *A. chinensis* re
sources, we focused our attention on *A. chinensis* diapause.

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WILEY Full Text Article

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Identification and profiling of Sogatella furcifera microRNAs and their potential roles in regulating the developmental transitions of nymph-adult

Xi-Bin Yang [1] [2], Cao Zhou [3], Jia-Peng Yang [1] [2], Ming-Fu Gong [1] [2], Hong Yang [1] [4] [2], Gui-Yun Long [1] [2], Dao-Chao Jin [1] [2]

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Abstract

Sogatella furcifera is one of the most serious insect pests that affect rice in Asia. One class of small RNAs (sRNAs; ~22 nt long) is miRNAs, which participate in various biological processes by regulating the expression of target genes in a spatiotemporal manner. However, the role of miRNAs in nymph-to-adult transition in S. furcifera remains unknown. In this study, we sequenced sRNA libraries of S. furcifera prepared from individuals at three different developmental stages (pre-molt, molting, and early adult). A total of 253 miRNAs (134 known and 119 novel) were identified, of which 12 were differentially expressed during the nymph-to-adult developmental transition. Moreover, RT-qPCR analysis revealed that all 12 miRNAs were differentially expressed among five different nymph tissues and 14 different developmental stages (1st -5th instar nymphs and 1-d-old adults). Injection of miR-2a-2 mimic/antagomir and miR-305-5p-1 mimic/antagomir into 1-d-old 5th instar nymphs significantly increased the mortality rate. In addition, a defective molting phenotype was observed in nymphs injected with miR-2a-2 and miR-305-5p-1, suggesting that these miRNAs are involved in S. furcifera nymph-adult transition. In conclusion, these results reveal the function of critical miRNAs in S. furcifera nymph-adult transition, and also provide novel potential targets of insecticides for the long-term sustainable management of S. furcifera.

Keywords: Small RNAs sequencing; Sogatella furcifera; Temporal expression; functional analysis; miRNAs.

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Article

Two New Species of *Betacixius* Matsumura, 1914 (Hemiptera: Fulgoromorpha: Cixiidae) from Southwestern China, with an Updated Checklist and Key to Species †

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† The LSID (Life Science Identifier) for this publication is: urn:lsid:zoobank.org:pub:CE7A6CA9-B96C-435B-AFC0-7834BD064B18.

Simple Summary: *Betacixius* Matsumura, 1914 is a small genus of cixiid planthoppers distributed throughout China, Japan and Vietnam. Despite its rich biodiversity in Southwest China, *Betacixius* has not been taxonomically well studied in this region. Here, two new species, *Betacixius gongshanensis* sp. nov. from Yunan Province and *B. guizhouensis* sp. nov. from Guizhou Province, are described, giving the genus 27 species in total. We believe that the discovery in this study will contribute to further studies on the classification and phylogeny of Cixiidae.

Abstract: In this study, two new species of genus *Betacixius* Matsumura, 1914 (Fulgoromorpha, Cixiidae), *Betacixius gongshanensis* sp. nov. from Yunnan Province and *B. guizhouensis* sp. nov. from Guizhou Province, are described and illustrated. An updated checklist and identification key to known species of the genus *Betacixius* are provided.

Keywords: Auchenorrhyncha; new species; planthopper; taxonomy

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Citation: Zhi, Y.; Wang, X.-Y.; Yang, L.; Chen, X.-S. Two New Species of *Betacixius* Matsumura, 1914 (Hemiptera: Fulgoromorpha: Cixiidae) from Southwestern China, with an Updated Checklist and Key to Species. *Insects* **2022**, *13*, 512. https://doi.org/10.3390/insects13060512

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1. Introduction

The cixiid planthopper genus *Betacixius* Matsumura, 1914, in the tribe Semonini (Hemiptera: Cixiidae: Cixiinae), currently consists of 25 species and two subspecies distributed throughout China, Japan and Vietnam [1]. Following our previous works [2,3], we aim to revise the species from Southwest China in the present study. The specimens from Guizhou and Yunnan provinces brought to our attention another two new species, *Betacixius gongshanensis* and *B. guizhouensis*, which are described and illustrated here. The total number of *Betacixius* species is thus increased to 27, with 25 occurring in China. An updated checklist and identification key of *Betacixius* are given.

2. Materials and Methods

The morphological terminology follows Bourgoin [4] for male genitalia, Bourgoin et al. [5] for wing venation, and Bourgoin [6] for female genitalia. Body length was measured from the apex of the vertex to the tip of the forewing; vertex length represented the median length of the vertex (from the apical transverse carina to the tip of basal emargination). Fuchsin staining was used to highlight the female genitalia structures we studied. External morphology and drawings were visualized and created with the aid of a Leica MZ 12.5 stereomicroscope. Photographs were taken with the KEYENCE VHX-6000 system. Illustrations were scanned with a CanoScan LiDE 200 and imported into

insects MDPI

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Copper Chaperone for Superoxide Dismutase *FoCCS1* in *Frankliniella occidentalis* May Be Associated with Feeding Adaptation after Host Shifting

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Nabil Killiny, Academic Editor

Abstract

Simple Summary

Western flower thrips (*Frankliniella occidentalis*) have a wide range of hosts. Therefore, they can colonize new host plants with each seasonal change. This study examined whether the superoxide dismutase (*SOD*) gene regulates the feeding adaptation of *F. occidentalis* after host shifting. The coding sequences for *CCS1* and *MnSOD2* in *F. occidentalis* were cloned and the corresponding amino acid sequence was predicted, and the mRNA expression levels of these two genes at different developmental stages were determined. Further, the mRNA expression levels of *FoCCS1* and *FoMnSOD2* in second-instar larvae and adult females transferred to kidney bean and broad bean plants for rearing were analyzed. Decreasing the mRNA levels of *FoCCS1* and *SOD* activity by RNA interference significantly reduced the survival rate and fecundity of adult *F. occidentalis* females. These findings provide a reference for analyzing the adaptive mechanism of *F. occidentalis* after host shifting.

Abstract

Western flower thrips (*Frankliniella occidentalis*) pose a serious threat to the global vegetable and flower crop production. The regulatory mechanism for superoxide dismutase (SOD) in the feeding adaptation of *F. occidentalis* after host shifting remains unclear. In this study, the copper chaperone for SOD (*CCS*) and manganese SOD (*MnSOD*) genes in *F. occidentalis* were cloned, and their expression levels at different developmental stages was determined. The mRNA expression of *FoCCS1* and *FoMnSOD2* in *F. occidentalis* second-instar larvae and adult females of F_1, F_2, and F_3 generations was analyzed after shifting the thrips to kidney bean and broad bean plants, respectively. The F_2 and F_3 second-instar larvae and F_2 adult females showed significantly upregulated *FoCCS1* mRNA expression after shifting to kidney bean plants. The F_1 second-instar larvae and F_2 adult females showed significantly upregulated *FoCCS1* mRNA expression after shifting to broad bean plants. The RNA interference significantly downregulated the *FoCCS1* mRNA expression levels and adult females showed significantly inhibited SOD activity after shifting to kidney bean and broad bean plants. *F. occidentalis* adult females subjected to RNA interference and released on kidney bean and broad bean leaves for rearing,

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Mitogenomic phylogeny of Typhlocybinae (Hemiptera: Cicadellidae) reveals homoplasy in tribal diagnostic morphological traits

Bin Yan,[1] Christopher H. Dietrich,[2] Xiaofei Yu,[3] Meng Jiao,[1, 4] Renhuai Dai,[1] and Maofa Yang[1, 3]

Abstract

The subfamily Typhlocybinae is a ubiquitous, highly diverse group of mostly tiny, delicate leafhoppers. The tribal classification has long been controversial and phylogenetic methods have only recently begun to test the phylogenetic status and relationships of tribes. To shed light on the evolution of Typhlocybinae, we performed phylogenetic analyses based on 28 newly sequenced and 19 previously sequenced mitochondrial genomes representing all currently recognized tribes. The results support the monophyly of the subfamily and its sister-group relationship to Mileewinae. The tribe Zyginellini is polyphyletic with some included genera derived independently within Typhlocybini. Ancestral character state reconstruction suggests that some morphological characters traditionally considered important for diagnosing tribes (presence/absence of ocelli, development of hind wing submarginal vein) are homoplastic. Divergence time estimates indicate that the subfamily arose during the Middle Cretaceous and that the extant tribes arose during the Late Cretaceous. Phylogenetic results support establishment of a new genus, *Subtilissimia* Yan & Yang gen. nov., with two new species, *Subtilissimia fulva* Yan & Yang sp. nov. and *Subtilissimia pellicula* Yan & Yang sp. nov.; but indicate that two previously recognized species of *Farynala* distinguished only by the direction of curvature of the processes of the aedeagus are synonyms, that is, *Farynala dextra* Yan & Yang, 2017 equals *Farynala sinistra* Yan & Yang, 2017 syn. nov. A key to tribes of Typhlocybinae is provided.

Keywords: ancestral character state reconstruction, Auchenorrhyncha, classification, high-throughput sequencing, Membracoidea, microleafhopper, mitochondrial genes, phylogenetic analysis

Abstract

We studied the evolutional relationships of Typhlocybinae based on 47 typhlocybine mitogenomic dataset representing all currently recognized tribes. The Ancestral character state reconstruction suggests that some morphological characters (fore- and hind wing patterns) traditionally considered important for diagnosing typhlocybine tribes are homoplastic. The divergence time estimates indicate that the subfamily Typhlocybinae arose during the Middle Cretaceous and that the extant tribes arose during the Late Cretaceous.

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Comparative Analysis of Mitochondrial Genomes among Twelve Sibling Species of the Genus *Atkinsoniella* Distant, 1908 (Hemiptera: Cicadellidae: Cicadellinae) and Phylogenetic Analysis

Yan Jiang,[1,2] Hao-Xi Li,[2,3] Xiao-Fei Yu,[2,3] and Mao-Fa Yang[1,2,3,*]

Nicolas Nègre, Academic Editor

Abstract

Simple Summary

Atkinsoniella is a large genus of 98 species across the world and 88 species recorded in China within the globally distributed subfamily Cicadellinae, which is phytophagous, and some of which have been reported as important agricultural pests. Some *Atkinsoniella* species are very similar in morphological characteristics, making accurate identification at species level confusing. To provide further evidence toward understanding the relationships within the genus *Atkinsoniella* and subfamily Cicadellinae, mitogenomes of 12 *Atkinsoniella* sibling species were obtained and annotated. Their characteristics were comparatively analyzed. In addition, the comprehensive phylogenetic relationship within the subfamily Cicadellinae was determined based on three mitochondrial datasets using both the maximum-likelihood (ML) and Bayesian inference (BI) methods. The results suggested that the genus *Atkinsoniella* was recovered as a monophyletic group. The branches of the 12 newly sequenced species were clearly separated, with most nodes receiving strong support in all analyses, indicating that mitogenomics is an effective method for identifying closely related species and understanding their phylogenetic and evolutionary relationships.

Abstract

The herbivorous leafhopper genus *Atkinsoniella* Distant, 1908 (Hemiptera: Cicadellidae: Cicadellinae), a large genus of subfamily Cicadellinae, consists of 98 valid species worldwide and 88 species recorded in China. Some species of the genus are very similar in morphological characteristics, so they are difficult to identify accurately. In this study, 12 mitochondrial genomes of *Atkinsoniella* species with similar morphological characteristics were first obtained through high-throughput sequencing, which featured a typical circular molecule of 15,034–15,988 bp in length. The arrangement and orientation of 37 genes were identical to those of typical Cicadellidae mitogenomes. The phylogenetic relationship within the subfamily Cicadellinae was reconstructed using maximum-likelihood (ML) and Bayesian inference (BI)

insects MDPI

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Effects of Nano-Graphene Oxide on the Growth and Reproductive Dynamics of *Spodoptera frugiperda* Based on an Age-Stage, Two-Sex Life Table

Cao Li,[1] Chaoxing Hu,[1,*] Junrui Zhi,[1,*] Wenbo Yue,[1] and Hongbo Li[2]

Clint Kelly, Academic Editor

Abstract

Simple Summary

Fall armyworm (FAW), *Spodoptera frugiperda,* is an important pest in a variety of different crops. Graphene oxide (GO) is a promising candidate used in a biological context because of its versatility. In agriculture, GO could be potentially used as a pesticide additive to improve the efficacy of insecticides. In this study, the effects of GO on the development and reproduction of FAWs were determined based on life table analysis. The results showed that GO could prolong the duration of the egg stage and instar larval stages, but shorten lifespan of male and female adults, and this effect was enhanced with increasing GO concentrations. GO also reduced the number of eggs laid by female moths. In addition, the expression of genes related to reproduction have also been affected by GO. In conclusion, GO prolonged the developmental period of FAWs, decreased fecundity, and may decline the population size. The study provides a basis for the rational use of GO as a pesticide synergist for FAW control.

Abstract

The development and reproduction of the fall armyworm (FAW), *Spodoptera frugiperda*, which were reared on artificial diets containing nano-graphene oxide (GO), were determined based on age-stage, two-sex life table analysis. The results showed that GO had adverse effects on FAWs. Compared with the control, the duration of the egg stage and first, second, and sixth instar larval stages increased with increasing GO concentrations; however, the lifespan of male and female adults decreased with increasing GO concentrations. Weights of FAW pupae that were supplied with GO-amended diets increased by 0.17–15.20% compared to the control. Intrinsic growth, limited growth, and net reproductive rates of FAWs feeding on GO supplemented diets were significantly lower than the control, while mean generational periods (0.5 mg/g: 38.47; 1 mg/g: 40.38; 2 mg/g: 38.42) were significantly longer than the control. The expression of genes encoding vitellogenin (*Vg*) and vitellogenin receptor (*VgR*) expression was abnormal in female FAW adults feeding on GO-amended diets; the number of eggs laid de-

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Herbivore-Induced Rice Volatiles Attract and Affect the Predation Ability of the Wolf Spiders, *Pirata subpiraticus* and *Pardosa pseudoannulata*

Jing Liu, Liangyu Sun, Di Fu, Jiayun Zhu, Min Liu, Feng Xiao, and Rong Xiao*

Gianandrea Salerno, Academic Editor, Manuela Rebora, Academic Editor, and Stanislav N. Gorb, Academic Editor

Abstract

Simple Summary

The spiders, *Pirata subpiraticus* Bösenberg *et* Strand (Araneae: Lycosidae) and *Pardosa pseudoannulata* Bösenberg *et* Strand (Araneae: Lycosidae) are important natural enemies of many rice pests. Herbivore-induced plant volatiles can attract natural enemies to pest locations and are becoming important in integrated pest management. This study assessed the effects of herbivore-induced rice volatiles on the selection behavior, predation ability and field attraction of two species of spiders. The selection frequency of spiders for methyl salicylate, linalool, and 2-heptanone were significantly greater than the blank group. Methyl salicylate can shorten the predatory latency of male *P. pseudoannulata* and can also trap more *P. pseudoannulata* in the field. Linalool may also shorten the predatory latency of male *P. subpiraticus* and increase the daily predation capacity of female *P. pseudoannulata*. In summary, herbivore-induced rice volatiles attract *P. pseudoannulata* and *P. subpiraticus*, and potentially increase their pest control capability. These results provide support for the practical use of herbivore-induced rice volatiles to attract and retain spiders in rice fields.

Abstract

Spiders are important natural enemies of rice pests. Studying the effects of herbivore-induced rice volatiles on spider attraction and predation ability may lead to safer methods for pest prevention and control. In this study, four-arm olfactometer, predation ability experiment, and field trapping experiment were used to evaluate the effects of herbivore-induced rice volatiles on *Pirata subpiraticus* Bösenberg *et* Strand (Araneae: Lycosidae) and *Pardosa pseudoannulata* Bösenberg *et* Strand (Araneae: Lycosidae). The 0.5 μg/μL linalool concentration was attractive, and also shortened the predation latency in male *P. subpiraticus* and female *P. pseudoannulata*. The 0.5 μg/μL linalool concentration increased the daily predation capacity of female *P. pseudoannulata*. Male *P. pseudoannulata* were attracted to 1.0 g/L methyl salicylate, which also shortened their predation latency. In field experiments, methyl salicylate and linalool were ef-

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Juvenile Hormone Synthesis Pathway Gene *SfIPPI* Regulates *Sogatella furcifera* Reproduction

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Lynn M. Riddiford, Academic Editor

Abstract

Simple Summary

The juvenile hormone is essential for insect growth, development, and reproduction. Isopentenyl pyrophosphate isomerase is a key isomerase involved in the synthesis of the juvenile hormone. This study evaluates the effect of the targeted silencing of the *SfIPPI* gene on the reproduction of *Sogatella furcifera* (white-backed planthopper). We found that *SfIPPI* silencing significantly inhibits the ovarian development and egg production in female adults of *S. furcifera* and significantly inhibits the transcription of downstream genes in the juvenile hormone synthesis pathway. Our data provide insight into the function of juvenile hormone biosynthetic pathway genes in insect reproduction, which could be a potential target to control and prevent agricultural pests.

Abstract

The juvenile hormone (JH) is crucial for insect reproduction, and isopentenyl pyrophosphate isomerase (IPPI) is a key enzyme in the JH synthesis pathway. However, few studies have investigated how IPPI regulates insect reproduction. This study identifies and characterizes the IPPI gene (*SfIPPI*) from the important agricultural pest *Sogatella furcifera*. A phylogenetic analysis reveals a high homology of *SfIPPI* with the *IPPI* amino acid sequences of *Laodelphax striatellus* and *Nilaparvata lugens* (Stål). Furthermore, *SfIPPI* is expressed at various developmental stages and in various tissues of *S. furcifera,* and is significantly higher on the 5th day of adult emergence and in integument tissue, while lower levels are found on the 3rd day of adult emergence and in fat body and gut tissue. After silencing *SfIPPI* using RNA interference, the ovarian development is significantly inhibited and the fecundity is significantly reduced when compared with the control group. Additionally, *SfIPPI* silencing significantly decreases the expression levels of downstream JH signal transduction pathway genes (*SfJHAMT*, *SfFAMeT*, and *SfKr-h1*) and *SfVg*. Our findings are helpful in elucidating the molecular mechanism underlying the regulation of insect reproduction through genes in the JH synthesis pathway, and they provide a theoretical basis for the development of pest control treatments targeting *SfIPPI*.

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SfDicer2 RNA Interference Inhibits Molting and Wing Expansion in *Sogatella furcifera*

Qing-Hui Zeng,† Gui-Yun Long,† Xi-Bin Yang, Ze-Yan Jia, Dao-Chao Jin, and Hong Yang*

Abstract

Simple Summary

Endoribonuclease 2 (Dicer2) plays various physiological roles in the RNA interference (RNAi) pathway by fragmenting double-stranded RNA to generate small interfering RNA, which then mediates gene silencing. In this study, the role of *Dicer2* in the regulation of molting and wing expansion in *Sogatella furcifera* (white-backed planthopper) was investigated. In particular, *SfDicer2*-mediated RNAi resulted in wing deformities and lethal modifications in *S. furcifera*, which are attributable to the significant inhibition of chitin synthesis and degradation and wing expansion genes. This study provides insights into the biological functions of *Dicer2* in insects, which can aid in RNAi-mediated pest control.

Abstract

Endoribonuclease 2 (Dicer2) is a key nicking endonuclease involved in the small interfering RNA biosynthesis, and it plays important roles in gene regulation and antiviral immunity. The Dicer2 sequence was obtained using the transcriptomic and genomic information of *Sogatella furcifera* (Horváth), and the spatiotemporal characteristics and functions of molting and wing expansion regulation were studied using real-time quantitative polymerase chain reaction and RNA interference (RNAi) technology. The expression of *SfDicer2* fluctuated during the nymphal stage of *S. furcifera*. Its expression decreased significantly over the course of molting. *SfDicer2* exhibited the highest transcript level in the nymphal stage and adult fat body. After *SfDicer2* was silenced, the total mortality rate was 42.69%; 18.32% of the insects died because of their inability to molt. Compared with the effects of ds*GFP* or water, 44.38% of the insects subjected to the silencing of *SfDicer2* exhibited wing deformities after successful eclosion. After *SfDicer2* RNAi, the expression of chitinase, chitin deacetylase, trehalase, chitin synthase 1, and wing expansion-related genes was significantly inhibited. These findings indicate that *SfDicer2* controls molting by affecting genes associated with chitin synthesis and degradation and regulates wing expansion by altering the expression of wing expansion-related genes in *S. furcifera*.

Keywords: *Sogatella furcifera*, *Dicer2*, RNA interference, molting, wing expansion

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Assessment of Suitable Reference Genes for qRT-PCR Normalization in *Eocanthecona furcellata* (Wolff)

Ying-Na Pan, Ru-Na Zhao, Di Fu, Chun Yu, Chun-Ni Pan, Wei Zhou, and Wen-Long Chen*

Kostas Iatrou, Academic Editor

Abstract

Simple Summary

Eocanthecona furcellata (Wolff) is an important polyphagous predatory natural enemy insect for agriculture and forestry production. In this paper, we screened nine commonly used reference genes *β-1-TUB*, *RPL4*, *RPL32*, *RPS17*, *RPS25*, *SDHA*, *GAPDH2*, *EF2*, and *UBQ*. Five methods, Ct value, geNorm, NormFinder, BestKeeper, and RefFinder, were used to assess the stability of gene expression at different developmental stages, in different tissues of male and female adults, under different temperatures and starvation treatments. Finally, stable reference genes were screened under different experimental conditions, which laid the foundation for further study of *E. furcellata* gene function.

Abstract

Quantitative reverse transcription–polymerase chain reaction (qRT–PCR) is a widely used tool for measuring gene expression; however, its accuracy relies on normalizing the data to one or more stable reference genes. *Eocanthecona furcellata* (Wolff) is a polyphagous predatory natural enemy insect that preferentially feeds on more than 40 types of agricultural and forestry pests, such as those belonging to the orders Lepidoptera, Coleoptera, and Hymenoptera. However, to our knowledge, the selection of stable reference genes has not been reported in detail thus far. In this study, nine *E. furcellata* candidate reference genes (*β-1-TUB*, *RPL4*, *RPL32*, *RPS17*, *RPS25*, *SDHA*, *GAPDH2*, *EF2*, and *UBQ*) were selected based on transcriptome sequencing results. The expression of these genes in various samples was examined at different developmental stages, in the tissues of male and female adults, and after temperature and starvation treatments. Five algorithms were used, including ΔCt, geNorm, NormFinder, BestKeeper, and RefFinder, to evaluate reference gene expression stability. The results revealed that the most stable reference genes were *RPL32* and *RPS25* at different developmental stages; *RPS17*, *RPL4*, and *EF2* for female adult tissue samples; *RPS17* and *RPL32* for male adult tissue samples; *RPS17* and *RPL32* for various temperature treatments of nymphs; *RPS17* and *RPS25* for nymph

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Fruit Fly in a Challenging Environment: Impact of Short-Term Temperature Stress on the Survival, Development, Reproduction, and Trehalose Metabolism of *Bactrocera dorsalis* (Diptera: Tephritidae)

Chun Yu, Runa Zhao, Wei Zhou, Yingna Pan, Hui Tian, Zhengyan Yin, and Wenlong Chen*

Susana Pascual, Academic Editor, Gloria Nombela, Academic Editor, and Francisco J. Beitia, Academic Editor

Abstract

Simple Summary

Bactrocera dorsalis (Hendel) is a widespread and economically important insect pest, infesting various fruits and vegetables. Due to the instability of climate change in early spring and autumn, extreme cold and hot temperatures were developed in a short period of time. Exposure to sudden short-term high or low temperatures may affect the reproduction, development, and physiological changes of *B. dorsalis*. In this study, we determined the effects of short-term temperature treatments on the growth, development, fecundity, and trehalose metabolism of *B. dorsalis*. The results showed that development and reproduction of the flies were negatively affected when temperature was below 10 °C; or more than 31 °C, even causing permanent sterility at extreme temperatures. The changes of glucose, glycogen, trehalose, and trehalose-6-phosphate synthase level had a correlation with the population dynamics of the fruit flies. Our present study can provide a scientific basis for population monitoring, prediction, and comprehensive prevention of the fruit fly.

Abstract

An understanding of physiological damage and population development caused by uncomfortable temperature plays an important role in pest control. In order to clarify the adaptability of different temperatures and physiological response mechanism of *B. dorsalis*, we focused on the adaptation ability of this pest to environmental stress from physiological and ecological viewpoints. In this study, we explored the relationship between population parameters and glucose, glycogen, trehalose, and trehalose-6-phosphate synthase responses to high and low temperatures. Compared with the control group, temperature stress delayed the development duration of all stages, and the survival rates and longevity decreased gradually as temperature decreased to 0 °C and increased to 36 °C. Furthermore, with low temperature decrease from 10 °C to 0 °C, the average fecundity per female increased at 10 °C but decreased later. Reproduction of the species was negatively affected during high-temperature stresses, reach-

insects

Communication

Discovery of the Genus *Anapleus* Horn, 1873 from Cretaceous Kachin Amber (Coleoptera: Histeridae) †

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† urn:lsid:zoobank.org:pub:131A5A42-CE3C-455C-97D8-75B46CE4F54B.

Simple Summary: Historically, researchers have suggested different resolutions of the basal relationships of the family Histeridae based on various datasets and methods of phylogenetic analysis. Phylogenetic analyses combining extant and fossil forms will doubtlessly shed further light on its early evolution. The present study describes the first fossil *Anapleus* species from mid-Cretaceous Kachin amber. This new discovery enriches the fossil record of histerid beetles and has important implications for efforts to understand their early evolutionary history.

Abstract: For the first time, an extant histerid genus *Anapleus* Horn, 1873 is described from a specimen found in mid-Cretaceous Kachin amber. *Anapleus kachinensis* sp. nov. Although the genus *Anapleus* has not been precisely defined by synapomorphies, the new species shares numerous features with extant species while differing in comparatively few external characteristics. *Anapleus kachinensis* represents the first record of an extant histerid genus from Cretaceous deposits and provides further evidence of the ancient origin of the genus.

Keywords: histeroidea; anapleini; new species; fossil species

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1. Introduction

The small histerid beetle genus *Anapleus* Horn, 1873 currently comprises 16 extant species and is widely distributed from Europe and Asia to North and Central America [1]. Members of *Anapleus* share a number of characteristics: (1) body small, oval and convex; (2) frontal stria of head absent, surface obliquely convex in front of eyes and feebly depressed on longitudinal median line; (3) labrum transverse, with a pair (or more) of setiferous punctures; (4) antenna stout, scape oblong and stout, pedicel somewhat elongate and thick, club consisting of the three apical antennomeres, of which the sutures are distinct; (5) pronotum transverse, sides usually strongly convergent to apices; (6) elytra usually coarsely punctate, sometimes strigose apically, dorsal striae absent, lateral margins carinate, apex of elytra truncate; (7) propygidium transverse and nearly vertical, pygidium curved downwards, prosternal keel quadrate and broad, truncate to shallowly emarginate at base, suture between lobe and keel indistinct; (8) antennal fissure longitudinal, deep and situated along prosternal lobe and process; (9) carinal striae of prosternal keel deeply impressed; (10) mesosternum short and transverse, meso-metasternal suture distinct and crenate, metasternum coarsely and densely punctate [2]. Though none of these characteristics has been hypothesized as an explicit autapomorphy of this genus, there has been little question of its monophyly in the literature to date. Yet, apart from isolated descriptions, and faunal

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Biological quality of *Anisopteromalus calandrae* (Hymenoptera: Pteromalidae) reared with cold-stored larvae of *Lasioderma serricorne* (Coleoptera: Anobiidae)

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ARTICLE INFO

Keywords:
Fitness
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ABSTRACT

An effective storage method for larvae of the tobacco beetle *Lasioderma serricorne* (F.) (Coleoptera: Anobiidae) would be useful for rearing and studying its larval parasitoid *Anisopteromalus calandrae* (Howard) (Hymenoptera: Pteromalidae), which is an idiobiont ectoparasitoid. In this study, we observed the survival of *L. serricorne* larvae that were refrigerated under different conditions (stored at 7 °C, 10 °C, and 13 °C for 30, 45, 60, and 75 days) and the number of emerging *A. calandrae* under these conditions, aiming to determine the optimal temperature for *L. serricorne* larvae storage. Our results showed that 10 °C was the optimum temperature for storing *L. serricorne* larvae, with no significant differences recorded in the number of parasitoids that emerged from *L. serricorne* larvae that had been refrigerated for 75 days compared with the control. After refrigeration at 7 °C for 45 days, *L. serricorne* larvae were almost dead, with no parasitoid emergence, suggesting that dead host larvae were not used for rearing *A. calandrae*. Interestingly, when stored for more than 45 days at 13 °C, *L. serricorne* larvae developed abnormally and died, and the number of parasitoids that emerged was also significantly reduced. Subsequently, we tested the adaptive parameters of *A. calandrae* reared with *L. serricorne* larvae after cold storage at 10 °C for different periods, including development time, sex ratio, longevity, adult body length, and fecundity. These parameters were not significantly different from those of the control with the exception of fecundity, which indicated that progeny production on refrigerated hosts gradually declined with storage duration. In summary, *A. calandrae* could successfully parasitize and utilize *L. serricorne* larvae as hosts for long-term refrigeration at 10 °C for up to 45 days without considerable undesirable effects on offspring suitability. These results may have practical implications regarding the development of efficient mass-rearing systems for *A. calandrae*.

1. Introduction

Biological control (biocontrol) is a safe and sustainable pest management technology that effectively uses natural enemies, such as predators, parasitoids, or pathogens, to prevent and control pests (Wang et al., 2019). There is an increasing tendency to use biological strategies to avoid the excessive employment of pesticides and ensure food safety in the prevention and management of storage pests (Ghimire and Phillips, 2014). The mass production of natural enemies is a prerequisite for applying biological control programs (Favetti et al., 2014). However, because of the relatively short shelf life of most natural-enemy insects, they must be produced shortly before use, thus making the cost of raising insects one of the main problems in the successful implementation of biological control programs (Cagnotti et al., 2018). Refrigeration is an important and valuable technology for the biological control of large-scale feeding and breeding of natural enemies (Colinet and Boivin, 2011). Moreover, it can provide a large number of stable suitable hosts when parasitic wasps need to multiply (Tiago et al., 2019).

There are three types of cold-storage condition of natural enemies: Constant low temperature (Bayram et al., 2005; Chen et al., 2013;

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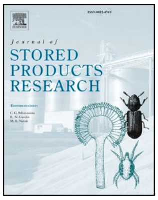

Life history traits of the parasitoid *Anisopteromalus calandrae* (Hymenoptera: Pteromalidae) on three beetle hosts

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Anisopteromalus calandrae
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ABSTRACT

Anisopteromalus calandrae (Howard) (Hymenoptera: Pteromalidae) is a wasp biocontrol agent used against larvae and pupae of coleopteran pests in warehouse settings. The objectives of this study were to assess the life history and life table parameters of *A. calandrae* reared on three coleopteran pests: *Acanthoscelides obtectus* (Say), *Callosobruchus chinensis* (L.), and *Lasioderma serricorne* (F.). The results suggest that host species identity influenced the developmental duration, fecundity, and body size of *A. calandrae*. When reared on *L. serricorne*, the parasitoid's pre-adult period was the shortest (15.68 d), but it had the highest female adult longevity (31.79 d) and fecundity (162.04 progeny per female). Higher values of net reproductive rate (R_0), intrinsic rate (r), and finite rate (λ) of *A. calandrae* were also recorded for its population reared on *L. serricorne*. Further, the *L. serricorne* host enabled *A. calandrae* females to attain a larger body size (2.59 mm) than those reared on *A. obtectus* (2.44 mm) or *C. chinensis* (2.48 mm). Our results demonstrated that, in comparison with *A. obtectus* and *C. chinensis*, the most suitable host for *A. calandrae* is *L. serricorne*. The implications of our results for biological control of these three host pests are discussed.

1. Introduction

The world population is estimated to reach 9.8 billion by 2050, which arguably imposes a rising demand for food (United Nations 2017). One of the most effective ways to resolve this pressing issue is by reducing post-harvest losses in the storage phase. Yet insect pests can damage stored food products for various reasons, causing economic damage that includes direct losses in terms of the products' weight and indirect losses via the products' contamination (Belda and Riudavets, 2010). As estimated by Sarwar (2015), about one-quarter to one-third of the world's grain crop is lost every year during storage mainly due to infestations from stored product pests. Thus, the importance of managing pests of stored grain is increasingly recognized. The major technique to control such stored grain pests is the application of chemicals. However, the number of chemical products permitted for controlling these pests is declining due to the evolution of insecticide resistance, enhanced environmental concerns, and consumers' mounting uneasiness about their residual effects in food products (Belda and Riudavets, 2010; Kavallieratos et al., 2015; Zhang et al., 2015). However, certain physical control techniques, such as treating food products in warehouses with inert gases, or the use of extreme temperature during storage, may not be suitable or even affordable for small-scale farmers in many developing countries (Niedermayer and Steidle, 2013). These problems suggest biological control could offer an effective alternative for the management of stored grain pests.

Anisopteromalus calandrae (Howard) (Hymenoptera: Pteromalidae) is a well-known idiobiont ectoparasitoid wasp that attacks late-instar larvae and pupae of numerous species of coleopteran pests, developing internally or concealed within the host substrate (Baur et al., 2014; Ghimire and Phillips, 2014). Because it has a wide variety of hosts, a short life history, and high productivity, *A. calandrae* is a promising biological control candidate for stored product pests (Ahmed, 1996).

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Immune function analysis of *LsSd*, a transcription factor of the Hippo signaling pathway, in the cigarette beetle *Lasioderma serricorne*

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The Scalloped (Sd) is a transcription factor that regulates organ size control in the Hippo-signaling pathway. Recent studies have showed that Hippo signaling also functions in the innate immune response. Although the Sd gene has been reported in many insects, their immune functions remain unexplored. In this study, the *LsSd* gene of *Lasioderma serricorne*, with a complete open reading frame that encodes a protein composed of 402 amino acids was identified. *LsSd* was predominantly expressed in early pupae. Tissue-specific analyses revealed that the highest concentrations of *LsSd* were detected in the midgut and brain. At 1–24 h after *Escherichia coli* infection, *LsSd* expression increased substantially. However, *LsSd* expression was downregulated 3–12 h after *Staphylococcus aureus* infection. RNA interference-mediated silencing of the *LsSd* transcript resulted in deformed, considerably smaller, and degenerated wings. Meanwhile, *LsCycE*, *LsDiap1*, and *LsVg*, which are involved in cell proliferation and wing development, were drastically reduced when *LsSd* was depleted. In a survival assay, the *LsSd* knockdown considerably decreased the susceptibility to *S. aureus*, a gram-positive bacterium. In addition, knockdown of *LsSd* remarkably downregulated the transcription of *LsCact* in response to *S. aureus* stimulation, while upregulating the expression of five immune-related genes. Our results provide conclusive proof for the important roles of *LsSd* in the immune response of *L. serricorne*.

KEYWORDS

***Lasioderma serricorne*, *LsSd* gene, Hippo-signaling pathway, wing development, immune response**

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Structural Features and Phylogenetic Implications of Four New Mitogenomes of Caliscelidae (Hemiptera: Fulgoromorpha)

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Klaus H. Hoffmann, Academic Editor

Abstract

To explore the differences in mitogenome variation and phylogenetics among lineages of the Hemiptera superfamily Fulgoroidea, we sequenced four new mitogenomes of Caliscelidae: two species of the genus *Bambusicaliscelis* (Caliscelinae: Caliscelini), namely *Bambusicaliscelis flavus* and *B. fanjingensis*, and two species of the genus *Youtuus* (Ommatidiotinae: Augilini), namely *Youtuus strigatus* and *Y. erythrus*. The four mitogenomes were 15,922–16,640 bp (base pair) in length, with 37 mitochondrial genes and an AT-rich region. Gene content and arrangement were similar to those of most other sequenced hexapod mitogenomes. All protein-coding genes (PCGs) started with a canonical ATN or GTG and ended with TAA or an incomplete stop codon single T. Except for two transfer RNAs (tRNAs; trnS1 and trnV) lacking a dihydrouridine arm in the four species and trnC lacking a dihydrouridine stem in the *Youtuus* species, the remaining tRNAs could fold into canonical cloverleaf secondary structures. Phylogenetic analyses based on sequence data of 13 PCGs in the 28 Fulgoroidea species and two outgroups revealed that Delphacidae was monophyletic with strong support. Our data suggest that Fulgoridae is more ancient than Achilidae. Furthermore, Flatidae, Issidae, and Ricaniidae always cluster to form a sister group to Caliscelidae.

Keywords: planthopper, Caliscelidae, mitogenome, phylogenetics, genomics

1. Introduction

Caliscelidae is a relatively small family within the large and diverse planthopper superfamily Fulgoroidea that comprises approximately 240 described species from 77 genera divided into five tribes (Caliscelini, Peltonotellini, Adenissini, Ommatidiotini, and Augilini) and two subfamilies (Ommatidiotinae and Caliscelinae) [1,2]. These species are extensively distributed worldwide. The genus *Bambusicaliscelis* was established by Chen and Zhang (2011) [3] and belongs to the tribe Caliscelini of the subfamily Caliscelinae. The genus *Youtuus* was established by Gong and Chen (2018) [4] and belongs to the tribe Augilini of the subfamily Ommatidio
These two genera are restrictively distributed in southern China and primarily inhabit b
They directly injure bamboo using their sucking and piercing mouthparts and indirectly
age bamboo by transmitting plant pathogens; this severely hampers bamboo productio

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Microbiome Structure of the Aphid *Myzus persicae* (Sulzer) Is Shaped by Different Solanaceae Plant Diets

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Abstract

Myzus persicae (Sulzer) is an important insect pest in agriculture that has a very broad host range. Previous research has shown that the microbiota of insects has implications for their growth, development, and environmental adaptation. So far, there is little detailed knowledge about the factors that influence and shape the microbiota of aphids. In the present study, we aimed to investigate diet-induced changes in the microbiome of *M. persicae* using high-throughput sequencing of bacterial 16S ribosomal RNA gene fragments in combination with molecular and microbiological experiments. The transfer of aphids to different plants from the Solanaceae family resulted in a substantial decrease in the abundance of the primary symbiont *Buchnera*. In parallel, a substantial increase in the abundance of *Pseudomonas* was observed; it accounted for up to 69.4% of the bacterial community in *M. persicae* guts and the attached bacteriocytes. In addition, we observed negative effects on aphid population dynamics when they were transferred to pepper plants (*Capsicum annuum* L.). The microbiome of this treatment group showed a significantly lower increase in the abundance of *Pseudomonas* when compared with the other Solanaceae plant diets, which might be related to the adaptability of the host to this diet. Molecular quantifications of bacterial genera that were substantially affected by the different diets were implemented as an additional verification of the microbiome-based observations. Complementary experiments with bacteria isolated from aphids that were fed with different plants indicated that nicotine-tolerant strains occur in Solanaceae-fed specimens, but they were not restricted to them. Overall, our mechanistic approach conducted under controlled conditions provided strong indications that the aphid microbiome shows responses to different plant diets. This knowledge could be used in the future to develop environmentally friendly methods for the control of insect pests in agriculture.

Keywords: insect microbiome, Solanaceae, *Nicotiana tabacum*, *Solanum melongena*, *Capsicum annuum*

Introduction

Microorganisms are ubiquitous in the environment and often associated with eukaryoti
During the last decades, it has been shown that microorganisms in plants and animals o
fulfill important functions (Van der Ent et al., 2009; Fuchs, 2010). Individual plants and
often harbor more than 1,000 different microbial species; some of them are crucial dete

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Disruption of the Serine/Threonine Kinase *Akt* Gene Affects Ovarian Development and Fecundity in the Cigarette Beetle, *Lasioderma serricorne*

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Serine/threonine kinase Akt, an important component of the insulin signaling pathway, plays an essential role in many physiological processes. In this study, we identified and characterized an *Akt* gene (designated *LsAkt*) from the cigarette beetle, *Lasioderma serricorne*. *LsAkt* contains a 1614 bp open reading frame encoding a 537 amino acid protein that possesses a conserved pleckstrin homology domain and a serine/threonine kinase domain. The expression of *LsAkt* was high in pupal stages and peaked in day-4 female pupae. In adult tissues, *LsAkt* was highly expressed in the thorax, ovary, and midgut. The expression of *LsAkt* was induced by methoprene or bovine insulin *in vivo*, but significantly decreased by 20-hydroxyecdysone. RNA interference-mediated knockdown of *LsAkt* resulted in severely blocked ovarian development and reduced fecundity and hatchability. The vitellogenin (Vg) content and juvenile hormone (JH) titers of *LsAkt*-depletion beetles were decreased, and expressions of *Vg* and four JH signaling and biosynthetic genes were significantly decreased. Silencing of *LsAkt* reduced the amounts of glucose, glycogen, and trehalose in female adults and affected the expressions of seven key carbohydrate metabolic genes. Taken together, it is inferred that *Akt* implicates in *L. serricorne* reproduction by modification of Vg synthesis, juvenile hormone production and carbohydrate metabolism.

Keywords: serine/threonine kinase, cigarette beetle, insulin, reproduction, juvenile hormone, carbohydrate metabolism

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INTRODUCTION

Insulins are multifunctional peptide hormones and consist of insulin-like peptide (ILP), insulin-like growth factor (IGF), and relaxin (Wu and Brown, 2006). Insulin structure, function, and signal transduction are evolutionary conserved in both vertebrates and invertebrates (Taniguchi et al., 2006; Das and Dobens, 2015). In insects, ILPs specifically activate the insulin receptors, which in turn, transmit a signal via the phosphoinostide 3-kinase (PI3K)-serine/threonine kinase (Akt) pathway or the mitogen-activated protein kinase (MAPK) pathway. This mediates diverse

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Endemism Patterns of Planthoppers (Fulgoroidea) in China

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Studies on endemism are always of high interest in biogeography and contribute to better understanding of the evolution of species and making conservation plans. The present study aimed to investigate the endemism patterns of planthoppers in China by delimiting centers of endemism and areas of endemism. We collected 6,907 spatial distribution records for 860 endemic planthopper species from various resources. Centers of endemism were identified using weighted endemism values at 1° grid size. Parsimony analysis of endemicity and endemicity analysis were employed to detect areas of endemism at 1°, 1.5°, and 2° grid sizes. Six centers of endemism located in mountainous areas were identified: Taiwan Island, Hainan Island, eastern Yungui Plateau, Wuyi Mountains, western Qinling Mountains, and western Yunnan. We also delimited six areas of endemism, which were generally consistent with centers of endemism. Our findings demonstrated that mountainous areas have an essential role in facilitating the high level of endemism and formation of areas of endemism in planthoppers through the combined effects of complex topography, a long-term stable environment, and geological events. Dispersal ability and distribution of host plants also have important effects on the patterns of planthoppers' endemism.

Keywords: areas of endemism, biogeography, centers of endemism, mountainous areas, planthoppers

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INTRODUCTION

The geographical distribution of endemic species (i.e., restriction of a species to a particular area) represents the highest degree of historical and ecological imprint of all biological entities (Casazza et al., 2008). Moreover, endemic areas have been generally recognized as priority areas for biodiversity conservation plans (Myers et al., 2000; Lamoreux et al., 2006; Huang et al., 2010, 2016; Gomes-da-Silva et al., 2017; Zhao et al., 2020a). Therefore, studies related to patterns of endemism have always been a central topic of biogeography and biodiversity conservation (Laffan and Crisp, 2003; Orme et al., 2005; Posadas et al., 2006; Sandel et al., 2011; Huang et al., 2012; Feng et al., 2016; Li et al., 2017).

Studies on the spatial patterns of endemics often delimit the main distribution areas, and these areas are frequently described as centers of endemism (CoEs) and areas of endemism (AoEs). Although the drivers causing formation of CoEs and AoEs may show similar ecological or

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RESEARCH ARTICLE

Fitness of fall armyworm, *Spodoptera frugiperda* to three solanaceous vegetables

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Abstract

The fall armyworm (FAW), *Spodoptera frugiperda* Smith (Lepidoptera: Noctuidae) is an important agricultural pest that invaded China in the middle of December 2018. As a polyphagous pest, FAW is identified as a serious threat to agricultural production and food security in China. Pepper (*Capsicum annuum* L.), tomato (*Solanum lycopersicum* Mill.) and eggplant (*Solanum melongena* L.) are three of dominant solanaceous vegetables of this country. To our knowledge, the effects of these plants on the performances of FAW have not been well studied. In this study we assessed the fitness of this pest to these three plants. Results showed that FAW can complete its life cycle when fed with tomato and pepper, but not on eggplant. The population parameters of FAW fed with maize (*Zea mays* L.) and the three solanaceous vegetables were compared using the age-stage two-sex life table method. Developmental duration was significantly different in the larval stage, but not in the pupae stage. FAW fed with pepper had the longest pre-adult period (41.73 d) and the lightest pupal weight (0.1134 g); the survival rate was lower than FAW fed with tomato. Significant differences were observed in the mean fecundity of female, with the highest (943.95 eggs) laid by FAW fed with tomato. FAW had the shortest mean generation time (T), the highest intrinsic rate of increase (r) and finite rate of increase (λ) on maize, and the highest net reproductive rate (R_0) on tomato. Overall, FAW fitness on the three solanaceous vegetables was: tomato>pepper>eggplant. This study provides the foundation for further assessment of FAW risk to solanaceous vegetables and for establishing corresponding control strategies in China.

Keywords: *Spodoptera frugiperda*, age-stage two-sex life table, adaptability, tomato, pepper, eggplant

1. Introduction

The fall armyworm (FAW), *Spodoptera frugiperda* Smith (Lepidoptera: Noctuidae) is a polyphagous pest native to tropical and subtropical America (Sparks 1979; Todd and Poole *et al.* 1980; Martinelli *et al.* 2006). In 2016, FAW invaded Nigeria, Ghana and other sub-Saharan African

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A Chromosome-Level Genome Assembly of *Ephestia elutella* (Hübner, 1796) (Lepidoptera: Pyralidae)

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Abstract

The moth *Ephestia elutella* (Hübner), is a storage pest that feeds on tobacco, cacao beans, cereals, dried fruits, and nuts. We generated a chromosome-level genome assembly containing 576.94 Mb using Nanopore long reads (approximately 130×) and Hi-C data (approximately 134×). The final assembly contained 804 scaffolds, with an N50 length of 19.00 Mb, and 94.96% (547.89 Mb) of the assembly was anchored into 31 pseudochromosomes. We masked 58.12% (335.32 Mb) of the genome as repetitive elements, identified 727 noncoding RNAs, and predicted 15,637 protein-coding genes. Gene family evolution and functional enrichment analyses revealed significantly expanded gene families primarily involved in digestion, detoxification, and chemosensation. Strong chromosomal syntenic relationships were also observed among *E. elutella*, silkworm, and tobacco cutworm. This study could provide a valuable genomic basis for better understanding the biology of *E. elutella*.

Key words: Phycitinae, genome annotation, comparative genomics, gene family evolution, synteny.

Significance

Genomic resources for the important storage pest *Ephestia elutella* are essentially nonexistent at present, making it difficult to understand the genomic architecture underlying this species' behavior, food preferences, and potential susceptibilities to various forms of management. In this study, we generated a high-quality, chromosome-level genome sequence for *E. elutella*, and performed an analysis of gene family evolution and synteny, respectively. Our work provides fundamental and valuable data for better understanding the tobacco moth and can contribute to improved moth management.

Introduction

Moths are one of the major super-radiations of Lepidoptera, comprising near 160,000 extant species in the world, which play key roles in many terrestrial systems. A total of 149 lepidopteran genomes were reported in NCBI database. *Ephestia elutella* (Hübner) (Lepidoptera: Pyralidae), the cacao moth, tobacco moth, or warehouse moth, is an important storage pest worldwide that preferring to feed on dried materials of plant origin, such as cereal products, cacao beans, dried fruits, and nuts (Athanassiou et al. 2018; Trematerra 2020). Current methods used to control *E. elutella* infestation in tobacco storage primarily include fumigation, using phosphine (PH_3), and contact insecticides (Ou et al. 2021). Until now, the whole genome of *E. elutella* has not been sequenced. High-quality moth genomes are important genetic resources for the study of pest biology, evolution, and pest control. Thus far, only four pyralid genomes have been published on NCBI (accessed April 25, 2021), including *Endotricha flammealis*, *Galleria mellonella*, *Plodia interpunctella*, and *Amyelois transitella*. Their genome sizes range from 382 Mb to 483 Mb. However, none of the chromosome-level assemblies for these species are available to the public, making this the first chromosome-level

Chromosome-Level Genome Assembly of *Nephotettix cincticeps* (Uhler, 1896) (Hemiptera: Cicadellidae: Deltocephalinae)

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Abstract

The green rice leafhopper, *Nephotettix cincticeps* (Uhler), is an important rice pest and a vector of the rice dwarf virus in Asia. Here, we produced a high-quality chromosome-level genome assembly of 753.23 Mb using PacBio (~110×) and Hi-C data (~94×). It contained 163 scaffolds and 950 contigs, whose scaffold/contig N50 lengths reached 85.36/2.57 Mb. And 731.19 Mb (97.07%) of the assembly was anchored into eight pseudochromosomes. Genome completeness was attained to 97.0% according to the insect reference Benchmarking Universal Single-Copy Orthologs (BUSCO) gene set ($n = 1,367$). We masked 347.10 Mb (46.08%) of the genome as repetitive elements. Nine hundred sixty-two noncoding RNAs were identified and 14,337 protein-coding genes were predicted. We also assigned GO term and KEGG pathway annotations for 10,049 and 9,251 genes, respectively. Significantly expanded gene families were primarily involved in immunity, cuticle, digestion, detoxification, and embryonic development. This study provided a crucial genomic resource for better understanding on the biology and evolution in family Cicadellidae.

Key words: Chiasmini, green rice leafhopper, insect genomics, comparative genomics, genome annotation, gene family evolution.

Significance

Most species of leafhoppers (Hemiptera: Cicadellidae) are important pests of food crops. A high-quality genome could play a key role in appreciating pest biology, evolution, and devising pest control strategies. Right now, only two cicadellid genomes are currently available, including *Homalodisca vitripennis* and *Empoasca onukii*. In this study, the genome of the green rice leafhopper, *Nephotettix cincticeps*, was sequenced and analyzed. The chromosome-level genome of *Nephotettix cincticeps* provides a valuable resource for studying the phylogeny and biology of leafhoppers.

Introduction

Leafhoppers (Auchenorrhyncha: Cicadellidae) are currently the largest family of sap-sucking herbivores and comprise the most abundant known vectors of plant pathogens of any insect family in the Hemiptera (Dietrich 2013). Many species in Cicadellidae feed on economically significant plants and are thus considered as important pests, mostly because of injuries incurred to plants from direct feeding injury. And some species can transmit plant pathogens (Weintraub and Beanland 2006). The green rice leafhopper (GRLH), *Nephotettix cincticeps* (Uhler) (Cicadellidae: Deltocephalinae), is a potent pest of rice. It is widely distributed among rice-producing areas in Asia, and able to transmit rice viral pathogens, notably the rice dwarf virus, in a

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Role of *SfJHAMT* and *SfFAMeT* in the reproductive regulation of *Sogatella furcifera* and its expression under insecticide stress

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ABSTRACT

The isoprene branching pathway is a unique downstream synthesis pathway of juvenile hormone (JH) in arthropods, which plays an important role in the growth, development, and reproduction of insects. Juvenile hormone acid *O*-methyltransferase (JHAMT) and farnesoic acid *O*-methyltransferase (FAMeT) are two key proteins that are regulated in the isoprene branching pathway. Based on the available transcriptomic and genomic data of *Sogatella furcifera*, full-length cDNAs of *SfJHAMT* and *SfFAMeT* were identified. In vitro injection of dsRNA targeted to silence *SfJHAMT* and *SfFAMeT* inhibited the fecundity, ovarian development, and transcription levels of *SfKr-h1* and *SfVg* significantly. Of note, The transcription levels of *SfJHAMT* and *SfFAMeT* are regulated mutually; i.e., silencing of *SfJHAMT* causes an increase in the *SfFAMeT* transcription level and vice versa, and the negative effect of simultaneous silencing on reproduction is greater. The results revealed a coordinated effect of *SfJHAMT* and *SfFAMeT* on the reproductive capabilities of *S. furcifera*. Furthermore, a JH analog (methoprene) partially rescued the negative effect of simultaneous silencing by *SfJHAMT* and *SfFAMeT* on reproduction. In addition, the expression profile analysis after insecticide stress showed that triazophos (LC_{25}) can induce the transcription of *SfMet* and *SfKr-h1* to promote JH signal transduction, which affects the transcription of *SfVg* and ultimately promotes the reproduction of *S. furcifera*. The results of the present study lay a foundation to further explain the isoprene branch pathway function in insect reproduction and can open up new avenues for sustainable pest control while expanding the current understanding of molecular mechanisms through which insecticides stimulate reproduction and lead to pest resurgence.

1. Introduction

Juvenile hormone (JH) is a sesquiterpenoid compound that is synthesized in the insect corpora allata and plays important regulatory roles in the physiological processes of insect growth and reproduction. The biosynthesis of JH primarily involves two pathways: the upstream mevalonate pathway, which is common to the biosynthesis of JH and cholesterol/sterols, and the isoprene branch pathway, which is unique to arthropods (Bellés et al., 2005). The isoprene branch pathway largely includes the following reactions: farnesyl pyrophosphate → farnesol → farnesal → farnesic acid (FA) → JH (Fig. S1). The FA → JH reaction involves one of two branched pathways: one involving the participation of farnesoic acid *O*-methyltransferase (FAMeT) (Goldstein and Brown, 1990) and the second involving the participation of juvenile hormone acid *O*-methyltransferase (JHAMT, Fig. S1) (Daimon et al., 2012).

The *JHAMT* and *FAMeT* genes encode two important enzymes, which are essential for the growth and reproduction of insects, in the isoprene branch pathway (Shinoda and Itoyama, 2003; Burtenshaw et al., 2008). For example, silencing of the *TcJHAMT3* gene in the larval stage of *Tribolium castaneum* resulted in precocious larval–pupal metamorphosis (Minakuchi et al., 2008), whereas silencing of the *FAMeT* gene in the parental female or male *Ceratitis capitata* significantly reduced fecundity of the female offspring (Vannini et al., 2010). Although *JHAMT* and *FAMeT* functions in insect reproduction have been relatively elucidated,

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GBE

Chromosomal-Level Genome Assembly of a True Bug, *Aspongopus chinensis* Dallas, 1851 (Hemiptera: Dinidoridae)

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Abstract

The true bug, *Aspongopus chinensis* Dallas, 1851 (Hemiptera: Dinidoridae), is a fascinating insect with prolonged diapause and medicinal properties but also a notorious pest. However, because of the lack of genomic resources, an in-depth understanding of its biological characteristics is lacking. Here, we report the first genome assembly of *A. chinensis* anchored to 10 pseudochromosomes, which was achieved by combining PacBio long reads and Hi-C sequencing data. This chromosome-level genome assembly was 1.55 Gb in size with a scaffold N50 of 156 Mb. The benchmarking universal single-copy ortholog (BUSCO) analysis of the assembly captured 96.6% of the BUSCO genes. A total of 686,888,052 bp of repeat sequences, 18,511 protein-coding genes, and 1,749 noncoding RNAs were annotated. By comparing the *A. chinensis* genome with that of 8 homologous insects and 2 model organisms, 213 rapidly evolving gene families were identified, including 83 expanded and 130 contracted gene families. The functional enrichment of Gene Ontology and KEGG pathways showed that the significantly expanded gene families were primarily involved in metabolism, immunity, detoxification, and DNA/RNA replication associated with stress responses. The data reported here shed light on the ecological adaptation of *A. chinensis* and further expanded our understanding of true bug evolution in general.

Key words: PacBio sequence, whole-genome sequence, genome annotation, gene family evolution, Hi-C.

Significance

True bugs (Hemiptera: Heteroptera) are vital insect pests that affect public health and agronomy, yet, the whole-genome assemblies of only five species are available. Here, we assembled a complete draft genome of the true bug *Aspongopus chinensis* using the PacBio sequencing technology and used Hi-C sequences to assist chromosomal assembly. The whole-genome assembly produced in this study could be a useful genomic resource for understanding the evolutionary biology and biological characteristics of true bugs in general and of *A. chinensis* in particular. This assembly can be used to develop effective pest control strategies.

Introduction

Hemiptera is an insect order that is distributed across the world and contains >8,000 nonholometabolous species (Capinera 2008). Hemiptera is classified into five suborders: Sternorrhyncha (aphids, scale insects, psyllids, and whiteflies), Fulgoromorpha (planthoppers), Cicadomoirpha (leafhoppers, cicadas, and spittlebugs), Coleorrhyncha (moss bugs), and Heteroptera (true bugs) (Wang et al. 2019). True bugs are sap-sucking insects that consume food from sources ranging from animals to plants (Sparks et al. 2020). *Aspongopus chinensis* Dallas, 1851 (supplementary fig. S1), a true bug species mainly distributed in Eastern South Asia, is a polyphagous insect that has a prolonged diapause (Luo et al. 2012; Li et

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Ecology and Evolution Open Access WILEY

RESEARCH ARTICLE

Two sexes respond equally to food restriction in a sexually dimorphic but not body mass dimorphic jumping spider

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Abstract

Natural selection favors animals that evolve developmental and behavioral responses that buffer the negative effects of food restrictions. These buffering responses vary both between species and within species. Many studies have shown sex-specific responses to environmental changes, usually in species with sexual size dimorphism (SSD), less found in species with weak or no SSD, which suggests that sizes of different sexes are experiencing different selections. However, previous studies usually investigated development and behavior separately, and the balanced situation where males and females of sexually dimorphic species respond in the same way to food restriction remains little known. Here, we investigated this in *Phintelloides versicolor* (Salticidae) that presents sexual dimorphism in color and shape but weak SSD. We examined whether food restriction induced the same responses in males and females in development duration, adult body size and weight, daily time allocated to foraging, and hunting. We found food restriction induced similar responses in both sexes: both exhibited longer development duration, smaller adult body size and weight, higher probability of staying outside nests and noticing prey immediately, and higher hunting success. However, there were sexual differences regardless of food condition: females showed faster development, smaller adult body size, higher probability of staying outside of nests, and higher hunting success. These indicated the differential selection on male and female sizes of *P. versicolor* could be under a balanced situation, where males and females show equal developmental and behavioral plasticity to environmental constraints.

KEYWORDS

fecundity selection, life history traits, sex role, sex-specific response, sexual difference

1 | INTRODUCTION

Food resources are indispensable to survival and reproduction for animals. Food restriction has effects on a series of life history traits, including development duration (Berrigan & Charnov, 1994; George et al., 2002; Nylin & Gotthard, 1998; Uhl et al., 2004), daily time allocated to foraging (Lenski, 1984) and hunting behavior (Aguilar-Argüello & García-Chávez, 2015). However, in the wild, animals usually experience a lack of food resources, which favors the evolution of adaptive strategies that mitigate the effects of food or nutrition

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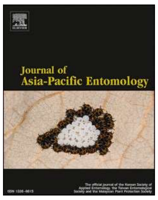

Full length article

Cloning and differential expression of three heat shock protein genes associated with thermal stress from the wolf spider *Pardosa pseudoannulata* (Araneae: Lycosidae)

Liang-Yu Sun, Jing Liu, Qin Li, Di Fu, Jia-Yun Zhu, Jian-Jun Guo, Rong Xiao *, Dao-Chao Jin *

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ABSTRACT

Pardosa pseudoannulata is the main predatory natural enemy of crop pests in a paddy ecosystem. When *P. pseudoannulata* is exposed to unfavorable temperature conditions, the response of heat shock proteins could resist the damage, and is therefore, conducive to the organism's rapid adaptation to the surrounding stress environment. In this study, we explored the roles of *hsp70* and *hsp90* genes in response to heat stress, using the rapid amplification of cDNA ends technique and cloned full-length cDNAs of *Pphsp70, Pphsp83*, and *Pphsp90*. The mRNA expression levels of the three genes under different temperature stresses (25, 28, 31, 34, 37, 40, and 43 °C) and with different duration stresses (4, 8, 12, 16, and 20 h) were analyzed by quantitative real-time polymerase chain reaction. The full-length cDNA of *Pphsp70*, *Pphsp83*, and *Pphsp90* was 2331 base pair (bp), 2466 bp, and 2663 bp, respectively. Phylogenetic analysis of amino acid sequences of *Pphsp70*, *Pphsp83*, and *Pphsp90* showed that the sequences had high homology with that of other spiders. The mRNA expression of all three genes was extremely significantly up-regulated at 43 °C. Moreover at 43 °C, the expression of all three genes in both female and male spiders at the duration of 4 h was the highest compared to that of other stress duration groups. Therefore, it can be inferred that the three genes of *P. pseudoannulata* play a crucial protective role in resistance in a high-temperature environment.

Introduction

Rice is one of the food crops on which people depend for survival. China's rice yield ranks the first in the world (Lou et al., 2013). However, the rice brown planthopper, rice borers, and other insect pests are factors that affect the rice yield (Kamolsukyeunyong et al., 2019). There are various rice paddy spider species with strong fecundity and adaptability, which could attack pests in most agricultural ecosystem of Asia (Heong et al., 1991; Meng et al., 2016). As the main predatory natural enemies, also known as "guardians of rice fields," spiders play an irreplaceable role in biological control (Huang et al., 2018). *Pardosa pseudoannulata* (Bösenberg *et* Strand), belonging to family Lycosidae, order Araneae, is an important natural predatory enemy of rice pests (Wang, 2007). It is a dominant species with favorable characteristics such as active, predatory, strong reproductivity, and stress resistant (Wang and Shi, 2002), and tends to survive in a relatively humid environment (Li et al., 2016).

Temperature is a crucial environmental factor affecting the growth, development, survival, and distribution of spiders in paddy fields (Zhao, 2001; Gao et al., 2011). *P. pseudoannulata*, like other arthropods, is heterothermic, that is, the body temperature varies with the temperature of its environment. Therefore, the external environment temperature can directly affect the metabolic rate of the spider, thus affecting its growth, reproduction rate, and life vitality. Thus, environmental temperature is an important factor affecting the survival of *P. pseudoannulata* (Li and Jackson, 1996; Zhao, 2001).

The favorable temperature range for the growth of *P. pseudoannulata* is 20–30 °C with relative humidity conditions of 75–85% (Sun et al., 2007). However, in the south of China, the temperature often exceeds 40 °C in summer (Xiao et al., 2016). Thus, *P. pseudoannulata* in the rice field system are often subjected to extreme temperature stresses. When spiders are exposed to higher temperatures, for their survival, heat shock proteins (HSPs) are rapidly synthesized in their cells as a response. Indeed, high temperature-induced expression of HSPs is one of the

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ORIGINAL RESEARCH

Ecology and Evolution Open Access WILEY

Structural features of the mitogenome of the leafhopper genus *Cladolidia* (Hemiptera: Cicadellidae: Coelidiinae) and phylogenetic implications in Cicadellidae

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Abstract

The first two complete mitogenomes of the leafhopper genus *Cladolidia* (*C. biungulata* and *C. robusta*) were sequenced and annotated to further explore the phylogeny of *Cladolidia*. Both the newly sequenced mitogenomes have a typical circular structure, with lengths of 15,247 and 15,376 bp and A + T contents of 78.2% and 78%, respectively. We identified a highly conserved genome organization in the two *Cladolidia* spp. through comparative analysis that included the following assessments: genome content, gene order, nucleotide composition, codon usage, amino acid composition, and tRNA secondary structure. Moreover, we detected the base heterogeneity of Cicadellidae mitogenomic data and constructed phylogenetic trees using the nucleotide alignments of 12 subfamilies of 58 leafhopper species. We noted a weak heterogeneity in the base composition among the Cicadellidae mitogenomes. Phylogenetic analyses showed that the monophyly of each subfamily was generally well supported in the family Cicadellidae; the main topology was as follows: (Deltocephalinae + (Treehoppers + ((Megophthalminae + (Macropsinae + (Hylicinae + (Coelidiinae +Iassinae)) + (Idiocerinae + (Cicadellinae + (Typhlocybinae + (Mileewinae + (Evacanthinae +Ledrinae)))))))))). Within Coelidiinae, phylogenetic analyses revealed that *C. biungulata* and *C. robusta* belong to Coelidiinae and the monophyly of *Cladolidia* is well supported. In addition, on the basis of complete mitogenome phylogenetic analysis and the comparison of morphological characteristics, we further confirm the genus *Olidiana* as a paraphyletic group, suggesting that the genus may need taxonomic revisions.

KEYWORDS

Cicadellidae, heterogeneity, leafhopper, mitochondrial phylogenomics, structure

1 | INTRODUCTION

In contrast to nuclear DNA, the mitogenome has a maternal mode of inheritance and is usually minimally recombinogenic; it carries genes with comparatively rapid evolutionary rates (Ballard & Whitlock, 2004; Cameron, 2014; Moritz & Brown, 1987; Wolstenholme, 1992). The entire mitogenome is a valuable source of extensive information compared with single genes. Moreover, it exhibits genome-level characteristics, including gene content, base composition, gene organization, and gene secondary structure.

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Article

Different Host Plants Distinctly Influence the Feeding Ability of the Brown Citrus Aphid *Toxoptera citricida*

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Simple Summary: The brown citrus aphid, *Toxoptera citricida,* is an important pest of citrus and causes serious damage in the main production areas. Host plant resistance is an environmentally friendly method to manage aphid infestations and is becoming increasingly important as aphids develop greater resistance to insecticides. The aim of this study was to assess *T. citricida* resistance on seven widespread and common hosts using electropenetrography combined with a population development test. We showed that the feeding parameters of the brown citrus aphid differed significantly depending on the host plants. *Toxoptera citricida* spent more time in the pathway stage and less time in the phloem stage on Eureka, while the opposite was observed on Yuzu and Rough Lemon. Measurements of population development of aphids showed that on the Eureka, aphids developed more slowly. Our data suggest that different host plants distinctly influence the ability of *T. citricida* to feed. The brown citrus aphid did not prefer to feed on Eureka Lemon compared to the other six host plants.

Abstract: Piercing–sucking insects are important crop pests, and an understanding of their feeding behavior and population development plays a crucial role in studying insect population dynamics and crop resistance. In our study, we examined the probing behavior of the brown citrus aphid, *Toxoptera citricida*, using electropenetrography and assessed its population development after 8 days on seven host plants: Yuzu, *Citrus junos* Sieb. ex Tanaka; Rough Lemon, *C. jambhiri* Lush.; 'Luofu' kumquat, *Fortunella margarita* Swingle; 'Olinda' valencia orange, *C. sinensis* (L.) Osbeck; 'Yanxiwanlu' Ponkan, *C. reticulata* Blanco; 'Rohde Red' valencia orange, *C. sinensis*; and 'Eureka' lemon, *C. limon* (L.) Osbeck. The results demonstrated that probing by the brown citrus aphid differed significantly according to the target hosts. *Toxoptera citricida* produced significantly more pathway activities on Eureka than on Rough Lemon and Yuzu. *Toxoptera citricida* spent more time from the first probe to first salivation into phloem sieve elements on Eureka compared to Yuzu. In addition, the total duration of ingestion from sieve cells of each aphid in the phloem-feeding phase was shortest on Eureka, and this was significantly shorter than that on Yuzu, Rough Lemon, Luofu, and Olinda. The population number of *T. citricida* on Eureka after 8 days was significantly lower than that on the other hosts. Overall, Eureka was found to have obvious resistance to *T. citricida*, whereas Yuzu and Rough Lemon were susceptible host plants. These results provide a theoretical basis for exploring aphid-resistant fruit tree resources using resistant varieties.

Keywords: *Toxoptera citricida*; electropenetrography; host plants; feeding behavior; plant resistance

Citation: Zhao, R.; Wu, C.; He, Y.; Yu, C.; Liu, J.; Li, T.; Zhou, C.; Chen, W. Different Host Plants Distinctly Influence the Feeding Ability of the Brown Citrus Aphid *Toxoptera citricida*. *Insects* **2021**, *12*, 864. https://doi.org/10.3390/insects12100864

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Article

Does Larval Rearing Diet Lead to Premating Isolation in *Spodoptera litura* (Fabricius) (Lepidoptera: Noctuidae)?

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Simple Summary: *Spodoptera litura* Fabricius (Lepidoptera: Noctuidae) is a serious polyphagous pest. Most studies focus on the effects of natural hosts on *S. litura*. However, progressively more laboratory studies *S. litura* involve feeding the larvae with an artificial diet. We compared the life performance and observed mating choice of *S. litura* reared on tobacco, Chinese cabbage, and an artificial diet. The results revealed that diet had a significant effect on the duration of each stage of development. In the multiple-choice test with individual males consuming tobacco, Chinese cabbage, or an artificial diet, females fed on the artificial diet preferred to mate with males that were fed on the same diet and rarely mated with males fed on tobacco or Chinese cabbage. We suggest that the diet of *S. litura* has a potential impact on mate choice and sexual isolation.

Abstract: Host plant preference during the larval stage may help shape not only phenotypic plasticity but also behavioral isolation. We assessed the effects of diet on population parameters and mate choice in *Spodoptera litura*. We raised larvae fed on tobacco, Chinese cabbage, or an artificial diet, and we observed the shortest developmental time and highest fecundity in individuals fed the artificial diet. However, survival rates were higher for larvae on either of the natural diets. Population parameters including intrinsic rate of increase and finite rate of increase were significantly higher with the artificial diet, but this diet led to a lower mean generation time. Copulation duration, copulation time, and number of eggs reared significantly differed between diets. In terms of mate choice, females on the artificial diet rarely mated with males fed on a natural host. Our results support the hypothesis that different diets may promote behavioral isolation, affecting mating outcomes. Thus, findings for populations fed an artificial diet may not reflect findings for populations in the field.

Keywords: diet; mate choice; assortative mating; *Spodoptera litura*; life table

Citation: Di, X.-Y.; Yan, B.; Wu, C.-X.; Yu, X.-F.; Liu, J.-F.; Yang, M.-F. Does Larval Rearing Diet Lead to Premating Isolation in *Spodoptera litura* (Fabricius) (Lepidoptera: Noctuidae)? *Insects* **2021**, *12*, 203. https://doi.org/10.3390/insects12030203

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1. Introduction

Selection for behavioral differences in insect species impacts the evolution of host plant specificity [1], and the behavioral choices of those insects reflects evolutionary adaptation [2]. Different host plants provide different levels of nutritional quality for different insect species [3], and they can have cascading effects on their life histories [4] including fitness, growth, and fecundity [5]. This phenomenon is common in polyphagous herbivores [6,7] such as cotton bollworms, which exhibit significant differences in population development among the various host plants [8].

An increasing number of studies are using insects reared on artificial diets, which can affect their life history traits [9,10]. For example, *Bactrocera cucurbitae* (Coquillett) larvae fed on an artificial diet produce significantly fewer ovarioles than individuals in natural host

insects

Article

Characterization of Two Complete Mitochondrial Genomes of *Atkinsoniella* (Hemiptera: Cicadellidae: Cicadellinae) and the Phylogenetic Implications

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Simple Summary: *Atkinsoniella* is a large genus of almost 99 species across the world within the subfamily Cicadellinae, which is a large subfamily, comprising more than 2400 species of approximately 330 genera. Some of the Cicadellinae distributed worldwide are known as important agricultural pests. To better understand the mitogenomic characteristics of the genus *Atkinsoniella* and reveal phylogenetic relationships, the complete mitochondrial genomes of *Atkinsoniella grahami* and *Atkinsoniella xanthonota* were sequenced and comparatively analyzed in this study. The mitogenomes of these two *Atkinsoniella* species were found to be highly conserved, similarly to other Cicadellidae, except for the secondary structure of trnaS1, which formed a loop with the dihydrouridine (DHC) arm. This phenomenon has also been observed in other insect mitogenomes. Phylogenetic analyses, based on mitogenomes using both the maximum likelihood (ML) and Bayesian inference (BI) methods of three datasets, supported the monophyly of Cicadellinae, as well as the other subfamilies, and produced a well-resolved framework of Cicadellidae and valuable data for the phylogenetic study of Cicadellinae.

Abstract: The complete mitochondrial genomes of *Atkinsoniella grahami* and *Atkinsoniella xanthonota* were sequenced. The results showed that the mitogenomes of these two species are 15,621 and 15,895 bp in length, with A+T contents of 78.6% and 78.4%, respectively. Both mitogenomes contain 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (rRNAs), and a control region (CR). For all PCGs, a standard start ATN codon (ATT, ATG, or ATA) was found at the initiation site, except for *ATP8*, for which translation is initiated with a TTG codon. All PCGs terminate with a complete TAA or TAG stop codon, except for *COX2*, which terminates with an incomplete stop codon T. All tRNAs have the typical cloverleaf secondary structure, except for *trnS*, which has a reduced dihydrouridine arm. Furthermore, these phylogenetic analyses were reconstructed based on 13 PCGs and two rRNA genes of 73 mitochondrial genome sequences, with both the maximum likelihood (ML) and Bayesian inference (BI) methods. The obtained mitogenome sequences in this study will promote research into the classification, population genetics, and evolution of Cicadellinae insects in the future.

Keywords: leafhopper; mitogenome; *Atkinsoniella*; phylogeny

Citation: Jiang, Y.; Li, H.-X.; Yu, X.-F.; Yang, M.-F. Characterization of Two Complete Mitochondrial Genomes of *Atkinsoniella* (Hemiptera: Cicadellidae: Cicadellinae) and the Phylogenetic Implications. *Insects* **2021**, *12*, 338. https://doi.org/10.3390/insects12040338

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1. Introduction

The leafhopper subfamily Cicadellinae is distributed worldwide and contains around 2400 species, represented by approximately 330 genera [1]. In China, 26 genera and 315 species of Cicadellinae have been recorded [2]. Some Cicadellinae insects are of considerable economic importance as they feed on sap in the xylem of woody and herbaceous plants and, via this process, are able to transmit phytopathogenic bacterium and plant viruses to crops, ornamental plants, and weeds [3–6]. Accurate identification of insects

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Article

Life Table and Preference Choice of *Frankliniella occidentalis* (Thysanoptera: Thripidae) for Kidney Bean Plants Treated by Exogenous Calcium

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Simple Summary: Western flower thrips, *Frankliniella occidentalis*, is an invasive key pest that damages vegetables and ornamentals worldwide. The activation of induced resistance by chemicals may provide a simple and feasible way of achieving improvement of resistance to stress in crop plants, which is an important technology for the development of sustainable agriculture. Calcium (Ca) is an essential element for plants; numerous studies have shown that Ca can confer crop plants with resistance to abiotic and biotic stresses. For the first time, we report the negative effects of exogenous Ca on kidney bean plants in relation to the performance of *F. occidentalis*, including a reduced preference of thrips. Therefore, Ca could potentially be used to control *F. occidentalis*.

Abstract: Exogenous calcium (Ca) has been used to induce host plant resistance in response to abiotic and biotic stresses, including from thrips attack. The aim of this study was to determine whether exogenously applied Ca affects the performance of *Frankliniella occidentalis*. We assessed the development time, total longevity, reproduction, and population parameters of *F. occidentalis*, and its preference choice on Ca-treated or untreated control kidney bean plants under laboratory conditions. The results showed that *F. occidentalis* fed on Ca-treated leaves had a longer developmental time but lower longevity (female and male) and fecundity than *F. occidentalis* fed on control leaves. Population parameters, including the intrinsic rate of increase (r), finite rate of increase (λ), and net reproductive rate (R_0), were all found higher in control leaves than in Ca-treated leaves, and the mean generation time (T) was shorter. In preference choices, the number of thrips on control plants was higher than the number of thrips on Ca-treated kidney bean plants. Overall, our results indicated that exogenous Ca pretreatment on kidney bean plants affected the life history and preference choice of *F. occidentalis*, suggesting Ca might be used as a promising elicitor of inducible plant defense against thrips.

Keywords: *Frankliniella occidentalis*; exogenous calcium; inducible plant defense; life table; preference choice

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Citation: Zeng, G.; Zhi, J.-R.; Ye, M.; Xie, W.; Zhang, T.; Li, D.-Y.; Liu, L.; Wu, X.-B.; Cao, Y. Life Table and Preference Choice of *Frankliniella occidentalis* (Thysanoptera: Thripidae) for Kidney Bean Plants Treated by Exogenous Calcium. *Insects* **2021**, *12*, 838. https://doi.org/10.3390/insects12090838

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1. Introduction

Frankliniella occidentalis (Pergande) (Thysanoptera: Thripidae) is a significant agricultural invasive pest worldwide due to its broad host range and rapid reproduction, and it poses a great threat to crops [1,2]. Thrips feeding results in damaged areas with a silvery appearance because of thrips piercing and sucking plant leaves and the increased possibility of destructive disease that causes serious yield losses [3,4]. In China, *F. occidentalis* has quickly spread to more than 10 provinces in the last 10 years since its initial occurrence

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Article

Functional Response and Predation Potential of *Carabus elysii* Adults against the Terrestrial Slug *Agriolimax agrestis*

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Simple Summary: *Agriolimax agrestis* is one of the most important cash crop pests in China, widely affecting tobacco, vegetables, edible mushrooms, and other crops. Not only does it cause direct damage to plants but it also spreads bacteria that are harmful to plants and humans. Currently, the control of *A. agrestis* relies mainly on chemical agents; however, the heavy application of chemicals often leads to ecological damage. In this study, using *Carabus elysii* as a natural enemy, the predatory ability of adult *C. elysii* on *A. agrestis* was assessed under indoor conditions for the first time. The results show that *C. elysii* adults have a strong predatory ability on different sizes of slugs, especially juvenile slugs, and the female adults have a better predatory ability than the male adults. In general, *C. elysii* has strong potential to control *A. agrestis* and can be used as an effective control measure.

Abstract: Terrestrial slugs are a prominent agricultural pest worldwide. To mitigate the negative effects of chemical pest control, biological control involves the use of natural enemies to reduce the impact of target pests. Numerous insects are natural predators of slugs. This study evaluated potential of the predatory species, *Carabus elysii* Thomson (Coleoptera: Carabidae) to biologically control the terrestrial slug, *Agriolimax agrestis*. Laboratory experiments were conducted to investigate the functional response, searching efficiency, and interference effect of female and male *C. elysii* adults regarding adult, immature, and juvenile *A. agrestis* individuals. The results show that both female and male ground beetle adults are functionally capable of preying on different sizes of terrestrial slugs. *C. elysii* exhibited Holling type II functional responses when preying on *A. agrestis*. The maximum daily prey consumption was 35.5 juveniles, 25.1 immatures, and 17.1 adults for adult females and 26.9 juveniles, 20.3 immatures, and 11.6 adults for adult males. The searching efficiency of female *C. elysii* adults regarding *A. agrestis* was always higher than that of male adults for identical ages and densities of *A. agrestis*. Moreover, the predation of *C. elysii* on slugs was affected by predator density. The disturbance coefficient of male *C. elysii* were the highest on adult *A. agrestis*. The results of this study suggest that female *C. elysii* exhibit a high potential for the biological control of *A. agrestis*.

Keywords: *Carabus elysii*; *Agriolimax agrestis*; predation; intraspecific interference

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1. Introduction

Slugs (Mollusca: Gastropoda: Stylommatophora) are prominent agricultural and horticultural pests in temperate and tropical regions worldwide. In addition to feeding on all parts of plants, they are vectors for numerous plant pathogens that can reduce both the aesthetic appearance of plants and crop yields [1,2]. Furthermore, they disseminate parasites that can be harmful for humans, domestic animals, and wild mammals. Slugs of

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Artificial diet significantly enhance fitness and be applicable in mass-rearing of *Ephestia elutella* (Hübner) (Lepidoptera: Pyralidae)

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ABSTRACT

Ephestia elutella (Lepidoptera: Pyralidae) is a cosmopolitan and polyphagous pest attack a wide variety of stored products. To better understand the effect of an artificial diet and tobacco leaves on mass-rearing performance of *E. elutella*, the developmental times of preadult and adult stages, total longevity, reproduction, and life table parameters were analyzed from the data gathered from individual and group reared *E. elutella* under laboratory conditions according to age–stage, two-sex life table theory. The intrinsic rate of increase (r) and finite rate of increase (λ) of group-reared data were found significantly lower than individual-reared data on same rearing medium. Both of these parameters of *E. elutella* reared on artificial diet were significantly higher than tobacco leaves regardless of whether they were reared individual or group-reared. Moreover, high preadult survival rates and fecundity values were recorded from *E. elutella* reared on artificial diet. In addition, the mass-rearing system of late instar larvae of *E. elutella*, which are suitable for mass-rearing an effective parasitoid, *Habrobracon hebetor* (Say) (Hymenoptera: Braconidae), demonstrate that rearing 10,000 daily *E. elutella* 5th instar larvae on artificial diet is cheaper than rearing 5th and/or 6th instar larvae on tobacco leaves. Overall, artificial diet used in present study can be used for continuous mass rearing *E. elutella*.

1. Introduction

Ephestia elutella (Hübner) (Lepidoptera: Pyralidae), the warehouse moth or tobacco moth, is a cosmopolitan and polyphagous pest of tobacco, wheat, cocoa, dried nuts (Ashworth, 1993; Deng et al., 2018). It ranks second only after *Lasioderma serricorne* (F.) (Coleoptera: Anobiidae) which together cause a yearly loss amounts to approximately 1% of stored tobacco worldwide (Ryan, 1999). Beside the direct damage on dried tobacco leaves by the larvae feeding, *E. elutella* reduce the quality of tobacco by contaminating with excreta, spinning silken webs, exuvia and body parts (Deng et al., 2018; Trematerra, 2020). Larvae especially prefer to feed tobacco with high sugar and low nicotine content (Ashworth, 1993).

The control of *E. elutella* has predominantly been achieved through the phosphine fumigation (Bell, 1979, 1992; Ryan, 1999; Coresta, 2019), application of residual insecticides (Massey, 1999; Ryan, 1999), and insect growth regulators (Ryan, 1999; Mondal and Parween, 2000). Alternative control approaches including sulfuryl fluoride fumigation (Baltaci et al., 2009), insecticide (alpha-cypermethrin)-coated net protection (Rumbos et al., 2018; Athanassiou et al., 2019), pheromone trapping (Trematerra, 2012; Athanassiou et al., 2018; Ou et al., 2018), controlled atmosphere treatments (Coresta, 2020), physical control with higher (Bell, 1983), and lower temperatures (Collins and Conyers, 2010) have produced promising results against the moth.

Efforts to utilize biological control by larval parasitoid, *Habrobracon hebetor* (Say) (Hymenoptera: Braconidae) have great potential in providing the desired level of suppression of *E. elutella* on tobacco (Schöller and Prozell, 2001; Ou et al., 2019). *H. hebetor* is a cosmopolitan, gregarious ectoparasitoid that prefer to attack late instars of lepidopteran pests infesting especially stored products (Benson, 1973, 1974) and able to parasitise *E. elutella* larvae hidden between tobacco leaves and parasitization rates ranged between 65 and 75% (Schöller and Prozell, 2001; Ou et al., 2019). The release of large number of *H. hebetor* is essential to achieve rapid and high level of pest control in stored

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Comparative analysis of twelve mitogenomes of Caliscelidae (Hemiptera: Fulgoromorpha) and their phylogenetic implications

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ABSTRACT

Here, the complete mitochondrial genomes (mitogenomes) of 12 Caliscelidae species, *Augilina tetraina*, *Augilina triaina*, *Symplana brevistrata*, *Symplana lii*, *Neosymplana vittatum*, *Pseudosymplanella nigrifasciata*, *Symplanella brevicephala*, *Symplanella unipuncta*, *Augilodes binghami*, *Cylindratus longicephalus*, *Caliscelis shandongensis*, and *Peltonotellus* sp., were determined and comparatively analyzed. The genomes varied from 15,424 to 16,746 bp in size, comprising 37 mitochondrial genes and an A+T-rich region. The typical gene content and arrangement were similar to those of most Fulgoroidea species. The nucleotide compositions of the mitogenomes were biased toward A/T. All protein-coding genes (PCGs) started with a canonical ATN or GTG codon and ended with TAN or an incomplete stop codon, single T. Among 13 PCGs in 16 reported Caliscelidae mitogenomes, *cox1* and *atp8* showed the lowest and highest nucleotide diversity, respectively. All PCGs evolved under purifying selection, with *atp8* considered a comparatively fast-evolving gene. Phylogenetic relationships were reconstructed based on 13 PCGs in 16 Caliscelidae species and five outgroups using maximum likelihood and Bayesian inference analyses. All species of Caliscelidae formed a steadily monophyletic group with high support. Peltonotellini was present at the basal position of the phylogenetic tree. Augilini was the sister group to Caliscelini and Peltonotellini.

Subjects Biochemistry, Entomology, Genomics, Molecular Biology, Zoology
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INTRODUCTION

The family Caliscelidae (Insecta: Hemiptera: Fulgoroidea) includes a diverse group of phytophagous insects, including two subfamilies (Ommatidiotinae and Caliscelinae), five tribes (Caliscelini, Peltonotellini, Ommatidiotini, Adenissini, and Augilini), and >240 species (*Bourgoin, 2021*). The group is relatively small but widely distributed worldwide. Similar to other hemipteran insects, those belonging to the family Caliscelidae use piercing and sucking mouthparts to consume plant juice. Such feeding activities result in proliferation of plant cells which can further affect plant growth and development, spread

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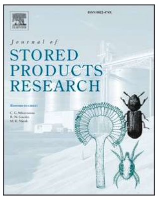

Stability evaluation of candidate reference genes for RT-qPCR normalization in *Lasioderma serricorne* (F.)

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ABSTRACT

Lasioderma serricorne (Fabricius) is an important insect pest of stored products worldwide. The real-time quantitative polymerase chain reaction (RT-qPCR) is a reliable technique commonly used to analyze gene expression across various biological processes. For accurate gene expression analyses using RT-qPCR, selection of stable reference genes to normalize RT-qPCR data is a prerequisite. However, the lack of studies on validation of reference genes in *L. serricorne* limits application of RT-qPCR in *L. serricorne*. In this study, the expression stability of eleven candidate reference genes (*Actin*, *ARF1*, *β-Tubulin*, *EF1α*, *SYN6*, *TBP1*, *RPL3*, *RPL12*, *RPL13a*, *RPL32*, *18S rRNA* using five algorithms (geNorm, NormFinder, BestKeeper, ΔCt and RefFinder) in *L. serricorne* under different experimental and biotic conditions was assessed. The results showed that the best combinations of reference genes that could be used as internal controls in *L. serricorne* were *18S rRNA* and *RPL13a* for different development stages; *18S rRNA* and *RPL3* for different larval tissues; *RPL3* and *RPL13a* for different temperatures; *RPL32*, *RPL12* and *Actin* for starvation. These results provided for the first time a comprehensive list of stable reference genes for the normalization of RT-qPCR analyses in *L. serricorne* and will benefit the in-depth molecular biology research in the future.

1. Introduction

The cigarette beetle, *Lasioderma serricorne* (Fabricius) (Coleoptera: Anobiidae), is one of the most important storage insect pests worldwide that infests various stored products, including grain, spices, herbs, yeast, dried fruits, and tobacco leaves (Abdelghany et al., 2016). Although the adults of cigarette beetle do not feed, they can infiltrate food storage containers and make holes in wrappers and packaging to enter and exit from packaged commodities. The larvae directly feed on the food, and dead beetles and excreta remain inside, causing loss of quality in stored products (Koo et al., 2020). In addition, the overreliance on a limited number of pesticides and lack of insecticides with alternate modes of action has led to serious problem of insect resistance (Saglam et al., 2015).

Recently, the molecular biology of *L. serricorne* has received extensive attention and been studied in depth. For example, several genes involved in molting, wing development, immunity were identified (Yang et al., 2019, 2020a, 2020b). Real-time quantitative polymerase chain reaction (RT-qPCR) is a sensitive technique for the quantitative analysis of target genes expression under different experimental conditions (VanGuilder et al., 2008). However, RT-qPCR is influenced by some factors including RNA integrity and quality, primer amplification efficiency, and the stability of reference gene expression levels across control and treatment groups. To reduce these variations, reference genes are used to calibrate and standardize the experimental samples. The expression levels of ideal reference genes should be relatively stable in various developmental stages and physiological conditions (Wang et al., 2014). Usually, the basic metabolism genes including *Actin*, ribosomal protein (*RPL*), glyceraldehydes 3-phosphate dehydrogenase (*GAPDH*), elongation factor (*EF*) have been used as RT-qPCR analysis of coleopterans (Lu et al., 2018). However, the transcript levels of many reference genes are condition-specific and accordingly, no one reference gene will work for all RT-qPCR experiments and it is necessary to test several options prior to making a selection (Ponton et al., 2011).

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Research

Biological and Microbial Control

Host Deprivation Effects on the Functional Response and Parasitism Rate of *Habrobracon hebetor* (Hymenoptera: Braconidae) on *Ephestia elutella* (Lepidoptera: Pyralidae) in the Laboratory

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Abstract

Habrobracon hebetor (Say) is an important biological control agent for lepidopteran pests of stored products. In this study, the age-specific functional response, paralysis rate, and parasitism rate of *H. hebetor* under different host deprivation treatments (PC: without host deprivation, used as the control, P1d: host deprivation, but the host was removed after 1 d contact, and PW: host deprivation from beginning) were evaluated at different larval densities (5, 10, 20, 40, and 80) of the *Ephestia elutella* (Hübner) at 28 ± 1°C, 75 ± 5% RH and 16:8 h L:D. Ages of parasitoid females used were 2, 5, 10, and 20 d old. The logistic regression results indicated that the functional response of *H. hebetor* females under different host deprivation treatments was type II. The longest handling time was observed in 20-d old females, while the shortest handling time and highest maximum attack rate (*T/Th*) were estimated at the age of 2 d in all treatments. The paralysis and parasitism rates of *H. hebetor* were the highest at 2, 5, and 10-d old in all treatments. The results of this study suggest that *H. hebetor* females up to 10-d old can be used as an efficient biological control agent against *E. elutella*. The data of this study can also be used to predict the efficacy of different aged *H. hebetor* females in controlling *E. elutella* populations.

Key words: tobacco moth, larval ectoparasitoid, functional response, paralysis rate, parasitism rate

The tobacco moth *Ephestia elutella* (Hübner) is a major insect pest affecting stored tobacco leaves (Athanassiou et al. 2019, Ou et al. 2018, 2019). It causes serious damage to tobacco leaves stored within one year by reducing the quality of tobacco through larval feeding and producing contaminates (Deng et al. 2018). In general, the *E. elutella* management in tobacco is typically based on the use of fumigants containing phosphine, which presents several risks, such as poisoning, fire, and high degrees of corrosion to equipment and electronics, as well as contributing to the further development of resistance (Valizadegan et al. 2012). Due to these deleterious effects, alternative eco-friendly means of pest control are needed. Biological control is considered one of the key strategies in alternative pest control.

The first step in the preparation and implementation of biological control applications is the search for effective biological control agents. The braconid wasp, *Habrobracon hebetor* (Say), which is a cosmopolitan, gregarious, idiobiont, and synovigenic ectoparasitoid (Gündüz and Gülel 2010), is considered among the most effective biological control agents of lepidopteran pests of stored products such as *Plodia interpunctella* (Hübner) (Lepidoptera: Pyralidae), *Ephestia kuehniella* Zeller (Lepidoptera: Pyralidae), and *Sitotroga cerealella* (Olivier) (Lepidoptera: Gelechiidae) (Sanower et al. 2018,

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Two lysozymes are involved in the larva-to-pupa transition and the antibacterial immunity of *Lasioderma serricorne* (coleoptera: Anobiidae)

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ABSTRACT

Lysozymes play important roles in the innate immune response against pathogen infections of insects. In this study, i-type and c-type lysozymes (*LsLysI* and *LsLysC*) were identified from the cigarette beetle, *Lasioderma serricorne*. Both genes were highly expressed in late larvae and pupae, especially in the fat body and integument. The expression of *LsLysI* and *LsLysC* was induced by 20-hydroxyecdysone. The expression levels of both *LsLys* genes were significantly upregulated after peptidoglycan (PGN) exposure and gram-positive bacterium *Staphylococcus aureus* infections. RNA interference (RNAi)-mediated knockdown of *LsLysI* or/and *LsLysC* in 5th instar larvae reduced lysozyme levels and disrupted the larva-to-pupa molt. Knockdown of *LsLysI* or *LsLysC* alone, and co-suppression of both genes, increased larval mortality by 13.3%, 21.1%, and 43.3% after *S. aureus* infection. The results demonstrated that *LsLysI* and *LsLysC* play key roles in a successful larva-to-pupa transition and in the innate immune response of *L. serricorne*.

1. Introduction

Lysozymes (E.C. 3.2.1.17), also known as muramidases, are important effectors in the innate immune system of both vertebrates and invertebrates (Dobson et al., 1984; Callewaert and Michiels, 2010). Lysozymes are ubiquitous enzymes that hydrolyze the β-1, 4-glycosidic linkage between *N*-acetylmuramic acid and *N*-acetylglucosamine in the peptidoglycan layer of bacterial cell walls and cause bacterial cell lysis (Nayduch and Joyner, 2013). Based on sequence structures and catalytic characters, animal lysozymes are divided into three types, including the chicken-type (c-type), goose-type (g-type), and invertebrate-type (i-type) (Bathige et al., 2013). Lysozymes participate in many physiological processes, such as digestion (Cançado et al., 2008), antiviral (Ly-Chatain et al., 2013), antibacterial (Liao et al., 2018), and antifungal activities (Sherman et al., 2016), anti-inflammatory (Smedowski et al., 2017), and inhibition of tumor growth and metastasis (Mahanta et al., 2015).

Since the first insect lysozyme was reported in honey bees (Mohrig and Messner, 1968), many lysozyme genes have been found in insects, including Lepidoptera (Yu et al., 2002), Coleoptera (Beckert et al., 2015), Orthoptera (Mohamed et al., 2016), Hemiptera (Gerardo et al., 2010), and Hymenoptera (Evans et al., 2006). The c-type and i-type lysozymes are predominately identified in insects (Ito et al., 1999). In most cases, both c-type and i-type lysozymes participate in innate immunity against pathogenic microorganisms (Callewaert and Michiels, 2010). For example, the expressions of two lysozymes in *Tribolium castaneum* were significantly

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Abbreviations: PGN, peptidoglycan; LPS, lipopolysaccharide; PCR, polymerase chain reaction; ORF, open reading frame; RT-PCR, reverse transcription PCR; qPCR, quantitative real-time PCR; cDNA, complementary DNA; 20E, 20-hydroxyecdysone; dsRNA, double-stranded RNA; RNAi, RNA interference; GFP, green fluorescent protein.

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Fast Recognition of *Lecanicillium* spp., and Its Virulence Against *Frankliniella occidentalis*

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Background: *Frankliniella occidentalis* (Thysanoptera: Thripidae) is a highly rasping-sucking pest of numerous crops. The entomogenous fungi of *Lecanicillium* spp. are important pathogens of insect pests, and some species have been developed as commercial biopesticides. To explore *Lecanicillium* spp. resources in the development of more effective *F. occidentalis* controls, efficient barcode combinations for strain identification were screened from internal transcribed spacers (ITS), *SSU*, *LSU*, *TEF*, *RPB1*, and *RPB2* genes.

Results: Six genes were used to reconstruct *Lecanicillium* genus phylogeny. The results showed that ITS, *TEF*, *RPB1*, and *RPB2* could be used to identify the strains. All phylogenetic trees reconstructed by free combination of these four genes exhibited almost the same topology. Bioassay studies of a purified conidial suspension further confirmed the infection of second-instar nymphs and adult female *F. occidentalis* by seven *Lecanicillium* strains. *L. attenuatum* strain GZUIFR-lun1405 was the most virulent, killing approximately 91.67% *F. occidentalis* adults and 76.67% nymphs after a 7-day exposure. *L. attenuatum* strain GZUIFR-lun1405 and *L. cauligalbarum* strain GZUIFR-ZHJ01 were selected to compare the fungal effects on the number of eggs laid by *F. occidentalis*. The number of *F. occidentalis* nymphs significantly decreased when *F. occidentalis* adults were treated with *L. cauligalbarum* strain GZUIFR-ZHJ01.

Conclusions: The combination of ITS and *RPB1* could be used for fast recognition of *Lecanicillium* spp. This is the first report of the pathogenicity of *L. attenuatum*, *L. cauligalbarum*, *L araneogenum*, and *L. aphanocladii* against *F. occidentalis*. Additionally, *L. cauligalbarum* strain GZUIFR-ZHJ01 caused high *F. occidentalis* mortality and inhibited the fecundity of the pest.

Keywords: entomopathogenic fungi, fast recognition, *Frankliniella occidentalis*, *Lecanicillium*, pathogenicity

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Abbreviations: Spp., species pluralis; GZAC, the Institute of Fungal Resources of Guizhou University; rDNA, ribosomal DNA; LSU, the large subunits of the rDNA; SSU, the small subunits of the rDNA; TEF, the transcription elongation factor-1α; ITS, ITS1–5.8S rDNA–ITS2 region, the first and the internal transcribed spacers; RPB1, DNA-directed RNA polymerase II subunit rpb1; RPB2, DNA-directed RNA polymerase II subunit rpb2.

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Microbiome-Guided Exploration of the Microbial Assemblage of the Exotic Beverage "Insect Tea" Native to Southwestern China

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Insect tea is a unique beverage that is native to Southwestern China and traditionally produced by local farmers in an elaborate process. It consists of insect larvae excrements that are commonly obtained from meal moths (*Pyralis farinalis* Linnaeus 1758) reared on a specific plant-based diet. We have reconstructed the whole production process under laboratory conditions in order to obtain microbiome-level insights into this uncommon beverage and to trace back the origin of the prevalent bacteria in the final product. The bacterial community composition was specific for each production stage, with a high proportion of *Streptomycetacea*, *Pseudonocaridaceae*, *Enterococcaceae*, and *Enterobacteriaceae* in the insect tea. A large proportion of the constituents was traced back to the producing insect (13.2%) and its excrements (43.8%), while the initial plant-based substrate for tea production was found to contribute only 0.6% of the traceable bacteria in the final product. Moreover, an enrichment of *Enterobactericeae* was observed during the analyzed process steps and verified with complementary analyses. The cultivation experiments indicated a high occurrence of viable bacteria in the tea at $2.7 \times 10^5 \pm 1.2 \times 10^5$ cfu g^{-1}. The isolated bacteria included *Bordetella petrii* and *Enterococcus* spp. that were recovered from a commercial product. By implementing an integrative approach, the insect tea was shown to harbor a species-rich bacterial community that can be traced back to certain plant and insect microbiome constituents from distinct production steps. Moreover, the microbial profile of the insect tea was found to be unique for a food product so far and contained several bacterial groups that are considered from the current perspective as food contaminants or yet unreported in other beverages. Due to the high number of viable bacteria, the tea harbors a so far undescribed dynamic component that might have implications for human health.

Keywords: insect tea, tea microbiome, food microbiome, *Pyralis farinalis*, *Enterobacteriaceae*, Chong Cha

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Molecular Characterization and Expression of *OfJNK* and *Ofp38* in *Ostrinia furnacalis* (Guenée) Under Different Environmental Stressors

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Ostrinia furnacalis, an important pest of corn, has substantial detrimental effects on corn production. The mitogen-activated protein kinase (MAPK) signaling pathway plays a pivotal role in an insect's resistance to environmental stress. The expression levels of *JNK* and *p38* have been well recorded in several insects under different environmental stressors, at different developmental stages, and in various tissue types; however, there is limited information on *JNK* and *p38* in agricultural insects. To clarify the mechanism whereby *O. furnacalis* responds to environmental stress, we cloned *JNK* and *p38* from *O. furnacalis* and subsequently named them *OfJNK* and *Ofp38*, respectively. Further, we examined the expression levels of *OfJNK* and *Ofp38* under different environmental stressors. In this study, we obtained full-length sequences of *OfJNK* and *Ofp38*, and RT-qPCR results showed that these genes were expressed at all developmental stages, in various tissues (head, chest, abdomen, leg, wing, antennae, compound eye, midgut, and ovary) and under different environmental stressors (4°C and ultraviolet A treatment for 0, 30, 60, 90, and 120 min). The expression levels of *OfJNK* and *Ofp38* were relatively higher in eggs and 3-day-old adult females than in other developmental stages. Moreover, the expression level of *OfJNK* was higher in the wings than in other tissues, whereas that of *Ofp38* was significantly higher in the ovaries than in other tissues. *OfJNK* and *Ofp38* showed high expression 90 min after being subjected to treatment at 4°C and ultraviolet A irradiation; the expression of *Ofp38* peaked at 30 min, whereas that of *OfJNK* peaked at 60 min. These results indicate that *O. furnacalis* differs in terms of its response under different environmental stressors. In summary, our results will provide a foundation for additional research needed to determine the role of the MAPK signaling pathway and the underlying mechanisms by which it shows resistance to environmental stresses in insects.

Keywords: *Ostrinia furnacalis*, c-Jun N-terminal kinase, p38 mitogen-activated protein kinase, gene cloning, expression analysis, environmental stressors

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RESEARCH ARTICLE

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Genomic content of chemosensory receptors in two sister blister beetles facilitates characterization of chemosensory evolution

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Abstract

Background: More than 2500 species belong to the Meloidae family (Coleoptera: Tenebrionoidea), members of which produce the potent defensive blistering agent cantharidin and are commonly known as blister beetles or *Spanishflies*. Cantharidin has recently been used for cancer therapy. *Hycleus cichorii* and *Hycleus phaleratus* have been used in traditional Chinese medicine for more than 2000 years due to their ability to biosynthesize cantharidin. To understand the role of the chemosensory system in beetle evolution, we comparatively analysed the chemosensory receptor families of both blister beetle species and compared them with those of other beetles.

Results: We identified 89 odorant receptors (ORs), 86 gustatory receptors (GRs), and 45 ionotropic receptors (IRs) in *H. phaleratus* and 149 ORs, 102 GRs and 50 IRs in *H. cichorii*. Nine groups of beetle ORs were recovered, and a similar pattern of ORs in Coleoptera emerged. Two evident expanded clades in *Hycleus* (Groups 5A and 3) were reconstructed in the phylogenetic tree. Four of eight genes with evidence of positive selection were clustered in the expanded clades of Group 5A. Three, eight and three orthologous pairs of CO_2, sugar and fructose receptors, respectively, were identified in both blister beetles. Two evident expanded clades of putative bitter GRs in *Hycleus* were also found, and the GR in one clade had notably low divergence. Interestingly, IR41a was specifically expanded in blister beetles compared to other insects identified to date, and IR75 was also clearly expanded in both blister beetles based on our phylogenetic tree analysis. Moreover, evidence of positive selection was detected for eight ORs, three GRs and two IRs, half of which were from five duplicate clades.

Conclusions: We first annotated the chemosensory receptor families in a pair of sister beetle genomes (Meloidae: *Hycleus*), which facilitated evolutionary analysis of chemosensory receptors between sibling species in the Coleoptera group. Our analysis suggests that changes in chemosensory receptors have a possible role in chemical-based species evolution in blister beetles. Future studies should include more species to verify this correlation, which will help us understand the evolution of blister beetles.

Keywords: Blister beetle (*Spanishfly*), Chemosensory, Gustatory receptor, Odorant receptor, Ionotropic receptors

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The Phylogenetic Implications of the Mitochondrial Genomes of *Macropsis notata* and *Oncopsis nigrofasciata*

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Macropsinae are forest pests that feed on woody plants. They can damage the growth of trees and crops, and some species can also spread plant pathogens. Due to their widespread effects, these leafhoppers are of great economic significance, which is why there is a need to study their genomes. To fill the gap in the mitochondrial genomic data of the subfamily Macropsinae, we sequenced the complete mitochondrial genomes of *Macropsis notata* and *Oncopsis nigrofasciata* (which were 16,323 and 15,927 bp long, respectively). These two species are representative species of the leafhoppers group (Cicadellidae); the mitochondrial genomes of these species range from a length of 15,131 bp (*Trocnadella arisana*) to 16,811 bp (*Parocerus laurifoliae*). Both mitogenomes contained 37 typical insect mitochondrial genes and a control region; there were no long non-coding sequences. The genes within the mitogenome were very compact. The mitogenomes from both species contained two kinds of parallel repeat units in the control region. The whole mitogenomes of Macropsinae showed a heavy AT nucleotide bias (*M. notata* 76.8% and *O. nigrofasciata* 79.0%), a positive AT Skew (0.15 and 0.12), and a negative GC Skew (–0.14 and –0.08). Upon comparative ML and BI analysis, some clade relationships were consistent among the six trees. Most subfamilies were reconstructed into monophyletic groups with strong support in all analyses, with the exception of Evacanthinae and Cicadellinae. Unlike the results of previous research, it was shown that although all Deltocephalinae species are grouped into one clade, they were not the sister group to all other leafhoppers. Further, Cicadellinae and Evacanthinae were occasionally reconstructed as a polyphyletic and a paraphyletic group, respectively, possibly due to the limited numbers of samples and sequences. This mitogenome information for *M. notata* and *O. nigrofasciata* could facilitate future studies on the mitogenomic diversity and evolution of the related Membracoidea, and eventually help to control their effects on plants for the betterment of society at large.

Keywords: leafhopper, *Macropsis notata*, *Oncopsis nigrofasciata*, mitogenome, phylogenetic analyses

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insects

MDPI

Article

Testing Seven Hypotheses to Determine What Explains the Current Planthopper (Fulgoridae) Geographical and Species Richness Patterns in China

Zheng-Xue Zhao [1,2,3], Lin Yang [1,2,3], Jian-Kun Long [4], Zhi-Min Chang [4], Zheng-Xiang Zhou [1,2,3], Yan Zhi [1,2,3], Liang-Jing Yang [1,2,3], Hong-Xing Li [1,2,3], Yong-Jin Sui [1,2,3], Nian Gong [1,2,3], Xiao-Ya Wang [1,2,3] and Xiang-Sheng Chen [1,2,3,*]

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Simple Summary: Although there are many described species and ample geographical distribution data available on planthoppers (Fulgoridae) in China, the research on the underlying mechanisms of macro-scale richness patterns is still scant. To contribute to unraveling these mechanisms, we tested seven hypotheses related to contemporary environments and historical climate stability by relating the species richness to 15 environmental variables. The historical climate stability, ambient energy, and productivity hypotheses are superior to other hypotheses in explaining the current richness patterns of planthoppers. Based on these main hypotheses, we narrowed the mechanisms underlying contemporary planthopper distribution in China. Furthermore, other factors not included in this study (i.e., orogenic processes and geological isolation) may significantly contribute to richness patterns identified here.

Abstract: Although many hypotheses have been proposed to understand the mechanisms underlying large-scale richness patterns, the environmental determinants are still poorly understood, particularly in insects. Here, we tested the relative contributions of seven hypotheses previously proposed to explain planthopper richness patterns in China. The richness patterns were visualized at a 1° × 1° grid size, using 14,722 distribution records for 1335 planthoppers. We used ordinary least squares and spatial error simultaneous autoregressive models to examine the relationships between richness and single environmental variables and employed model averaging to assess the environmental variable relative roles. Species richness was unevenly distributed, with high species numbers occurring in the central and southern mountainous areas. The mean annual temperature change since the Last Glacial Maximum was the most important factor for richness patterns, followed by mean annual temperature and net primary productivity. Therefore, historical climate stability, ambient energy, and productivity hypotheses were supported strongly, but orogenic processes and geological isolation may also play a vital role.

Keywords: ambient energy; biogeography; dispersal ability; historical climate stability; Last Glacial Maximum; planthoppers; productivity; species richness

insects

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Article

Biological Traits of the Pincer Wasp *Gonatopus flavifemur* (Esaki & Hashimoto) Associated with Different Stages of Its Host, the Brown Planthopper, *Nilaparvata lugens* (Stål)

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Abstract: *Gonatopus flavifemur* (Esaki & Hashimoto) is a common parasitoid of the most important rice pest, the brown planthopper (BPH) *Nilaparvata lugens* (Stål), in eastern and southeastern Asia. We investigated the parasitism rates, feeding rates, and offspring development of *G. flavifemur* in association with five instars of BPH nymphs and male and female adults under laboratory conditions (27 ± 1 °C and 70 ± 5% Relative Humidity). The results showed that the life stage of the host significantly affects parasitism, host feeding, and offspring development by *G. flavifemur*. The parasitism rate was highest on 4th instar nymphs, and the feeding rate was highest on 1st instar nymphs. The cocooning rate on male adult BPHs was significantly lower than that on other stages; however, emergence rates did not significantly differ among the BPH stages. The rate of female offspring upon emergence from 5th instars was higher than other stages. Both the parasitism and host-feeding functional responses of *G. flavifemur* to different BPH stages fit well with Holling type II models, supporting the results of parasitism and feeding rates and indicating that *G. flavifemur* would be a good agent for BPH control. In conclusion, *G. flavifemur* prefers to feed on young nymphs but prefers to parasitize older nymphs. In addition, 5th instar nymphs are favorable to female offspring of the pincer wasp.

Keywords: *Gonatopus flavifemur*; *Nilaparvata lugens*; host stage; parasitism; host feeding; development

1. Introduction

Dryinids are the main parasitic wasps of planthoppers in rice fields and can parasitize and feed on both nymphs and adults [1]. Approximately 12 dryinid species have been reported to parasitize rice planthoppers in China. Among them, *G. flavifemur* (Esaki & Hashimoto), *Gonatopus nigricans* (R.C.L. Perkins), *Haplogonatopus oratorius* (Westwood), *Haplogonatopus apicalis* R.C.L. Perkins, and *Echthrodelphax fairchildii* R.C.L. Perkins are reported to be common species in rice fields [2–5]. In addition, *Gonatopus flavifemur* (Esaki & Hashimoto, 1932) (synonym: *Pseudogonatopus flavifemur* Esaki & Hashimoto) is one of the most common natural enemies of rice planthoppers (Delphacidae) in China [6]. This species is consistently characterized by sexual dimorphism [7], and the wingless, ant-like female (Figure 1B) wasps lay eggs and feed on planthoppers (Figure 1C). The mode of reproduction in *G. flavifemur* is sexual and parthenogenetic. Typically, females lay eggs on a live host, and the wasp larvae hatch

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New potential strains for controlling *Spodoptera frugiperda* in China: *Cordyceps cateniannulata* and *Metarhizium rileyi*

Ye-Ming Zhou · Wen Xie · Jia-Qin Ye · Tao Zhang · Ding-Yin Li · Jun-Rui Zhi · Xiao Zou

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Abstract *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae), an invasive pest, was identified in China in early 2019. This pest is a serious threat to food, especially maize production. Consequently, it is necessary to use biological control to reduce the damage caused by *S. frugiperda.* Furthermore, it is important to find new entomopathogenic fungi or a local wild parasitic isolate to control this pest. Here, one fungus was found infecting *S. frugiperda* larvae in China. Isolated colonies were identified as *Metarhizium rileyi* (Farlow) Kepler, S.A. Rehner & Humber (Hypocreales: Clavicipitaceae) using morphological and molecular methods. Bioassay studies with purified conidial suspensions further confirmed the infectivity to 4th instar *S. frugiperda* larvae. The results showed that no *S. frugiperda* larvae survived after being treated with a spore suspension of *M. rileyi* GZUIFR-LS01 or *Cordyceps cateniannulata* (Z.Q. Liang) Kepler, B. Shrestha & Spatafora (Hypocreales: Cordycipitaceae) GZUIFR-S22 for seven days at 90% RH. However, at 75% RH, 13% and 48% of larvae survived after seven days of exposure to *M. rileyi* GZUIFR-LS01 and *C. cateniannulata* GZUIFR-S22, respectively. Additionally, *C. cateniannulata* strain GZUIFR-S22 led to a survival rate of less than 50% in *S. frugiperda* larvae after two days of treatment at 90% RH. This is the first report of the pathogenicity of *C. cateniannulata* against *S. frugiperda*.

Keywords Entomopathogenic fungi · Biological control · *Metarhizium rileyi* · *Cordyceps cateniannulata* · Cordycipitaceae · Hypocreales · *Spodoptera frugiperda* · Pathogenicity

Introduction

Maize is a major staple crop in China, with the total output of corn having surpassed that of rice to become the top food crop (Grijalba et al. 2018; China Grain Industry Association 2019). However, the recent invasion of *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae) in China has caused a serious

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Determinants of Delphacidae richness and endemism in China

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Abstract. 1. Identifying the macro-scale patterns and the underlying mechanisms of species richness are key aspects of biodiversity-related research. In China, previous studies on the mechanisms underlying insect richness have primarily focused on the current ecological conditions. Therefore, the impact of historical climate change on these mechanisms is less well understood.

2. Here, we use members of the Delphacidae family to evaluate the relative impact of the current environmental conditions and that of the Last Glacial Maximum on total species richness and endemism. Total species richness and endemic species richness were summed in $1° \times 1°$ grid cells that the insects occupied. Generalised linear models, simultaneous autoregressive models, and random forest models were used to assess the effects of different environmental factors on total species richness and endemism.

3. The two patterns of species richness are jointly regulated by the current environment and the Last Glacial Maximum, but their key determinants differ. Winter coldness and the temperature annual range strongly affected the total species richness, but temperature variation during the Last Glacial Maximum also played an important role in the development of species richness. The distribution of endemic species was most strongly affected by the Last Glacial Maximum temperature change.

4. The studies confirm that historical climate change contributes to patterns of insect species richness, particularly patterns of endemism. Considering that China was mildly affected by the last glacial period, we propose that the incorporation of historical climate data into such studies will provide a better understanding of the underlying mechanisms.

Key words. Delphacidae, endemism, historical climate, species richness, temperature annual range, winter coldness.

Introduction

Understanding the patterns of species richness and the mechanisms that underlie these phenomena is a popular research topic in the field of ecology and biogeography (Rosenzweig, 1995; Buckley *et al.*, 2010; Jetz & Fine, 2012). Investigations on the mechanisms driving the macro-scale patterns of species richness will help us better understand the evolution of species and aid conservation efforts (Pennisi, 2005; Kreft & Jetz, 2007). Current environmental conditions are commonly thought to govern spatial variation in species richness, as highlighted by several recent studies (Hawkins *et al.*, 2003; Field *et al.*, 2009; Qian, 2013; Torres-Romero & Olallatarraga, 2015; Godoy-Bürki *et al.*, 2017). Nevertheless, patterns of species richness are also regulated by the interaction between present-day factors and evolutionary processes (Ricklefs, 2004), such as those stemming from historical climatic conditions richness patterns (Araújo *et al.*, 2008; Kissling *et al.*, 2012; Rakotoarinivo *et al.*, 2013; Svenning *et al.*, 2015). The historical climate hypothesis suggests that regions severely affected by climate change host fewer species, whereas regions with greater

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Characterization and phylogenetic implications of the complete mitochondrial genome of Idiocerinae (Hemiptera: Cicadellidae)

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Protective and Detoxifying Enzyme Activity and *ABCG* Subfamily Gene Expression in *Sogatella furcifera* Under Insecticide Stress

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Sogatella furcifera, an important migratory pest of rice, has substantial detrimental effects on rice production. To clarify the mechanism whereby *S. furcifera* responds to insecticide stress, we measured the activity of its protective [superoxide dismutase (SOD); peroxidase (POD); catalase (CAT)] and detoxifying [carboxylesterase (CarE); glutathione *S*-transferase (GST); mixed-function oxidase (MFO)] enzymes and the expression levels of its ATP-binding cassette subfamily G (*ABCG*) transporter genes in response to sublethal concentrations (LC_{10} and LC_{25}) of the insecticides thiamethoxam, buprofezin, and abamectin. On the bases of the transcriptome data and the *ABCG* genes of *Laodelphax striatellus*, we obtained 14 full-length *ABCG* sequences for *S. furcifera*. RT-qPCR results showed that 13, 12, and 9 *sfABCG* genes were upregulated in the presence of thiamethoxam, buprofezin, and abamectin, respectively, at LC_{10}. Moreover, 13 and 7 *sfABCG* genes were upregulated following treatment with thiamethoxam and abamectin, respectively, at LC_{25}. Enzyme activity assays showed that although thiamethoxam, buprofezin, and abamectin induced GST, CarE, CAT, POD, and SOD activity, they did so at different concentrations and exposure times. The activity of MFO was generally inhibited with prolonged exposure to the three insecticides, with the inhibitory effect being most significant at 72 h. These results indicate that *S. furcifera* differs in its response to different types or concentrations of insecticides. Taken together, our results lay the foundations for gaining a deeper understanding of the mechanisms underlying the adaptation of *S. furcifera* to different types of insecticides, which would be of considerable significance for the development of effective pest management strategies.

Keywords: white-backed planthopper, detoxifying enzyme, protective enzyme, ATP-binding cassette transporter, insecticide stress, response mechanism

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INTRODUCTION

Sogatella furcifera, an important pest of rice, causes serious problems in rice production by sucking phloem sap from the rice plant, inflicting damage through oviposition, and transmitting viral diseases (Zhou et al., 2008). Although the use of insecticides has traditionally been an important means of control for this rice pest (Endo and Tsurumachi, 2001; Nizamani et al., 2002), recent

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RESEARCH ARTICLE

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Lecanicillium cauligalbarum sp. nov. (Cordycipitaceae, Hypocreales), a novel fungus isolated from a stemborer in the Yao Ren National Forest Mountain Park, Guizhou

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Abstract

A new species of entomopathogenic fungi, *Lecanicillium cauligalbarum*, was discovered from a survey of invertebrate-associated fungi in the Yao Ren National Forest Mountain Park in China. The synnemata of this species emerged from the corpse of a stemborer (Lepidoptera), which was hidden amongst pieces of wood on the forest floor. It differs from morphologically similar *Lecanicillium* species mainly in its short conidiogenous cells and ellipsoid to ovoid and aseptate conidia. Phylogenetic analysis of a combined data set comprising ITS, *SSU*, *LSU*, *TEF*, *RPB1* and *RPB2* sequence data supported the inclusion of *L. cauligalbarum* in the *Lecanicillium* genus and its recognition as a distinct species.

Keywords

Entomopathogenic fungi, *Lecanicillium*, multiple genes, phylogeny, new species

Introduction

The entomopathogenic fungal genus *Lecanicillium* W. Gams & Zare belongs to Ophiocordycipitaceae. It is typified by *Lecanicillium lecanii* with *Torrubiella confragosa* as the sexual morph (Zare and Gams 2001, Wijayawardene et al. 2017). *Lecanicillium lecanii*

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Research Article

OXFORD

Ecology and Behavior

Delay in Mating Reduces Reproductivity but Increases Life Span in Tobacco Cutworm, *Spodoptera litura* Fabricius (Lepidoptera: Noctuidae)

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Abstract

A pheromone-mediated mating disruption is a vital tool in the management of insect population dynamics that not only prevents mating but also delays mating in the target insect. Here, we examined the effect of delayed mating on the longevity and reproductive performance of the global pest, *Spodoptera litura* Fabricius (Lepidoptera: Noctuidae). Delayed mating was imposed on both sexes simultaneously, males only, and females only. The results showed that a 30–40% reduction in the successful mating rate of *S. litura* was caused by 7-d delay in mating. Increased mating ages of both sexes of *S. litura* resulted in a significant decrease in 3-d-old delayed mating, followed by an increase in mean duration of copulation. Furthermore, delayed mating had a significantly negative influence on the number of *S. litura* eggs produced. Mating delay imposed on both sexes simultaneously had a significantly greater effect on longevity and the number of eggs than when it was applied to either sex alone, and females were more severely affected by delayed mating than males in terms of longevity. Percentage of mating, fecundity, and female longevity were all significantly correlated with the number of days delayed mating. However, the hatching rate of eggs was not significantly affected by an increased delay in mating. Overall, our results indicated that delayed mating in both females and males drastically reduced the females' reproductive output, which itself was affected more by increasing the age at mating of females than males.

Key words: delayed mating, egg number, longevity, *Spodoptera litura* Fabricius, survival rate

Synthetic sex pheromones are an effective way to control mating events and monitor the insect population dynamics of lepidopteran pests (Arn and Louis 1997, Sanders 1997, Witzgall et al. 2010). Mating control methods mediated by pheromones mainly entail mass trapping of males and mating disruption. Applying mating disruption techniques to protect commercial crops and insect population control has proven successful in several cases, such as for *Pectinophora gossypiella* (Lepidoptera: Gelechiidae) (Brooks et al. 1979), *Epiphyas postvittana* (Walker) (Lepidoptera: Tortricidae) (Shaw et al. 1993), and *Cydia pomonella* (L.) (Lepidoptera: Tortricidae) (Angeli et al. 1999). Several possible mechanisms are thought to explain how mating disruption occurs via an artificially released pheromone (Cardé and Minks 1995), including its effects on the target insect's peripheral and central nervous system (Bartell 1982), the inability of responding insects to distinguish individual odor trails from an odor background, an imbalance in the pattern of sensory inputs, and by insects following a false trail (Welter et al. 2005, Fitzpatrick 2006, Witzgall et al. 2010, Kawazu et al. 2014). The false-trail-following mechanism results in either an asynchrony in sexual behavior or a delay in mating (Cardé and Minks1995). Some reports suggested that the latter resulted in only a moderate level of mating disruption (Cardé and Minks 1995, Srinivas and Rao 1999, Miller et al. 2006), yet the delayed mating of female moths of various lepidopteran pests by 2–7 d was shown to improve the efficacy of mating disruption (e.g., Torres-Vila et al. 2002). Moreover, many previous laboratory studies show that delayed mating can negatively affect the reproductive potential of several lepidopteran insects by reducing their numbers of offspring and the hatchability of eggs (Kehat and Gordon 1977, Ellis and Steele 1982, Walker 1991, Rogers and Marti 1994, Karalius and Buda 1995, Proshold 1996, Knight 1997, Fadamiro and Baker 1999, Torres-Vila et al. 2002). In those cases where mate finding is not completely inhibited, inevitably significant mating may still occur (Torres-Vila et al. 2002, Jiménez-Pérez and Wang 2003), but the significant population

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Research article

Insecticide Resistance and Resistance Management

Expression Differences of Resistance-Related Genes Induced by Cycloxaprid Using qRT-PCR in the Female Adult of *Sogatella furcifera* (Hemiptera: Delphacidae)

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Data Availability Statement: The raw reads from the transcriptome of *Sogatella furcifera* have been uploaded and placed in the NCBI SRA database (accession number: SRR4294200 and SRR4294203).

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Abstract

As a newer cis-nitromethylene neonicotinoid pesticide at present, cycloxaprid has good industrialization prospects, including the management of imidacloprid-resistant populations, because this chemical have an excellent efficiency against rice planthoppers. *Sogatella furcifera* (Horváth) is the most economically important pest of rice worldwide and has developed resistance to many insecticides. This study focused on the expression change of these resistance genes, induced by cycloxaprid, involved in metabolic detoxification and receptor protein. Twenty-two differentially expressed genes (DEGs) that may be related with the insecticide resistance were found in the transcriptome of *S. furcifera*, including 2 cytochrome P450 genes, 2 glutathione S-transferase (GST) genes, 1 acid phosphatase (ACP) gene, 12 decarboxylase genes, 2 glycolipid genes, 1 cadherin gene, and 2 glycosyltransferase genes, which were up- or downregulated in response to an exposure of cycloxaprid. Furthermore, two P450 genes (CYP4 and CYP6 family, respectively), two decarboxylase genes, and one glycosyltransferase gene were validated by qRT-PCR. Expression differences of these genes verified successfully by qRT-PCR in response to different concentrations and times treated with cycloxaprid could explain the insecticide resistance mechanism under cycloxaprid stress in *S. furcifera*.

Key words: *Sogatella furcifera* (Horváth), P450, decarboxylase, glycosyltransferase, qRT-PCR

As a novel neonicotinoid insecticide, cycloxaprid was first reported in 2008 (Shao et al. 2008, 2010, 2011) and named in 2011 (Li et al. 2011), and its mode of action was similar to that of imidacloprid and nitenpyram. Because of a broad spectrum of insect pests and low toxicity to mammals, cycloxaprid has been regarded as a replacement for imidacloprid to control important pests, especially imidacloprid-resistant insects, on various crops in China (Shao et al. 2010, 2011). This new insecticide is strongly recommended for managing piercing–sucking insect pests such as aphids, whiteflies, leafhoppers, and planthoppers especially *Sogatella furcifera* (Horváth) in future (Yang et al. 2016).

Sogatella furcifera is one of the most serious migratory pests on rice crops around Asia, even worldwide (Kisimoto 1971, Cheng 2009, Sogawa et al. 2009). It mainly attacks rice, *Oryza sativa* L., and causes damage by directly feeding and ovipositing on rice stems, a characteristic yellowing of tissues known as "hopperburn." Moreover, it is a vector transmitting several rice viruses, especially the southern rice black streaked dwarf virus causing a huge loss of rice yield (Zhang et al. 2008, Zhou et al. 2008, Yin et al. 2011, Xu et al. 2012, International Rice Research Institute website 2012, Zhou et al. 2013). It is reported that this pest is mainly distributed throughout south Asia countries and south-east Asia countries, such as Vietnam, Indonesia, Philippines, China, Japan, Korea, South Pacific Islands, and northern Australia (Khan and Saxena 1985, Salim and Heinrichs 1987).

Induction, as a universal phenomenon, is one of the nature's most basic adaption mechanisms to environmental pressure. Many chemicals could lead to the inductive response, and those chemicals, which are of interest in entomology, include plant allelochemicals, insecticides, insect hormones, and their analogs (Leon 1984). And

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Research article

Insecticide Resistance and Resistance Management

Monitoring Trends in Insecticide Resistance of Field Populations of *Sogatella furcifera* (Hemiptera: Delphacidae) in Guizhou Province, China, 2012–2015

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Abstract

Sogatella furcifera (Horváth) is a migratory insect that is one of the most important pest species on rice in many Asian countries. Control of *S. furcifera* (Hemiptera: Delphacidae) primarily depends on the use of chemical insecticides, and with this extensive reliance on pesticides, determining the degree of resistance of *S. furcifera* populations to the chemicals used for its control is essential. In this study, the resistance level to six conventional insecticides in five populations of *S. furcifera* from Guizhou Province was monitored yearly using the rice-stem dipping method in 2012–2015 to precisely understand current resistance levels and to estimate trends in the development of insecticide resistance in *S. furcifera* in Guizhou. Overall, *S. furcifera* from five regions in Guizhou showed a trend toward decreased susceptibility to isoprocarb (resistance ratio [RR] 0.82–3.59), susceptibility to low resistance against thiamethoxam (RR 0.27–9.69), susceptibility to moderate resistance to imidacloprid (RR 0.71–26.06), and decreased susceptibility to moderate resistance to chlorpyrifos (RR 4.63–19.58). The resistance to pymetrozine (RR 10.48–84.65) was moderate to high, and that to buprofezin (RR 6.36–412.43) was low to very high. In conclusion, the use of buprofezin and pymetrozine to control *S. furcifera* should be reduced in Guizhou Province, whereas prudent use at a reasonable frequency of chlorpyrifos and imidacloprid can continue. Isoprocarb and thiamethoxam are the best choices for effective management of *S. furcifera*. Rotations using alternative insecticides with different modes of action are recommended for regions in which resistance is at a moderate level.

Key words: *Sogatella furcifera*, neonicotinoid, pyridine, insect growth regulator, resistance monitoring

Sogatella furcifera (Horváth) (Hemiptera: Delphacidae) is one of the most serious migratory pests on rice crops throughout South and Southeast Asia (Atwal et al. 1967, Kisimoto 1971, Kisimoto 1976, Khan and Saxena 1985, Wu et al. 1997, Sogawa et al. 2009, Heong 2009, Lakshmi et al. 2010, Suri and Singh 2011, Matsumura et al. 2013). In addition to causing direct damage, *S. furcifera* is a vector of several rice pathogens, particularly the Southern rice black-streaked dwarf virus, which causes large yield losses (Shen et al. 2003, Wang et al. 2010, Pu et al. 2012, Zhou et al. 2013, Li et al. 2013, Tu et al. 2013, Lei et al. 2014).

Resistance of *S. furcifera* to the pesticides used for its control has gradually increased since the 1980s (Fukuda and Nagata 1969, Nagata and Masuda 1980, Endo et al. 1988, Endo and Tsurumachi 2001). Insecticide resistance may be one of the primary contributors to population surges, such as occurred with *Nilaparvata lugens* (Stål) (Wang et al. 2008). Before the 1990s, organophosphates, carbamates, and pyrethroids, including dichlorvos, isoprocarb, carbaryl, deltamethrin, and cypermethrin, were used to control *S. furcifera* and *N. lugens*. From the 1970s to the 1990s, these species of rice planthopper developed a remarkable degree of resistance to the commonly used insecticides across China, Thailand, southern Vietnam, and Malaysia (Nagata and Masuda 1980, Krishnaiah and Kalode 1988, Mao and Liang 1992, Endo and Tsurumachi 2001, Nagata et al. 2002). Neonicotinoid insecticides were developed after the 1990s (Jeschke and Nauen 2008) and were used intensively against rice planthoppers, including *S. furcifera*, in many rice-growing regions (Matsumura et al. 2013). However, since 2003, these neonicotinoids have been less effective. Imidacloprid, registered for use on rice in 1991, played a key role in the management of rice planthoppers in Japan, China, and Vietnam (Liang et al. 2007, Cheng 2009). However, the high resistance to imidacloprid in *N. lugens* eventually led to control failure in China in 2005 (Wang et al. 2008, 2009a; Li et al. 2009;

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Ecology and Behavior

Effects of Temperature on Development and Survival of *Orthopygia glaucinalis* (Lepidoptera: Pyralidae) Reared on *Platycarya strobilacea*

JIAN-FENG LIU,[1] MAO-FA YANG,[1,2] JI-FENG HU,[3] AND CHANG HAN[4]

J. Econ. Entomol. 1–11 (2015); DOI: 10.1093/jee/tov003

ABSTRACT The larvae of *Orthopygia glaucinalis* (L.) (Lepidoptera: Pyralidae) are used to produce insect tea in Guizhou, China. We investigated the development and survival of *O. glaucinalis* reared on dried leaves of *Platycarya strobilacea* under laboratory conditions at 19, 22, 25, 28, 31, 34, and 37°C. The duration of development from egg deposition to adult emergence decreased significantly with increasing temperature from 19 to 31°C, whereas the duration of egg and overall development significantly increased at 34°C. Based on the extreme-value distribution function, the optimal temperature for survival of overall development was 24.89°C, and the larval stage was most susceptible to temperature extremes. The common linear model and the Ikemoto and Takai linear model were used to determine the relationship between temperature and the developmental rate, and estimated the low-temperature threshold (11.44 and 11.62°C, respectively) and the threshold constant (1220.70 and 1203.58 degree-days, respectively) of *O. glaucinalis*. Nonlinear models were used to assess in fitting the experiment data and to estimate the high temperature thresholds (34.00 to 39.08°C) and optimal temperatures (31.61 to 33.45°C). An intrinsic optimal temperature of 24.18°C was estimated for overall development using the Sharpe–Schoolfield–Ikemoto (SSI) model. Model-averaged parameter estimates and the unconditional standard error were also estimated for the temperature thresholds. Based on the biological parameters and model selection, we concluded that common linear, Lactin-1, and SSI models performed better for predicting the temperature-dependent development of *O. glaucinalis*. Our findings enable breeders to optimize the developmental rate of *O. glaucinalis* and improve the yield of insect tea.

KEY WORDS *Orthopygia glaucinalis*, insect tea, developmental rate, critical threshold, model selection

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Insect tea is a unique specialty tea produced from the frass of certain insect larvae that have fed on particular plant species (You and Zhao 1979, Gao 1996, Xu et al. 2013, Liu et al. 2014). The use of insect tea was first documented in 1578 during the Ming Dynasty in "Compendium of Materia Medica" (Li 1982). The Chengbu Local Records (V) office in Hunan Province also has a record from 1906 related to the use of insect tea during the reign of Emperor Guangxu of the Qing Dynasty. Insect tea is a source of high quality protein and amino acids, and is often used to relieve summer heat, protect the spleen and stomach, and improve digestion (Wu 1997, Xu et al. 2013, Liu et al. 2014). Insect tea is extremely popular in the provinces in southwestern China and in certain Southeast Asian countries (Gao 1996).

Temperature is a critical abiotic factor that influences the dynamics of insect populations and that of their natural enemies (Huffaker et al. 1999, Nelson et al. 2013). The developmental rate of insects increases almost linearly below the limit of sublethal high temperatures (Wen 1997; Shang et al. 2012, 2013; Liu et al. 2014). The common and Ikemoto and Takai linear models have been used to predict the egg, larval, and pupal development of insects using physiological data (Wen 1997; Shang et al. 2012, 2013; Liu et al. 2014). Linear approximation and reduced major axis methods allow the estimation of low-temperature thresholds and thermal constants within a limited temperature range (Campbell et al. 1974, Ikemoto and Takai 2000). The developmental rate is essentially nil at the low-temperature threshold, and increases with increasing temperature. It reaches at a maximum at the optimal temperature, and decreases rapidly as the high-temperature threshold is approached (Roy et al. 2002, Aghdam et al. 2009).

Although the relationship between temperature and the developmental rate is approximately linear at moderate temperatures, it is curvilinear near the high- and

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BMC Genomics

RESEARCH ARTICLE Open Access

Fragmented mitochondrial genomes of the rat lice, *Polyplax asiatica* and *Polyplax spinulosa*: intra-genus variation in fragmentation pattern and a possible link between the extent of fragmentation and the length of life cycle

Wen-Ge Dong[1,2], Simon Song[3], Dao-Chao Jin[1*], Xian-Guo Guo[2] and Renfu Shao[3]

Abstract

Background: Blood-sucking lice (suborder Anoplura) parasitize eutherian mammals with 67% of the 540 described species found on rodents. The five species of blood-sucking lice that infest humans and pigs have fragmented mitochondrial genomes and differ substantially in the extent of fragmentation. To understand whether, or not, any life-history factors are linked to such variation, we sequenced the mt genomes of *Polyplax asiatica* and *Polyplax spinulosa*, collected from the greater bandicoot rat, *Bandicota indica*, and the Asian house rat, *Rattus tanezumi*, respectively.

Results: We identified all of the 37 mitochondrial genes common to animals in *Polyplax asiatica* and *Polyplax spinulosa*. The mitochondrial genes of these two rat lice are on 11 circular minichromosomes; each minichromosome is 2–4 kb long and has 2–7 genes. The two rat lice share the same pattern for the distribution of the protein-coding genes and ribosomal RNA genes over the minichromosomes, but differ in the pattern for the distribution of 8 of the 22 transfer RNA genes. The mitochondrial genomes of the *Polyplax* rat lice have 3.4 genes, on average, on each minichromosome and, thus, are less fragmented than those of the human lice (2.1 and 2.4 genes per minichromosome), but are more fragmented than those of the pig lice (4.1 genes per minichromosome).

Conclusions: Our results revealed distinct patterns of mitochondrial genome fragmentation within the genus *Polyplax* and, furthermore, indicated a possible inverse link between the extent of mitochondrial genome fragmentation and the length of life cycle of the blood-sucking lice.

Keywords: Mitochondrial genome, Genome fragmentation, Minichromosome, Chromosome evolution, Sucking lice

Background

Lice in the suborder Anoplura are wingless, exclusive blood-sucking insects and are permanent ectoparasites of eutherian mammals [1,2]. Blood-sucking lice evolved from chewing lice ~100 million years ago (Mya) and diversified rapidly ~65 Mya with their mammalian hosts [3]. More than 540 species of blood-sucking lice have been described and are classified into 15 families and 50 genera [4-7]. Twelve of the 29 recognized mammalian orders and ~840 mammalian species are hosts of blood-sucking lice. The diversity of blood-sucking lice mirrors that of their mammalian hosts with 67% of the described species found on rodents [2,5,7]. Each species of mammalian host is usually parasitized by a single species of blood-sucking lice, but there are exceptions as many mammalian species are hosts of multiple species of blood-sucking lice (up to seven species) [7]. Vice versa, each species of blood-sucking lice usually parasitizes only one species of mammals, but many species of blood-sucking lice parasitize multiple

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RESEARCH ARTICLE **Open Access**

Fragmented mitochondrial genomes are present in both major clades of the blood-sucking lice (suborder Anoplura): evidence from two *Hoplopleura* rodent lice (family Hoplopleuridae)

Wen-Ge Dong[1,2], Simon Song[3], Xian-Guo Guo[1*], Dao-Chao Jin[2], Qianqian Yang[4], Stephen C Barker[5] and Renfu Shao[3*]

Abstract

Background: The suborder Anoplura contains 540 species of blood-sucking lice that parasitize over 840 species of eutherian mammals. Fragmented mitochondrial (mt) genomes have been found in the lice of humans, pigs, horses and rats from four families: Pediculidae, Pthiridae, Haematopinidae and Polyplacidae. These lice, eight species in total, are from the same major clade of the Anoplura. The mt genomes of these lice consist of 9–20 minichromosomes; each minichromosome is 1.5–4 kb in size and has 1–8 genes. To understand mt genome fragmentation in the other major clade of the Anoplura, we sequenced the mt genomes of two species of rodent lice in the genus *Hoplopleura* (family Hoplopleuridae).

Results: We identified 28 mt genes on 10 minichromosomes in the mouse louse, *Ho. akanezumi*; each minichromosome is 1.7–2.7 kb long and has 1–6 genes. We identified 34 mt genes on 11 minichromosomes in the rat louse, *Ho. kitti*; each minichromosome is 1.8–2.8 kb long and has 1–5 genes. *Ho. akanezumi* also has a chimeric minichromosome with parts of two rRNA genes and a full-length tRNA gene for tyrosine. These two rodent lice share the same pattern for the distribution of all of the protein-coding and rRNA genes but differ in tRNA gene content and gene arrangement in four minichromosomes. Like the four genera of blood-sucking lice that have been investigated in previous studies, the *Hoplopleura* species have four minichromosomes that are only found in this genus.

Conclusions: Our results indicate that fragmented mt genomes were present in the most recent common ancestor of the two major clades of the blood-sucking lice, which lived ~75 million years ago. Intra-genus variation in the pattern of mt genome fragmentation is common in the blood-sucking lice (suborder Anoplura) and genus-specific minichromosomes are potential synapomorphies. Future studies should expand into more species, genera and families of blood-sucking lice to explore further the phylogenetic utility of the novel features associated with fragmented mt genomes.

Keywords: Mitochondrial genome, Genome fragmentation, Minichromosome, Chromosome evolution, Sucking lice

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