Regulation of lipid metabolism in Spodoptera frugiperda by the symbiotic bracovirus of the gregarious parasitoid Cotesia ruficrus

Li Xian[1], Zhang Shi-Ze[1*]
1. College of Plant Protection, Northwest A&F University, Yangling, Shaanxi, China
* shzzhang@nwafu.edu.cn

摘要：Parasitoids alter host energy homeostasis to create a favorable environment for their own development. However, the mechanisms underlying this process remain largely unexplored, especially for gregarious parasitoids. Cotesia ruficrus, a gregarious endoparasitoid native to China, targets the invasive pest Spodoptera frugiperda (fall armyworm, FAW) and has been shown to its effectively control FAW populations. This study investigates the role of the polydnavirus (PDV) produced by C. ruficrus in regulating lipid metabolism of FAW larvae. The results demonstrated that, following PDV injection for 5 days, both triglyceride concentrations and lipid droplet diameters in the fat bodies of FAW larvae significantly increased. RNA interference (RNAi) targeting the PDV gene CrBV3-31 led to a reduction in triglyceride concentrations and lipid droplet size, along with an upregulation of the LSD1 gene. Furthermore, silencing CrBV3-31 decreased triglyceride levels in C. ruficrus pupae and lowered its eclosion rate. These findings suggest that the PDV gene CrBV3-31 plays a crucial role in enhancing lipid accumulation in FAW larvae, thereby supporting the survival of C. ruficrus offspring. This study uncovers a novel mechanism by which gregarious endoparasitoids exploit symbiotic bracovirus genes to regulate host energy metabolism, increasing lipid levels to meet the developmental needs of their multiple offspring.

关键词：Cotesia ruficrus;Spodoptera frugiperda;Polydnavirus;CrBV genome;lipid metabolism

The pseudogerm in polyembryonic M. cingulum functions to modulate host physiology

Jian Hu[1*]
1. School of Agriculture and Biotechnology, Sun Yat-sen
University, Shenzhen, Guangdong, China
* lsshj@mail.sysu.edu.cn

摘要：Endoparasitoid wasps have evolved diverse strategies to counter host immune defenses. While the functional mechanisms of certain parasitic factors have been well characterized, the broader strategies employed by most endoparasitoids remain largely unexplored. Here, we report a novel parasitic factor—the pseudogerm, a syncytial structure likely derived from the polar body in the polyembryonic wasp Macrocentrus cingulum and its function.

We first examined DAPI staining during cleavage and early embryogenesis. The results showed that the polar bodies are retained and contribute to the formation of both embryos and pseudogerms. The syncytial nuclei of the pseudogerm are noticeably larger than the egg nuclei and divide more slowly during early cleavage. Secondary embryonic cells containing only polar body nuclei develop into syncytial pseudogerms, whereas cells containing both polar body nuclei and egg nuclei give rise to embryos. In this process, the egg nucleus directs the formation of the embryonic body, while the polar body nuclei guide the development of the syncytial extraembryonic membrane.

The cytoplasm of the pseudogerm is densely packed with endoplasmic reticulum and mitochondria and covered externally with microvilli, indicating strong secretory and absorptive capacities. In vitro culture and ultrastructural analyses indicate that pseudogerms can secrete exosomes. Sequencing of microRNAs from pseudogerms, embryos, and host hemolymph at different time points after parasitization shows that both pseudogerms and embryos release large amounts of microRNAs into the host hemolymph, among which 37 microRNAs are significantly upregulated post-parasitization and 26 are detected within exosomes secreted by pseudogerms. Proteomic and transcriptomic analyses further confirm that pseudogerms express a wide range of secretory proteins.

Embryo transplantation experiments demonstrate that pseudogerms can inhibit host cellular immune responses against wasp larvae. When five pseudogerms were co-transplanted with wasp embryos into naïve larvae of Ostrinia furnacalis, the encapsulation rate of the hatched wasp larvae decreased from 99% to 0%, furthermore, the pupation rate of host larvae decreased to 0 too, indicating that pseudogerm can inhibit host immune attack to wasp larvae and modulate the development of host larva to promote wasp larval survival within the host hemocoel. Further investigations revealed that miR-281-5p can suppress the expression of its target gene Apolipophorin in the host across species boundaries, thereby reducing its regulatory effect on hemocyte adhesion and inhibiting hemocyte encapsulation of wasp larvae. Additionally, pseudogerms can disrupt the host prothoracic gland, leading to decreased 20E production and suppression of host pupation (Zhang et al., 2025). miR-281-5p also downregulates E93 expression in the host, further interfering with pupation (under revision). These results indicate that microRNAs secreted by pseudogerms play an important role in manipulating host physiological processes, although the functions of many other microRNAs remain to be elucidated. Moreover, during the late developmental stages of the wasp larvae, pseudogerms can serve as a nutritional resource when consumed by the larvae, providing supplemental nourishment (Hu et al., 2015).

Our findings uncover a unique strategy that polar body originate parasitic factor, pseudogerm, manipulates host immunity and development to promote the survival of wasp larvae in host. These results provide further insights into the co-evolutionary mechanisms between parasitoid wasps and their hosts.

关键词：Parasitoid;parasitic factor;pseudogerm;microRNAs;modulation

Genetic Improvement of Fecundity Traits and Molecular Mechanisms in Trichogramma dendrolimi

HUI DONG[1], Wunan Che[2]

1. plant protection,Shenyang Agricultural University,Shenyang,Liaoning,China
2. plant protection,Shenyang Agricultural University,Shenyang,Liaoning,China

摘要：Trichogramma dendrolimi is an egg parasitoid and natural enemy widely employed for the biological control of various lepidopteran pests. The Wolbachia-induced thelytokous reproductive strain of T. dendrolimi exhibits significant pest control potential and holds promising applications in biological control. The reproductive traits of Trichogramma serve as crucial indicators for assessing its effectiveness in field pest control. Therefore, elucidating the molecular regulatory mechanisms underlying fecundity in Trichogramma is of paramount importance. Additionally, achieving targeted genetic enhancement of fecundity in the thelytokous strains of the pine caterpillar red-eye wasp is crucial for improving the efficacy of Trichogramma biocontrol in field conditions. This study compares the reproductive capacities of T. dendrolimi from different geographical populations to identify high-fertility (TdH) and low-fertility (TdL) strains. Hybridization and backcrossing experiments were conducted to determine the genetic inheritance patterns of reproductive traits in T. dendrolimi. BSA-seq analysis was employed to identify candidate genes regulating the reproductive traits in T. dendrolimi. RNAi technology was applied to silence the expression of candidate genes associated with reproductive capacity, thereby assessing their effects on fertility and exploring the regulatory roles of JH and 20E in the reproductive capacity of T. dendrolimi. Gradual introgression hybridization and molecular marker-assisted selection were employed to achieve targeted genetic improvement of the reproductive capacity in the thelytokous strain of T. dendrolimi. This thesis provides a theoretical foundation for the genetic improvement research on other natural enemy insects.

关键词：Trichogramma dendrolimi;Fecundity;Genetic improvement

The Dual Regulation of Insulin Signaling and Juvenile Hormone Pathway in Reproductive Diapause of the Natural Enemy, Seven-Spotted Ladybeetle (*Coccinella septempunctata*)

Junjie Chen[1], Yuyan Li[1], Nicholas M. Teets[2], Shunda Han[1], Lisheng Zhang[1 3]

(1 State Key Laboratory for Biology of Plant Diseases and Insect Pests, Key Laboratory of Natural Enemy Insects, Ministry of Agriculture and Rural Affairs, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, No. 2, West Yuan Ming Yuan Road, Beijing 100193, P. R. China; 2 Department of Entomology, University of Kentucky, Lexington, KY 40546, USA; 3 Plant Protection College, Shenyang Agricultural University, Shenyang 110866, P. R. China.)

Abstract

Understanding the regulation of diapause in natural enemy insects is crucial for improving the long-term storage, transportation, and field deployment of biological control agents. This study investigates the dual regulation of insulin signaling (IIS) and juvenile hormone (JH) pathways in reproductive diapause of the seven-spotted ladybeetle (*Coccinella septempunctata*), a key aphid predator. We demonstrate that enhanced JH degradation plays a critical role in diapause induction. Applying methoprene (a JH analog) to pre-diapause females elevated JH signaling and reversed the diapause program, confirming that low JH levels are essential for diapause induction. Conversely, RNAi knockdown of JH degradation genes increased expression of JH-inducible gene (*Kr-h1*), reduced diapause characteristics, and promoted reproduction (accelerated ovary growth, yolk deposition, suppressed lipid accumulation). Further, we show that IIS regulates diapause via the transcription factor FoxO. In diapausing beetles, exogenous insulin application or RNAi knockdown of *CsFoxo* terminated diapause. Conversely, in non-diapausing beetles, RNAi knockdown of the insulin receptor (*CsInR*) arrested ovarian development and decreased JH levels, inducing a diapause-like state. Collectively, these results reveal that shutdown of insulin signaling activates CsFoxO, driving the diapause phenotype, while reduced JH titer facilitates reproductive arrest. This dual regulatory mechanism provides fundamental insights into *C. septempunctata* diapause control.

Neonicotinoid insecticide imidacloprid induces chemosensory deficits in a nontarget parasitoid wasp

Wenqi Shi[1], Jianhua Huang[1]*
1. Institute of Insect Sciences, Zhejiang University, Hangzhou, Zhejiang, China
* jhhuang@zju.edu.cn

摘要：Chemical pesticides are widely used to manage the population of arthropod pests. Their increasing use in agriculture has raised concerns about their harmful effects on nontarget organisms, particularly some beneficial insects such as parasitoid wasps. To assess the potential risk and ecological safety of chemical pesticides, it is necessary to understand their impacts on the physiology and behaviour of those important natural enemies of arthropod pests. Here, we applied the Drosophila parasitoid Leptopilina drosophilae as a study model to investigate the effects of sublethal doses of imidacloprid, a widely used neonicotinoid insecticide. Our results demonstrated the detrimental effects of imidacloprid on the host-searching behaviour of L. drosophilae females and the courtship behaviour of L. drosophilae males. Comparative transcriptome and functional analysis provided further insights into the potential mechanisms underlying the impaired behaviours, with the downregulated expression of certain chemoreception genes in both female and male exposed wasps. Our findings thus emphasize the importance of understanding the risks associated with the use of chemical pesticides and the need to develop more eco-friendly pest management strategies for a sustainable balance between chemical and biological control.

关键词：Parasitoid wasps;Imidacloprid;Host-searching behaviour;Courtship behaviour;Comparative transcriptome;Chemoreception genes

Nanocarrier-mediated transdermal delivery of Lmidgf4 dsRNA expedites biological control of locusts by Beauveria bassiana

Kong Xue[1], Tan Shuqian[1], Guan Mei[1], Lin Xiaoxin[1], Shen Jie[1], Shi Wangpeng[1], Wang Dan[1]*

1. College of Plant Protection, China Agricultural University, Beijing, Beijing, China

* dwang@cau.edu.cn

摘要：Locusts have been a major global agricultural pest that poses a serious threat to crop and livestock production. Entomopathogenic fungi (EPF) provide an eco-friendly control method; however, their efficacy usually takes slow and is unstable. To achieve an enhancement of the biocontrol efficacy of Beauveria bassiana (B. bassiana) against locusts, we developed a new strategy by which B. bassiana and nanocarrier-mediated dsRNA are co-applied across the locust cuticle. The nanocarrier star polycation (SPc) effectively delivers Lmidgf4 dsRNA (dsLmidgf4) into the locust, which targets Locusta migratoria imaginal disc growth factor 4 (Lmidgf4). SPc protects dsLmidgf4 from degradation by the hemolymph and enables efficient gene silencing. Furthermore, SPc has no adverse effects on B. bassiana spore germination and growth. Lmidgf4 interference leads to a thinner layer of endocuticle, thus facilitates infection of B. bassiana, and finally reduces the median lethal time of locusts infected with B. bassiana. In conclusion, the combination of B. bassiana and dsRNA/SPc complex overcomes the slow action of fungi, providing a novel strategy for field control of locusts.

关键词：Nanocarrier;Transdermal delivery;Fungi;Imaginal disc growth factor 4;DsRNA;Locust

Effects of host age, parasitoid age, and superparasitism on reproductive fitnss of Macrocentrus cingulum (Hymenoptera:Braconidae), a larval polyembryonic parasitoid

Qianqian Mi;[1], Feng Zhang[2,3*], Jian Hu[1*]
1. School of Agriculture and Biotechnology, Sun Yat-sen Universsity, Shenzhen, Guangzhou, China
2. MARA-CABI Joint Labortary for Bio-safety, Institute of Plant Protection, Chiese Academy of Agricultural Sciences, Beijing, Beijing, China
3. CABI East & South-East Asia, CABI, Beijing, Beijing, China
* f.zhang@cabi.org, lsshj@mail.sysu.edu.cn

摘要：The Asian corn borer, Ostrinia furnacalis (Guenée), is an important pest of maize that is found throughout Asia, Australia, Africa, and the Western Pacific Islands. Larvae of O.furnacalis feed all parts of corn plants, and boring in ears and stalks can cause severe damage. Several reports indicate this pest has caused 40-60% yield losses in the Philippines and 6-9 million tons of lost yield annually in China . Macrocentrus cingulum Brischke (Hymenopetera: Braconidae) is a polyembryonic endoparasitoid that is a promising species for control of O.furnacalis larvae. M.cingulum can deposit more than one egg in one host larvae, producing several hundred embryos and early-instar larvae through clonal division inside the host, but only 40-90 progenies emergence from the host eventually. Thus, intraspecific competition among immature larvae for host resources occurred frequently.

We investigated the main factors likely to influence progeny production by M. cingulum when reared in O. furnacalis, i.e., host age and parasitoid age, focus on effects on the parasitism rate, brood size, and progeny sex ratio. We also examined the influence of superparasitism on brood size during both the larval and adult periods. These findings facilitate the mass rearing of M. cingulum, and suggest conditions useful to maximize production of this polyembryonic parasitoid for releases against O. furnacalis.

关键词：biological control; reproductive efficiency;polyembryonic parasitoid

Multi-level Investigation of Diapause in *Arma chinensis*: Transcriptomics, Metabolomics, and Functional Studies

Maosen Zhang[1#], Junjie Chen[1#], Yuyan Li[1*], Nicholas M Teets[3], Lisheng Zhang[1,2 *]

[1]State Key Laboratory for Biology of Plant Diseases and Insect Pests, Key Laboratory of Natural Enemy Insects, Ministry of Agriculture and Rural Affairs, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, No. 2, West Yuan Ming Yuan Road, Beijing 100193, P. R. China;

[2]Key Laboratory of Animal Biosafety Risk Prevention and Control (North) of Ministry of Agriculture and Rural Affairs, Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Shanghai 200241, China;

[3]Department of Entomology, University of Kentucky, Lexington, KY 40546, USA

[#]Contributed equally

[*]Correspondence

Abstract

The predatory stinkbug Arma chinensis is an important biological control agent whose diapause mechanisms are crucial for storage and field application. We conducted an integrated multi-omics study combining transcriptomic, metabolomic, and functional analyses to elucidate diapause regulation in this species. Transcriptomic and metabolomic profiling revealed 9,254 differentially expressed genes and 493 altered metabolites across diapause stages. Major metabolic pathways including glutathione metabolism, TCA cycle, glycolysis, and lipid metabolism underwent significant reorganization. Pre-diapause was characterized by increased lipid accumulation and energy consumption, while maintenance phase showed amino acid and glucose metabolism restructuring.

We identified the dopamine D2-like receptor (AcDD2R) as a key neuroendocrine regulator. AcDD2R expression peaked in head tissue during pre-diapause. RNA interference demonstrated that AcDD2R negatively regulates lipid accumulation by suppressing lipogenic genes (acetyl-CoA carboxylase and fatty acid synthase). DD2R knockdown not only increased lipid storage but also enhanced post-diapause reproductive fitness, shortening pre-oviposition period and increasing egg production and hatchability. This comprehensive characterization reveals coordinated metabolic reprogramming and neuroendocrine control of diapause in A. chinensis. The identification of DD2R as a regulator of both lipid metabolism and reproductive fitness provides potential targets for optimizing diapause manipulation in biological control programs.

Sorbitol Suppression in Spodoptera frugiperda Enhances Parasitoid Development and Fitness

Yu-Si Chen[1], Zhi-Wei Wu[1], Xiao-Han Shu[1], Jia-Chen Zhu[1], Li-Cheng Gu[1], Xi-Qian Ye[1], Zhi-Zhi Wang[1*], Xue-Xin Chen[1*]
1. Institute of Insect Sciences,College of Agriculture and Biotechnology,Zhejiang University,Hangzhou,Zhejiang,China
* zzwang0730@zju.edu.cn,xxchen@zju.edu.cn

摘要：Parasitoid parasitism reprograms host metabolism to nourish the developing offspring, yet its impact on alternative carbohydrate pathways, such as the polyol pathway, is poorly understood. Here, we demonstrate that a generalist parasitoid wasp Meteorus pulchricornis suppresses sorbitol contents in its host Spodoptera frugiperda larvae, by downregulating polyol metabolism in the fat body. Two aldose reductase genes, AKR1B1-1 and AKR1B1-2, responsible for catalyzing glucose-to-sorbitol conversion, are identified as key mediators of this metabolic shift. Furthermore, sorbitol restoration in hosts disrupts parasitoid larval development and reduces its fitness, including a decrease in pupation rate, reduced cocoon weight, smaller adult size and lower parasitism rates. Transcriptomic analysis and the fluctuating wasp ROS level suggest that the elevated host circulating sorbitol may disrupt redox homeostasis in developing wasp larvae. These findings provide new insights into host-parasite metabolic interactions centered on polyol metabolism and lay the groundwork for enhancing parasitoid-based biological control strategies.

关键词：Host-parasite interaction;sorbitol;polyol pathway;aldose reductase;parasitoid fitness

The application of SPP in insects: Resistance Breeding and Biological Control

Yuting Feng[1], Chunyan Yang[1], Qianlan Tan[1], Lin Wu[1], Xi Qin[1], Yuancheng Wang[1], Qingyou Xia[1], Ping Lin[1]*, Guanwang Shen[1]*

1. Integrative Science Center of Germplasm Creation in Western China (Chongqing) Science City, Biological Science Research Center, Southwest University, Beibei, Chongqing, China

* linpingswu@swu.edu.cn, gwshen@swu.edu.cn

摘要：Signal peptide peptidase (SPP) is an intracellular lysate aspartate protease with significant evolutionary conservation and a broad spectrum of biological functions. It regulates normal immune surveillance of cells, hydrolyzes signal peptides, promotes the release of epitope-containing fragments, and prevents natural killer cells (NK) from erroneously damaging normal cells. Additionally, it interacts with glycoproteins on the virus surface, influencing its processing and reproduction. It can also be utilized by the virus to evade the killing of the host immune system. SPP plays an important role in human immunity, but its role in silkworms remains unclear. Here, we obtained the $BmSPP^{KO}$ knockout strain using CRISPR/Cas9-based gene editing. We found that the DNA content of Bombyx mori nucleopolyhedrovirus (BmNPV) was significantly decreased in $BmSPP^{KO}$ silkworms compared to the control, resulting in an 12.4% lower mortality. It indicates that BmSPP plays a negative regulatory role in silkworm resistance to BmNPV infection and is a target gene of BmNPV virus resistance in silkworm. In addition, we also found that $BmSPP^{KO}$silkworms showed a susceptibility phenotype to Beausteria bassiana. This was caused by the inhibition of chitin synthesis in the epidermis of Bombyx mori, leading to a reduction in the thickness of the chitin layer in the epidermis. These results indicate that SPP can serve as an important target gene, it can not only play a significant role in the breeding of BmNPV resistance in silkworms, but also act as a target gene to improve the biological control effect of Beausteria bassiana and establish a solid research foundation for the broad-spectrum synergism of Beausteria bassiana in pest control.

关键词：SPP;antiviral;BmNPV;Beauveria bassiana;biological control

Estrogen-Related Receptor Potential Target Genes in Silkworm (Bombyx mori): Insights into Metabolic Regulation

Luyu Hou[1], Jinxin Wu[1], Die Liu[1], Haoran Xu[1], Hongbo Yao[1], Yiwen Liang[2], Qingyou Xia[1], Ping Lin[1], Guanwang Shen[1]*
1. Biological Science Research Center, Southwest University, Chongqing, Chongqing, China
2. College of Sericulture, Textile and Biomass Sciences, Southwest University, Chongqing, Chongqing, China
* gwshen@swu.edu.cn

摘要：Estrogen-related receptors (ERRs) are important transcription factors within the nuclear receptor family that regulate cellular energy storage and consumption by binding to estrogen-related receptor response elements (ERREs) on gene promoters. While ERRs' role in vertebrates is well-studied, their molecular mechanisms in insect metabolism and development remain unclear. This study systematically summarizes the functions of ERRs in insects, focusing on silkworms by analyzing gene functions and comparing databases. ERRE-like elements were identified in the 2000 bp upstream promoter regions of 69 metabolism-related silkworm genes. Furthermore, electrophoretic mobility shift assays (EMSAs) revealed that ERREs within the promoters of 15 genes related to sugar, fat, and protein metabolism specifically bind to ERR. Notably, an ERRE in the promoter of the trehalose transporter 1 gene (BmTret1), crucial for trehalose homeostasis in insect hemolymph, exhibited significantly enhanced activity in ERR-overexpressing cells. These findings suggest that ERR is a potential regulatory factor in silkworm metabolism and refine its metabolic regulatory network. This study highlights the broader and more critical role of ERR in insects than that previously recognized, contributing to a deeper understanding of insect metabolism and its potential applications in related fields.

关键词：estrogen-related receptor; estrogen-related receptor response element; metabolic regulation; physiological function; silkworm

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

Xi-Yu Bao[1], Jun-Bo Luan[1*]
1. College of Plant Protection, Shenyang Agricultural University, Shenyang, Liaoning, China
* jbluan@syau.edu.cn

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

关键词：amino acids;hormone;HTGs;reproduction;Rickettsia;symbiont;TOR;whitefly