

0001

## Olfactory Response and Feeding Preference of the *Liriomyza huidobrensis* (Blanchard) (Diptera: Agromyzidae) to Potato Varieties

**Rameswor Maharjan and Chuleui Jung**

Department of Bioresources Science, Graduate School, Andong National University

The potato leafminer fly, *Liriomyza huidobrensis* (Blanchard) (Diptera: Agromyzidae) is a polyphagous pest attacking many vegetables and ornamental plants. We found *L. huidobrensis* were infesting potato crop in Miryang and Goreyong in 2011. Five potato (*Solanum tuberosum*) varieties (*Ghowun*, *Daeri*, *Sumi*, *Chubeak*, and *Seohong*) were tested for the preference of *L. huidobrensis*. In the olfactometer bioassay, leafminers chose the *Ghowun* variety most (55%) followed by *Sumi* (18%). Remaining 3 varieties were chosen less than 10%. When leafminers choose and move toward the preferred variety, movement speed was faster. In the plant choice test in the laboratory, as expected, *Ghowun* was the most chosen but the choice of the other 4 varieties was not different. The same pattern as found in the plant choice test conducted in the greenhouse. Feeding frequency was the highest in *Ghowun* variety followed by *Sumi* > *Daeri* = *Seohong* > *Chubaek* in the laboratory test but *Ghowun* > *Sumi* > *Chubaek* > *Daeri* = *Seohong* in greenhouse test. When measured in 2 weeks after release, plant damage rates and number of mines were in congruence to the preference results. Further study is needed to clarify the factor responsible for the choice of the plants and also the ways to manage this new pest.

**Key words:** Potato leafminer fly, five-arm olfactometer, varieties, feeding behavior

## Novel Histopathological and Molecular Effects of Natural Compound Pellitorine on Larval Midgut Epithelium and Anal Gills of *Aedes aegypti*

**Haribalan Perumalsamy<sup>1,2</sup>, Jun-Ran Kim<sup>1,2</sup>, Sang Mi Oh<sup>2</sup>, Je Won Jung<sup>2</sup>,  
Hyung Wook Kwon<sup>2</sup> and Young-Joon Ahn<sup>2</sup>**

<sup>1</sup>Research Institute for Agriculture and Life Science, Seoul National University

<sup>2</sup>WCU Biomodulation Major, Department of Agricultural Biotechnology,  
Seoul National University

The yellow fever mosquito, *Aedes aegypti*, is a vector for transmitting dengue fever and yellow fever. An assessment was made of the histopathological and molecular effects of pellitorine, an isobutylamide alkaloid, on third instar *Ae. aegypti* larvae. At 5 mg/L concentration of pellitorine, whole body of the treated larvae became dark in color, particularly damaged thorax and abdominal regions. Pellitorine targeted mainly on midgut epithelium and anal gills, indicating variably dramatic degenerative responses of the midgut through a sequential epithelial disorganization. The anterior and posterior midgut was entirely necrosed, bearing only gut lumen residues inside the peritrophic membranes. Pellitorine caused comprehensive damage of anal gill cells and branches of tracheole and the debris was found in hemolymph of anal gills. RT-PCR analysis indicates that the compound inhibited gene expression encoding V-type H<sup>+</sup>-ATPase and aquaporine 4 after treatment with 2.21 mg/L pellitorine. The results provide a fact that pellitorine merits further study as a potential larvicide with a specific target site or a lead molecule for the control of mosquito populations.

**Key words:** *Aedes aegypti*, pellitorine, histopathology, midgut, anal gill, target site, V-type H<sup>+</sup>-ATPase, aquaporine

0003

## Gene cloning of a Putative Plasmatocyte-spreading Peptide-binding Protein and its Function In Immune Responses of *Spodoptera exigua*

**Jiyeong Park and Yonggyun Kim**

Department of Bioresources Sciences, Andong National University

Immune defense is indispensable for insect survival. However, uncontrolled and excessive immune responses would be highly detrimental and energy-consuming processes. An insect cytokine, plasmatocyte-spreading peptide (PSP), induces hemocyte-spreading behavior as well as activating phenoloxidase (PO) in the beet armyworm, *Spodoptera exigua*. A hemocyte transcriptome of *S. exigua* contains a partial sequence of a putative PSP-binding protein (SePSP-BP). *SePSP-BP* was expressed in all developmental stages especially in hemocytes and fat body. A quantitative RT-PCR showed that the bacterial infection significantly up-regulated the expression level of *SePSP-BP*. A double-stranded RNA specific to *SePSP-BP* (dsRNA<sup>SePSP-BP</sup>) was injected and suppressed *SePSP-BP* expression even in response to bacterial challenge. The larvae treated with dsRNA<sup>SePSP-BP</sup> suffered high mortality to infection of nonpathogenic bacteria and prolonged high PO activity after the immune challenge. These results suggest that SePSP-BP may play a role in suppressing immune responses as a negative controller.

**Key words:** PSP-binding protein, PO, Immune, *Spodoptera exigua*

## Comparative Analysis of Common Host Two Baculoviruses Genomes Isolated from *Hyphantria cunea* in Korea

**Jae Bang Choi, Tae Young Shin, Sung Min Bae, Mi Ra Yu and Soo Dong Woo**

Department of Agricultural Biology, Chungbuk National University

*Hyphantria cunea* is a fall webworm is considered an agricultural pest. It is a major pest of many board-leaved trees. *H. cunea* nucleopolyhedrovirus (HcNPV) and *H. cunea* granulovirus (HcGV) were isolated from the fall webworm cadavers in Korea. To better understand HcNPV and HcGV, their genomic sequences were determined, analyzed and compared to two viruses together. The entire nucleotide sequence of the HcNPV genome was fully sequenced using 454 pyrosequencing. The genome of the HcNPV was 131,302 bp with a 45 % G+C content. Computer assisted analysis predicted 146 open reading frames (ORFs) of 50 or more amino acids that showed minimal overlap. Further more, when the phylogenetic relationship was analyzed, HcNPV was closely related to *Orgyia pseudotsugata* MNPV (OpMNPV) which belong to Group I NPV. The HcGV genome was 114,557 bp with a 39% G+C content and contained 130 putative ORFs of 50 or more amino acids. When phylogenetic relationships were analyzed, HcGV was closely related to *Xestia c-nigrum* granulovirus, which belong to the Type-II GV. HcNPV shares 48 ORFs with HcGV. The most significant difference between HcNPV and HcGV is *fgf* gene. HcNPV contains one *fgf* gene, whereas HcGV contains three *fgf* genes. The presence of *fgf* reduces the time and efficient systemic infection it takes the virus to kill its host. The difference of *fgf* number from HcNPV and HcGV suggested that different affect for the speed of systemic infection.

**Key words:** *Hyphantria cunea*, HcNPV, HcGV, genome sequence, *fgf* gene

O005

## **Polyhedrin Fusion Expression Enhance the Production of Foreign Protein in Baculovirus Expression System**

**Sung Min Bae<sup>1</sup>, Hee Jung Kim<sup>1</sup>, Tae Young Shin<sup>1</sup>, Jae Bang Choi<sup>1</sup>, Yeon Ho Je<sup>2</sup>,  
Byung Rae Jin<sup>3</sup> and Soo Dong Woo<sup>1</sup>**

<sup>1</sup>Department of Agricultural Biology, Chungbuk National University (sdwoo@cbnu.ac.kr)

<sup>2</sup>Research Institute for Agriculture and Life Sciences, Seoul National University

<sup>3</sup>College of Natural Resources and Life Science, Dong-A University

To enhance the production efficiency of foreign protein in baculovirus expression system, the effects of polyhedrin fragments were investigated by fusion expression them with the enhanced green fluorescence protein (EGFP). Recombinant viruses were generated to express EGFP fused with polyhedrin fragments based on the minimal region for self-assembly and the KRKK nuclear localization signal (NLS). The increase of EGFP production by fusion expressions was confirmed through protein and fluorescence intensity analyses. The importance of nuclear localization for enhanced production of EGFP was shown by the mutation of the NLS within the fused polyhedrin fragment. Among the fusion expressed protein in cytoplasm, the most hyper-expression was observed in the fusion of amino acids 32 to 59 of polyhedrin. Polyhedrin fragment fusion expression with classical swine fever virus E2 protein also resulted hyper-enhanced expression of E2 protein. However, the fusion expression of porcine circovirus ORF2 with polyhedrin fragment did not show significant enhance of ORF2 production. These results suggested that the enhancement of foreign protein production when fused with polyhedrin is caused by the enhanced stability of expressed protein.

**Key words:** Baculovirus, Polyhedrin, Fusion expression, Localization

## Sequential Immunosuppressive Activity of Bacterial Metabolites of an Entomopathogenic Bacterium, *Xenorhabdus nematophila*

**Seonghyeon Eom, Youngjin Park and Yonggyun Kim**

Department of Bioresource Sciences, Andong National University, Andong 760-749, Korea

An entomopathogenic bacterium, *Xenorhabdus nematophila*, secretes at least eight bacterial metabolites, which have suppressive effects on insect immunity. This study quantified their sequential production during bacterial growth and analyzed their individual immunosuppressive activities against an insect host, *Spodoptera exigua*. *X. nematophila* exhibited a typical bacterial growth in both insect host and culture medium, in which eight metabolites were secreted in different time points. At early growth phase (6 to 12 h), Ac-FGV, Cis-cPY, PHPP and indole metabolites were detected in the culture broth. During early growth phase, PHPP was highly potent to inhibit phenoloxidase activity as well as nodule formation. At late growth phase (24 to 48 h), BZA, HPA, PY were detected at 10 – 140 ppm in the culture broth, their metabolites were highly potent to inhibit phospholipase A2 and to induce cytotoxicity to hemocytes. These results suggest that *X. nematophila* sequentially produces the immune suppressive metabolites, which cooperatively inhibit different steps of insect immune responses.

**Key words:** Insect immune, immunosuppression, *Xenorhabdus nematophila*, hemocyte, benzylideneacetone.

0007

## Screening and Characterization of Antimicrobial Metabolites from Entomopathogenic Fungi

**Tae Young Shin, Seung Hyun Ko, Won Woo Lee, Jae Bang Choi, Sung Min Bae and Soo Dong Woo**

Department of Agricultural Biology, Chungbuk National University

Entomopathogenic fungi are natural pathogens of insects and contribute to the regulation of host insect populations in the environment. Several these fungi produce a wide range of secreted enzymes, secreted protein toxins and secondary metabolites to overcome host defenses and ultimately kill the host, and to defend host resources against competing pathogens and saprophytes. This study was performed to evaluate the antimicrobial activity of 207 entomopathogenic fungi from Korea soils against plant pathogenic bacteria *Ralstonia solanacearum* and plant pathogenic fungi *Botrytis cinerea* using dual culture technique on SDYA. As results, twelve isolates (5.7%) and six isolates (2.8%) showing the greatest inhibition against *R. solanacearum* and *B. cinerea*, respectively. The culture supernatant of these selected isolates completely suppressed the growth of the pathogen, indicating that suppression was due to the presence of antimicrobial compound in the culture filtrate. The stability test of the culture filtrate showed that the antimicrobial component was heat stable and not protein. These entomopathogenic fungal metabolites may be a good feature to be used in the development of a new biocontrol method of *R. solanacearum* and *B. cinerea*.

**Key words:** entomopathogenic fungi, antimicrobial activity, dual culture, culture filtrate

## **Selection and Evaluation of Acaropathogenic fungi to the Bulb mite, *Rhizoglyphus echinopus***

**Seung Hyun Ko, Tae Young Shin, Won Woo Lee, Jae Bang Choi,**

**Sung Min Bae and Soo Dong Woo**

Department of Agricultural Biology, Chungbuk National University

The bulb mite (*Rhizoglyphus echinopus*) damages garlic, shallot and onion in the bulbs, corms and tubers. It has recently become a serious problem because of the continuous use of acaricides resulting in resistance among bulb mite population. Thus, there is need to find alternative control measures to suppress bulb mite population. Here, we report the screening result of pathogenic fungi for the control of *R. echinopus*. Initial screenings were performed using 352 isolates of entomopathogenic fungi from Korea soils. As results, 15 isolates of acaropathogenic fungi showed the pathogenicity to bulb mite supporting fungal conidiation. These isolates were identified as 3 isolates of *Metarhizium flavoviride* var. *pemphigi* and 12 isolates of *Metarhizium pingshaense* by microscopic examination and genetic sequencing of the ITS region and elongation factor-1 alpha. Selected 15 isolates were tested for their virulence against adult *R. echinopus* and the thermotolerance and the activity to UV-B irradiation of conidia. Additionally, the activities of chitinases and proteases produced by *M. pingshaense* were compared according to the medium. These acaropathogenic fungi would be considered promising for biological control of bulb mite.

**Key words:** *Rhizoglyphus echinopus*, bulb mite, acaropathogenic fungi



0009

## 초생재배와 합성피레스로이드계 조합처리가 굴응애의 발생양상에 미치는 단기효과

현승용, 김동순\*

제주대학교 생명자원과학대학 식물자원환경전공(교신저자dongsoonkim@jejunu.ac.kr)

굴응애(*Panonychus citri* McGregor)는 감귤의 중요한 응애류 해충으로 다른 잎응애류(Tetranychidae)와 같이 재배환경에 따라 발생양상이 달라지는 것으로 알려져 있다. 본 연구에서는 감귤원에서 초생재배 유무(초생재배 W, 청정재배 NW)와 합성피레스로이드계 살포유무(살포 P, 무살포 NP)를 조합하여 처리하고 2011년 6월 8일부터 2013년 11월 24일 까지 굴응애 및 천적발생밀도를 조사하여 비교하였다. 응애의 발생밀도를 누적응애일수(CMD)로 환산하여 비교한 결과, 2011년에는 가을 응애 개체군을 기준으로 했을 때 NW+NP 처리구에서 CMD가 가장 높았으며, 다음으로 W+NP, NW+P, W+P 순이었다. 전체적으로 합성피레스로이드계를 살포한 경우 기대와는 달리 굴응애 밀도가 낮았고 반대로 무살포구에서 굴응애 발생이 높았다. 2012년 처리별 가을 응애 개체군의 CMD도 2011년의 결과와 동일한 경향이였다. 관측된 천적 개체군(주로 이리응애류와 마름응애류)은 가정에 근거한 기대치와 크게 다르지 않았다. 2011년의 경우 NW+NP 처리구와 W+NP 처리구에서 차이가 있었으나, 2012년 실험에서는 기대치와 관측치가 거의 일치하였다. 전체적으로 약제효과가 뚜렷하게 나타나서 합성피레스로이드계 살포시 천적이 유의하게 감소하였다. 잡초효과는 엇갈리는 결과를 보였는데, 봄 개체군 대비 가을 개체군의 증가 등을 고려할 때 초생재배를 하는 경우 천적의 발생이 증가하였다. 본 연구결과는 합성피레스로이드계가 천적에 대한 독성뿐만 아니라 잎응애에 대한 기피작용을 유발하여 잡초-천적-응애의 선순환적 상호작용 시스템을 교란시킬 수 있음을 보여주고 있다.

**검색어:** 굴응애, 초생재배, 합성피레스로이드계, 이리응애, 천적효과

## 수출화훼 박스높이별 해충에 미치는 전자빔의 영향

윤승환, 이선우, 김현경, 구현나, 김길하\*

충북대학교 식물의학과

수출용 화훼박스에 장미와 국화를 각각 채운 후 화훼관련 해충 6종(아메리카잎굴파리, 담배거세미나방, 복숭아혹진딧물, 점박이응애, 담배가루이, 대만총채벌레)에 대한 전자빔 (200 Gy, 300 Gy) 영향을 박스의 높이에 따라 조사하였다. 200 Gy 선량의 전자빔 조사 시 점박이응애, 담배가루이, 대만총채벌레의 알은 모든 높이에서 부화가 억제되었지만 아메리카잎굴파리와 담배거세미나방은 박스하부 위치에서 일부 부화가 되었다. 아메리카잎굴파리 유충, 담배거세미나방 유충과 담배가루이의 약충은 모든 높이에서 용화 및 우화가 억제되었다. 그러나 점박이응애와 복숭아혹진딧물 약충은 박스상부에서조차도 우화가 억제되지 않았다. 번데기에 조사 시 아메리카잎굴파리의 번데기는 모든 높이에서 우화가 억제되었고 담배거세미나방은 상부에서도 완전히 억제되지 않았다. 성충에 조사 시 점박이응애는 장미박스 중부에서  $F_1$ 세대의 부화율이 100% 억제되었지만 국화박스에서는 완전히 억제되지 않았다. 200 Gy 선량에서 완전히 억제되지 않은 해충의 발육단계를 300 Gy로 조사하였을 때는 200 Gy 보다 높은 억제효과를 보였다. 따라서 화훼수출 시 전자빔 조사선량은 화훼종류별, 대상해충별에 따라 달라질 수 있다.

**검색어:** 전자빔, 수출화훼, 검역해충

0011

## **“Hidden” Warning Coloration: Predators Learn to aVoid Distasteful Prey with Hidden Conspicuous Display**

**Chang Ku Kang<sup>1</sup>, Hyun Joon Cho<sup>1</sup>, Sang im Lee<sup>1</sup> and Piotr G. Jablonski<sup>1</sup>**

<sup>1</sup>Laboratory of Behavioral Ecology and Evolution, School of Biological Sciences,  
Seoul National University

Defended (distasteful or toxic) prey are often characterized by conspicuous coloration and this phenomenon is called "aposematism". The main advantage of aposematism is that it promotes faster learning by predators to avoid the prey. Some defended prey species use a different strategy; they remain cryptic in the normal state, but display conspicuous aposematic signal (which is normally hidden) in response to a predator's approach/attack. This anti-predator strategy of a defended prey has not been well studied yet although it can theoretically give the benefits of both camouflage and aposematism. Here, we investigated the effectiveness of this 'hidden-aposematic signal' as a warning signal. Using wild tits (*Parus minor*) as predator and novel artificial prey models (which mimics wings of insects), we tested whether hidden conspicuous signal of a defended prey enhances the avoidance learning rate of predators and how does it compare with the typical conspicuous/non-conspicuous signal. We found that hidden conspicuous signal indeed enhances the avoidance learning rate of predators in comparison with the non-conspicuous signal. However the overall learning rate by predators to avoid the defended prey was slower than for the normal conspicuous signal. Our results suggest that the prey with hidden-aposematic signals could enjoy both the benefits camouflage and the benefits of aposematism that are however lower than benefits from a typical aposematic signal. We, for the first time, highlight the functional aspect of a unique, but yet largely ignored, defensive coloration of prey.

**Key words:** aposematism, wing coloration, predator-prey, avoidance learning

## Intercepted Hitchhiking Moths through International Vessel at the Korean Port of Entry

Minyoung Kim<sup>1,2</sup>, Heung-Sik Lee<sup>1</sup>, Jong-Ho Lee<sup>1</sup>, Ki-Jeong Hong<sup>3</sup> and Seunghwan Lee<sup>2</sup>

<sup>1</sup>Animal and Plant Quarantine Agency, Korea

<sup>2</sup>Department of Agricultural Bio-Technology, Seoul National University, Korea

<sup>3</sup>Department of Plant Medicine, Sunchon National University, Korea

Six unknown hitchhiking moths intercepted at the Korean port of entry were detected from an international vessel by the personnels of the International Plant-Quarantine Accreditation Board (PQA) in 2012. Among them, there was a noctuid moth, *Noctua pronuba* (Linnaeus), which is a quarantine pest in Korea. Other five species are three erebids (*Lophocampa maculata* Harris, *Lemyrarhodo philodes* (Hampson), and *Trigonodes cephise* (Cramer)), one sphingid (*Hippotion rosetta* Swinhoe), and one zygaenid (*Histia flabellicornis nigrinus* Jordan). They are mostly distributed in the subtropical regions. In addition to these hitchhiking moths from the vessel, other interception records from inanimate pathways are provided here on the bases of Pest Information System, Animal and Plant Quarantine Agency (QIA). Thus, it is necessary to monitor inanimate pathways and to adopt comprehensive border surveillance system, in order to protect further invasions of alien insect species.

**Key words:** Hitchhiking, moth, vessel, port, inanimate pathway, Korea

## Temperature-dependent Development of *Paromius exiguus* (Distant) (Hemiptera: Lygaeidae) On Two Host Plants

Myo Than Tun<sup>1</sup>, Seung-Tae Kim<sup>2</sup>, Soo-Yeon Lee<sup>2</sup>,  
Jong-Kook Jung<sup>1</sup> and Joon-Ho Lee<sup>1,2</sup>

<sup>1</sup>Entomology Program, Department of Agricultural Biotechnology, Seoul National University

<sup>2</sup>Research Institute for Agriculture and Life Sciences, Seoul National University

The developmental time of immature stages of *Paromius exiguus* (Distant) was studied at eight different constant temperatures (17.5, 20, 22.5, 25, 27.5, 30, 32.5 and 35°C) with a photoperiod of 14:10 (L:D) h on two host plants, *Imperata cylindrica* and *Calamagrostis epigeios*. On both host plants, the developmental time decreased with increasing temperatures. A significant difference in the developmental times was observed between two host plants for each nymphal stage and for the total nymphal stage as well. For completion of the total nymphal stage, the development time at 17.5 and 35°C were 69.6 and 16.6 days on *I. cylindrica* and 38.6 and 13.8 days on *C. epigeios*, respectively. The relationship between developmental rate and temperature was fitted to a linear regression model and the six nonlinear models (Lactin 1, Lactin 2, Briere 1, Briere 2, Logan 6 and Taylor). Except for the Taylor model, all of the five nonlinear models fitted the data for the total nymphal stage of the current study well, according to the high  $r^2$  value, on both host plants. The distribution of completion of each development stage was well described by the two-parameter Weibull function.

**Key words:** *Paromius exiguus*, developmental time, temperature-dependent development models

## Damage and Seasonal Occurrence of *Arbordia* spp. in Grapevine Export Complexes in Korea

Chae Min Lee<sup>1</sup>, Dong Woon Lee<sup>1</sup>, Suk Jun Lee<sup>1</sup> and Jin Sun Song<sup>2</sup>,  
Tae Heon Lim<sup>1</sup>, Sang Sub Han<sup>3</sup>, Sang Myeong Lee<sup>1</sup>, Hyeong Hwan Kim<sup>2</sup>  
and Myoung Rae Cho<sup>2</sup>

<sup>1</sup>Department of Ecological Science, Kyungpook National University

<sup>2</sup>Horticultural & Herbal Crop Environment Division, National Horticulture of  
Horticultural & Herbal Science

<sup>3</sup>Department of Forest Science, Chonbuk National University.

This report is a part of research on pests occurring in grapevine orchards in export complexes (Hwangsung in Gyeonggi, Sangju and Yeongcheon in Gyeongbuk, Namwon in Junbuk and Yeongdong in Chungbuk) from 2010 to 2012. This research was conducted to evaluate the distribution and difference in damage rates depending on management types of grapevine orchards (domestic sale farm vs. export farm). Damage by *Arbordia* spp. occurred only in 2010 and differed depending on localities and individual farms in the same area. Numbers of orchards damaged by *Arbordia* spp. were one, two and four in Hwasung, Namwon and Sangju, respectively, and the damage rate was below 6.2%. There was no damage in the orchards in 2011 and 2012, however, *Arbordia* spp. were collected on sticky traps in the orchards. *A. nigrigena* and *A. kakogawana* were the dominant species in Yeongcheon and Yeongdong, respectively, in 2011. *A. kakogawana*, *A. maculifrons* and *A. nigrigena* were collected on sticky traps in 2012. Collected numbers of *Arbordia* spp. were different depending on localities and management types of the orchards (domestic sale vs. export). *A. kakogawana* was the dominant species in all the survey sites and the densities were higher in the domestic sale farms than in the export farms.

**Key words:** *Arbordia kakogawana*, *A. maculifrons*, *A. nigrigena*, grapevine

0015

## Genetic Variation of the Asian Cavity-Nesting Honey Bee, *Apis cerana* (Hymenoptera: Apidae) in South Korea, as Revealed by An Internal Spacer Sequence of Mitochondrial DNA

Joo Young Lee<sup>1</sup>, Ah Rha Wang<sup>1</sup>, Yong Soo Choi<sup>2</sup>, Ratna Thapa<sup>2</sup> and Iksoo Kim<sup>1</sup>

<sup>1</sup>College of Agriculture & Life Sciences, Chonnam National University

<sup>2</sup>Department of Agricultural Biology, National Academy of Agricultural Science

Worldwide studies on *Apis cerana* variation for biogeography and genetic diversity depended largely on a 86~93 bp-long mitochondrial non-coding region (internal spacer region) located between tRNA<sup>Leu</sup> and COII (named as NC2), possibly due to higher variability among available markers. In order to incorporate the *A. cerana* occurring in South Korea into world extensive data, we also sequenced the NC2 from 118 *A. cerana* samples collected over nine Korean localities and 66 *A. cerana* samples over seven Asian localities, such as China, Vietnam, and Thailand. These data were combined with preexisting world data to scrutinize genetic relationships of *A. cerana* in South Korea to outside distributional range. Sequencing of 184 samples provided a total of ten haplotypes: five from Korea, six from China, one from Vietnam, and two from Thailand. Among them eight were new, whereas two were previously reported ones. Phylogenetic analysis of *A. cerana* NC2 haplotypes so far found including ours has confirmed the presence of four major groups of *A. cerana* (Asian mainland group, Sundaland group, Palawan group, and Luzon-Mindahnao group) and all haplotypes found in this study also were included in the Asian mainland group. In order to find further variable regions that can be used as sequence-based marker several mitochondrial non-coding regions and nuclear intron regions are in the middle of testing.

**Key words:** Genetic variation, *Apis cerana*, internal spacer sequence

## 형태분류와 DNA 바코드의 통합을 이용한 난분류군 종진단 효율성-주둥이방아벌레아과의 경우

한태만<sup>1,2</sup>, 이영보<sup>1</sup>, 김남정<sup>1</sup>, 박해철<sup>1</sup>, 이승환<sup>2</sup>

<sup>1</sup>국립농업과학원 농업생물부 곤충산업과

<sup>2</sup>서울대학교 농업생명과학대학

주둥이방아벌레과는 종간의 형태가 매우 유사하면서, 지역적 종 분화가 많이 이루어진 분류군의 하나임으로 형태학적 종 동정이 어려운 경우가 많다. 이번 연구에서 직접형태분류가 완료된 국내외의 종과 NCBI에 등록된 염기서열을 대상으로 총 83종 408개체에 대한 DNA 바코드를 분석한 후 각 종에 대한 DNA 바코드 특성 및 형태형질과의 연관성을 진단하고자 하였다. 그 결과, DNA 바코드와 형태분류와의 일치는 63종(75%)에 불과 하였다. 특히, 형태분류에서 동일종으로 결론지었던 4종으로부터 8종(9.6%)의 동소적 또는 이소적 은밀종을 새롭게 확인 하였고, 형태적 난분류군 4종(4.8%)은 명료한 종 진단이 가능하게 되었다. 또한 형태분류를 통한 2종(2.4%)에서 신종을 재확인 할 수 있었고, 2종(2.4%)에 대해서는 각각 지리적 신아종에 대한 가능성이 진단되었다. 2종(2.4%)에서는 형태적 차이가 명료하나 단일 종 묶음이 형성되었으며, 2종(2.4%)에서는 종내 지역집단에서 유전적 차이가 모호하여 별종 가능성을 제시하기 어려운 경우도 있었다. 결론적으로 형태분류와 DNA 바코드 분석을 통합 적용하여 총 83종 중 81종(97.6%)에 대한 명료한 종 진단이 가능함을 확인 할 수 있었다.

**검색어:** 주둥이방아벌레아과, 형태분류, DNA 바코드, 한국



0017

## 멸종위기종 큰자색호랑꽃무지의 적용 학명은 올바른 것인가?

박창선<sup>1</sup>, 한태만<sup>1</sup>, 이영보<sup>1</sup>, 김기경<sup>2</sup>, 서홍렬<sup>2</sup>, 김진일<sup>3</sup>, 박해철<sup>1</sup>

<sup>1</sup>국립농업과학원 농업생물부 곤충산업과

<sup>2</sup>국립생물자원관 동물자원과

<sup>3</sup>성신여자대학교 생물학과

큰자색호랑꽃무지속(*Osmoderma*)은 구북구와 신대륙에 걸쳐 12종이 분포하며, 대다수 종들은 희소성으로 각국에서 보호종으로 지정되어 있다. 국내에서도 큰자색호랑꽃무지 1종이 기록되어 멸종위기야생동식물 2급 종으로 보호받고 있으며, 현재까지는 *Osmoderma opicum* Lewis, 1887이란 학명을 적용해 왔다. 하지만 과연 국내 종이 일본산 *O. opicum*과 동일한 종인지는 분류학적으로 재분석할 필요성이 제기되어 왔고 최근 중국 및 극동러시아지방에서 새롭게 *O. caeleste* (Gusakov, 2002)란 종도 발표된 바 있다. 이에 따라 지리적 분포영역의 근연종들과 최근 COI염기서열이 분석된 유럽산 종들을 포함하여 국내 큰자색호랑꽃무지의 형태 및 분자분류를 통합적으로 진행하고자 한다. 1차 연구 결과로서 한국산 개체와 일본산 개체는 DNA 바코드 분석을 통해 별종으로 판단될 정도로 큰 바코딩 갭이 나타났을 뿐 아니라 형태적인 차이도 확인되었다. 따라서 국내 종은 그에 적합한 학명을 찾아 주어야 할 것으로 판단된다. 향후 추가적인 표본 확보와 DNA 바코드 마커의 추가 등 보다 정확한 종 동정을 위한 통합적인 분석과 검증이 수행될 예정이다.

검색어: 큰자색호랑꽃무지, 형태분류, 분자분류, 한국

## mtCOI과 16S rRNA분석을 통한 국내 사슴풍뎡이 집단의 분류학적 위치 재검토

안하영<sup>1</sup>, 한태만<sup>1</sup>, 이영보<sup>1</sup>, 김남정<sup>1</sup>, 김성현<sup>1</sup>, 정종철<sup>2</sup>, 박해철<sup>1</sup>

<sup>1</sup>국립농업과학원 농업생물부 곤충산업과

<sup>2</sup>서대문자연사박물관

사슴풍뎡이는 꽃무지아과 중에서 수컷이 유일하게 특이한 뿔을 갖고 있을 뿐 아니라 긴 앞다리를 가진 모습으로 주목을 받아왔다. 이 종은 베트남 북부, 티벳동부, 중국 서부와 중북부를 거쳐 한반도에 이르기까지 아종의 분화 없이 단일 종으로 다루어왔다. 특히, 국내 집단은 1914년에 북한 개체를 통하여 처음으로 *Dicronocephalus admasi* 학명이 부여된 이래, 이 학명에 대한 논란 없이 지금까지 받아들여 왔다. 하지만, 사슴풍뎡이속(*Dicronocephalus*)은 동양구에서 한반도와 극동러시아 지역에 걸쳐 8종 7아종이 분포하는데, 종 또는 아종 사이에 형태적으로 매우 유사하여 이들 종간에 유연관계는 아직까지 알려지지 않은 실정이다. 또한, 국내 집단과 형태적으로 유사한 종이 타이완에 분포하는 등 지리적 격리의 가능성을 진단할 필요성이 있었다. 이에 따라 1차적으로 국내 사슴풍뎡이 집단을 포함하여 5종 5아종을 대조 분류군으로 삼아 mtCOI과 16S rRNA마커를 이용한 분자분류를 시도하였다. 그 결과, 한국산 사슴풍뎡이 집단은 중국산 사슴풍뎡이 집단과 유전적 차이가 없는 것으로 확인되었다. 다만, 형태분류학자의 주장과 달리 대만산 *D. yui*와 sister group을 형성하는 것이 확인되었다. 따라서 향후 추가적인 샘플의 확보를 통해 사슴풍뎡이 종의 분화를 밝히고, 사슴풍뎡이속의 지리적 분포와 더불어 새로운 종의 발굴 가능성을 타진하는 연구를 계속하고자 한다.

**검색어:** 사슴풍뎡이속, 사슴풍뎡이, 분자분류, 한국

0019

## 형태적 난분류군, 연노랑풍뎡이와 등얼룩풍뎡이의 분자마커를 이용한 분류학적 재검토

이연희<sup>1</sup>, 강태화<sup>1</sup>, 한태만<sup>1</sup>, 이영보<sup>1</sup>, 김진일<sup>2</sup>, 박해철<sup>1</sup>

<sup>1</sup>국립농업과학원 농업생물부 곤충산업과

<sup>2</sup>성신여자대학교 생물학과

국내 연노랑풍뎡이속(*Blitopertha*)에는 어깨무늬풍뎡이(*B. conspurcata*), 연노랑풍뎡이(*B. pallidipennis*), 등얼룩풍뎡이(*B. orientalis*) 3종이 분포한다. 이 중 연노랑풍뎡이와 등얼룩풍뎡이는 외부형태가 극히 유사하고 두 종간 수컷의 교미기 형태도 변이가 심하면서 서로 이행현상을 나타내는 등 정확한 종 동정이 어려운 분류군으로 알려져 왔다. 이와 같이 형태적 분류가 어려운 종들에 대하여 형태분석과 더불어 분자분석까지 통합한 연구로 극복해 보고자 이번 연구를 시도하였다. 우선, 국내산 표본뿐 아니라 등얼룩풍뎡이의 기산지인 일본표본과 연노랑풍뎡이의 기산지인 극동 러시아 표본들을 포함하여 mtCOI과 Histone H3 마커를 이용한 분자분석을 수행하였다. 그 결과, 두 종은 뚜렷이 분화된 종으로 진단되었으나, 등얼룩풍뎡이 계열에서 제3의 새로운 종이 국내에 존재하는 것으로 추정되었다. 아울러 분자 분석된 표본의 분포를 보면, 두 종은 동소적으로 혼재된 분포를 보이는 것으로 나타났다.

**검색어:** 연노랑풍뎡이, 등얼룩풍뎡이, 통합분류, DNA 바코드, 형태적 난분류군

## Revision of Tribe Archipini (Tortricidae: Tortricinae) from Northern part of Vietnam

**XuanVi Le, Pham Thi Vuong<sup>1</sup>, Yang-Seop Bae**

Division of Life Sciences, Incheon National University, Korea

<sup>1</sup>Plant Protection Research Institute, Vietnam Academy of Agricultural Sciences, Vietnam

The tribe Archipini occurring mainly in the Holarctic, Afrotropical and Oriental Regions; scarcely represented in the Neotropical with more than 500 described species of 150 genera (Razowski, 2003). The tribe Archipini in Vietnam was studied by several authors. Kuznetsov (1992) described two new species, *Homona superbana* and *Neocalypsis sodaliana*, besides 28 known species were recorded, and he (1997) also recorded four species, *Homona encausta* (Meyrick), *Neocalypsis tricensa* (Meyrick), *Meridemis furtiva* Diakonoff and *Lumaria probolias* (Meyrick). In a study on Tortricidae fauna from Vietnam (2000), 43 of 208 Tortricidae species belong to the tribe Archipini were annotated. Based on the collection of the Berlin Museum, Razowski (2008a) reported seven known species and described 13 new species belong to four genera, *Gnorismoneura* Issiki & Stringer, 1932, *Terthreutis* Meyrick, 1912, *Synochoneura* Obraztsov, 1955, and *Terricula* Falkovitsh, 1965, he also reported ten known species and described five new species belong to three genera, *Choristoneura* Lederer, 1859, *Homona* Walker, 1863 and *Meridemis* Diakonoff, 1976 (2008b). In the year of 2009, he described one new genus, *Chirapsina* Razowski, 15 new species, besides 37 known species were recorded (2009a), he (2009b) also described five new species and four known species from Vietnam. In the present study, we focused on Archipini fauna in the northern part of Vietnam, a total of 19 species belong to 13 genera are recorded. Among them, five species *Adoxophyes tetraphracta* Meyrick, *Meridemis bathymorpha* Diakonoff, *Pademis corylana* Fabricius, *Terthreutis bulligera* Meyrick, and *Ulodemis hyalura* Diakonoff are recorded for the first time.

**Key words:** Lepidoptera, Tortricidae, Tortricinae, Archipini, Vietnam

0021

## Three Species of Water Striders from Different Types of Habitats Exhibit Different Types of Anti-predator Strategies

**Jae Hak Son<sup>1</sup>, Sang-Im Lee<sup>1</sup> and Piotr G. Jablonski<sup>1</sup>**

<sup>1</sup>Laboratory of Behavioral Ecology and Evolution, Department of Biological Sciences,  
Seoul National University

Prey species should avoid areas where predation risk is high. However, if this is impossible, prey should reduce activities that may make them conspicuous and attract predators, such as foraging or mating. Thus, predation risk should change behavioral pattern of prey species. Not all species have same anti-predator behavioral patterns because they have evolved in the presence of different types or number of predators in their habitat. In this study we measured microhabitat use and escape initiation distance to identify how sensitive each species is to approaching predators. We measured jumping performance and morphological characteristics to reveal the relationship between jumping and morphology and whether jumping is helpful for escaping from predators' attack. Finally, we compared the survival rate among three species to identify how survival rate is affected by anti-predator behavioral patterns. The survivorship was related to microhabitat use and to the escape initiation distance, rather than on the jumping ability. We predicted that a species with the best survival rate will have superior jumping ability in order to escape from predators at the moment when they were attacked by predators. The jumping ability, however, was probably limited by hydrodynamic and morphological constraints, so jumping appears to contribute little to successfully escaping from predators' attacks.

**Key words:** Predation risk, Anti-predator behavior, Predator avoidance, Water striders.

## ***Chlaenius (Ocybatus) junceus* Andrewes (Coleoptera: Carabidae: Chlaeniini), New to Korea.**

**Ik Je CHOI, Jinyoung PARK and Jong Kyun PARK**

Department of Ecological Science, Kyungpook National University

Genus *Chlaenius* Bonelli, 1810 of the tribe Chlaeniini is a cosmopolitan group distributed in all zoogeographical region. General characteristics of *Chlaenius* are with pubescent or metallic luster on the pronotum and elytra, and antennal second segment shorter than third segment.

Members of subgenus *Ocybatus* are similar to those of subgenera *Lissauchenius* and *Chlaenioctenus* in having a round yellow spot on each elytron, but it showed difference from them having apical segment of labial palpi strongly securiform.

Subgenus *Ocybatus* Laferté-Sénéctere, 1851 belonging to the genus *Chlaenius* were reported three species from Palearctic region: *Chlaenius (Ocybatus) junceus* Andrewes, 1923, *Chlaenius (Ocybatus) aspercollis* Bates, 1873, *Chlaenius (Ocybatus) bioculatus* Chaudoir, 1856, among them *Chlaenius (Ocybatus) bioculatus* Chaudoir, 1856 has been recorded in Korea. In here *Chlaenius (Ocybatus) junceus* Andrewes reported firstly from Korea. Description and photo of adult are provided.

**Key words:** Coleoptera, Carabidae, *Chlaenius*, Palearctic region, Korea

## A New Cryptic Species of Genus *Aphis* (Hemiptera: Aphididae) Sharing Primary and Secondary Host with the Cotton-melon Aphid, *Aphis gossypii* Glover

Yerim Lee<sup>1</sup>, Seunghwan Lee<sup>1</sup> and Hyojoong Kim<sup>2</sup>

<sup>1</sup>Insect Biosystematic Laboratory, Research Institute for Agricultural and Life Sciences,  
Seoul National University

<sup>2</sup>Animal Phylogeny and Systematics Lab., Department of Biology, Kunsan National University

In terms of aphid species identification, both host plant association and morphological characteristics are crucial factors. However, aphids in the genus *Aphis* Linnaeus (Hemiptera: Aphididae) often are cryptic in morphology due to their rapid radiation. Moreover, overlapping host plant species can make difficult situation worse. Three cryptic species *Aphis gossypii* Glover, *Aphis glycines* Matsumura, and *Aphis rhamnicola* **sp. nov.** occur together on the Buckthorn, *Rhamnus* spp. in the overwintering season in Korea. Due to lacking informative morphological characters and host plant sharing, the new species recently has been recognized as a distinct species. In this study, *A. rhamnicola* **sp. nov.** on various host plants was compared with the primary host sharing species, *A. gossypii* and *A. glycines*, based on morphological and molecular characteristics. In the results, there were significant genetic differences between three species, despite the high similarities in morphology. Our results provide strong evidence for establishing new species, which seems to be a typical heteroecious species that alternates between only primary host, *Rhamnus* spp., and various secondary hosts. We describe a new species, *A. rhamnicola* **sp. nov.**, for apterous and alate vivipara, fundatrix, ovipara, and gynopara, including diagnostic key for host sharing species in genus *Aphis*.

**Key words:** Aphididae, *Aphis*, cryptic species, COI, *Rhamnus*, *Commelina*

## **Taxonomic Study of Phycitinae (Lepidoptera, Pyraloidea, Pyralidae) in Jilin Province, China**

**Mu-Jie Qi, Xuan-Vi Le, Yong-Don Ju, Bayarsaikhan Ulziijargal, Bo-Sun Park, Hee-Jo Lee, Min-Seon Kim, Sol-moon Na, Jae-won Kim and Yang-Seop Bae**

Department of Life Sciences, Incheon National University, Korea

Phycitinae is one of the subfamilies of Pyralidae, about 4000 phycitinae species in the world (Solis and Mitter 1992), and around 300 species of 110 genera have been reported in China (Li and Ren 2005). The subfamily of Phycitinae is characterized by the following characteristics: both wings are long and narrow, chaetosema present; forewing with 11 veins or less, R3 and R4 stalked at base or fused completely, both male and female with only one frenulum; gnathos rod-shaped or coniform; valva with costa well developed, transtilla free or connected at top, aedeagus cylindrical, male usually with culcita; ductus bursae from corpus bursae. The larvae of phycitinae are leafrollers, leafminers or products pests. Their distribution is throughout the world (Munroe and Solis, 1999).

As a NE region, Jilin province lies in the center of northeast part of China, borders by North Korea, Far East of Russia, Heilongjiang, Liaoning and Inner Mongolia. Until now, only 20 species of phycitinae have been reported from here, accordingly, the faunistic inventory is by no means completed, and to survey the diversity of phycitinae is significant for systematic study in China.

In this study, we identified 35 species belonging to 19 genera, of them, 2 species are reported for the first time in China, and 12 species are newly reported from Jilin Province. The materials examined come from the collection of Incheon National University and Northeast Forestry University.

**Key words:** Pyralidae, Phycitinae, fauna, new record, Jilin



## A Molecular Phylogeny of the Odonata (Insecta) Occurring in South Korea Inferred from COI, 16S rRNA, 28S rRNA, and EF1- $\alpha$ Sequences

**Min Jee Kim<sup>1</sup>, Kwang Soo Jung<sup>2</sup> and Iksoo Kim<sup>1</sup>**

<sup>1</sup>College of Agriculture & Life Sciences, Chonnam National University

<sup>2</sup>College of Natural Sciences, Andong National University

Previously, several levels of phylogenetic relationships in an insect order Odonata have been estimated using morphological and molecular markers. For the molecular phylogeny rRNA sequences were mainly, but other markers were not frequently employed. In this study, we sequenced both two mitochondrial genes (COI and 16S rRNA) and nuclear genes (28S rRNA and elongation factor-1 $\alpha$ ), composed of ~4,002 bp from 71 species of Odonata, occurring mostly in South Korea. These concatenated sequences were utilized to test the previous phylogenetic hypotheses of Odonata via Bayesian Inference (BI) and Maximum Likelihood (ML) algorithms, along with the data partition option available in BI method. Each families and superfamilies represented by multiple taxa consistently supported monophylies with the highest nodal supports in both Anisoptera and Zygoptera. A close relationship of Anisozygoptera to Anisoptera represented by a single species was obvious. On the other hand, familial relationships within each suborder of Anisoptera and Zygoptera have shown two compelling topologies. The topology obtained by BI method with partitioning of the four genes showed an unresolved relationship among Gomphidae, Aeshnidae, and the suborder Anisozygoptera in Anisoptera clade, presenting the relationships (((Libellulidae + Corduliidae) + Macromiidae) + (Gomphidae + Aeshnidae + Anisozygoptera)) + (((Coenagrionidae + Platycnemididae) + Calopterygidae) + Lestidae)). Another topology obtained by both BI and ML methods without partitioning, on the other hand, placed Anisozygoptera the basal lineage of Anisoptera, but Lestidae in Zygoptera was placed as the sister to Anisoptera + Anisozygoptera, presenting the relationships (((((((Libellulidae + Corduliidae) + Macromiidae) + Aeshnidae) + Gomphidae) + Anisozygoptera) + Lestidae) + ((Coenagrionidae + Platycnemididae) + Calopterygidae)). Topological test to find out better supported tree turned out a slight higher support for the former topology, but the monophyly of Zygoptera with the inclusion of Lestidae was supported only poorly (BPP = 0.68) in the former topology.

**Key words:** Odonata phylogeny, COI, 16S rRNA, 28S rRNA, elongation factor-1 $\alpha$

## The Complete Mitochondrial Genome of *Erynnis montanus* (Lepidoptera: HesperIIDae): A New Gene Arrangement in Lepidoptera

**Ah Rha Wang, Heon Cheon Jeong, Yeon Soo Han and Iksoo Kim**

College of Agriculture & Life Sciences, Chonnam National University

Gene arrangement in the mitochondrial genome (mitogenome) has been regarded as an important evolutionary event that is useful as a phylogenetic signal. The mountainous duskywing, *Erynnis montanus*, belongs to a lepidopteran family HesperIIDae. We sequenced 15,530-bp long complete mitogenome of the species. The genome has the typical gene content of animals (13 protein-coding genes, two rRNA genes, 22 tRNA genes, and one major non-coding A+T-rich region). Further, *E. montanus* mitogenome also contained a high A/T content in the whole genome (81.7%) and the CGA (arginine) as the start codon for the COI gene, as typical in lepidopteran mitogenome. However, unlike other lepidopteran species, including two sequenced skippers, the *E. montanus* mitogenome has a unique arrangement tRNA<sup>Ser</sup>-tRNA<sup>Asn</sup>, instead of the tRNA<sup>Asn</sup>-tRNA<sup>Ser</sup> found unanimously in other lepidopteran species, providing a new gene arrangement in Lepidoptera. Such rearrangement probably was likely caused by duplication of gene block tRNA<sup>Ser</sup>-tRNA<sup>Asn</sup> and subsequent random loss of tRNA<sup>Asn</sup> in the first copy and tRNA<sup>Ser</sup> in the second copy, resulting in the arrangement tRNA<sup>Ser</sup>-tRNA<sup>Asn</sup>. Considering current phylogenetic relationships among available lepidopteran groups in connection with lepidopteran gene arrangement the new gene arrangement found in *E. montanus* seems to be apomorphy, requiring cautious interpretation as a phylogenetic signal.

**Key words:** Mitogenome, *Erynnis montanus*, gene arrangement, Lepidoptera

## Molecular Phylogeny of Oecophoridae (Lepidoptera: Gelechioidea)

Sora Kim<sup>1</sup>, Sunghoon Jung<sup>1</sup> and Seunghwan Lee<sup>1</sup>

<sup>1</sup>Department of Agricultural Bio-Technology, Seoul National University, Korea

Oecophoridae (Lepidoptera: Gelechioidea), the concealer moths, is worldwide in distribution and comprises more than 4,000 described, particularly in Australia with over 3,000 endemic species. To date, the phylogenetic relationships of Oecophoridae have been poorly known, except a few works on the higher-level phylogeny of the superfamily Gelechioidea which includes some species of Oecophoridae.

This study is the first comprehensive molecular phylogenetic analysis of Oecophoridae, based on 4,395 base pairs of mitochondrial protein coding gene (COI), nuclear ribosomal RNA genes (18S and 28S) and nuclear protein coding genes (IDH, MDH, Rps5, EF1a and wingless) for 82 taxa. Data were analysed using maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI) phylogenetic frameworks. The results are shown that the family Oecophoridae is not monophyletic, as the genus *Casmara* is closely clustered with Stathmopodidae far from the Oecophorid lineage and the genera *Tyrolimnas* and *Phaeosaces* are closely clustered with Depressariinae in the Elachistid lineage. Main clade of Oecophoridae comprises Xyloryctinae previously assigned to Xyloryctidae, closely claded with New Zealandian Oecophorids including the genera *Hierodoris*, *Gymnobatra* and *Izatha*; the problematic position group, *Acryptolechia* spp., Deuterogoniinae and Oecophorinae.

**Key words:** Lepidoptera, Gelechioidea, Oecophoridae, Phylogeny

## 캄보디아 Samkos지역의 곤충상: 나비목 Faunal Study of Lepidoptera in Samkos Area, Cambodia

박보선, 주영돈, 레수안비, 올지자르갈, 이희조, 배양섭

인천대학교 생명과학기술대학 생명과학과

캄보디아는 동양구에 위치한 국가로 북동쪽으로 라오스, 동쪽과 남동쪽으로 베트남, 북쪽과 서쪽으로 태국과 접하고 있다. Samkos지역은 캄보디아 서쪽에 위치한 산림지역으로 1997년 유네스코 생물권 보호구역으로 지정된 바 있다. Samkos산은 1750m 높이로, 산림이 우거지며 야생동물이 다양하게 서식하는 지역이다. 현재 Samkos지역은 화전에 의한 화재와 개발로 인해 산림이 심각하게 훼손되고 있으며, 그에 따라 생물다양성 감소에도 큰 영향을 미칠 것으로 예상되는 지역이다. 본 연구는 2012년 7월 12일 ~ 7월 23일, 2013년 2월 13일까지 캄보디아 서부지역에 위치한 Samkos산에서 실시하였다. 연구방법은 Sweeping, Light trap, Bucket trap 등 다양한 방법을 이용하여 곤충상을 조사한 결과, 나비목은 총 7과 81속 98종이 채집되었다.

검색어: Samkos, 캄보디아, 나비목, 생물권보호구역

## Diversity of Oribatid Mites (Acari: Oribatida) in Organic and Conventional Apple Orchards

**Jiwon Kim, Eunsun Keum and Chuleui Jung**

Department of Bioresource Sciences, Graduate School, Andong National University

Soil biodiversity is important for proper functioning of soil ecosystem. Soil microarthropods play roles in cycling of nutrients and decomposition of organic matter. We compared the diversity of oribatid mites in organically and conventionally managed apple orchards. Sampling were done from 10 orchards; 5 from organic and 5 from conventional, in spring season of 2011 and 2012. Species richness and abundance were higher in conventional (25, 4,222/m<sup>2</sup>) than organic orchard (21, 1,906/m<sup>2</sup>). Diversity index was higher in conventional than organic orchard. Common dominant species present in orchards were *Perglumna duplicata nipponica* and *Scheloribates latipes*. Only observed in apple orchards were *Pilogalumna tenuiclava*, *Protoribates agricola*, *Hypochothonius luteus*, *Punctoribates manzanoensis*, *Punctoribates sphaericus*, and *Scheloribates corpusculum*. In organic orchard, *Suctobelbella naginata* and *Tectocepheus cuspidentatus* were only present. *Pergalumna altera*, *Galumna longiporosa*, and *Protoribates lophotrichus*, *Galumna* sp. were found only in conventionally managed apple orchard. Further study on the functional aspects and association with other soil biotic and abiotic factors are demanding.

**Key words:** Diversity, Organic, Conventional, Species richness

## **Predatory Gamasid Mites (Acari: Mesostigmata) on Organic and Conventional Apple Orchards**

**Eun Sun Keum, Ji Won Kim and Chuleui Jung**

Department of Bioresource Science, Graduate School Andong National University

Predatory gamasid mite (Acari: Mesostigmata) is living in soil and litter. They feed on nematode, collembolan and insect larvae. This research compared diversity of gamasid mite in organic and conventional apple orchards. Soil samples were collected in spring season of 2011 to 2012 (5 for each orchard system). Fifteen families, 54 species and 15 families, 50 species were collected from organic and conventional orchards, respectively. In total 18 families and 77 species of gamasid mite were collected. Shannon Diversity was average 2.5 in organic orchard and 2.3 in conventional orchard. Major dominant species was *Eugamasus fujisanus* (Parasitidae) in organic orchard and *Uropoda hokkaidoensis* (Uropodidae) in conventional orchard. Parasitidae and Uropodidae were preferred in soil surface, large soil pores and decaying organic material litter. Future, more research on composition of gamasid mite, biotic and abiotic factors in orchard system are demanded.

**Key words:** Organic, Mesostigmata (gamasid mite), Diversity

0031

## Deep Sequencing based Transcriptome Analysis of *Plutella xylostella* Larvae Parasitized by *Diadegma fenestrale*

**Ju Il Kim, Min Kwon, Jae Dong Shim, Seong Hee Kim, Eun Ju Hong, Jeom Soon Kim, Yong Gyu Lee, Sam Nyu Jee and Si Hyeock Lee<sup>1</sup>**

Highland Agriculture Research Center, NICS, RDA

<sup>1</sup>Department of Agricultural Biotechnology, Seoul National University

The physiology of parasitic wasp control of their lepidopteran hosts' not only includes injecting their egg but also various factors such as symbiotic virus. This study was focused on the investigation of sophisticated interaction between parasitoid (*Diadegma fenestrale*) and their host (*Plutella xylostella*) in *P. xylostella* larva at transcriptome level, to check whether it is parasitized or not. Short-read deep sequencing method (Hiseq2000) was used for the transcriptome analysis. De novo assembly of cDNA sequence data generated 196,081 contigs between 201bp and 15,853bp in length. Some detoxification enzymes such as cytochrome P450 and Immune-related genes such as antimicrobial peptides were up-regulated after parasitism. Expression of symbiotic ichnovirus genes was detected in parasitized larvae with 55 contigs identified from five ichnovirus gene families including vankyrin, viral innexin, repeat elements, a cysteine-rich motif, and polar residue rich protein. This investigation provides a detailed information on differential expression of *P. xylostella* larval genes and symbiotic ichnovirus genes following parasitization.

**Key words:** *Diadegma fenestrale*, ichnovirus, deep sequencing, *Plutella xylostella*

## Microbiome of Two Morphs of *Vollenhovia emeryi* (Hymenoptera: Myrmicinae)

Gilsang Jeong<sup>1</sup>, Soyeon Park<sup>1</sup>, Pureum Noh<sup>1</sup>, Seung-Yoon Oh<sup>2</sup>, Hwakyung Hwang<sup>1</sup>, Yongwhan Kim<sup>3</sup> and Jae Chun Choe<sup>1</sup>

<sup>1</sup>Division of EcoScience, Ewha Womans University

<sup>2</sup>School of Biological Sciences, Seoul National University

<sup>3</sup>Sunchang High School

The hologenome theory of evolution proposes that an organism is simply not an individual but the totality of numerous microbial symbionts to the host. In fact, the evidence of biochemical and physiological associations between the symbionts and the host has been growing fast in all major taxa.

The *Vollenhovia emeryi* ant is tiny and found nationwide in Korea. The ant can be further categorized by its wing morphology, eg. long-winged and short-winged. Our initial screening process showed that the microbial reproductive manipulator, the *Wolbachia* bacterium, only infected the long-winged morph. This gave us a good opportunity to investigate the effect of the *Wolbachia* infection on the bacterial community diversity using the next generation sequencing technique.

We find that there are about 180 bacterial symbionts in the short-winged morph. On the other hand, the long-winged morph has only about 10 bacterial symbionts. This implies that the bacterial community diversity may be subject to the existence of *Wolbachia*. Furthermore, the *Wolbachia* strain diversity is unexpectedly high. The results and future research direction will be discussed from the hologenome theory perspective.

**Key words:** *Vollenhovia emeryi*, bacterial diversity, next generation sequencing, *Wolbachia*, hologenome theory



## The Pyrosequencing Approach Reveals Very High Strain Diversity of the Endosymbiont, *Wolbachia* in *Vollenhovia emeryi*

Soyeon Park<sup>1</sup>, Haewon Shin<sup>1</sup>, Pureum Noh<sup>1</sup>, Seung-Yoon Oh<sup>2</sup>, Hwakyung Hwang<sup>1</sup>, Bitna Lee<sup>1</sup>, Yongwhan Kim<sup>3</sup>, Jae Chun Choe<sup>1</sup> and Gilsang Jeong<sup>1</sup>

<sup>1</sup>Division of EcoScience, Ewha Womans University

<sup>2</sup>School of Biological Sciences, Seoul National University

<sup>3</sup>Sunchang High School

*Wolbachia* is one of the most common endosymbionts best known to induce several reproductive alterations in its insect hosts. In some cases, the insect hosts harbor more than two strains of the bacterium. The *Vollenhovia emeryi* ant lives in dead trees and is morphologically subdivided into the long-winged and the short-winged. Interestingly the short-winged morph is free of *Wolbachia*, but only the long-winged morph is multiple- infected with the *Wolbachia* bacterium.

We sampled four populations of the long-winged morph in Korea and performed pyrosequencing in Multilocus Sequence Typing (MLST), to determine the bacterial strain diversity. Six different gene regions (*coxA*, *fbpA*, *ftsZ*, *gatB*, *hcpA* and *wsp* gene) were targeted and amplified. However, the result shows that diversity of haplotypes is very high. The pyrosequencing approach in MLST, a new method of discriminating *Wolbachia* strains, is promising to effectively detect multiple infections and rare haplotypes.

**Key words:** *Wolbachia*, *Vollenhovia emeryi*, MLST and pyrosquencing

## RNA Interference of Glycerol Production Patterns a Rapid Cold Hardiness of the Beet Armyworm, *Spodoptera exigua*

Youngjin Park and Yonggyun Kim

Department of Bioresource Sciences, Andong National University, Andong 760-749, Korea

The beet armyworm, *Spodoptera exigua*, is a freeze-susceptible species and overwinters without diapause in temperate zone. Depression of supercooling point (SCP) and rapid cold hardiness (RCH) allow *S. exigua* to survive at low temperatures. This study reports a polyol which is responsible for the cold hardiness of *S. exigua*. Pre-exposure of *S. exigua* larvae to 4°C for 6 h significantly enhanced survival under a freezing temperature (-10°C). This pre-exposure treatment also significantly depressed larval SCPs. Analysis of polyols indicated that glycerol titers significantly increase with increase of pre-exposure time. Glycerol kinase (GK) and glycerol-3-phosphate dehydrogenase (GPDH) are involved in glycolysis pathway of insect. The *S. exigua* GK (*SeGK1*) and G3PDH (*SeG3PDH1*) genes were predicted from 454 pyrosequencing transcripts from fifth instar larvae of the beet armyworm, *S. exigua*. The *SeGK1* and *SeG3PDH1* genes both were expressed in all larval stage by RT-PCR analysis. Expression of *SeGK1* and *SeG3PDH1* genes were suppressed by its specific dsRNA<sup>*SeGK1*</sup> or dsRNA<sup>*SeG3PDH1*</sup> injection into hemocoel of 5th instar larva. Each 200 ng of dsRNA<sup>*SeGK1*</sup> or dsRNA<sup>*SeG3PDH1*</sup> injection also significantly decreased glycerol amount in hemolymph. Larval treated by either dsRNA<sup>*SeGK1*</sup> or dsRNA<sup>*SeG3PDH1*</sup> significantly lost the RCH under -10°C exposure. These results indicate that glycerol is a crucial RCH agent and its synthesis is regulated by *SeGK1* and *SeG3PDH1* genes in *S. exigua*.

**Key words:** Glycerol, glycerol kinase, glycerol-3-phosphate dehydrogenase, rapid cold hardiness, RNA interference, *Spodoptera exigua*

O035

## **(E)-5-Hexadecenyl Acetate: A Novel Moth Sex Pheromone Component from *Stathmopoda auriferella***

**Chang Yeol Yang, Kyung San Choi and Myoung Rae Cho**

National Institute of Horticultural and Herbal Science, Rural Development Administration

The sex pheromone of *Stathmopoda auriferella* (Walker) (Lepidoptera: Stathmopodidae), an important pest of kiwifruit in Korea, was studied. Two candidate pheromone components detected in the gland extracts of females were identified as (E)-5-hexadecenyl acetate (E5-16:OAc) and (E)-5-hexadecenol (E5-16:OH) in a ratio of 75:25 by mass spectral analysis of natural pheromone components and dimethyldisulfide adducts, and retention index comparisons with synthetic standards. In the kiwifruit orchards, E5-16:OAc alone was attractive to *S. auriferella* males and caught significantly more males than live virgin females. However, addition of E5-16:OH strongly inhibited attraction to E5-16:OAc. These results suggest that the major component of the female-produced sex pheromone of *S. auriferella* is E5-16:OAc. This hexadecenyl acetate is a novel moth sex pheromone component.

**Key words:** *Stathmopoda auriferella*, Sex pheromone, (E)-5-hexadecenyl acetate, Lepidoptera, Stathmopodidae, Insect pest

## Origin and Biological Function of E94k Polydnalviral Gene

**Rahul P. Hepat and Younggyun Kim**

Department of Bioresource Sciences, Andong National University, Andong 760-749 Korea

A polydnavirus, *Cotesia plutellae* bracovirus (CpBV), is symbiotic to an endoparasitoid wasp, *C. plutellae*, which specifically parasitizes young larvae of the diamondback moth, *Plutella xylostella*. CpBV contains some genes originated from other insect viruses. CpBV-E94k1 and CpBV-E94k2 are homologous to corresponding baculovirus gene E94k, and may play an important role in host-parasitoid interactions. This study was conducted to confirm the origin and function of CpBV-E94k by analyzing its sequence and functional assays. Our phylogenetic analysis indicates that CpBV acquires these E94k genes from baculoviruses. These two genes were expressed during entire period parasitization period. Expression of these E94ks was also tissue-specific because they were expressed in the hemocyte and fat body, but not in the other tissues. Subsequent analysis of gene function by RNA interference showed that it clearly inhibited host immune and developmental processes.

**Key words:** E94k, *Cotesia plutellae*, bracovirus, *Plutella xylostella*

## Evolutionary Aspects and Enzymatic Properties of Two Acetylcholinesterases in Insects

Young Ho Kim<sup>1</sup> and Si Hyeock Lee<sup>1,2</sup>

<sup>1</sup>Research Institute for Agriculture and Life Sciences, Seoul National University

<sup>2</sup>Department of Agricultural Biotechnology, Seoul National University

Most insect possess two AChEs (i.e., AChE1 and AChE2 encoded by *ace1* and *ace2* gene, respectively). Due to its higher transcription level and responsibility for insecticide resistance, it is believed that AChE1 is likely the main catalytic AChE, between two AChEs of the insects having both AChE1 and AChE2 studied to date. However, Cyclorrhaphan flies have only AChE2, suggesting the evolutionary scenarios for the takeover of *ace2* and the loss of *ace1* during Diptera evolution (Huchard et al., 2006). Therefore, it is essential to investigate the evolutionary distribution of AChE1 and AChE2 in Insecta. In this study, among 100 insect species examined, we found 33 species expressing AChE2 as the catalytic major enzyme by Western blotting using AChE1- and AChE2 specific antibodies. These findings are contrary to the common expectation that AChE1 is dominant synaptic enzyme in all insect species with the exception of Cyclorrhapha. In this study, we compared the characteristics of both AChE1 and AChE2 from the German cockroach and the honey bee, in which AChE1 and AChE2 were expressed as major catalytic enzyme, respectively. In addition, we presented a unique case of a damselfly, which expresses both AChEs exhibiting almost identical enzymatic activities, along with the fruit fly, where AChE1 is not present but multiple forms of AChE2 appear to replace the function of AChE1. The current study will provide valuable insights into the evolution of AChE.

**Key words:** acetylcholinesterase, insect, evolution, synaptic function, non-neuronal function

## RNA Interference of Cadherin Gene Expression in *Spodoptera exigua* by Oral Ingestion of dsRNA<sup>SeCad1</sup>

Youngjin Park and Yonggyun Kim

Department of Bioresource Sciences, Andong National University, Andong 760-749, Korea

Cadherin gene, which is a receptor of the *Bacillus thuringiensis* toxins, was predicted from 454 pyrosequencing transcripts from fifth instar larvae of the beet armyworm, *Spodoptera exigua*. The *S. exigua* cadherin gene (*SeCad1*) encodes 9 cadherin repeats and a transmembrane domain. The *SeCad1* gene was expressed in all developmental stage specifically in gut tissue by RT-PCR analysis. Expression of *SeCad1* gene was suppressed by both injection and feeding of its specific dsRNA<sup>SeCad1</sup> in 5th instar larval stage. The suppression of *SeCad1* expression did not significantly influence on pupal and adult development of *S. exigua*. However, the larval treated with dsRNA<sup>SeCad1</sup> (100 ng/larva) significantly reduced susceptibility to *B. thuringiensis* ssp. *aizawai* ( $3 \times 10^6$  CFU/larva). By contrast, the dsRNA<sup>SeCad1</sup>-treated larvae did not show any change in susceptibility to *B. thuringiensis* ssp. *krustaki* ( $4 \times 10^7$  CFU/larva). These results suggest that SeCad1 is a specific receptor of Cry1A toxin from *B. thuringiensis* in *S. exigua*, but not Cry1C toxin.

**Key words:** *Bacillus thuringiensis*, cadherin, gut, receptor, RNA interference, *Spodoptera exigua*

## Residual Contact Vial Bioassay for the Selection of Effective Acaricides against the Two-spotted Spider Mite

**Deok Ho Kwon<sup>1</sup>, Ji Hyun Park<sup>2</sup>, Taek Jun Kang<sup>3</sup> and Si Hyeock Lee<sup>1,2</sup>**

<sup>1</sup>Research institute for Agriculture and Life Science, Seoul National University

<sup>2</sup>Department of Agricultural of Biotechnology, Seoul National University

<sup>3</sup>Department of Horticultural Crop Research, National Institute of Horticultural and Herbal Science, RDA

Emergence of resistant two-spotted spider mite (TSSM) can induce the over usage of standard amount of acaricides and result in various side effects. Rapid resistance monitoring is essential step for the efficient management of resistant populations by enabling the selection of appropriate acaricides. Here, we evaluated the 10 acaricides to determine its suitability on residual contact vial bioassay (RCV) by using PyriF strain as standard. Five acaricides (Abamectin, monocrotophos, tebufenpyrad, bifentazate and cyflumetofen) revealed the dose-dependent mortality within 8 h, whereas other remaining acaricides (Fenbutatin oxide, fenpyroximate, flufenoxuron, spiromesifen and etoxazole) did not. This finding suggests that the application of RCV method is limited depending on the mode of action and physicochemical properties of each acaricide. Resistance levels to five acaricides (Abamectin, monocrotophos, tebufenpyrad, bifentazate and cyflumetofen) were determined for four field populations of TSSM by using RCV diagnostic kit. All TSSM populations showed the highest sensitivity to cyflumetofen, indicating that it would be most effective in controlling field populations. RCV diagnostic kit would enable to provide crucial information for choosing the most appropriate acaricides in the field.

**Key words:** *Tetranychus urticae*, RCV, Acaricide selection, Resistance

## Mutation in *nAChR* Beta Subunit Is Associated with Imidacloprid Resistance in the *Aphis gossypii*

Ju Il Kim, Min Kwon, Sangeun Park<sup>1</sup>, Jeong-Jin Ahn<sup>1</sup>, Young-Uk Park<sup>1</sup>, Seonwoo Lee<sup>1</sup>, Hyun-Na Koo<sup>1</sup>, Gil-Hah Kim<sup>1</sup>, Si Young Kim<sup>2</sup> and Si Hyeock Lee<sup>3</sup>

Highland Agriculture Research Center, NICS, RDA

<sup>1</sup>Department of Plant Medicine, Chung buk National University

<sup>2</sup>Crop protection research team, Dongbu Hannong Co., Ltd

<sup>3</sup>Department of Agricultural Biotechnology, Seoul National University

The cotton aphid, *Aphis gossypii* (Glover), is one of the most serious pests in various vegetable crops. In Korea, some field populations of *A. gossypii* especially in greenhouse showed high resistance against neonicotinoids. The imidacloprid-resistant strain (IR) selected from one of the greenhouse strains was found to be about 3,800 folds more resistant to imidacloprid, compared to the susceptible strain (S), as judged by LC<sub>50</sub> values. To identify differentially expressed genes in IR, an isogenic strain, reverse susceptible strain (IRS) was generated from IR and comparative transcriptome analyses based on GS-FLX were conducted using total RNAs extracted from both IR and IRS. Also we confirmed protein expression patterns by 2DE and detoxification enzyme over-expression by synergist test. However there was no significant variation among IR, IRS and S. Comparison of the nucleotide sequence of seven nicotinic acetylcholine receptor (nAChR) subunit (alpha 1-5,7 and beta 1) genes from S and IR strain revealed a point mutation causing an arginine to threonine substitution (R81T) in the loop D region of the nAChR beta 1 subunit of the IR. These mechanisms were also reported in *M. persicae* and this amino acid change confers a vertebrate-like character to the insect nAChR and results in reduced sensitivity to neonicotinoids. Moreover an extra point mutation, L80S (leucine to serine substitution) was also detected nearby R81T mutation in nAChR beta 1 subunit variant. These mutations can be an additive factor in imidacloprid resistance in *A. gossypii*. This is the first report of imidacloprid resistance mechanism in *A. gossypii*. Further, this would be helpful in managing *A. gossypii* resistant populations in field.

**Key words:** *Aphis gossypii*, Imidacloprid, nicotinic acetylcholine receptor



## Contact and Fumigant Toxicity of Hiba Oil Constituents and Efficacy of spray Formulations Containing the Oil to American House Dust Mite and Copra Mite

**Jun-Ran Kim<sup>1,2</sup>, Haribalan Perumalsamy<sup>1,2</sup>, Min Jung Kwon<sup>2</sup>,  
Hyung Wook Kwon<sup>2</sup> and Young-Joon Ahn<sup>2\*</sup>**

<sup>1</sup>Research Institute for Agriculture and Life Science, Seoul National University

<sup>2</sup>WCU Biomodulation Major, Department of Agricultural Biotechnology,  
Seoul National University

An assessment was made of the toxicity of hiba, *Thujopsis dolabrata* var. *hondai*, oil and 24 oil constituents and control efficacy of four experimental spray formulations containing the oil (0.5, 1, 2, and 3% sprays) to adult American house dust mite (AHDM), *Dermatophagoides farinae*, and copra mite (CM), *Tyrophagus putrescentiae*. Results were compared with those of three conventional acaricides benzyl benzoate, *N,N*-diethyl-3-methylbenzamide (deet), and permethrin. Based on 24 h LC<sub>50</sub> values, (-)-thujopsene was the most toxic constituent against AHDM (9.82 µg/cm<sup>2</sup>) and CM (10.92 µg/cm<sup>2</sup>) and the toxicity of the compound was nearly identical to that of benzyl benzoate (9.33 and 10.14 µg/cm<sup>2</sup>). High toxicity was also observed with (-)-(*E*)-pinocarveol, carvacrol, (+)-terpinen-4-ol, β-thujaplicin, cedrol, α-terpineol, (+)-ledene, thymol, and 2,4-di-tert-butylphenol against both mite species (LC<sub>50</sub>, 11.92–19.19 and 12.49–22.97 µg/cm<sup>2</sup>). These constituents were more toxic than deet (LC<sub>50</sub>, 35.53 and 38.42 µg/cm<sup>2</sup>). Hiba applied as 2 and 3% sprays provided >95% mortality against both mite species, whereas permethrin (*cis:trans*, 25:75) 2.5 g/L spray treatment resulted in ca 11% mortality. Global efforts to reduce the level of highly toxic synthetic acaricides in indoor environments justify further studies on hiba oil preparations containing the constituents described as potential contact-action fumigants or lead molecules for the control of mite populations.

**Key words:** *Dermatophagoides farinae*, *Tyrophagus putrescentiae*, *Thujopsis dolabrata* var. *hondai*, hiba oil, botanical acaricide, spray formulation

## Larvicidal Activity of Ajowan (*Trachyspermum ammi*) and Peru Balsam (*Myroxylon pereira*) Oils and Blends of Their Constituents against *Aedes aegypti*, Acute Toxicity on Water Flea, *Daphnia magna*, and Aqueous Residue

Seon-Mi Seo, Il-Kwon Park, Yoon-Mi Jeon, Sung-Woong Kim,  
Hyo-Rim Lee and Hwa-Jeong Yeom

<sup>1</sup>Division of Forest Insect Pests and Diseases, Korea Forest Research Institute, Seoul 130-712,  
Republic of Korea

We evaluated the larvicidal activity of 20 plant essential oils and components from ajowan (*Trachyspermum ammi*) and Peru balsam (*Myroxylon pereira*) oils against *Aedes aegypti*. Of the 20 plant essential oils, ajowan and Peru balsam oils at 0.1 mg/mL exhibited 100% and 97.5% larval mortality, respectively. At this same concentration, the individual constituents, (+)-camphene, benzoic acid, thymol, carvacrol, benzyl benzoate and benzyl *trans*-cinnamate caused 100% mortality. The toxicity of blends of constituents identified in 2 active oils indicated that thymol and benzyl benzoate were major contributors to the larvicidal activity of the artificial blend. We also tested the acute toxicity of these 2 active oils and their major constituents against the water flea, *Daphnia magna*. Peru balsam oil and benzyl *trans*-cinnamate were the most toxic to *D. magna*. Two days after the treatment, residues of ajowan and Peru balsam oils in water were 36.2% and 85.1%, respectively. Less than 50% of benzyl *trans*-cinnamate and thymol were detected in the water at 2 days after treatment. Our results show that the essential oils of ajowan and Peru balsam and some of their constituents have potential as botanical insecticides against *Ae. aegypti* mosquito larvae.

**Key words:** plant essential oils, *Trachyspermum ammi*, *Myroxylon pereira*, larvicidal activity, mosquito, *Daphnia magna*, residue in water

## Damage of Grapevines by *Apolygus spinolae* ( Hemiptera : Miridae) in Grape Export Complex Area in Korea

**Jin Sun Song<sup>2</sup>, Dong Woon Lee<sup>1</sup>, Suk Jun Lee<sup>1</sup>, Chae Min Lee<sup>1</sup>, Tae Heon Lim<sup>3</sup>,  
Dongpyeo Lyu<sup>4</sup>, Hyeong Hwan Kim<sup>2</sup> and Myoung Rae Cho<sup>2</sup>**

<sup>1</sup>Department of Ecological Science, Kyungpook National University,

<sup>2</sup>Horticultural Environment Division, Nation Institute of Horticultural & Herbal Science,

<sup>3</sup>Research Institute of Agri-Bio Science, Samhoub, Co., Ltd.,

<sup>4</sup>Department of Forest Science, Sangji University, Wonju, Gangwon.

The green pale plant bug, *Apolygus spinolae* was one of the main insect pests that damaged leaves and fruit in grapes and its damage status was firstly reported in 2000 in grape orchards. This research was conducted to evaluate the distribution and difference in damage rate depending in management type of grapevine orchards (domestic sale farm vs export farm) in the export complex area of Korea (Hwangsung in Gyeonggi, Sangju and Yeongcheon in Gyeongbuk, Namwon in Junbuk and Yeongdong in Chungbuk) from 2010 to 2012. Damage by *A. spinolae* occurred in all 62 survey farms and damage rate differed depending on locality and individual farms in the same area. Damage rate was lower in export farms than in domestic sale farms, and damage rate of leaves was highly correlated with damage rate of new shoots. 15 species of hemipteran insect were attracted to sticky traps and *A. spinolae* was the dominant species. The attracted number of *A. spinolae* in the sticky traps differed depending on locality, and more occurred in domestic sale farms than expert farms. *A. spinolae* was continually attracted to sticky traps in the harvest period in grapevine orchards.

**Key words:** *Apolygus spinolae*, damage rate, export agricultural products, grapevine, quarantine

0044

## **Enhansive Effect of Two Fumigants, Ethyl formate and Phosphine Gas, to Both Control Cotton Aphid and Two-Spotted Spider Mite in Applying Export Strawberries**

**Byung-ho Lee\*, Bong-su Kim, Sun-ah Jung and Eul-jai Myung**

Dongbu ARI, Dongbu Farm Hannong Co., Ltd.

For replacement of methyl bromide(MB) in Korea, Vapormate<sup>TM</sup>, a gas formulation of ethyl formate(EF) with carbon dioxide, are firstly introduced in import bananas and Vivakil<sup>TM</sup>, a gas formulation of phosphine(PH3) with carbon dioxide, are ready to commercial use in export cut flowers. Their applications are being extended for other import and export commodities. Ethyl formate have been shown to have effectiveness short exposure time(<4hr) but it has a limited application at low temperature for TSM(Two spotted spider mites) due to some phytotoxic to strawberry. Phosphine gas has demonstrated their efficacy to TSM at low temperature but only meets quarantine requirement when applying longer fumigation time(>24hr) to control CA(cotton aphids). We firstly evaluated two MB alternatives, EF and PH3, have enhansive effect within short exposure time(4hr) at low temperature(5°C) for controlling both TSM and CA without any injury to export strawberries.

**Key words:** ethyl formate, phosphine, methyl bromide alternative, enhansive effect, cotton aphid, two-spotted spider mite

0045

## **The Effect of a single Blood Meal on Insecticide Resistance of the Major West Nile Virus Vector, *Culex pipiens pallens* (Diptera: Culicidae), in the Republic of Korea**

**Kyu-Sik Chang, Dae-Hyun Yoo, Seong Yoon Kim, Mi Yeoun Park, E-Hyun Shin, Wook-Gyo Lee, Jong Yul Roh,**

Div. of Medical Entomology, Center for immunology and pathology, National Institute of Health

Insecticide resistance and activation of the metabolic detoxification enzymes of female *Culex pipiens pallens* by the blood meal were assessed using a micro-application bioassay and micro-plate enzyme activity assays. Four group of *Cx. pipiens pallens* were used, a susceptible non-engorging group at seven days after emerging, SNE7 Cp; a resistant non-engorging group at seven days after emerging, RNE7 Cp; a resistant engorged group at one day after blood feeding and a resistant engorged group at seven days after blood feeding, REG7 Cp.

Insecticide resistance of *Cx. pipiens pallans* was increased by the blood feeding. Based on LC<sub>50</sub> values, SNE7 Cp demonstrated >50 fold of higher susceptibility to all tested insecticides when compared with RNE7 Cp. RNE7 Cp showed higher susceptibility to all tested insecticides than REG1 Cp and REG7 Cp with a relative susceptibility LC<sub>50</sub> (SRLC<sub>50</sub>) of 25.8 to 50.0 and 25.0 to 48.8.

In micro-plate enzyme assays, the metabolic detoxification enzyme activity of *Cx. pipiens pallans* adult females was increased by the blood feeding. Activation of non-specific esterases (EST), glutathione-S-transferase (GST) and mixed function oxidase (MFO) in RNE7 were higher than in SNE7 and the all tested enzymes in REG1 and REG7 demonstrated significantly higher enzyme activation than RNE7, except for activation of GST in REG1. Activation of MFO in REG1 and REG7 were 209.4- and 74.6- fold higher than in REG7, respectively. Non-specific esterases (EST) and glutathione-S-transferase exhibited < 10 fold of higher Rr values.

These results may be significant in terms of the criteria that are used to evaluate resistance, because blood fed female mosquitoes may show enhanced expression of the resistance phenotype, possibly allowing for earlier detection of insecticide resistance.

**Key words:** Metabolic detoxification enzymes, *Culex pipiens pallens*, Insecticide resistance, a blood meal.

## Japanese Encephalitis Virus Detected from *Culex orientalis* and *Culex pipiens* Complex in Korea

**Hyunwoo Kim<sup>1</sup>, Young Eui Jeong<sup>2</sup>, Go-Woon Cha<sup>2</sup>,  
Mi Yeoun Park<sup>1</sup> and E-hyun Shine<sup>1</sup>**

<sup>1</sup>Division of Medical Entomology, Korea National Institute of Health, Osong

<sup>2</sup>Division of Arboviruses, Korea National Institute of Health, Osong

Japanese encephalitis virus (JEV), a mosquito-borne pathogen, is the most important cause of viral encephalitis worldwide. The major vector mosquito of this virus, known as *Culex tritaeniorhynchus*, is mainly live in paddy rice field in Korea. So Japanese encephalitis (JE) is a disease of rural areas. During urbanization, rice cultivated land has decreased also resulting the number of JE patients has decreased. However, recent outbreak of JE in Korea 2010, the patients distribution was not related with that of the mosquito. Therefore, this study was conducted to evaluate involving other mosquito species in the transmission of JEV. Five localities, JE reported in 5 years, have been selected to collect mosquitoes according their habitats (mountain, swap, cow shed, and downtown area) in 2012. Total 22,774 collected mosquitoes were pooled by species, date and site of collection. Of the 1,282 pools, eight (five were from *Culex orientalis*, one from *Culex pipiens* complex, and two from *Aedes vexans*) were found positive for flavivirus RNA in SYBR Green I-based real-time RT-PCR assay. The results of sequences blasting on NCBI showed that the flaviviruses from *Cx. orientalis* and *Cx. pipiens* complex were identified as JEV genotype V.

**Key words:** Japanese encephalitis virus (JEV), *Culex orientalis*, *Culex pipiens* complex, genotype V

0047

## 애완학습용 곤충 소비자의 행동 모니터링

김남정, 김소윤, 김성현, 최원호, 박해철, 이영보

국립농업과학원 곤충산업과

우리나라는 1988년 이후 장수풍뎅이, 사슴벌레, 나비류 등 50여 종류의 곤충이 학습과 취미용으로 상품화되어 시장규모가 증가하고 있는 추세에 있으며, 곤충의 체험학습장 및 곤충생태공원, 곤충박물관 등에는 연 200만명 이상이 관람하는 것으로 나타났다(특허청, 2011). 따라서 점차 규모가 커지고 있는 애완학습용 곤충시장을 올바르게 이해하고 적절히 대응하기 위해서는 소비자의 욕구를 파악할 필요가 있기 때문에 실제 이용자의 행동 모니터링을 시행하였다.

‘곤충’으로 검색된 블로그의 게시물을 대상으로 내용분석을 실시한 결과, 방문시기는 1월과 2월, 자녀의 체험학습을 위해 초등학교 저학년 이하의 자녀를 동반한 가족형 방문인 것으로 나타나 방학을 이용한 자녀교육 목적의 방문형태가 주를 이루는 것을 확인할 수 있었다. 방문지역은 서울 및 경기도의 수도권지역에 집중되어 있으며, 사진 게시물의 내용을 분석한 결과를 살펴보면 곤충과 관련된 전시품사진과 체험활동위주의 사진이 가장 높은 비율을 보였다. 만족스러웠던 경험은 교육적 효과가 높은 다양한 체험활동이 많았다는 것이며, 불만족스러웠던 경험은 곤충을 보는 것만으로도 징그럽고 무섭다는 내용이 가장 많은 것으로 나타났다. 따라서 보다 누구나 쉽게 다가갈 수 있도록 친근한 이미지를 형성할 필요가 있으며, 교육적 가치가 높으면서 직접 체험할 수 있는 보다 다양한 형태의 전시 및 프로그램 개발에 대한 연구가 필요할 것으로 보인다.

**검색어:** 곤충, 블로그(blog), 소비자

## **Applying Hidden Markov Model for the Traveling Behaviors of Subterranean Termites in the Artificial Tunnels with Varying Width and Curvature**

**Seungwoo Sim<sup>1</sup>, Seungho Kang<sup>1</sup> and Sang-Hee Lee<sup>1</sup>**

<sup>1</sup>Department of Mathematical Model Research, National Institute for Mathematical Sciences

In the real world, most of biological systems that follow Markov process have internal states which are unobservable, so called hidden states. However, although the states could not be directly observed, events emitted under any hidden states would often be observable. It infers that a lot of biological systems might be simulated by hidden Markov model (HMM). To date, many studies tried to apply the HMM for monitoring and describing of animal behaviors. In this study, we attempted to build a HMM that emulates the traveling behavior of subterranean termites in the artificial tunnels with varying width and curvature, based on the empirical data obtained from our previous study that explored the relationship between subterranean termite's movement efficiency and the geometric pattern of their tunnels.

**Key words:** *Subterranean termite, tunnel, traveling behavior, HMM*



## Analysis of the Responses of Termites to Tunnel Irregularity

Sang-Hee Lee<sup>1</sup>, Sook Jung Ku<sup>2</sup>

<sup>1</sup>Department of Mathematical Model Research, National Institute for Mathematical Sciences

<sup>2</sup>Kangwon National University

Subterranean termites build extensive underground galleries consisting of elaborate tunnels and channels to forage food resources. Diverse soil conditions surrounding the tunnels, such as soil density, may cause irregularities in the size and shape of the tunnels, and termites are likely to encounter a number of tunnel irregularities while traveling. Considering the tunnel length, how termites respond to an irregularity is likely to affect their movement efficiency, and this in turn is directly correlated to their foraging efficiency. To understand the response of termites, we designed an artificial linear tunnel with rectangular irregularities in a 2-D arena. The tunnel widths,  $W$ , were 3 and 4 mm. The rectangular irregularities were 2 mm in width and of varying heights  $H$  (2, 1, 0, -1, and -2 mm). The positive and negative sign of  $H$  represents a convex and concave structure, respectively. We systematically observed the movement of termites, *Coptotermes formosanus* Shiraki, at the irregularity and quantified the time needed,  $\tau$ , for a termite to pass the irregularity. The time  $\tau$  was shorter for  $(W, H) = (3, 0)$  and  $(3, -1)$  than for  $(W, H) = (3, 1)$ ,  $(3, 2)$ , and  $(3, -2)$ . The time  $\tau$  was longer for  $(W, H) = (4, -1)$ , and  $(4, -2)$ , than for  $(W, H) = (4, 0)$ ,  $(4, 1)$  and  $(4, 2)$ . Four types of behaviors explained the response to the irregularity. The implications of these findings are briefly discussed in relation to termite foraging efficiency.

**Key words:** Termite movement efficiency, Tunnel surface irregularity, Termite tunnel network, Foraging efficiency

## 가지 길이 유사성 엔트로피를 이용한 나비 영상 인식

강승호, 이상희

국가수리과학연구소 수리생물학연구팀

생물 종 다양성 및 보존에 대한 필요성은 곤충과 같은 생물 개체의 정확하고 효율적인 인식 방법에 관심을 불러 일으켰다. 특히 스마트 폰과 같은 디지털 정보기전의 발달과 보급으로 인해 영상 매체를 이용한 곤충 종의 자동인식에 대해 많은 연구가 이루어지고 있다. 본 논문은 나비 영상 인식을 위해 가지 길이 유사성 엔트로피(Branch Length Similarity Entropy)를 이용한 특징 추출 방법을 제안한다. 제안한 특징 추출 방법은 나비의 윤곽으로부터 높은 곡률을 가진 특징점들을 추출한 다음 이들 사이를 네트워크로 구성하고 특징점 간의 길이 분포를 엔트로피로 표현한 것이다. 제안한 특징 추출 방법의 성능을 평가하고자 15종의 나비 영상을 대상으로 지도학습 기반 기계학습 방법인 베이지안 분류기, 인공 신경망 및 서포트 벡터 머신을 이용해 기존에 제시된 푸리에 기술자 및 웨이블릿 기술자와 비교하였다.

**검색어:** 나비 분류, 가지 길이 유사성 엔트로피, 기계학습

## What Determines Densities of Cicada Species in Central Korea?

**Yikweon Jang<sup>1</sup>, Tae Eun Kim<sup>1</sup> and Seung-Yoon Oh<sup>2</sup>**

<sup>1</sup>Department of Life Sciences, Ewha Womans University

<sup>2</sup>School of Biological Sciences, Seoul National University

In some cicada species, male calling songs are so loud that they become a nuisance to city dwellers in Korea. To understand the abundance of cicada species in central Korea, we conducted complete enumeration surveys of exuviae in *Hyalessa fuscata*, *Cryptotympana atrata*, *Meimuna* spp, and *Graptopsaltria nigrofuscata*. Exuviae collection was conducted in three representative habitats in central Korea: metropolitan, suburban, and country. We collected the exuviae twice with a 10-day interval between samplings in August 2010. Resource-weighted density of each species was calculated based on the area and the number of trees. *H. fuscata* was the dominant species in all three regions. Resource-weighted densities in metropolitan and suburban regions were much higher than those in the country region, due to *H. fuscata* and *C. atrata*. The results of the multivariate general linear models showed that region, date, and the interaction between these two variables were all significant for population densities of cicada species. Unlike the resource-weighted densities, the organism-weighted densities that indicated the intensity that an individual had to share its host with others were much larger than tree-weighted densities for cicada exuviae. Furthermore, there was no significant difference in organism-weighted densities among habitats. The difference between resource-weighted and organism-weighted densities implied that larger proportions of trees were not used by cicada juveniles in the country. Thus, the distributions and abundance of tree host species could be an important factor for cicada density in Korea.

**Key words:** *Hyalessa fuscata*, *Cryptotympana atrata*, resource-weighted density, organism-weighted density

## 대구지역에서 사회성 말벌에 의한 피해 양상

최문보, 장갑수, 김슬옹, 김태수, 권관익, 이종욱

영남대학교 생명과학과

2001-2012까지 대구지역에서 119 구조대에 의한 사회성 말벌의 벌집제거 출동건수를 보면 총 11,948건으로 나타났으며 이 건수는 매년 증가하고 있는 추세이다. 특히 2008년 이후로 그 증가세가 급격하게 증가하였는데 2001년 147건에 비해 2012년에는 4,979건으로 약 34배 증가하였다. 이들 출동은 주로 7-9월에 가장 높게 나타내었는데 이는 벌집이 가장 성숙된 시기와 일치한다. 대구 내 상습 피해 지역은 12년 동안 북구 지역이 2,825건으로 가장 많은 신고건수를 나타내었으나 단위면적당으로 보면 남구 지역이 33.60으로 가장 높게 나타나 실질적인 피해가 가장 높은 지역으로 나타났다. 따라서 도시 내 말벌의 피해에 대한 방제 및 조절은 남구가 가장 우선적으로 그 대상지가 되어야 할 것이다.

대구 도심지에서 나타나는 말벌종은 13종으로 나타났으며 그중 왕바다리(*Polistes rothneyi koreanus*)가 집중적으로 피해를 일으키는 것으로 나타났으며 최근 아열대 침입종 등검은말벌(*Vespa velutina nigrithorax*)이 도시 내에서 그 분포를 늘려가고 있어 피해가 예상된다.

대구지역에서 말벌의 영소가 급격히 증가하는 원인은 도시 내 녹지대의 증가가 가장 큰 원인으로 생각되어지며, 그 외 영소 장소의 안전성, 도시 내 높은 온도에 따른 콜로니 발육 증대, 낮은 빈도의 포식 및 기생률 등으로 보여 진다.

**검색어:** 사회성 말벌, 대구, 도시, 119구조대 출동

O053

## A New Species of *Phyllotreta* Chevrolat (Coleoptera, Chrysomelidae, Alticinae) from South Korea

Jinyoung PARK<sup>1\*</sup>, Jong Eun LEE<sup>2</sup> and Jong Kyun PARK<sup>1</sup>

<sup>1</sup>Department of Applied Biology, Kyungpook National University, Sangju, Korea

<sup>2</sup>Department of Biological Science, Andong National University, Andong, Korea

The genus *Phyllotreta* Chevrolat belonging to the subfamily Alticinae (Coleoptera: Chrysomelidae). One of the largest alticine genera with approximately 150 species in the Palearctic region and more than 250 species worldwide. In Korea a total of 6 species were known by Lee and An (2001).

New species of *Phyllotreta* Chevrolat, 1837 are described: *P. hamata* Park sp. nov. from South Korea. The relationships of the new species with the actual species groups of *Phyllotreta* are discussed. Also, illustrations of diagnostic characteristics of the new species including male aedeagus and spermatheca are provided with a key to South Korean *Phyllotreta* species.

Up to now 7 species of *Phyllotreta* have been recorded from the South Korea, including the present species.

**Key words:** Chrysomelidae, Alticinae, *Phyllotreta hamata* Park sp. nov.

## 한반도 서식 자생 곤충종의 확증표본 시스템 구축

서홍렬, 김기경, 안능호, 박선재

국립생물자원관 동물자원과

지구 생물다양성의 보전과 함께 생물자원의 지속가능한 이용과 생물자원을 이용하여 얻어지는 이익을 공정하고 공평하게 분배할 것을 목적으로 유엔환경개발 회의에서 만들어진 생물다양성협약은, 2010년 생물유전자원의 접근과 이익공유에 관한 나고야의정서(ABS)를 채택하면서, 세계 각국이 가지고 있는 생물자원의 이용에 대한 국제적 규범을 만들었다. 따라서, 향후 의정서 발효 이후 여러 분야에서 이용될 수 있는 우리 생물자원의 주권적 권리를 지키기 위해서는 국가 생물종 목록에 근거해 자생 생물종에 대한 확증표본(voucher specimens)의 현황과 증거표본을 조속히 확보하는 일이 무엇보다 시급하게 되었다. 확증표본이란 우리나라 자생생물을 채집하여 표본으로 제작한 것으로 전문가가 정확히 동정하여 우리나라 생물종의 서식 증거로 이용하는 생물표본을 말하는데, 그간 우리나라에서는 많은 종들에 대한 확증표본 자료가 체계적으로 정리되지 않았고 일부 종들만 대학 및 연구기관에서 부분적으로 정리 및 보존하는 정도였다. 환경부 국립생물자원관은 이러한 국제적 규범에 선제적으로 대응하여 2008년부터 국가 생물종 확증표본 정보 시스템을 구축해 왔는데, 곤충분야에서는 5년간의 조사 연구를 통해 2012년 12월까지 기록된 곤충류 14,145종 중 8,245종에 대한 확증표본 정보를 구축하였다. 지금까지 구축된 확증표본 정보는 우리 곤충자원의 권리를 주장하는 근거뿐만 아니라, 생물다양성 연구, 생물지리학적 연구, 형태학적 연구 및 계통분류학적 연구 등 다양한 연구 분야에서 기초자료로 귀중하게 이용될 수 있을 것이다.

**검색어:** 생물주권, 곤충, 확증표본, 생물다양성협약, 나고야의정서

## 한반도 서식 자생 곤충의 인벤토리 구축

서홍렬, 안능호, 김기경, 박선재

국립생물자원관 동물자원과

지구 생물다양성의 보전과 함께 생물자원의 지속가능한 이용과 생물자원을 이용하여 얻어지는 이익을 공정하고 공평하게 분배할 것을 목적으로 유엔환경개발회의에서 만들어진 생물다양성협약은, 2010년 생물유전자원의 접근과 이익공유에 관한 나고야의정서(ABS)를 채택하면서, 세계 각국이 가지고 있는 생물자원의 이용에 대한 국제적 규범을 만들었다. 따라서, 향후 의정서 발효 이후 여러 분야에서 이용될 수 있는 우리 생물자원의 주권적 권리를 지키기 위해서는 가장 기초적 자료인 우리 생물종에 대한 인벤토리(Inventory)를 종합적으로 빨리 구축하는 것이 중요하게 되었고, 정부는 이에 대응하기 위해 「생물다양성 보전 및 이용에 관한 법률」을 2013년 2월부터 시행하면서 국가의 생물종 목록 구축을 의무화 하였다. 한반도에 자생하고 있는 생물종의 수는 국토의 면적과 위도가 비슷한 일본과 영국의 경우를 고려하여 약 10만종 이상으로 학자들은 추정하고 있는데, 환경부 국립생물자원관은 2008년부터 각 분류군별 전문가들의 도움을 받아 각종 문헌기록들을 분석·정리하여 한반도에 서식하는 생물종 인벤토리를 지속적으로 구축해 왔다. 2012년에는 그간 5년간의 인벤토리 구축 결과를 종합하여 한반도의 생물종수를 39,150 분류군으로 정리하였는데, 이 중 곤충류는 14,145 분류군을 차지하였다. 이 중에서 분류학적으로 체계가 변경된 것들은 최신의 정보를 반영하였는데, 툴토기목은 3개의 목으로 재분류하여 뿔툰툰목, 둥근툰툰목, 툰툰목으로 정리하였고, 이목은 이목과 새털이목으로 분리하였다. 국립생물자원관은 지금까지 정리된 곤충 인벤토리를 분류군별로 나누어 2015년까지 국가 생물종 곤충분야 목록집으로 발간할 예정이다.

**검색어:** 인벤토리(Inventory), 생물주권, 곤충, 생물다양성협약, 생물종목록집

## Northward Range Shifts of Korean Butterflies

**Tae-Sung Kwon<sup>1</sup>, Cheol Min Lee<sup>1</sup> and Sung-Soo Kim<sup>2</sup>**

<sup>1</sup>Division of Forest Ecology, Korea Forest Research Institute, 57 Hoegi-ro, Dongdaemun-gu, Seoul 130-712, Republic of Korea

<sup>2</sup>Research Institute for East Asian Environment and Biology, Gangdong-gu, Seoul 134-852, Republic of Korea

In the Northern Hemisphere, northward shifts due to global warming are apparent in various organisms such as butterflies, birds, and plants. In South Korea, ranges of butterflies are expected to shift northwards. We tested whether distribution limits of Korean butterflies shift northwards. We used two Korean butterfly atlases (1938-1950, 1977-2011) for analysis of the range shifts. Northern limits of southern species moved significantly northward (ca. 60 km) for 50 years, whereas southern limits of northern species did not significantly move northwards nor southwards. This finding parallels with other studies on butterflies and birds in Europe and North America.

**Key words:** Butterfly, range shift, distribution, Korea, climate change, global warming



## Effects of Forest Degradation on Butterfly Communities in the Gwangneung Forest

Cheol Min Lee<sup>1</sup>, Tae-Sung Kwon<sup>1</sup>, Sung-Soo Kim<sup>2</sup>, Jeong-Dal Shon<sup>3</sup>, Bong-Woo Lee<sup>3</sup>

<sup>1</sup>Division of Forest Ecology, Korea Forest Research Institute, Seoul 130-712, Republic of Korea

<sup>2</sup>Research Institute for East Asian Environment and Biology, 293-27, Amsa 3 dong, Gangdong-gu, Seoul 134-852, Republic of Korea

<sup>3</sup>Korea National Arboretum, 51-7 Jikdong-ri, Soheul-eup, Pocheon-si, Gyeonggi-do 487-821, Republic of Korea

This study was carried out to clarify the response of butterfly communities on forest degradation in the Gwangneung Forest, Korea. We monitored butterfly communities with varying degrees of human activities by conducting line transect twice a month in 2011. A total of 70 species and 4,676 individuals butterflies were observed in four sites: natural forest, plantation forests, and Korea National Arboretum. Species richness increased with increasing open land. The result on niche breadth and habitat type of butterfly was consistent with our predictions; specialist species and forest interior species were abundant in natural forest, whereas generalist species and grassland species were abundant in Korea National Arboretum, the most modified area. Also, habitat breadth of butterflies clearly indicated the difference on the degree of forest degradation. Butterfly diversity associated with landscape patterns based on aerial photographs supported mosaic concept which indicates that species diversity increases as habitat heterogeneity and variability increase. Forest management plan that maintains various habitats and ensures grasslands is necessary to increase butterfly diversity in forest.

**Key words:** forest degradation, butterfly, niche breadth, habitat type, habitat breadth

## Taxonomic Notes on the Genus *Clerus* Geoffroy (Coleoptera: Cleridae) with a New Species from South Korea

**Jongok Lim<sup>1</sup>, Roland Gerstmeier<sup>2</sup>, Bongwoo Lee<sup>1</sup> and Seunghwan Lee<sup>3</sup>**

<sup>1</sup>Division of Forest Biodiversity, Korea National Arboretum, Republic of Korea

<sup>2</sup>Institute of Animal Ecology, Germany

<sup>3</sup>Department of Agricultural Biotechnology, Seoul National University, Republic of Korea

Two families of checkered beetles (Cleridae and Thanerocleridae) contain approximately 3,600 described species.

*Clerus* is one of genera belonging to the *Omadius* genus-group (Cleridae: Clerinae: *Clerus* series), and distributed in Palaearctic, Indo-Australian and Afrotropic regions containing 17 species. Among the known species, 11 species have been recorded from Palaearctic region (seven from East Asian countries).

Through a taxonomic study on the Korean *Clerus* species, a total of three species, *C. dealbatus* (Kraatz, 1879), *C. pilosellus* (Gorham, 1878) and *Clerus* sp. nov. are recognized.

From the present study, it was confirmed that *C. dealbatus* was misidentified as *Thanasimus lewisi* (Jacobson, 1911) in the country, due to the similarity of the body coloration. The presence of the latter species in Korean insect fauna is very doubtful.

Diagnostic characters of three Korean *Clerus* species are presented.

**Key words:** Coleoptera, *Clerus*, new species, predator, South Korea

0059

## 한란(*Cymbidium kanran* Makino)을 포함한 난초과의 주요 해충 *Japanagromyza tokunagai* (Sasakawa) (파리목: 굴파리과)에 대한 연구

임종수, 김일권

국립수목원 산림생물조사과

한란(*Cymbidium kanran* Makino)은 개화기가 보통 11~1월로, 추울 때 꽃이 핀다하여, ‘한란(寒蘭)’이라 불린다. 우리나라의 제주도를 비롯하여, 일본 남부, 중국 남부, 대만 등에 분포하는 동북아시아 온대기후대의 표식종으로 알려져 있다.

본 연구는 천연기념물 제 432호로 지정된 “제주 상호동 한란자생지”(제주도 서귀포시 돈내코 위치)에 자생하는 한란이 2011년에 꽃을 거의 못피우는 피해가 발생하여 이를 야기한 해충을 규명하기 위하여 2012년 2월-10월에 걸쳐 현지 방문 조사를 실시하였다.

본 연구를 통하여, 해당 해충 종은 굴파리과(Agromyzidae)의 국내 미기록종인 *Japanagromyza tokunagai* (Sasakawa)로 확인되었다. 한란의 꽃대에 1-3마리 정도의 *J. tokunagai* 유충이 굴을 파면서 자라는데, 꽃이 피기 전에 꽃대가 부러지는 피해를 입힌다. 본 연구를 통해 이 굴파리는 한란 뿐만 아니라 보춘화(*C. goeringii*)의 꽃대와 자방, 금난초(*Cephalanthera falcata* (Thunb.) Blume), 은난초(*Ce. erecta* (Thunb.) Blume), 두잎감자난초(*Oreorchis coreana* Finet) 그리고 복주머니란(*Cypripedium macranthos* Sw.)의 자방에 피해를 입히는 것을 확인하였다. 이와 더불어 이 굴파리의 피해를 입은 한란 꽃대와 금난초 자방에서 좀벌과(Eulophidae)의 *Pediobius* sp. cf. *P. metallicus*, 금좀벌과(Pteromalidae)의 *Sphegigaster* sp. 그리고 검정알벌과(Scelionidae)의 *Telenomus* sp., 총 3종의 기생벌이 같이 우화하였다. 굴파리의 피해를 막기 위해 꽃대가 올라오는 시기부터 개화 직전까지 망을 씌우는 방법을 제시하였다.

**검색어:** 난초과, 한란, 파리목, 굴파리과, 기생벌, 기주식물

## **Developmental Characteristic of Yellow Spotless Ladybug, *Illeis koebelei* Timberlake (Coleoptera: Coccinellidae: Psylloborini) and the Biological Control Effect on the Cucumber Powdery Mildew**

**Young-su Lee, Soon-sung Hong, Jin-young Kim,  
Soon-jae Kim and Hee-dong Kim**

Gyeonggi-do Agricultural Research and Extension Services

The yellow spotless ladybug (YSL), *Illeis koebelei* is a kind of aboriginal ladybug in Korea. YSL feed on the fungi and extraordinary prefer to powdery mildew (PM). This study was conducted to investigate the developmental characteristic and the biological control effect on the cucumber PM by the YSL from 2010 to 2012.

YSL were detected on the 12 species of host plants infected with PM. and occurrence was observed from the early of July to the early of November in Gyeonggi area. The feeding amount of YSL on the cucumber PM was in order of 4<sup>th</sup> larva, adult, 3<sup>rd</sup> larva, 2<sup>nd</sup> larva and 1<sup>st</sup> larva. The optimum developmental temperature and photoperiod for YSL was 20~25°C and 16L:8D respectively. Three species of fungi were selected as the short term substitution feed for YSL. Control effect on cucumber PM under 2.5% of occurrence rate was linearly increased in proportion to increased numbers of 3<sup>rd</sup> larva were applied. Combination treatment of the fungal agent with YSL enhanced suppression of cucumber PM more than either agent used alone. The safety agricultural chemicals were selected harmless to the survival of larva and adult of YSL. The survival rate of pupae and adult was over 80% after storage at 10~12°C for 30 days. Five species of banker plant were selected for maintenance of YSL during growing season in greenhouse.

**Key words:** Mycophagous, Natural enemy, Yellow spotless ladybug, Control, Powdery mildew

## Study on the Hatching Characteristics and Diet of Stick Insect, *Baculum elongatum* (Phasmida : Phasmatidae) for Artificial Mass Rearing

JinGu Lee<sup>1</sup>, HeeDong Kim<sup>1</sup>, ChangSung Kang<sup>1</sup>, AeGyeong Seo<sup>1</sup>, SangHyun Lee<sup>2</sup>,  
YoungKyu Park<sup>3</sup> and YoungBo Lee<sup>4</sup>

<sup>1</sup>Gyeonggi-do Agricultural Research and Extension Services

<sup>2</sup>Sunyou. Co. Ltd.

<sup>3</sup>Korea Beneficial Insects Lab. Co. Ltd. <sup>4</sup>National Academy of Agricultural Science

*Baculum elongatum* has a long, thin shape that resembles a twig, propagates by parthenogenesis, changes body color, and drops eggs, all of which suggests its potential in the commercial market, especially as an educational pet insect. This study was carried out to determine the best hatching environment and an alternative or artificial diet for rearing *B. elongatum* to be developed as a commercial and educational pet insect.

Oviposition was performed by females without fertilization by the sperm of males. The oviposition period was  $42.2 \pm 22.7$  days and the number of eggs per female was  $109.5 \pm 70.5$  eggs. The hatch rate was 73.3% at 25°C and 66.7% after low temperature treatment (8°C for 60 days). In nature, *B. elongatum* overwinters as an egg, but it can be assumed from the results that cold temperatures were not required for hatching. The hatch rate was 98.2% in the treatment using floral foam, fermented sawdust, and leaves.

Clover(*Trifolium repens*) was an excellent diet as it was similar to the host plant and could be used as an alternative diet. The rate of reaching adulthood for the insects was 66.7% on an artificial diet containing 25% acacia leaves. For sustainable mass rearing of nymphs or adults of *B. elongatum*, a natural diet could be used such as acacia (*Robinia pseudoacacia*), white oak (*Quercus aliena*), chestnut (*Castanea crenata* var. *dulcis*), and bush clover (*Lespedeza bicolor*), or an alternative diet such as clover or artificial diet. To rear nymphs and adults of *B. elongatum*, natural diet such as acacia, white oak, chestnut, or bush clover leaves, or an alternative diet such as clover or an artificial diet can be used.

**Key words:** Stick insect, *Baculum elongatum*, insect