

Insect Neuropeptide Hormone, Pheromone and Pest Management

Man-Yeon Choi

Center of Medical, Agricultural, and Veterinary Entomology, USDA-ARS

Neuropeptides are the largest group of neurohormones that act in intercellular communication to regulate various physiological and behavioral events during development and reproduction in animals. One of these families is Pyrokinin/PBAN (P_heromone B_iosynthesis A_ctivating N_europeptide) family defined by a similar 5-amino-acid C-terminal sequence (FXPRLamide) that is the active core fragment for these peptides. This motif has been identified from a variety of insect orders, and even a crustacean species. This family of peptides has been implicated in various physiological functions: 1) moth pheromone biosynthesis, 2) larval melanization, 3) moth embryonic and pupal diapause, 4) visceral muscle contraction in the cockroach, 5) fly puparium formation in different insect species. To date, ~159 PBAN/Pyrokinin family peptides have been identified from 40 species. It is one of the largest neuropeptide families in insects; however, the physiological function of most of these peptides is unknown. The mechanism of PBAN control over pheromone production is only well defined for sex pheromone biosynthesis in a limited number of lepidopteran moths. No other insect groups have been reported to regulate pheromone biosynthesis using PBAN.

Conventional insecticides target synapses and/or sodium channels that result in neurotoxicity in the nervous system. Unfortunately, this mode of action affects non-target animals as well. These methods remain the major tool for pest control, and the side effects cause many global problems that result in increased environmental and human health expenses. Therefore, *we are faced with a requirement to develop new targeted control agents that will lead to pesticides with new modes of action.* This is not impossible, but not easy. Every species-specific neuropeptide is expected to play a critical physiological function in metamorphosis and development of insects. There are no exceptions.

Our long-standing question is – “*how can interference/disruption of the insect (neuro)hormonal system be used to discover novel control tools*”. To solve this question a novel approach is being applied for finding and screening novel agonist and/or antagonist to gene products, neuropeptide and receptor, from the in vitro system and through virtual modeling. *This concept will be a new paradigm opening the window for the next generation of the pest control, and the principle method will be adapted for insect specific pests.*

Another research interest here will be presented on exocrinal products, such as semiochemicals produced from insects and plants for chemical communication that regulates insect/insect and insect/host interactions. These studies have included the identification of pheromones and the biosynthetic pathway of their production from insects. *The ultimate goal of this research is to discover novel biologically-based green pesticides that are environmental-friendly pest control alternatives.*

Molecular Mechanism and Evolution of Female Post-mating Behavior: Insights from *Drosophila* Sex Peptide Receptor

Young-Joon Kim¹ & Barry J. Dickson²

¹School of Life Sciences, Gwangju Institute of Science and Technology (GIST), Gwangju 500-712, Republic of Korea

²Research Institute of Molecular Pathology (IMP), Dr. Bohr-Gasse 7, A-1030 Vienna, Austria

Upon mating, females of many animal species undergo dramatic changes in their behavior. In *Drosophila melanogaster*, post-mating behaviors are triggered by sex peptide (SP), a key modulatory substance produced in the male seminal fluid and transferred to female during copulation. SP modulates female behaviors by acting on the sex peptide receptor (SPR) located in a small subset of internal sensory neurons that innervate the female uterus and project to the central nervous system (CNS). Interestingly, however, SPR is also expressed broadly in the CNS of both sexes. Moreover, SPR is also encoded in the genomes of insects that lack obvious SP orthologs. Based on these observations, we speculated that SPR may have additional ligands that are only distantly related to SP, if at all. If so, then this also raises questions on the evolution of SP-SPR signaling. To begin to address these questions, we set out to identify additional ligands for SPR. Here, we identify myoinhibitory peptides (MIPs) as a second family of SPR ligands that is conserved across a wide range of invertebrate species. MIPs are potent agonists for *Drosophila*, *Aedes* and *Aplysia* SPRs *in vitro*, yet are unable to trigger post-mating responses *in vivo*. In contrast to SP, MIPs are not produced in male reproductive organs, and are not required for post-mating behaviors in *Drosophila* females. We conclude that MIPs are evolutionarily conserved ligands for SPR, which are likely to mediate functions other than the regulation of female reproductive behaviors. Therefore, we propose that SPR has a different ancestral function, with a role in post-mating behavior arising only recently in *Drosophila* evolution, concomitant with the emergence of its novel SP ligand.

Key words: Female post-mating behavior, Sex peptide receptor, Evolution

Mitochondrial genomics approaches to insect identification and species delimitation

Stephen L. Cameron¹

¹Australian National Insect Collection, Commonwealth Scientific and Industrial Research Organisation, Black Mountain Laboratories, Canberra, AUSTRALIA

Due to their ease of sequencing and high levels of nucleotide diversity mitochondrial (mt) genes have long been favoured targets for investigations of species level issues in systematic entomology particularly species delimitation and diagnostic identification. Advances in sequencing technology and price reductions have now made routine sequencing of whole insect mt genomes feasible and thus the application of much larger datasets to these perennial problems can be attempted. I will present two examples – the development of diagnostic targets within forensically important blowflies (Diptera: Calliphoridae) from scans of whole mt genome variability and the determination of species status within the cotton bollworm (Lepidoptera: Noctuidae: *Helicoverpa*) – to illustrate the ease and comparative cheapness of genomics level approaches to these age old problems.

Key words: DNA diagnostics, Species delimitation, Calliphoridae, Noctuidae

Hsc70B*, An Antiviral Gene in *Anopheles gambiae

Seokyoung Kang and Young Seok Hong

Department of Tropical Medicine, Tulane University, New Orleans, Louisiana, USA

Mosquito-borne viral pathogens infect millions of people worldwide, often resulting in fatal infections. Our research interests in mosquito vector biology focuses on understanding of the molecular and genetic basis of mosquito resistance to arbovirus infections. Unlike mammalian cells including humans, for instance, mosquito cells do not show pathologic symptoms when infected by arboviruses. This observation led us to embarking a microarray study to investigate mosquito-virus interactions using *Anopheles gambiae* and o'nyong-nyong virus (ONNV) as a model system. As a result, we found that transcription of the *hsc70B* gene is increased about 2.6-fold in ONNV-infected *An. gambiae* compared to non-infected controls. Subsequently, *in vivo* RNAi silencing of the *hsc70B* transcript caused enhanced ONNV replication in female mosquitoes. Therefore, these results suggest that the *hsc70B* protein has an inhibitory effect on ONNV replication. A promoter analysis of the *hsc70B* locus further demonstrated that the *hsc70B* promoter is able to induce transcription of *hsc70B* in response to ONNV infection. In addition, *hsc70B* transcription was also induced by West Nile or La Crosse virus infection. Collectively, our findings indicate that *hsc70B* plays a role in suppressing virus replication as a general antiviral mechanism. Implications of *hsc70B* research and our other research endeavors toward the control of mosquito-borne infectious diseases will be discussed.

Key words: *Anopheles gambiae*, mosquito-borne infectious, o'nyong-nyong virus, RNAi silencing

진딧물 기생봉 *Aphelinus asychis*의 기능반응과 공간분포

변영웅, 김정환, 최만영, 김성현

국립농업과학원 곤충산업과

진딧물 기생봉 *A. asychis*의 기능반응을 구명하기 위해 페트리디쉬 내의 가지잎에 복숭아혹진딧물과 감자수염진딧물을 각각 밀도별(5, 10, 20, 30, 50마리)로 접종하고(9반복) 25°C, 16L:8D 조건에서 24시간 동안 기생당한 진딧물 수를 이용하여 기능반응을 분석하였다. Type I, Type II, Type III (Hassell, 1978) 기능반응식에 데이터를 fitting한 결과, Type III 기능반응 그래프와 동일하였으며, BIC (Bayesian Information Criterion)의 값도 Type III에서 가장 낮아서 *A. asychis*는 두 진딧물에 대해 Type III 기능반응을 나타내었다. 기생봉의 두 진딧물에 대한 탐색효율(a)과 핸들링타임(T_h)은 유의한 차이가 없었다. *A. asychis*의 기능반응과 공간분포를 구명하기 위하여 포트에 정식한 가지유묘를 망사케이지(120×120×70cm)에 넣고 복숭아혹진딧물을 가지유묘의 상, 중, 하 위엽에 고르게 밀도별(3, 6, 9, 12마리)로 접종하고 교미한 암컷 *A. asychis* 1마리를 정중앙 유묘에 방사한 후 3일 간격으로 머미와 진딧물의 수를 조사하였다(3반복). 3가지 기능반응식에 데이터를 fitting한 결과, Type II 기능반응 그래프와 동일하였고 BIC값도 Type II에서 가장 낮았으므로, 페트리디쉬 시험과는 달리 *A. asychis*는 Type II 기능반응을 보였다. 진딧물의 주내 공간분포는 접종 3일째부터 시험 종료일까지 상위엽에 많이 분포하였고, 조사 15일째에 밀도가 가장 높았다. *A. asychis* 머미는 6일째부터 상위엽에서 관찰되었고, 그 수가 서서히 증가하다가 21일째 밀도가 가장 높았으며 그 후 급격히 진딧물 밀도가 감소하였다.

검색어: *Aphelinus asychis*, 복숭아혹진딧물, 감자수염진딧물, 기능반응, 공간분포

What Can Population Genetics Tell Us About Insect Dispersal?

Kyung Seok Kim

BK Program for Veterinary Science, College of Veterinary Medicine, Seoul National University

Population genetics is the study of genetic constitution of Population across space and over time. Population genetics plays a pivotal role in characterizing dispersal behavior of insects and provides important clues to questions in the field of insect behavior and ecology. Understanding dispersal behavior of insects is of important issue not only for academic interests but also for application purposes including management and eradication. Dispersal is one of major evolutionary forces that can influence genetic variation of population. Dispersal is mostly driving genetic homogenization of diverging populations. Moreover, understanding dispersal pattern and capacity of insects is a key component for designing effective management and resistance management strategies of many insect pests since dispersal ability determines the spread rate of disease and resistance gene. The capability of predicting insect movement therefore is an essential component of agricultural production management systems. Here I introduce application of population genetics to insect dispersal study with the case studies of three agricultural insect pests, cotton boll weevil (*Anthonomus grandis*), Western con rootworms (*Diabrotica vergifera*) and European corn borer (*Ostrinia nubilalis*). These insects all are invasive and major pests of crops of U.S.A during the last ~100 years.

Key words: Population genetics, dispersal behavior, management, invasive, *Anthonomus grandis*, *Diabrotica vergifera*, *Ostrinia nubilalis*

Control efficiency of the predatory mites, *Neoseiulus californicus* and *Phytoseiulus persimilis*, for *Tetranychus urticae* on a spatially-structured strawberry leaf disc arena

Jeong Joon Ahn¹ and Joon-Ho Lee²

¹Division of Applied Entomology, Department of Agricultural Biology, National Academy of Agricultural Science, Rural development administration

²Entomology Program, Department of Agricultural Biotechnology, Seoul National University

Strawberry, *Fragaria ananassa* Duchesne, is one of the important horticultural crops cultivated in greenhouses. *Tetranychus urticae* is one of major strawberry pests, and *Neoseiulus californicus* and *Phytoseiulus persimilis* have been used as biological control agents for control of *T. urticae*. The interactions between *T. urticae* and *N. californicus* and between *T. urticae* and *P. persimilis* were investigated to compare their control efficiency for *T. urticae* on a spatially-structured strawberry leaf disc area at different temperatures and on different treatments. The experimental arena was an array of leaf discs (3 cm diameter) placed upside down on a water-saturated cotton pad in an aluminum pan (17.4 x 21.5 cm). Twenty leaf discs (4 x 5) were placed adjacent each other for allowing dispersal of *T. urticae* and its predatory mites. The temperature conditions were 20, 25, and 30°C and there were six different treatments. The overall population densities of *T. urticae* were influenced by temperature (20, 25, and 30°C) in *N. californicus* treatment. In the same temperature condition, *P. persimilis* was more effective than *N. californicus* to control *T. urticae*. Two predator systems were better than one predator systems to suppress the population density of *T. urticae* at 25°C. Some results of this study could be used to understand the spatial association of *T. urticae* and its predatory mites in greenhouse crops and fields.

Key words: Strawberry, *Tetranychus urticae*, *Neoseiulus californicus*, *Phytoseiulus persimilis*, temperature