Insect science for new approaches to pest management and exploitation of beneficial insects

John A. Pickett
School of Chemistry, Cardiff University, Wales, UK

Abstract: The study of insect science offers new approaches and products for management of pests and particularly improved exploitation of beneficial insects for biological pest control. In initially addressing the young scientists in the audience, I will offer some advice and also ideas on my approach to science and specifically insect science. Studying the natural induction of chemically based defenses against herbivores by crop plants has proved valuable and can provide direct reduction of herbivory in addition to increasing foraging by natural pest enemies, including hymenopterous wasps. These approaches are intrinsically more sustainable than traditional approaches of using insecticides with toxic modes of action to which there is rapid selection for resistance and because of potential non-target effects on beneficial insects including both biological control agents and pollinators. There is inevitably a very strong likelihood of the selection for resistance to the new products acting behaviorally against pests and in promoting foraging by biological control agents. However, by understanding and exploiting the evolutionary nature of these new resistance traits, rational solutions will be readily available. The ultimate goal is to promote the sustainability potential of the creation of perennial arable crops and to use the types of inducible defense developed for crop protection to manage the wider needs of crops by means of sentinel plants. This would minimise current intensive energy consumption in crop cultivation by obviating ground preparation and seasonal sowing which would promote a more productive crop rhizosphere including nutrient and water conservation.

New functions of venom and domesticated endogenized viruses (DEVs) in host-parasitoid interactions

Xuexin Chen
Agriculture, Life and Environmental Sciences, Zhejiang University, China.

Neofunctionalization of Toll signaling: Evolution of dorsoventral axis formation in insects

Siegfried Roth

Institute of Zoology, University of Cologne, Germany.

Abstract: Toll signaling plays a crucial role in pathogen defense throughout the animal kingdom. It was discovered, however, for its function in dorsoventral (DV)axisformation in Drosophia. In all other insects studied so far but not outside the insects, Toll is also required for DV patterning. However, in insects more distantly related to Drosophila,Toll's patterning role is frequently reduced and substituted by an expanded influence of BMP signaling, the pathway implicated inDV axis formation in all major metazoanlineages. This suggests that Toll was integrated into an ancestral BMP-based patterning system at the base of the insects or during insect evolution. The observation that Toll signaling has an immune function in the extraembryonic serosa, an early differentiating tissue of most insect embryos, suggests a scenario of how Toll was co-opted from an ancestral immune function for its new role in axis formation.

Nutritional specialization and social evolution in woodroaches and termites

Sheng Li
Guangdong Provincial Key Laboratory of Insect Developmental Biology and Applied Technology, Institute of Insect Science and Technology & School of Life Sciences, South China Normal University, Guangzhou, China.

Abstract: Woodroach biparental-care and termite sibling-altruism evolved from solitary cockroach ancestors following nutritional specialization on dead-wood, but the genomic changes during these transitions are unclear. We sequenced eight Blattodea species showing increasingly contracted genomes. Woodroach brood-rearing remained constrained by deactivated oxidative phosphorylation and peroxisome genes, explaining slow immature growth. The termites lost key genes mediating sperm motility, confirming that reproductive division of labor required monogamous colony-founding. They also co-opted many genes from fundamental nutrition-sensitive juvenile hormone, insulin, EGFR and Dpp signaling pathways, enabling that most larvae develop as workers via high energy-metabolism early in development, while reproductive nymphs highly express energy-metabolism genes late in development. These pathways are consistent with obligate dependence on provisioning by sterile workers and feedback loops allowing large homeostatic colonies to evolve.

Gene editing reveals novel functions of a caterpillar salivary enzyme

Gary W. Felton
Department of Entomology, The Pennsylvania State University, University Park, Pennsylvania, USA
gwf10@psu.edu

Abstract: Glucose oxidase is a prevalent enzyme found in the saliva of many caterpillar species, and intriguingly, its interaction with host plants yields contrasting outcomes. In some plants, the enzyme suppresses direct defensive mechanisms — such as toxin production or wound-induced proteins — thus facilitating herbivory. However, in other host plants, the very same enzyme appears to activate defensive responses, ultimately increasing resistance to caterpillar feeding. This dual effect presents a fascinating evolutionary puzzle: why do caterpillars consistently produce glucose oxidase in such abundant quantities, despite its potentially counterproductive impact? From an evolutionary standpoint, this raises critical questions about the net fitness benefits conferred by the enzyme. If glucose oxidase can trigger harmful defenses in certain plants, why hasn't natural selection favored caterpillars that modulate or reduce its expression? To explore this evolutionary conundrum, we employed CRISPR-Cas9 gene editing to generate *Helicoverpa zea* (tomato fruitworm) mutant lines lacking functional glucose oxidase activity. Through targeted bioassays, we discovered unexpected roles for the enzyme beyond plant interaction—including enhanced protection against microbial pathogens and parasitoids, as well as alternative mechanisms for mitigating direct plant defenses.

Molecular insights into insect cuticle formation

--------Recent advances in our lab

Qing Yang
Agricultural Genomics Institute at Shenzhen, Chinese, Academy of Agricultural Sciences

Abstract: The insect cuticle is a multifunctional exoskeleton essential for protection, development, and environmental interaction. Its formation involves highly coordinated processes of chitin, cuticle protein-assisted assembly and lipid transport. Qing Yang's lab has made significant advances in uncovering the molecular underpinnings of insect cuticle formation, with a focus on identifying novel components, regulatory mechanisms, and potential targets for pest control. Through a combination of transcriptomics, proteomics, and functional genetics, the lab has identified key enzymes and structural proteins involved in cuticle biosynthesis, including previously uncharacterized chitin synthases, chitin deacetylases, and cuticular protein families. These findings highlight the importance of molecular self-organization in forming mechanically robust yet flexible cuticular layers. Additionally, Qing Yang's lab has pioneered structure-guided strategies to explore the interaction networks among cuticle components, providing insight into how chitin fibers are embedded within proteinaceous matrices. This work has led to the discovery of molecular features unique to insect cuticles, offering promising avenues for the development of species-specific, environmentally safe pesticides.

How Parasitoid Wasp Venoms Manipulate the Development and Physiology of Their *Drosophila* Hosts

Ryusuke Niwa

Life Science Center for Survival Dynamics, Tsukuba Advanced Research Alliance (TARA) at the University of Tsukuba, Japan

Abstract: Parasitoid wasps are one of the most diverse groups of animals. They inject various venoms into their hosts to control their development and physiology, achieving successful parasitism. However, the molecular mechanisms of venom-induced host manipulation at the molecular and cellular levels remain largely unexplored.

To address this issue, we use *Asobara japonica*, a Braconidae endoparasitoid wasp, and the host species *Drosophila* as a model. The adult wasp lays a single egg inside the larval body of the host *Drosophila*. The wasp larva preys on its host body after the host becomes a pupa, and then the adult wasp emerges from the host fly pupal case. We found that *A. japonica* infection rapidly induced imaginal disc degradation (IDD), which was mediated by apoptosis, autophagy, and inhibition of cell proliferation, while other tissues appeared intact. IDD was caused by the venom injected into the host by the wasp. To identify and characterize responsible wasp venoms for IDD, we performed whole genome sequencing of *A. japonica* [Kamiyama et al. (2022) PMID 35686927], followed by transcriptomics, proteomics, comparative genomics, and wasp RNAi approaches. We eventually identified two responsible genes encoding novel secretory proteins, designated IDD factor (IDDF)-1 and IDDF-2. RNAi of IDDF-1 or IDDF2 almost completely abrogated the venom-induced apoptosis, autophagy, and inhibition of cell proliferation in the host imaginal discs, significantly suppressing IDD. Notably, the RNAi wasps exhibited a lower parasitism success rate than the control wasps. Our study highlights the hacking strategy of the endoparasitoid wasp, which contributes to successful parasitism by preventing host metamorphosis [Kamiyama et al. (2025) PMID 39879297].

In this presentation, we will also introduce our ongoing comparative experimental and genomic approaches using not only *A. japonica* but also other Asobara parasitoids.

Diversified Seasonal Adaptations in Insects

Shuai Zhan
CAS Center for Excellence in Molecular Plant Sciences (CEMPS) in China.

Abstract: Seasonal adaptation is crucial for insects from around the globe, particularly for those living in temperate regions. Insects have evolved highly diversified strategies for seasonal adaptation, including various forms of migration and diapause. We have applied integrative approaches to characterize a suite of genes involved in seasonal migration and phase changes across several representative systems. For studying diapause, we recently utilized the domestic silkmoth, which exhibits characteristic voltinism phenotypes across strains, as a system to identify the genetic basis underlying diapause variations. We applied forward genetic and GWAS approaches across hundreds of strains, and localized the most effecting locus to the 5′ region of a central clock gene, Cycle. We identified a 1-bp deletion unique to non-diapause strains as the key causal allele, which disrupts one specific isoform of CYC (CYC-C). We further showed that this isoform controls diapause in silkmoths, while the other isoforms (A and B) appear to play the native role of CYC as a fundamental component of circadian regulation. The functional diversity of CYC has been conserved across a wide range of Lepidoptera taxa for over 100 million years. Our findings highlight the importance of circadian clock genes in seasonal adaptation and suggest diverse scenarios regarding how these genes link seasonal rhythms to daily rhythms.

Receptor-mediated specificity in tritrophic plant-pest-predator interactions

Adam D. Steinbrenner
Department of Biology, University of Washington, Seattle, WA, USA
astein10@uw.edu

Abstract: Plants deploy direct and indirect defenses in response to insect herbivory. The specific antiherbivore responses involve cell surface immune receptors that recognize herbivore associated molecular patterns (HAMPs), yet the ecological relevance of this molecular interplay remains unexplored. We demonstrate that the Inceptin Receptor (INR) encoded by common bean (Phaseolus vulgaris), upon recognition of inceptin, a HAMP in caterpillar oral secretions, orchestrates a defense response mediated by tritrophic interactions with predatory wasps. Laboratory and field experimentation in Mexico using a naturally occurring inceptin-insensitive mutant (BC6F2 inr-1) and its near-isogenic line (NIL) INR equivalent, revealed that inceptin recognition by INR activates an herbivore-specific immune pathway, and triggers the emission of a volatile blend of methyl salicylate and homoterpenes that recruits predatory wasps. In the field, we found that pairs of the responsive parent line PI 311785 and inr-1/inr-1 NIL plants treated with oral secretions derived from fall armyworm demonstrated 40% reduction of attack to sentinel caterpillars by predatory Polybia sp and Mischocyttaurus sp wasps to inr-1/inr-1 plants. Similarly in 2024, pairs of NILs treated with a physiologically relevant concentration or excess of In11 showed a 40% reduction of attack to inr-1/inr-1 across two independent experiments, while there was no difference in visitation for mock treated plants (w + H2O). Our findings establish a direct link between the molecular recognition of herbivores and ecologically relevant tritrophic outcomes, providing insight into the potential mechanistic basis for the effectiveness of traditional intercropping systems such as the Mesoamerican Milpa and push-pull agriculture. Findings from this Phaseolus vulgaris case study may also translate to other Integrative Pest Management (IPM) practices, e.g. companion planting and agroecosystems relevant to soybean agriculture in regions prone to outbreaks of lepidopteran pests.

Deciphering the molecular mechanisms underlying high reproductive capacity in insects

Shutang Zhou
State Key Laboratory of Cotton Bio-breeding and Integrated Utilization, School of Life Sciences,
Henan University

Abstract: Insects are characterized by their high fecundity. A hallmark of female insect reproduction is vitellogenesis, a heterosynthetic process by which vitellogenin (Vg) is synthesized in the fat body, transported through patency on the follicular epithelium, and deposited into developing oocytes. We found that UDP-glucosyltransferase mediates detoxification of the plant defense chemical DIMBOA, allowing insects to utilize poaceous plants for growth and reproduction. Insulin and gonadotropic juvenile hormone (JH) coordinately promote Vg expression by respectively regulating USF expression and phosphorylation-dependent activation. A duplicated paralogue of insulin receptor that is predominantly expressed in adult fat body functions distinctively for massive Vg synthesis required for synchronous oocyte maturation. Epigenetic regulation by succinylation at H3K23, triggered by the GPCR-PLC-PKC-GCN5 cascade, is indispensable for reproductive capacity. Moreover, JH acts via its receptor and the LCMT1-PP2A-FoxO pathway, inducing endoreplication and polyploidization for enhanced Vg synthesis. While patency is opened by Na+/K+-ATPase activated by the PLC-IP3R-PKC signaling, it is enlarged by GPCR-Cdc42-aPKC-Par3 modulated remodeling of zonula adherens between follicle cells. In addition, JH activates the GPCR-PLC-PKCι cascade for Vg receptor (VgR) phosphorylation that is prerequisite for VgR-mediated endocytosis of Vg into oocytes. Collectively, the findings advance our understanding of how insects possess high reproductive capacity and lay a large number of eggs.