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정기총회 및 춘계학술발표회

주제: 삶의 질 향상을 위한 응용곤충학의 역할

일시 : 2010년 5월 13일(목) ~ 15일(토)
장소 : 경상대학교 농업생명과학관

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Program and Abstracts

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2010년도 한국응용곤충학회 정기총회 및 춘계 학술발표회

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<공지 사항>
※ 5월14일(금) 중식 식권은 특강 종료 후 등록대에서 지급합니다.
※ 주차권은 소모임 종료 후 등록대에서 지급합니다.
※ 특강발표는 30분 발표에 10분 질의. 발표시간은 총 40분입니다.
※ 구두발표는 10분 발표에 5분 질의. 발표시간은 총 15분입니다.
※ 소모임 발표는 15분 발표에 5분 질의. 발표시간은 총 20분입니다.

	농업생명과학관 (101호)	농업생명과학관 (102호)	농업생명과학관 (305호)	농업생명과학관 (306호)	농업생명과학관 (307호)	농업생명과학관 (1층, 3층 복도)
13-May						
12:30-	등록					poster presentation
13:00-13:50	정기총회					
13:50-14:00	Coffee break					
14:00-14:40	특강 Ⅰ 최만연 박사 (ARS-USDA)					
14:40-15:20	특강 Ⅱ 김영준 박사 (광주과학기술원)					
15:20-16:00	특강 Ⅲ Dr. Stephen Cameron (CSIRO)					
16:00-16:10	Coffee break					
16:10-17:10		일반학술 구두 발표회 (곤충분류)	일반학술 구두 발표회 (곤충생리)	일반학술 구두 발표회 (선충, 곤충생태)	일반학술 구두 발표회 (해충방제, 위생곤충 및 기타)	
17:10-17:30		Coffee break				
17:30-18:30		일반학술 구두 발표회 (곤충분류)	일반학술 구두 발표회 (곤충생리)	일반학술 구두 발표회 (선충, 곤충생태)	일반학술 구두 발표회 (해충방제, 위생곤충 및 기타)	
19:00-	간친회(Reception) ※ 장소 : 교육문화센터 2층 교직원식당					

	농업생명과학관 (101호)	농업생명과학관 (102호)	농업생명과학관 (305호)	농업생명과학관 (306호)	농업생명과학관 (307호)	농업생명과학관 (1층, 3층 복도)
14-May						
09:00-09:40	특강 Ⅳ 홍영석 박사 (Tulane University)					
09:40-10:20	특강 Ⅴ 변영웅 박사 (국립농업과학원)					
10:20-10:30	Coffee break					
10:30-11:10	특강 Ⅵ 김경석 박사 (서울대학교)					
11:10-11:50	특강 Ⅶ 안정준 박사 (국립농업과학원)					
11:50-13:00	중식 ※ 장소 : 교육문화센터 2층 교직원식당(식권 제공)					
13:00-13:45		일반학술 구두 발표회 (곤충분류)	일반학술 구두 발표회 (곤충생리)	일반학술 구두 발표회 (선충, 곤충생태)	일반학술 구두 발표회 (해충방제, 위생곤충 및 기타)	
13:45-14:00		Coffee break		Coffee break	Coffee break	
14:00-15:00		일반학술 구두 발표회 (곤충분류)		일반학술 구두 발표회 (선충, 곤충생태)	일반학술 구두 발표회 (해충방제, 위생곤충 및 기타)	
15:00-16:40		소모임 (곤충분류, 산업곤충 연구회)		소모임 (살충제, 위생해충 연구회)		

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특별 강연

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 (Pheromone Biosynthesis Activating Neuropeptide) 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 ofthe insect (neuro)hormonal system be used to discover novel control tool*s”. 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 Behaivor: Insights from *Drosophila* Sex Peptide Receptor

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[2]Research 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. Cameron[1]

[1]Australian 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: Noctuiidae: *Helicoverpa*) – to illustrate the ease and comparative cheapness of genomics level approaches to these age old problems.

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

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

Functional Response and Spatial Distribution of Aphid Parasitoid *Aphelinus asychis*

Young Woong Byeon[1], Midori Tuda[2], Jeong-Hwan Kim[1], and Man-Young Choi[1]

[1]Applied Entomology Division, National Academy of Agricultural Science (NAAS)
[2]Institute of Biological Control, Faculty of Agriculture, Kyushu University

The functional response and spatial distribution of parasitoid may be useful for understanding host-parasitoid dynamics because information on these will give knowledge of the host-parasitoid interaction, which could lead to the development of strategy for biological control of insect pests.

The functional responses of *A. asychis* on the green peach aphid and potato aphid was investigated in eggplant leaf-disc arena. As a result, among the three types of functional response, type III best described the *A. asychis* response to the aphid densities, according to the Bayesian Information Criterion (BIC).

Functional response and spatial distribution of *A. asychis* on green peach aphid, *Myzus persicae*, was investigated on 5x5 eggplants in the net cage. After *M. persicae* were inoculated uniformly at the densities of 1, 3, 6, 9 and 12 (per plant) on upper, middle and lower leaves of each 25 eggplants, one mated female of *A. asychis* was introduced on the central eggplant. Each aphid density was duplicated. *A. asychis* showed a type II functional response different from that estimated on the eggplant leaf-disc arena. Although the initial distribution of the aphids in the 25 eggplants was uniform vertically and horizontally, the aphids became gradually concentrated on the upper leaves of eggplants, so did immature *A. asychis*.

Key words: *Aphelinus asychis*, *Myzus persicae*, functional response, spatial distribution

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 *Tetranychu urticae* on a spatially-structured strawberry leaf disc arena

Jeong Joon Ahn[1] and **Joon-Ho Lee**[2]

[1]Division of Applied Entomology, Department of Agricultural Biology, National Academy of Agricultural Science, Rural development administration
[2]Entomology 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. uritcae.* 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

구두 발표

제주도에서 곤충병원성 선충, *Steinernema longcaudum*과 *S. monticolum*의 재발견

정영학[1], 이동운[2], 추호렬[1], 박정규[1], 신창훈[2]

[1]경상대학교 응용생명과학부(BK21), [2]경북대학교 생물응용학과, 제주도 한라수목원

2005년 제주도 30지역에서 곤충병원성 선충 분포 조사를 실시하였다. 미끼곤충인 꿀벌부채명나방 유충을 이용하여 토양 내 곤충병원성 선충을 조사하였는데 1차적으로 치사유충의 색깔 변화로 *Steinernema*속과 *Heterorhabditis*속을 구별하였다. 30곳의 토양 시료들 중 곤충병원성 선충이 검출된 지역은 5지역으로 검출율은 16.7%였다. 분리 된 곤충병원성 선충은 모두 *Steinernema* spp.였는데 형태학적, 분자학적, 생물학적 특징으로 분류, 동정 한 결과 *Steinernema monticolum*과 *S. longicaudum*으로 동정 되었다. *Steinernema monticolum*은 조천읍, 어리목, 성판악, 1100도로 주위 산림에서 발견 되었고, *S. longicaudum*은 성산읍 한 곳에서 발견되었다. 곤충병원성 선충의 서식처로는 산림에서 28.6%, 해안가에서 12.5% 발견되었고, 토성은 모두 사양토였다. *S. longicaudum*은 공주와 논산지역에서 발견 된 바 있고, *S. monticolum*은 지리산에서 발견 되었었는데 제주도에서 발견 된 것은 처음이다. 분리한 곤충병원성 선충의 계통과 접종 농도는 병원성에 영향을 주었다.

검색어: 곤충병원성 선충, *Steinernema monticolum*, *S. longicaudum*, 제주도

Chimerical nature of the ribosomal RNA gene of a *Nosema* species

Gilsang Jeong[1], Yonggu Lee[2], Jonggill Kim[1], Wontae Kim[1], Kwanho Park[1], Youngcheol Choi[1], Kyoung Sang Cho[3], Sungwoo Bae[1], and Jiyoung Choi[1]

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Taxonomic resolution of the *Nosema/Vairimorpah* clade has been augmented with DNA sequences of the small subunit (SSU) and large subunit (LSU) ribosomal RNA (rRNA) and the arrangement of SSU and LSU. Based on the two characteristics, the clade is largely divided into two, i.e. 'true' *Nosema* sub-group and 'non-true' *Nosema* sub-group within the clade. Our study shows that a novel *Nosema* species isolated from Pieris rapae has mixed characteristics of the 'true' and non 'true' *Nosema* sub-group based on the topology of SSU and LSU sequences, and rRNA of the isolate is normally organized. Additionally, the length of ITS can be a diagnostic tool to distinguish 'true' *Nosema* from non 'true' *Nosema* in the *Nosema/Vairimorpha* clade based on its nucleotide length as reported before. To our knowledge, this is the first report of recombination event in the *Nosema/Vairimorpha* clade.

Key words: small subunit (SSU), large subunit (LSU), internal transcribed spacer (ITS), cophylogeny of SSU and LSU, organization of rRNA

A Taxonomic Review of the Subfamily Dendrometrinae (Coleoptera, Elateridae) in Korea

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The subfamily Dendrometrinae is a large group in Elateridae with about 2000 species world wide. However, this subfamily were not taxonomically reviewed in the Korean fauna. As the result of taxonomic review, 40 species are confirmed from Korea, with the description of two new genera, 11 new species, and one new subspecies. A total of 11 species are also recognized for the first time from Korea.

Key words: Taxomomy, Coleoptera, Elateridae, Dendrometrinae, Korea.

A new entedonine parasitoid (Hymenoptera: Eulophidae) parasitizing eggs of *Pachynematus itoi* (Hymenoptera: Tenthredinidae) in South Korea

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A new species of *Closterocerus* (Hymenoptera: Eulophidae: Entedoninae) is described from South Korea. The species is reported for the first time as an egg parasitoid of *Pachynematus itoi* Okutani (Hymenoptera: Tenthredinidae), of which recent sudden outbreak caused severe damage in larch forests. In total 61 species in Chalcidoidea are recorded as primary parasitoids of various tenthredinid sawflies in the Palaearctic area. However, no chalcidoid parasitoids have previously been recorded from *P. itoi*. The genus *Closterocerus* is cosmopolitan in distribution, and with an extremely wide host range from Symphyta, leaf-mining and gall-inducing insects to scale insects and plant lice. In Korea, one species of *Closterocerus*, three *Chrysonotomyia*, two *Desmatocharis*, one *Neochrysocharis* and one *Teleopterus* were known; most of them, except *Chrysonotomyia sudoensis* Paik, now are placed under *Closterocerus*. The new species is compared with 13 other species of *Closterocerus* that are known from the Far East.

Key words: Eulophidae, Entedoninae, *Closterocerus*, egg parasitoid, the Far East

Review of the Korean species of the genus *Scolytus* and a new record of *Scolytus frontalis* (Coleoptera: Scolytidae) from Korea

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The genus *Scolytus* of the family Scolytidae comprises more than 120 species through the world. Fifteen species of the genus *Scolytus* are revised from Korean peninsula. The genus *Scolytus* can be distinguished from the other genera by combination of following characteristics: frons slightly concave or convex with vertical wrinkles; club longer than 7-segmented funicle; pronotum fairly large, shining, punctured, narrowed towards the front, turning into a more slight or distinct neck-like constriction; vicinity of scutellum deeply impressed; elytra flat with punctures densely or sparsely arranged in rows; abdominal sternites from 2nd to 5th obliquely, convexly, concavely or vertically ascendant and with or without process or tubercles at middle.

Scolytus frontalis Blandford, 1894 is new record to Korea. This species was collected from living Zelkova tree, *Zelkova serrata* which were planted along the street. We provide the habitus of this species and its biological informations.

Key words: Coleoptera, Scolytidae, *Scolytus frontalis*, Korea.

Study on the molecular identification of Dark-winged fungus gnats (Diptera: Sciaridae) using mitochondrial COI gene

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In the family Sciaridae, only 3 species have been recorded in Korea, as the pests on various crops and mushrooms in glasshouse (*Bradysia difformis* Frey, 1948, *Bradysia procera* (Winnertz, 1868), *Lycoriella ingenua* (Dufour, 1839)), even though Sciaridae is one of the species-rich families in the order Diptera. There are plenty of species unknown in Korea which are very hard to identify by morphological characters in the larval, pupal stages and also female adults as well. Therefore, using the sequences of cytochrome oxidase I gene (COI) from adult male, we tested the utilities of DNA barcode to identify the species of sciarid flies.

Key words: Sciaridae, *Bradysia, Lycoriella,* DNA barcode, molecular identification

A new aphid genus *Neoaulacorthum* (Hemiptera: Aphididae: Macrosiphini), determined by molecular and morphometric analyses

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We performed molecular and morphological analyses to determine generic limit of the genus *Aulacorthum* including several species with controversial taxonomic histories. The sequences of four mitochondrial genes, *COI*, *COII*, *srRNA* and *lrRNA*, and one nuclear gene, *EF1a*, implied that *Aulacorthum* is not monophyletic, with *Aulacorthum magnoliae* and *Aulacorthum nipponicum* forming a clade that is not sister to other currently recognized *Aulacorthum* species. Morphometric analysis based on 20 morphological characters also showed that *A. magnoliae* and *A.nipponicum* exhibited morphological characteristics distinct from congeneric species. Based these results, we propose a new genus, *Neoaulacorthum* ge. n. for *A.magnoliae* and *A.nipponicum*.

Key words: *Aulacorthum*, *Aulacorthum magnoliae*, *Aulacorthum nipponicum*, Macrosiphini, *Neoaulacorthum*

Ancestral Character States and Correlated Evolution of the Flower Bugs (Heteroptera: Anthocoridae) using Bayesian Analysis of Multistates and Discrete Characters

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Investigating the molecular clock, the ancestral character states, and the correlated evolution of discrete binary traits on phylogenetic trees, we studied the evolutionary history of the family Anthocoreidae, using ~3000bp of the mitochondrial 16S rRNA and nuclear 18S rRNA and 28S rRNA genes for 44 taxa. The BEAST and BayesTraits were used to examine the divergence times, cladogenesis, and historical habitat patterns. The correlated evolution of discrete characters was tested by reversible-jump Markov chain Monte Carlo. Our results suggest that (i) the ancestral habitat patterns of dead plants may have served as an important rule for the stem group of anthocorids; (ii) the radiation of angiosperms and the prey insect in the mid-Cretaceous might have provided anthocorids with more habitat options; and (iii) the transition of habitats played an important role for the change of ovipositor patterns in the family Anthocoreidae.

Key words: Anthocoridae, Phylogeny, Molecular dating, Ancestral character states, Correlated evolution

Phylogenetic correlation between DNA and morphology and morphological trait evolution in the species-rich genus *Aphis* (Hemiptera: Aphididae)

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The species-rich genus *Aphis* consists of more than 500 species, many of them host-specific on a wide range of plants, yet very similar in general appearance due to morphological resemblance toward particular morphological types. Most species have been historically clustered into four main phenotypic groups (*gossypii*, *craccivora*, *fabae*, and *spiraecola* groups). To confirm whether these morphological relationships are correlated with the genetic relationships, we compared the morphometric dataset of 28 characters measured/counted from 33 representative species with a phylogeny reconstructed from the combined dataset of four DNA regions (3,842 bp). The correlation of the rates of evolution between morphological and DNA datasets was highly significant in their diversification. Analysis of trait evolution revealed that the morphological traits found to be significant based on the ANOVA were confidently correlated with the phylogeny. The dominant patterns of trait evolution resulting in increased rates in short branches and temporally later evolution are likely suitable for the modality of *Aphis* speciation because they have adapted species-specifically, rapidly, and more recently for many different host plants.

Key words: *Aphis*, morphology, phylogenetic correlation, trait evolution

Divergence in calling songs and genetic sequences in three cryptic cricket species (Genus *Loxoblemmus*) in Korea

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The genus *Loxoblemmus* has three speices in Korea: *L. doenitzi, L. campestris* and *L. equestris*. Males of *L. doenitzi* have flat heads and triangular horns on both sides of their frons, whereas males of *L. campestris* and *L. equestris* have flat heads and no horns. The latter two species are not clearly distinguished based on morphology and thus may constitute cryptic species. We studied the divergence in morphology, calling songs, and genetic sequences to understand patterns of differentiation of these three species. Distributions of the number of file teeth and wing morphology overlapped in *L. campestris* and *L. equestris*. In calling songs, the number of pulses in a chirp was four in *L. campestris*, but that was greater than or equal to six in *L. equestris*. The genetic sequence analyses using 16S rRNA and COI barcode revealed that *L. doenitzi* diverged off earlier from the other two species. Thus, the genetic data were congruent with the calling song data in three *Loxoblemmus* species. Our results suggest that the speciation processes may be closely related to differentiation in calling songs in the *Loxoblemmus* complex.

Description of Two Complete Mitochondrial Genomes of the Endangered Lycaenids, *Spindasis takanonis* and *Protantigius superans* (Lepidoptera: Lycaenidae), and Phylogenetic Relationships among Lepidopteran Insects

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Two complete mitochondrial genomes (mitogenomes) of the endangered, lycaenid butterflies, *Spindasis takanonis* and *Protantigius superans* (Lepidoptera: Lycaenidae), were sequenced. Each 15,349 bp and 15,248 bp-long genome contained both the lepidopteran specific gene arrangement that differ from the most common arrangement of insects by the movement of tRNA^{Met} to a position 5'-upstream of tRNA^{Ile}. Neither of the species have typical COI start codon. Instead, the CGA (arginine) sequence that is commonly present in all other lepidopterans was also found in both lycaenids. The possible binding site for the transcription termination peptide, TACTA sequence, also was well retained in both species. The high A+T-content, which is a characteristic of insect mitogenomes was well reflected in the genomes in the form of higher frequency of codons with A/T nucleotides, severe A/T bias in 3rd codon position, and extremely high A/T content in the A+T-rich region. The 19 bp-long poly-T stretch and the downstream conserved motif ATAG, which were suggested previously to function as a structural signal for minor-strand mtDNA replication, was also well conserved in the A+T-rich region of both lycaenids. Phylogenetic analysis among lepidopteran superfamilies supported the relationships of either (((((Bombycoidea + Geometroidea) + Noctuoidea) + Papilionoidea) + Pyraloidea) + Tortricoidea) by concatenated amino acid sequence or (((((Bombycoidea + Geometroidea) + Noctuoidea) + Pyraloidea) + Papilionoidea) + Tortricoidea) by concatenated nucleotide sequences of 1st and 2nd codon positions of 13 protein-coding genes, two rRNA genes, and 22 tRNA genes, revealing fluctuating positions of Papilionoidea and Pyraloidea between the two data sets.

Deliberately Unequal Gene Sampling, A Design of Molecular Studies Tested in Lepidoptera

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Seeking to improve the weak resolution of deeper divergences in an initial study based on five nuclear genes (6.6kb total) in 123 exemplars, we nearly tripled the total sequence (to 26 genes, 18.4 kb total) in one third (41) of the taxa. The expanded, deliberately incomplete data matrix consistently increased bootstrap support for previously-identified groupings, while introducing no contradictory groupings of the kind that missing data have been predicted to produce. To test the relative effectiveness of “more genes” versus “more taxa” sind that we compared two largely complete matrices, the initial 5 gene × 123 taxon and the 26 gene × 41 taxon data sets, that contain roughly equal amounts of sequence. The “more genes” data set yielded consistently, sometimes dramatically higher bootstrap support that is generally not attributable to taxon number alone. We also found that a gene-rich taxon subset provides reassuring evidence of strong underlying signal that is not obvious in subsequent larger analyses, helping to encourage and guide the search for deep relationships amid the noise of expanded taxon sampling.

Key words: Ditrysia, nuclear genes, molecular systematics, gene sampling, taxon sampling

Identification and Field Bioassays of the Sex Pheromone of *Synanthedon haitangvora*

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Synanthedon haitangvora (Lepidoptera: Sesiidae) is an economically important pest of apple trees in Korea and China. We report here the identification of compounds in pheromone gland extracts of female *S. haitangvora*, and the male responses to blends of different components and ratios in the field. Two major components from pheromone gland extracts of *S. haitangvora* females were identified as *Z*3,*Z*13-18:OAc and *E*2,*Z*13-18:OAc, and the average ratio of these components was about 1:1. Seven minor components, *Z*9-16:OAc, *Z*11-16:OAc, *Z*9-18:OAc, *Z*13-18:OAc, *E*3,*Z*13-18:OAc, *Z*3,*Z*13-18:OH, and *E*2,*Z*13-18:OH, also were identified from gland extracts. Field tests showed that male *S. haitangvora* were attracted to *Z*3,*Z*13-18:OAc alone, but the maximum number of males was attracted to the binary blend of *Z*3,*Z*13-18:OAc and *E*2,*Z*13-18:OAc mimicking the blend found in female extracts. The addition of minor components to a 1:1 blend of *Z*3,*Z*13-18:OAc and *E*2,*Z*13-18:OAc did not increase the numbers of moths captured. The only significant effect of minor components was the strong inhibitory effect of adding *Z*3,*Z*13-18:OH to the primary binary blend. Increasing doses of the optimum pheromone blend in the lures from 0.1 to 2.0 mg increased trap catches of male *S. haitangvora*.

Key words: *Synanthedon haitangvora*, *Z*3,*Z*13-18:OAc, *E*2,*Z*13-18:OAc, Lepidoptera, Sesiidae

A Sodium-Potassium-Chloride Channel is Involved in Oenocytoid Cell Lysis in Response to PGE_2 in *Spodoptera exigua*

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Sodium-potassium-chloride co-transporter (NKCC) is a membrane bound channel protein that plays a prominent role in a variety of epithelial absorptive, secretory processes and a direct role in cell volume regulation, in which NKCC transports sodium, potassium, and chloride ions across the cell membrane. It has been known that prostaglandin E_2 (PGE_2) induces an acute cell lysis of specific hemocyte type, oenocytoid, to release prophenoloxidase into the plasma and ouabain (a specific sodium pump inhibitor) inhibits the oenocytoid cell lysis resulting in preventing phenoloxidase activation. However, it is not clear how the intracellular signaling pathway leads to oenocytoid cell lysis in response to PGE_2. This study was designed to analyze functional role of NKCC in the cell lysis to release prophenoloxidase. A gene structure of NKCC was derived from cDNA library of *Spodoptera exigua* hemocyte, NKCC was expressed in all developmental stages and tissues. A real time quantitative RT-PCR showed that bacterial challenge significantly induced its expression. Specific inhibitors of NKCC, bumetanide and chlorothiazide, clearly prevented the cell lysis in a dose dependent manner. When RNA interference using double stranded RNA (dsRNA) specific to NKCC suppressed its expression, the oenocytoid lysis and PO activation was significantly inhibited in response to PGE_2. It also reduced nodule formation to bacterial challenge. These results indicate that NKCC is associated with oenocytoid cell lysis probably by increasing cell volume through inward transport of ions in response to PGE_2.

Key words: Sodium-potassium-chloride channel, Prostaglandin E_2 Oenocytoid, Cell lysis, Prophenoloxidase, *Spodoptera exigua*

Host translation inhibitory factor of a polydnavirus discriminates host mRNAs by specific secondary structure of their 5'UTRs

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A polydnavirus, *Cotesia plutella* bracovirus (CpBV), encodes host translation inhibitory factors (HTIFs). Two HTIFs have been identified and named as CpBV15α and CpBV15β. HTIFs specifically inhibit host gene expression at post transcriptional level. This suggests that HTIFs can discriminate host mRNAs for their inhibition. To test this hypothesis, we chose a storage protein 1 (SP1) for a target and CpBV15β for non-target genes. Both target and non-target genes were constructed in a cloning vector by cloning their 5'UTR+ORF and *in vitro* transcribed. The capped partial mRNAs were *in vitro* translated using rabbit reticulocyte lysate in the presence or absence of HTIFs. Translation of SP1 mRNA was significantly inhibited by the HTIF, but those of CpBV15α and CpBV15β were not. We prepared chimeric mRNAs by exchanging 5'UTR and ORF of both target and non-target genes. Inhibitory activity of HTIFs was dependent on the 5'UTR structure. Target 5'UTR had more complicated secondary structure than non-target 5'UTR in terms of free energy required for unwinding. To identify the target molecule of HTIF to discriminate 5'UTR, an immunoprecipitation using HTIF antiserum was conducted. HTIF was co-precipitated with eIF4A that would be required for unwinding the secondary structure of mRNA. These results suggest that HTIF of CpBV can sequester host eIF4A, any mRNAs possessing complicated secondary structures in their 5'UTRs would be difficult to recruit initiation complex for efficient translation.

Key words: Host translation inhibitory factors, *Plutella xylostella*, *Cotesia plutella*, CpBV, Translation regulation, mRNA secondary structure

복숭아순나방(*Grapholita molesta*) 방제를 위한 한국형 교미교란제 처리 기술

김용균

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국내 사과 및 복숭아의 과실류에 피해를 주고 있는 복숭아순나방(*Grapholita molesta*)은 과실 내부 가해라는 서식 습성에 따라 화학적 방제에 어려움이 있다. 따라서 야외 노출 발육 시기인 성충을 대상으로 교미교란 처리 기술이 대체 기술로서 제안되었다. 본 해충의 성페로몬을 기반으로 교미교란제를 처리한 포장에서 뚜렷한 교미교란 효과를 얻을 수 있다. 그러나 국내 과수의 소규모 경영규모에 따라 인접한 농가에서 교미한 암컷의 유입으로 방제의 실효를 거두지 못하게 되었다. 이를 해결하기 위해 교미한 암컷을 포획할 수 있는 먹이트랩과 처리 효과의 사각지대를 줄이기 위한 교미교란제의 테두리 처리가 병행될 필요가 있었다. 먹이트랩과 테두리처리가 투입된 교미교란제 처리는 교미교란제의 단독 처리에 비해 우수한 방제 효과를 나타냈다. Paste 형태의 교미교란제를 3월과 7월의 2회 처리로 연중 방제 효과를 거둘 수 있었다. 추후 교미교란제의 투입량을 줄이는 기술과 교미한 암컷의 포획 효율을 높이는 유인제 개발 기술이 필요하다.

Key words: *Grapholita molesta*, sex pheromone, RAPD, movement, apple

A Broad - Complex gene responsible for larval-pupal metamorphosis of the beet armyworm, *Spodoptera exigua*

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To clarify the molecular mechanism of metamorphosis, we analyzed the Broad-Complex (BR-C) gene in the beet armyworm, *Spodoptera exigua*. We obtained a partial BR-C sequence from a pyrosequencing cDNA library. The BR-C of *S. exigua* was expressed only in the final larval instar, at which its expression was clearly detected in the epidermis. A treatment of a juvenile hormone analog, pyriproxyfen, inhibited larval-pupal metamorphosis and suppressed the BR-C expression. The hormonal treatment also inhibited expression of two storage protein genes that were usually expressed during a final larval instar. RNA interference of the BR-C using its double strand RNA suppressed BR-C expression and inhibited the larval-pupal metamorphosis. These results suggest that the BR-C is critical to induce larval-pupal metamorphosis of *S. exigua*.

Key words: *Spodoptera exigua*, juvenile hormone, epidermis, Broad - Complex, metamorphosis

Transient expression of a putative RNase containing BEN domain encoded in *Cotesia plutellae* bracovirus induces an immunosuppression of the diamondback moth, *Plutella xylostella*

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A polydnavirus, *Cotesia plutellae* bracovirus (CpBV), possesses segmented genome located on chromosome(s) of an endoparasitoid wasp, *C. plutellae*. An episomal viral segment (CpBV-S3) consists of 11,017 bp encoding two putative open reading frames (ORFs). ORF301 shows amino acid sequence homologies (28~50%) with RNase T2s of various organisms. It also contains BEN domain in C-terminal region. ORF302 is a hypothetical gene, which is also found in other bracoviruses. Both genes were expressed in larvae of *Plutella xylostella* parasitized by *C. plutellae*. ORF301 and ORF302 were transiently expressed in hemocyte, fat body, gut, and epidermis of *P. xylostella*. To analyze effects of these genes on the parasitism, the segment of CpBV-S3 was injected to non parasitized larvae of *P. xylostella*, in which the two genes were expressed at least for four days post-injection. The *P. xylostella* larvae injected with CpBV-S3 exhibited significant immunosuppression, such as reduction in total hemocyte population, suppression of immune associated genes including cecropin, pro-phenoloxidase (PO) and serpin1, and impairment in nodule formation behavior of hemocytes in response to bacterial challenge. Each gene expression in the treated larvae was inhibited by co-injecting respective double strand RNA (dsRNA) specific to each ORF. Injection of dsRNA of ORF301 could rescue the immunosuppression by the viral segment-treated larvae, but not by ORF302 specific dsRNA. The larval injected with CpBV-S3 exhibited an enhanced susceptibility to baculovirus infection. These results indicate that ORF301 of CpBV-S3, which containing BEN domain, suppresses both cellular and humoral immune responses in *P. xylostella*.

Key words: *Cotesia plutellae,* Polydnavirus, RNaseT2, RNA interference, Immunosuppression, *Plutella xylostella*

Antifungal activity of gallerimycin encoded in the beet armyworn, *Spodoptera exigua*

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Antimicrobial peptides (AMPs) are a group of immune proteins that protect the host from microial infection. Gallerimycin is one of the AMPs most commonly found in *Galleria mellonella* and *Spodoptera frugiperda*. In this paper, we found Gallereimycin in *Spodoptera exigua* by expressed sequence tag library 0analysis. The gallerimycin of *S. exigua* gene is 332 bp long and the predicted open reading frame contains 75 amino acids with a signal peptide. After removing signal peptide, *S. exigua* gallrimycin was estimated to be 5.9 kDa and pI at 8.53. The gallerimycin of *S. exigua* shared maximum sequence homology with that of *S. frugiperda*. In naive *S. exigua* larvae, not much gene expression was detected, but strongly induced in fat body and hemocytes following immune challenge with entomopathogenic bacteria and fungus. A recombinant gallerimycin was prepared using a bacterial expression system and showed significant antibacterial and antifungal activities. RNA interference using double stranded RNA could knock down the expression of gallerimycin and significantly suppressed immune capacity.

Key words: *Spodoptera exigua,* Gallerimycin, Antimicrobial peptides, RNA tinterference, Immune

A high effective IBC (integral biological control) technique using two entomopathogenic bacterial mixture to control the diamondback moth, *Plutella xylostella*

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Bacillus thuringiensis (Bt) is effective to control the diamondback moth, *Plutella xylostella*. However, its relative slow and unstable control efficacy limits its wide use by farmers. To facilitate pathogenic rate of Bt, a bacterial mixture technique has been developed in this study. Two entomopathogenic bacteria, *Xenorhabdus nematophila* (Xn) and *Photorhabdus temperata temperata* (Ptt), possess high immunosuppressive activity against several lepidopteran insects. The mixture treatments using Bt + Xn or Bt + Ptt significantly enhanced Bt pathogenicity in median lethal concentration and time. Though live Xn and Ptt bacterial cells gave significant effect on the pathogenicity, their 48 h culture broth after removing the bacterialcells still possessed the synergistic effect on the Bt pathogenicity. The larvae fed with the bacterial culture broth suffered significant immunosuppression in response bacterial to infection.

Key words: *Xenorhabdus nematophila, Photorhabdus temperata temperata, Plutella xylostella*, Bt, Pathogenicity, Immunity

Applicability of CATTS as a postharvest phytosanitation technology against the peach fruit moth, *Carposina sasakii*

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As an environment-friendly phytosanitary measure, CATTS (controlled atmosphere temperature treatment system) has been developed to kill several quarantine insect pests infesting subtropical agricultural commodities. This study tested any possibility to apply CATTS to apples to effectively eliminate the peach fruit moth, *Carposina sasakii*, which has been regarded as a quarantine insect from the imported countries. When the larvae of *C. sasakii* were directly exposed to 46℃ (an installed lethal temperature of CATTS), they showed a median lethal time at 14.66 min. Addition of high carbon dioxide to the temperature treatment enhanced the thermal limit susceptibility of *C. sasakii* to 46℃. The larvae internally infesting apples were tested using this CATTS device and showed 100% lethality after 60 min exposure to a treatment of 46℃ under 15% CO_2 in the chamber. This study suggests a possibility that CATTS can be applied as a quarantine measure to kill the larvae of *C. sasakii* locating inside the apples. To understand the CATTS effect, a heat shock protein was cloned. Hsp90 was partially sequenced and showed its expression in response to heat treatment. CATTS was likely to suppress hsp90 expression.

Key words: apple, *Carposina sassakii*, CATTS, quarantine, sanitation, heat shock protein

Identification of Toll and Imd signals in the hemocytes of *Spodoptera exigua*

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Based on *Drosophila* model, Toll and Imd signals have regared as central intracellular pathways in insect immune cells in response to various pathogens. Current insect genome studies have identified the corresponding orthologs in other insets. This study reports two immune signaling genes, Se-Toll-1 and Se-Relish-1, and suggests Toll and Imd pathways in the hemocytes of *Spodoptera exigua*. Partial Se-Toll-1 and Se-Relish-1 share high sequence homologies with known Toll and Relish genes of lepidopteran and dipteran species. Their expressions were detected from all developmental stages. In larval stage, there two genes were expressed in all tested tissues including hemocytes. Real time quantitative RT-PCR indicates that expression of both genes were highly up-regulated by bacterial and fungal infections. Various antimicrobial peptides (AMPs) were expressed in the hemocytes of *S.exigua*, in which their expressions appeared to be controlled by Se-Toll-1 and Se-Relish-1. However, Se-Toll-1 and Se-Relish-1 were proved to controlled different AMP genes from their RNA interference assays. These results suggest Toll and Imd signals in the hemocytes of *S. exigua*.

Key words: Antimicrobial peptides (AMPs), Imd, RNA interference, RT-PCR, *Spodoptera exigua,* Toll

Confusing Aspects in Species Identification for Sex Pheromone Study of *Matsumuraeses phaseoli* and *M. falcana*

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Previous studies indicated that *Matsumuraeses phaseoli* and *M. falcana* (Lepidoptera: Tortricidae) are separate species since a few differences were observed in genitalia morphology and female sex pheromone composition. A clear difference was detected in the DNA sequences of cytochrome oxidase I of the two species separately collected in different plants and regions. A hybridization test also showed that a post-zygotic reproductive isolation occurred between the species. In field monitoring, however, both species have been caught simultaneously and together in the separate sex pheromone traps installed for the two species around neighboring soybean and red bean fields. Molecular marker-assisted identification with several adults sampled from the trapped insects showed that only ca. 40% of *M. phaseoli* adults identified as the species by genitalia morphology was the *M. phaseoli*, while ca. 97% of *M. falcana* adults identified as the species was the *M. falcana*. The result indicated that the observation of genitalia did not make a decisive criterion for classification of the insects. Conclusively, it suggested that the sex pheromones of the two species should be studied more precisely although there is a possibility that the two species are hybridized in fields as in laboratory, and speciation is under process.

Key words: *Matsumuraeses phaseoli*, *M. falcana*, sex pheromone, classification, genitalia, molecular markers

Molecular and Biochemical Characterization of Three Acetylcholinesterases from the Pinewood Nematode, *Bursaphelenchus xylophilus*

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Three acetylcholinesterases (AChEs) were identified from the pinewood nematode, *Bursaphelenchus xylophilus*. Sequence comparison with known AChEs in conjunction with three-dimensional structure analysis suggested that all BxAChEs share typical characteristics of AChE at the major catalytic structures. BgAChE3 was most predominantly transcribed and then followed by AChE1 and AChE2. Immunohistochemistry using anti-BxAChEs antibodies revealed that BxAChE1 is most widely distributed whereas BxAChE2 exhibits more localized distribution in neuronal tissues. BxAChE3 was detected from entire body together with some limited tissues, including mouth parts and alimentary lining, and determined to be the only soluble AChE, suggesting its localization in hemolymph or/and extracellular space. Kinetic analysis of in vitro expressed BxAChEs revealed that BxAChE1 has the highest substrate specificity whereas BxAChE2 has the highest catalytic efficiency with BxAChE3 having the lowest catalytic efficiency. Interestingly, presence of BxAChE3 in the pool of BxAChEs significantly reduced the inhibition of BxAChE1 and BxAChE2 by inhibitors. Knockout of BxAChE3 by RNAi significantly increased the toxicity of nematicides, suggesting the protective role of BxAChE3 against these toxicants. Based on several features, including tissue distribution, expression level, substrate kinetics and inhibition property, it appeared that BxAChE1 is the major AChE with the function of postsynaptic transmission whereas BxAChE3 has been evolved to acquire the function of chemical defense, perhaps intrinsically against secondary toxic compounds from host pine trees, such as α-pinene and limonene. BxAChE2 appears to play a role in post-synaptic transmission in specialized neurons but its detailed physiological function still remains to be elucidated.

Key words: Acetylcholinesterase, *Bursaphelenchus xylophilus*, sequencing comparison, kinetics, inhibition assay, RNAi

A combination of biochemical and proteomic analyses reveals *Bx*-LEC-1 as an antigenic target for the monoclonal antibody 3-2A7-2H5-D9-F10 specific to the pinewood nematode

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Diagnosis and confirmation of pinewood nematode (PWD) are time consuming tasks that require nematode extraction and microscopic examination. To develop a more efficient detection method for *Bursaphelenchus xylophilus*, we first generated monoclonal antibodies (MAbs) specific to *B. xylophilus*. Among 2,304 hybridoma fusions screened, a hybridoma clone named 3-2A7-2H5 recognized a single protein from *B. xylophilus* specifically. We finally selected the MAb clone 3-2A7-2H5-D9-F10 (D9-F10) for further studies. To identify the antigenic target of MAb-D9-F10, we analyzed proteins in spots, fractions or bands via nano liquid chromatography electrospray ionization quadrupole ion trap mass spectrometry (nano-LC-ESI-Q-IT-MS). Peptides of galactose-binding lectin-1 of *B. xylophilus* (*Bx*-LEC-1) were commonly detected in several proteomic analyses, demonstrating that this LEC-1 is the antigenic target of MAb-D9-F10. The localization of MAb-D9-F10 immunoreactivities at the area of the median bulb and esophageal glands suggested that the *Bx*-LEC-1 may be involved in food perception and digestion. The *Bx*-LEC-1 has two non-identical galactose-binding lectin domains important for carbohydrate binding. The affinity of the *Bx*-LEC-1 to D-(+)-raffinose and N-acetyllactosamine were much higher than that to L-(+)-rhamnose. Based on this combination of evidences, MAb-D9-F10 is the first identified molecular biomarker specific to the *Bx*-LEC-1.

Key words: *Bursphelenchus xylophilus*, *Bx*-LEC-1, biomarker, *monoclonal antibody*

자운영답에서 알팔파바구미 발생생태

이홍수, 권진혁, 정부근, 김태성, 송원두, 노치웅
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경남지역 진주, 하동, 고성 자운영 재배지에서 알팔파바구미의 발생을 포충망조사, 육안조사, 식물체 수거 후 밀도조사를 통해 년중 발생생태를 조사하였다. 자운영 포장에서 효과적인 알팔파바구미의 초기 유충의 조사방법으로 초기 발생하는 유충은 포충망 조사로 확인이 어려우므로 10×10cm 넓이 면적의 식물체를 자른 후 용기에 담아 흔들어서 떨어진 유충 및 식물체에 남은 유충을 조사하는 것이 효과적이었다. 초기에 발생하는 유충은 식물체의 아래부분에 발생하고 크기가 작아서 포충망 조사로는 4월중순까지 발생확인이 안되었으나 식물체 수거후 용기에 흔들어서 조사하는 방법으로는 3월중순부터 확인이 되었다.

산란을 위해 자운영답으로 이동한 성충을 조사하는데는 Pitfall trap을 이용하는 것이 좋은 결과를 얻었다. 육안조사와 포충망 조사로는 확인할 수 없었으나 Pitfall trap에서는 1월부터 발생을 확인할 수 있었다.

알파파바구미의 발생생태는 이동성충이 전년도 10월 하순경 자운영답으로 이동하여 산란을 시작하였고 유충은 3월상중순, 번데기는 4월하순, 1세대 성충은 5월중순부터 발생하며 벼의 정식이 시작되면 주변 새로운 기주로 옮겨가서 서식하다가 다시 10월하순경 자운영이 올라오면 이동하여 산란을 개시하였다.

검색어: 자운영, 알팔파바구미, 발생, pitfall trap, 포충망조사

제주도 녹차 재배지에서 풍뎅이류에 의한 녹차 피해와 발생 생태

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2008년과 2009년 제주도 녹차 재배지(도순, 한남, 서광)에서 발생하는 풍뎅이류의 피해와 밀도 및 발생 생태를 조사하였다. 세 지역 모두 홈줄풍뎅이(*Bifurcanomala aulax*)가 우점하였고, 청동풍뎅이(*Anomala albopilosa*)와 꽃무지(*Eucetonia pilifera*)가 발생하였다. 세 종 모두 유충은 차나무의 뿌리를 가해하였고, 청동풍뎅이는 차 잎을 가해하였다. 홈줄풍뎅이는 2령 또는 3령으로 월동하였고, 5월 하순에 번데기가 된 후 6월 하순에 성충이 출현하였다. 부화 된 1령충은 8월 하순에 발견되었다. 녹차 재배지에서 청동풍뎅이의 우화는 6월 25일 최초로 이루어졌고, 7월 14일까지 계속 되었으나 이후 8월 중순까지는 우화되는 개체가 없었다. 유아등에서는 7월 5일 유인 된 후 8월 초순부터 2차 유인이 된 후 9월 초순까지 계속 되었고, 유인 최성기는 9월 초순이었다.

검색어: 차나무, 굼벵이, 홈줄풍뎅이, 청동풍뎅이, 꽃무지

Comprehensive soil quality assessment in urban forests using biological indices

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Soil quality, as the capacity of a soil to function, are currently characterized and evaluated mainly physico-chemical properties. In the present study, several biological indices were applied to determine whether biological indices could provide a more comprehensive understanding in terms of soil quality assessment in urban forests. Microbe and invertebrate biological indices (i.e. biodiversity of both microbe and invertebrate, enzyme activity of microbe, feeding activity of invertebrate) were examined at 6 urban forests with different levels of disturbance in Seoul, Korea. The results showed that feeding activity and biodiversity were significantly and positively intercorrelated, but not with the enzyme activity. We also examined whether these biological indices could be modeled as functions of soil physico-chemical characteristics. To develop a predictive model, we applied principal component regression. The results showed that first principal component represented more than 33% of the total variance of biological indices and gave a good relationship with soil physico-chemical characteristics (R^2=0.71). The predictive model developed in this study can be used for qualitative but not for quantitative assessment of soil quality.

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Key words: Soil quality assessment, biodiversity, feeding activity, enzyme activity

Released eggs of *Riptortus pedestris* (Hemiptera: Alydidae) enhances parasitism in Agakong field

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Riptortus pedestris (Fabricius) (Hemiptera: Alydidae) causes losses in several crops in Korea. Release of non-viable refrigerated eggs of *R. pedestris* is known to enhance natural parasitism by *Ooencyrtus nezarae* Ishii (Hymenoptera: Encyrtidae) and *Gryon japonicum* (Ashmead) (Hymenoptera: Scelionidae) in soybean fields. In this study, we conducted an experiment of cage-exclusion design to verify the former results in more manipulative approach in a soybean field. Agakong field (45×26 m^2) located at Songcheon, Andong was divided into 15 plots (10×6 m^2) with each experimental arena of 3×2 m^2 in the center. There were three treatments: (1) release of refrigerated eggs of *R. pedestris*, (2) release of refrigerated eggs with one time spray of thiamethoxam, and (3) untreated control. A fine mesh cloth with iron poles was used to encircle the arenas. Refrigerated eggs of *R. pedestris* were released (100/arena) twice before sampling. One-day old eggs of *R. pedestris* were released (60/arena) in all the experimental arenas at an interval of 6 days, and 30 eggs from each were collected to record parasitism. We found no significant difference in the eggs and nymphs population of *R. pedestris* among the treatments. However, adult density was significantly reduced in the treated plots during final two sampling days compared to the control. We found significantly higher parasitism by *G. japonicum* on the eggs collected from treated plots (9-25%) compared to the control plots (1-9%). It is verified that releasing non-viable eggs of *R. pedestris* help to enhance natural parasitism in soybean field.

Key words: *Ooencyrtus nezarae*; *Gryon japonicum*; refrigerated eggs; thiamethoxam

Flower model trap helps to reduce thrips infestation on red pepper in field

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Chrysanthemum flower model trap developed by modifying an artificial yellow chrysanthemum flower was reported to be more attractive to flower thrips than a commercial yellow sticky trap. The installation of the traps (20 traps per 50 m^2 plot), especially, reduced the seasonal populations of *Frankliniella intonsa* Trybom (Thysanoptera: Thripidae) on strawberry flowers in greenhouse by 82% compared to the untreated control. In this study, we tested if the installation of the flower model traps can reduce thrips population on a red pepper field located in Seokdong, Andong. The pepper field was treated two times with pesticides during the period of experiment. The traps were installed in plant canopy at different densities (0, 5, 10, 20 traps) in 20 plots (3×5 m^2 each) using a completely randomized design. Population of thrips was examined on the collected pepper flowers from 1 July to 29 July in 2009. Thrips found on the flowers were all *F. intonsa*. Significance effect of treatment and sampling date was found from repeated-measure analysis of variance. The highest density of traps significantly reduced female and male *F. intonsa* population by 60% and 46% compared to the control, respectively. However, no difference in immature population was found among the treatments. These results indicate flower model trap can be an additional tool for the management of flower thrips on field red pepper.

Key words: *Frankliniella intonsa*; sticky trap; visual attraction; Thripidae

Frame work of the adaptive population dynamic model of Varroa mite in Korean beekeeping environment

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Modeling the complex system often provide better understanding of the behavior of the system given that parameters for the modeling are appropriate. The honeybee mite, *Varroa destructor* Anderson and Trueman, is one of the most serious pests of honeybees in Korea. Even with vast amount of ecological information of this parasite and its host, *Apis mellifera*, in the world, limited information is available in Korean environment. This paper provides some basic framework of the varroa mite population dynamics modified from published works in western world to adapt to Korean beekeeping environment. Overall population growth rate was in agreement to those previous published. However the detail behavior was quite different mainly because of splitting honeybee colony during the summer season. Although this framework provide reasonable, logical theoretical linkage to varroa mite population growth, implementation of the results provided from this model is not appreciated mainly because this paper is intended to show the basic framework, not the simulated results. Thus, further incorporation of realistic parameters from honey bee and its parasites in Korean environment would provide better insight of the population behavior and management options. Also, research gaps which need to be filled are further discussed.

Key words: *Varroa destructor*, *Apis mellifera*, population dynamics, model, swarming, phoresy

상주지역 배 과원에서 복숭아순나방과 복숭아심식나방의 발생 동태

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관행관리와 친환경관리를 하는 경북 상주시 공검면 일대 10개의 배과원에서 2005년부터 5년간 복숭아순나방과 복숭아심식나방의 발생을 페로몬트랩을 이용하여 모니터링하였다. 복숭아심식나방은 5월말 1세대 성충이 발생이 시작되어 7월 중순 최성기를 보였으며 9월 중순 이후 성충은 급감하였다. 년간 누적 발생량의 변이계수는 20% 이내로 과원별로 발생량의 차이가 매우 적은 것으로 나타났다. 반면 년차별 발생량의 차이는 누적온일도와 정의 상관을 보였다. 또한 관행관리과원에 비하여 약제가 적게 처리되는 친환경관리 과원에서 발생량이 많았다. 반면 복숭아순나방은 월동 세대 성충이 5월말에 발생 최성기를 이루고, 누적온일도 모델에 적용시킨 결과 4세대의 성충이 발생하는 것으로 파악되었다. 복숭아순나방은 매년 발생이 증가하는 패턴을 보였으며 이는 누적온일도와는 상관이 없었다. 과원별 연간 누적 발생량의 변이계수는 5-46%로 과원별로 발생량의 차이가 매우 다. 상주지역 배 과원에서 복숭아순나방과 복숭아심식나방의 발생량 간에는 상관관계가 나타나지 않았다.

검색어: 배, 복숭아순나방, 복숭아심식나방, 온일도 모델, 상관관계

DNA Sequence Variation of the Tobacco Cutworm, *Spodoptera litura* (Lepidoptera: Noctuidae) Determined by Mitochondrial A+T-rich Region and Nuclear ITS2 Sequences

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In an effort to gain a better understanding of the nature of the population genetic structure of the pest insect, *Spodoptera litura* (Lepidoptera: Noctuidae), tobacco cutworms were collected from six Korean and five Chinese localities and their mitochondrial A+T-rich region and nuclear internal transcribed spacer 2 (ITS2) regions were cloned and sequenced. A total of 106 A+T-rich region haplotypes and 92 ITS2 sequence types were obtained from 158 individuals. Compared to the preliminary mitochondrial COI gene sequence data that provided all identical sequence types in all samples, the A+T-rich region and nuclear ITS2 are highly variable. Overall, a low level of genetic fixation in the A+T-rich region (F_{ST} = 0 ~ 0.02965) and nuclear ITS2 (F_{ST} = 0 ~ 0.34491), and no discernable isolated population was noted to exist among most *S. litura* populations. The presence of a majority of within-population variations, rather than variations among populations or between China and Korea, indicates that the *S. litura* populations are composed of heterogeneous individuals. The fixation index at hierarchical level of among regions shows no significance, suggesting that the *S. litura* populations in both Korea and China are profoundly interrelated with one another. This finding is in accord with the current knowledge that *S. litura* has sufficient flight capacity for dispersal.

An ethogram for the pre-reproductive stages of the green peach aphid, *Myzus persicae*

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The green peach aphid, *Myzus persicae,* is one of the most widespread insect pest worldwide. We documented all behaviors of this species during the pre-reproductive period to understand the behavioral repertoire, organization of behaviors, and the context in which they occur. The behaviors that we observed include honey-dew production, walking, wagging, and molting. Honey-dew production occurred regularly at every 30-60 min throughout all nymphal stages. Walking seemed to occur when the host condition was not good, probably related to searching for a new host. Wagging, which was the turning of abdomen with the stylet in the plant, was also frequently observed, but the function of this behavior was unclear. We also noted the frequency and the amount of time for each behavior at different nymphal stages.

Key words: *Myzus persicae,* aphid, ethogram, pre-reproductive period

Analysis of DNA Sequence Variation of the Bumblebee, *Bombus ignitus* (Hymenoptera: Apidae), Based on Mitochondrial COI Gene and Nuclear Ribosomal ITS2 Sequences

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The bumblebee, *Bombus ignitus* (Hymenoptera: Apidae), is a valuable natural resource that is one of the most notably utilized for greenhouse pollination in Korea. In order to understand the nature of genetic relationships, gene flow, and population structure of the species we sequenced a partial COI gene of mitochondrial DNA (mtDNA) corresponding to "animal barcode" region and the complete internal transcribed spacer 2 (ITS2) of the nuclear ribosomal DNA (nrDNA) collected from Korean localities. Although the 658-bp long mtDNA sequence provided only six haplotypes with the maximum sequence divergence of 0.61% (4 bp), the ITS sequences provided 84 sequence types with the maximum sequence divergence of 1.02% (21 sites), confirming better applicability of the ITS sequences to the study of intraspecific variation. The complete ITS2 sequences of *B. ignitus* were shown to be longest among known insects, ranging in size from 2,034 bp ~ 2,052 bp, harboring two duplicated repeats. Overall, a very high per generation migration ratio, a very low level of genetic fixation, and no discernable hierarchical population/ population group were noted to exist among populations of *B. ignitus* on the basis of both molecules, thus suggesting that the *B. ignitus* populations on the Korean peninsula are panmictic, which is consistent with our understanding of the dispersal capability of the species.

수출 단감원에서 주요 깍지벌레의 수체와 과수원에서 발생과 분포

정부근, 이홍수, 권진혁, 김태성, 송원두
경남농업기술원 친환경연구과

단감 수출재배단지에서 발생하는 깍지벌레류의 주요 우점종과 이들의 단감 수체 내에서와 과수원내에서 분포를 조사하여 방제에 활용코자 조사를 수행하였다. 단감 재배단지는 순천시 외곽의 농가, 진주시 문산면, 창원시 동읍에서 단감재배 10농가 선정하여, 농가 당 10주 정도를 깍지벌레가 주로 활동하는 5월부터 10월까지 매월 간격으로 조사하였다. 감나무 수체에서 발생하는 깍지벌레류는 과실, 잎, 가지, 주간에서 조사하였다. 과원 내에서 발생하는 깍지벌레류는 과원 중심에서 외곽으로 3방향을 나누고 다시 각각의 방향 별로 5등분한 지점을 중심으로 9월에 조사하였다. 주로 발생하는 깍지벌레 종은 식나무깍지벌레로 향후 주요해충으로 방제할 필요가 있었다. 그 외 깍지벌레류로 감나무주머니깍지벌레, 거북밀깍지벌레, 뿔밀깍지벌레가 조사되었고 검역해충인 온실가루깍지벌레는 관찰되지 않았다. 단감 수체 내에서 식나무깍지벌레는 잎, 과실, 4년생 이하의 가지(세지)에서 주로 발생하였고 주간에서는 발생하지 않았다. 종전까지 주요해충으로 인식되던 감나무주머니깍지벌레는 잎, 과실, 가지, 주간 등에서 모두 발생하나 주로 주간에서 발생하였다. 과원 내 발생은 외관상 관찰되는 과수원 외곽과 달리 비교적 골고루 분산하여 발생하는 것으로 나타났다.

검색어: 감나무주머니깍지벌레, 식나무깍지벌레, 단감, 분포, 주요종

단감원에서 식나무깍지벌레의 발육과 방제

정부근, 이흥수, 권진혁, 김태성, 송원두
경남농업기술원 친환경연구과

단감 수출에서 종종 문제를 일으키며 주요 해충으로 등장한 식나무깍지벌레의 방제법을 구명하기 위하여 발육조사를 2009년에 수행하였다. 과원에서 발육조사를 위하여 2009년 4월 초순부터 11월까지 매주 간격으로 진주시 문산에서 수행하였다. 발육조사는 식나무깍지벌레가 발생하는 현장에서 감나무의 가지, 잎, 과실 등을 채취하여 실내에서 실체현미경으로 조사하였다. 식나무깍지벌레에 대한 방제약제 시험은 사천시 용현에서 2009년 6월 9일부터 일주일 간격으로 2회 방제후 7월 21일 방제결과를 조사하였다. 월동성충의 산란은 4월 8일부터 14일 사이에 시작하여 산란 최성기는 5월 8일에 도달하는 것으로 나타났다. 이때부터 약충이 부화하여 가지나 잎으로 이동하는 것으로 나타났고 5월 14일에 월동세대로부터 부화약충의 발생이 최성기에 도달하는 것으로 나타났다. 깍지벌레의 특성을 감안하여 방제기간은 이시기를 기준으로 비교적 잔효력이 우수한 약제를 선정하여 방제하면 방제효과가 높을 것으로 생각되었다. 1세대 성충에 의한 산란최성기와 가지에서 약충이동 최성기는 7월 27일로 여름철 고온임을 감안하면 거의 동시적으로 이루어지는 것으로 나타났다. 잎에서 수컷의 우화는 9월 3일 전후로 발생하여 9월 29일경까지 거의 모두 우화하는 것으로 나타났다. 방제시험 결과 뷰프로페진·디노테퓨란 수화제가 방제가 90% 이상이었다. 당해연도에 발육조사와 방제시험을 동시에 수행한 결과 여타약제 등에서 약효가 다소 낮았던 것을 고려하면 적기방제로 방제가를 제고할 수 있을 것으로 생각된다.

검색어: 식나무깍지벌레, 발육, 단감, 방제

Oral toxicity of symbiotic bacteria *Photorhabdus temperata* ssp. *temperata* against immature stages of insects

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Oral toxicities of 5 *Photorhabdus temperata* ssp. *temperata* (Ptt) strains collected in different regions of Korea were determined against the larvae of *Plodia interpunctella, Galleria mellonella, Lucilia caesar, Culex pipiens pallens* and *Paratlanticus ussuriensis*. When a diet or water containing culture media of 5 different Ptt strains were ingested to immature insects, mortalities of the first instar larvae of *G. mellonella, L. caesar, P. ussuriensis* and young nymphs of *C. pipiens pallens* were rapidly increased and 100% within 3-5 days after treatments. However, mortality of *P. interpunctella* neonate larvae was slightly slower and 94.4-100% within 7 days after treatments. As controls, a diet containing either water, the medium without culturing bacteria, or *E. coli* culture medium did not effective on their mortalities. As another control group, the culture medium of *P. temperata* ssp. *laumondii* (KACC) were variously effective to mortalities of 4 species, namely, 100, 45.3, 2.8 and 0% to *Galleria, Lucilia, Plodia* and *Culex*, respectively. Culture media of Ptt strains inhibited developmental late of late larvae of *P. interpunctella*. Our results suggest that the oral administration of the culture medium of Ptt symbiotic bacteria was highly effective to control various immature insects.

Key words: Developmental inhibition, Entomopathogenic nematodes, Insecticidal toxins, Oral toxicity, *Photorhabdus temperata*, Symbiotic bacteria

여름형과 월동형 점박이응애에 대한 Vapormate의 훈증효과

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훈증제 vapormate를 처리하여 여름형과 월동형 점박이응애에 대한 살충효과를 비교하였다. 여름형 점박이응애는 실험실에서 누대 사육한 것을, 월동형 점박이응애는 경남 산청군의 사과 과수원에서 채집한 것을 사용하였다. Vapormate처리농도는 용적률 0%에서는 65.8, 117.4, 170, 284.4 mg/ℓ, 단감을 채운 용적률 30%에서는 65.2, 118.9, 163.7, 265.8 mg/ℓ이었다. 용적률 0%에서 100% 사충률을 보인 vapormate 농도는 여름형 성충에 대해서는 117.4 mg/ℓ이상, 월동형 성충에 대해서는 170 mg/ℓ이상이었다. 용적률을 30% 채웠을 경우에는 여름형이 163.7 mg/ℓ이상에서, 월동형이 265.8 mg/ℓ에서 100% 사충률을 보였다. 두 용적률 모두 여름형보다 월동형이 vapormate에 대해 내성이 높았으며 훈증처리 후 24, 48시간 간에 사충률 차이는 없었다. 여름형 점박이응애 알의 부화율은 무처리에서는 94%이었으나 용적율 0%와 30%에서 처리한 모든 농도에서 0%이었다. 훈증용기의 용적을 채울 때 사용한 단감에 대한 약해(무름정도, 반점발생, 색도변화)는 상기의 모든 처리농도에서 나타나지 않았다.

검색어: 점박이응애, 검역, Vapormate, 훈증 , Ethyl formate

Fumigant antitermitic activity of plant essential oils and components from ajowan (*Trachyspermum ammi*), allspice (*Pimenta dioica*), caraway (*Carum carvi*), dill (*Anethum graveolens*), geranium (*Pelargonium graveolens*) and litsea (*Litsea cubeba*) oils against Japanese termite (*Reticulitermes speratus Kolbe*)

Junheon Kim, Seon-Mi Seo, Eunae Kim, Hwa-Jeong Yeom, Il-Kwon Park, and Sang-Chul Shin

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Plant essential oils from 26 plant species were tested for their insecticidal activities against the Japanese termite, *Reticulitermes speratus* Kolbe, using a fumigation bioassay. Responses varied with source, exposure time, and concentration. Among the essential oils tested, strong insecticidal activity was observed with the essential oils of ajowan (*Trachyspermum ammi*), allspice (*Pimenta dioica*), caraway (*Carum carvi*), dill (*Anethum graveolens*), geranium (*Pelargonium graveolens*), and litsea (*Litsea cubeba*). The composition of six essential oils was identified by using gas chromatography-mass spectrometry. The compounds thus identified were tested individually for their insecticidal activities against Japanese termites. Responses varied in a dose-dependent manner for each compound. Phenol compounds exhibited the strongest insecticidal activity among the test compounds further, alcohol and aldehyde groups were more toxic than hydrocarbons. The essential oils and compounds described herein merit further study as potential fumigants for termite control.

Key words: Plant essential oils, *Reticulitermes speratus*, antitermitic activity, fumigant, ajowan, allspice, caraway, dill, geranium, litsea, thymol, carvacrol, eugenol

Larvicidal activity of Myrtaceae essential oils and their components against *Aedes aegypti*, acute toxicity on the water flea, *Daphnia magna*, and aqueous residue

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The larvicidal activities of 11 Myrtaceae essential oils and their components against Aedes aegypti were tested by the immersion method. We also tested the acute toxicity of 4 active oils and their components against the water flea, Daphnia magna. Further, the aqueous residues of these oils and their components were determined at 2 and 7 days after suspending in water. Among the 11 oils tested, 0.1 mg/mL of *Melaleucalinariifolia, M. dissitiflora, M. quinquenervia,* and *Eucalyptus globulus* oils showed strong larvicidal activity against A. aegypti. Among the test compounds, allyl isothiocyanate, ɣ-terpinene, p-cymene, (+)-limonene, (-)-limonene, ɣ-terpinene, and (E)-nerolidol showed strong larvicidal activity against A. aegypti. The acute toxicity test revealed *M. linariifolia* was the most toxic to *D. magna*. Among test compounds, allyl isothiocyanate was the most toxic to D. magna. Two days after treatment, the residues of *M. dissitiflora, M. linariifolia, M. quinquenervia*, and *E. globulus* oils in water were 55.4, 46.6, 32.4, and 14.8%, respectively. Low concentrations of allyl isothiocyanate, ɣ-terpinene, p-cymene, (-)-limonene, (+)-limonene, and ɣ-terpinene were detected in the water at 2 days after treatment. Therefore, Myrtaceae essential oils and their components could be developed as control agents against mosquito larvae.

Key words: Myrtaceae plant essential oils, larvicidal activity, mosquito, water flea, *Daphnia magna*, aqueous residue

The efficacy of Bistrifluron UG to control the mosquito, *Culex pipiens molestus* (Diptera: Culicidae)

A point mutation in a glutamate-gated chloride channel confers abamectin resistance in the two-spotted spider mite, *Tetranychus urticae* Koch

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The molecular mechanisms and genetics of abamectin resistance mediated by target site insensitivity in the two-spotted spider mite, *Tetranychus urticae*, were investigated by comparing two isogenic AbaS and AbaR strains. Cloning and sequencing of full-length cDNA fragments of GABA-gated chloride channel genes revealed no polymorphisms between the two strains. However, sequence comparison of the full-length cDNA fragment of a *T. urticae* glutamate-gated chloride channel gene (*TuGluCl*) identified a G323D point mutation as being tentatively related with abamectin resistance. In individual F2 progenies obtained by backcrossing, the G323D genotype was confirmed to correlate with abamectin resistance. Bioassays using progeny from reciprocal crossings revealed that the abamectin resistance trait due to TuGluCl insensitivity is incompletely recessive.

Key words: glutamate-gated chloride channel, target site insensitivity, macrocyclic lactone, abamectin, *Tetranychus urticae*

Toxicity of compounds identified in *Cnidium officinale* Rhizome to *Bemisa tabaci* (Hemiptera: Aleyrodidae)

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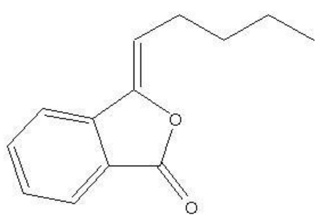
The toxicity of materials derived from rhizome of *Cnidium officinale* Makino to adults from B and Q biotype of *Bemisia tabaci* was examined using a leaf-dipping bioassay. Results were compared with those of two currently used insecticides: acetamiprid and thiamethoxam. The active principles of *C. officinale* rhizome were identified as butylidenephthalide (**1**), ligustilide (**2**), and 3-butylphthalide (**3**) by spectroscopic analysis. These compounds exhibited 100% mortality against both B and Q biotype adults at 2.5 mg/ml. At a concentration of 1.25 mg/ml, butylidenephthalide produced 88 and 92% mortality against B and Q biotype adults, respectively. 3-butylphthalide showed 100 and 89% mortality against B and Q type adults, respectively. Ligustilide exhibited 97 and 100% mortality against B and Q type adults, respectively. The toxicity of these compounds to B type adults was almost equal to that of thiamethoxam and acetamiprid, whereas two insecticides exhibited 40% mortality to Q biotype. *C. officinale* rhizome-derived materials merit further study as potential insecticides for the control of *B. tabaci* populations due to global efforts to reduce the level of highly toxic synthetic pesticides.



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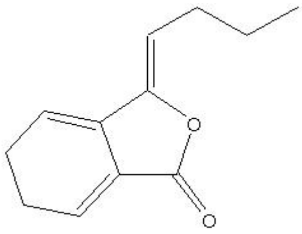

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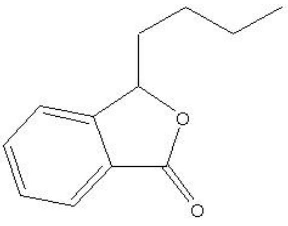

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Key words: *B. tabaci*, *C. officinale,* butylidenephthalide, ligustilide, 3-butylphthalide

Vapor Phase Repellency and Toxicity of *Zanthoxylum piperitum* Pericarp Steam Distillate, *Zanthoxylum amartum* Seed Oil, and their Constituents to *Stomoxys calcitrans* Orientation Responses

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The vapor phase repellency and toxicity of *Zanthoxylum piperitum* pericarp steam distillate (ZP-SD), *Z. armatum* seed oil (ZA-SO), and their 29 constituents to the adult female stable fly, *Stomoxys calcitrans* (Diptera: Muscidae), were examined using filter paper fumigation bioassay. Results were compared with those of the currently used repellent: DEET. Both of ZP-SD and ZA-SO exhibited vapor phase repellency and toxicity to female flies at 5 to 40 mg/filter paper (0.23 to 1.82 mg/cm^3 air) during a 120-min exposure, whereas DEET exhibited neither repellency nor toxicity to the stable fly. At 5 mg/filter paper, vapor phase of ZP-SD and ZA-SO repelled 50 to 67% and 61 to 51% flies, respectively, to control area during 30 to 120 min. At 40 mg/filter paper, vapor phase of ZP-SD and ZA-SO caused 100% and 81% mortality, respectively, after 120 min of exposure. Among the tested volatile constituents, cuminaldehyde was the strongest repellent and toxic compound to the fly and was four times more toxic than ZP-SD and ZA-SO. Cuminaldehyde vapor phase repelled 62% flies to control area after 30 min at 2.5 mg/filter paper and caused 100% mortality after 120 min at 10 mg/filter paper. Based on the structure-activity relationships, the toxicity and repellency of constituents having aldehyde moiety were better than those of alcohol or ether one. Overall, ZP-SD, ZA-SO, and their bioactive constituents could be useful as potential vapor repellents to control stable fly population.

Key words: vapor phase repellent, toxicity, orientation responses, *Stomoxys calcitrans*, *Zanthoxylum armatum*, *Zanthoxylum piperitum*

Larvicidal activity of compounds identified in *Pongamia pinnata* against *Aedes aegypti* and *Culex pipiens pallens*

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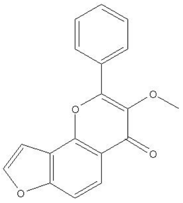
The toxicity of materials derived from seed of *Pongamia pinnata* Pierre toward to third instar larvae of *Aedes aegypti* and *Culex pipiens pallens* was examined using direct contact bioassay. Results were compared with those of the currently used insecticides: fenthion and temephos. The active principles of *Pongamia pinnata* were identified as the karanjin (**1**), pongamone (**2**), palmitic acid (**3**) and karanjachromene (**4**), by spectroscopic analysis. Based on 24h LC_{50} values, karanjin (14.61 and 16.13 ppm) was the most toxic compound but less effective than fenthion (0.0031 and 0.068 ppm) and temephos (0.016 and 0.056 ppm) against *Ae. aegypti* and *Cx p. pallens*. Moderate toxicity was produced by pongamone (34.50 and 39.53 ppm), palmitic acid (36.93 and 42.96 ppm), and karanjachromene (43.05 and 48.95 ppm). *P. pinnata* seed derived materials, particularly karanjin, merit further study as potential mosquito larvicides for the control of mosquito populations in light of global efforts to reduce the level of highly toxic synthetic larvicides in the aquatic environment.



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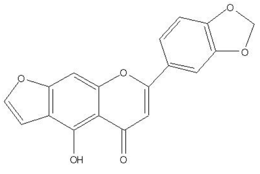

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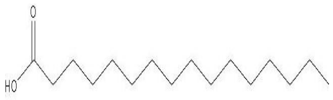

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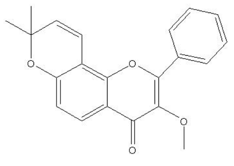

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Key words: Karanjin, *Pongamia pinnata*, *Aedes aegypti*, *Culex pipiens pallens*

비타민 A 강화벼의 곤충 및 생물상 변화양상 및 비교

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2009년 경북 군위군 소재 경북대학교 벼 GMO 격리포장에서 곤충 및 생물상 조사가 이루어졌다. 조사는 유전자 조작된 비타민 A 강화벼(황금벼)와 대조벼인 낙동벼에서 동력흡충기와 포충망을 이용하여 정기적으로 이루어졌고, 두 포장간에 발생밀도, 우점종 구성, 종 다양도 지수등이 비교되었다. 채집된 생물들은 대부분이 거미강과 곤충강에 속하였고, 낙동벼에서 13목 57과 1,234.2개체, 황금벼에서 12목 52과 1,369.7 개체가 채집되었다. 두 포장에서 시기별 출현빈도나 밀도의 변화경향은 유사했다. 분류군수는 본답 후기로 갈수록 증가한 반면, 개체수는 7월 10일, 8월 25일 조사에서 최고밀도 기록 후, 감소하였다. 두 조사지간에 분류군수와 개체수에서 유의한 차이는 없었다. 이중에서 거미류는 낙동벼에서 8과 44.8개체, 황금벼에서 8과 54.2개체가 채집되었다. 시기별로 두 포장간의 거미군집 발달 패턴의 큰 차이는 보이지 않았다. 황금벼와 낙동벼 모두에서 깔따구, 멸구, 노랑굴파리, 진딧물, 실잠자리가 공통적으로 우점했다. 종 다양도 지수분석에서 낙동벼에서 생물상이 풍부도, 균등도 다양도등이 황금벼에 비해 다소 높았다. 주요 해충인 애멸구 발생동태는 두 포장간에 유의한 차이가 없었다. 흰등멸구의 경우도 8월 25일 조사결과를 제외하고는 비슷한 밀도변동을 보였다. 본 발표는 1년차 연구결과로 앞으로 추가연구를 통해 GM벼의 영향을 정밀하게 평가할 예정이다.

검색어: 비타민 A 강화벼, 곤충상 비교, 종 다양도, 군집분석

Identification and Characterization of Chlorpyrifos-Methyl degrading *Chryseobacterium* sp. Strain KR200

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The Organophosphorus pesticides are widely used for agricultural and domestic purposes due to their relatively low persistence in the environment. Chlorpyrifos-methyl (CM) is used at a rate of over 14 million pounds per year in US agriculture, ranking it as the second most heavily used pesticide. This study aimed at isolating bacteria from soil and determining their ability to degrade CM and identify the intermediates in culture broth. Bacteria capable of degrading CM was isolated by enrichment culture. *Chryseobacterium* sp. strain KR200 degraded CM up to 91.58% in 7days. Studies with CM in liquid culture of *Chryseobacterium* sp. strain KR200 demonstrated that the isolate hydrolyzed CM to 3,5,6-trichloro-2-pyridinol, and utilized this compound for growth and energy. We performed SDS-PAGE and two-dimensional gel electrophoresis and identified proteins whose expression pattern is affected by CM using mass spectrometry. The results revealed various proteins that can be grouped according to their respective cellular function. These results highlight the potential of this bacterium to be used in the clean up of contaminated pesticide waste in the environment.

Key words: Insecticide, Insecticide degrading bacteria, Chlorpyrifos-methyl, *Chryseobacterium* sp.

Easy and Rapid Quantification Method of *Plutella xylostella* Granulovirus

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The diamondback moth, *Plutella xylostella* is a one of the most important pests of various cruciferous crops and has a geographically wide ranging habitat. The heavy dependence on chemical pesticides has created severe pesticide resistance problems. In recent years, *Bacillus thuringiensis* product have been widely used for *P. xylostella* control bus genetic resistance in populations to some *B. thuringiensis* strains, compounded by cross-resistance to several different *B. thuringiensis* toxins, has also been identified. Such recent resistance problems serve to emphasize the urgent need for alternative control agents and their use within an integrated pest management approach. Baculoviruses have been used as agents for the biological control of certain insect pest species. the granuloviruses (GVs), based on the structure of the occluded virus and the occlusion body (OB). Several reports have showed *P. xylostella* granulovirus (PxGV) as a promise control agent for *P. xylostella*. However, it is very difficult to study GV because its OB, granule, has very small size and could be observed exactly under the electron microscopy (EM). This study was performed to develop rapid quantification method for granule of PxGV. After the exact quantification of granule with latex beads using EM, the universal extraction method of viral DNA was established for consistent experiment. The number of granules was calculated by the quantification of PCR products for granuline gene using spectrophotometer and densitometer. This novel calculation method for granule would be useful to study GV.

Key words: *Plutella xylostella*, PxGV, quantification, PCR, electron microscopy

소모임

Development of microsatellite loci from the soybean aphid, *Aphis glycines* Matsumura (Hemiptera: Aphididae)

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Ten novel microsatellite loci were isolated and characterized from the soybean aphid, *Aphis glycines.* The soybean aphid was recently introduced into North America where it has become a serious pest of soybeans. This invasive pest has rapidly spread throughout the midwestern United States and southern Canada since 2000. The isolated loci were polymorphic, with two to 18 alleles in 20 individuals from a single population in Korea. The analyses revealed that 19 individuals had different multilocus genotypes, showing expected heterozygosity values ranging from 0.180 to 0.891. We report the development of microsatellite markers for *A. glycines* potentially suitable for further studies of population structure, dispersal, and host alternation.

Key words: aphid, *Aphis glycines*, microsatellite, population genetics, soybean aphid

The analysis of hexapod mitochondrial sequences for assaying the utility of DNA barcode

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DNA barcode projects in Hexapoda have been initialized and progressed accumulating large number of mitochondrial gene sequences. However, due to large number of data, overview of DNA barcode projects was not conducted until now. Here we reported the current status of DNA barcode projects with the aid of Insect Mitochondrial Genome Database (IMGD; http://www.imgd.org/) which archives 128,562 partial mitochondrial gene sequences (PMEs) of Hexapoda. Among 37 mitochondrial genes, *COI* has been used popularly (22,379 PMEs;17.40 %) through all 33 orders. Through 513 researches, different parts of *COI* PME have been utilized differently along with hexapod orders. Inaddition, by calculating genetic divergences of *COI* PMEs, intra-species and inter-species in 21 hexapod orders were distinguished by 5% divergence and some of mitochondrial genes in certain order present higher genetic divergences than that of *COI*. Based on these results, we confirmed that DNA barcode is a use ful tool to identify hexapod species and several mitochondrial genes can be good molecular markers to support *COI*.

Key words: Hexapoda, DNA barcode, *COI*, and mitochondrial genes

산림곤충자원 보호·이용 관리의 장기발전 전략

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산림곤충이란 산림으로 규정되는 지역에 서식하는 모든 곤충으로써 중요한 생물자원이며, 그 중요성이 점차 증대되고 있는 실정이다. 산림곤충에 관한 연구는 현재까지 해충위주로 수행되어 왔으며, 이를 제외한 희귀곤충, 산림생태계의 토양분해자 역할, 화분매개자로서의 역할 등 유용곤충이나 의약용으로 활용되는 다양한 여러 산림곤충에 대한 보호관리 차원의 연구 접근은 아주 드물다. 국내 곤충자원 연구는 농촌진흥청을 중심으로 잠업, 양봉, 애완곤충 분야 등, 농가소득증대 차원의 응용분야나 환경부의 법적보호종 중심의 생물다양성 조사 및 보전방안에 관한 연구, 국립수목원의 생물표본 및 종의 DB사업 등을 통해서 부분적으로 활발하게 진행되고 있다. 그러나, 국가적인 곤충자원의 종합적인 보호와 관리·이용을 위해서는 곤충의 주서식지인 산림을 중심으로 체계적인 분포조사, 수집, 분류, 활용방안, 보호·관리 등의 종합적·장기적인 기반사업 추진이 절실함에도 현재까지 산림청내 곤충업무는 산림병해충과를 중심으로 해충 생태 및 방제위주의 연구를 주로 수행 중이며 국립수목원에서 자생곤충종의 분포연구, 주요 산림곤충의 분류연구 및 정보화 등 기초연구 수행이 부분적으로 이루어지고 있을 뿐이다. 한편 선진국에서는 국가기관을 중심으로 자국내 곤충자원의 탐색조사 및 활용성에 대한 연구개발이 활발히 이루어지고 있어서, 미국은 농무성 산하「경제곤충연구소」에서 곤충자원의 조사 및 확보업무가 추진되며, 영국은 국가생물기록센터가 주축이 되어 곤충을 포함한 다양한 생물의 조사 및 이들에 대한 정확한 데이터를 수집·관리함으로써 생물다양성 관리에 활용하며, 일본은 국책연구과제인「곤충기능이용기술개발연구(1993-)」를 추진하고 있으며, 네덜란드 등 유럽에서는 친환경농업을 위한 곤충자원의 활용기술 개발 등 다각적인 곤충연구가 활성화되어 있다. 또한 유엔 생물다양성협약 (CBD)이 발효된 이후 곤충의 이용 및 자원화를 위한 국가간 경쟁이 치열해 지고 있다. 우리나라의 곤충은 90% 이상이 산림 내에 서식하는 주요 산림자원이지만 이들의 활용, 자원화 및 보전에 대한 체계적 관리정책이 미약하며, 산림 곤충자원에 대한 조사, 분류, 산업화, 보호·관리에 관한 연구를 위한 연구 인프라가 극히 취약한 실정이다. 따라서 산림청 등 산림을 관리하는 부처에서는 산림곤충을 대상으로 이들의 보호관리와 이용방안에 대한 체계적인 조사연구를 통해서 산림자원의 보전과 지속적

인 활용이란 측면에서 적극 검토되어져야 할 것이다.

본 발표에서는 다음과 같은 내용에 초점을 두고 발표 및 논의하고자 한다: 산림내에 서식하는 곤충에 대한 보호·관리 및 자원화를 위한 중장기 마스터플랜 수립; 국토의 64%인 산림의 생물다양성 유지관리를 위한 산림곤충의 종합적·체계적 조사 가이드라인 마련; 종합적인 산림곤충의 조사·수집, 보호·증식 등을 위한 연구인프라 강화 및 민간네트워크 구축방안 연구; 희귀곤충 및 그 서식지 보호를 위한 정책개발 제안; 국내·외 곤충시장의 조사분석 및 활용기술 적용범위 분석을 통한 유용한 산림곤충의 이·활용 방안 제안. 이상의 원활한 수행을 위한 산림곤충 업무 추진을 위한 법적·제도적 근거 마련, 특히「산림자원법」,「산림보호법」 등 관련 현행법의 문제점 및 개선할 분야에 관해서 심도있는 분석이 이루어져야 할 것이다.

Year-Round Production System of the Korean Native Bumblebee *Bombus ignitus* for Crop Pollination

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The bumblebee is an important pollinator of various greenhouse crops, especially for tomatoes and there has been increasing interest in commercial use of the insects for pollination. Recent advances in commercial rearing of the European bumblebee (*Bombus terrestris*) made it possible to package bumblebee for crop pollination. Bumblebees are distributed world widely including alpine, cool temperate and even arctic environments of the northern continents. We chose *B. ignitus* out of seven Korean native bumblebees, because the species showed the best results both in artificial multiplication and in pollinating ability. Now, we are studying an artificial year-round mass rearing of *B. ignitus* selected as the most reliable native species in crop pollination. Therefore, we investigated the optimum temperature and humidity, effect of photoperiod and CO_2-treatment, facilitating effects of helper, and artificial hibernation of *B. ignitus* to establish year-round mass rearing of *B. ignius*.

The experimental regimes of temperature and humidity were defined as 23℃, 27℃ and 30℃ under a constant humidity of 65% R.H., and 50%, 65% and 80% R.H. under a constant temperature of 27℃, respectively. Among the temperature regimes, 27℃-rearing showed the best results, i.e., the rates of colony initiation, colony foundation and progeny-queen production at 27℃ were 83%, 63% and 46%, respectively, which corresponded to 2.2-5.5 times the respective values at other temperature regimes. The numbers of progeny produced at 27℃-rearing, 164±33 workers, 553±174 males and 33±48 queens were also higher, corresponding to 21.8 and 1.5 times those at 23℃ and 30℃, respectively. In terms of humidity, 65% R.H. was favorable for big colony formation. Under the same humidity, the rates of colony initiation, colony foundation and progeny-queen production were 85%, 70% and 50%, respectively, and the number of progenies reached 180±30 workers, 578±179 males and 35±38 queens. Therefore, 27℃ and 65% R.H. were determined to be the favorable environmental conditions for colony development of *B. ignitus* in indoor rearing.

It was investigated whether developmental characteristics of foundation queens of *B. ignitus* collected in the 4 localities in Korea would be affected by the first oviposition days of them. The first ovipostion day was classified as 1 - 4 days (immediate early), 5 - 6 days (early), 7 - 10 days (delayed early), 11 - 20 days (medium), 21 - 40 days (late), and above 41days (very late). The queen that had the early first oviposition day, i.e., laid eggs so early after starting to be raised indoors, showed much higher rate of colony foundation and progeny-queen production and much shorter period of colony foundation and worker emergence. Besides, the numbers of worker and progeny-queen emerged from the queen that had the early first oviposition day were higher than those of the queen that had the late first oviposition. In results, the queen that had the early first oviposition day could make colony stronger and could make colony formation period shorter, therefore, the first oviposition day of foundation queen was proved to be a criterion for the selection of super colonies when *B. ignitus* is raised indoors.

It was investigated whether or not such helpers as worker bee, bee-cocoon and egg-cup etc, have any effects on oviposition and colony foundation of the bumblebee queen, *B. ignitus*. Among the helpers tested, the callow workers of B. ignitus and B. terrestris showed the most remarkable effects on the oviposition rates to 92% and 88%, respectively. The live cocoon as a helper improved oviposition rate over 60%. A narcotized old worker 10 days-aged after emergence, showed similar effects to a callow worker on the colony development such as oviposition rate, colony foundation and progeny-queen production. On the other hand, dried cocoon, callow honeybee worker or egg-cup did not show a positive effect as a helper. In the number of workers recruited to a foundation queen, two workers showed better effect than one worker on the colony development, with no difference between two and more.

The effect of photoperiodic regimes on the oviposition and colony development of *B. ignitus* queens was examined with 0L, 8L, and 16L under 2 7℃ and 65% R. H. Among these photoperiod regimes, the oviposition rate at 8L and 16L was 80.2% and 83.1%, respectively, which was 12-15% higher than that at the dark condition (0L). Duration up to first oviposition at 8L and 16L was 17.5 days and 16.5 days, respectively, which was 2-3 days shorter than that at 0L. The colony foundation rate at 8L and 16L was 9.2% and 10.4%, respectively, which corresponded to 1.7-2.0 fold the value at 0L. In addition, the rate of progeny-queen production at 8L and 16L was also two fold higher than that at 0L. Taken there together, the light conditions (8L and 16L) rather than dark condition (0L) were more suitable for oviposition and colony development for *B. ignitus* in the indoor rearing condition.

We investigated mating conditions of photoperiod, illumination and temperature during mating periods, care temperature of queen before mating, mating period and number of queen per mating cage to improve mating rate of *B. ignitus*. Among photoperiodic regimes of 12L, 14L and 16L during mating periods, queen mated at 14L showed better results than at 12L and 16L in egg-laying characteristics and colony development. In case of illumination during mating periods, intensity of 1000 lux was more effective than at intensity of 100 lux and 2000 lux in mating *B. ignitus* queen. Mating temperature and care temperature of queen before mating favorable for *B. ignitus* queen were 22-25? and 19?, respectively. The period need to mating *B. ignitus* queen was 3 days, and the number of queen suitable per mating cage of 55× 45× 65 ㎝ was 30.

The effect of CO_2-treatment on interrupting diapause of *B. ignitus* was examined to provide a means for year-round rearing of the bumblebee. When mated young queens were exposed to 65% or 99% CO_2 for 30 min daily during two consecutive days, oviposition rate increased to 75% and 77%, respectively, comparing 50% in CO2-untreated queens. At the same time, the days needed to first oviposition shortened to 17-18 days in CO_2-treated queens, comparing to 30 days in CO_2-untreated queens. CO_2-treatment at the second day after mating was appropriate to the oviposition and colony development. CO_2-treatment showed a positive effect on the oviposition and colony development, but less than them of over-wintered queen in numbers of produced progeny. It can be concluded that CO_2-treatment to *B. ignitus* is insufficient to produce commercial grade bumblebee colony in spite of its capability for promoting oviposition, because the treatment failed to form a big colony.

Artificial hibernation is essential for year-round rearing of the bumblebee, *B. ignitus* that undergoes one generation per year. It is known that keeping the queens in low temperature for two or three months is effective to terminate their diapause and develop the colony. Temperature, time and surroundings to keep the queens during artificial hibernation were investigated. Among the tested temperatures, -2.5°C, 0°C, 2.5°C, and 5°C, the optimum temperature was 2.5°C. At the temperature (2.5°C), survival rate after chilling of the queens was high and colony development thereafter was enhanced. The proper time to initiate chilling queen was 10 to 14 days after adult eclosion, and the survivability of the queens after chilling was good during the upper period. For the surrounding to keep the queen during artificial hibernation, we proposed the method to preserve them in a bottle filled with perlite and keep it around 80% R. H.

Key words: Bumblebee, *Bombus ignitus*, Temperature, Humidity, Photoperiod, Helper, Mating, Preoviposition, CO_2-treatment, Artificial hibernation. Oviposition, Colony development

살충제 등록시험법

김시용
동부하이텍 농생명연구소 작물보호연구팀

살충제 등록시험법을 최근에 발생하고 있는 주요 해충과 재배방법 및 살충제 특성을 고려하여 합리적인 시험방법을 제시하고, 살충제 등록시험의 신규 담당자가 쉽게 이해하여 시험을 수행할 수 있도록 아래의 순서로 정리하여 제시합니다.

1. 수도(벼) 등록시험법
2. 과수 등록시험법
3. 잔·특작 등록시험법
4. 화훼 등록시험법
5. 수목·잔디 등록시험법

검색어: 등록시험법, 수도, 과수, 잔·특작, 화훼, 수목·잔디

살충제 등록시험 합리적 추진방향

이종섭

작물보호협회

한국작물보호협회에서는 농약품목등록시험을 주관하여 추진하고 있다. 외부위탁시험일 경우 하작물은 약 170여 항목에 400여개 약제를, 동작물은 약 50여 항목에 60여개 정도의 약제에 대하여 매년 시험을 추진하고 있다. 그러나 이제는 수년간 걸쳐 진행되고 있는 농약품목등록 절차 및 추진현황에 대하여 면밀히 고찰하고 문제점과 개선방안을 도출, 시험 신청자 및 시험 담당자, 평가자에게 제안함으로써 높은 시험의 신뢰성을 확보하여야 할 중요한 시점에 이르러 있다. 농약등록시험이 보다 합리적이고 투명하게 이루어졌을 때 사용자는 물론 더 나아가 농산물 소비자에게 안전과 안심을 전해 줄 수 있을 것이다.

Registrational setbacks in Insecticide Items failed in Reviews

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In pesticide registration, the most of applicants are manufacturing companies which have richly experience in applying registration. With their experience, registration applications of pesticide shows excellent ratio of pass, but still some of application still fail to pass, and are judged as disqualifications or to be returned for supplement. In 2009, There were 6 items failed in registrational reviews. Two of them were for their active ingredient contents lower than specifications, Other two were for trials conducted wrong, so sent back to applicants to add supplement. But the rest of them, two items showed low efficiency in one trial, and were judged as disqualifications, which mean that ingredient cannot be registered for that target crop forever. Disqualification from low efficiency has highly strict criterion and usually don't have any flexibility to lower efficiency than criteria, unless there was no pesticide available for that pest. The way to remedy this criterion is very delicate and controversial issue, and needs more reconciliation of various views.

Key words: pesticide registration, registrational criteria, disqualification

Considering Insecticide Resistance to Insecticides

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Insecticide resistance development of insect pests is one of the main threatening factors against stable crop production and keeping human life safe from insect pest disease vector. To know properties of insecticides resistance is very important to develop a management program against insecticide resistance pests. Insecticide resistance development is an event of evolutionary process. We have to deal with insecticide resistance of insect pests by interaction between insecticide and insect pests in their chemical, physical and biological environment. We can glimpse at and infer the evolutionary process of insects from investigating and comparing the resistance level of insect pests to insecticides. Huge amount and many kinds of insecticides have been sprayed to control insect pests. Development of insecticide resistance of insect such as housefly and mosquito, known as most common medical insect, is a result of adaptation to environment covered with insecticides. We can easily assume that the amount and kind of insecticides sprayed the evolutionary force to the diversity of insecticide resistance. The resistance diversity will be very good character of good markers for determining geographical isolation.

Key words: Insecticde, Resistance, Vector, Evolution, Development

나방파리(moth flies)의 생물학적 특징과 방제

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- 일반적 특징 -

나방파리를 보통 drain fly 그리고 sewer fly 또는 filter fly 라고도 부르며, 몸과 날개에 많은 털을 가지고 있다. 주로 하수구 주변에서 볼 수 있고, 소형 곤충으로 몸 길이는 3-4mm 정도인데, 체색은 대체로 검은색을 띄나 갈색으로 보이기도 한다. 분류는 날개시맥의 독특한 특징으로 종을 구별한다.

나방파리의 주요 서식처는 하수구(관), 정화조, 오물로 오염된 토양에서 주로 발생한다.

- 생물학적 특징 -

1. 완전변태를 하며 생활사 기간은 8-24일 정도이다.
2. 적절한 유기물과 습기가 있는 곳에 약 30-100개의 알을 집단으로 산란한다.
3. 알은 48시간 이내에 부화한다.
4. 알을 불규칙하게 세워 산란하는데: 더러운 음식쓰레기를 모은 곳, 배관시설에 고인 물, 오수 필터, 유기물이 부패한 장소에 주로 산란한다.
5. 유충과 번데기는 하수, 정화조 안의 얇은 젤라틴 같은 막에서 볼 수 있으며, 침전물이나 썩은 식물체 그리고 미세한 식물성과 동물성 물질을 먹고 산다.
6. 유충기간은 9-15일 이며, 번데기 기간은 20-40시간 정도이고, 우화한 성충은 성적으로 성숙해지고 수 시간 내에 교미하며, 성충의 수명은 보통 2주이다.
7. 성충은 비행력이 약하고, 휴식하는 벽면에 기어가는 듯이 보이기도 하며, 비상할 때는 짧은 거리를 날고 높이 날지 못한다.
8. 휴식은 배관시설물이나 벽면의 그늘진 곳에서 휴식하며, 야간활동성이다.

- 관리 -

1. 서식처(발생원)를 파악하는 것이 매우 중요
2. 욕실바닥의 잦은 청소 및 물이 고이지 않도록 관리

3. 반 밀폐된 발생원 주변에 공간살포: 정화조 내 물이 차 있지 않은 벽면에 휴식하는 나방파리도 방제할 수 있도록 조치해야함
4. 발생원에 고농도의 IGR(성장억제제) 처리: 물 사용을 자제해야 함
5. 욕조 하부의 빈 공간에 물이 고이면 발생원이 되므로 공간 내 에어로솔 살포
6. 제한된 공간 내에는 전기살충기, 유인등을 이용한 끈끈이 활용
7. 성충과 유충을 동시에 방제할 수 있는 시스템 운영

포스터 발표

P001

Insect Diversity of Cambodia II: Coleoptera

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Cambodia covers an area of 181,035 sq km among them, forests cover 53 percent. As a tropical monsoon climate, average annual rainfall is about 1,400 mm(about 55 in) on the central plain and increases to as much as 3,800 mm (150 in) in the mountains and along the coast. The average annual temperature is about 27°C (about 80°F). There are many wildlife diversity in Cambodia, but regulated or unregulated logging and mining have diminished the country's wildlife rapidly. This expedition was conducted three times in 2009 (7.2-7.11, 10.16-22, 12.25-12.30). Central Cadamon Protected Forest (N 11° 41' 13" E 103° 26' 31.3") and Seima Biodiversity Conservation Area (N 12° 08' 20.8", E 106° 55' 2.7") were main area surveyed by pitfall trap, light trap and sweeping etc. As the result, totally 611 individuals of 11 families in Coleoptera was collected, among them *Gonocephalum*species of Tenebrionidae was highest number and species in Melonthidae, Chrysomelidae and Dynastidae etc., were collected, specially kind of Hydrophilidae species from wetland was surved in the expedition.

Key words: Insect diversity, Coleoptera, Seima, Cadamom, Cambodia

P002

월출산국립공원에서 확인된 미기록 맵시벌 3종에 대한 연구

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2009년 2월부터 10월까지 실시된 월출산국립공원 자연자원조사 결과 미기록 맵시벌 3종이 발견되었다. 본 조사지점은 다양한 곤충상을 확인할 수 있을 것으로 판단되는 큰골, 도갑사, 천황사, 무위사, 성전저수지 계곡을 선정하여 조사를 실시하였으며 비행성 곤충의 조사를 위해 쓸어잡기(Sweeping)와 말레이즈트랩(Malaise trap)을 이용하였다. 조사지점 중 무위사, 천황사, 성전저수지 계곡에서 각각 *Brussinocryptus orientalis rufomaculatus* (Uchida) 누런다리동양뾰족맵시벌(가칭), *Eurycryptus sakaguchii* (Uchida) 검정무늬단색뾰족맵시벌(가칭), *Colpotrochia pilosa sinensis* (Uchida) 어리누런방패뭉툭맵시벌(가칭)이 처음으로 발견되었다. 본 연구에서는 미기록 맵시벌 3종의 기재문과 외부 형태학적 특징을 나타내는 사진을 제공하고자 한다.

검색어: 검정무늬단색뾰족맵시벌, 누런다리동양뾰족맵시벌, 어리누런방패뭉툭맵시벌, 월출산국립공원

P003

극동아시아산 오색나비(*Apatura ilia*)와 황오색나비(*Apatura metis*)의 DNA barcoding을 통한 분류학적 재평가

박해철[1], 강태화[1], 한태만[1], 정종철[2], 김성수[3], 이영보[1]

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오색나비(*Apatura ilia*)와 황오색나비(*Apatura metis*)는 과거로부터 동일종, 또는 동일종의 아종관계, 별종 등으로 분류학적 위치에 대한 논란이 있어왔다. 이 두 종은 주로 날개 무늬로 구분되는데, 오색나비와 황오색나비의 중간적 양상을 나타내는 경우가 빈번하여 생물학적 종을 식별하는데 혼란이 있어왔다. 이에 따라서 일부 전문가는 두 종의 공유 분포 지역에서는 잡종이 형성될 수 있다는 주장을 제시하였다. 또한 최근 아마추어 나비전문가에 의하여 사육된 황오색나비는 2세대에서 2가지 형이 모두 나타났다는 보고도 있었다. 따라서 형태형질을 바탕으로 동정된 표본을 근거로 DNA barcoding을 이용하여 오색나비와 황오색나비의 생물학적 실체를 검증해 보고자 하였다. 오색나비류의 전세계 분포지 중, 우선 중국, 극동러시아, 한국, 일본에서 확보된 극동아시아산 오색나비류 총 60 개체들을 대상으로 시도하였다. 그 결과, 오색나비 집단과 황오색나비 집단의 유전적 차이는 개체에 따라 0.0%에서 1.0%까지 밖에는 차이가 나지 않는 것으로 확인되었으며, NJ tree에서도 두 집단이 각각 별도의 묶음으로 구분되지 않았다. 특히, 형태적으로 오색나비로 동정된 북방계 개체들의 일부가 단계통 묶음을 형성하는 듯한 양상을 보이나, 그의 나머지 개체들과 남부집단 그리고 황오색나비의 전 개체들은 모두 하나의 섞긴 묶음을 형성하였다. 또한 두 묶음과는 0.5% 정도의 극히 미미한 서열 차이만 보였고, 특정 지역 집단으로 구성된 무리도 존재하지 않았다. 따라서 기존의 오색나비와 황오색나비의 극동아시아산 개체들은 오색나비 한 종이며, 황오색나비로 알려진 개체들은 오색나비의 변이체로 진단하는 것이 분류학적 당위성을 가질 것으로 판단되었다.

검색어: 오색나비, 황오색나비, 네발나비과, DNA barcoding, 분자분류

P004

DNA barcoding을 이용한 은밀종 *Asiopodabrus* sp. nov. (딱정벌레목: 병대벌레과)의 생물학적 종진단

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지난 10여 년간의 한국산 병대벌레과에 대한 분류학적 연구를 통하여 연노랑목가는병대벌레(*Asiopodabrus fragiliformis*)는 체색이나 앞가슴등판의 형태에 의해 2개의 무리로 뚜렷하게 구분되었지만, 수컷 개체의 부족으로 생식기에서는 명확한 차이를 충분히 확인할 수 없어서 형태 변이폭이 큰 종으로만 인식해 왔다. 최근 한국산 병대벌레과의 전종에 대한 DNA barcoding 분석에서 9개체의 연노랑목가는병대벌레가 각각 5개체와 4개체로 나누어져 2개의 단일 집단으로 구분되어 새로운 은밀종이 있을 가능성이 제시되었다. 특히, 두 집단 사이에서는 3.9-5.2%의 큰 서열 차이를 보였고, 이들 각각의 집단 내 서열 차이를 보면 기존 연노랑목가는병대벌레집단은 0.0-2.0%, 신종 추정집단은 0.3-2.0%으로 차이를 나타내었다. 따라서 두 집단 모두 2.0%의 divergence threshold를 보여주면서 뚜렷한 barcoding gap이 형성됨을 확인하였다. 이를 근거로 각 집단의 형태 형질을 재검토하였으며, 그 결과로 신종 추정집단에서는 수컷 생식기에서 화살모양의 ventral process가 개체마다 동일하게 나타남을 확인하였다. 반면에 기존 연노랑목가는병대벌레집단에서는 기부에서 두껍다가 점점 가늘어지는 형태의 ventral process를 가짐을 볼 수 있었다. 결과적으로 과거 형태적 분류로서 연노랑목가는병대벌레의 개체변이는 체색과 앞가슴등판의 형태적 차이를 가진 2종으로 구분될 수 있었다. 따라서 신종추정집단을 기존 연노랑목가는병대벌레에서 독립된 *Asiopodabrus* sp. nov.로 명명하여 신종으로 보고하고자 한다.

검색어: *Asiopodabrus* n. sp., 병대벌레과, DNA barcoding, 은밀종, 분자분류

P005

Taxonomy of the subfamily Acaenitinae (Ichneumonidae: Hymenoptera) from Korea

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The subfamily Acaenitinae Föster, 1869 is a small-sized subfamily belonging to the family Ichneumonidae. Members of Acaenitinae distributes in Ethiopian, Oriental, and Palearctic Regions. Twenty six genera have been recorded in the World, and six genera are known from Korea.

The biology of the Acaenitinae is not well known, however, some hosts are recorded from Cerambycidae in Coleoptera (Gardiner, 1960), Sesiidae and Tortricidae in Lepidoptera (Ulbricht, 1909; Starke, 1956).

Generally female is easily distinguished from that of other subfamily of Ichneumonidae. They can be recognized by their very elongate subgenital plate, and by the auxiliary tooth on the tarsal claws. Male can be also easily recognized by the form of the claws and the facial shape.

In this study, we found a newly recorded genus *Yezoceryx*, belonging to the Tribe Acaenitini, with two species in Korean fauna. Illustrated key of species and genera, diagnosis and photographs of each species are provieded.

Key words: *Yezoceryx*, Acaenitinae, Ichneumonidae, Hymenoptera

P006

Is a Natural Monument, *Chrysochroa fugidissima* (Coleoptera; Buprestridae) a Novel or Not?

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Chrysochroa fulgidissima is the most beautiful Korean beetle and valuable insect in traditional culture because of ancient *fulgidissima*'s adornments in Korea and Japan. The species is also recognized as very rare in the Korean fauna. However, we recently realized that the Korean population has been applied to *Ch. fulgidissima* without detailed taxonomic approaches since Japanese colonial rule of Korea. Therefore, we investigated 76 dried specimens belonging to seven populations collected from N. Vietnam, E. China, Taiwan, Japan, and Korea through morphological and molecular taxonomy using DNA barcoding of COI and 16S rRNA. As the result, the Korean population is strongly formed a monophyletic branch divided from other populations by genetic divergence of each 10.2%~11.7% in DNA barcoding and 6.4%~7.9% in 16S rRNA, and as well as fine structure in the male genitalia. It is allowed to us that the Korean population, which has been underestimated at species discrimination in morphology, may be considered as a novel species.

Key words: *Chrysochroa fulgidissima*, *Chrysochroa* n. sp., Buprestidae, DNA barcoding, 16S rRNA, molecular taxonomy, Korea.

P007

한국산 하늘소과(딱정벌레목) 연구현황

김경미[1], 변봉규[1], 이봉우[1], 안승락[2], 임종옥[3], 한영은[3],
박신영[1], 임종수[1], 박종균[4], 이승환[3], 류동표[5], 김철학[6], 조동광[1]

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하늘소과(Cerambycidae)는 산림내 대표적인 천공성 해충인 동시에 천연기념물인 장수하늘소가 포함되어 있는 중요한 산림곤충류 중 하나로 전세계적으로 약 25,000여종이, 국내에는 306종이 보고되어 있다.

본 연구는 중요 산림곤충 중 하나인 하늘소과(Cerambycidae)의 분류학적 체계를 수립하여 관련 응용 및 활용분야에 제공할 기초자료를 확보키 위한 국립수목원의 연구과제의 일환으로 수행되었다. 금번연구에서는 향후 하늘소과의 분류연구과제를 체계적으로 수행키 위해 우리나라에서의 현재까지 연구현황을 중심으로 조사하여 분석하였다. 이를 위해 그동안의 연구자료를 확보하여 분석함과 동시에 산림청의 국가생물종정보시스템의 DB정보도 함께 활용하여 종합적인 하늘소류의 연구현황을 파악하도록 노력하였다.

우리나라 하늘소과(Cerambycidae)에 대한 연구는 Kolbe(1886)이 16종을 보고한 것이 최초이며 이후 다양한 종들이 보고되었고, Cho(1962)가 한국산 241종의 목록을 제시한 것이 최초의 종합기록이라 할 수 있다. 1960년대 이후에는 Cho를 비롯하여 Lee, An 등의 여러 학자들의 연구를 통하여 정리된 하늘소류는 296종에 이른다 (한국곤충명집, 1994). 금번조사를 통해 Lee(1982)의 1종 등 총 3종이 한국곤충명집(1994)에 누락되었음이 확인되었고, 1994년도 이후에는 Danilevsky(1996)에 의해 3신종을 비롯한 총 10종이 추가된 것으로 파악되었다. 그러나 이와같은 수치는 향후, 보다 집중적인 문헌 및 표본조사를 통해 늘어날 것으로 전망된다.

최근에는 동호인들을 중심으로 많은 관심과 활발한 연구활동이 이루어지고 있는 실정이다. 반면에 국가적인 차원의 종합적인 분류연구나 표본의 수집·보존 등은 앞으로의 시급한 과제로 판단되었다.

검색어: 하늘소과, 연구사, 표본

P008

백석봉의 나비목 곤충상

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국립수목원 산림생물조사과

본 연구는 국립수목원에서 수행 중인 우리나라 자생 산림생물에 대한 분포조사를 통해 특정종별 보전 및 자원화를 위한 기초 자료 확보를 목적으로 조사되었다. 백석봉은 해발 1,170m로 강원도 정선군 북평면에 가리왕산의 동쪽에 위치하며 동강으로 흘러가는 오대천이 있다. 현재까지 인근 가리왕산 등 주요 산림지역은 생물상 조사가 이루어져 있으나 백석봉의 경우 정확한 곤충분포상 등 기초조사가 이루어지지 않은 지역 중 하나이다. 이 지역의 식생으로는 대부분이 신갈나무림으로 구성되어 있으며, 능선부에는 소나무림이, 서남향 사면부에는 신갈나무-소나무 혼효림이 분포하고 있으며, 등산로 외에는 접근할 수가 없을 만큼 지형이 매우 험준하다. 해발 600m 이하에 소규모 조림지와 경작지가 분포하고 있다.

금번조사는 2009년 4월부터 7월까지 4회에 걸쳐 주간채집 및 야간조사를 병행하여 실시하였으며, 산림지역에 우점분류군 중 하나인 나비목 곤충을 중점적으로 조사하였다. 본 조사에서 확인된 나비목 곤충은 30과 267종 1,066개체로 나타났다. 계절별로는 5월에 122종 496개체가 6월에 157종 468개체 등으로 조사되어 다른 시기에 비해 높은 종다양성을 보였다. 분류군별로는 자나방상과(Geometroidea)가 2과 95종으로 가장 많은 종들이 확인되었으며 그 다음으로 밤나방상과(Noctuoidea)가 3과 91종으로 나타나 종다양성이 높은 분류군으로 확인되었다. 이와같이 조사된 분포상 정보는 산림생물종의 보존 및 자원화를 위한 기초자료와 향후 기후변화 등에 의한 밀도변동 추이의 경향 파악 등에 활용될 것으로 기대된다.

검색어: 생물상, 곤충상, 백석봉, 강원도, 국립수목원

P009

A First Report of *Artona martini* Efetov (Lepidoptera, Zygaenidae) from Korea

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In this study, a zygaenid speies, *Artona martini* Efetov, was reported for the first time from Korea. Recently we collected numerous larvae of the species, feeding on bamboo, *Pseudosasa japonica* (Siebold & Zucc. ex Steud.) Makino, in Hongneung arboretum of Korea Forest Research Institute, Seoul.

This species is very similar to *Artona* (*Balataea*) *funeralis* (Butler) in appearance, which was recorded first from Korea by Witt (1985). Because the two species is very similar to each other in appearance and host plants, it will be need to examine and compare the Korean materials of the two species. But there is no available specimen of *Artona* (*Balataea*) *funeralis* (Butler), which was reported by Witt (1985) for the time being.

They have two generations per year in Korea: The moths of first generation fly during the middle of May to middle of June and the second generation during the late of July to the early of August respectively. Also *Sasa borealis* (Hack.) Makino was recorded as host plants of the species from Japan (Yamaguchi & Arita, 1960).

The external morphology was examined and illustrated. Materials examined herein are now preserved in the Korea National Arboretum.

Key words: *Artona martini* Efetov, Zygaenidae, Lepidoptera, new record, Korea

P010

Epermeniidae (Lepidoptera) of Korea, with two unknown species

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The family Epermeniidae (Lepidoptera) is a small family with more than 100 described species in the world (Gaedike, 1996). It is divided into two subfamilies, Epermeniinae and Ochromolopinae (Dugdale *et al*., 1999). Although this family comprises species with variously shaped wings from broad to narrow lanceolate, it is characterized by stiff bristles on the whole surface of the hind tibia. Another character, one or more scale teeth on the dorsum of the forewing seems to be another apomorphy for the family. However, some species lack these teeth by secondary loss (Kuroko, 2006).

The family has been poorly known from Korea to date. The first record of Epermeniidae in Korea was *Epemenia strictella* (Wocke), by Park (1983), on the basis of specimen collected in the Suwon, Province Gyeonggi. Since this report, no research has been conducted on this family in Korea. This study is based on the recent survey on the Microlepidoptera by Korea National Arboretum(KNA) to clarify the fauna of microlepidoptera of Korea.

In this study, we report two species of the family Epermeniidae, *Phaulernis chasanica* and *Ochromolopis* sp., for the first time from Korea along with illustraton of adults.

Key words: *Phaulernis chasanica*, *Ochromolopis* sp., Epermeniidae, Korea

P011

A Taxonomic Revision of the Genus *Linnaemya* Robineau-Desvoidy (Diptera, Tachinidae) in Korea

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Linnaemya Robineau-Desvoidy (Diptera, Tachinidae) is one of the largest genera of the subfamily Tachininae with more than 149 described species in the world. In Korea, only three species have been known to date. In this study, the genus *Linnaemya* in Korea was reviewed. All available material was examined to identify the species of the genus. Based on the present study, we described a new species. Also ten species are reported for the first time from Korea: *L. comta*, *takanoi*, *tessellans*, *ambigua*, *kanoi*, *zachvatkini*, *picta*, *pallidohirta*, *scutellaris*, and *lateralis*. We provide a generic key, illustrations, and photos of the species of the genus. A phylogenetic analysis was also conducted to infer interspecific relationships among Korean *Linnaemya* species using a software, PAUP, with an outgroup *Lypha dubia*.

Key words: Diptera, Tachinidae, *Linnaemya*, phylogenetic analysis, Korea

P012

New Records of Phyline Plant Bugs from Korea (Heteroptera: Miridae: Phylinae)

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In phyline plant bugs, four genus each with one species are recognized new to Korea: *Atractotomoidea castanea* Yasunaga, 1999; *Moissonia befui* Yasunaga, 1999; *Monosynamma* bohemanni (Fallen, 1829) and *Pseudophylus stundjuki* (Kulik, 1973). Diagnosis and keys to species are provided with the clear dorsal images and the illustrations of male genitalia. Also the brief biology is discussed.

Key words: Heteroptera, Miridae, Phylinae, new records, Korea.

P013

Systematic study of the genus *Athetis* (Lepidoptera: Noctuidae: Xyleninae) from the Korea

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The genus *Athetis* is a cosmopolitan genus of the subtribe Athetina (Noctuidae: Xyleninae (Fibiger & Lafontaine 2005; Lafontaine & Fibiger 2006). It comprises about 211 described species from the world to date, with about 150 species known from South Palaearctic and Oriental Regions (Kononenko 2005). In the Korean peninsula, 12 species was reviewed by Kononenko & Han (2007).

In this study, key to the Korean *Athetis* species is provided with the photos of adults and genitalia for each species.

Key words: Lepidoptera, Noctuidae, Xyleninae, *Athetis*, Korea.

P014

Six New Species of the Genus *Promalactis* Meyrick (Lepidoptera, Oecophoridae) from Vietnam

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The genus *Promalctis* Meyrick, 1908 is the largest genus of the family Oecophoridae, with more than 150 described species in the world (Wang *et al*., 2009; Du *et al*., 2009). The genus is mainly distributed in the Palaearctic and Oriental regions, probably with the highest diversity in the South and East Asia. However it has been very poorly studied to date, with only with only 4 publications which were based on very limited collecting. In total, 76 were reported from China, which is more than half of the known species in the Palaearctic region(Wang, 2006; Du *et al*., 2009), 14 species known from Korea (Park & Park, 1998), 12 species from Japan (Fujusawa, 2002), 8 species from Russian Far East (Lvovsky, 1976, 1985, 1986), and 3 species from Nepal (Lvovsky, 2000a). In the Oriental region, since Meyrick (1908a, 1908b) described 14 species from India and Myanmar, Lvovsky (2000a, 2000b) described 25 additional species from the southern Asia, including the southern part of China, Malaysia, Indonesia, and the Philippines. In Vietnam, only 4 species, *Promalactis albiapicalis* Lvovsky 1997, *P. buonluoi* Lvovsky 1997, *P. fansipanella* Lvovsky 2007, and *P. suzukiella* (Matsumura 1931), have been described to date(Lvovsky, 1997, 2007a).

The aim of this study is to describe six new species of *Promalactis* based on material mainly collected in the northern part of Vietnam. Adults, head parts, wing venations, and the male or female genitalia of the new species are illustrated.

Key words: Taxonomy, Lepidoptera, Oecophoridae, new species, *Promalactis,* Vietnam

P015

Taxonomic Review of the Genus *Periphyllus* (Hemiptera: Aphididae) in the Korean peninsula

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The genus *Periphyllus* is tree-dwelling group, mostly on maple tree (*Acer* spp.). In this study, we discovered one species new to Korea, *P. loricatus* (Pashtchenko 1987) on *A. ginalla*. In prior to Pashtchenko(1987), *Periphyllus ginallae* Paik in Szelegiewicz (1974) seems the same species, nevertheless, treated as 'nomen nudum' without any description. As a result of our revision, totally seven species belong to this genus in the Korean peninsula.

Key words: Aphididae, *Periphyllus loricatus*, *Acer ginallae*, Korea

P016

New Records of bark beetles (Coleoptera: Scolytidae) from Korea

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Up to days, 31 species of 7 genera of the tribe Xyleborini have been recorded from Korean peninsula. We have collected the bark beetles with Malaise traps from 2007 to 2009 in the central part of the Korean peninsula.

As a result of this study, we report 2 species, *Xyleborus japonicus* Nobuchi, 1981 and *X. pelliculosus* Eichhoff, 1878, for the first time from Korea with brief descriptions and illustrations of diagnostic characters.

Key words: Scolytidae, Xyleborini, *Xyleborus japonicus*, *Xyleborus pelliculosus*, Korea.

P017

Three new records of the subfamily Epyrinae (Hymenoptera: Bethylidae) from Korea

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Three species, *Allobethylus tomoae* Terayama, *Cephalonomia tarsalis* (Ashmead), and *Laelius yamatonis* Terayama of the subfamily Epyrinae are recorded for the first time in Korea. Both sexes of *A. tomoae* Terayama, *C. tarsalis* (Ashmead) and female of *L. yamatonis* Terayama are briefly described with diagnostic morphological illustrations for each species based on the Korean specimens. Male of the genus *Allobethylus* is discovered for the first time from the word.

Key words: *Allobethylus tomoae* Terayama, *Cephalonomia tarsalis* (Ashmead), *Laelius yamatonis* Terayama, Epyrinae, Korea

P018

Taxonomy review of the subgenus *Uromelan* Mordvilko with one new record (Hemiptera: Aphididae) from Korea

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A total of six species in the subgenus *Uroleucon* (*Uromelan*) is revised from the Korean Peninsula. *Uroleucon adenophora* (Matsumura, 1918) is recognized for the first time in Korea, collected on the young upper stem of *Adenophora* sp. (Campanulaceae). It is described, illustrated, and measured for apterous viviparous females.

Key words: *Uroleucon*, Aphididae, Korea.

P019

A new species of the genus *Clytus* Laicharting (Coleoptera: Cerambycidae) from Korea

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Up to days, 5 species belonging to the genus *Clytus,* one of the large genera among the tribe Clytini have been recorded from Korean peninsula.

The genus *Clytus* can be distinguished from the other genera by combination of following characteristics: width of head between each antennal socket longer than length of scape; carinae on frons absent; 1st segment of hind-tarsus 2 times shorter than combined length of 2nd+3rd segments; hind-femora weekly swelled in middle part; posterior part of metasternum without process in ventral view.

Clytus sp. nov. is most similar to *C. clavicornis* Reiche, an endemic species to Sicily island in Southern Italy, having thickened 5th or 6th to apical antennal segment. However, this species can be distinguished from the latter species by specific morphological characteristics.

As a result of this study, we report *Clytus* sp. nov. as new to science with brief description and illustrations diagnostic characteristics with key to the Korean *Clytus* species.

Key words: Cerambycidae, Cerambycinae, Clytini, *Clytus*, Korea.

P020

A newly recorded species *Gonatopus dromedarius* (A. costa) (Gonatopodinae: Dryinidae: Hymenoptera) from Korea.

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The Gonatopodinae is the most diverse subfamily among the Dryinids subfamilies. It is recognized about 381 described species in the world. A total three genera and seven species have been reported from Korea (He, J. and Xu, Z., 2002).

Generally *Gonatopus* is easily distinguished from other Gonatopodinae genera by the combination of the following characters: Palpal fomula 6/3, or 5/3 or, or 5/2 , or 4/3, or 4/2, or 3/2; enlarged claw with a subapical tooth, or with a small subapical tooth; Tibial spurs 1, 0, 1.

Also, Genus *Gonatopus* Ljungh, 1810 ranks as the most commonly distributed genus in the world and parasitoids of leaf hopper, Cicadellidae (except for Typhlocybinae, Idiocerinae, Macropsinae) (Olmi, 1984).

In this study, we found one newly recorded species, *Gonatopus dromedarius* (A.costa) and provide a key to the species of genus *Gonatopus* from Korea.

Key words: *Gonatopus*, *Gonatopus dromedarius*, Gonatopodinae, Dryinidae, newly recorded species, parasitoids

P021

Taxonomic Study of the Genus *Eriborus* Föster (Hymenoptera: Ichneumonidae: Campopleginae) from Korea

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The genus *Eriborus* which is a small-sized campoplegine genus was firstly described by Föster in 1869 based on *Campoplex perfidus*. Members of this genus included 52 species in the world. Among them, 11 species are distributed in Eastern Palaearctic region, and only two species, *E. molestae* (Uchida, 1933) and *E. terebrans* (Gravenhorst, 1829) have been recorded in Korea(Yu *et al*., 2005). Most species of this genus are specialized parasitoids of 17 lepidopteran families, Cerambycidae(Coleoptera) and Tenthredinidae(Hymenoptera), and more particularly attack most of Noctuidae and Pyralidae(Lepidoptera) larvae as koinobiont endoparasitoids. This genus is easily distinguished from other campoplegine genera by the combination of the following characters: Carinae of propodeum usually strong, areola longer than wide; propodeal spiracles circular or short elliptic; fore wings without areolet; thyridium subcircular or longitudinally elliptic. In this study, we found two newly recorded species, *Eriborus vulgaris* (Morley, 1913) and *Eriborus sinicus* (Holmgren, 1868) from Korea. A revised key to the species of Korean *Eriborus* Föster, redescriptions and photographs of diagnostic characters are provided.

Key words: Campopleginae, *sinicus, vulgaris,* Ichneumonidae, Korea

P022

First record of the Family Ciidae (Coleoptera: Tenebrionoidea), represented by Genus *Octotemnus* Mellié, in Korea with new host fungi

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The beetle family Ciidae, represented by *Octotemnus laminifrons* Motschulsky, 1860 and *Octotemnus japonicus* Miyatake, 1954 is presented for the first time in Korea.

The beetle family Ciidae Leach is a relatively moderate family, which comprises about 640 described species in 42 genera worldwide. This family is distributed throughout the world.

Ciids are minute fungus-feeding beetles, which are associated with the mycelia and fruiting bodies of wood-rotting fungi. These beetles are considered mycetobiont because they depend upon the basidiocarps for food and breeding throughout their life span. And also ciids are important components of the saproxylic fauna of many forests ecosystems and a number of species are considered rare or threatened and are associated with old growth forests or undisturbed forest conditions.

A habitus photographs of adults, description, illustrations of diagnostic characters, and host fungi are provided.

Key words: *Octotemnus laminifrons* Motschulsky, *Octotemnus japonicus* Miyatake, Ciidae, Coleoptera, taxonomy, host fungi, new record, Korea.

P023

Faunal overview of Mongolia (I): Lepidoptera (Insecta)

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Mongolia is a land-locked country which covers an area of 1,564,116 km^2 in North East Asia. It is one of the largest land-locked countries and the world's seventh largest country. The climate of Mongolia is extremely continental with long, cold, and dry winters, and with relatively short, mild and dry summers. The mid-winter, temperatures averages -26℃ with extremes recorded as low as -58℃. Summer temperatures in the Gobi desert may reach ±40℃. Annual precipitation ranges from 600 mm in the Khentii, Altai and Khovsgol mountains to less than 100 mm in the Gobi. On the biodiversity side, more than 3,000 species of vascular plants, 927 lichens, 437 mosses, 875 fungi, and numerous algae have been recorded with many more yet to be classified. The fauna of the country includes 136 species of mammals, 436 species of birds, 8 species of amphibians, 22 species of reptiles, 75 species of fishes and about 13,000 species of insects. The insect fauna is not definitively explored up to date. In the present study, we briefly reviewed for the Lepidoptera diversity of Mongolia. Many entomologists from various contries have been described or recorded more than 900 species of butterflies and moths belonging to 30 families, such as: Tineidae 27 spp. (Zagulyaev, 1979), Aegeriidae 2 spp. (Daniel, 1975), Tortricidae 190 spp. (Razowski, 1972), Cossidae 5 spp. (Yakovlev, 1968), Gelechiidae 50 spp. (Piskunov, 1979), Pterophoridae 19 spp. (Zagulyaev, 1968), Ethimdae 11 spp. (Zagulyaev, 1968), Athihiidae 2spp.(Kuznetsov, 1980), Morphidae 1sp. (Reidl, 1960), Pyralidae 27 spp. (Whalley, 1979), Hesperiidae 19 spp. (Korshunow, 1977), Papilionidae 10 spp. (Yakovlev, 1923), Pieridae 20 spp. (Korshunov, 1972), Lycaenidae 56 spp. (Bailint, 1989), Satyridae 57 spp. (Goltz, 1939), Nymphalidae 60 spp. (Fruhstofer, 1908 Korshunov, 1976; Korshunov & Soljanikov, 1977 Bayartogtokh & Enkhbayar, 2009), Lasiocampidae 11 spp. (Dubatolov & Zolotuhin, 1992); Sphingidae 12 spp. (Daniel, 1971); Geometridae 196 spp. (Wehrli, 1922); Noctuidae 130 spp. (Sukharev, 1982).

Key words: Diversity, Insecta, Lepidoptera, Mongolia, species.

P024

Taxonomic Notes of Subfamily Olethreutinae (Lepidoptera: Tortricidae) in the North Vietnam

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Leaf roller moths Olethreutinae is the second largest subfamily in Tortricidae, comprising worldwide more than 4,300 species (Horak, 2006). Of which, 465 species of 88 genera in South Asia (Diaknoff, 1973). In Vietnam, when studying on fauna of the agricultural pests, National Institute of Plant Protection (NIPP) recorded only 4 Tortricidae species (1977-1978), and 3 Tortricidae species (1997-1998). From 1996 to 2001. Kuznetzov reported two new genera *Fibuloides* gen. nov., *Pammenpsis* gen. nov., and 19 species of Olethreutinae. He also has created a list of 208 Tortricidae species in the North Vietnam. Recently, Razowski recorded 33 species, 11 genera (2008), he (2009) also reported 107 species, 61 genera, of which 61 species of 41 genera belong to Olethreutinae in the North Vietnam. Of which, 25 species are described as new to science, 13 species are new to Vietnam.

In the present study, we are briefly reviewed of subfamily Olethreutinae in North Vietnam. We recognized 105 species of 51 genera. Of them, 50 species are reported for the first time from North Vietnam such as: *Andrioplecta pulverula* Meyrick, 1912; *Cryptophlebia repletana* Walker, 1863; *Dactylioglypha tonica* (Meyrick, 1909); *Lobesia aelopa* Meyrick, 1997; *Lobesia ambigua* Diaknoff, 1954, etc. The materials identification base on the collection of University of Incheon, which has collected in North Vietnam from 2004-2009.

Key words: Lepidoptera, Olethreutinae, Taxonomy, Fauna, North Vietnam.

P025

A new record of *Dichrorampha gueneeana* Obraztsov (Lepidoptera, Tortricidae, Olethreutinae) from Korea

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The genus *Dichrorampha* Guenée, 1845 belong to subfamily Olethreutinae, family Tortricidae described about 110 species in the Holarctic region (Brown, 2005). In Palaearctic region, there are about 90 species and about 20 species found in Nearctic region; 54 species are recorded from Europe (Razowski, 2003).

Danilevesky and Kuznetsov (1968) established the subtribe Dichroramphae by the genus *Dichrorampha* Guenée. Razowski (1989), proposed the usage of Lipoptychina instead of Dichroramphae since the former name is older. Komai (1999) referred to the group as the *Dichrorampha* genus-group and added *Pammenemima* Diakonoff (= *Titanotoca* Diakonoff) to the group (Horak, 2006).

Since Park (1983) reported two species of the genus for the first time from Korea, they are mainly studied by Park and Ahn (1986), Byun, Bae and Park (1998), Oh, Bae and Park (2001). Four species have been reported to present from the Korean peninsula.

In this study, *Dichrorampha gueneeana* Obraztsov, 1953 is report for the first time from Korea. *D. gueneeana* Obraztsov, 1953 resembles with *D. latiflavana* Caradja, 1916 superficially, but the former is easily distinguished from the latter by following characters: dorsal patch of forewing color pale yellowish, and smaller than *D. latiflavana* Caradja, 1916; sclerite of colliculum slender; bent proximally and ductus bursae broader than *D. latiflavana* Caradja, 1916. Morphological characters of this species are redescribed with illustrations of wing venation and genitalia.

Key words: *Dichrorampha*, *gueneeana*, Olethreutinae, Tortricidae, Lepidoptera, genitalia, new record, Korea

P026

Microsatellite DNA as Potential Markers for Strain Identification of the Silkworm (*Bombyx mori*)

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The silkworm (*Bombyx mori*), as an industrial insect, possesses a high economic value. Casual discrimination and accumulated genetic information of silkworm varieties are essential ground for the practical utilization and long-term conservation. In this study, nine available microsatellite loci were successfully genotyped from ~50 silkworm strains preserved in Korea. According to genotyping analysis, we obtained 3 ~ 16 alleles per locus, with an average of 7.4, the observed heterozygosity ranging from 0.04 to 0.98, and the polymorphic information content (PIC) ranging from 0.06 to 0.88, revealing that some loci are highly variable. Among 54 strains 13 strains were casually identified by the presence of 17 strain-specific apomorphic alleles. Furthermore, 30 among remaining strains contained strain-specific allele combinations that are also apomorphic to each strain, allowing us to discriminate each of these from other strains by genotyping of multiple loci. These results collectively suggest that the silkworm microsatellite DNA is actually and potentially important molecular marker for the discrimination of the silkworm strains that are preserved as hundreds in Korea, as more loci are genotyped.

P027

Phylogenetic Relationships of True Butterflies (Lepidoptera: Papilionoidea) Inferred from COI, 16S rRNA and EF-1α Sequences

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The phylogenetic relationships among true butterfly families (superfamily Papilionoidea) have been a matter of substantial controversy, and that debate has led to several competing hypotheses. Two of the most compelling of those hypotheses involve the relationships of (Nymphalidae + Lycaenidae) + (Pieridae + Papilionidae) and (((Nymphalidae + Lycaenidae) + Pieridae) + Papilionidae). In this study, approximately 3,500 nucleotide sequences from cytochrome oxidase subunit I (COI), 16S ribosomal RNA (16S rRNA), and elongation factor-1 alpha (EF-1α) were sequenced from 83 species belonging to four true butterfly families, along with those of eight outgroup species belonging to the skipper family (superfamily Hesperioidea). These sequences were subjected to phylogenetic reconstruction via Bayesian Inference (BI), Maximum Likelihood (ML), and Maximum Parsimony (MP) algorithms. All phylogenetic analyses among the four true butterfly families strongly indicated a sister relationship between the Nymphalidae and Lycaenidae on one hand, and relatively strongly indicated a sister relationship between the Pieridae and Papilionidae on another hand, thus supporting the hypothesis: (Nymphalidae + Lycaenidae) + (Pieridae + Papilionidae).

P028

A Taxonomic Study of the Genus *Micromus* (Neuroptera: Hemerobiidae: Microminae) from Korea

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The genus *Micromus* is a large group, belongs to the family Hemerobiidae with a worldwide distribution. This genus was named by Rambur, 1842 based on the type species *Hemerobius variegates* Fabricius, 1793. Eighty five species have been described from the world. Among them only one species, *M. numerosus* (Navás), has been recorded from Korea. Morphologically, *Micromus* is easily distinguished from other hemerobiid genera by the combination of the following characteristics: maxillary palpus 5 segments, labial palpus 3segments; forewing with costal area quite narrow at base and one prestigmal Sc-R crossvein, without recurrent humeral vein and crossvein 2M-Cu. Members of the genus *Micromus* are generally considered to be beneficial as predators of various aphids, particularly on sugar cane and corn plants. This genus occurs in a variety of habitats including both trees and grasses. It is often found in alfalfa fields where both larvae and adults feed on aphids. Adults are also highly attracted to lights at night. In this reviewing study about the Korean *Micromus*, we study two species. *M. angulatus* (Stephens) and *M. numerosus* (Navás). Among them *M. angulatus* is newly included in Korean fauna. We also provide a key to the Korean species of *Micromus*, description, illustrations of diagnostic characters and distributional data.

Key words: Hemerobiidae, Microminae, *Micromus angulatus*, Korea

P029

External Morphology and Distribution of Antennal Sensilla of *Aphidius colemani*

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Several species of the genus *Aphidius* are used in biological control programs against aphid pests throughout the world and their behavior and physiology are well studied. But despite knowing the importance of sensory organs in their behavior, their antennal structure is largely unknown. In this study, the external morphology and distribution of the antennal sensilla on the antennal of both female and male adults of *A. colemani* were described using scanning electron microscopy (SEM). Generally, the filaform antennae of males (1,565.60± 194.64㎛) are longer than females (1,303.83±156.41㎛). Antennae of this species is made up of scape, pedicel and flagellomeres. Male and female antennae differed in the total number of flagellomeres as 15 in males and 13 in females. Female and male antennae of *A. colemani* has samely ten types of sensilla. We classified 3 types of sensilla trichodea as without pores, with a tip pore and with wall pores, 3 types of sensilla coeloconica, 1 sensilla placodea and 1 Bohm bristles. In addition, the possible functions of the above sensilla types are discussed in light of previously published literature; mechanoreception (Bohm bristles and sensilla coeloconica) and olfaction (sensilla trichodea and sensilla placodea). Future studies on the functional morphology of the antennal sensilla of *A. colemani* using transmission electron microscopy (TEM) coupled with electrophysiological recordings will likely confirm the functions of the different sensilla identified in this study.

Key words: *Aphidius colemani*, antennal sensilla, SEM.

P030

New Record of The Leek Moth, *Acrolepiopsis nagaimo* (Lepidoptera:Acrolepiidae) in Korea

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Acrolepiopsis nagaimo (Yasuda, 2000) belonging to the family Acrolepiidae (Lepidoptera) is newly discovered in Korea. The species was first collected wild at Wol-ak-san [Mt.] a few years ago and they were recently found to infest Chinese yam, *Dioscoreabatatas* at a Chinese yam experimental field of the Institute for Bioresources Research located at Andong. Diagnostic characteristics of the adult are described and photographs of adult and male and female genitalia are provided.

P031

Distinguishing *Actias artemis* and *A. gnoma* by morphology and by molecules

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Actias artemis and *A. gnoma* are the two saturniid species of which their gracious morphology often attracts butterfly collectors. The two species, however, have similar wing patterns, even with considerable amount of variations, making difficult to distinguish between the two. We gathered about a hundred specimens of either of the species and tried to distinguish them by their wing morphology as indicated in many books and webpages. This was definitely not easy and we were not even sure if our distinction was right. We changed our plan and we first tried to sequence their COI barcode region and found that the two have more than enough difference and could easily distinguish the two by sequence similarity. Then we compared their outer morphological characters that are often used by people between the two to see if any morphological character can distinguish the two. We concluded that no one characteristic can separate the two although combination of several characteristics may do so. We also made a comparison of their genitalia and they were distinctly different. With the help of genitalic dissection, we found that they can be distinguished without actual dissection by comparing their genital end after just brushing off some scales at the end. For female comparison, a further study with more material is needed as we found the proportion of females among the samples was very low.

Key words: *Actias artemis*, *Actias gnoma*, COI, barcode, morphology, wing pattern.

P032

Undescribed species, *Micromus angulatus* (Neuroptera:Hemerobiidae) new to Korea

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Study of the Korean Hemerobiidae has been so scarce that only three species in two genera were recorded in Korea. Here we report an undescribed species, *Micromus angulatus*, new to Korea. A brief description and images of the wing pattern, and adult and genitalia of both sexes are provided.

Key words: Neuroptera, Hemerobiidae, *Micromus*, *M. angulatus*, fauna

P033

LepTree - A Genomics-Inspired Community Collaboration

Soowon Cho[1], and the Leptree team members[2]

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Lepidoptera includes over 160,000 species of butterflies and moths worldwide. They have enormous ecological and economic impact as pests, pollinators, and food sources for other organisms. We are using Assembling the Tree of Life (AToL) NSF funding to: 1. generate a backbone phylogeny of the entire order, 2. date major subclade divergence by re-evaluating fossils (fossil project), 3. create a rich taxonomic resource (taxon template) and 4. create a glossary of morphological terms and associated images to synergize tree-building using morphological characters - all within a worldwide online venue. Our project goal is to galvanize the broader lepidopterist community towards constructing a comprehensive and fully resolved tree. Here we present the fossil project, taxon template and morphology projects.

Key words: Lepidoptera, phylogenetics, Tree of Life, morphology, molecular systematics

P034

A new species morphologically similar to *Bromius obscurus* (Coleoptera: Chrysomelidae) infesting grape vines

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Western grape rootworm, *Bromius obscurus* is a well-known pest of grape vines in Europe although it was originated from America. Although this species was originally described in America, its distribution became pandemic and are known to occur in Korea (포도꼽추잎벌레) as well. We recently compared their morphologies and COI sequences and found that the Korean species is not *B. obscurus*, but a similar species either within the same genus, or possibly in a different genus of Eumolpinae of Chrysomelidae as their sequence similarity is less than 90%. Preliminary comparison between the two species is given with outer morphology and COI barcode sequences.

Key words: Western grape rootworm, Eumolpinae, COI barcode, fauna

P035

Hyphantria cunea hemocytic STAT is activated in response to microorganism infection

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A new insect member of the STAT family of transcription factors (HcSTAT) has been cloned from the lepidopteran, *Hyphantria cunea*. The domain involved in DNA interaction and the SH2 domain are well conserved. The gene is transcribed at a low level during all stages of development, and transcribed in hemocyte, fat body, midgut, epidermis, and Malpighian tubule. Especially, hemocyte and Malpighian tubule showed transcriptional activation of HcSTAT upon Gram-negative and -positive bacteria challenge. Gram-negative and -positive bacteria challenge specifically results in nuclear translocation of HcSTAT protein and induction of DNA-binding activity that recognizes a STAT target site in *H. cunea* hemocyte. *In vivo* treatment with sodium orthovanadatetranslocates HcSTAT to the nucleus in hemocyte cells.

Key words: *Hyphantria cunea* STAT SH2 domain hemocyte Malpighian tubule Gram-negative and positive

P036

Knockdown of apolipophorin-III is caused disruption of mitochondrial membrane potential in *Hyphantria cunea*

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Apolipophorin-III (apoLp-III) is a hemolymph protein whose function is to facilitate lipid transport in an aqueous medium in insects. Recently, apolipophorin-III in *Galleria mellonella* and *Hyphantria cunea* was shown to play an unexpected role in insect immune activation. We show here a novel possible function/role of the apoLp-III in insects. To investigate the genes which have a relationship with apoLp-III in fall webworm larvae, we reduced endogenous Hc apoLp-III mRNA levels in larvae via RNA interference (RNAi).

The RNAi-mediated Hc apoLp-III reduction resulted in the reduction of antioxidants, like MnSOD, catalase, and glutathione S transferase as well as immune proteins. In particular, expression of MnSOD commonly decreased in fat body, midgut, and hemocytes following the knockdown of Hc apoLp-III, which induced an elevated level of superoxide anion in *Hyphantria cunea* larvae. The observed effect of Hc apoLp-III RNAi suggests that Hc apoLp-III is related to the action/expression of antioxidants, especially MnSOD.

Key Words: *Hyphantria cunea* apolipophorin-III RNAi MnSOD; antioxidant ROS superoxide

P037

Comparative analysis of MnSOD and Cu/ZnSOD genes by various stress from *Hyphantria cunea*

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A MnSOD gene was cloned from the fall webworm, *H. cunea*. The MnSOD cDNAs encode precursor proteins of 215 amino acid residues. The deduced amino acid sequences of the *H. cunea* MnSOD cDNA showed 76% identity to *B. mori* MnSOD and 62-56% to MnSOD sequences from other organisms. MnSOD and Cu/ZnSOD in *H. cunea* is expressed from all tissues. MnSOD expression is changed at a trace level in infected larvae, while Cu/ZnSOD expression is strongly changed against bacteria, and fungi. The expression level of Cu/ZnSOD increased by different artificial photoperiod (24L:0D), UV irradiation (312nm), and starvation condition, while the expression level of MnSOD only increased by starvation condition. Also, expression of MnSOD and Cu/ZnSOD showed no significant change in 0L:24D condition. In addition to expression levels of Cu/ZnSOD in *H. cunea* significantly increased by temperature stress and injection with paraquat, but reduced by injection with 10% H_2O_2. The expression level of MnSOD significantly increased by temperature stress and reduced by injection with 10% H_2O_2 and paraquat.

Key words: Antioxidant enzyme, superoxide dismutase *Hyphantria cunea* reactive oxygen species Cu/ZnSOD; MnSOD; stress.

P038

Development of *Artophaneura alcinous*(Lepidoptera: Papilionidae) reared on different temperature and survivorship after storage at low temperature for diapause termination

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In order to establish an indoor-rearing system for *A. Alcinous,* the effect of temperature and pupal diapause was investigated. Temperature has been suggested as an important factor in determining the developmental rate, Lifespan and mortality in invertebrates. As temperature increase, the developmental period was gradually reduced. The developmental period of *A. alcinous* larvae was 12.9 days and 25.8 days at 30℃ and 20℃, respectively. And we investigated the effect of different chilling days on diapause termination. Under longday condition(LD 16:8h, 20℃) oxygen consumption gradually increase. But oxygen consumption on the first day of pupa was the highest and rapidly fell down the next day and attained lowest point after 7days, with average value of 1.92mol/min/g under shortday condition(LD 8:16h). Diapause pupae were chilled for 60, 75, 90, 105 days at 8℃ and thereafter subjected to LD 16:8h at 25℃. And emergence rate at 60~90days was 57.1~80.7%.

Key words: indoor-rearing system, *Artophaneura alcinous*, diapause, temperature

P039

Characterization of digestive enzymes in *Hermetia illucens* (Diptera: Stratmyidae) larva reveals its biochemical basis as a garbage scavenger

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The black soldier fly (BSF), *Hermetia illucens*, is known as a beneficial insect and feeds on organic materials derived from animals and human, resulting in reduction of food waste and conversion of organic materials. Despite of a lot of study about the BSF, there is a less information about composition of digestive enzyme of the BSF larva. Experimentally, there is no evidence about characterization of digestive enzyme of the BSF. We investigated biochemical property of digestive enzyme released from the salivary and gut of the BSF. Through digestive enzyme assay, we found that the BSF has amylase, lipase and protease activity in gut extracts, resulting in that the BSF belong to polyphagous insect group. In the BSF gut, trypsin-like protease activity showed one peak at various temperature and pH condition. This result means the BSF has probably a similar form of trypsin-like enzymes. On study of comparison of enzyme activity between the BSF and the housefly using the apiZYM kit, the BSF had more strongly digestive enzyme activity than one of the housefly about leucine arylamidase, alpha-galactosidase, beta-galactosidase, alpha-mannosidase and alpha-fucosidase. This finding supports that the BSF can ingest raw waste far more efficiently than any other known species of fly as reported previously.

Key words: Digestive enzyme, *Hermitia illucens*, BSF, protease activity

P040

Wake-up Conditions for Improving Oviposition and Colony Development of the Bumblebees *Bombus terrestris and B. ignitus*

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Bumblebees are widely used to pollinate crops in greenhouses and fields. Here, we investigated whether different wake-up treatments during a short period of 1-3 days just before indoor rearing has any effects on oviposition and colony development of CO_2-treated *Bombus ignitus* queens and artificially hibernated *B. terrestris* queens The wake-up regimes were defined as 16L for 1 day (16L-1), 16L per day for 3 days (16L-3), 24L for 1 day (24L-1), or 24D for 1 day (24D-1). Among these wake-up treatments, the oviposition rate and pre-oviposition period of *B. ignitus* queens reared at 24L-1 were 16.7-25.1% higher and 1.0-3.5 days shorter than other wake-up treatments. *B. terrestris* queens reared at 24L-1 also showed the best results for egg-laying characteristics, which were 8.9-18.8% higher for oviposition and 0.6-3.5 days shorter for preovipostion period than other wake-up treatments. Furthermore, *B. terrestris* queens reared at 24L-1 were 17.5% and 13.8% higher in rate of colony foundation and queen production, respectively, than other wake-up treatments. These results show that the most favorable wake-up treatment just before rearing for egg-laying and colony developmental characteristics of *B. ignitus* and *B. terrestris* queens was 24L-1. Overall, our findings indicate that a wake-up treatment just before rearing was effective for colony initiation and colony development of bumblebee queens.

Key words: Bumblebee, *Bombus ignitus*, *B. terrestris*, Wake-up, Photoperiod, Oviposition, Colony development

P041

Neural Endocrine Interaction in a Peripheral Olfactory System in the American Cockroach Associated with Circadian Olfactory Modulation

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An olfactory system is one of the complicatedly-equipped sensory facilities in the insect sensory systems, which is most essential for insect olfactory-driven behaviors relevant to survival such as finding hosts, mates, oviposition sites, and food resources. These behaviors are mostly controlled by circadian rhythm. The american cockroach, *Periplaneta americana*, has been an ideal model to extensively study olfactory system associated with complex behavioral repertoires and circadian controls of certain behaviors, respectively. Even though it is known that olfactory-related physiology in peripheral and central olfactory systems seems to be highly variable by circadian rhythms, little is known about how these are controlled at the neuronal and molecular levels. It has been reported that the plasticity in the olfactory system is modulated by a set of neuropeptides. However, it remains still elusive how these neuropeptides and neuroendocrine system interact in the peripheral systems to change olfactory responses in cockroaches. Here, current study focuses on the localization of neuropeptides and their receptors by using in situ hybridization and immunostaining methods. Also, expression level of these genes are evaulated by qRT-PCR methods. Circadian fluctuation of these genes seem to be important neurotransmission machineries in the periphery. Our current study suggests that microcircuits of neuronal systems in the peripheral olfactory organ play an important in olfactory modulation by circadian rhythm.

P042

Nutrient regulation by a generalist caterpillar of *Spodoptera exigua*

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The aim of this research was to demonstrate whether generalist-feeding caterpillars of *Spodoptera exigua* (Hübner) regulate their nutrient intake when faced with nutritionally variable food conditions. Six, chemically-defined diets were prepared that differed in the composition of protein and digestible carbohyrate:42% protein with 0% carbohydrate by dry mass(p42:c0), p35:c7, p28:c5.6, p7:c35, p5.6:c28 and p0:42. A total of 288 newly-ecdysed final instar(5th) caterpillars were collected and assigned randomly into 7 food pairing treatments, in which they were allowed to choose between two diet block:one with high P:C ratio and the other with low ratio [1) p42:c0 vs. p0:c42, 2) p42:c0 vs. p7:c35, 3) p35:c7 vs. p0:c42, 4) p35:c7 vs. p7:c35, 5) p35:c7 vs. p5.6:c28, 6) p28:c5.6 vs. p7:c35 and 7) p28:c5.6 vs. p5.6:c28]. Various aspects of food intake and larval performance variables were measured for each insect, including larval survival, stadium duration, pupal mass and body lipid composition. Results showed that the intake of protein and carbohydrate self-composed by caterpillars in all treatments converged to a point in a bivariate nutrient plot and the ratio of protein to carbohydrate averaged over these converging intake points was close to 1:1. This indicates that *S. exigua* caterpillars have capacity to balance their nutrient intake by defending their species-specific 'intake target' despite the differences in amount and proportion of nutrients available in each food choice treatment.

Key words: carbohydrate, Feeding behavior, Geometric Framework, Intake target, *Spodoptera exigua*, Protein

P043

Wing form dimorphism in reaction to nymphal density in the brown planthopper, *Nilaparvata lugens*

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An expression of adult wing form in reaction to rearing density during nymphal stage was investigated in the brown planthopper, *Nilaparvata lugens*. Under mass rearing condition, the S-BPH and the 2007-BPH population predominantly showed a short-winged, brachypterous, form and a long-winged, macropterous, form, respectively. At rearing density of less than 5 nymphs in the 2007-BPH, 90% of females showed brachypterous form, but all males became macropterous form. The ratio of macropterous form in the 2007-BPH males decreased by 75% in 10 to 15 rearing density, but increased by more than 95% again at 20 to 30 rearing density. In the case of the 2007-BPH females, the ratio of macropterous form gradually grew from 31% at 10 nymphal density to 92% at 20 nymphal density. All females originated from the S-BPH showed brachypterous form, regardless of nymphal density. The ratio of macropterous males in the S-BPH rapidly went down from 74% at 1 nymphal density to 10% at 10 nymphal density. At 20 nymphal rearing density, all males of the S-BPH showed brachypterous form. On the other hand, other brachypterous (OJ67-BPH) and macropterous (2006-BPH) population produced similar results with above the two populations at 1 nymphal rearing density. In summary, these results demonstrate that wing form dimorphism in *N. lugens* is largely influenced by nymphal density and the wing form at a specific density (low or high) can be different by sex or *N. lugens* populations.

Key words: *Nilaparvata lugens*, nymphal density, wing form dimorphism

P044

Molecular Cloning of Prophenoloxidase Genes from the Multicolored Asian Lady Bird Beetle, *Harmonia axyridis*

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The multicolored Asian ladybird beetle, *Harmonia axyridis*, is a generalist predator of aphids also, shows a high level of phenotype polymorphism in color pattern of elytra. Although, it is not sure about genetic information of color polymorphism, it has been confirmed that this phenomenon comes from their genetic traits. The color of *H. axyridis* elytra is mainly composed of black and red pigment. Phenoloxidase (PO) plays an important role in many insect physiological functions, i.e. sclerotization and pigmentation of cuticle and melanization of parasites. Following activation, PO catalyses the hydroxylation of tyrosine and subsequent oxidation of phenolic substance into quinines, which are further converted to melanin. However, the molecular bases of *H. axyridis* color pattern formation are almost unknown but it may be that the different pro-POs have different expression. In this study, total RNA samples from four each color pattern individuals, for example, succinea 1, succinea 2, conspicua and spectabilis was extracted. A cDNA enconding pro-PO was molecular cloned from each color pattern of *H. axyridis* and its putative amino acid sequence shared homology with pro-PO of other insects. We are pursuing to elucidate that their pro-PO sequence will be similar with those other insect PPO sequence. There are also regions of high sequence similarity, including putative activation site and two copper binding sites.

Key words: *Harmonia axyridis,* prophenoloxidase, color polymorphism, RT-PCR, cloning

P045

EMS와 UV-A가 무당벌레 번데기와 자손세대에 미치는 영향

강은진, 윤규식, 강민아, 권혜리, 박민우, 서미자, 유용만, 윤영남
충남대학교 농업생명과학대학 농생물학과

EMS(ethyl methansulphonate)는 alkylalting 물질로 초파리를 비롯하여 꼬마선충, 애기장대, 모기 등에 single-site mutation을 일으키는 것으로 알려져 있으며, 자외선은 노출량을 쉽고 정확하게 조절할 수 있어 곤충의 돌연변이 유발에 사용된다. 본 연구에서는 무당벌레의 번데기에 0.1과 1%농도의 EMS를 처리한 것과 UV-A(360mm)에 1시간과 12시간 노출시킨 것을 대상으로 발육기간과 성비, 색상패턴별 출현비율을 조사하였다. 이와 더불어 돌연변이원 처리가 무당벌레의 자손세대에 미치는 영향을 조사하기 위해 돌연변이원을 처리한 번데기에서 우화한 성충의 자손세대를 처리농도, 처리시간별로 동일한 진딧물을 공급하여 F2세대까지 사육하여 결과를 얻었다. EMS-1%와 UV-A 12시간처리구의 경우, 우화 세대의 성충이 산란한 알이 부화되지 않는 경우가 있었으며, 발육기간은 EMS-0.1%처리구와(무처리: 20.24±1.90; 0.1%: 23.39±1.83; P=0.00), UV-A 1시간, 12시간 처리구에서 무처리구에 비해 발육기간이 증가하였다(무처리: 21.43±1.79; 1Hr: 22.30±1.68; 12Hr: 22.75± 1.76; P=0.00). 우화 세대의 성비는 EMS와 UV-A에 따른 차이없었고, 생존율은 EMS-1% 처리에서 크게 감소하였다(무처리: 95.23±8.24; 1%: 42.70±19.15; P=0.05). EMS와 UV-A 처리를 하면 발육기간동안 비정상적 탈피현상이 많았다. UV-A를 처리한 비멜라닌계통 모세대의 자손세대는 모든 개체가 비멜라닌계통으로 출현된 반면, EMS-1% 처리구에서는 비멜라닌계통의 출현비율이 70%로 EMS에 의한 자손세대의 색상패턴의 변화를 확인하였다.

검색어: 무당벌레, EMS, UV-A, 성비, 발육기간, 색상패턴 출현비율

P046

The Effects of gut bacteria to ladybird, *Harmonia axyridis*

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Gut symbiotic microorganisms of insects are known that play important roles in the digestion, development, survival, and reproduction of host insects, and it is widely accepted that symbionts synthesize essential amino acids or vitamins for host insect among these relationship. More recently, however, it has become increasingly apparent that symbiont's contribution to their host are not limited to nutrition. Actually, these symbionts are frequently observed near an insect's digestive tract. In this study, we isolated and identified gut bacteria of ladybird, *Harmonia axyridis*, which is a predator and used the factor for biological control of aphids, and was aimed to survey gut bacteria affecting to ladybird's biological or ecological characteristics.

We separated the guts of larvae and adults ladybird and cultured them in 4 media, such as NA, skim-milk, CMC and CMA. About 33 isolates including genus Arthrobacter were identified in this study. These were cultured in NA media with several antibiotics. We selected ofloxacin and penicillin that inhibited these bacteria growth in media, and reared ladybirds as prey with aphids treated ofloxacin and penicillin 1000ug/1ml concentration. After that, weight of pupae, larval stage, emergence stage, fecundity and hatching rate were investigated. It was shown that, ofloxacin and penicillin treatment was caused by weightless of pupae, fecundity and delay of larval stage, and the affected hatching rate as well.

Key words: *Harmonia axyridis*, Gut bacteria, ofloxacin, penicillin

P047

Comparison of Cuticular Hydrocarbons on Developmental Stages of the Bean Bug, *Riptortus pedestris*

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Cuticular hydrocarbons (CHCs) were analyzed using GC and GC-MS, and compared with developmental stages of the bean bug, *Riptortus pedestris*. Carbon numbers on each developmental stages differed from 14-19 in eggs to 4th nymph, 25 in 5th nymph, and over 30 in last nymph that until adult emergence. Carbon numbers are increased to 16-17 carbons over time in newly emerged adults, 18-22 in 1 and 3 days after emergence, respectively; 23-27 in 6 days after emergence; approximately 30 in over 10 days after emergence. Carbon numbers increased as passed days after emergence. *Riptortus pedestris* consisted of *n*-nonacosane on almost all developmental stages, and followed by *n*-hentriacontane and 13,17-;15,19-demethyltritriacontane. Eggs, however, consisted of unknown compounds with high proportion and followed by *n*-heptacosane, and newly emerged adults also has a high proportion of *n*-heptacosane. From the above results, CHCs on developmental stages of the bean bug consist of *n*-alkane with saturated hydrocarbons (36-65 %), followed mono- or di- methylalkanes. However, newly emerged female and male adults mostly consisted of methyl-alkane. The major constituents of CHCs on the developmental stages of *Riptortus pedestris* is differently proportioned, but hardly showed the difference in their composition.

Key words: Cuticular hydrocarbons (CHC), Bean bug, *Riptortus pedestris*

P048

한국산 목거위벌레아과 10종의 요람구조 및 잎의 재단 패턴

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‘잎을 마는 바구미(leaf-rolling weevils)’로 알려져 있는 거위벌레류(Rhynchitidae, Attelabidae)는 식식성 곤충(obligatory phytophagous)이다. 전 세계적으로 주둥이거위벌레과(Rhynchitidae) 1,110종과 거위벌레과(Attelabidae) 1,000종이 보고되어 있다(Legalov, 2003).

거위벌레류는 뉴질랜드와 하와이를 제외하고, 전 세계적으로 분포하고 있으나, 대부분의 종은 아열대지역과 열대지역에 서식하고 있다. 가장 많은 종수는 동양구(Oriental), 열대아프리카(Afrotropical), 신열대구(Neotropical)에서 관찰된다. 거위벌레류의 특징은 ‘자손을 위한 특별한 보살핌’이라고 할 수 있다. 어떤 거위벌레류는 유충의 성장과 먹이를 위해 독특한 재단법을 이용하여 잎덩이(요람, leaf rolls, cradle)를 만들기도 하고, 다른 종들은 식물의 과실이나 꽃, 줄기 등을 유충의 성장을 위해 이용한다. 특히 **목거위벌레아과(Apoderinae)**는 신열대구, 신북구에서는 전혀 분포하지 않고, 오스트리아구에서는 소수의 종을 제외하고는 역시 분포하지 않으며, 거위벌레과에서 가장 나중에 분화된 분류군(Legalov, 2005)으로 요람을 다른 종에 비해 섬세하게 대부분 짧은 원통형 요람을 만드는 것이 특징이다.

본 연구에서는 목거위벌레아과 10종의 요람형을 기재하는 동시에 요람의 형태와 잎의 재단선에 따라 요람형 분류를 시도하여 그 결과를 보고하는 바이며 요람형의 용어는 Suzuki and Uehara(1996a)에 따랐다.

검색어: 목거위벌레아과, 요람구조, 잎의 재단선

사 사 : 이 논문는 2009년 정부(교육과학기술부)의 재원으로 한국연구재단의 지원을 받아 수행된 연구임. [NRF-2009-351-C00151]

P049

Effects of functional GM Chinese cabbage on the life history of Diamondback moth (*Plutella xylostella*)

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The life table statistics of diamondback moth on the transgenic Chinese cabbage (line: SKCP) with myrosinase gene was compared with that on the non transgenic Chinese cabbage (line: SC) at 25±1℃. Adult life span and number of progeny of *P. xylostella* on the SC and SKCP lines were similar to each other. The sex ratio, developmental period, intrinsic rate of increase and finite rate of increase of *P. xylostella* on SC and SKCP were not significantly different in both treatments (sex ratio: t=-1.60; df=220; P=0.1108, developmental period: t=-0.55; df=220; P=0.5803, intrinsic rate of increase: t=-0.11; df=45; P=0.9172). However, the finite rate of increase and net reproduction were significantly different in between SC and SKCP lines (finite rate of increase: t=2.26; df=45; P=0.0287, net reproduction: t=2.08; df=45; P=0.0442).

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Key words: myrosinase gene, life table statistic, *Plutella. xylostella,* GMO.

P050

Prediction of population dynamics of *Myzus persicae*, *Heliothis assulta* and *Frankliniella occidentalis* as climate changes: modeling approach

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Myzus persicae, *Heliothis assulta* and *Frankliniella occidentalis* are the most severe pests of pepper in Korea. IPCC (Intergovernmental Panel on Climate Change) reported that the temperature would increase 7℃ at the end of this century. According to the elevated temperature, the pest population will be grow dramatically. We need to predict the pest-population size to maintain good crop productivity. DYMEX and CLIMEX are commercial software developed by CSIRO in Australia, to build and simulate population dynamics models. Using this software, we predicted population dynamics of *M. persicae*, *H. assulta* and *F. occidentalis* applying past climate data (1970) and future climate data (2070) which were generated by National Institute of Meteorological Research (NIMR). The population growth rates of *M. persicae*, *H. assulta* and *F. occidentalis* were 6300, 16 and 950 times, respectively, with 5 degree elevation. Therefore pest management should be conducted intensively in the future.

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Key words: global warming, DYMEX, ecological model, pest management, pepper

P051

Effects of genetically modified virus-resistant pepper on the insect community in the pepper cultivation area.

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The effects of the genetically modified virus-resistant pepper (line: H15) and the Non-GM pepper (line: P2377) on the insect community in the pepper cultivation area were evaluated. Sampling was conducted using yellow sticky traps and pheromone funnel traps in Anseong and Deokso fields.

Total number of insects caught on sticky trap were 3924 individuals at GM pepper and 3670 individuals at Non-GM pepper in Anseong and 2362 individuals at GM and 2528 individuals at Non-GM in Deokso, respectively. The total number of the insect individuals caught by sticky trap was not shown significant differences between GM and Non-GM pepper at Anseong and Deokso fields, respectively.

The number of aphids per sticky trap ranged from 11.60±2.02 to 1.92±0.96 at Non-GM and from 11.56±2.15 to 0.33±0.23 at GM in Anseong, and from 2.78±1.22 to 0.11±0.08 and from 2.73±0.84 to 0.11±0.08 at Non-GM and GM pepper in Deokso, respectively. There were no significant differences in seasonal occurrences of aphids caught on sticky traps in GM and Non-GM pepper at both fields, and significant differences in aphids population density between Non-GM and GM were not observed.

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Key words: Virus-resistant GM pepper, Aphid, *Myzus persicae* GMO.

P052

끝동매미충(*Nephotettix cincticeps*) 발생시기 변화 연구

김광호, 이상계, 김정준, 이시우, 박창규, 박홍현
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현재 우리나라의 수도해충으로는 114종이 기록되어 있다. 그 중 12종이 주요 해충으로 알려져 있으며 최근에는 애멸구를 비롯한 멸구류와 매미충류의 발생 빈도가 증가하고 있으며, 혹명나방의 비래밀도가 격년으로 증감하고 있다. 벼애나방 및 줄점팔랑나비가 국지적으로 다량 발생하여 보고가 접수되고 있는 실정이다.

끝동매미충의 피해는 간접적으로 벼위축병, 및 누른 오갈병의 매개와 직접 흡즙에 의한 벼잎의 황변, 분얼수 감소 및 염실장애 등으로 피해를 주고 있으며, 발생이 많은 남부지방에서 피해 및 방제가 문제가 되고 있는 실정이다(엄 등 1978).

우리나라에서는 끝동매미충의 방제를 위해 내충성 품종육성(최 등 1973, 최, 1975, 김 1978), 약제저항성 검정(최, 1976), 우수살충제선발(최 등 1977, Hokyo 1971)등의 연구가 이루어져 있으나, 최근 지구온난화에 따른 끝동매미충의 본답으로의 이동시기 등에 관한 연구는 전무한 실정이다.

한편 해충의 적절한 방제 및 관리를 위해서는 대상해충의 발생경과를 포장을 중심으로 한 생활사와 개체군 동태에 관한 기초성적의 누적이 필요하다. 따라서 본 연구는 주요 지역의 과거 30여년간의 유아등 자료를 바탕으로 월동 후 1세대의 본답으로의 50% 이동 일수 변화를 살펴봄으로써 향후 이들의 발생시기 및 방제전략 수립의 기초자료로 활용함을 목적으로 하고 있다.

P053

국내 몇몇 지역의 꽃매미 월동난의 시기별 부화율 조사

김광호, 이상계, 김정준, 이시우, 박창규, 박홍현

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2000년대 초 중국으로부터 국내에 유입되었으리라 추정되는 꽃매미(*Lycorma delicatula* White)는 김 등(2006)이 국내의 천안, 연기, 서울 관악산 등지에서 최초 발생 보고한 이래, 해마다 그 발생면적이 급증하고 있다.

최근 5년 동안의 포도원과 그 주변의 발생 면적을 상황을 살펴보면 2006(1ha)→2007(7ha)→2008(81ha)→2009(2,946ha)→2010(8,478ha)로 해마다 7배에서 30배 이상으로 발생면적이 예측할 수 없을 정도로 급증하고 있다.

이렇게 꽃매미가 급증하는 원인은 이들은 1년에 1세대가 경과함으로써 국내에 서식하고 있는 다른 매미류(4~7년)에 비해 세대기간이 짧고, 암컷 한마리당 산란수가 400~500(왕 등 1981)개 정도로 매우 많으며, 현재 국내에 이들의 밀도를 억제할 수 토착천적의 부재가 주요한 요인으로 알려져 있다.또한 월동난의 생존율이 매우 높아 이듬해 밀도 급증의 큰 원인이 되고 있다.

현재 국내의 꽃매미 발생현황은 9개 시도 49개 시군(2010년 농식품부 총조사)에서 발생이 되고 있으므로 국내의 전 지역에서 월동이 가능한 것으로 추측된다.

따라서 본 연구에서는 지역별로 꽃매미 월동난의 생존율을 조사 분석함으로써 이후 확산가능 지역을 추정할 수 있고, 또 2008년과 2009년의 월동 생존율을 비교함으로써 동계 혹한이 꽃매미 월동난의 생존율에 미치는 영향을 분석하고자 함에 있다.

P054

꼬마잠자리 서식지의 식물상 및 생활형

김명현, 한민수, 방혜선, 정명표, 강기경, 나영은, 이덕배

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현재 우리나라에서 멸종위기보호야생동식물로 지정되어 있는, 꼬마잠자리는 습지의 식생천이나 대규모 개발에 의해서 서식지가 감소하고 있는 실정이다. 본 연구에서는 꼬마잠자리의 독특한 서식지에 출현하는 식물상을 조사함으로서 향후 꼬마잠자리의 서식지 복원 및 보전을 위한 기초자료를 제공하고자 한다. 조사지역은 꼬마잠자리가 높은 밀도로 서식하고 있는 3곳(문경 농암면, 문경 산북면, 영동)으로 하였다. 서식지의 환경적 특성은 사면의 하부에서 상부까지 서식지의 위치에 상관없이 연중 수심이 2-10cm로 유지되면서, 직사광선이 차단되지 않는 개방된 습지에서 주로 서식하고 있었다. 꼬마잠자리 서식지에 분포하는 관속식물은 29과 50속 62종 9변종 2품종으로 총 73분류군으로 조사되었다. 조사된 식물들의 각 과별 구성종은 사초과와 벼과가 각각 21.9%와 13.7%로 많이 나타났다. 조사 지역별로는 영동에서 37분류군, 문경 산북에서 48분류군, 문경 농암에서 43분류군이 확인되었다. 이들 3곳에서 공통으로 출현한 식물종은 버드나무, 고마리, 벼룩나물, 좀고추나물, 매듭풀, 바늘꽃, 통발, 골등골나물, 별날개골풀, 골풀, 청비녀골풀, 사마귀풀, 뚝새풀, 조개풀, 도깨비사초, 방동사니대가리, 쇠털골로 총 17분류군이었다. 출현한 관속식물 73분류군의 생활형을 살펴보면, 휴면형은 수생식물(HH)이 24종, 1년생식물(Th)이 15종, 1년생수생식물(HH(Th))이 14종으로 많이 출현했다. 번식형에서 산포기관형은 풍력산포와 중력산포를 가지는 것(D1,4)이 25종, 중력산포형(D4)이 23종으로 많이 출현했다. 지하기관형은 영양번식형(R5)이 34종, 자동산포형(R3)이 15종으로 많이 출현했다. 생육형은 직립형(e)과 총생형(t)이 각각 21종으로 많이 출현했다.

검색어: 꼬마잠자리, 식물상, 생활형, 멸종위기보호야생동식물, 복원

P055

참딱부리긴노린재(*Geocoris pallidipennis* (Costa))의 발육과 산란에 미치는 온도의 영향

김정환, 변영웅, 김황용, 최만영, 김성현, 황석조
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가루이류, 응애류, 나방류 알과 어린유충 등을 포식하는 참딱부리긴노린재에 대한 발육과 산란에 미치는 온도의 영향을 구명하기 위하여 25, 30, 35, 37.5, 40℃와 습도 70±10% 조건에서 조사하였다. 참딱부리긴노린재의 알 부화율은 25～35℃에서 80%이상이었으나, 37.5℃는 59.98%였고, 40℃는 전혀 부화하지 않았다. 알 발육기간은 25℃가 13.22일로 가장 길었고, 37.5℃가 4.98일로 가장 짧았다. 약충(1～5령)의 발육기간은 25, 30, 35, 37.5℃에서 각각 30.68 18.95, 14.34, 12.35일로 온도가 높을 수 록 짧아졌으며, 40℃에서는 발육하지 못하는 것으로 나타났다. 약충 발육기간 동안 생존율은 25℃에서 56.1%로 가장 높았으나, 나머지 온도에서는 28.4%이하로 매우 낮아 대량사육과정에서 생존율을 높일 수 있는 기술이 필요하다. 성충의 평균 산란기간은 25℃가 37.93일로 가장 길고, 40℃가 6.46일로 가장 짧았으며, 성충 우화 후 70%산란기간은 25, 30, 35, 37.5, 40℃에서 각각 39, 23, 19, 11, 5일이었다. 총 산란수는 35℃에서 111.19개로 가장 많았고, 40℃가 22.11개로 가장 적었다. 성충의 수명은 25, 30, 35, 37.5, 40℃에서 각각 62.45, 39.32, 33.81, 17.00, 9.31일로 온도가 높을 수 록 짧아지는 것으로 나타났다. 참딱부리긴노린재는 35℃의 고온에서 정상적인 발육과 산란을 하는 것으로 보아 비닐하우스 고온 조건에서 재배되는 참외 등 포복성 작물에 발생하는 가루이류 등의 해충 생물적방제 천적으로 이용이 가능할 것으로 추정된다.

검색어: 참딱부리긴노린재, 천적곤충, 온도발육, 산란수, 수명

P056

Black Soldier Flis(Diptera: Stratiomedae): Seasonal Molting, adult Emergence and Mating of in Artificial Rearing System

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The black soldier fly, Hermetia illucens (BSF), has a worldwide distribution in the tropics and warm temperate regions and is active in the Korea from May through October. This species colonize a wide variety of decomposing vegetable and animal matter and oviposit in a variety of decomposing materials.

In this study, how the BSF molting, adult emergence and mating rate changed by seasonal condition at the artificial rearing system was investigated.

The black soldier fly larvae and pupae were reared under laboratory condition (27℃, 60% R.H.). Under the laboratory condition, molting and adult emergence were not influenced by seasonal factors such as climate, radiation intensity. But it is known that the sunlight is the most important factor of the mating. In the previous study the time of day, temperature, and humidity is significantly correlated with oviposition and mating. The rearing of BSF throughout the year is restricted by sunlight. In this study, the data shows definitely different mating numbers throughout whole year. The time of the day and sunlight density are changed with season and it influence on artificial rearing. To culture the black soldier fly throughout the year in Korea needs a more deep study under the artificial rearing system.

Key words: Black soldier fly, artificial rearing, oviposition, mating, seasonal factors

P057

담배거세미나방(*Spodoptera litura*) 성충발생 예측을 위한 몇가지 온도 의존적 발육 모형의 모수 추정 및 평가

박창규, 정유림, 윤지은, 염기홍, 이지은
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담배거세미나방 (*Spodoptera litura* (Fabricius))을 8개 항온 조건(13, 16, 19, 22, 25, 28, 31, 34℃)에서 사육하며 충태별 발육 기간을 조사한 후, 온도별 발육율을 설명하는 5가지 선형 및 비선형 발육모형의 모수를 추정하였다. 비선형 모형의 경우 16, 34℃ 값을 임의적으로 설정하여 모수를 추정하였으며, 변온조건에서 조사된 성충 발생시기 자료를 이용하여 성충 발생시기 예측을 위한 발육모형들의 적합성을 평가하였다.

항온조건에서 발육시험 결과 13, 34℃에서 난 발육은 불가능하였고, 16℃에서는 용까지는 발육하였으나 성충으로 우화하지는 못하였다. 난부터 성충까지 전체 발육기간은 31℃에서 27.6일로 가장 짧았으며, 온도가 낮아짐에 따라 발육기간이 길어져 19℃에서는 82.2일로 가장 길었다. 난부터 성충까지 발육할 때 발육영점온도와 유효적산온도는 각각 13.1℃, 500온일도(DD)로 추정되었다. 분석된 4개의 비선형 발육 모형들의 결정계수는 0.98∼0.99로 높았으며, 유충부터 성충까지 누적발육완료 패턴을 3-parameter Weibull 함수를 이용하여 분석한 결과 높은 결정계수(r^2=0.92)를 보였다.

5개의 온도에 따른 발육모형과, 3-parameter Weibull 함수를 이용하여 일자별 누적 성충 발생율을 예측하였다. 날짜별 발육율을 계산할 때 사용한 일 평균기온은 일 최저온도에 3배하고 일 최고온도에 4배하여 더한 후 7로 나눈 값을 사용하였을 경우 성충 누적 발생 패턴을 가장 잘 설명할 수 있었다. 2회에 걸친 성충 누적 발생율 실측치를 예측치와 비교한 결과 5개의 발육 모형 중 Schoolfield 등 (1981)의 모형이 유충부터 성충까지 누적 발육완료율을 가장 잘 설명하였다.

검색어: 담배거세미나방, 온도 의존적 발육 모형, 발육완료 모형, 평가

P058

복사나무잎에 대한 갈색여치의 먹이 선호특성

방혜선, 김명현, 정명표, 한민수, 강기경, 나영은, 이덕배

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곤충의 성장속도, 산란량 등에 영향을 미치는 중요 인자 중 하나가 먹이로 하는 식물의 질과 양의 변화이다. 특히 메뚜기목 곤충은 단백질과 동시에 수분을 포함한 다른 영양원을 먹이에서 얻는다. 메뚜기류는 다른 곤충에 비해 체내 조직의 총 질소 함량이 높기 때문에 그 높은 수준을 유지하기 위해서는 지속적으로 질소함유량이 높은 먹이원을 섭취해야만 하는 것으로 알려져 있다. 따라서 기주식물의 질적인 변화는 메뚜기의 성장과 산란에 영향을 미쳐 전반적으로 밀도변화를 가져오는 주요인으로 작용한다.

충북 영동지역을 중심으로 지난 2006년 및 2007년 대발생하여 농작물에 피해를 준 갈색여치는 주로 야산에서 부화한다. 부화한 갈색여치는 서식지의 식물이 개엽하기 전까지는 부식질을 섭식하며, 갈참나무를 포함한 참나무류가 개엽을 하면 이들의 어린잎을 섭식한다. 갈색여치가 산림지역에서 과수원으로 이동하는 시기는 5월 초순경으로 복사나무 잎이 개엽하는 시기와 일치하였다. 복숭아 잎에 대한 선호성에는 갈색여치의 성장과 발육에 직접적으로 관계되는 질소함량 차이와 상관성이 높은 것으로 조사되었다. 야외에서 갈색여치가 과수원으로 이동 하는 시기와 갈참나무 잎의 질소함량이 급격히 감소하는 시기가 일치하며, 동일시기 복사나무 잎의 질소함량은 갈참나무 잎보다 항상 높은 값을 유지하였다. 또한 실내실험에서 3가지(갈참나무 잎, 복사나무 잎, 어린 복숭아) 먹이 중 복사나무 잎 > 복숭아 > 갈참나무 잎의 순으로 먹이를 선호하는 것으로 관찰되었다.

검색어: 갈색여치, 복사나무잎, 먹이, 선호특성

P059

Insecticidal capacity of novel recombinant baculoviruses to *Plutella xylostella* and *Spodoptera exigua* larvae

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This study was conducted to investigate the insecticidal capacity of several recombinant baculoviruses to *P. xylostella* and *S. exigua* larvae. NeuroBactrus was constructed as follows: the cry1-5 of *Bacillus thuringiensis* 2385-1 was inserted into *Autographa californica* multicapsid nucleopolyhedrovirus (AcMNPV) genome by fusion of *polyhedrin-cry1-5-polyhedrin* under the control of *polyhedrin* gene promoter, and insect-specific neurotoxin from the scorpion *Androctonus australis* (AaIT) under the control of early promoter from *Cotesia plutellae* bracovirus was introduced by fusion of *orf603* partial fragment in the opposite direction of *polyhedrin* gene, respectively. Other recombinant baculoviruses derived from the NeuroBactrus - NBt-DelA (deleted AaIT), NBt-Del5 (deleted cry1-5), and NBt-DelA5 (deleted AaIT and cry 1-5) - were manufactured in serial passages in vitro. The data were analyzed by SPSS. The value of LC_{50} was lower when *P. xylostella* larvae fed on cabbage coated with NeuroBactrus (4068.4) than when it fed on cabbage coated with AcMNPV ($4.5x10^6$). Survival time (ST_{50}) of *P. xylostella* larvae (2.54days) was shorter when it fed on cabbage coated with NeuroBactrus than when it fed on cabbage coated with other recombinant baculoviruses (7.54days, 7.68days, and 8.26days) and AcMNPV (9.67days). *S. exigua* larvae presented the same results.

Key words: AcMNPV, Insecticidal capacity, NeuroBactrus, *Plutellaxylo stella, Spodoptera exigua*

P060

Border Effect of Spatial Distribution of *Rice Stripe Virus* Disease Caused by Vector Insect, *Laodelphax striatellus*

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In many cases over the years, we failed to forecast accurately outbreak of *Rice stripe virus* (RSV) disease using population density of overwintering small brown planthopper (SBPH), *Laodelphax striatellus*. What is the source of error in this viral disease assessment? For answering the question, spatial distribution of RSV in paddy fields was investigated in relation to the yield of rice grain, and the population density of overwintering SBPH in ridge of paddy fields. Total 14 paddy fields in 5 regions were surveyed in June, 2008. Disease assessment was carried out with each of 30 rice plants in the one of the borders, 5th, 10th line from ridge, and 90 rice plants in diagonal line for conventional method. The ears of rices from 18 plants in the same surveyed line were collected in the late of August for the weights of 100 rice grains. The infection rate of RSV was decreased by the distance from ridge; on the contrary, the increase tendency was shown in the yield of rice grains in the middle of paddy field. It is suggested that the border effect of viral distribution between ridge and paddy field is caused by the spatial distribution of the vector insect. Thus, in this case, the narrow border effect could represent that the SBPH migrated short distance from the ridge to paddy field. The conventional method, observing the disease in middle area of diagonal line, showed no correlation to the population density of overwintering vector generation in ridge. It might cause underestimation of the regional disease rate. The counting of RSV-diseased plant in border line only overestimated it also. However, the RSV infection rate in the near border had highly positive linear relationship (R^2=0.91) to the regional average values by regression analysis. Therefore, the near border sampling method can improve the RSV disease risk assessment.

Key words: *Rice stripe virus*, Small brown planthopper, *Laodelphax striatellus*, border effect, spatial distribution, disease risk assessment

P061

Characterization of cricket song patterns and the behavior observation of *Teleogryllus emma* (Orthoptera:Grylloidea)

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We analyzed the chirp sound and behavior of *Teleogryllus emma* with observation system, which was consisted of computer, ccd-camera and microphone. Computational methods of wavelet transformation and Self-Organizing Maps (SOM) were utilized to characterized the chirp sound of insect species for automatic counting in this study. Wavelets were initially applied to feature extraction of the chirp sound. Wavelet coefficients were accordingly calculated based on the basis function (e.g., Morlet). The obtained coefficients were subsequently provided to count number of chirps in each song. Sound structure of insect specimens consisted with long chirp and short chirp and the patterns of song were grouped by frequency of long chirp and short chirp. The song patterns of insect specimens were divided by Self-Organizing Map (SOM) that was used number of chirp as input data. Application of computational methods to automatic detection of chirp sound was further discussed for obtaining objective assessment in behavior science.

검색어: *Teleogryllus emma,* Number of chirp, Automatic counting, Song pattern, Behavior

P062

Influence of trap types and locations in tree trunk on trapping efficiency against *Platypus koryoensis* (Coleoptera: Platypodidae)

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Trapping efficiency by trap types, colors and positions in the trunk was evaluated for monitoring and the integrated pest management of *Playtpus koryoensis*, known as a vector of Korean oak wilt disease. The experiments were conducted in oak forest located in Gwangtan-myeon, Paju-si, Gyeonggi-do, Korea using two types of trap: sticky trap and multi-funnel trap. Trapping efficiency of two trap types was not significantly different. Trapping efficiency of the sticky trap was not affected by four trap colors: yellow, black, white and transparent. The number of caught by the traps, regardless of trap types, was higher in the traps facing upper slope than lower slope.

Key words: *Platypus koryoensis*, Korean oak wilt disease, Trap efficiency, sticky trap, multi-funnel trap

P063

벼 재배지 해충과 천적의 발생양상 구명

이건휘, 백채훈, 노태환, 이두구, 심형권, 김시주
국립식량과학원 간척지농업과

벼 재배지에서 천적을 보호하고 이용하는 기술을 개발하고자 벼 재배논과 주변 논둑에 발생하는 해충과 천적의 종류와 발생양상을 조사하였다. 논에서 발생하는 해충은 끝동매미충(*Nephotettix cinciticeps*) 등 7종, 천적은 거미류 등 14종이 발생한 반면, 논둑에서는 해충은 애멸구(*Laodelphax striatellus*) 등 10종, 해충은 기생봉류 등 20종이 발생되었다. 논에서 발생하는 해충 종류는 논둑에서 발생하는 해충종 보다 적었지만 발생량은 월등히 많았다. 그러나 천적은 논보다 논둑에서 발생하는 종류와 발생량이 많은 경향이었다. 논에서 해충이 발생된 이후 논둑에 서식하는 천적이 논으로 이동하는 양상을 보였으나 일부 거미와 같은 포식성 천적은 논으로 이동하지 않고 논둑에서 배회하는 종류도 많았다. 10월 하순이후에는 일부 해충과 천적이 논에서 다시 논둑으로 이동하는 양상을 나타냈다. 또한, 논둑을 제초한 지역보다는 제초하지 않은 지역에서 천적 발생량이 월등히 많아 논둑이 천적의 서식처 역할을 할뿐만 아니라 천적의 먹이가 되는 해충의 서식처역할을 하는 것으로 구명되어 벼 재배지에서 해충의 생물적 방제를 위해서는 논둑관리가 중요한 요인으로 생각된다.

검색어: 벼, 해충, 천적, 발생양상, 생물적 방제

P064

조 노린재류의 발생종류, 조 피해 및 약제방제효과

김현주, 배순도, 윤영남, 최병렬, 남민희, 박정규[1]

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조에 발생하는 노린재의 종류는 애긴노린재, 알락수염노린재, 흑다리잡초노린재, 풀색노린재, 시골가시허리노린재, 썩덩나무노린재 및 가시점둥글노린재 이었으며, 그 가운데 애긴노린재, 흑다리잡초노린재 및 알락수염노린재의 발생량이 많았다. 조에서 노린재류는 6월 하순부터 10월 하순까지 발생하며, 발생최성기는 결실기부터 등숙기까지라 할 수 있다. 노린재류는 주로 조 이삭을 흡즙하여 알맹이를 검게 변색시키거나 기형으로 만들어 피해를 준다.

애긴노린재, 알락수염노린재 및 썩덩나무노린재에 대한 Clothianidin 액상수화제 등 5종 약제의 처리효과를 조사하였다. 분무처리에 의한 생물검정에서 애긴노린재는 처리 후 3일에 100%의 살충률을 나타내었으나, 알락수염노린재는 처리 후 7일에 Fenthion 유제와 Clothianidin 액상수화제에서 각각 95.2%와 79.2%의 살충률을 나타내었고, 타 약제의 살충률은 50%이하로 나타났다. 하지만 충체침지처리에 의한 노린재류의 살충률은 5종 약제 모두 처리 후 3일에 100% 살충률을 나타내었다. 따라서 약제처리간에 노린재류에 대한 살충률의 차이를 나타내었다. 한편, 조 포장에서 노린재류에 대한 약제처리효과는 3일차 및 7일차에 Fenobucarb 유제를 제외하곤 90%이상의 방제효과를 나타내어 조 노린재 방제약제로 이용할 수 있다.

검색어: 조, 노린재, 발생, 피해, 약제방제

P065

산림지와 농경지에서 톱다리개미허리노린재의 발생양상

배순도, 김현주, 최병렬, 윤영남, 남민희

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산림지(밀양 화악산)와 농경지(밀양, 식량과학원 기능성작물부 내)에서 톱다리개미허리노린재의 발생양상을 조사하였다. 집합페로몬을 이용한 톱다리개미허리노린재의 발생은 봄철(4～6월)에는 농경지보다 산림지에서 약 3배 이상 많았으며, 여름철(7～9월)에는 산림지보다 콩 포장에서 약 2.5배 많았고, 콩 포장 침입 최성기는 8월 상순 이었다. 집합페로몬에 의한 시기별 일중(日中) 시간대별 톱다리개미허리노린재 암컷과 수컷의 발생비율은 8월 중순 및 하순 14:00～16:00에 각각 50～53% 및 38～39%로 가장 높았으며, 9월 하순에는 12:00～14:00에 36～41%로 가장 높았다. 불출법(Flushing method)에 의한 톱다리개미허리노린재의 9월 상순 시간대별 발생량은 14:00>16:00> 12:00>10:00>08:00>06:00순으로 많았다. 따라서 톱다리개미허리노린재는 봄철에 산림지에서 여름철에서 가을까지는 콩 등의 농경지에서 많이 발생되었으며, 노린재의 활동은 오전보다 오후에 활발하였고, 시간대별 발생비율은 낮의 길이에 따라 영향을 받았다.

검색어: 톱다리개미허리노린재, 산림지, 농경지, 발생, 시간대, 발생비율

P066

자운영과 헤어리베치에서 알팔파바구미의 발생과 작물피해

배순도, 김현주, 최병렬, 윤영남, 남민희
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국내에서 자운영과 헤어리베치는 화학농약 사용절감과 친환경 농산물 생산을 위해 많이 재배되는 녹비작물이다. 겨울철 내한성 등의 이유로 자운영은 남부지방에서 헤어리베치는 중부지방에서 주로 재배된다. 국내에서 알팔파바구미는 1994년 제주도에서 처음으로 발생되었으며, 2005년 경남 사천에서 대량으로 발생된 이후 전국적으로 그 분포가 확산되고 있다. 따라서 알팔파바구미의 발생지역 확산은 녹비작물의 안정 및 안전생산에 가장 큰 장애요인으로 인식되고 있다. 그러므로 알팔파바구미의 친환경 관리는 자운영과 헤어리베치에서 알팔파바구미의 발생양상과 그로 인한 녹비작물의 피해를 정확히 조사하는 것이 우선적이라 할 수 있다.

본 연구는 자운영과 헤어리베치에서 알팔파바구미의 유충과 성충발생 및 그로 인한 녹비작물의 피해를 조사하였다. 포충망 조사법에 의한 월동성충의 발생최성기는 4월 상순경 이었으며, 유충발생 최성기는 4월 중순경 이었고, 신성충은 4월 하순부터 발생되었다. 알팔파바구미에 의한 녹비작물의 피해는 헤어리베치보다 자운영에서 심하였으며, 5월 하순경 자운영과 헤어리베치의 피해엽수률은 80%이상 이었다. 따라서 녹비작물의 안정생산에 가장 큰 위협이 되는 알팔파바구미를 친환경적으로 관리할 수 있는 방제제 개발이 시급히 요구되는 바이다.

검색어: 알팔파바구미, 자운영, 헤어리베치, 발생, 피해, 조사법

P067

친환경 시설오이에서 긴털가루응애의 피해 증상과 실태 보고

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2009년 공주와 2010년 천안의 친환경 시설오이 재배지에서 잎과 과실이 원인모를 해충에 의해 피해를 받았으며 그 원인을 몰라 많은 피해를 입고 있었다. 오이 잎의 피해는 초기에는 잎에 하얀색 반점이 생기다가 피해가 진전되면서 잎의 곳곳이 찢어지는 증상을 보였다. 또한 과실의 피해는 어린과실때는 과실의 일부분이 물에 데친것 같은 증상이 나타나다가 과실이 생육할수록 그물망의 코르크화가 진행되어 결국에는 과실 전체가 코르크화 되었다. 잎과 과실의 피해 원인을 알아보기 위하여 잎과 과실을 채취하여 실내에서 현미경으로 관찰한 결과 긴털가루응애에 의한 피해로 밝혀졌다. 긴털가루응애의 피해는 육묘 중에는 나타나지 않았으나, 정식 후 부터 잎이 하얗게 되고 찢어지는 피해를 나타내면서 피해를 보이다가 수정 후 과실이 형성되는 시기부터는 과실에 피해를 주고 있었다. 두 지역의 시설오이 재배지에서 긴털가루응애에 의한 피해를 받은 농가의 특징은 대부분의 농가가 볏짚을 웃그름으로 사용하고 있었으며, 긴털가루응애는 볏짚에 의해 시설하우스로 이동한 것으로 판명되었다. 반면 볏짚을 사용하거나, 사용하지 않는 관행농가에서는 긴털가루응애의 발생과 피해가 없었다. 공주와 천안 시설오이 농가 중 피해가 심한 농가를 선정하여 긴털가루응애의 잎, 과실 피해와 볏짚, 잎에서의 발생밀도를 조사한 결과 공주의 농가에서는 잎 피해률이 9%, 과실 피해률이 3%, 오이 잎과 볏짚에서의 긴털가루이응애 발생밀도는 잎당 4.3마리, 10cm 길이의 볏짚 당 4.1마리였다. 천안의 농가에서는 잎과 과실 피해률이 각각 평균 13%, 5%였으며, 잎과 볏짚에서의 발생밀도는 평균 4.6마리, 4.7마리였다. 따라서 향후 친환경 시설오이 재배지에서 짚을 웃거름으로 사용할 때는 사전에 볏짚에 긴털가루응애의 발생유무를 확인 후 사용하는 것이 바람직할 것으로 사료된다.

검색어: 오이, 긴털가루응애, 코르크화, 과실 피해률, 볏짚

P068

중부지역 배과원 발생하는 잎말이나방 종류와 성충 발생소장

양창열, 김형환, 조명래, 김성종, 조경호, 최동로

농촌진흥청 국립원예특작과학원

중부지역 배 과수원에서 채집된 잎말이나방 종류는 애모무늬잎말이나방류(*Adoxpohyes* spp.), 사과무늬잎말이나방(*Archips breviplicanus*), 사과잎말이나방(*Hoshinoa longicellana*), 갈색잎말이나방(*Pandemis heparana*), 매실애기잎말이나방(*Rhopobota naebana*) 등이었으며, 애모무늬잎말이나방류가 82.3%를 차지하였다. 애모무늬잎말이나방(*A. orana*)의 암컷 성페로몬 성분은 *Z*9-14:OAc (80%)과 *Z*11-14:OAc (20%)이었으며 사과애모무늬잎말이나방(*A. paraorana*)은 *Z*11-14:OAc (97%)과 *Z*9-14:OAc (3%)이었다. 사과무늬잎말이나방의 경우에는 *E*11-14:OAc (70%)과 *Z*11-14:OAc (30%)를 성페로몬 성분으로 이용하는 반면에, 사과잎말이나방은 *Z*11-14:OAc (80%)과 *E*11-14:OAc (20%)이었다. 갈색잎말이나방은 3가지 성분(*Z*11-14:OAc, *Z*9-14:OAc 및 *Z*11-14:OH)을 95:3:2의 비율로 이용하였다. 성페로몬 트랩을 이용하여 수원지역에서 수컷 성충의 발생소장을 조사한 결과, 사과애모무늬잎말이나방의 발생 최성기는 5월 하순, 7월 상순, 9월 중순이었으며, 사과무늬잎말이나방의 경우에는 6월 상순과 7월 중순에 발생최성기를 보였다. 한편 사과잎말이나방의 발생최성기는 6월 하순과 9월 중순이었다.

검색어: 배, 잎말이나방, 성페로몬, 발생소장

P069

Damages in horticultural crops by *Tyrophagus putrescentiae*

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A storage mite (cheese mite), *Tyrophagus putrescentiae,* is known as the pest in storing grains and common health pest species in the dust around home. The mite directly affect our well-being as parasites, vectors of disease, and producers of allergens. But recently we found damages in horticultural crops especially in greenhouses. It is very difficult to diagnose the damage by the mite because of the tiny size of the mite. And the symptom is not clear at the beginning stage. In this study, observations were done on the mite and the crop damage symptoms in several horticultural crops under dissecting microscope and scanning electron microscope (SEM). The mite body size was 0.3~0.5㎜ and they had long hairs all around their body when observed under SEM. The characteristic damage symptoms in some horticultural crops are as follows. In phalaenopsis, the flower buds became yellow and the lower side of the leaves had white spots. The surface of young cucumber fruits became shiny and soft at the early damage stage. In the crops, the damaged surfaces became corky as the plants grew up. In peach tree, whole the trees lost vigor and flower drops were observed when the mite density was very high in greenhouse cultivation.

Key words: *Tyrophagus putrescentiae*, Symptom, Horticultural crop

P070

Pasteuria penetrans endospore attachment on root-knot nematode juveniles affected by temperature and nematicides treatments

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This study was conducted to evaluate the effects of temperature and nematicides on endospore attachment characteristics of 2 Korean isolates of nematode-parasitic bacteria, *Pasteuria penetrans*. *P. penetrans* CJ-1 and 98-35 isolates and 3 species of root-knot nematodes in U. of Florida were used ; *Meloidogyne incognita* (MI), *M. arenaria* (MA), and *M. javanica* (MJ). Three nematicide levels of 2, 4, and 6 ppm were compared by treating Vydate and Nemacur in the endospore containing soils.

The endospores were attached to the root-knot nematode juveniles by centrifugal method. Reproduction of the isolates was checked by observing root-knot nematode females harvested from inoculated tomato roots.

1. Among the two Korean isolates, 98-35 showed attachments to MI, MA, and MJ juveniles, but it could not reproduce in any species. CJ-1 reproduced on all the 3 tested root-knot nematode species.
2. Endospores pretreated in -14°C showed higher attachment rate than those pretreated in 4, 24, and 40℃.
3. Nemacur treatments significantly suppressed the attachment of the endospores to the juveniles, while Vydate treatment effects were negligible.

Key words: nematode-parasitic bacteria, *Pasteuria penetrans*, *Meloidogyne incognita*, *M. arenaria*, *M. javanica*

P071

이른 봄 지역적 나방 종 다양성 변화를 통한 기후변화 연구

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본 연구는 나방개체군의 일별 종다양성에 영향을 미치는 비생물적(abiotic) 요인을 알아보기 위하여, 전라남도 무안군 청계면에 위치한 승달산 지류에서, 2007년부터 2009년까지 4월3일부터 4월 30일까지 매일 채집을 실시하였다. 조사일은 총 84회 이며, 채집이 되지 않은 10회는 분석에서 제외하였다. 74회의 조사에서 나방은 총 4과 52종 686개체가 채집되었으며, 과별로는 밤나방과(Noctuidae)가 27종 85개체, 자나방과(Geometridae)가 23종 137개체, 쌍꼬리나방과(Epiplemidae)와 재주나방과(Notodontidae)가 각 1종, 463개체, 1개체로 나타났다. 우점종은 쌍꼬리나방과의 검은띠쌍꼬리나방(*Epiplema plagifera*)으로 463개체로 전체 개체수의 67.5%를 차지하였다. 채집된 종 가운데 singleton은 24종이며, doubleton은 8종으로 나타났으며 각 46%, 15%로 나타났다. 기상정보는 최고온도, 평균온도, 최소온도, 강수량, 평균풍속, 상대습도, 일사량, 운량을 이용하였다. 일별 출현 종수와 상관관계 분석결과 평균온도, 최고온도, 풍속, 상대습도, 일사량과 유의한 결과($p<0.05$)를 나타냈으며, 선형회귀분석결과 일별 최고온도만 유의함($F_{1,72}=11.947$, $p<0.005$)을 나타냈다. 나방의 활동에 가장 큰 영향을 주는 요인은 기온으로 볼 수 있으며, 기온이 상승하면 나방의 활동도 활발해진다. 기후변화로 인한 봄의 동식물상의 변화가 예상되며, 봄 개체군의 장기적인 조사는 변화경향을 제시할 것이다.

검색어: 나방, 다양성, 이른 봄, 기후, 최고온도

P072

한라산국립공원에 분포하는 나방의 종 다양성 및 고도별 분포 양상

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한라산국립공원에 분포하는 나방의 종 다양성 및 분포 양상을 알아보기 위하여 2009년 5월부터 10월까지 8개의 조사지점을 고도별로 선정하였다. 조사는 UV Light 트랩을 이용하여 매월 1회씩 실시하였다. 그 결과 총 13과 321종 4462개체가 채집되었다. 과별로는 자나방과 120종 2490개체, 밤나방과 123종 1102개체, 재주나방과 17종 219개체가 채집되었다. 월별로는 6월이 163종 2882개체, 7월이 121종 593개체, 8월이 102종 357개체가 채집되었다. 종별로는 털뿔가지나방(*Alcis angulifera)* 1322개체, 넓은띠담흑수염나방(*Hydrillodes morosa)* 395개체, 아지랑이물결가지나방(*Aethalura ignobilis)* 160개체 순으로 우점하였다. 고도별로는 636m지점이 116종 1038개체, 499m지점이 104종 753개체, 744m 지점이 111종 672개체로 채집되어 최저고도(264m)와 최고고도(1109m)의 중간 지점에서 종수와 개체수의 분포가 상대적으로 크게 나타났다. 또한 8개의 조사지점에서 종 다양성을 Fisher's Alpha로 분석한 결과는 264m에서 42.77, 1109m에서 29.47으로 고도가 낮을수록 종 다양성이 높게 나타났다. 조사지점을 사면별로 보면 남사면(264m, 499m, 636m, 953m)에서 243종 2691개체, 북사면 (701m, 744m 966m, 1109m)에서 215종 1771개체가 채집되었다. 두 사면간 종수(t-test, t=0.364, p=0.728)와 개체수(t-test, t=1.257, p=0.256)는 차이가 없었다. 고도간 나방군집 유사도를 Sørensen 지수로 분석한 결과 고도가 나방군집에 영향을 미치는 것으로 분석된다.

검색어: 나방, 종 다양성, 한라산, 고도, 사면

P073

Comparative Analysis of Benthic Macroinvertebrates in Lakes and Streams in Different Levels Disturbances

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Benthic macroinvertebrates are considered as a representative group in presenting ecological states and water quality in freshwater ecosystems. Although much study has been not conducted in stream, relatively few cases were comparatively reported in community responses to disturbances in lake and stream. Benthic macroinvertebrate were sampled in 12 lakes and 8 streams in different trophic and saprobic state. The sampled communities were accordingly grouped according to degree of disturbance. Species abundance distribution (SAD) was used for illustrating ecological states, and the fitness was accordingly checked with the proposed models. SADs were divided according to saprobic states in stream while SADs were clearly separated based on trophic levels.

Key words: benthic macroinvertebrate, species abundance distribution, trophic level, saprobic state

P074

꽃매미의 포도원에서의 산란 위치

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천안시 입장면에 위치한 두 곳의 포도원에서 꽃매미의 산란위치에 따른 난괴수를 조사하였다. 또한 합판과 부직포, 인삼용 차광천을 이용하여 인위적인 산란장소를 제공하여 경사유무, 차광 정도, 표면 특성에 따른 산란 정도를 조사하였다. 포도원 내부보다는 외곽에(F=1860.97, p<.0001), 수직보다는 경사진 곳에(F=1941.73, p<.0001), 포도나무보다는 시멘트 지주에(F=905.71, p<.0001), 노출된 곳보다는 식물체에 가려진 곳에(F=4785.73, p<.0001) 더 많이 산란을 하는 것으로 나타났다. 포도원 외곽에 위치하고 경사져 있으며 식물체로 가려진 시멘트 지주에서 평균 51.1개의 난괴가 발견되었으며, 수직이지만 식물체로 가려진 시멘트 지주에서도 평균 23.5개의 난괴가 발견되었다. 인위적인 산란장소를 제공한 실험에서도 차광정도(F=6.76, p=0.0026), 표면특성(F=66.76, p<.0001), 경사유무(F=7.98, p=0.0069)에 따라 산란된 난괴수에 유의한 차이가 존재하여 포도원에서의 결과와 동일하였으며 차광정도와 표면특성(F=4.45, p=0.0169) 그리고 표면특성과 경사유무(F=4.90, p=0.03160) 사이에는 유의한 상호작용이 존재하였다.

검색어: 꽃매미, 산란위치, 포도

P075

Spider Communities between Traditional farming and Environmental friendly farming in Rice fields

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Field survey was conducted to determine the differences of spider community between traditional farming and environmental friendly farming at 17 localities, Korea in 2008. In guild structure, The occupancy rate of pest group, general group and natural enemy group was 37.3%, 41.0% and 21.6% respectively in environmental friendly farming, and 36.9%, 35.6% and 27.5% respectively in traditional farming. Among natural enemy group, parasitoids and predators were 15.8% and 84.2% respectively in environmental friendly farming, and 28.1% and 71.9% respectively in traditional farming. Among natural enemy group, rice field spiders were 74.4% and 62.2% in environmental friendly farming and traditional farming respectively. Among predators, rice field spiders were 86.7% in environmental friendly farming and 84.9% in traditional farming. Rice field spider community comprises 28 species of 24 genera belonging to 10 families and 30 species of 24 genera belonging to 10 families in environmental friendly farming and traditional farming respectively. Dominant families were Lycosidae, Linyphiidae and Tetragnathidae and dominant species were *Pirata subpiraticus*, *Ummeliata insecticeps*, *Tetragnatha maxillosa*, *Gnathonarium dentatum* and *Packygnatha clercki* in both agricultural practices. The ratio of hunting spiders and webbing spiders was similar between agricultural practices.

Key words: spider, community, traditional farming, environmental friendly farming, rice field

P076

Temperature-dependent development of overwintered eggs of *Lycorma delicatula* (Hemiptera: Fulgoridae)

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We studied to develop a forecasting model to predict the hatching time of overwintered eggs of *Lycorma delicatula.* We collected overwintering egg masses on 1st February, 17th February and 4th March. After chilling them at 5℃ for 15 days, development of eggs was investigated at six constant temperature (35, 31, 27, 23, 19, 15℃). The hatching rate of egg was highest at 23℃ (87.88±19.32%) followed by 19℃ (87.71±21.47%), 27℃ (75.96±24.82%), and 31℃ (30.92±24.81%). Eggs did not survive at 35℃. The developmental duration of eggs was 39.47±2.24, 22.96±3.25, 17.56±1.58 and 12.15±6.29, at 19, 23, 27 and 31℃, respectively. The egg developmental rate was described with a linear model (eq. $Y=0.0034X-0.0364$ ($r^2=0.9649$)) between 19℃ and 31℃. The lower developmental threshold temperature was 10.71℃ and effective accumulated temperature for egg development was 286.40 Degree days.

Key words: *Lycorma delicatula*, egg development, lower developmental threshold

P077

갈색여치 분포의 과거, 현재, 미래

정명표, 방혜선, 김명현, 한민수, 강기경, 이덕배
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갈색여치는(*Paratlanticus ussuriensis*) 메뚜기목 여치과에 속하는 곤충으로 2001년 충북 충주 및 단양 지역의 과수농가에 피해가 보고된 이후로, 충북 영동 지역을 중심으로 해마다 지속적으로 발생하고 있으며, 2006년 및 2007년 충북 영동지역에 대발생하여 과수농가에 많은 피해를 주었다. 갈색여치와 같은 메뚜기목 곤충들이 대발생하여 농작물에 피해를 준 사례는 국내에서는 흔치 않아 갈색여치 방제에 어려움이 많기 때문에, 최근 국내에서 갈색여치의 생태 및 방제 방법에 대한 연구가 이루어지고 있다. 본 연구에서는 갈색여치의 과거 및 현재 분포 정보를 제공하고, 향후 갈색여치 분포를 예측함으로 해서 갈색여치 방제를 위한 기초 자료를 제공하고자 한다. 2001년도까지 보고된 자료에 따르면 갈색여치는 전국 41개 시군에서 발생이 보고되었다. 2006년부터 2009년까지 갈색여치 분포 조사 결과 경기도, 강원도, 충북, 경북 북부 지방을 중심으로 11개 시군에서 갈색여치 발생이 새롭게 확인되었다. 이 중 충북 영동, 옥천, 전북 무주, 전남 구례, 경북 문경, 강원 홍천 대관령 일대에서 많은 개체가 확인되어, 이들 지역은 갈색여치 피해위험 지역으로 판단할 수 있다. 갈색여치 분포는 활엽수 분포 지역과 상당히 밀접한 관계를 보였으며, 향후 지구 온난화에 따라 활엽수 분포 지역이 넓어질 것으로 예측되기 때문에 갈색여치의 분포 지역 또한 넓어질 것으로 예상된다.

검색어: 갈색여치, 분포, 활엽수, 지구 온난화

P078

Sensitivity of sympatric parasitoids of *Riptortus pedestris* (Hemiptera: Alydidae) to different temperature and relative humidity

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Ooencyrtus nezarae Ishii (Hymenoptera: Encyrtidae) and *Gryon japonicum* (Ashmead) (Hymenoptera: Scelionidae) are major egg parasitoids of *Riptortus pedestris* (Fabricius) (Hemiptera: Alydidae), a mobile pest on several crops in Korea and Japan. We compared the sensitivity of the two parasitoids to different temperature and relative humidity (RH) conditions to understand their phenological relations. Less than 6 hours old naïve female adult *O. nezarae* and *G. japonicum* were individually kept in 50 ml tubes without food and water sources. The tubes were placed in three humidity conditions (50-55, 70-75, and 90-95% RH) in desiccators. These desiccators were then maintained at 20, 25, and 30°C. In each temperature and RH combination 75-76 individuals were assessed for the mortality every 8 hours. *G. japonicum* was found to survive longer (37-116 hours) in all the temperature and RH combinations than *O. nezarae* (31-103 hours). Both the two parasitoids survived better in higher RH in all temperatures. The reduced sensitivity to lower humidity by *G. japonicum* compared to *O. nezarae* may explain the earlier occurrence of *G. japonicum* in the spring. The relations with seasonal occurrence of the two parasitoids were discussed.

Key words: *Ooencyrtus nezarae*; *Gryon japonicum*; survivorship; Encyrtidae; Scelionidae; mortality

P079

아스파라거스 해충 발생 및 피해양상

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아스파라거스(*Asparagus officinalis*)는 어린 순을 식용으로 이용하는 작물로 전국적으로 약 20ha면적에서 재배되고 있다. 현재 이 작물에 발생하는 해충에 대한 연구가 미비하여 농가에서 방제에 어려움이 있다.

2007년부터 제주시 애월과 오등동, 서귀포시 동홍동의 시설 아스파라거스 재배원에서 조사를 수행한 결과, 파총채벌레(*Thrips tabaci*), 담배거세미나방(*Spodoptera litura*)과 파밤나방(*S. exigua*), 아스파라거스잎벌레(*Crioceris asparagi*), 달팽이류가 아스파라거스 재배에 가장 문제가 되는 해충이었다.

아스파라거스에 발생하는 총채벌레종류는 파총채벌레로, 전시기에 발생하나 봄 수확기에 밀도가 낮게 유지되다가 6월 입경이후 밀도가 급증하는 경향을 보였다. 피해는 봄 수확기에는 순의 탈색 및 곡경을 유발하였고, 입경 후에는 잎과 줄기에 다량의 흡침자국을 만들고 병 발생을 심화시켰다. 나방류 해충으로는 파밤나방과 담배거세미나방, 왕담배나방(*Helicoverpa armigera*), 네눈쑥가지나방(*Ascotis selenaria*), 도둑나방(순으로 많이 발생하였고, 이 중 파밤나방과 담배거세미나방은 매년 8월 이후 가을철에 다량 발생하는 양상을 보였다. 피해증상은 줄기의 표면이나 잎을 갉아먹었다. 봄 수확기에 문제가 되는 해충으로 아스파라거스잎벌레와 달팽이류가 있다. 아스파라거스잎벌레는 순의 잎 비늘 사이에 주로 산란하였고, 부화한 약충과 성충이 모두 가해하였다.

검색어: 아스파라거스, 해충, 발생양상, 피해

P080

Sexually dimorphic male horns and their use in agonistic behaviors in the horn-headed cricket *Loxoblemmus doenitzi*(Orthoptera:Gryllidae)

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Sexual dimorphism, the difference between sexes in secondary sexual characters, is in general driven by processes of sexual selection. The horn-headed cricket, *Loxoblemmus doenitzi*, exhibits sexual dimorphism in head shape, in which males have flat heads and triangular horns on both sides of their heads, whereas females have rounded heads and no horns. We hypothesized that male horns have been evolved due to intra-sexual selection in which males use these horns as weapons in aggressive interactions. To test this hypothesis, we conducted agonistic trials of field-caught males in *L.doenitzi*. Horn length was significantly correlated with thorax length and hind femur length. During agonistic males aggressively used their horns by beating the opponent's horns with their horns or by poking the opponent's body with their horns. However, the result of logistic regression analysis revealed that horn length or horn point frequency were not significant factors for contest outcome. Instead, body size was significant for determining contest outcome.

P081

Agonistic interactions between nymphs of the lantern fly, Lycorma delicatula (Hemiptera: Fulgoridae)

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The nymphs of the lantern fly, *Lycorma delicatula*, typically aggregate on tree branches for feeding. We studied the agonistic interactions between nymphs in the field and investigated the effects of residence and size asymmetries on contest outcome. Resident nymphs took positions and engaged in feeding on tree branches, whereas intruding nymphs moved along tree branches. When intruders approached, residents typically raised their front legs as a threat sign. Intruders would decide to either move away or palpate residents, and residents often lowered their position when palpated. Then, intruders would attempt to shake residents back and forth, and the number of attempts varied from once to several. Residents either maintained its position or fled away. After a contest, the winner was determined as the one which occupied the position it fought over. Resident nymphs won 84.2 % of the agonistic encounters, and nymphs with bigger body size won 63.2 % of the agonistic encounters. The result of the logistic regression analysis revealed that residence was a significant factor for contest outcome, but body size was not.

P082

시화호 주변 곤충 비오톱의 장기 모니터링에 관한 연구

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방조제 건설에 의한 인공호수이자 기수호인 시화호는 면적 43.80㎢에 달하며, 행정구역상 경기도 시흥시, 안산시, 화성시에 걸쳐 있고, 지리적으로 위도 37° 11' - 37° 20', 경도 126° 34' - 126° 50' 에 포함된다. 기후조건은 연평균기온 11.9℃, 연평균강우량 1,252.3mm, 연평균상대습도는 72.8%이다. 본 연구는 시화호 주변지역의 육상곤충 비오톱 6곳에서 2005년 4월부터 2009년 9월까지 매년 주간 4회, 야간(6월) 1회 조사를 수행하여 5년간 총 25회 조사하였다. 주간조사는 전 지역에서 실시하였으며, 야간조사는 음도(INS-3)지역에서 시행하였다. 조사결과 2005년 10목 76과 255종, 2006년 10목 83과 273종, 2007년 13목 86과 282종, 2008년 13목 110과 354종, 2009년 12목 107과 338종이 출현하며 지속적으로 종다양성이 향상되는 양상을 나타냈으나 2009년 최초로 감소하였다. 목별 우점도는 1차년도 최우점 목이던 파리목의 우점도가 24.71%에서 14.79%까지 지속적으로 감소하였으며, 딱정벌레목의 경우 8.63%에서 17.46%로 두드러진 증가 추세를 나타냈다. 지역별로는 당재(INS-6)지점의 다양도가 가장 높아졌으며, 방아머리나루터(INS-7)지역은 개선이 필요한 것으로 나타났다. 전체적으로 교란에 강한 파리목의 우점도가 감소 추세를 보이는 것을 볼 때 환경이 점차 개선되고 곤충 개체군도 안정되어가는 것으로 사료된다. 또한 경기 서북부 국지종인 큰주홍부전나비가 당재(INS-6)지점에서 발견되어서 서식지 보호가 필요한 것으로 사료된다.

검색어: 시화호, 비오톱, 곤충상, 장기 모니터링

P083

Temperature-Dependent Development of *Maruca vitrata*, and Estimated Adult Occurrence Time in A Red Bean Field

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The legume pod borer, *Maruca vitrata* (Fabricius) (Lepidoptera: Crambidae) causes serious damage to some legume crops of genus *Vigna* and *Sesbania* in Korea. In the current study, laboratory studies on the temperature-dependent development of the insect were performed at 8 constant temperatures ranging from 13℃ to 34℃ at 3℃ intervals. Lower developmental threshold (LDT) for eggs, larvae, and pupae were calculated as 10.0, 12.5 and 13.3℃, respectively, using the linear-regression equations of the developmental rates. Degree-days required to complete a stage were estimated as 48, 187, and 94, for egg, larval, and pupal stages, respectively. The larvae couldn't survive at 13 and 16℃, and the larval survival rate was the highest at 28℃. The egg hatching rate was the lowest at 13℃. In the adult stage, the pre-oviposition period was the shortest at 22℃, and the total egg number was the most with ca. 500 at 25℃. Degree-days for the stages of 1st-4th larval instars, egg, and adult emergence-50% oviposition were calculated during the reproductive development season of red bean using single sine method and Suwon weather station data based on LDTs, respectively. Finally, the adult occurrence time was estimated after the degree-days were cumulated reversely from the distribution data of larval stages observed in a red bean field.

Key words: *Maruca vitrata*, temperature-dependent development, linear regression model, lower development threshold, degree-day, estimation for field occurrence

P084

Development of the Perilla Leaf Pyralid Moth, *Pyrausta panopealis* (Lepidoptera: Pyralidae), at Different Temperatures and Test of Larvicidal Effect of Some Commercial Natural Products

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The perilla leaf pyralid moth, *Pyrausta panopealis* Walker (Lepidoptera: Pyralidae), is a serious pest damaging to leaf perilla. In order to establish the life parameters of P. panopealis for eventual purpose of control, the developmental span of each stage were investigated under five temperature regimes (20℃ ~ 3 0℃). In addition, the larvicial efficacy of several on-the-market environment-friendly agricultural materials (EFAMs) was tested. The width of head capsule at each larval stage measured to be the mean of 0.21, 0.32, 0.47, 0.64, and 0.98 mm, respectively. The larval period of *P. panopealis* was longest at 20ºC as 27.0 days and shortened as temperature goes up to 30ºC as 11.3 days. Survivorship of the larval *P. panopealis* was the highest at 30ºC as 80%, whereas that of other temperatures ranged from 40% (20ºC) to 62.5% (27.5ºC), indicating that the *P. panopealis* appears to favor higher temperature. In addition to larval period, the duration of egg, prepupa, and pupa stages also shortened as temperature goes up, whereas the duration of adult stage increased as temperature goes up: from 4.1 days at 20 ºC to 6.1 days at 30ºC. After the perilla leaf pyralid moths were successfully stabilized in indoor environment the larvicidal efficacy of the ten EFAMs that were previously selected from the result of other moth species was tested aimed at 4th instar larvae for 48 hrs. Seven of the ten tested showed more than 90% of mortality within 12 hrs and reached nearly up to 100% within 24 hrs, but the remaining three showed less than ~70%.

P085

Mitochondrial DNA Sequence Variation of the Rice Leaf Roller, *Cnapahalocrocis medinalis* (Lepidoptera: Pyralidae) and Structural Analysis of the A+T-rich Region

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The rice leaf roller, *Cnaphalocroci smedinalis* Guenée (Lepidoptera: Pyralidae) is a leaf-feeding pest of rice world-widely distributed. For better understanding of the pest insect, geographic sequence variation of the species were performed using the mitochondrial A+T-rich region, with the samples collected from seven Korean and six Chinese localities. A total of 94 haplotypes obtained from 187 individuals showed the length variation, ranging from 339 bp to 348 bp. The maximum divergence of 4.57% appears to evidence a substantial sequence variation, indicating the applicability of this molecular marker to the study of geographic variation. Overall, a high per generation migration ratio (Nm = 3.67742 ~ infinite), a low level of genetic fixation (F_{ST} = 0 ~ 0.11969), and no discernable isolated population were noted in the most *C. medinalis* populations. AMOVA analysis to find out allocation of genetic variability of *C. medinalis* populations has shown allocation of majority of variation to the within-population, rather than among-populations and between-region, suggesting that the *C. medinalis* populations in both China and Korea are largely well connected. This result is consistent with current knowledge of the dispersal ability of the species. The structure analysis of the A+T-rich region has shown that the typical structural elements found in other lepidopteran insects also is well preserved in the *C. medinalis* A+T-rich region (i.e., a poly-T stretch and a microsatellite-like A/T repeat).

P086

허브식물에서 발생하는 수종의 해충 보고

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최근 허브식물는 기능 및 건강식품으로 각광받고 있는 식품 제조 원료로 사용되고 있으나, 소면적 작물로 그동안 허브 병해충에 대한 기존 자료가 부족한 상태이다. 이에 고품질 허브생산을 위해 요구되는 해충 종합관리체계를 구축하기 위한 사전조사로 허브에 발생하는 해충의 종류 및 발생소장이 규명되어야 한다. 이에 준고냉지에 20종의 허브식물을 식재하여 해충발생 특성을 2008년과 2009년 2년간 육안조사한 결과를 아래와 같이 보고하고자 한다. 발생한 해충은 총채벌레목 1종, 노린재목 4종, 매미목 4종, 나비목 8종, 딱정벌레목 1종, 파리목 1종, 거미강 1종, 기안목 1종 등 총 21종이었다. 허브식물별 해충발생수를 조사하였을 때, 바질 8종, 페퍼민트와 레몬밤, 7종, 세이지, 로켓샐러드 6종, 배초향, 구절초 5종, 벨가못, 펜넬, 한련화 3종, 로즈마리, 오레가노, 백리향 2종, 라벤더, 케모마일, 에키네시아, 고수, 쳐빌, 로즈제라늄 1종이었고, 노지에서 재배할 경우는 피해 해충 종수는 더욱 감소하였다. 해충피해가 발생하지 않은 허브식물은 재배환경에 따라 다르게 나타났다. 비가림하우스에서는 마조람 1종에서, 노지에서 재배한 허브식물에서는 라벤더, 케모마일, 오레가노, 마조람, 백리향, 에키네시아, 고수, 로즈제라늄에서는 해충 피해가 발생하지 않았다. 이후 해충발생특성 및 피해정도에 대한 지속적인 조사가 요구되며, 이러한 자료를 기반으로 해충방제체계를 구축하여 농가의 안정적인 생산을 유도하여야 할 것이다.

Key words: 허브식물, 준고냉지, 해충 발생 특성

P087

Age-specific population dynamics of cottony cushion scale, *Icerya purchasi* (Hemiptera: Margarodidae), in citrus orchards in Jeju, Korea

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The cottony cushion scale, *Icerya purchasi* Maskell (Hemiptera: Margarodidae), is a destructive pest on citrus. This study was conducted to obtain the stage-specific phenology of *I.purchasi* for use in field application. The crawlers (hatched nymphs) from the egg sac of overwintered female began to move from late May and peaked in early to mid-June with most crawlers completed the movement till late June. The 1st nymph population peaked in mid June in 1stgeneration and early October in 2ndgeneration. The 2nd nymphs showed peak activity in late July and late October during the 1st and 2nd generation, respectively. The 3rd nymphs peaked in early September in 1st generation, while it kept a plateau without forming a peak after mid October in 2nd generation. The 1st generation adults peaked in mid September, and the tail was overlapped with 2nd generation adult population. Consequently, two life cycles were competed in Jeju area. An average of 20.7% of citrus orchards was infested with *I. purchasi* with a 3.9% of mean infested trees in Jeju. The present results should be useful in establishing management strategies for *I. purchasi* in citrus orchards.

Key words: Citrus pest, Age-structure, Crawlers, Fecundity, Hatching frequency

P088

애넓적밑빠진벌레의 연간 생활사 구명

장용석, 강성혁, 김수빈, 송상헌, 양지순, 송진영, 김동순
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애넓적밑빠진벌레(*Epuraea domina* Reitter)는 딱정벌레목(Coleoptera) 밑빠진벌레과(Nitidulidae) 속하는 곤충으로 감귤에서는 개화기 성충이 꽃에 모여 꽃잎과 암술을 먹고 자방에 상처를 내어 과실의 표면에 긁힌 자국의 콜크화 피해를 유발하는 해충으로 알려져 있다. 본 연구는 애넓적밑빠진벌레의 연중 생활사를 구명하고자 2009년 5월부터 2010년 4월까지 제주도 감귤원에서 성충 및 알, 번데기 등의 발생 동태를 조사하였다. 애넓적밑빠진벌레 성충은 낙과되어 반부패된 감귤에서 주로 발견되었으며, 5월 중순경 감귤개화기에 개화한 꽃으로 유인되어 발생한 후 6월에서 10월 중순까지는 낙과과실 등 주요 서식처에서 발견되지 않았고 10월 중순이후부터 낙과 감귤에서 다시 발견되기 시작하였다. 이때 발생한 성충은 초겨울(12월 초순)부터 토양에 산란을 시작하였으며 최고 산란 시기는 12월에서 2월경이었고 4월 상순까지 산란이 관찰되었다. 겨울철 낙과감귤에서 발육한 유충은 4월 상순부터 토양에서 번데기로 되었으며 4월 하순경부터 성충으로 우화하였다. 항온조건인 12℃와 25℃에서 산란 여부를 조사한 결과 두 온도 조건에서 산란이 가능하였으며, 25℃에서 산란수가 약 3배 많았고 산란기간은 짧았다.

검색어: 애넓적밑빠진벌레, 감귤, 생활사, 우화, 산란

P089

제주도 수서곤충류의 분포와 군집 분석

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제주도 지역 화구호를 비롯한 담수습지 24곳 습지에 서식하고 있는 수서곤충의 분포와 군집의 특성에 대해 분석한 결과 총 7목 31과 68속 92종 3327개체가 출현하였다. 조사지 중 가장 다양한 종이 출현한 장소는 동백동산못 50종이었다. 국내 최대형종 수서곤충이며 멸종위기동물인 물장군은 저지대 6곳에서 출현하였고 한국미기록과 곤충인 Hydrochidae의 *Hydrochus japonicus* Sharp는 이번에 조사지 6곳에서 확인되었다. 이와 함께 지금까지 국내에 보고 되지 않았던 노린재목의 Omaniidae *Corallocoris*의 1개체가 1100습지에서 확인되었다.

조사지간 유사도를 분석한 결과 유사도가 0.19인 사라악과 백록담의 거리가 가장 가까운 것으로 나타났고 유사도지수가 1이내에서는 크게 12개의 군집으로 구별되었는데 대다수가 해발고도가 유사한 조사지별로 유사한 그룹을 형성하고 있었다. 한편 걸월이못 등 5개 지점은 다른곳과는 거리가 멀게 나타나 독자적인 수서곤충군집 특성을 가지고 있는 것으로 나타났다. 우점도 등 군집지수에 대해 강, 하천, 계곡, 늪, 농경지 등 그 동안 이루어져 왔던 다른 곳의 습지와 비교하여 본 결과 우점도는 다소 낮은편이었고 종 풍부도는 아주 높은 편이었으며 균등도 지수는 높은 편이었다. 반면에 종 풍부도와 상대 밀도는 비교 자료가 없었다.

검색어: 제주도, 우점도, 종 다양도, 노린재목, 딱정벌레목

P090

Utilization of Trap for Efficient Management of Cryptic Mealybug, *Pseudococcus cryptus*, in Citrus Orchards, Jeju

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The males of cryptic mealybug, *Pseudococcus cryptus*, were attracted on trap baited with or without a synthetic sex pheromone. The attractiveness of sex pheromone trap was higher than yellow-color sticky trap, but both phenologies were similar. There was a positive relationship between mean density of 2nd nymph to adult cryptic mealybug and the density of the male caught on trap. The density of cryptic mealybug per tree was higher correlated with yellow-color sticky trap than sex pheromone trap. The pattern of cryptic mealybug male occurrence had two to three cohorts in a generation resulted from overwintering stage. The maximum occurring time of 1st to 2nd nymph stage could be estimated from the peak time of trap catch by effective temperature accumulation. The higher and lower threshold temperature was estimated as 10.9 and 32.6℃, respectively and its thermal constant was 360 degree-day. The cryptic mealybug parasitoid, *Anagyrus* sp., which was first recovered in Jeju in 2009, was well attracted on yellow-color sticky trap. There was a high correlation between the density of *Anagyrus* sp. and of cryptic mealybug males caught on trap.

Key words: *Pseudococcus cryptus*, sex pheromone, trap, monitoring, *Anagyrus* sp.

P091

Density and infection rate of Malaria vector mosquitoes from 24 sites in Gyeonggi and Gwangwon province and Incheon city, malaria epidemic areas, the Republic of Korea, 2009

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Density of malaria vector mosquito was monitored at 24 sites in Korea to estimate malaria epidemic from 2004 to 2009. Twenty four locations include six in Gwangwon province and nine in Kyonggi province and nine in Incheon metropolitan city. Mosquitoes collected by public health centers in 24 sites were sent to each RIPHE(Research Institute of Public Health & Environment) then the RIPHE identified the malaria vector mosquitoes. KCDC analysed the results. Number of malaria vector mosquito collected in 2009 shapely decreased over 33 % when compared with number of mosquito collected from 2004 to 2009.

In 2009, malaria vector mosquitoes firstly were collected at Injegun on 2nd week of April (6-13, April) and the highest peak of collected mosquito was demonstrated on 3rd week of August. Number of collected mosquito sharply decreased below 10 at 3rd week of september and None of mosquito was collected 2nd week October.

Decrease of number of malaria vector mosquito collected in 2009 seem to be related with lowest temperature around midnight and precipitation days per month.

Key words: vector mosquitoes, malaria, temperature, precipitation days, the Republic of Korea

P092

Effect of Temperature and Host Stage on Performance of *Aphelinus varipes* Parasitizing the Green Peach Aphid, *Myzus persicae*

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Developmental time, mummification, pupal mortality, sex ratio of a South Korean strain of *Aphelinus varipes* Förster parasitizing the green peach aphid, *Myzus persicae* were studied at 20, 25 and 30℃ in controlled climate cabinets. Plastic container with sweet pepper(*Capsicum annuum* L.) were used as experimental units. Green peach aphid in different larval instars and as adults, reared at the three different temperatures, were presented to *A. varipes* in a 'no-choice' and 'choice' situation for 6h. These presentations were done at 25℃ in each experiment to avoid an influence of temperature on parasitization rate. In case of no-choice test, more 1st(24%), 2nd(22%) and 3rd(38%) instar aphids were parasitized than 4th(14%) instar and adult(10%) among the aphids reared at 25℃. In case of choice test, more 1st(41%), 2nd(42%) and 3rd(29%) instar aphids were parasitized than 4th(13%) instar and adult(0%) among the aphids reared at 25℃. Pupal mortality of the parasitoid was not influenced by temperatures. The sex ratio of *A. varipes* was male-biased, and varied between 49.4% females developed from aphids reared at 30℃ and 42.8% from aphids reared at 20℃. The sex ratio was not significantly influenced by host stages. The developmental time of *A. varipes* parasitizing the green peach aphid ranged from 26.1days at 20℃ to 11.1days at 30℃.

Key words: *Aphelinus varipes*, Performance, Parasitoid, *Myzus persicae*

P093

파프리카 품종별 복숭아혹진딧물의 생물학적 특성 및 섭식행동차이 비교

윤규식, 강민아, 권혜리, 박민우, 강은진, 서미자, 유용만, 윤영남
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파프리카 품종별 복숭아혹진딧물의 기주섭식 행동패턴과 생명표작성을 통한 생물학적 특성차이를 비교하기 위해, 현재 시판되고 있는 파프리카 4품종(그린에이스, 오로벨, 퍼플, 스마트 고추)에서 복숭아혹진딧물(*Myzus persicae*)의 생식개시일, 수명, 생식일, 총 산자수, 평균세대기간(Tc), 순증가율(R0), 내적자연증가율(rm)을 25±℃, 상대습도60-70%, 광주기16L:8D 조건에서 조사하여 생명표를 작성하고 EPG기술을 이용하여 섭식행동의 차이도 비교하였다. 파프리카 품종간 복숭아혹진딧물의 수명은 17.2~17.7일, 생식일은 11.9~12.4일, 총 산자수는 42.6~45.3마리, 내적증가율에서0.364~0.365로 품종 간에 차이는 있었으나 통계적으로 유의하지 않았지만, 생식개시일, 평균세대기간(Tc), 순증가율(R0)은 오로벨에서 각각5.6일, 10.29일, 42.86마리였고 그린에이스에서는 각각6.6일, 10.46일, 45.27마리로 품종간 차이가 확인되었다. EPG를 이용한 체관부 섭식시간 분석에서 첫 번째 탐침시간은 158~386초, 총 구침을 빼고 있는 시간은 6675~7096초, 체관부 섭식횟수는 7.67~8.33회, 총 체관부섭식시간에서 9116~10871초로 품종간 차이는 있었으나 통계적으로 유의하지 않았지만, 탐침횟수, 구침활성시간, 첫 번째 체관부섭식시간은 오로벨에서 17.67회, 714초, 639초였고 그린에이스에서는 31.33회, 1460초, 1426.33초로 품종간 차이를 보이는 경향을 나타냈다.

검색어: EPG, 복숭아혹진딧물(*Myzus persicae*), 파프리카, 품종, 생식개시일, 수명, 생식일, 총 산자수, 평균세대기간(Tc), 순증가율(R0), 내적자연증가율(rm)

P094

Economic Injury Level of *Bemisia tabaci* Infesting Greenhouse Tomato

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Economic injury level was estimated for the sweetpotato whitefly, *Bemisia tabaci* on greenhouse tomato (*Lycopersicon esculantum* cultivar pinktop). In the greenhouse, seedling tomato transplanted at mid-April and inoculated *B. tabaci* at late-April with the densities of 0, 1, 3, 9, 27, 54, 108 and 216 per plant. Only 108 and 216 inoculation densities increased until mid-July. Total weight of fruits was not showed the differences by initial whitefly density; however, the total weight of marketable fruits decreased significantly among plots by higher initial whitefly density. The rates of yield loss increased with increasing whitefly density, resulting in 8.3, 14.0, 29.7, 29.7, 25.7, 40.4, and 69.4% reduction in each of the plots, respectively. The relationship between initial whitefly densities and yield losses was well described by a linear regression, $Y= 18.09X+6026.5$, $R^2=0.8504$. Based on the relationship, the number of adults per plant which can cause 5% loss of yield was estimated to be approximately 17.

Key words: Economic injury level, Sweetpotato whitefly, *Bemisia tabaci*, Yield loss

P095

Distribution and Damage induced by Population Densities of sweetpotato whitefly, *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Tomato

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Insect pest may move to near area to forage the food by adverse changes of their environments. Understanding these behaviors of searching the host will be helpful for further control. This study was performed to investigate the host preference and distribution of *B. tabaci* in a host plant when they needs. Once entered an area including hosts, *B. tabaci* will select a host rather than non-host and stayed for living. Dispersal within a niche (in a whole plant), *B. tabaci* was observed in lower part in tobacco and middle in tomato when seedlings, but they dispersed throughout the whole fully grown tomato plants with irregular inclined to the under, outer stretched leaves. *Bemisia tabaci* was also caught massively in yellow sticky traps in height of 30 cm above soil, and 30 cm above a plant. There was no attraction effect by flower model traps and fly catcher. When introduced with different densities (0, 10, 50, 100, 200, and 400) in square cages, the *B. tabaci* do damaged at the densities of 200 with mild and 400 with severe symptom on plants in two weeks and four weeks after inoculation.

Key words: Damage, Population density, Sweetpotato whitefly, *Bemisia tabaci*

P096

A Long-Term Comparative Study on Macrolepidoptera Diversity in Three Types of Vegetations from Worak-san [Mt.] in 2009

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With the help of KLTER/ME and KLPS in Woraksan, we have surveyed monthly diversity and seasonal prevalence of Macrolepidoptera in Wol-ak-san [Mt.] for the period of five months from May to September since 2005. Since 2007, to reduce variation, we chose two monitoring points, instead of one, for each of the three representative vegetations: *Quercus mongolica*-, *Quercus variabilis*- and *Pinus densiflora*-formations, abbreviated as QM, QV and PD, respectively, and collected exclusively larger moths with bucket-type of light traps for quantified survey. In 2009, as a result, QV showed higher species diversity and specimen number than QM or PD although the differences between QV and QM are subtle. The number of individuals collected may not be a good indicator, e.g., *Idaea biselata* collected in QM in June was over 200 in 2007, which is more than twice the number of specimens in all other sites per month, while the number in 2008 was dropped to only 10 specimens. In 2009, they became a dominant species again, showing biennial dominancy trend. It also seems that we are experiencing major decline of specimen numbers: 651 specimens collected in 2009 while 874 specimens collected in 2008, which was already a big reduction compared to over 2500 specimens in 2007.

Key words: Mt. Worak, Macrolepidoptera, biodiversity monitoring

P097

수출 선인장 주요 해충 발생정도 및 피해양상

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선인장은 대표적인 수출작목으로 선인장에 발생하는 해충의 효율적인 관리를 위해 2008년 10월부터 2009년 9월까지 수출 선인장 주요재배지인 고양에서 해충의 발생정도와 피해양상을 조사하였다. 비모란과 삼각주에 발생하는 해충은 담배거세미나방, 파밤나방 등 나방류, 작은뾰족민달팽이, 명주달팽이 등 달팽이류와, 귤가루깍지벌레, 꽃노랑총채벌레, 복숭아혹진딧물, 온실가루이 등이었다. 특히, 비모란에는 나방류, 삼각주에는 나방류와 민달팽이류가 주요 해충이었다. 해충 종류별 피해양상을 보면 담배거세미나방은 선인장을 갉아먹었으며, 작은뾰족민달팽이는 표면을 핥는 듯이 가해하여 엷게 코르크화되고 피해부 주위에 달팽이 점액이 묻어 있었다. 귤가루깍지벌레는 선인장 표면에 하얀 가루가 묻어 있는 듯하고, 꽃노랑총채벌레는 흡즙하여 표면에 긁힌 흔적을 볼 수 있었다. 복숭아혹진딧물은 수액을 빨아 가해하였으며 선인장에서 나타나는 피해는 고사보다는 이차적인 그을음증상이었다. 이상의 연구결과 선인장재배시 발생하는 해충의 피해진단은 가능하였으나 효과적인 방제를 위한 약제가 등록되어 있지 않아 향후 방제약제 등록이 절실히 요구된다.

검색어: 선인장, 비모란, 삼각주, 담배거세미나방, 작은뾰족민달팽이

P098

침투성 약제의 근부처리를 통한 착색단고추의 해충 방제

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착색단고추의 중요 해충에 대한 침투성 약제의 근부처리 효과를 검증하기 위하여, 경상대학교 농장 온실에서 약제선발실험을 실시하였다. 착색단고추의 플러그묘를 큐브로 이식할 때, 큐브당 침투성 약제(이미다클로프리드, 치아메톡삼, 디노테퓨란, 아세타미프리드)의 입제를 큐브당 2g, 1.5g, 1g씩 각각 6반복 처리한 후 정식하여 착색단고추에 발생하는 진딧물류, 총채벌레류, 가루이류의 밀도 변화 및 약해 유무를 조사 하였다. 그 결과 큐브 당 처리약량 2g에서는 약해가 경미하게 발생하였으나 처리약량 1.5g과 1g처리구에서는 약해도 없고 약효도 뛰어났다. 특히 이미다클로프리드와 치아메톡삼이 효과가 좋아 농가에 적용 한다면 직접적인 효과를 볼 수 있을 것으로 생각되었다. 큐브 당 1.5g과 1g을 처리하여도 약해도 없고 효과가 좋았으나 보다 안정적인 착색단고추 재배를 위해서 큐브 당 입제 1g을 처리약량으로 선정하여 진주시 대곡면에서 농가실증실험을 실시하였다. 그 결과, 해충이 충분히 유입될 수 있는 환경을 유지했던 경상대학교 농장의 온실에 비해 대곡의 실험농가에서는 담배가루이만 주로 발생하였으며, 무처리구와 농가의 관행 약제처리구에 비해 이미다클로프리드 근부처리구에서 담배가루이의 약충, 성충 모두에 대하여 방제효과가 뛰어나고 약해도 없는 것을 알 수 있었다.

검색어: 착색단고추, 근부처리, 담배가루이, 이미다클로프리드, 치아메톡삼

P099

Bionomics of *Diadromus sp.* (Hymenoptera: Ichneumonidae), an internal and solitary pupal parasitoid, and the characteristics of its parasitism on diamondback moth, *Plutella xylostella* (L.)

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Diamondback moth (DBM, *Plutella xylostella* L.), the most destructive pest of cruciferous crops, is well-known as typical subtropical insect pest. A number of biological agents such as diseases, parasites and predators can affect populations of DBM in the fields negatively. In previous reports, we suggested *Cotesia glomerata, Diadegma semiclusum,* and *Microplitis plutellae* as promising natural enemies to DBM control at highland areas, but these species are larval parasitoids. In 2004~2009, we searched highland fields cultivating various cruciferous crops for PUPAL parasitoids which can supplement the unsatisfactory parasitism in the augmentative release of larval parasitoids. We obtained adults of hymenopteran parasitoid from DBM pupae in early July at Hoengseong region (asl 540 m), and then identified as *Diadromus sp.*, although being a critical species so far. This parasitoid showed high rate of parasitism, about 13.2%, in mid October at the same region. Development period from oviposition to emergence of *Diadromus sp.* ranged from 14 to 18 days under 23℃ condition. Adult longevity, > three weeks, was longer when it was provided with 10% sugar solution as food than with water only or without food. Male adults mated as soon as emerging from parasitized DBM pupae, and laid eggs into DBM pupae for a week. Parasitism by *Diadromus sp.* was highest on 7th day after emergence. In contrast, lethality of DBM pupae which were not parasitized by wasps showed 60% on average for seven days. Parasitized DBM pupae could be stored at 10℃ for two weeks. The simultaneous augmentative release of larval parasitoids and pupal parasitoids can be an important component to integrated DBM management program in the future.

Key words: pupal parasitoid, *Diadromus sp.*, parasitism, longevity, *Plutella xylostella*

P100

Biochemical and molecular diagnosis of Insecticide resistance conferred by esterase and MACE based mechanisms of the *Myzus Persicae* (Hemiptera: Aphididae)

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The green peach aphid, *Myzus persicae* (Sulzer), is one of the most serious pest in cabbage cultivation. Field survey was carried out to know the insecticide resistance levels in five main cabbage cultivation regions (Pyeong-chang, Hong-cheon, Bong-wha, Mu-ju and Je-ju) in 2009. The green peach aphid can resist a wide range of insecticides in five surveyed local populations. Among the nine tested insecticides, four chemicals (methomyl, bifenthrin, pymetrozine and flonicarmid) showed less than 50% mortality in the recommended concentration in all populations. Multi resistant (MR) strain was selected from these populations and esterase over-expression, modified AChE (MACE) and mutation(s) in para-type sodium channel were analysed using native IEF and quantitative sequencing with five local populations. Esterase over-expression and MACE (StoF mutation) were observed in all populations including MR strain. LtoF mutation is well known as a *kdr* mutation in para-type sodium channel. However, even though LC_{50} values of MR strain noted over 2,000 times higher than that of susceptible strain against bifenthrin, any mutation was not detected in para type sodium channel and also local populations. These results suggested that unusual case could be existed in pyrethroid resistance mechanism in green peach aphid.

Key words: green peach aphid, *Myzus persicae* (Sulzer), insecticide resistance, esterase over-expression, modified AChE (MACE)

P101

미생물살충제 (뷰베리아바시아나) 활용을 위한 환경조건

박종호, 윤여준, 한은정, 홍성준, 김용기, 지형진
국립농업과학원 유기농업과

유기농 토마토 시설재배에서 온실가루이가 대량 발생하지만 친환경적인 방제 방법이 부족한 상황이다. 온실가루이 방제를 위하여 곰팡이(뷰베리아바시아나)를 원료로한 미생물 살충제가 개발되어 있으나 현재 국내에서는 효과적인 활용 기술에 대한 자료가 부족하여 미생물 살충제의 현장 활용이 미미한 상태이다. 미생물 살충제로 사용되는 뷰베리아바시아나의 생육과 곤충에 대한 감염은 온도와 습도에 영향을 받는다. 상용화된 두 가지의 미생물제에서 원균주를 순수분리하여 PDA 배지에 15℃, 20℃, 25℃, 30℃, 35℃에서 배양하여 균사의 생장을 확인한 결과 25℃까지 생육속도가 증가했으나 이후 30℃부터 감소하여 35℃에서는 거의 성장을 하지 못했다. 온실가루이에 대한 미생물제(뷰베리아바시아나)의 효과를 습도조건을 달리하여 검사한 결과 포화습도에서 100% 65.5%의 감염살충률을 보여주었던 두 제제가 60%의 상대습도에서는 10%미만의 감염 살충률을 보여주었다. 온도와 습도가 다른 온실가루이가 발생한 토마토 두 하우스에서 곰팡이성 미생물제의 효과를 비교하였을때 높은 습도와 30도 미만의 최고온도를 보인 온실에서는 미생물제가 온실가루이에 대해 81.4%의 감염률을 보였으나 낮은 습도와 높은 최고온도를 보인 온실에서는 감염된 온실가루이를 발견하지 못했다.

검색어: 미생물살충제, 토마토, 온실가루이, 뷰베리아바시아나

P102

조선왕조실록DB 분석을 통한 황충(蝗蟲)의 실체에 대한 재논의

박해철[1], 한만종[1], 이영보[1], 이관석[1], 강태화[1], 한태만[1], 김태우[2]
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우리나라 해충의 역사에서 가장 많이 등장하는 해충명이 황(蝗), 황충(蝗蟲), 또는 비황(飛蝗)이다. 황충은 어떤 특정종의 이름이 아니며, 중국을 비롯한 한자문화권에서 흔히 이주형 풀무치 또는 메뚜기의 총칭으로 흔히 알려져 있다. 하지만, 한반도의 문헌을 비교하여 일찌기 Saigo(1916), Maramatsu(1921), Okamoto(1924)는 군거성 풀무치, 멸구류, 또는 일부 다른 종이 섞여있다는 주장들을 제기한 바 있다. 이에 백(1976과 1977)은 조선왕조실록에서 38건의 황충에 대한 기사를 추출해 분석하여 황충은 멸강나방이 주를 이루고, 일부는 벼멸구이고, 풀무치는 1건만 확인되며 나머지는 종류미상이라 하였다. 하지만 최근에 윤과 문(2003과 2006)은 황충으로 풀무치와 대발생이 가능한 메뚜기류를 중심에 놓고 다른 곤충류의 가능성도 열어둔 바 있다. 이들 주장사이에는 한반도의 황충이란 것이 중국대륙처럼 풀무치를 비롯한 메뚜기류가 중심무리인지 또는 멸강나방 같은 과거에서 현대까지 이어 발생하는 주요 농업해충이 중심무리인지를 놓고 해석의 차이가 벌어지게 된다. 따라서 우선 조선시대 관료들이 황충을 어떻게 이해했는지 문헌을 통해 고증하고자 한다. 아울러 조선왕조실록 원문DB에서 찾아볼 수 있는 황충 관련기사 229건를 분석하였고, 그 가운데 해석이 가능한 범위에서 현재의 생물학적 실체를 밝히고자 시도하였다. 이를 통해 볼 때, 조선시대의 황충의 실체는 미확인 종이 다수를 차지하였지만, 분석된 기사 중에는 멸강나방 유충을 대표로한 농업해충이 대부분을 차지하고, 진정한 메뚜기류로 볼 수 있는 기록은 2건에 불과하였다. 아울러 문헌 비고를 통해 조선의 황충이란 것은 농업생태계에서 주로 집단적으로 발생하는 해충을 일컫는 용어로 보는 것이 타당할 것으로 판단되었다.

검색어: 황(蝗), 황충(蝗蟲), 비황(飛蝗), 조선왕조실록DB

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갈색여치에 대한 백강균의 살충활성

방혜선, 정명표, 김명현, 한민수, 강기경, 이덕배, 남성희[1]
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최근 충북 영동지역 과수원에 갈색여치(*Paratlanticus ussuriensis*)가 대발생하여 복숭아, 포도, 자두 등의 잎과 줄기, 열매 등을 갉아 먹는 등 많은 피해를 유발하고 있다. 이와 같은 현상은 2006년 및 2007년도 같은 지역에 높은 밀도로 발생하여 과수 생산에 많은 손실을 주었는데, 영동뿐만 아니라 옥천, 청원, 보은에서도 예년보다 높은 밀도로 발생하였다. 친환경적 갈색여치 방제를 위한 일환으로 야외 및 실내에서 분리된 백강균(*Beauveria bassiana*)을 이용하여 갈색여치에 대한 감염여부와 방제 가능성을 검토하였다.

야외채집 및 실내에서 분리된 백강균을 이용하여 갈색여치에 대한 살균활성을 검정하였다. 사용된 모든 백강균은 갈색여치에 대해 80~100%의 강한 살균활성을 나타냈으며, 접종 후 3~6일내 갈색여치가 사망하였다. 각 지역에서 채집된 백강균 및 실내에서 분리한 백강균간의 살균활성 차이는 통계적으로 유의하지 않았다. 본 실험을 통해, 백강균은 갈색여치에 대해 살균활성을 나타내는 것으로 확인되었다.

검색어: 갈색여치, 백강균, 살충활성

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화학살균제가 미생물살충제(*Bacillus thuringiensis*)에 미치는 영향

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Bacillus thuringiensis(B.t.)는 해충방제용으로 가장 많이 사용되고 있는 미생물제이며, 배추재배 농가현장에서 *B. thuringiensis*를 제형화한 미생물 살충제와 함께 배추 병 방제를 위하여 화학살균제를 사용하고 있다. *B. thuringiensis*의 미생물 살충제를 안정적으로 사용하기 위하여 이들 농약과 *B. thuringiensis*간의 상호작용을 규명하고 혼용 및 교호살포하기에 적절한 농약을 선발하기 위하여 본 연구를 수행하였다. 현재 유통되고 있는 *B. thuringiensis* 살충제 7종에 대하여 수행되었으며, 화학살균제는 배추에서 노균병과 무름병에 등록되어 있는 코퍼하이드록사이드 수화제 등 12종을 대상으로 수행하였다. 추천농도의 화학농약을 첨가한 TSA배지에 대상미생물살충제를 도말하여 형성된 콜로니를 비교하였으며, 대상 미생물살충제 7종과 화학살균제를 각각 추천농도로 혼합하여 30분 shaking 한 후 배추 잎침지하여 배추좀나방에 대한 살충력을 petri-dish에서 조사하였다. 7종의 *B. thuringiensis* 살충제는 화학농약을 함유한 배지에서의 *B. thuringiensi*의 콜로니는 옥시테트라사이클린 수화제, 스트렙토마이신 수화제, 발리다마이신에이 수화제, 옥솔린산 수화제를 함유한 TSA배지에서 콜로니가 형성되지 않았다. 미생물 살충제와 화학살균제의 혼합액을 배추좀나방에 처리한 결과 5종의 *B. thuringiensis* 살충제(TB-WP, SC, SB, BG)는 12종의 화학살균제의 혼합에 따른 살충력에 차이가 없었으나, TB-SO와 플루오피콜라이드 · 프로파모카브하이드로클로라이드 액상수화제, TH와 코퍼하이드록사이드 수화제의 혼합액처리에서 배추좀나방의 살충력이 유의하게 감소하는 결과를 보였다.

검색어: *Bacillus thuringiensis,* 화학살균제, 배추좀나방

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황벽나무 열매 추출물에 대한 쌀바구미의 살충활성 및 항산화활성

정미화, 조창욱, 홍진영, 최정은, 김영희
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유기질 문화재 보존 천연 살생물제 개발을 위한 후보물질 조사를 위해 국내에 자생하는 황벽나무(*Phellodendron amurense*) 열매의 메탄올 조추출물 및 분획물을 대상으로 쌀바구미(*Sitophilus oryzae*) 성충에 대한 살충활성 및 항산화 활성을 조사하였다.

조추출물은 극성 차이를 이용하여 n-hexane(Hex), dichloromethane(MC), ethylacetate(EA)로 순차적으로 분획되었으며, 농도별로 24시간동안 접촉 및 훈증 방법에 의해 쌀바구미의 치사율을 측정하였다. 그 결과, 황벽나무 열매의 EA 분획물에서 쌀바구미에 대해 상대적으로 높은 치사율을 나타내었다. 그러나 조추출물 및 Hex, MC 분획물에서는 낮은 치사율을 나타내었다.

또한, 추출물 및 분획물의 항산화 활성을 측정한 결과, 100㎍/㎖의 농도에서 조추출물, Hex, MC 분획물의 항산화 활성이 각각 19.6%, 12.4%, 22.5%로 약하게 나타난 반면, EA 분획물은 62.8%의 강한 항산화 활성을 나타내었다.

위의 결과로부터 황벽나무 열매 EA 분획물은 쌀바구미에 대한 살충활성과 항산화 활성이 우수한 물질로 조사되었기 때문에, 이들에 의해 야기되는 생물학적 열화에 대한 유기질 문화재 보존 천연 살생물제 개발을 위한 후보물질로 사용가능할 것으로 사료된다.

검색어: 쌀바구미, 황벽나무 열매, 살충활성, 천연 살생물제, 해충열화

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세신추출물의 살충활성

조창욱, 최정은, 김영희, 정미화, 홍진영
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세신(*Asarum sieboldii*)은 쥐방울과(Aristolochiaceae)에 속하는 다년생 식물로서, 민족두리풀(*Asarum heterotropoides* F. Maekawa var. *mandshuricum* F. Maekawa) 또는 족두리풀(*Asarum sieboldii* var. seoulensis)의 뿌리를 약용으로 한다. 세신의 성분으로는 methyleugenol, cineol, safrole, limonene, eucarvone (azulene), elemicin, kakuol, 1,8-cineol, γ-asarone, asarylketone 등을 함유한다고 보고되어 있으며, 세신의 추출물은 해열, 진정, 진통, 항염증, 항균작용 등을 나타낸다고 보고되고 있다. 우리나라 목조문화재 가해 및 저장해충으로 알려진 권연벌레(*Lasioderma serricorne*, Fabicius)는 크기가 작고 방제가 매우 어려운 해충으로 알려져있다. 목조문화재는 특성상 직접 약제처리를 하기가 어렵기 때문에 권연벌레를 방제하기 위하여 주로 훈증처리를 통한 방제 방법을 활용하고 있다. 따라서 본 연구에서는 이러한 권연벌레의 방제법의 일환으로서 활용하고자 세신의 메탄올추출물과 디클로로메탄추출물을 이용하여 훈증처리와 기피 실험을 통하여 권연벌레에 대한 세신의 살충활성과 기피효과를 알아보았다. 각각 원액을 포함한 추출물을 농도를 달리하기 위하여 70% 에탄올로 희석시킨 후 0.3g/ml부터 0.1g/ml씩 더 농도를 높게 하여 추출물 원액까지 8개 농도로 훈증 실험을 수행하였다. 그 결과 50% 이상의 살충활성을 나타내는 농도가 에탄올 추출물은 0.8g/ml로 나타났으며, 디클로로메탄 추출물은 0.4g/ml로 에탄올 추출물보다 높게 나타났다. 이는 세신의 주요 살충활성을 나타내는 성분이 디클로로메탄 용매에 많이 용출되는 것으로 사료된다. 그러나 세신의 기피효과 실험에서는 효과를 나타내지 않았다.

검색어: 세신, 권연벌레, 목조문화재, 천연추출물

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몇 가지 살충제와 Emamectin benzoate와 Imidacloprid 혼용처리의 솔껍질깍지벌레에 대한 비효용적 효과

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솔껍질깍지벌레는 소나무재선충에 의한 소나무 재선충병과 더불어 남부해안지역의 곰솔림에 심각한 피해를 주는 해충으로 일부 지역에서는 두 병해충이 동시에 발생하고 있다. 산림 내 병해충 방제는 대면적이고, 방제의 제한점이 많아 두 종 이상의 병해충을 동시방제 할 필요성이 높은 편이다. 본 연구에서는 동일 기주에서 나무주사를 통한 솔껍질깍지벌레 방제효과가 우수한 약제를 선발하고, 소나무재선충병의 동시 방제를 위하여 2종의 유효성분을 혼합 처리하여 그 효과를 검정 하였다. Thiamethoxam 유제 (2.15%)와 Imidacloprid 분산성 액제 (20%)를 단독 처리한 결과 86.5%, 89.7%로 솔껍질깍지벌레에 대한 살충효과가 뛰어났으며 효과가 우수한 두 가지 살충제와 소나무재선충병 수간주사 약재인 Emamectin benzoate 유제 (2.15%)를 한 기주에 각각 주사한 결과 Thiamethoxam 유제 (2.15%) 혼합 처리구에서는 97.1%의 방제효과를 보였으나 Imidacloprid 분산성 액제 (20%) 혼합 처리구는 9.4%로 방제효과가 감소하였고, 두 약제를 섞어 한번에 주사한 경우에도 6.2%의 낮은 살충효과를 나타내었다. 따라서 솔껍질깍지벌레와 소나무재선충병 동시 방제를 위하여 Emamectin benzoate와 Imidacloprid를 혼합 처리하는 것은 부적합 한 것으로 나타났다.

검색어: 솔껍질깍지벌레, 소나무재선충병, Thiamethoxam, Imidacloprid, Emamectin benzoate, 살충효과, 나무주사

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Fenitrothion의 솔껍질깍지벌레 (*Matsucoccus thunbergianae*)에 대한 살충활성

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남부 해안 지방 해송에 심각한 피해를 주는 솔껍질깍지벌레(*Matsucoccus thunbergianae*)는 2령충 시기인 3월경에 Buprofezin을 항공 또는 지상살포하고 있다. 본 연구에서는 처리 시기의 조절을 통한 효율적 방제를 위해 솔껍질깍지벌레 2령충, 번데기, 성충의 각 발육단계별에 대한 Fenitrothion 유제 (50%)의 살충활성을 spray법으로 검정하였다. 암컷 2령충에 Fenitrothion 500ppm을 처리하였을 때 탈피저해율은 84.0%, 250ppm에서는 81.4%로, 대조약제로 Buprofezin 액상수화제 (40%) 4000ppm을 처리했을 때 탈피저해율인 28.7%, 무처리구의 15.4%보다 높았고, 암컷 성충에 Fenitrothion 500ppm, 50ppm 처리했을 때 산란율은 각각 1.0%, 23.3%로, Buprofezin 65.7%, 무처리 82.9%의 산란율보다 높은 산란억제율을 보였다. 한편, 수컷은 2령충과 번데기에 Fenitrothion 500ppm을 처리했을 때 각각 0%, 6.4%의 우화율을, Buprofezin 4000ppm처리시 각각 0.6%, 23.0%의 우화율을 나타내어 무처리에서의 62.7%와 94.5% 우화율보다 높은 우화억제율을 보였다.

검색어: 솔껍질깍지벌레, Buprofezin, Fenitrothion, 산란율

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사막이리응애(*Neoseisulus californicus*)에 대한 원예용 살충제의 저독성 및 잔효독성 평가

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시설채소 재배농가에서 생물적 방제와 상호보완적으로 사용할 수 있는 저독성약제에 대한 정보 요구가 증가되고 있어 착색단고추 및 딸기재배지의 주요 해충인 점박이응애의 포식성 천적인 사막이리응애에 대해 착색단고추와 딸기에 방제약제로 등록되어 있는 주요 살충제 50종을 저독성 및 잔효독성을 평가하였다. 원예용 농약을 추천농도로 희석하여 사막이리응애 성충에 분무처리한 결과 IOBC기준으로 저독성(사충율, 30% 이하)인 살충제는 아세타미프리드(수), 인독사카브(수), 피메트로진(수), 루페루론(유), 플로니카미드(입상), 플루벤디아마이드(액상), 노발루론(액상), 메톡시페노자이드(액상), 아세퀴노실(액상), 플루페녹수론(분산성액제), 에톡싸졸(액상), 헥시티아족스(수) 등 12종이었다. 착색단고추에서 약제 살포 1일후 보정사충율이 30%이하인 살충제는 스피노사드(액상), 인독사카브(액상), 클로티아니딘(수), 클로티아니딘(액상), 티아클로프리드(액상), 티오디카브(수), 피리다벤(수), 피리프록시펜(유), 스피네토람(입상) 등 9종으로 평가되었다.

검색어: 사막이리응애(*Neoseisulus californicus*), 저독성, 잔효독성

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친환경유기농자재별 벼 주요해충에 대한 살충효과

백채훈, 이건휘, 노태환, 강미형[1], 이두구, 김시주
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시판되는 몇 가지 친환경유기농자재를 대상으로 실내에서 혹명나방(*Cnaphalocrocis medinalis*), 벼애나방(*Narana aenescens*), 멸강나방(*Pseudaletia unipuncta*) 및 줄점팔랑나비(*Parnara guttata*)의 살충효과를 조사하였다. 19개 친환경유기농자재에 대해 각 나방류 2-3령 유충의 각각 처리 후 1, 3일차의 실내 살충효과를 조사한 결과, 90% 이상의 살충률을 나타낸 친환경유기농자재는 혹명나방은 1일차에서 EFAM-B 1개, 3일차에서는 EFAM-A 등 10개, 벼애나방은 1일차에서 EFAM-A 등 11개, 3일차에서는 EFAM-A 등 12개, 멸강나방은 1일차에서 EFAM-A 등 3개, 3일차에서는 EFAM-A 등 9개, 줄점팔랑나비는 1일차에서 EFAM-A 등 12개, 3일차에서는 EFAM-A 등 15개였다.

또한, 국내에 자생하는 은행나무의 부위별 추출물에 대한 벼멸구 약충의 살충효과를 조사한 결과, 뿌리 > 잎 > 가지의 순으로 살충효과가 높았다.

검색어: 혹명나방, 벼애나방, 멸강나방, 줄점팔랑나비, 벼멸구, 친환경유기농자재

P111

Economic Injury Level of *Thrips tabaci* (Thysanoptera: Thripidae) on Welsh onion (*Allium fistulosum* L. var)

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This study was conducted to develop economic injury level (EIL) and economic threshold (ET) of onion thrips, *Thrips tabaci* on welsh onion (*Allium fistulosum* L. var). The changes of welsh onion biomass and *T. tabacci* density were investigated after introductions of *T. tabacci* at different densities and days: By the results of the experiment in the early welsh onion cultivation periods (30d after transplanting), the biomass of welsh onion significantly decreased with increasing the initial inoculated density of *T. tabacci*. The relationship between cumulative insect days (CID) and yield loss (%) of welsh onion was well described by a nonlinear logistic equation. Using the estimated equation, EIL and ET of *T. tabacci* on welsh onion were estimated at 24 and 20 CID per plant, respectively. By the results of the experiment in the late cultivation periods of welsh onion (about 120d after transplanting), the welsh onion biomass was also significantly different inoculation thrips densities to welsh onion. The EIL and ET were calculated as 35 and 28 thrips per welsh onion plant. Until a more elaborate EIL-model is developed, the present result may be useful for *T. tabacci* management during the cultivations of welsh onion.

Key words: *Thrips tabacci, Allium fistulosum* L., economic injury level, economic threshold, gain threshold

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고구마뿌리혹선충 저항성 토마토 품종 및 대목 선발

김형환, 전흥용, 조명래, 양창열, 강택준, 정재아, 한유경

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국내에서 시설원예작물에 발생하는 대표적인 뿌리혹선충은 고구마뿌리혹선충, 당근뿌리혹선충, 땅콩뿌리혹선충 등이다. 시설토마토에서 피해가 심한 고구마뿌리혹선충을 대상으로 51 계통의 토마토 품종과 대목의 저항성 정도를 알아보았다. 온실에서 증식한 고구마뿌리혹선충의 알을 분리하여 부화시킨 후 1,300g의 사질양토가 들어있는 포트에 유충을 1,000마리씩 접종한 후 45일째에 난낭수를 조사하였다. 저항성 정도는 토마토 뿌리에 형성된 난낭수가 감수성 품종(가장 난낭수가 많은 품종)과 비교하여 10% 이하이면 저항성, 11～25% 사이이면 중간 저항성, 25% 이상이면 감수성으로 판정하였다 (Fassuliots, 1985). 그 결과 일반 토마토의 홈런킹, 방울토마토의 레드체리, 대목의 부킹하계 및 스페셜이 주당 난낭수가 32.6개 미만인 저항성 품종으로 나타났다. 일반 토마토의 레젠드썸머, 레전드, 선명, 핑크탑, TPO3, 델리스, 타샤, 릴리앙스, 그리고 방울토마토의 텐텐, 디저트, 레드스타, 베리킹, 아리가또, 대목의 B-블로킹, 솔류션, 동반자, 그린파워 등이 주당 난낭수가 33.0～81.6개인 중간 저항성 품종으로 밝혀졌다. 로꾸산마루, 호용, 서광 등 30개 토마토 및 대목 품종은 주당 난낭수가 81.8개 이상인 감수성으로 판명되었다. 따라서, 고구마뿌리혹선충이 발생하는 포장에서 모종에 접을 붙이지 않고 토마토를 재배할 경우에는 홈런킹과 레드체리를, 접을 붙여 재배할 경우에는 대목인 부킹하계와 스페셜을 활용하는 것이 바람직할 것으로 사료된다.

검색어: 토마토, 대목, 고구마뿌리혹선충, 저항성, 중간 저항성

P113

고추와 배추에서 식물추출조성물을 이용한 복숭아혹진딧물의 방제

김형환, 조명래, 강택준, 정재아, 최성환[1], 천인규[1]

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고추와 배추에서 피해가 많은 해충인 복숭아혹진딧물의 친환경방제 방법에는 천적, 친환경자재 등이 이용되고 있다. 본 시험에서는 복숭아혹진딧물의 방제에 적용할 수 있는 식물추출조성물로 이루어진 친환경자재를 개발하는데 목적을 두고 연구를 수행하였다. 실내 페트리디쉬와 포트 검정에서는 1% Pyrethrin + 0.6% Matrine (PM), 1.5% Natural Pyrethrins (NP), 10% Nicotine (NI) 3종류의 식물추출조성물을 이용하였다. 페트리디쉬 검정에서 복숭아혹진딧물에 각 식물추출조성물을 500배, 1,000배, 2,000배 농도로 처리한 후 24시간째 살충력을 조사한 결과 PM, NP, NI 모두 500배와 1,000배 농도에서 95% 이상의 높은 치사율을 나타내었다. 포트 검정에서는 고추와 배추 유묘가 심겨져 있는 포트에 각 식물추출조성물을 각각 3일, 5일, 7일 간격으로 1회, 2회, 3회 살포한 후 5일째까지 24시간 간격으로 치사율을 조사한 결과 PM, NP, NI의 500배 농도 처리에서는 살포간격에 상관없이 90% 이상의 살충력을 보였다. 그러나 1,000배 농도로 3일과 5일 간격으로 처리하였을 때는 85% 이상의 살충력을 보였지만, 7일 간격 처리에서는 80% 이하의 살충력을 나타내었다. 2,000배 농도로 3일과 5일 간격으로 1회와 2회 처리에서는 살충력이 낮았으나, 3회 처리에서 80～85%의 살충력을 보였으며, 7일 간격 처리에서는 살충력이 매우 낮은 것을 확인하였다. 따라서 본 시험의 결과를 토대로 3종류의 친환경자재를 복숭아혹진딧물의 방제에 이용할 때는 1,000배 농도로 3일～5일 간격으로 살포하는 것이 가장 효과적이었다.

검색어: 고추, 배추, 식물추출조성물, 복숭아혹진딧물, 살충력

P114

시설오이에서 총채가시응애와 오이이리응애를 이용한 꽃노랑총채벌레의 방제

김형환, 전흥용, 조명래, 양창열, 강택준, 정재아
농촌진흥청 원예특작과학원 원예특작환경과

아산과 공주의 친환경 시설오이 재배지에서 꽃노랑총채벌레의 번데기를 포식하는 총채가시응애와 오이 지상부 꽃노랑총채벌레의 약충과 성충을 포식하는 오이이리응애를 활용하여 꽃노랑총채벌레의 방제효과를 조사하였다. 3월에 정식한 반촉성 시설오이 재배지에서 12∼14일 간격으로 조사하면서 꽃노랑총채벌레가 발생하는 초기에 총채가시응애와 오이이리응애를 방사량, 방사횟수, 방사간격을 달리하여 처리한 다음 꽃노랑총채벌레의 밀도 감소효과를 조사하였다. 그 결과 반촉성 시설오이(3월)를 정식 한 후 50엽당 꽃노랑총채벌레가 1∼10마리 사이에 발생하였을 때 총채가시응애를 m^2당 15.2마리(15,000마리/300평/10a) 밀도가 되게 하였고, 1회 방사한 후 예찰을 통하여 꽃노랑총채벌레가 50엽당 11∼20마리 사이에 발생하게되면 오이이리응애를 m^2당 38.0마리(75,000마리/300평/10a) 밀도가 되게 하여 12∼14일 사이의 간격을 두고 2회 방사하면 90% 이상의 방제효과가 있었다. 이러한 효과는 작기가 종료되는 7월 상순까지 지속되었다. 또한 초기 꽃노랑총채벌레의 발생밀도가 50엽당 20마리 이상 발생하였을 때는 총채가시응애를 m^2당 15.2마리 밀도로 방사하고 오이이리응애는 m^2당 38.0마리 밀도가 되게하여 12∼14일 사이의 간격을 두고 3회 방사하거나, 오이이리응애 밀도를 2배 증가시켜 m^2당 76.0마리(150,000마리/300평/10a) 밀도로 12∼14일 사이의 간격을 두고 2회 방사하면 85% 이상의 방제효과를 나타내었다.

검색어: 오이, 총채가시응애, 오이이리응애, 꽃노랑총채벌레, 방제효과

P115

오이, 토마토, 상추 재배지에서 녹비작물을 이용한 뿌리혹선충의 밀도 경감 효과

김형환, 전흥용, 조명래, 양창열, 강택준, 정재아
농촌진흥청 원예특작과학원 원에특작환경과

과채류 및 엽채류의 후작지 중간작물 재배에 의한 병해충 관리 기술을 개발하기 위한 일환으로 전작물인 오이, 토마토 및 상추 재배 후 중간작물로 헤어리벳치, 네마장황, 수단그라스를 20～30일 동안 재식하였다. 오이의 후작 중간작물로는 헤어리벳치(5kg/10a)를, 토마토는 네마장황(6kg/10a)을, 상추는 각각 헤어리벳치와 수단그라스(5kg/10a)를 재배한 다음 고구마뿌리혹선충과 당근뿌리혹선충의 밀도 경감 효과를 조사하였다. 헤어리벳치와 네마장황을 30일 동안 간작한 오이와 토마토 시설하우스에서 고구마뿌리혹선충의 밀도 감소 효과를 조사한 결과 헤어리벳치가 79.5%, 네마장황이 80.8%로 담수보다 선충의 밀도 경감 효과가 높았다. 시설상추 재배지에서 수단그라스와 헤어리벳치를 간작한 후 당근뿌리혹선충의 밀도 감소효과를 조사한 결과 수단그라스 재배구에서 64.6%, 헤어리벳치 재배구에서 63.1%의 효과를 나타내었다. 특히 상추재배지의 경우 수단그라스를 30일 이상 재배하면 다음 작기의 상추 정식을 위해 로터리 작업을 여러번 해야하는 번거로움과 함께 로터리 작업 후에 비닐멀칭을 하게 되면 잘게 부숴지지 않는 뿌리, 줄기, 잎으로 인하여 비닐이 찢어지거나, 정식 작업시 애를 먹는 것을 볼 수 있었다. 따라서 오이, 토마토, 상추 재배 후 휴작기인 20～30일 동안 헤어리벳치, 네마장황, 수단그라스를 이용하여 토양속 뿌리혹선충의 밀도를 감소시킬 수 있었다.

검색어: 고구마뿌리혹선충, 당근뿌리혹선충, 헤어리벳치, 네마장황, 수단그라스

P116

시설상추에서 총채가시응애와 미끌애꽃노린재를 이용한 꽃노랑총채벌레의 방제

전흥용, 김형환, 조명래, 양창열, 강택준, 정재아

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시설상추에서 문제가 되고 있는 해충에는 싸리수염진딧물, 꽃노랑총채벌레, 검은은무늬밤나방 등이 알려져 있다. 본 연구는 토양 속 꽃노랑총채벌레의 번데기를 포식하는 총채가시응애(*Hypoaspis aculeifer*)와 상추 잎에 서식하는 꽃노랑총채벌레의 약충과 성충을 포식하는 미끌애꽃노린재(*Orius laevigatus*)를 이용하여 보다 효율적으로 꽃노랑총채벌레를 방제하기 위하여 수행되었다. 꽃노랑총채벌레의 피해가 증가하는 7월～8월에 정식하는 시설상추에서 꽃노랑총채벌레의 발생초기에 총채가시응애는 1회 방사하고, 미끌애꽃노린재는 방사량, 방사횟수를 달리하여 방제효과를 조사한 결과, 7월 하순～8월 초순 중 정식하는 3작기 시설상추에서 꽃노랑총채벌레가 상추 100엽당 1~10마리 사이에 발생할 때 총채가시응애를 m^{2}당 15.2마리(15,000마리/300평/10a) 밀도로 1회 방사한 후 예찰을 통하여 꽃노랑총채벌레가 100엽당 15~25마리 사이에 발생하면 미끌애꽃노린재를 m^{2}당 0.8마리(750마리/300평/10a) 밀도로 15~30일 사이의 간격을 두고 2회 방사하면 90% 이상의 밀도감소 효과가 있었다. 그리고 꽃노랑총채벌레가 100엽당 25마리 이상 발생하였을 때는 총채가시응애를 ㎡당 15.2마리 밀도로 1회 방사하고 미끌애꽃노린재는 m^{2}당 0.8마리 밀도가 되게하여 15~30일 사이의 간격을 두고 3회 방사하거나, 미끌애꽃노린재 밀도를 2배 증가시켜 m^{2}당 1.6마리 밀도로 15~30일 사이의 간격을 두고 2회 방사하면 80% 이상의 효과를 보였다.

검색어: 상추, 총채가시응애, 미끌애꽃노린재, 꽃노랑총채벌레, 방제효과

P117

Insecticidal activities of Various Plant Extract against Four Agricultural Insect Pests

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The toxicity of methanol extract from 28 plants toward four agricultural insect pests were examined using contact toxicity bioassay with spray methods.

At a concentration of 1,000 ppm *Achyranthes japonica* whole body was observed strong activity against *Myzus persicae. Paeonia lactiflora* root and *Corydalis turtschaninovii* rhizome methanol extract were observed strong activity toward Tetranychus urticae. *Catalpa ovata* leaf and *Ginkgo biloba* leaf and stem methanol extracts were revealed high activity toward *Nilaparvata lugens. Actium lap* root methanol extract was observed moderate activity against *Plutella xylostella*. High or moderate insecticidal activity of plant extracts were listed in Fig.1.

These plant resource, particularly plant methanol extract or insecticidal constituents, merit further as potential insect pest control agents or leads because of their great activity as a insecticide.

Key words: botanical insecticide, agricultural insect, *Tetranychus urticae, Nilaparvata lugens, Myzus persicae, Plutella xylostella*

P118

Seasonal phenology and spatial distributions of *Plodia interpunctella*, *Lasioderma serricorne* and *Trogoderma variabile* in two warehouses in Korea

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Insect pest monitoring program in subsistence warehouses can detect pest problems in early infestation stages. Temporal and spatial distributions of pests produced by monitoring allows facility managers and pest control operators to visualize pest problems and evaluate effectiveness of cleaning, sanitation and pest management practices.

Pheromone-based insect monitoring traps were placed to study temporal and spatial distribution of Lepidopteran and Coleopteran stored product pests in two central distribution centers of United States Military Forces in the Republic of Korea, from March to December 2008. The two distribution centers receive store and issue subsistence and they are located in two different cities, Seoul and Taegu. As a result, three pests, *Plodia inter punctella* Hübner (Indian meal moth), *Lasioderma serricorne* F. (cigarette beetle), and *Trogoderma variabile* Ballion (warehouse beetle), were detected on the traps. *P. interpunctella* was most abundant, followed by *L. serricorne* and *T. variabile.* Different phenologies and spatial distribution of each species were seen from the two warehouses, that were related with internal temperature of the two warehouses and food availability.

The program benefited to lead a better understandings for existence and extent of local pest problems in the two subsistence distribution centers, and also helped to find effective pest management periods and locations.

Key words: *Plodia interpunctella*, *Lasioderma serricorne*, *Trogoderma variabile*, pheromone trap, phenology, spatial distribution, Korea

P119

Mathematical models applied to dispersal of pest populations in greenhouse

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A genome project has been launched and aims to sequence total genome of *Cotesia plutellae* bracovirus. On this process, several open reading frames (ORFs) have been identified. This study was intended to clone and express protein tyrosine phosphatase genes, PTP1 and PTP6. The ORFs of these two genes consist of 900 and 891 bp, respectively. PTP1 and PTP6 are genes of a group of genes that has been implicated as important regulatory components in cell growth, differentiation and malignant transformation by certain viruses. In this work,we studied the cloning and expression patterns of these genes in *Plutella xylostella,* a lepidopteran host of *C. plutellae*. A polymerase chain reaction (PCR) produced the corresponding products of PTP1/6. These PCR products were cloned and expressed using an expression vector pBAD-TOPO, and then over-expressed using an inducer, L-arabinose. Then the purified proteins were confirmed using Western blotting (immunoblotting using V5 antibody) and the apparent molecular weights of both proteins were about 40 kDa. Expression of PTP genes were analyzed in the parasitized *P. xylostella* by realtime RT-PCR, which indicated late expression pattern of both PTPs during parasitization. We are pursuing to elucidate their physiological function in the parasitized host insect.

Key words: *Cotesia plutellae,* polydnavirus, CpBV, protein tyrosine phosphatase, RT-PCR, cloning, expression, *Plutella xylostella*

P120

Automatic Pest Detection Implemented in Robotics in Green House

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Accurate estimation of pest density is a prerequisite in achieving efficient pest management. An automatic pest detection system with image processing was installed on a robot to recognize brown marmorated stink bug (*Halyomorphahalys*) on leaves of paprika(*Capsicumannuumvar.angulosum*). The shape of pest was recognized and subsequently the robot arm was moved toward the leaves to spray pesticides. The detection system was efficient along with increasing population densities increased. The robot with image processing system was useful for estimating population densities in spatial and temporal domain efficiently.

Key words: pest detection, greenhouse, robotics, image processing

P121

The putative role of carboxylesterase 2 in insecticide tolerance in *Bemisia tabaci*

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The hemipteran whitefly *Bemisia tabaci* (Gennadius) is one of the most destructive pests damaging more than 600 agricultural crop species worldwide. The B and Q biotypes are most widely spread in Korea but they are not distinguishable based on morphological characters. Carboxylesterase 2 (Coe2) was determined to be 5.9 times more expressed in B biotype compared to Q biotype. Comparison of deduced amino acid sequences of Coe2 (595 a.a.) showed a total of 3.85% polymorphisms between B and Q types but no differences in major active sites. Quantitative real-time PCR revealed that both B and Q biotypes possess a single copy of *coe2*, suggesting that the overexpression of Coe2 in B biotype is likely due to overtranscription. To determine the putative role of Coe2 in insecticide tolerance, esterases were separated by native isoelectric focusing (IEF) and inhibited by various insecticides. The putative Coe2 band was apparently inhibited by pyrethroid and organophosphate insecticides, but not by imidacloprid. These findings suggest that overexpression of Coe2 confers chemical defense against pyrethroid and organophosphate insecticides, perhaps by sequestration.

Key words: *Bemisia tabaci*, whitefly, carboxylesterase, overexpression, insecticide tolerance

P122

Toxicity and Repellency of Origanum Essential Oil and Its Components against *Tribolium castaeneum* (Coleoptera: Tenebrionidae) Adults

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Origanum essential oil [*Origanum acutidens* (Hand.-Mazz.)] showing insecticidal activity and repellency against red flour beetle, *Tribolium castaneum* (Coleoptera: Tenebrionidae) adults was analysed by GC-MS. All constituents of the oil were identified, and the main components were carvacrol (67.2%), *p*-cymene (16.2%), *γ*-terpinene (5.5%), thymol (4.9%),and linalool(2.1%). In vapor phase fumigant assay, the origanum oil was more effective in closed condition (LD50 = 0.555 mg/cm^3) than in open one (LD50 = 0.353 mg/cm^3).This result suggests that the toxicity of the oil to red flour beetle is exerted largely by vapor phase. Based on 24-h LD50 values, the toxicity of caryophyllene oxide (0.00018 mg/cm^3) was comparable with that of dichlorvos (0.00007mg/cm^3) as a positive insecticide. In addition, thymol, camphene, *α*-pinene, *p*-cymene, and *γ*-terpinene gave good insecticidal activity (LD50 = 0.012 - 0.195 mg/cm^3). In repellent test using 9 constituents of origanum oil, caryophyllene oxide showed 100% repellent activity at 0.0158 and 0.0032 mg/cm^2. These results indicate that the origanum oil and its some components could be potential candidates as a fumigant and repellent for managing *T. castaneum* adults. Potential molecular target of repellents will be discussed.

Key words: Origanum essential oil, *Tribolium castaneum*, fumigant, repellent activity, caryophyllene oxide

P123

PCR-based restriction fragment length polymorphism (RFLP) screening of three aminopeptidase N (APNs) from diamondback moth (*Plutella xylostella*) in Korea

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The diamondback moth, *Plutella xylostella*, is one of the most important pests of cole crops in the world and is the first insect to evolve resistance to Bt toxins in open-field populations. To search for useful molecular markers for Bt reistance monitoring, the PCR-based restriction fragment length polymorphism (RFLP) profiles of three aminopeptidase N (PxAPN1, PxAPN2 and PxAPN4) were determined for 15 representative regional field populations of *P. xylostella*. Most regional samples had similar RFLP patterns, whereas PxAPN1 from four regions and PxAPN4 from two regions showed different banding patterns after restriction enzyme treatment, but no differences were found in PxAPN2 among populations. The DNA sequence analysis revealed that a point mutation at the restriction site was responsible for the polymorphism of PxAPN1 but no mutations were observed in PxAPN4. Comparing amino acid sequences of PxAPNs from regional populations with reference PxAPNs (GenBank accession no. AAB70755) revealed that four regional populations possessed a point mutation in the Cry1A binding site of PxAPN1 and five regional populations possessed a deletion of eight amino acids in PxAPN4. These RFLP patterns were consistently observed in Southern regions of Korea, including Kyungsangnam-Do and Jeju-Do. The functional association of these RFLP with Bt resistance is currently under investigation.

P124

Construction of A Recombinant *Bacillus thuringiensis* 19-22 Strain Exhibiting Antifungal and Dual Insecticidal Activities

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A new *Bacillus thuringiensis* isolate 19-22 (Bt 19-22) exhibited high anti-fungal activity against barley powdery mildew (*Blumeria graminis* f. sp. *hordei*). The *cry* gene content of Bt 19-22 comprised *cry1Aa*, *cry1Ab*, *cry1Ac* and *cry1D* which have high insecticidal activity against lepidopteran larvae. We tried to confer a dipteran insecticidal activity to Bt 19-22 for constructing a recombinant strain which has multiple functions, anti-fungal and dual insecticidal activity. The insecticidal *cry11Aa* gene of *B. thuringiensis* was constructed under *cry1Ac* promoter in an *E. coli*-*B. thuringiensis* shuttle vector (pPro11A). The plasmid, pPro11A was introduced into Bt 19-22 isolate by electroporation and four transformants which had different *cry* gene contents were identified by PCR with *cry11Aa* and *cry1*-type specific primers. Among them, a Bt 19-22 transformant (11A/19-22 No. 7) expressed Cry11A protein (approximately 70 kDa) successfully without change of its inherent characteristics such as Cry protein expression and antifungal activity. The insecticidal activity of 11A/19-22 No. 7 was checked against *Plutella xylostella* and *Culex pipiens*. These results suggests that the recombinant strain shows dual insecticidal activity against lepidopteran and dipteran larvae as well as antifungal activity.

Key words: *Bacillus thuringiensis* 19-22, antifungal activity, barley powdery mildew, *cry11Aa*, dual insecticidal activity

P125

Molecular Characterization of A Genomic DNA of *Bacillus thuringiensis* Bacteriophage and Its Distribution in *Bacillus thuringiensis* Type Strains

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Through an application of plasmid capture system (PCS) to *Bacillus thuringiensis* plasmid DNAs, we acquired 21 polymorphic clones of putative genomic DNA of bacteriophage. The genome size of phage 1-3 (PhBT1-3) was determined to be 46,517 base pairs (bp) with 35.43% G + C content and 83% coding region. Sixty-five putative open reading frames (ORFs) with more than 50 codons were found in the new phage genome. In accordance with this genome finding, the phage particles and its DNA were confirmed from the supernatant of *B. thuringiensis* 1-3. Morphological characterization and infectivity assay demonstrated that PhBT1-3 belongs to the family *Siphoviridae* and it showed infectivity to three *B. thuringiensis* type strains, *galleriae*, *entomocidus*, and *morrisoni*. Based on these results, we screened the existence of phages in *B. thuringiensis* type strains by PCR with terminase small subunit-specific primers. Ten of 67 type strains showed PCR products and the similarity of those putative amino acids was more than 70%. Furthermore, we verified the existence of various shaped phages from the supernatants of 10 *B. thuringiensis* type cultures. In conclusion, we characterized a putative genome of phage, PhBT1-3 from *B. thuringiensis* 1-3, and confirmed the distribution of phages in the group of 67 *B. thuringiensis* type strains.

Key words: plasmid capture system (PCS), *Bacillus thuringiensis*, genomic DNA, bacteriophage, phage distribution

P126

Generation and characterization of *Autographa californica* nucleopolyhedrovirus single ORF-turncated mutants

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Autographa californica nucleopolyhedrovirus (AcMNPV) has a large double-strand DNA genome of approximately 134 kbp and comprises 156 open reading frames (ORFs). To elucidate DNA replication cascade of AcMNPV, we developed a novel baculovirus genome that can be maintained in *Escherichia coli* as a plasmid and can infect susceptible lepidopteran insect cells. This genome, named bAc-MK, contains a mini-F replicon and a kanamycin resistance marker. Using a convenient Tn7 transposon-based system, pPCS-S, which contains an ampicillin resistance gene, 56 single ORF-truncated mutants were generated by random insertion into bAc-MK genome. These single ORF-truncated mutants were independently transfected into Sf9 cells to verify viral replication. Interestingly, both *lef-1* and *p48* knockout mutants showed normal viral replication in infected cells, which are reported to essential for viral replication. These results suggest that these single ORF-truncated mutants are useful for elucidation of viral replication cascade.

Key words: AcMNPV, bAc-MK, pPCS-S, single ORF-truncated mutants, replication cascade

P127

Insecticidal activity of the chitinase A from the *Spodoptera lirura* nucleopolyhedrovirus

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Baculovirus chitinase gene (*ChiA*) is a late gene and is essential for liquefying host insect at the late stage of infection for its hydrolyzing chitin function. In previous report, baculovirus ChiA can offer many interseting new opportunities for pest control. Recently, a putative chitinase gene (*ChiA*) was identified in the *Spodopter litura* nucleopolyhedorvirus (SlMNPV-K1) genome. The open reading frame (ORF) contains 1,692 nucelotides (nt) and encodes a protein of 563 amino acids (aa) with a predicted molecular weight of 62.62 kDa. To conform the insecticidal activity of ChiA from SlMNPV-K1, we constructed a baculovirus transfer vector, pBac-SlChiA, and this transfer vector was co-transfected with the bApGOZA DNA into sf9 cell to generate corresponding recombinant viru which designed Ap-SlChiA. Western blot analysis indicate that SlMNPV-K1 *ChiA* was successfully expressed. We found the chitinase activity of recombinant virus was enhanced 53% than wide type AcMNPV by chitinase assay, and the recombinant virus showed higher evidently insecticidal activity against 3rd instar larvae of *Spodotera exigua* than wide type AcMNPV (4.5 time). These results suggested that the chitinase gene from SlMNPV-K1 could be successfully applied to improve pathogenicity of bauclovirus.

Key words: chitinase A (*ChiA*), *Spodopter litura* nucleopolyhedorvirus (SlMNPV-K1), insecticidal activity

P128

Characterization of a strain of *Bacillus thuringiensis* serovar aizawai which harbors a Rolling-Circle Replicating Plasmid, pBt1-3

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Bacillus thuringiensis 1-3 (Bt 1-3) which was isolated from a Korean soil sample showed high insecticidal activity against *Aedes aegypti* as well as *Plutella xylostella*. The isolate was determined to belong to ssp. *aizawai* (H7) type by an H antiserum agglutination test and produced bipyramidal-shaped crystal proteins with a molecular weight of 130 kDa. PCR analysis with *cry* gene specific primers showed that Bt 1-3 contained *cry1Aa*, *cry1Ab*, *cry1C*, *cry1D* and *cry2A* gene, differing from spp. *aizawai* (reference strain) which contains *cry1Aa*, *cry1Ab*, *cry1C* and *cry1D*. We modified the plasmid capture system (PCS) to clone plasmid from Bt 1-3 through in vitro transposition. Fifty-three clones were acquired and their sizes were approximately 10 kb. Based on the sequence analysis, they were classified according to similarities with four known Bt plasmids, pGI3, pBMB175, pGI1 and pGI2, respectively. One of pGI3-like clones, named as pBt1-3, was fully sequenced and its 20 putative open reading frames (ORFs), Rep-protein, double-strand origin of replication (dso), single-strand origin of replication (sso), have been identified. The structure of pBt1-3 showed high similarity with pGI3 which is one of rolling-circle replication (RCR) group VI family.

Key words: *Bacillus thuringiensis, aizawai, cry2A, Aedes aegypti* bioassay, plasmid capture system, RCR group VI

P129

Synergistic Effect of *Beauveria bassiana* SFB-205 Culture Broth on the Insecticidal Activity against Lepidopteran Pests

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Entomopathogenic fungi are widely available as biological control agents for controlling insect pests in agriculture and forestry. The fungal culture broth contains various pathogenesis-related components such as blastospores, mycelium and insecticidal enzymes such as chitinase, Pr1- and Pr2-proteases, which have been reported to play an important role in penetrating insect cuticles. In this study, we tried to evaluate the utility of culture broth from *Beauveria bassiana* SFB-205 to control lepidopteran pests. High level of insecticidal activity correspond to over 90% of mortality were observed when the culture broth of *B. bassiana* SFB-205 was inoculated to the *Spodoptera litura* larvae together with the *B. thuringiensis* K1. The freeze-dried culture broth showed synergistic effects in insecticidal activity against larvae of *S. exigua* and *S. litura* when treated with corresponding baculoviruses, SeNPV and SlNPV. Active ingredient of the *B. bassiana* SFB-205 culture broth was identified to chitinase, which have truncated form by insertional mutation compared to previously reported chitinases.

Key words: *Beauveria bassiana* SFB-205, culture broth, chitinase, synergistic effect, lepidopteran pest

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Olfactory Responses of *Stomoxys calcitrans* to *Zanthoxylum piperitum* Pericarp Steam Distillate, *Zanthoxylum armatum* Seed Oil, and their Volatile Constituents Alone or in Combination with 1-Octen-3-ol

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Electroantennogram techniques (EAGs) were employed to record olfactory responses in the antennae of the adult female stable fly, *Stomoxys calcitrans* (Diptera: Muscidae), to *Zanthoxylum piperitum* pericarp steam distillate (ZP-SD), *Z. armatum* seed oil (ZA-SO) and their 29 volatile constituents alone as well as binary mixture of the ZP-SD and ZA-SO with 1-octen-3-ol. The electrophysiological responses of the test materials were compared with those of DEET and 1-octen-3-ol. At concentration of 10^{-1} (v/v) in mineral oil, ZP-SD, ZA-SO, and all volatiles elicited EAG responses in the fly antennae except for DEET, which is extremely low volatile. ZP-SD, ZA-SO, and some of the test volatiles elicited EAG responses rather lower than 1-octen-3-ol, which showed vapor phase repellency and toxicity to the fly in our previous behavioral research. This suggests that the stable fly possesses olfactory receptor neurons responding to given repellent compounds *per se*. In binary mixture with 1-octen-3-ol at concentration of 10^{-1}, ZP-SD and ZA-SO elicited 16±0.55 and 18±0.63 mV while ZP-SD, ZA-SO, and 1-octen-3-ol alone elicited responses of 14±0.45, 15.8±0.37 and 16.2±0.58 mV, respectively. Among the volatile compounds, terpinen-4-ol, β-myrcene, α-phellanderene, citronellal, and limonene oxide elicited 80 – 96% relative EAG amplitude compared to 1-octen-3-ol as a reference (100%). Based on structure-activity relationships, constituents having aldehyde moiety elicited bigger EAG responses than those of alcohol or ether one. The perception in the fly antenna to plant volatile compounds exhibited complicated patterns of olfactory responses. Current and future directions of this study on sensory processing mechanisms underlying repellent behaviors will be discussed.

Key words: EAG responses, natural insect repellent, *Stomoxys calcitrans*, *Zanthoxylum armatum*, *Zanthoxylum piperitum*

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점박이응애(*Tetranychus urticae*) 천적으로서 사막이리응애(*Neoseiulus californicus*)의 생물적 특성

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천적의 성공적인 정착과 산란력은 천적의 능력을 판단하는 중요한 기준이 다. 점박이응애를 방제하기 위해 사막이리응애를 사용함에 있어 천적과 해충사이의 적절한 밀도관리를 통한 해충 발생억제기작이 장기간 유지되는 것이 이상적이라 할 수 있다. 본 연구에서는 실험실에서 강낭콩과 장미, 딸기를 기주로 하여 IOBC quality control guideline에 따라 산란력 및 생존율을 조사하여 점박이응애의 생물적 방제인자로서 사막이리응애의 적용 가능성을 확인하고자 하였다. 온도 20, 25, 30℃, 상대습도 70%RH, 광조건 16L:8D에서 각 작물별 산란력을 조사한 결과, 사막이리응애는 20℃에서 산란수는 적고 생존율은 높았으며, 30℃에서 산란수는 증가고 생존율이 급속히 감소하여 산란력과 생존율 간에 반비례의 관계를 보였다. 작물별로는 온도에 관계없이 장미에서 산란수 및 생존율이 높았으며, 강낭콩과 딸기에서의 산란수 및 생존율은 비슷하였다. 따라서 연중 20~28℃의 온도 조건에서 재배되는 장미에 사막이리응애를 사용했을 때 좋은 방제효과를 얻을 수 있을 것으로 기대되며, 딸기의 경우에도 주간 17~20℃, 야간 10℃ 내외로 서늘하여 사막이리응애의 방사밀도를 조절하면 높은 방제 효과를 기대할 수 있을 것으로 생각된다.

검색어: 사막이리응애, 점박이응애, 온도, 산란력

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오미자 줄기를 가해하는 주요 문제 해충

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최근 DDA, FTA 협상 등으로 인해 국가간 경제교류와 통합 등이 활발하게 진행되고 있으며 국제적으로 통용될 수 있는 우수농산물관리제도(Good Agricultural Practices, GAP)등의 농산물의 식품안전성 문제가 대두되고, 농산물을 안전하게 생산하는 것은 건강 유지뿐만 아니라 환경에 미치는 위해요소를 제거하여 생태계 보존 및 청결한 과원 관리가 절실하게 요구되고 있다.

오미자는 주로 해발 300m이상 되는 고랭지 지역에서 재배되고 있는 덩굴성 식물로 수명은 8-12년 정도 되는 우리나라 약용작물 중의 하나다. 특히 최근에 오미자의 맛과 효능이 소비자로부터 인정을 받으면서 재배면적이 전북 동부산악권(무주, 진안, 장수, 남원, 순창)을 중심으로 날로 증가하고 있는 실정이다. 그러나 오미자 재배면적이 집단화 규모화 되면서 병해충의 발생양상도 다르게 나타나-오미자에 대한 주요 병해충을 파악하여 방제의 기초자료 제공 및 병해충의 위험도를 평가하고자 이에 대한 실태를 조사 한 결과 오미자에 주로 발생하는 해충은 오미자 식나무깍지벌레가 피해가 많았으나 오미자 식재년수가 늘어나고 노후화 과원이 증가하면서 포도유리나방 및 신종 해충으로서 검은점애바구미 (*Dendrobaris maculata*(Roelofs, 1879))가 발생하였으며, 그밖에도 거위벌레, 노린재류, 자나방, 주머니나방, 열매를 가해하는 깍지벌레가 발생함을 알 수 있었다. 또한 해충이 아니었던 검거세미나방도 돌발해충으로 발생되어 많은 잎을 가해하기도 했다. 따라서 오미자 신종해충인 검은점애바구미의 사진자료와 피해증상을 보고하고, 오미자 줄기를 가해하는 주요 해충에 대한 정보를 공유하며, 병해충별 정확한 생리생태와 방제방법, 친환경 방제자재 선발 등을 연구함으로서 농가의 안정생산에 기여하고자 한다.

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점착트랩을 이용한 담배가루이 유인효과

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2009년 5월에 전라북도농업기술원 수경재배 비닐하우스에 가지를 정식하고 황색 등 8종의 색상지에 점착액을 도포하여 담배가루이 유인효과를 살펴보았으며, 트랩 점착액에 포도당, 과당, 올리고당, 물엿, 설탕 등을 첨가하여 당류 첨가에 따른 유인효과를 살펴보았다. 또한, 점착트랩을 지제부 30cm 위, 중간부, 정단부, 정단 30cm 위에 설치하고 담배가루이 유인 효과를 조사한 결과 색상지에 따른 담배가루이 유인효과는 황색이 100cm^2 당 87.9마리로 가장 많았고, 연두>주황>녹색>검정>적색>청색>백색순이었다. 점착액 당류 첨가효과는 포도당과 과당이 100cm^2 당 각각 159.3, 159.0마리로 유인량이 가장 많았고, 올리고당>물엿>설탕 순이었으며, 설치위치에 따라서는 정단부가 100㎠ 당 103.3마리로 가장 많고, 지제부 30cm 위 지점이 85.0마리였으며, 정단부 30cm 위와 중간부는 각각 51.9마리, 55.4마리로 가장 적었다. 따라서 담배가루이 유인을 위한 점착트랩은 포도당 또는 과당을 첨가한 점착액을 황색지에 도포하고 정단부와 지제부 30cm 위 지점에 설치하는 것이 좋을 것으로 판단된다.

검색어: 담배가루이(*Bemisia tabaci* Gonnadius), 색상지, 당, 유인효과

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Control effect of *Thrips tabaci* Lindeman using Parasitic natural and plant extracts in korean leek(*Allium tuberosum*) and green onion(*Allium fistulosum*)

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To control *Thrips tabaci* in Korean leek and green onion which grow at vinyl house in IKSAN, Jeollabuk-do, the non-treatment was set as negative control. In general treatment group, 120 mesh gauze was installed on the side window after planting(May, 2nd) and, in spring, *Orius strigicollis* (1.0/m^2) was grazed 3 times every 7 days from mid of May which is early development stage and In the mid of June, which is the peak stage, plant extracts were sprayed one time. In autumn, *O. strigicollis* was grazed 3 times every 7 days from mid of September which is early development stage, and in the mid of October, which is the peak stage, plant extracts were sprayed one time. The result shows that the leaf damage ratio was decreased by 22% in Korean leek and by 27% in green onion compared to the untreatment. And the control value of *Thrips tabaci* shows 78.7% in korean leak and 90.6% in green onion. The density control effect of *Thrips tabaci* was significantly controlled under max 6.2/plant in general treatment group compared max 25/plant in the untreatment and this result was similar in green onion. The yields by general treatment was increased by 85% in Korean leek and 56% in green onion, compared with non-treatment yields, which was 900kg/10a in Korean leek and 1,287kg/10a in green onion.

Key words: *Thrips tabaci*, *Orius strigicollis*, Green onion, Korean leek, The leaf damage ratio, Control value

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A general management effect of cruciferous vegetables pest

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To control pest of Brassicaceae leafy vegetable(leaf broccoli, Red Mustard Leaf, Tatsoi) which grows at vinyl house in IKSAN, Jeollabuk-do, the non-treatment was set as negative control, and treatment was divided into Parasitic natural treatment group and general treatment group. And incidence density of pest was surveyed and control effect was analyzed. As a result, in case of spring plants, the leaf damage ratio was decreased by 31% in Leaf broccoli, 30% in Red mustard leaf and 27% in Tatsoi compared to untreatment. In case of autumn plants, it was decreased by 32%, 41% and 17% respectively. The key pests were *Plutella xylostella*, *Pieris rapae*, *Myus persicae* Sulzer, *Thrips palmi* and Striped cabbage flea-beetle. Compared with the untreatment, the incidence density of each was significantly controlled. Other pests include *Spodoptera exigua*, *Macdunnoughia purissima*, *Macdunnoughia purissima* which showed high incidental density sometimes. In case of spring plants, the number by treatment was increased by 117% in Leaf broccoli, 85% in Red mustard leaf and 1,000% in Tatsoi. In autumn plants, it was increased by 132%, 257% and 1,077% respectively. The used Parasitic natural and eco-friendly materials were *Cotesia glomerata*, lacewing, ladyburg, *Orius laevigatus*, *Encarsia formosa*, Entomopathogenic nematode, Chungjigi and Togkaki. During early development of each pest, the Parasitic naturals were grazed 2~3 times at the interval of 7~10days. During the peak time, eco-friendly materials were sprayed 1~2 times. Based on this, comprehensive management model was drafted by period for each Brassicaceae vegetables pest.

Key words: Leaf broccoli, Red Mustard Leaf, Tatsoi, Comprehensive management model, Parasitic natural, Eco-friendly materials

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Monitoring for insecticide resistance in field-collected populations of *Culexpipienspallens*(Diptera:Culicidae)

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Five field-collected populations (TR-CP, UR-CP, JR-CP, GR-CP, and BR-CP colonies) of northern house mosquito, *Culex pipiens pallens*, identified by polymer chain reaction (PCR) were tested for susceptibility to 10 different insecticides by direct-contact mortality bioassay in comparison with an insecticide-susceptible KS-CP strain. Marked regional variations of insecticide susceptibility were observed. Extremely high to high levels of resistance were obtained: bifenthrin, resistance ratio (RR) = 1–520; β-cyfluthrin, RR = 16–397; α-cypermethrin, RR = 9–343; deltamethrin, RR = 1–40; etofenprox, RR = 2–42; permethrin, RR = 2–12; chlorpyrifos, RR = 2–675; fenitrothion, RR = 0.5–364; and fenthion, RR = 2–360. All of the colonies were susceptible to one or more of the insecticides examined. These results indicate that careful selection and rotational use of these insecticides should result in continued satisfactory control against field populations of northern house mosquito.

Key words: *Culexpipiens pallens*, Northern house mosquito, Insecticide resistance, Resistance monitoring, Regional variation

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Bacillus thuringiensis subsp. *israelensis* CAB191 균주를 이용한 모기유충의 친환경적 방제

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파리목 모기과에 속하는 모기는 인간에게 질병을 매개하는 위생해충으로 세대기간이 짧으며, 번식력이 강한 특성을 가지고 있다. 인간에게 피해를 주는 모기에 대한 국내의 모기 방제는 대부분 성충을 대상으로 분무식 화학농약을 처리하였으나성충의 휴식 및 행동습성 그리고 정확한 서식처에 직접 접촉을 해야 방제효과를 얻을 수 있다는 점에서 방제에 어려움이 있다. 본 연구에서는 피해의 본질적인 원인이 되는 모기 유충을 대상으로 곤충 살충성 단백질을 생성하는 *Bacillus thuringiensis*(이하Bt)균주를 선발하여 친환경적인 모기 방제에 대한 실험을 수행하였다.

국내의 토양에서 Spherical type의 Crystal을 형성하는 19개 균주를 위상차 현미경으로 확인 후 모기에 가장 높은 활성을 보인 *B.thuringiensis* subsp. *israelensis* CAB191균주를 선발 대량배양하였다., 생물검정은 현재 시판중인 *B.t.i* 약제(B제품)와 에스메토프렌을 주성분으로 하는 천연 식물성 테르페노이드 화합물인 약제(A제품)를 대조구로 사용하였다. 대상 해충은 이집트숲모기(*Aedes aegypti*), 이나도미집모기(*Culex inatomii*), 지하집모기(*Culex pipiens molestus*)의 3령 유충으로 생물 검정을 수행하였다. CAB191균주와 B제품은 10^3cfu/ml에서 이집트숲모기, 이나도미집모기, 지하집모기에 90%이상의 높은 사충률을 보였다. 반면 A제품은 1,000배 희석액에서 48시간 후 검정시 10%정도의 사충률을 보였다. 이로써 CAB191균주와 B제품이 활성이 높음을 알 수 있었다. 또한 *B.t.i*와 B제품, CAB191, 대조 균주로 *B.t.morrisoni*의 단백질 패턴을 분석하기 위하여 SDS-PAGE한 결과 CAB191, B제품이 *B.t.i*와 동일한 130, 72, 27KDa의 밴드를 형성함을 알 수 있었다.

검색어: *Bacillus thuringiensis*, Spherical type, SDS-PAGE

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곤충 사체에서 분리한 *Bacillus thuringiensis*균주에 의한 살충활성 검정

<u>범종일</u>, 문청원, 강동균, 길영종, 김기수, 문윤영, 서미자, 윤영남, 유용만

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해충에 대한 화학농약의 오남용으로 인하여 해충의 저항성이 발달되고 환경오염, 인축에 대한 위험 등의 이유로 화학농약의 사용을 줄이게 되었다. 그래서 친환경적인 방제인자인 미생물농약 *Bacillus thuringiensis*(이하 *B.t*)가 현재 전 세계적으로 널리 사용되고 있다. *B.t*는 그람 양성의 호기성 간균으로 토양, 곡물의 분진, 낙엽, 곤충의 사체등 다양한 곳에서 분리되는 것으로 알려져 있는데 본 연구에서는 풍뎅이류 곤충의 사체로부터 *B.t*를 분리하여 딱정벌레목 및 나비목 해충에 대한 생물활성 검정을 하여 살충활성이 우수한 균주를 선발하였으며 SDS-PAGE를 수행하였다.

파밤나방에 대한 생물활성 검정 결과, CAB530 균주는 처리 48시간 후에 90%가 넘는 사충률을 보여주었으나 CAB533 균주는 6%의 사충률을 보여주었다. 반면에 장수풍뎅이 유충과 배추벼룩잎벌레 성충에 대해서는 살충활성을 나타내지 않았다. SDS-PAGE 수행 결과 파밤나방에 살충활성이 있는 CAB530 균주는 *B.t* subsp. *kurstaki*와 비슷한 130kDa의 밴드를 나타냈으며 파밤나방 중장액으로 소화를 시킨 후에 약 65kDa의 밴드를 확인할 수 있었다. 파밤나방에 대해 살충활성이 적은 CAB533 균주는 65kDa의 독소단백질 밴드를 나타냈지만 파밤나방에 대해서 살충활성이 높지는 않았다.

검색어: *Bacillus thuringiensis*, 파밤나방, 딱정벌레목

P139

Occurrence and Distribution of Entomopathogenic fungi from Soils in Korea

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In agricultural fields, the entomopathogenic fungal species have been investigated for their potential as the biological control agents due to their role of natural enemies for insects. To address the requirements of a potential South Korea based biocontrol effort using entomopathogenic fungi, we investigated the occurrence of various entomopathogenic fungi in 1080 soil samples representing from various area and locations in South Korea. Entomopathogenic fungi were isolated from soils using semiselective medium SDA-D50 contained saboraund dextrose agar, 50 ug/ml dodine, 100 ug/ml chloramphenicol and 50 ug/ml streptomycin. The isolated putative fungi were identified by the determination of internal transcribed spacer (ITS) region sequences of the nuclear ribosomal analysis. As a result, entomopathogenic fungi were found to occur in 30.8% of the soil samples studied. The most abundant species were *Beauveria bassiana* (Bals.) Vuill. and *Metarhizium anisopliae* (Metschn.) Sorok. Isolates of *B. brongniartii*, *Cordyceps* sp., *Lecanicillium* sp., *Isaria* sp. and *Tolypocladium cylindrosporum* were also found. The occurrence of entomopathogenic fungi was analyzed by the area and soil types. These positive entomopathogenic fungi may have potential against variety pests in agriculture and forest.

Key words: dodine, entomopathogenic fungi, natural occurrence, Korea

P140

Cross Resistance and Synergistic effect of Acequinocyl Resistance in Twospotted Spider Mite, *Tetranychus urticae*

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Twospotted spider mite, *Tetranychus urticae* was collected from the rose greenhouse in Gimhae, Gyeongnam province in Jan, 2001. Resistant strain was reared over nine years treated with Acequinocyl (over 400 times), and increased 614 folds as compared to susceptible strain (S). Cross resistance of acequinocyl-resistant strain adults to eight acaricide was showed high in Cyflumetofen (108 folds) and expressed low in Abamectin (16 folds), Tebufenpyrad (7.6 folds), Fenpyroximate (6.1 folds). Against Chlorfenapyr (0.5 folds), however, showed negatively correlated cross resistance. Synergistic effects with PBO (piperonyl butoxide), an oxygenase inhibitor, DEF (*S,S,S*-tributyl phosphorotrithioate), an esterase inhibitor, and DEM (diethymaleate), an inhibitor of glutathion S-transferase were also investigated. Synergistic effect showed low in DEM (4.2 folds) but showed high in PBO (12 folds) and DEF (23 folds).

Key words: *Tetranychus urticae*, Twospotted spider mite, Cross resistance, Acequinocyl, Acaricide

P141

Attraction Effect and Electrophysiological Response of Spearmint Oil against Lantern Fly, *Lycorma delicatula*

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This study was performed to investigate attraction effect of six plant essential oils and to confirm their electrophysiological response against *Lycorma delicatula.* Among the tested oils, spearmint oil (94.1%) significantly attracted *L. delicatula* at a dose of 1.25㎕/cm^2 by using an olfactometer. In dose response to spearmint oil, a dose of 2.5㎕/cm^2 was very effective. GC-MS analysis revealed that the active components responsible for the effective attraction effect of spearmint oil were carvone (70.6%) and limonene (54.8%). Of the two active components, carvone was more significant than limonene with reference to attraction activity against *L. delicatula*. Analysis by GC-EAD showed, major components of spearmint oil that elicited response in *L. delicatula* antennae, indicating the potential role of the essential oil as attractant that determine the choice of the attraction material. In the field test, spearmint oil exhibited attraction effect up to 5 days. This effect was different in accordance with test places and treatment dose.

Key words: Lantern fly, *Lycorma delicatula*, attraction effect, electrophysiological response

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Effect of Electron-beam Irradiation on the Development and Reproduction of Agricultural Insect Pests

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On the development and reproduction of four major agricultural insect pests including *B. tabaci, M. persicae, P. xylostella* and *T. urticae*, electron-beam was irradiated with different doses of 30, 50, 70, and 100 Gy. The effect of electron beam was investigated with respect to the longevity, egg hatching, emergence, and fecundity. Eggs hatching of *B. tabaci, P. xylostella* and *T. urticae* were more inhibited as increased irradiation doses. Especially *B. tabaci* and *T. urticae* eggs were perfectly inhibited to hatch at a dose of 100 Gy. However, these pests showed no lethal effect on the nymph/larva, pupa, and adult stages. When irradiated on the eggs of *B. tabaci, P. xylostella* and *T. urticae*, the emergence was inhibited from nymphs/larvae to adults. Individually, *B. tabaci* emerged adult did not lay eggs at a dose of 70 Gy. Besides, fecundity of *P. xylostella* emerged adult decreased at a dose of 100 Gy. On the contrary, irradiation did not affect the longevity of *P. xylostella* adult. When irradiated on *B. tabaci, P. xylostella, Myzus persicae* and *T. urticae* nymphs/larvae, emergence was inhibited at doses of 70 and 100 Gy, and decreased the fecundity and inhibited the hatching of laid eggs. However, the longevity of adults did not affect.

Key words: *B. tabaci, M. persicae,* Electron beam, Irradiation

P143

Mass Production and Formulation of *Mamestra brassicae* Nucleopolyhedrovirus-K1

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Mamestra brassicae (cabbage moth) is a common European moth of the order Lepidoptera and the family Noctuidae. The larval stage is highly polyphagous and is known to feed on more than 70 species of host plants from 22 families, including Brassica species, lettuce, onion, potato, pea, tomato and apple. *M. brassicae* has become a significant pest also in Asia due to the damage caused to agriculturally and economically important Brassica crops. It is difficult to control *M. brassicae* using chemical insecticide because of its rapid development of resistance. The objective of our study, therefore, was the mass production and formulation of a local strain of *M. brassicae* nucleopolyhedrovirus-K1 (MabrNPV-K1) for the development of viral insecticide to control it. In production efficiency of MabrNPV-K1 using *M. brassicae* larvae, the mortality of the 3rd instar larvae was 100% when inoculated with 1.0×10^5 PIBs/larva and the yield of MabrNPV-K1 was maximal. Regarding the mortality, yield of polyhedra, inoculation doses and required time, the 1.0×10^4 PIBs/larva at 30°C was determined as optimal conditions producing polyhedra efficiently. To formulate MabrNPV-K1, feeding toxicities of various supplements including spreader and ultraviolet (UV) -protectant were determined. Tinopal UNPA-GX which is UV-protectants was effective for protection of polyhedra from UV and showed the increased mortality when added with 1% concentration. Other supplements did not influence significantly the mortality of MabrNPV-K1. Formulated MabrNPV-K1 with several supplements showed higher pathogencity than un-formulated MabrNPV-K1.

Key words: *Mamestra brassicae*, MabrNPV-K1, formulation, UV-protectant, Tinopal

P144

유충사육을 통한 산림해충 형태 및 생활사 구명

권영대, 지은미, 우건석, 김경환
경기도산림환경연구소 나무연구팀

산림에 발생하여 피해를 주는 돌발해충의 조기진단을 위하여 유충발생 시기인 5월부터 9월까지 수목을 가해하고 있는 유충을 기주와 함께 채집하여 플라스틱 사육용기에 넣어 온도 23℃, 습도 70%, 명암 16L:8D이 일정하게 유지되는 항온항습실 조건에서 실내사육을 실시하였다. 기주는 냉장보관하면서 공급하였으며, 유충의 충태별 형태와, 생육기간 등 생활사를 조사하였다. 이번 조사를 통하여 채집된 유충은 총 192종으로 이 중 75종이 확인되었으며, 117종은 사육중 폐사되었거나 번데기상태로 아직 미확인되었다. 분류군별로 정리하면 나비목이 22과 170종으로 가장 많이 조사되었으며, 그 다음이 딱정벌레목, 벌목의 순으로 조사되었다. 나비목에서는 자나방과가 45종, 밤나방과가 35종으로 가장 많이 조사되었으며, 그 다음으로 명나방과, 잎말이나방과, 재주나방과, 독나방과의 순으로 조사되었다. 기타 분류군에서는 잎벌레와 잎벌 등 식엽성 해충이 대부분 조사되었다.

또한 채집·사육된 유충들을 기주별로 분석한 결과 총 41종의 기주식물이 조사되었으며, 그 중 참나무류가 21종으로 가장 많이 조사되었다. 그 다음으로 버드나무, 벚나무, 밤나무 등의 순으로 많았다. 그리고 2종 이상의 기주식물을 가해한 유충으로는 미국흰불나방, 사과독나방, 무늬독나방, 긴금무늬밤나방, 꾕비름집나방, 줄점불나방, 줄고운가지나방 등이 조사되었다. 앞으로 이러한 기주식물별 유충자료는 산림해충 동정에 중요한 자료로 활용할 것으로 판단된다.

검색어: 유충형태, 생활사, 유충사육, 기주식물, 산림해충

P145

A Stong Ubiquitous Activity of *Bombyx mori* Heat Shock Protein 70 Promoter

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For stable germline transformation, the promoter of B. mori cytoplasmic actin gene (BmA3) was used to ubiquitous expression of transgenes. Except for BmA3 promoter, promoters used to regulate gene expressionin all tissues and developmental stages of *B. mori* were not nearly developed. To identify more powerful promoter than previously reported BmA3 promoter (Mange et al., 1997), we introduced a new dot blot hybridization method, and isolated nine clones that show stronger dot signal compared to the control, BmA3by this method. Among these 9 clones, we focused on one clone which has high amino acid homology (94%) with heat shock protein 70 gene of *Trichoplusia ni*. This resulting positive clone, named bHsp70 (*B. mori* heat shock protein 70) was ubiquitiously expressed in tissues and developmental stage of fifth instar B. mori larvae,and stimulated bythermal and ER stress. As result of promoter assay using dual luciferase assay system, we found the highest transcription activity region (-1003/+147) in the 5'-flanking region of bHsp70 gene that has 264-fold more intensive promoter activity than BmA3 promoter. Moreover, transcription activity of bHsp70 promoter under heat shock condition (42 ℃, 4 hr) was increased over 2-fold than normal condition. Therefore, we suggest that bHsp70 promoter may be used more effective candidate for transgene expression in B. mori.

Key words: *Bombyx mori*, Heat shock protein 70, Luciferase assay, Promoter

P146

Characterization and functional expression of attacin, an antibacterial protein, from the swallowtail butterfly, *papilio xuthus*

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Attacin is a well-studied glycine-rich antibacterial protein in insect immune response, which has limitary antibacterial effect to some Gram-negative bacteria. A cDNA encoding the attacin gene was screened and isolated from the immunized larvae of the swallowtail butterfly, *Papilio xuthus*. The complete *P. xuthus* attacin cDNA is 949 nucleotides encoding a 250 amino acid precursor that contains a putative 18-residue signal peptide, a common 42-residue pro-peptide sequence and a presumed 190-residue mature protein with a theoretical mass of 19904.01 and a pI of 9.13. The putative mature protein of *P. xuthus* attacin showed 48%~52% and 24%~30% identity in amino acid sequences with that of lepidopteran and dipteran insects, respectively. The attacin transcript was induced at significant level after injection with bacterial lipopolysaccharide (LPS). Recombinant attacin was highly expressed in *E. coli* BL21 (DE3) cells by fusing with an N-terminal S-tag/thrombin cleavage site configuration protein to avoid the cell death during induction. The expressed fusion protein was purified by Ni-NTA immobilized metal affinity chromatography (IMAC). After desalting and cleavage with thrombin, the recombinant attacin was released and showed considerably antibacterial activity against Gram-negative bacteria, *E. coli* ML 35. Our results proved that this protein family with a potent antibacterial activity may play a role in the immune response of butterflies.

Key words: *Papilio xuthus, Attacin*, antibacterial protein, expression, *E. coli*

P147

Development and characterization of microsatellite loci in the small-brownplanthooper(*Laodelphax striatellus*)

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The Laodelphax striatellus(SBPH: Small Brown Plant Hopper) is known to be not overwintering in South Korea and migrate from China to Korea every year by now, but these days many evidence support the possibility of SBPH over-wintering. These insects do considerable damage to the rice production in Korea. If they will come from China, identification of origin of migration is very important to make countermeasure against SBHP outbreak. So we want to know exact the route of long-distance migration of them. In this study, we have developed some microsatellite markers for basic population genetic analysis of SBPH. We will show the genetic characteristics of them

Key words: *Laodelphax striatellus*, molecular marker, Microsatellite, population genetics, SBPH

P148

Comparison of Pollinating Effect using 3 Species of Insects, *A. mellifera, O. cornifrons, B. terrestris*, in Japanese apricot Field

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To increase the fruit quality of the Japanese apricot, 3 species of insects, *Apis mellifera, Bombus terrestris* and *Osmia cornifrons* were used for pollination in Japanese apricot field in Jinju and Sancheong province. And also economical effect for crops of Japanese apricot fruit pollinated with same insect was analyzed. This study was also conducted using 3 kinds of methods for pollination effect, natural condition, net-house and control method. Because blooming period of Japanese apricot was different from the other fruit tree(Blooming time of Japanese apricot shows always in the middle of the March), foraging behavior of insects used in this examination showed different tendency each other. Especially *O. cornifrons* was not adapted to wind and lower temperature compared with *A. mellifera* and *B. terrestris* in this field condition. Rate of fruit set pollinated with *A. mellifera* and *B. terrestris* was showed 14.9% and 13% respectively. But *O. cornifrons* was lower than another 2 kinds of insects with 6% of fruit setting rate. Total rate of fruit set of Japanese apricot showed lower tendency compared with other kinds of fruit tree with under 30%. Quality of fruit pollinated with *A. mellifera* and *B. terrestris* showed higher than *O. cornifrons* in natural field condition in fruit weight. Economical income of Japanese apricot fruit producted by *A. mellifera* showed highest with 185% of benefit effect, and *B. terrestris* with 143% compared with natural field condition.

Key words: Japanese apricot, Pollination, *Apis mellifera, Bombus terrestris* , *Osmia cornifrons*

P149

Microarray expression profiling of oxidative stress responsive genes in *Spodoptera litura*

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To examine the expression profile of oxidative stress responsive genes in Spodoptera litura, we constructed a cDNA library from *S. litura* injected with hydrogen peroxide (H_2O_2). Using a microarray chip composed of 2,964 cDNAs, we screened gene expression at 1, 3, 5, 7, and 9 h post H_2O_2 injection. Data were clustered into 15 groups of genes that behave similarly across each time course. Seventy-three genes were identified as being at least 2-fold up- or downregulated after treatment with H_2O_2 in *S. litura*. We constructed expressed sequence tags (ESTs) for genes that changed at least 2-fold after treatment with H_2O_2. The functional classification of these ESTs based on Gene Ontology showed that the ESTs are rich in genes involved in oxidoreductase activity (5.7%), defense (14.3%), cellular process (22.9%), and development (17.1%).

Key words: microarray, oxidative stress, *Spodoptera litura*

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Molecular mechanism of T-lymphocyte apoptosis caused by coprisin

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Our previous study demonstrated that Coprisin, a peptide from Copris tripartitus infected with bacterial pathogens, has an antibacterial activity. We assessed in this study whether Coprisin caused cellular toxicity in various mammalian cell lines. Coprisin selectively caused a marked drop of cell viability in Jurkat T cells, U937 cells and AML-2 cells belonging to the human leukemia cells but not in Caki cells and Hela cells. Fragmentation of DNA, a maker of apoptosis, was also confirmed in theleukemia cell lines but not in other cells. The Coprisin-induced apoptosis in leukemia cells was mediated by AIF (apoptosis inducing factor), a caspase -independent pathway.

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농약사용 조건에 따른 배 병해충 방제 효과

조영식, 송장훈, 최장전, 최진호, 황해성
국립원예특작과학원 배시험장

배 병해충 방제시 농약사용 절감과 방제효율 개선을 위해 고속살포기(SS기; Speed Sprayer; HA-1000SCA)를 사용하여 2개 시험포장을 대상으로 각 포장에 동일한 시험구로 관행구(노즐:ø1.0mm 표준노즐; 분무압력 : 20kg/cm^2; 표준농도; 살포량 : 1L/3.3m^2), 관행저물량구(노즐:ø1.0mm 표준노즐; 분무압력 : 20kg/cm^2; 표준농도; 살포량 : 0.7L/3.3m^2), 저물량-1구(노즐:ID노즐(Lechler사; 스위스); 분무압력 : 10kg/cm^2; 1.5배 고농도; 살포량 : 0.5L/3.3m^2), 및 저물량-2구(노즐:ID노즐(Lechler사; 스위스); 분무압력 : 10kg/cm^2; 1.5배 고농도; 살포량 : 0.7L/3.3m^2)로 설정하여 방제하였는데, 시험포장에 따라 병해충의 발생 정도는 달랐지만 배 생육기 동안 검은별무늬병, 붉은별무늬병, 꼬마배나무이, 사과애모무늬잎말이나방의 방제 효과는 관행구와 저물량-2구에서 적은 병해충 발생량을 보였다. 관행저물량구와 저물량-1구의 병해충 발생량의 전자의 두 처리구보다 많은 경향을 보였다. 수확과실에 대해 검은별무늬병과 붉은별무늬병의 피해과율은 재배기와 유사한 경향을 보였지만 복숭아순나방 등 심식충류와 사과애모무늬잎말이나방의 피해과율은 처리구간 큰 차이가 없었고, 시포험포장 I과 II의 관행저물량구에서 깍지벌레류에 의한 피해과율이 각각 2.1과 7.5%로 가장 많았고, 다른 처리구에서는 0.9~1.4%의 피해과율로 큰 차이가 없었다. 따라서, 단위면적당 농약사용량(A.I.)은 일정하게 유지하여야 할 것으로 생각된다.

검색어: 배, 방제력, 방제효과, 병해충, 농약살포조건, 피해율

P152

Molecular characterization of a venom serine protease from the bumblebee *Bombus terrestris*

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Bee venom contains a variety of peptides and enzymes, including serine proteases. Here we describe the molecular cloning and characterization of a serine protease (Bt-VSP) isolated from the venom of the bumblebee *Bombus terrestris*. The *Bt-VSP* gene consists of six exons encoding a 358-amino acid protein. The form of Bt-VSP detected in bee venom was the 34-kDa mature protein, which is created by cleavage of the catalytic domain of Bt-proVSP between Arg111 and Val112. Bt-VSP activates prothrombin and directly degrades fibrinogen into fibrin degradation products, defining roles for Bt-VSP as a prothrombin activator, a thrombin-like protease, and a plasmin-like protease. The finding that Bt-VSP acts as a fibrin(ogen)olytic enzyme is similar to a previous finding that Bi-VSP, a venom serine protease of *B. ignitus*, exhibits fibrin(ogen)olytic activity. We also compared major venom components in honeybee and bumblebee, and found that bumblebee venom contains a larger amount of serine protease. Furthermore, unlike bumblebee venom, which exhibits fibrin(ogen)olytic activity owing to the presence of a serine protease, it is likely that honeybee venom lacks fibrin(ogen)olytic activity.

P153

Molecular cloning and characterization of a short peptidoglycan recognition protein (PGRP-S) with antibacterial activity from the bumblebee *Bombus ignitus*

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Peptidoglycan recognition proteins (PGRPs) are pattern recognition molecules of the innate immune system that recognize peptidoglycan, a unique cell wall component of bacteria. Here we cloned and characterized PGRP-S from the bumblebee *Bombus ignitus* (*BiPGRP-S*). The *BiPGRP-S* gene consists of four exons encoding 194 amino acid residues. Comparative analysis indicates that the predicted amino acid sequence of BiPGRP-S shares high identity with enzymatically active PGRP-S proteins and contains the amino acids required for amidase activity. BiPGRP-S in *B. ignitus* worker bees is constitutively expressed in boththe fat body and epidermis, and it is secreted into the hemolymph. Quantitative real-time PCR assays revealed that in both the fat body and epidermis, the *BiPGRP-S* gene is highly induced by an injection of *Bacillus thuringiensis*. In addition, recombinant BiPGRP-S expressed as a 19-kDa protein in baculovirus-infected insect cells can bind to *B. megaterium* and *B. thuringiensis* but not to *Staphylococcus aureus*, *Escherichia coli* or *Beauveria bassiana*. Consistent with these data, BiPGRP-S shows antibacterial activity against *B. megaterium* and *B. thuringiensis*. These results indicate that BiPGRP-S is an inducible protein that may be involved in the immune response against bacterial infection of the genus *Bacillus* as an amidase-type PGRP-S.

P154

cDNA Cloning and Genomic Structure of Glyceraldehyde-3-Phosphate Dehydrogenase from the Entomopathogenic fungus, *Paecilomyces tenuipes*-Jocheon.

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Fungi belonging to the *Paecilomyces* spp. have recently been used as food and herbal medicines in Korea and are greatly popular as commercially available powdered supplement or dried fruiting body. Despite this acceptance and its use, little is known of the genes related to its reactive agents. Presently, We have constructed an olig-d(T) primed directional cDNA library from the silkworm Dongchunghacho, an entomopathogenic fungus, of which species is belonging to *Paecilomyces* spp. based on the previous identification of ITS1 and ITS2 at the molecular level and collected from Jocheon Miryang, Korea. To isolate and screen genes in the fungus, 626 expressed sequence tags(ESTs) were generated by a partial sequencing from the cDNA library. cDNA encoding the glyceraldehyde-3-phosphate dehydrogenase(Pt-GAPDH) of *Paecilomyces tenuipes*-Jocheon was cloned from the above cDNA library. The complete cDNA sequence of Pt-GAPDH is comprised of 1,014bp encoding 338 amino acid residues. The deduced protein sequence of Pt-GAPDH showed higher homology with *Beauberia bassiana*-GAPDH(93% amino acid identity). Hydropathy analysis revealed that Pt-GAPDH protein is hydrophilic. The major three amino acids in its composition of amino acid residues were alanine(11.54%), valine(9.47%) and glycine(8.88%). The Pt-GAPDH gene of *Paecilomyces tenuipes* entomopathogenic fungus consisted of three exons and two introns coding for 338 amino acid residues, and the genomic DNA length of the gene spans 1302bp. The accession number of the gene in GenBank are GU997099 for Pt-GAPDH cDNA and GU997102 for Pt-GAPDH genomic DNA. More investigation works including gene expression, immunological analysis etc. will be carried continuously without hesitation after this presentation.

P155

Identification and Characterization of Venom Components of Two Solitary Hunting Wasps, *Orancistrocerus drewseni* and *Eumenes pomiformis*

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To search for novel biologically active venom components, secretory venom proteins of two solitary hunting wasps, *Orancistrocerus drewseni* Saussure (1857) and *Eumenes pomiformis* Fabricus (1781), were identified by SDS-PAGE in conjunction with mass analysis with the aid of venom gland and sac-specific EST libraries constructed by suppression subtractive hybridization. Arginine kinase was the most predominant protein in both wasp venoms. Along with the full-length arginine kinase, a truncated form, which was known to have paralytic activity on a spider, was a common predominant protein in the two wasp venoms. Insulin/insulin-like peptide-binding protein was abundantly found only in *E. pomiformis* venom and the EST library, which might be due to its unique behaviors of oviposition and provision. It seemed that some venom proteins are secreted into venom fluid from venom gland cells via exosomes, not by signal sequence-mediated transport processes. Amphipathic α-helical peptides (10-15 amino acids) were predominantly transcribed in the venom gland/sac than protein components, and showed cell lytic activities against insect cells, mammalian cells, bacteria, and fungi. Phospholipase A2 and hyaluronidase, which are known to be the main components of wasp venoms, were found in both wasp venoms. In addition, a dendrotoxin-like peptide known to be a K^+ channel blocker was also found in the venom of *E. pomiformis*.

Key words: *Orancistrocerus drewseni*, *Eumenes pomiformis*, solitary hunting wasp, venom, EST library, secretome

P156

Rapid detection of novel Cry proteins of *Bacillus thuringiensis* isolates by electrospray ionization of Quadrupole time of flight mass spectrometry

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Bacillus thuringiensis (*B. t.*) strains are important microorganism because they produced a large amount of δ-endotoxin protein per bacterial cell and their toxins are highly toxic to Lepidoptera, Coleoptera, and Diptera depending on *B. t.* To date, more than a hundred Cry proteins have been identified and classified into 195 holotypes, based on the amino acid sequence identity. The Cry proteins or cry genes from the Korean native *B. t.* isolates in this study were not identified yet. The electrospray ionization of quadrupole time of flight mass spectrometry (ESI Q-TOF MS) was used to get the internal amino acid sequences of the endotoxin-spore culture mixtures of *B. t.* isolates, for which polymerase chain reaction (PCR) techniques were unable to detect the cognate genes. Most of Cry proteins seperated, excized, and extracted from the one dimensional - polyacrylamide gel electrophoresis (1D-PAGE), instead of 2D-PAGE, were matched with protein databases using MS-MASCOT search program. The internal amino acid sequences which were submitted to protein BLAST (basic local alignment search tool) had partially homology with the Cry protein databases. Hence, present data strongly suggest that the *de novo* amino acid sequencing and ESI Q-TOF/MS analysis along with MASCOT search could be used as a simple and rapid method for detection of novel Cry toxins from *B. t.* isolates and identification of *B. t.* isolates.

Key words: *Bacillus thuringeinsis* isolates, Cry proteins, ESI Q-TOF MS, *de novo* sequencing, MASCOT search

P157

진디혹파리 알에 대하여 오이에 등록된 51종 살균제의 독성평가

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원예용 오이방제 약제로 등록된 51종 살균제에 대하여 진디혹파리(*Aphidoletes aphidimyza*) 알에 대한 독성을 조사하였다. 농약보조제에 대한 독성평가는 실시하지 않았다. ethaboxam+Famoxadone, Copper oxychoride+dithianon, dimethomorph+ dithianon 에서 각각 21.5%, 18.6%, 16.4%의 살충독성을 보였을 뿐, 실험에 사용된 모든 약제는 30% 이하의 낮은 살충독성을 나타내었다. 10% 이상의 독성을 보인 약제는 5종 뿐이었으며 나머지 46종의 약제는 10% 이하의 독성을 보였다. Flucioxonile과 Kresoxim-methyl의 경우 콜레마니진디벌 성충에 대하여 각각 90.6%와 53.1%의 살충률을 보이나 진디혹파리 알에 대하여는 각각 3.1%와 9.7%의 낮은 살충률을 보였다.

검색어: 진디혹파리, 살균제, 오이, 독성

P158

High-level expression of the PRRSV structural proteins by SUMO fusion in *Bombyx mori* cells and larvae

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The porcine reproductive and respiratory syndrome virus (PRRSV) has three major structural proteins which designated as GP4, GP5, and M. They have been considered very important to arouse the humoral and cellular immune responses against PRRSV infection and proposed to be the excellent candidate proteins in the design of PRRS bioengineering vaccine. However, the PRRSV structural proteins are produced in low levels in the infected cells because it forms insoluble protein and possesses several transmembrane regions. To overcome this problem, we fused the GP4, GP5, and M with SUMO (Small ubiquitin-related modifier), and expressed the fused gene in Bm5 cells and silkworm larvae. Expression of the proteins were analyzed by 12% SDS-PAGE and western blotting using 6xHis tag and porcine anti-PRRSV antibodies. In results, SUMO fused proteins were expressed at a high level in Bm5 cells. The levels of protein using the silkworm larvae is higher than that using Bm5 cells. The fused protein was purified by Ni-NTA affinity chromatography. This study demonstrated that SUMO, when fused with PRRSV structural proteins, was able to promote its soluble expression. This may be a better method to produce PRRSV structural proteins for vaccine development.

Key words: PRRSV, SUMO, Bm5 cells, *Bombyx mori*

P159

왕우렁이의 집단폐사와 수서곤충상

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왕우렁이는 국내에서는 유기농법의 하나로 활용되고 있으나 최근에 일부 지역에서 이앙 후 살포된 왕우렁이들이 며칠 내에 집단폐사되는 경향을 보이고 있다. 이에 동지역에서 수서생물상을 조사함과 함께 왕우렁이의 폐사와 관련성이 있을 만한 원인을 조사하였다. 수서곤충상의 경우 특별한 관련성은 없었으나 수서생물 중 개형충의 일종인 참씨벌레는 왕우렁이 살포시기에 이미 개체수의 급격한 증가를 보이는 한편 참씨벌레에 대해 왕우렁이가 극도의 회피성을 나타내는 점이 파악되었다. 그 외에 왕우렁이에 미칠 수 있는 여러 요인들에 대한 사전조사를 실시하였다.

검색어: 유기농법, 왕우렁이, 개형충, 참씨벌레, 액비

P160

총채벌레에 의한 감귤의 피해 증상 및 발생 생태

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지금까지 총채벌레에 의한 감귤 과피에서의 전형적인 피해 증상은 개화기에 가해되어 과경부 또는 과정부위의 동그란 회갈색 띠가 형성되는 증상이었으며 꽃노랑총채벌레에 의해 가해된다고 알려져 있지만 확실치 않다. 최근들어 큰 피해를 주고 있는 증상은 노지재배 감귤에 볼록총채벌레에 의한 햇빛에 검붉게 그을린 듯한 증상(검은점무늬병 후기 증상 및 녹응애 피해 증상과 매우 유사)으로써 2007년부터 서귀포시 남원읍 일부지역에 크게 발생하여 큰 피해를 주고 있다. 또한 부지화 및 세토카 등의 하우스 감귤의 경우 과피가 하얗게 탈색되고 유통 및 저장 시 그 부위로부터 썩어들어 가는 증상들이 발생하고 있는데 이들 증상은 꽃노랑총채벌레에 의해 가해되는 것으로 확인되고 있다. 또한 노지 감귤에서도 극조생 밀감을 중심으로 이와 유사한 증상들이 발생되고 있는데 아직까지 어떤 종이 가해하고 있는지는 확실치가 않다. 볼록총채벌레는 6월 하순경부터 밀도가 증가하기 시작하여 7월 부터는 우점하며 5월 부터 10월 하순까지 최소 7회 이상 번식하였으며 끈이 트랩에 포획된 개체수는 2008년의 경우 7월 하순, 2009년의 경우 8월 하순경에 가장 큰 밀도를 보였다. 과실에서의 유충은 7월 하순부터 발견되었으며 피해 증상은 9월 중순부터 관찰되기 시작하였다

검색어: 감귤, 총채벌레, 피해 증상, 밀도