

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

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

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

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

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

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

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

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

**Key words:** Taxonomy, Coleoptera, Elateridae, Dendrometrinae, Korea.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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*Synanthedon haitangvora* (Lepidoptera: Sesiidae) is an economically important pest of apple trees in Korea and China. We report here the identification of compounds in pheromone gland extracts of female *S. haitangvora*, and the male responses to blends of different components and ratios in the field. Two major components from pheromone gland extracts of *S. haitangvora* females were identified as Z3,Z13-18:OAc and E2,Z13-18:OAc, and the average ratio of these components was about 1:1. Seven minor components, Z9-16:OAc, Z11-16:OAc, Z9-18:OAc, Z13-18:OAc, E3,Z13-18:OAc, Z3,Z13-18:OH, and E2,Z13-18:OH, also were identified from gland extracts. Field tests showed that male *S. haitangvora* were attracted to Z3,Z13-18:OAc alone, but the maximum number of males was attracted to the binary blend of Z3,Z13-18:OAc and E2,Z13-18:OAc mimicking the blend found in female extracts. The addition of minor components to a 1:1 blend of Z3,Z13-18:OAc and E2,Z13-18:OAc did not increase the numbers of moths captured. The only significant effect of minor components was the strong inhibitory effect of adding Z3,Z13-18:OH to the primary binary blend. Increasing doses of the optimum pheromone blend in the lures from 0.1 to 2.0 mg increased trap catches of male *S. haitangvora*.

**Key words:** *Synanthedon haitangvora*, Z3,Z13-18:OAc, E2,Z13-18:OAc, Lepidoptera, Sesiidae

## A Sodium-Potassium-Chloride Channel is Involved in Oenocytoid Cell Lysis in Response to PGE<sub>2</sub> in *Spodoptera exigua*

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Sodium-potassium-chloride co-transporter (NKCC) is a membrane bound channel protein that plays a prominent role in a variety of epithelial absorptive, secretory processes and a direct role in cell volume regulation, in which NKCC transports sodium, potassium, and chloride ions across the cell membrane. It has been known that prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) induces an acute cell lysis of specific hemocyte type, oenocytoid, to release prophenoloxidase into the plasma and ouabain (a specific sodium pump inhibitor) inhibits the oenocytoid cell lysis resulting in preventing phenoloxidase activation. However, it is not clear how the intracellular signaling pathway leads to oenocytoid cell lysis in response to PGE<sub>2</sub>. This study was designed to analyze functional role of NKCC in the cell lysis to release prophenoloxidase. A gene structure of NKCC was derived from cDNA library of *Spodoptera exigua* hemocyte, NKCC was expressed in all developmental stages and tissues. A real time quantitative RT-PCR showed that bacterial challenge significantly induced its expression. Specific inhibitors of NKCC, bumetanide and chlorothiazide, clearly prevented the cell lysis in a dose dependent manner. When RNA interference using double stranded RNA (dsRNA) specific to NKCC suppressed its expression, the oenocytoid lysis and PO activation was significantly inhibited in response to PGE<sub>2</sub>. It also reduced nodule formation to bacterial challenge. These results indicate that NKCC is associated with oenocytoid cell lysis probably by increasing cell volume through inward transport of ions in response to PGE<sub>2</sub>.

**Key words:** Sodium-potassium-chloride channel, Prostaglandin E<sub>2</sub> Oenocytoid, Cell lysis, Prophenoloxidase, *Spodoptera exigua*

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

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A polydnavirus, *Cotesia plutella* bracovirus (CpBV), encodes host translation inhibitory factors (HTIFs). Two HTIFs have been identified and named as CpBV15 $\alpha$  and CpBV15 $\beta$ . HTIFs specifically inhibit host gene expression at post transcriptional level. This suggests that HTIFs can discriminate host mRNAs for their inhibition. To test this hypothesis, we chose a storage protein 1 (SP1) for a target and CpBV15 $\beta$  for non-target genes. Both target and non-target genes were constructed in a cloning vector by cloning their 5'UTR+ORF and *in vitro* transcribed. The capped partial mRNAs were *in vitro* translated using rabbit reticulocyte lysate in the presence or absence of HTIFs. Translation of SP1 mRNA was significantly inhibited by the HTIF, but those of CpBV15 $\alpha$  and CpBV15 $\beta$  were not. We prepared chimeric mRNAs by exchanging 5'UTR and ORF of both target and non-target genes. Inhibitory activity of HTIFs was dependent on the 5'UTR structure. Target 5'UTR had more complicated secondary structure than non-target 5'UTR in terms of free energy required for unwinding. To identify the target molecule of HTIF to discriminate 5'UTR, an immunoprecipitation using HTIF antiserum was conducted. HTIF was co-precipitated with eIF4A that would be required for unwinding the secondary structure of mRNA. These results suggest that HTIF of CpBV can sequester host eIF4A, any mRNAs possessing complicated secondary structures in their 5'UTRs would be difficult to recruit initiation complex for efficient translation.

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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As an environment-friendly phytosanitary measure, CATTS (controlled atmosphere temperature treatment system) has been developed to kill several quarantine insect pests infesting subtropical agricultural commodities. This study tested any possibility to apply CATTS to apples to effectively eliminate the peach fruit moth, *Carposina sasakii*, which has been regarded as a quarantine insect from the imported countries. When the larvae of *C. sasakii* were directly exposed to 46°C (an installed lethal temperature of CATTS), they showed a median lethal time at 14.66 min. Addition of high carbon dioxide to the temperature treatment enhanced the thermal limit susceptibility of *C. sasakii* to 46°C. The larvae internally infesting apples were tested using this CATTS device and showed 100% lethality after 60 min exposure to a treatment of 46°C under 15% CO<sub>2</sub> in the chamber. This study suggests a possibility that CATTS can be applied as a quarantine measure to kill the larvae of *C. sasakii* locating inside the apples. To understand the CATTS effect, a heat shock protein was cloned. Hsp90 was partially sequenced and showed its expression in response to heat treatment. CATTS was likely to suppress hsp90 expression.

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

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

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

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

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

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

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

## 자운영답에서 알팔파바구미 발생생태

이홍수, 권진혁, 정부근, 김태성, 송원두, 노치웅

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

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

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

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



## 제주도 녹차 재배지에서 풍뎡이류에 의한 녹차 피해와 발생 생태

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

**검색어:** 차나무, 굴벵이, 흙줄풍뎡이, 청동풍뎡이, 꽃무지

## Comprehensive soil quality assessment in urban forests using biological indices

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

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

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

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

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

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

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

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

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

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

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

## 상주지역 배 과원에서 복숭아순나방과 복숭아심식나방의 발생 동태

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

**검색어:** 배, 복숭아순나방, 복숭아심식나방, 온일도 모델, 상관관계

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

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

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

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

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



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

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

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

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

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

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

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

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

## 수출 단감원에서 주요 깍지벌레의 수체와 과수원에서 발생과 분포

정부근, 이흥수, 권진혁, 김태성, 송원두

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

**검색어:** 감나무주머니깍지벌레, 식나무깍지벌레, 단감, 분포, 주요종

## 단감원에서 식나무깍지벌레의 발육과 방제

정부근, 이홍수, 권진혁, 김태성, 송원두

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

**검색어:** 식나무깍지벌레, 발육, 단감, 방제

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

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

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

## 여름형과 월동형 점박이응애에 대한 Vapormate의 훈증효과

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

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

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

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

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



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

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

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

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

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

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

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

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

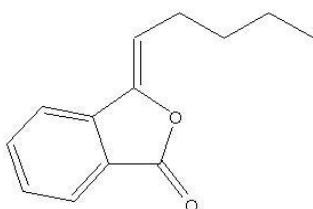
**Song-Hwa Chae<sup>1</sup>, Soon-Il Kim<sup>2</sup>, Si-Woo Lee<sup>3</sup>, and Young-Joon Ahn<sup>2</sup>**

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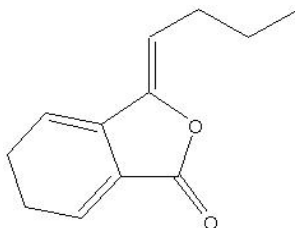
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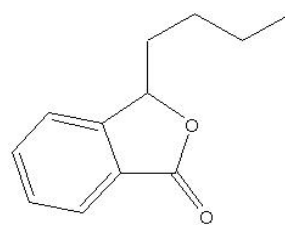
The toxicity of materials derived from rhizome of *Cnidium officinale* Makino to adults from B and Q biotype of *Bemisia tabaci* was examined using a leaf-dipping bioassay. Results were compared with those of two currently used insecticides: acetamiprid and thiamethoxam. The active principles of *C.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



(1)



(2)



(3)

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

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

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

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

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

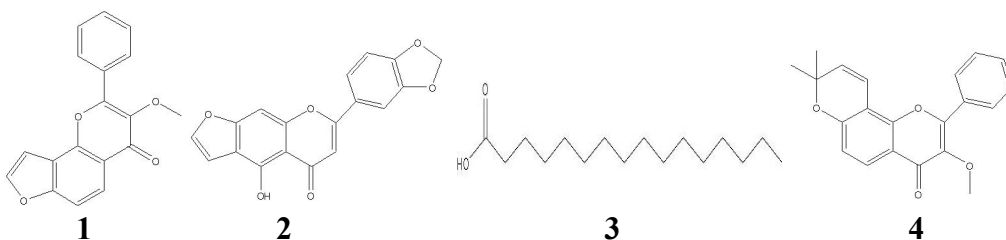
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The toxicity of materials derived from seed of *Pongamia pinnata* Pierre toward to third instar larvae of *Aedes aegypti* and *Culex pipiens pallens* was examined using direct contact bioassay. Results were compared with those of the currently used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



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

## 비타민 A 강화벼의 곤충 및 생물상 변화양상 및 비교

박홍현, 김광호, 이상계, 안정준

국립농업과학원 곤충산업과

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

**검색어:** 비타민 A 강화벼, 곤충상 비교, 종 다양도, 군집분석

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

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

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



## Easy and Rapid Quantification Method of *Plutella xylostella* Granulovirus

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

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