Oral Presentation

PD1

Identification of two diamondback moth parasitoids, *Diadegma fenestrale* and *Diadegma semiclausum*, using LAMP for application in biological control

Hwa Yeun Nam[1] and Juil Kim[1,2]

[1]Agriculture and Life Science Research Instituite, Kangwon National University

[2]Program of Applied Biology, Division of Bio-resource Sciences, CALS, Kangwon National University

The diamondback moth, *Plutella xylostella* L., is known as a widely distributed destructive pest of Brassica vegetables worldwide. Various biological controls, such as parasitoid wasps, have been used to control this pest. Among these parasitoid wasps, *Diadegma semiclausum* and *Diadegma fenestrale* are widely used globally. The taxonomy of these two species based on morphological characteristics is very similar, and they are both parasitic on *P. xylostella* larvae. Therefore to be able to accurately differentially identify these species, in this study, we developed a molecular diagnostic method using loop-mediated isothermal amplification (LAMP). *D. fenestrale* species-specific primers for LAMP were designed in COX3, and the optimal diagnostic conditions for the four primers (F3, B3, FIP, BIP) was at 63 °C for 35 min. A species-specific primer capable of classifying *D. semiclausum* was established from the ITS2 region, and the optimal condition for diagnosis was 40 min at 63 °C. The diagnostic limit concentration was up to 10 pg under both optimal conditions; therefore, it was feasible to detect even very low concentrations. The developed LAMP diagnostic method can be used in a variety of ways to diagnose whether *P. xylostella* has been parasitized in the process of field research and mass breeding, and to accurately distinguish the species that are parasitic on *P. xylostella* larvae.

Key words: *Plutella xylostella*, *Diadegma semiclausum*, *Diadegma fenestrale*, LAMP, diagnostic method

PD2

Simultaneous control of sacbrood virus (SBV) and *Galleria mellonella* utilizing an improved Bt strain that producing dsRNA targeting the SBV *vp1* gene

Min Gu Park[1], Jae Young Choi[1], Dong Hwan Park[2], Minghui Wang[2], Sang Hee Kim[2], Ho Yeon Lee[2] and Yeon Ho Je[1,2]

[1]Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea

[2]Department of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea

The Asian honey bee, *Apis cerana*, is threatened by sacbrood virus (SBV) and by the greater wax moth, *Galleria mellonella*. Recently, RNA interference (RNAi) has been suggested as a promising strategy for the suppression of honey bee viruses. In addition, *Bacillus thuringiensis* (Bt) has been widely used for the control of lepidopteraen pests, such as *G. mellonella*. For the simultaneous control of both SBV and *G. mellonella* utilizing an improved Bt that produces dsRNA targeting the vp1 gene of SBV, the plasmid pMBD-1ABC-dsVP1 was introduced into the Bt strain 4Q7, which expresses various from Cry1Ac, Cry1Be, and Cry1C toxins. SBV replication was suppressed in A. cerana worker bees when they ingested dsRNA produced by the Bt transformant. Crystal proteins from the transformant Bt showed a high level of insecticidal activity against the 4th instar larvae of *G. mellonella*. These results demonstrated that a Bt-based, dsRNA-producing system could be efficiently exploited for the control of both SBV and *G. mellonella* simultaneously.

Key words: *Bacillus thuringiensis*, insecticidal proteins, *Apis cerana*, sacbrood virus, *Galleria mellonella*

PD3

A systematic and ecological study on the collembola in well-preserved habitats (Focusing on caves)

Gyu-Dong Chang
Department of Agricultural Biology, National Institute of Agricultural Sciences

본 연구에서는 제주도 거문오름용암동굴계에 속하는 13개의 용암동굴과 평창, 문경, 정선 지역에 위치한 석회암동굴 8개, 국립공원 및 DMZ 지역을 조사하여 총 3목 23과 47종의 톡토기를 동정하였다. 이중 총 13종 (신종 6종, 미기록 4종, 재기재 3종)을 새롭게 기재하였고, 종의 명확한 분류학적 위치지정을 위하여 필요한 경우 형태분석뿐만 아니라 미토콘드리아 COI gene을 이용하여 분자계통분석을 수행하였다. 특히 장암굴 (강원도 평창군)에서는 분류학적 연구를 바탕으로 생태학적 연구도 함께 수행하여 동굴 내부에 서식하는 톡토기와 환경인자 (토양온도, 토양습도, 토양 pH, 대기온도, 대기습도) 간의 상관관계를 분석하였다. 그 결과 장암굴 내부의 환경인자와 톡토기의 분포 및 종 다양성에는 상관관계가 없는 것으로 나타났다.

검색어: 용암동굴, 석회암동굴, 가시톡토기, 동굴생태연구, 유전적 거리 분석

PD4

Sampling unit of *Ricania* sp. (Hemiptera: Ricaniidae) eggs in persimmons

Sunghoon Baek, Miji Jeon, Seunghwan Lee, JiSu Jeong and Chang-Gyu Park
Department of Industrial Entomology, Korea National College of Agriculture and Fisheries

This study was conducted to determine an optimal sampling unit of *Ricania* sp. (Hemiptera: Ricaniidae) eggs in persimmons. First of all, the within-tree distribution pattern of its eggs was characterized with 60 persimmon trees by cutting 12 branches at four horizontal criteria (east, west, south, and north) in three vertical levels (basal, middle, and terminal parts) per tree. In numbers of egg masses, there was no significant difference ($P > 0.05$) horizontally, but significant ($P < 0.05$) difference vertically (more eggs were found at the tips of branches). Then, the sample unit of the selected branches was determined based on coefficient variation and coefficient of determination calcuated from egg mass numbers per 10 cm from the tip within a branch. The 60-cm branch tip was selected as the optimal sampling unit for *Ricania* sp. in persimmons. Finally, the required number to satisfy the sampling purpose was determined by using Reusink's equation. By considering damage recognizable level of *Ricania* sp., three 60-cm branch tips per tree would be generally acceptable in its management in persimmon fields.

Key words: *Ricania sp.*, persimmon, within-tree distribution, sampling unit

PD5

Establishment of control strategy using entomopathogenic fungi to forest pest Japanse pine sawyer beetle, *Monochamus alternatus*

Jong-Cheol Kim[1], Tae Young Shin[1], So Eun Park[1] and Jae Su Kim[1,2*]
[1]Department of Agricultural Biology, College of Agriculture & Life Sciences, Jeonbuk National University
[2]Department of Agricultural Convergence Technology, Jeonbuk National University

Japanse pine sawyer, *Monochamus alternatus*, is the main pest that mediates pine wilt nematode, *Bursaphelenchus xylophilus*, that causes serious damage to pine forests. In this study, we studied the strategy to control *M. alternatus* using entomopathogenic fungi, *Beauveria bassiana* ERL836 and *Metarhizium anisopliae* JEF-197, that showed high virulence against *M. alternatus* adults. The fungal isolates were evaluated for insecticidal activity against *M. alternatus* by spray treatment on live pine trees and wintering trees. Both isolates showd a high insecticidal activity against JPS, and the possibility of replacing chemical fumigants was evaluated. In addition, the interaction of fungi and *M. alternatus* were analyzed by RNA-seq. This result can contribute to the development of insect control agents using entomopathogenic fungi.

Key words: biopesticide, control strategy, entomopathogenic fungi, *Monochamus alternatus*, RNA sequencing

PD6

Chromosomal level of the genome sequencing and genome wide discovery lncRNAs involved in insecticide resistance in *Helicoverpa armigera*

Md Mafizur Rahman[1], Hwa Yeun Nam[2], David G. Heckel[3] and Juil Kim[1,2]
[1]Program of Applied Biology, Division of Bio-resource Sciences, CALS, Kangwon National University
[2]Agriculture and Life Science Research Institute, Kangwon National University
[3]Department of entomology, Max Planck Institute for Chemical Ecology, Germany

Since, CYP337B3 which is one of the most deeply identified cytochrome P450 genes involved in pyrethroid insecticide resistance from Australasian of *H. armigera* (resistance ratio, RR, was around 40 folds), we tried to identify novel resistant related genes in Korean populations. Because Korean populations showed an extremely high level of resistance based on LC50 values (RR >1,000) than that of Australasian populations. From that point of view, we focused on the chromosomal level of the genome sequencing, and Illumina, nanopore platform was applied. About 390Gb and 1,211 Scaffolds of genome draft were set (ASM1716586v1). Combining Hi-C analysis, we finally set the 31 pseudo chromosomes. Based on this genome draft, a total of 8,394 long non-coding RNAs (lncRNA) were surveyed in 45 transcriptome data sets. Some of the lncRNAs showed a high level of inverse correlation to the insecticide-resistant related cytochrome P450 genes such as CYP337B3 and CYP321A1 genes. These results suggested that not only coding RNA but also lncRNA possibly involved in the pyrethroid insecticide resistance in *H. armigera*.

Key words: genome sequencing, lncRNA, trascriptome, *Helicoverpa armigera*

PD7

Modeling distribution and risk index of *Vespa velutina nigrothorax* in Korea

Min-Jung Kim[1,2], Seong bin Bak[3] and Chuleui Jung[1,3]
[1]Agricultural Science and Technology Research Institute, Andong National University
[2]Forest Entomology and Pathology Division, National Institute of Forest Sciences
[3]Department of Plant Medicals, Andong National University

등검은말벌은 2003년 국내에서 처음 보고된 이후 꿀벌 전문포식자로서 양봉농가 피해는 물론 토착 말벌 군집에 위협 등으로 2019년 환경부 생태계교란생물로 지정된 바 있다. 현재는 침입 이후 전국으로 확산되어 국내 생태계에 정착한 것으로 판단된다. 이에 국내 서식처 환경과 연관한 분포 특성을 파악하고자 전국 발생 상황을 트랩으로 조사하고, 기후 조건 및 경관 특성에 따른 밀도 발생 패턴을 분석하였다. 등검은말벌 조사지점의 밀도를 4단계의 발생 수준으로 변환 후 역거리가중법을 이용하여 시각화하였다. 변환된 발생 밀도를 설명하기 위해 9개의 생물기후변수와 각 지점당 1km 반경 내 7개의 경관 요소를 환경변수로 이용하여 다중 회귀분석을 실시하였다. 검토한 변수들 중 5개의 생물기후변수와 4개의 경관 요소가 등검은말벌의 밀도에 영향을 주는 것으로 추정되었다. 선정된 변수들을 입력 변수로 등검은말벌의 발생 확률 및 밀도 수준을 각각 랜덤포레스트 알고리즘을 이용하여 모형화하였다. 모형의 기여도는 기후변수 중에서 기온의 계절적 변동 수준이, 경관변수 중에서는 산림의 면적비율이 가장 중요한 설명 변수인 것으로 나타났다. 현재 등검은말벌은 경상도, 전라남도, 충청남도 지역에 발생 밀도가 높고 해안을 제외한 강원도와 제주도에서 발생 밀도가 낮을 것으로 예측되었다. 모형 예측 밀도와 양봉 농가 분포 자료를 바탕으로 등검은말벌 피해 위험 지수를 산출하였다. 이 결과는 양봉 농가의 등검은말벌 피해 방지 계획 도출 및 생태계교란 생물 국가 관리 전략에 활용될 수 있다.

검색어: 등검은말벌, 생물기후변수, 경관 요소, 발생밀도예측, 랜덤포레스트

PD8

Chronic exposure to field-realistic doses of imidacloprid resulted in biphasic negative effects on honey bee physiology

Sanghyeon Kim[1] and Si Hyeock Lee[1,2]
[1]Research Institute for Agriculture and Life Sciences, Seoul National University
[2]Department of Agricultural Biotechnology, College of Agriculture and Life Science, Seoul National University

In this study, in order to investigate the effects of chronic imidaclorpid (IMD) exposure on honey bees, honey bee colonies were chronically exposed to field-realistic doses (5, 20, and 100 ppb) of IMD, and the body weight, flight performance, and carbohydrate reserve of forager bees were analyzed. IMD induced a biphasic change in body weight of the forager bees: decrease at the low concentration range (5 and 20 ppb) but increase at the high concentration (100 ppb). Nevertheless, the flight capability of forager bees significantly decreased in a concentration-dependent manner. The effects of IMD on target genes in forager bees showed biphasic patterns, whereas nurse bees showed typical features of premature transition to foragers in a concentration-dependent manner. Taken together, these results suggest that field-realistic doses of IMD alters honeybee energy metabolism in distinctly different mechanisms at low and high concentrations, both of which negatively affect honey bee colony health.

Key words: honey bee, imidacloprid, chronic exposure, diabetes, carbohydrate metabolism, biphasic effect

O1

Sniffing mosquitoes: Transcriptomic analyses of olfactory gene evolution in Culicomorpha (Diptera)

Woo Jun Bang and Seunggwan Shin
School of Biological Sciences, Seoul National University, Seoul, 08826, South Korea

The infraorder Culicomorpha is one of the monophyletic groups in the lower Diptera and consists of eight families: Ceratopogonidae, Chaoboridae, Chironomidae, Corethrellidae, Culicidae, Dixidae, Simuliidae, and Thaumaleidae. It has four blood-sucking families referred to as mosquitoes (Culicidae), biting-midges (Ceratopogonidae), frog-biting midges (Corethrellidae), and black files (Simuliidae). Even though the vector species in families Ceratopogonidae and Culicidae have been well-studied medically, the phylogenetic studies were poorly conducted from a perspective of hematophagous in this group. In this study, the olfactory receptors, which are important for host-seeking function, were identified and analyzed based on the transcriptome data. The protein family annotation was conducted using at least two genus per families representatively, except for the family Thaumaleidae. The comparative transcriptomic analysis reveals the number of olfactory receptors in blood-sucking families is higher than that of non-bloodsucking families. Furthermore, it was estimated that the gain-loss of olfactory genes appeared diverse during speciation, also in family-level.

Key words: Culicomorpha, gene annotation, hematophagous, olfactory receptor, transcriptomics

O2

Comparative population genetics using DNA barcodes revealed an invasion of differential grasshopper from the United States to Korea

Jiseok Kim and Donghun Kim
Department of Vector Entomology, Kyungpook National University, Sangju, Rep. of Korea

Invasive species are unintentionally introduced into new areas through the international trade. They are able to cause a variety of impacts on agricultural environment as well as biodiversity. In 2018, the differentialis grasshopper, *Melanoplus differentialis,* was firstly identified in Ulsan, Korea. The spread of *M. differentialis* caused economic losses due to the lower quality of agricultural crop and costs for pest management. In order to identify the origin of *M. differentialis* population in Korea, the population genetics were analyzed using DNA barcodes from populations distributed throughout the North America. The 254 differential grasshoppers were collected from both Ulsan, Korea and America including eight states in the U.S. and two states in Mexico. The genetic variation among populations was analyzed by using four different mitochondrial genes: NADH dehydrogenase subunit 2 (ND2), mitochondrial cytochrome oxidase subunit I (mtCOI), mitochondrial cytochrome oxidase subunit II (mtCOII), and Cytochrome B (CytB). The populations in America were mainly divided into Southern and Northeastern U.S. populations on the basis of principal coordinate analysis (PCoA) using pairwise F_{ST} values. The TCS network and PCoA revealed that the Korean population were genetically close with Southern U.S. populations except Mississippi and shared more than one haplotype. The Korean population showed fewer haplotype diversity and the number of haplotypes was two, two, one, and four, respectively. Genetic variation between populations might be generated from the geographical separation, including mountains and geographical distance. Taken together, we suggest that Ulsan population of *M. differentialis* was likely invaded from the Southern U.S. including Texas and Louisiana via international trade.

Key words: DNA barcode, population genetics, the differential grasshopper, invasive insects

O3

Taxonomic revision of Hypenodinae from Korea, with annotated checklist (Lepidoptera: Erebidae)

Ji-Young Lee and Bong-Kyu Byun
Department of Biological Science and Biotechnology, Hannam University, Korea

This study was conducted to review of the subfamily Hypenodinae with taxonomic arrangement in Korea. Totally 13 species under 7 genera are recognized from Korea. Also, its phylogentic status of the subfamily, which has been confused to date, was reconstructed and discussed through molecular and phenetic analyses respectively. In this study, one species: *Hypenodes turfosalis* (Wocke, 1850), was treated as synonym of *H. humidalis* Doubleday, 1850. Also, one species and two subspecies: *Parens* sp. nov. 1, *Anachrostis* ssp. nov. 1 and *Micreremites* ssp. nov. 1 is described as new to science. Totally 2 subspecies of 13 species of 7 genera under 2 tribes was recognized from Korea. All the known species were redescribed with the adults and genitalic structure and key to the species was provided. Also their all available information, including the result of biological observation, distributional ranges and host plants is enumerated.

Key words: Lepidoptera: Erebidae, Hypenodinae, *Parens*, new species, new subspecies

O4

Differential evolution of Argonaute protein in the genus *Drosophila*

Won Hee Ko[1], Sangil Kim[1,2] and Seunggwan Shin[1*]
[1]School of Biological Sciences, Seoul National University, Seoul, 08826, Republic of Korea
[2]Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA

In invertebrates, innate immune system takes important immunity role because of a lack of adaptive immune systems such as antigen-specific antibodies and receptors. RNA interference (RNAi) is one of the most important innate immune systems in insects. Short interference RNA (siRNA) acts as an anti-viral role in the case of Diptera, and the Argonaute protein plays a critical role in it. We used the genus *Drosophila* (26 *Drosophila* species) to find a significant evolutionary signal in the antiviral immune system. We investigated Argonaute protein orthologs among the whole body CDS (coding sequence) from 26 *Drosophila* species using OrthoFinder v.2.5.4. The Ago2, which is one of the subfamily members of Argonaute protein, was noticeably duplicated in different *Drosophila* subgroups such as the *D. obscura* group. Therefore, Ago2 gene structural analyses showed that the evolutionary rate and sequence variation of Ago2 protein are relatively higher than the Ago1 in this study. Furthermore, unlike Ago1, we found specific domain differences contributing to the overall increase of Ago2 protein substitution rate.

Key words: Argonaute protein, *Drosophila*, Bioinformatics, innate immune system

O5

New suggestions for taxonomic position of Varroa mite

Jaeseok Oh[1] and Seunghwan Lee[1,2]

[1]Laboratory of Insect Biosystematics, Department of Agricultural Biotechnology, Seoul National University

[2]Research Institute of Agriculture and Life Sciences, Seoul National University

Genus *Varroa* is one of the most famous honeybee pests in the world. In 1904, Oudemans erected the genus *Varroa* in the family Laelapidae, since then many authors suggested its taxonomic positions through morphological analysis. Varroa mites have unique morphological characters such as hypertrichious setae, highly sclerotized broadened shields on both dorsal and ventral, reduction of the movable digit, and the absence of gnathosomal setae *h2*. For this reason, the genus *Varroa* was separated from the family Laelapidae to make their own family Varroidae by Delfinado & Baker (1974). In this study, we verified the taxonomic position of the genus Varroa through the phylogenetic analysis via 28s, 18s, ITS, and H3 genes, and morphological analysis to provide new suggestions that the family Varroidae returns to a tribe of the family Laelapidae.

Key words: *Varroa*, Varroidae, Laelapidae, Honeybee pest, Taxonomy

O6

Taxonomic notes on problematic species in Korean Nolinae (Lepidoptera: Nolidae)

Yeong-Bin Cha[1] and Yang-Seop Bae[1,2]

[1]Division of Life Sciences, College of Life Sciences and Bioengineering, Incheon National University, Academi–ro, Incheon 22012, South Korea.

[2]Bio–Resource and Environmental Center, Incheon National University, Academi–ro, Incheon 22012, South Korea.

The subfamily Nolinae Hampson, 1894 is the biggest group within the family Nolidae in Korea. Their small size, similar facies, and genitalia structure (especially *Nola* Leach) cause incorrect identify. As a result of recent study, several species are incorrectly identified until now, and discover as new species. Additionally, we discuss some of these species, with International Code of Zoological Nomenclature.

Key words: ICZN, review, misidentify

O7

Harrison's rule corroborated among nomadine Cuckoo Bees (Hymenoptera: Apidae: Nomadinae): Role of Body Size in Host-switching Dynamics

Kayun Lim[1], Seunghyun Lee[1,2], Michael C. Orr[2] and Seughwan Lee[1,3]
[1]Insect Biosystematics Laboratory, Department of Agricultural Biotechnology, Seoul National University
[2]Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences
[3]Research Institute of Agriculture and Life Sciences, Seoul National University

Harrison's rule, which represents the positive body size correlation between parasites and hosts, has been reported in a range of taxa, but whether the rule can be applied to cleptoparasitic insects is poorly understood. Subfamily Nomadinae, the largest cleptoparasitic bees, usurp the nests of host bees and lay their eggs. As the hosts prepare the cells with pollen balls for the offspring, the parasitic larvae consume the pollen and develop in the nest until they become adults. Nomadinae invade various host families and especially genus *Nomada* exploits the most diverse hosts in that ten genera have been documented as their host information. Not only the diverse hosts but the nomadine bees are also remarkably diverse in size, indicating the ideal model to test Harrison's rule. Here, we reassess the phylogeny of Nomadinae, including the expanded sampling of the genus *Nomada* to elucidate host shift fluctuation through the evolutionary dynamics and applicability of Harrison's rule in the subfamily.

Key words: Nomadinae, body size evolution, cleptoparasitism, Harrison's rule, phylogeny

O8

A review of the genus *Spulerina* (Lepidoptera: Gracillariidae) from Korea

Da-Som Kim[1], Jae-In Oh[2] and Bong-Kyu Byun[2]
[1]National Science Museum, Daejeon, Korea
[2]Department of Biological Science and Biotechnology, Hannam University, Daejeon, Korea

This study was conducted to review of the genus *Spulerina* Vári, 1961, belonging the subfamily Acrocercopinae of the family Gracillariidae, from Korea. The genus *Spulerina* was established by Vári in 1961, including 20 described species worldwide. In this study, a total of 6 species are recognized from Korea. Among them, three species, *Spulerina corticicola* Kumata, 1964, *S. parthenocissi* Kumata & Kuroko, 1988 and *S. virgulata* Kumata & Kuroko, 1988 is reported for the first time from Korea. All available information, including check list, host plants and images of adults and genitalia for species is provided.

Key words: Gracillaridae, *Spulerina*, new record, leaf-miners, Korea

O9

A systematic study based on the endophallic structure of the genus *Aulonocarabus* (Coleoptera: Carabidae), with new subspecies from Korea.

Taeyeong Kwon, Eun Young Choi, Jong Bong Choi, Myeong Cheol Kim, Hee Soo Lee and Jong Kyun Park
College of Ecology and Environmental Science, Kyungpook National University, Sangju, Korea

In Korea, a total of four species of the genus *Aulonocarabus* were recorded. Moreover, the species included in this group are known to be endemic to Korea only. However, external morphological characteristics of this group are highly similar, which makes morphological examination difficult. Therefore, morphological study was conducted based on the endophallic structure and molecular phylogenetic using the *ND5* sequence, a mitochondrial gene, was additionally performed. In addition, the methods mentioned above are used to report the new subspecies of *A. semiopacus*.

Key words: Carabidae, *Aulonocarabus*, Endophallus, Systematics, New subspecies.

O10

Cryptic diversity between specific populations and cases of sympatry of epigean leptonetid spiders (Araneae: Leptonetidae) in South Korea

Jong-Hwa Oh[1], Sora Kim[3] and Seunghwan Lee[1,2]
[1]Laboratory of Insect Biosystematics, Department of Agricultural Biotechnology, Seoul National University
[2]Research Institude of Agricultrue and Life Sciences, Seoul National University
[3]Laboratory of Insect Phylogenetics and Evolution, Department of Plant Protection & Quarantine, Jeonbuk National University

Leptonetidae are tiny (1-3mm) rarely encountered spiders, mainly inhabiting in moist environments such as caves, leaf litters, and rock piles. Because they are microhabitat specialists, most species are known to have a limited distribution range, rarely having sympatries only found in few epigean populations. In this study, we conducted a test of DNA barcoding with Korean Leptonetidae sampled from various mountains, islands, mines, and caves. 422 specimens representing 76 morphospecies were compared with number of MOTUs, generated by five species delimitation methods (ABGD, ASAP, GMYC, PTP, and bPTP). Our results also revealed many cases of multiple species sharing habitats, indicating sympatries occurring potentially on a nation scale, which are rare in leptonetids worldwide.

Key words: Leptonetidae, DNA barcoding, Species delimitation, Microhabitat, Sympatry

O11

Correlation of differential expression levels of NRRS and insecticidal activities of six different strains of *Xenorhabdus nematophila*

Eticha Abdisa and Yonggun Kim
Department of Plant Medicals, Andond National University

An entomopathogenic bacterium, *Xenorhabdus nematophila* is symbiotic to an entomopathogenic nematode, *Steinernema carpocapsae*. After entry to target insects, these nematodes release the symbiotic bacteria in the insect hemocoel. *X. nematophila* synthesizes various secondary metabolites using transcriptional activities of non-ribosomal peptide synthetase (NRPS) genes. This study demonstrated that the NRPS expression levels are correlated with the insecticidal activities using different bacterial strains of *X. nematophila*. Indeed, a mutagenesis to alter NRPS gene expression supports the functional correlation.

Key words: *Spodoptera exigua*, *Xenorhabdus nematophila*, NRPS, secondary metabolite, insecticidal activity

O12

Chymotrypsin as a molecular target of antibiotic resistance in three corn varieties by RNAi against Asian corn borer, *Ostrinia furnacalis*

Eun Young Kim[1,2], I Hyeon Kim[1], Jin Kyo Jung[1] and Yonggyun Kim[2]
[1]Crop Cultivation and Environment Division, Natl. Institute of Crop Science, RDA
[2]Department of Plant Medicals, Andong National University

조명나방(*Ostrinia furnacalis*)에 대해 해충 저항성을 보이는 세 가지 옥수수 품종 (일미찰, 광평옥, p3394)의 분자수준에서 내충성 기작을 이해하기 위해 본 연구를 수행하였다. 대조구로 사용한 인공사료 및 감수성 품종 (강원찰60호)으로 사육된 개체에 비해 유충 발육이 유의하게 저하되고, 유충 중장의 카이모트립신 활성이 50% 이상 감소하였다. 또한 카이모트립신 특이적 억제제 처리로 카이모트립신 활성을 억제시키면 유충 사망률이 증가되었다. 이를 통해 세 저항성 품종의 항생성 기작으로 카이모트립신을 분자 표적으로 설정하였다. 조명나방의 전사체에서 카이모트립신 유전자 9개를 얻었으며, 발현이 확인된 6개의 유전자 중 발현량이 가장 높은 *OfCHY3* 특이적 dsRNA를 유충에 주입 및 섭식시킨 결과 유전자 발현량이 크게 감소하였고, *OfCHY3* dsRNA를 발현하는 대장균 섭식실험에서도 유전자 발현량과 조명나방의 발육이 저하되었다.

검색어: 조명나방, RNAi, 카이모트립신, 항생성

O13

Diminished oxidative bioactivation is accountable for selective resistance to coumaphos in honey bees

Susie Cho[1], Kyungjae Andrew Yoon[2], Jiho Lee[3], Sanghyeon Kim[2], Joonhee Lee[1] and Si Hyeok Lee[1,2]
[1]School of Agricultural Biotechnology, Seoul National University
[2]Research Institute for Agriculture and Life Sciences, Seoul National University
[3]Korea Conformity Laboratories

Varroa destructor, an ectoparasitic mite, is a major threat to the western honey bees, *Apis mellifera*, which is the most important pollinator in agriculture. Varroa mites feed on honey bees and transmit viral infections to them. To combat varroa mites, a few synthetic miticides, such as fluvalinate, amitraz, and coumaphos, that meet the condition of high selectivity for varroa mites with low toxicity to honey bees are currently available for use in hives. The purpose of this research was to compare the toxicodynamic and metabolic properties of coumaphos in honey bees and varroa mites. To understand the molecular basis of selective coumaphos toxicity, we first investigated the toxicodynamic characteristics of AChEs from honey bees and varroa mites. We then examined the tissue distribution of representative P450s, the quantitative and qualitative profiles of coumaphos metabolites, and the functional properties of representative P450s in each species to compare the differences in coumaphos metabolism, with a particular focus on the differential detoxification and bioactivation of coumaphos between the two species. Finally, we evaluated the hypothesis that various phytochemicals can increase the varroa mite-specific toxicity of coumaphos by inducing the expression of the P450 responsible for coumaphos bioactivation in varroa mites. Thus, the possibility of further investigating the selective bioactivation mechanism in varroa mites for the development of novel synergists or/and additional proinsecticides with varroacidal action was explored.

Key words: honey bee, *Apis mellifera*, varroa mite, *Varroa destructor*, miticide, coumaphos, selective toxicity, cytochrome P450 (P450), metabolic factor, bioactivation, proinsecticide

O14

PGE_2 influence on chorion formation of Asian tiger mosquito, *Aedes albopictus*, through DEG transcriptome analysis during oogenesis

Du-yeol Choi and Yonggyun Kim
Department of Plant Medicals, College of Life Sciences, Andong National University

곤충 생식과정에서 알발육은 난모세포 생성 이후 난황형성과정이 일어난다. 이러한 과정에 인슐린유사펩타이드, 유약호르몬 및 탈피호르몬의 중개과정이 비교적 잘 알려져 있다. 그러나 이후 일어나는 난각형성과정에 관여하는 내분비 신호에 대해서는 잘 이해되고 있지 않다. 최근 아이코사노이드 가운데 PGE_2가 곤충의 생식과정에 관여한다는 것이 알려지고 있다. 본 연구는 흰줄숲모기(*Aedes albopictus*)의 난각형성과정에 관여하는 PGE_2의 영향을 분석하였다. 먼저 이 호르몬의 생합성을 억제하는 아스피린을 처리하면 난각형성이 둔화되는 것으로 관찰하였다. 다시 PGE_2를 추가하여 주면 난각형성이 회복되는 것을 관찰하여 PGE_2의 중개 기능을 증명하였다. PGE_2의 난각형성에 대한 기작을 알아보기 위해 난각형성관련 발현유전자들을 Illumina NovaSeq으로 분석하여 난각형성에 관여할 것으로 추정되는 864개의 DEG를 얻었다. 실제로 아스피린 처리 개체에서는 864개 중 57개 DEG들의 발현을 억제하였다. 이들 DEG에는 다수의 CRP, POX, CBP, VMP 등이 포함되었다.

검색어: 흰줄숲모기, 아스피린, PGE_2, 난각, 차세대 염기서열 분석, RNA 간섭

O15

An insect immunosuppressant, GameXPeptide, synthesis gene (*gxpS*) structure and its expression along with bacterial pathogenesis

Gahyun Jin and Yonggun Kim
Department of Plant Medicals, College of Life Sciences, Andong National University

A depsi pentapeptide called GameXPeptide (GXP) were identified in Xenorhabdus and Photorhabdus (X/P) bacteria, which are symbiotic to entomopathogenic nematode. GXP is synthased from a non-ribosomal peptide synthesis (NRPS) bacterial gene called *gxps*. Bacterial metabolite of 10 different X/P species produced GXP. *gxpS* genes were identifed in the 10 bacterial genomes. Expression of *gxpS* was increased along with bacterial growth. *gxpS* was highly expression at late bacterial growth phase. Manipulation of gxpS expression is now implemented by a mutagenesis using altering promoter activity.

Key words: entomopathogenic nematode, GameXPeptide, Xenorhabdus, Photorhabdus, *gxpS*, mutagenesis

O16

Functional analysis of olfactory receptors that detects disease (chalkbrood) smell in honey bees (*Apis mellifera*).

Seungha Lee, Sujin Lee, Dain Lee, Myeong-Lyeol Lee and Hyung Wook Kwon*
Department of Biological Sciences & Convergence Research Center for Insect Vectors, College of Life Science and Bioengineering, Incheon National University, Incheon, Republic of Korea

Chalkbrood is one of the rapidly spreading diseases in honeybees (*Apis mellifera*) that caused by fungal pathogen (*Ascosphaera apis*). The disease significantly repress brood growth and reproductivity of honey bee colonies. Phenethyl acetate has been known to a key compound associated with chalkbrood-infected larvae that induces hygienic behavior. The mechanism of hygienic action is triggered by the detection of chemical stimuli in diseased larvae and proceeds with the removal of diseased broods from the nest. Insect odorant receptors (ORs) are responsible for the detection of the relevant cues from diverse odorants including pheromones. Previous studies in *Drosophila melanogaster* odorant receptor (DmOr) have revealed that DmOr67a (NP_524005) and DmOr85d (NP_524281) act as phenethyl acetate receptor. The candidate odorant receptors in Apis mellifera (AmOrs) were selected via protein BLAST search (blastp) of those receptors. 6 candidate odorant receptors for phenethyl acetate were cloned and tested against 9 odorants stimuli by using *in vivo* cell calcium imaging after transfection into HEK-293 cells.

O17

Physiological role of 5-HT$_7$A and 5-HT$_7$B in salivary secretion and blood feeding behavior from the Asian tiger mosquito, *Aedes albopictus*

Seoyul Hwang and Donghun Kim
Department of Vector Entomology, Kyungpook National University

The success of mosquito blood feeding is accomplished by the secretion of saliva, which includes various bioactive molecules to suppress host's immune system as well as hemostasis including coagulation and platelet aggregation. Salivary secretion of mosquito is known to be controlled by serotonergic innervation into the salivary glands, where included proximal regions of both medial and lateral lobes. However, it is still unclear that which subtype of serotonin receptor (5-HT receptor) is mainly involved in the salivation of mosquito. In this study, two distinct 5-HT receptor subtype 5-HT$_7$, 5-HT$_7$A (1395bp) and 5-HT$_7$B (1431bp),were identified and characterized from the Asian tiger mosquito, *Aedes albopictus*. In heterologous expression system, Chinese hamster ovary (CHO) cells expressing 5-HT$_7$B were dose-dependently activated or inhibited by serotonin/agonists or antagonists, as indicated by elevated calcium mobilization. The transcripts of 5-HT$_7$A and 5-HT$_7$B were significantly higher in adult stages (minimum 1.2 to maximum 4.3-fold) than immature stages. Head and salivary glands of female mosquito were main tissues expressing 5-HT$_7$A and 5-HT$_7$B. The serotonin mediated mosquito salivary secretion was significantly decreased from female mosquitoes injected by dsRNA-5-HT$_7$A (46.5%), dsRNA-5-HT$_7$B (47.2%), and dsRNA-5-HT$_7$A and 5-HT$_7$B (58.2%), respectively. In addition, the blood feeding behavior of female mosquito such as probing and feeding was significantly prolonged up to 62.6% (13.8 seconds) and 62.7% (12.1 seconds) by RNAi, respectively. Thus, we suggested that 5-HT$_7$A and 5-HT$_7$B receptors play critical roles in the salivary secretion and feeding behavior of mosquito.

Key words: *Aedes albopictus*, salivation, 5-hydroxytryptamine receptor

O18

Bacterial metabolites of *Xenorhabdus hominickii* suppress cellular and humoral immune responses of *Spodoptera exigua* induced by *Bacillus thuringiensis* infection

Md Tafim Hossain Hrithik[1], Miltan Chandra Roy[1], Helge Bode[2] and Yonggyun Kim[1*]
[1]Department of Plant Medicals, Andong National University
[2]Max Planck Institute, Marburg, Germany

Different strains of *Bacillus thuringiensis* produce a diversity of Cry proteins that are selectively toxic to insect pests. Bacteria of *Xenorhabdus* and *Photorhabdus* can synthesize secondary metabolites to induce host immunosuppression. Insect immune responses play crucial role to combat with *B. thuringiensis* infection. This study hypothesized that bacterial secondary metabolites can enhance the pathogenicity of *B. thuringiensis* subsp. *aizawai* (BtA) against *S. exigua*. An addition of *X. hominickii* (Xh) culture broth significantly enhanced the insecticidal activities of BtA. Addition of Xh metabolites such as 3-ethoxy-4-methoxyphenol, oxindole, benzylideneacetone, and GameXPeptide significantly enhanced BtA toxicity. Oral administration of BtA significantly induced AMP gene expressions whereas Xh culture broth or secondary metabolites can suppress AMP gene expression. In the meantime, Xh culture broth or secondary metabolites significantly suppressed nodule formation. The enhanced BtA toxicity by Xh culture broth or secondary metabolites showed significant control efficacy against *S. exigua* compared to BtA alone in field condition.

Key words: *Bacillus thuringiensis* subsp. *aizawai*, *Spodoptera exigua*, *Xenorhabdus hominikii*, secondary metabolites

O19

Molecular evidence for TSWV entry to thrips gut epithelium through glycoprotein and cyclophilin

Falguni Khan, Jean Lee and Yonggyun Kim
Department of Plant Medicals, Andong National University

The western flower thrips, *Frankliniella occidentalis* is a devastating pest insect that is responsible for transferring TSWV in different crops throughout the world. Cyclophilin (Cp) is a peptidyl-prolyl cis-trans-isomerase and involved in different biological processes such as protein folding, cell signaling, and immune responses. Endocuticle structural glycoprotein (G_N) is an integral membrane protein which plays an important role in cell–cell interactions. Cp and G_N are abundant in midgut and salivary gland of the thrips, and are supposed to interact directly to TSWV during larval stage. Cp and G_N of *F. occidentalis* encode 205 and 284 amino acids, respectively. Their expressions in different developmental stages were confirmed by RT-PCR. Knockdown of Cp or G_N expression was performed by feeding gene-specific dsRNAs. This RNA interference altered TSWV titer in the thrips compared to control.

Key words: *Frankliniella occidentalis*, TSWV, glycoprotein, cyclophilin

O20

Physicochemical properties and volatile compound profiles of fermented *Protaetia brevitarsis* by lactic acid bacteria and yeast

Ji Yoon Cha[1,2], Tae-Kyung Kim[1], Min-Cheoul Kang[1], Hwanhee Yu[1] and Yun-Sang Choi[1]
[1]Research Group of Food Processing, Korea Food Research Institute
[2]Department of Biotechnology, Korea University

Edible insects can be approached in food security as the food of future, and have excellent nutritional properties. Also, edible insects emit less carbon and have environmental advantages, compared to livestock food. However, edible insect-processed foods have negative consumer preferences and need to raise consumer awareness. Consumers do not prefer the unique flavor of edible insects, which limits the use fo edible insects. In this study, *P. brevitarsis* larvae was fermented with lactic acid bacteria and yeast to investigate physicochemical properties and changes in volatile compounds. There were a total of 32 volatile compounds detected before fermentation, and the composition of volatile compounds changed after inoculation with lactic acid bacteria. It showed the possibility of improving flavor by showing an increase in esters with odor of fruity or sweetness and pyrazines with odor of roast and nutty. Therefore, the fermentation process of an insect can be a method capable of improving flavor.

Key words: *Protaetia brevitarsis*, fermentation, volatile compounds

O21

Morph-specific life-history correlations in a wing dimorphic water strider

Hyoseul Hyun and Chang S. Han
Department of Biology, Kyung Hee University

Life-history theory predicts a negative correlation between reproduction and survival because individuals differ in their investment in early reproduction at the expense of survival. However, life-history trade-offs can be masked when individual differences in resource allocation are smaller than those in resource acquisition. In polymorphic species, as distinct morphs exhibit differences in intrinsic physiology, the relative effects of resource acquisition and allocation on life-history traits will differ between morphs, contributing to morph-specific life-history correlations. In the wing-dimorphic water strider Aquarius paludum, wing morphs differed in within-morph individual-level life-history correlations. Longer-lived long-winged females produced fewer eggs per day and matured later, whereas life-history trade-offs were not observed in short-winged females. We suggest that morph-specific effects of resource allocation trade-offs, such as wing muscle histolysis, can shape the morph-specific extent of individual variation in life-history strategies.

Key words: life-history, resource acquisition, resource allocation trade-off, water strider, wing dimorphism

O22

Effects of curcumin and rosmarinic acid on the detoxification of pesticide poisoning of honey bees

Daniel Bisrat[1], Tekalign Begna[3], Delgramaa Ulziibayar[3], Yong-Rak Kang[3], Saeed Mohamadzade Namin[1,2] and Chuleui Jung[1,3]

[1]Agricultural Science and Technology Institute, Andong National University, Republic of Korea

[2]Department of Plant Protection, Faculty of Agriculture, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran

[3]Department of Plant Medicals, Andong National University, Republic of Korea

Honeybees pollinate around one third of the world's crop species, but their population decline has raised concerns about the sustainable food production. Agrochemicals are the major factor in honeybee mortality and while foraging, honeybees are exposed to variety of pesticides which are being applied in crop production. In addition, they may bring contaminated pollen and nectar into hive. Curcumin (CU) is the active ingredient of the dietary spice turmeric and has been consumed for medicinal purposes for thousands of years. Since the anti-inflammatory, anti-oxidant and pro-apoptotic characteristics of CU has been confirmed previously, the present study was designed to determine the effects of CU and other closely related chemicals such as rosmarinic acid (RA) on reduction of mortality of the worker bees intoxicated with different pesticides. In this study, CU and RA supplemented food were evaluated for their potential in reducing the mortality of worker bees intoxicated with three concentrations of four (imidacloprid, Acetamiprid, Fenitrothion, and Flupyradifurone) and seven different pesticides (carbaryl, amitraz, Bifenthrin, acetamiprid, imidacloprid, flupyrodifurone and fenitrothion) respectively. RA supplemented feeding reduced honey bee mortality across all intoxicated concentrations of acetamiprid, flupyradifurone and amitraz while it cause a significant lower mortality when honey bees were subjected to imidacloprid, fenitrothion, carbaryl and bifenthrin at lower dose intoxication. In the honeybees intoxicated with Acetamiprid and flupyradifurone, CU supplemented feeding was effective in reducing honey bee mortality across all intoxicated concentrations however, it cause a significant lower mortality when honey bees were subjected to imidacloprid and fenitrothion at lower dose intoxication. According to our results, CU and RA supplemented foods have potential to be applied as an antidote in intoxicated colonies however, more colony level studies is required for confirmation.

Key words: Detoxification, honeybee, *Apis mellifera*, curcumin, Rosmarinic acid.

O23

Species diversity of Burkholderiaceae family colonizing in *Riptortus pedestris* (Hemiptera: Alydidae) following environmental acquisition

Do-Hun Gook, Minhyung Jung, Jung-Wook Kho, Joo-Young Kim, Soowan Kim and Doo-Hyoung Lee
Department of Life Sciences, Gachon University, Gyeoggi-do, South Korea

Understanding of species diversity of bacteria colonizing in *Riptortus pedestris* (Hemiptera: Alydidae) is essential to better understand evolutionary relationships with symbionts acquired from soil environment where diverse microbes exist. Therefore, in laboratory conditions, 2nd instar nymphs were provided field-collected soil and reared to adult. Then, bacteria colonizing in midgut crypts of *R. pedestris* were cultured and subject to species identification for characterizing species richness and evenness of the symbionts. From the experiments, 87% of bacteria belong to genus *Caballeronia*; *Paraburkholderia* (10%), *Burkholderia* (2%), and *Pandoraea* (2%) were followed. At species level, 14 species were identified; *C. jiangsuensis* (35%) and *C. megalochromosomata* (22%) were dominant species.

Key words: Bean bug, Endosymbiosis, Environmental acquisition, Species identification

**This work was supported by the National Research Foundation of Korea(NRF) grant funded by the Korea government(MSIT)(2021R1A2C1010679).

O24

Additive interactions of mixture of acetamiprid and emamectin benzoate to honeybees (*Apis mellifera*) adult and larvae

Tekalign Begna[1], Delgrimaa Uzbaayer[1] and Chuleui Jung[1,2]
[1]Department of Plant Medicals, Andong National University
[2]Agricultural science & technology research institute, Andong National University

Honeybees are exposed to mixture of insecticides when collecting foods. The present study investigated the effects of formulation of two individual pesticides and their binary mixture in the A.meliifera. Results revealed that acetamiprid + emamectin benzoate (ACT + EB) had the highest toxicities to A.mellifera with LD50 0.00004 (spray) and 0.001μg/bee (oral) and LC50 value of 0.162μg/ml in larvae. Further risk assessment showed, the hazard potential of both ACT + EB and emamectin benzoate (EB) were higher, spray hazard quotient (cHQ) = 500 and 28, 038 and oral hazard quotient (oHQ) = 100 and 170 respectively. Furthermore, the estimated additive indices (AI) indicated acetamiprid and EB interact additively with AI of 0.01, 0.047, and 0.02 in contact, oral, and larvae respectively. Repeated larvae exposure to ACT + EB significantly reduce survival than solvent and negative control. Our findings indicated ACT + EB has adverse effects on honeybee suggesting further study in field to avoid increased toxic effects by mixture of pesticides.

Key words: Formulations; Additive effect; Spray toxicity; Oral toxicity; acute exposure; repeated exposure

O25

Environmentally-transmitted symbiotic microbe provides overall enhancement on adult feeding and dispersal, but negatively affects longevity of insects

Minhyung Jung, Joo-Young Kim, Soowan Kim and Doo-Hyung Lee
Department of Life Sciences, Gachon University, Gyeonggi-do, South Korea

Symbiotic microbe facilitates assimilation of nutrient in direct and indirect ways, thereby affecting behavior and fitness of host insects. In this study, we evaluated effect of symbiosis on host insects, especially on adult longevity, feeding and dispersal behaviors and female fecundity using *Riptortus pedestris* (Hemiptera: Alydidae) and *Caballeronia insecticola* as a model system. We found significantly enhanced food assimilation efficacy and dispersal behavior including horizontal walking and flight in symbiotic insects compared to apo-symbiotic ones. By contrast, longevity of symbiotic insects especially for female was significantly reduced, yielding survivorship as 56% during 60-day period compared to male and apo-symbiotic ones. When we measured titer of *C. insecticola* weekly over 8-weeks, titer of symbiotic microbe was maintained at 10^7 cell on average in female, whereas that of male gradually decreased from 10^7 to 10^5 cell over 8^{th} week.

Key words: insect-microbe symbiosis, feeding behavior, flight ability, survivorship

**This research was supported by Basic Science Research Program through the National Research Foundation of Korea(NRF) funded by the Ministry of Education(2020R1A6A3A13069963).

O26

Rapid cold hardening of small hive beetle *Aethina tumida* Murray

Muhammad Noor-ul-Ane[1*] and Chuleui Jung[1,2]
[1]Agricultural science & technology research institute, Andong National University, Andong, GB, Korea
[2]Department of Plant Medicals, Andong National University, Andong, GB, Korea

The small hive beetle (SHB) Aethina tumida Murray, (Coleoptera: Nitidulidae) is now a global invasive pest of honey bees. Insects use rapid cold-hardening (RCH) as a quick physiological response to increase their cold hardiness. Therefore, aim of study was to determine rapid cold-hardening in the small hive beetle and putative role of metabolites for rapid cold-hardening in most tolerant stage. The immatures stages of SHB were briefly exposed 12.5oC for 5 hours and then to 0oC for their respective lethal hours. All immature stages showed rapid tolerance to cold temperature. However, wandering larvae showed more survival because of rapid cold hardening as compared to other stages. Proline was highly elevated metabolite in wandering stage of SHB during rapid cold hardening. This study shows that SHB can tolerate sudden fluctuation of cold temperatures by initiating swift physiological change.

Key words: Honeybees; cold tolerance; metabolites; climate change

O27

Flash display increases prey survival against avian predators

Seong-Su No[1], Thomas N. Sherratt[2] and Chang-Ku Kang[1,2]
[1]Department of Biosciences, Mokpo National University
[2]Department of Agricultural Biotechnology, Seoul National University

위장색을 가지고 있는 피식자 중 일부는 화려한 색을 숨기고 있으며 이동 혹은 도주시에만 화려한 체색을 드러낸다. 이러한 숨겨진 화려한 체색은 포식자가 피식자의 평상시 체색이 화려한 색이라 착각하게 만들며, 피식자가 다시 정지하고 위장으로 몸을 숨기고 있을 때도 포식자가 눈에 띄는 색상을 계속 찾도록 혼란을 주는 효과가 있다. 이러한 피식자의 방어전략을 flash display라 부르며, 이러한 전략은 메뚜기, 나비, 조류 등 다양한 분류군에서 발견된다. 기존 연구에서 flash display 전략은 인간 포식자를 상대로 그 효용성이 검증되었지만, 실제 동물 포식자를 대상으로 그 효용성이 검증된 바가 없기에, 본 연구에서는 곤충의 주된 포식자인 조류(병아리)를 대상으로 flash display 전략의 효용성을 연구하였다. 조류 포식자에게 빔프로젝터를 이용하여 가상의 실험환경과 flash display를 보이며 도주하는 먹이를 보여준 뒤 생존율을 측정하는 방법을 활용하였으며, 1) flash display 가 조류 포식자에게 효과적인지, 화려한 색상을 가져야 효과가 있는지 2) 피식자의 몸 크기가 flash display 효용성에 영향을 주는지, 3) 포식자가 피식자의 위장한 모습을 확인하기 전 도주하는 것이 flash display 효용성에 영향을 주는지를 각각 독립적으로 검증하였다. 실험 결과 1) flash disiplay 는 조류 포식자를 상대로 생존율 증가 효과가 나타났고, 화려한 색상이 아니어도 효과가 있었다. 2) 크기가 큰 피식자와 작은 피식자에서 생존율 증가 효과는 큰 차이를 보이지 않았다. 3) 포식자가 피식자를 탐지 전 도주했을 때 생존율이 더 높았고, flash display 효과는 큰 차이를 보이지 않았다. 본 연구 결과는 flash display 가 실제 조류 포식자를 상대로 효과적인 방어전략이라는 것을 보여준다.

검색어: 위장색, 곤충 방어전략, 도주행동

O28

Escape behaviour is associated with hindwing coloration in grasshoppers

Won-Bin Lim[1,2] and Chang-Ku Kang[2]
[1]Department of Biosciences, Mokpo National University
[2]Department of Agricultural Biotechnology, Seoul National University

숨겨진 대비 색채 신호(hidden contrasting color signal) 중 하나인 flash display는 평상시에는 위장색을 가지고 있는 피식자가 포식자로부터 도주하는 중에만 화려한 색채를 보이는 것을 의미한다. 이러한 보호색은 곤충의 속날개에서 드물지 않게 진화하였으며, 도주 중에 화려한 색을 보임으로써, 포식자에게 자신의 평상시 색에 대한 혼동을 준다. 최근 연구에서, flash display는 긴 도주 시작 거리(FID; flight initiation distance)와 함께 작동할 때 효과적이며, 실제 조류를 상대로 한 연구에서 flash display를 가진 조류가 그렇지 않은 조류보다 더 긴 FID를 가진다는 것이 보고되었다. 본 연구에서는 이러한 관계가 flash display를 흔히 보이는 메뚜기과 곤충에서도 진화하였는지를 검증하였다. 이를 위해, 한국에 서식하는 메뚜기과 9종의 FID와 미국에서 보고된 9종의 메뚜기의 FID 자료를 이용하였다. 먼저 한국 메뚜기의 FID를 측정하기 위해 실험자가 메뚜기에게 다가가 도망가게 한 후 FID를 측정하였다. 미국 메뚜기의 FID는 기존에 출판된 Butler (2013)의 자료를 활용하였다. 연구 결과, 예측했던 바와 같이 flash display를 가진 종이 그렇지 않은 종보다 큰 FID 값을 가짐을 발견하였다. 또한 flash display가 상대적으로 큰 몸집을 가진 종에서 선택적으로 진화하였다는 사실도 밝혀내었다. 본 연구결과는 메뚜기과 곤충에서 도주행동과 flash display 가 공진화하였다는 것을 시사한다.

검색어: 메뚜기과, flash display, FID

O29

Sex differences in indirect effects on the escalation of aggressive displays of bean bugs *Riptortus pedestris*

Yi Hang Park and Chang Seok Han
Department of Biology, Kyung Hee University

최근 개체 수준의 행동 연구가 늘어나면서, 동물의 공격 행동이 개체마다 다른 수준으로 발현될 뿐만 아니라 (직접 영향, direct effect), 교류하는 상대방 개체에 따라서도 다르게 발현된다는 사실이 밝혀지고 있다 (간접 영향, indirect effect). 또한 같은 종 내에서의 공격 행동은 한 가지 형태가 아니라, 싸움이 진행되면서 공격 행동의 강도가 높아지며 순차적으로 여러 형태로 나타날 수 있다. 하지만 강도가 다른 여러 공격 행동에 대해 상대방 개체에 의한 간접 영향이 어떻게 다르게 나타나는지에 대한 연구는 아직 되어 있지 않다. 더 나아가, 강도가 다른 여러 공격 행동에서 나타나는 간접 영향 패턴이 수컷과 암컷에서 어떻게 다른지에 대해서도 아직 알려진 바가 없다. 본 연구는 톱다리개미허리노린재(*Riptortus pedestris*)를 대상으로 동성 개체 간에 무작위로 짝을 지어가며 반복적으로 1:1 대진을 기록했고, 수컷과 암컷 모두에서 나타나는 여러 공격 행동(1-leg kicking, 2-legs kicking, wing flaring, squeezing) 발현에 미치는 (1) 직접 영향과 (2) 간접 영향을 살펴보았다. 또한 각 공격 행동에 나타나는 직접 및 간접 영향에 양 성 차이가 어떻게 나타나는지에 대해서도 조사하였다. 연구 결과, 수컷은 암컷보다 모든 강도의 공격 행동이 더 높게 발현되었다. 수컷은 모든 공격 행동에 직접 영향이 존재했으며, 가장 강한 공격 행동(squeezing)을 제외한 나머지 공격 행동에 유의미한 간접 영향이 존재했다. 암컷은 일부 공격 행동(2-leg kicking and wing flaring)에만 직접 영향이 존재했으며, 가장 약한 공격 행동(1-leg kicking)에만 유의미한 간접 영향이 존재했다. 요약하면, 본 연구 결과는 공격 행동의 강도가 높아지면서 상대방이 공격 행동 발현에 미치는 영향(간접 영향)은 약해지며, 이러한 패턴은 양 성에서 모두 나타난다는 것을 보이고 있다. 이러한 사실은 공격 행동의 진화에 미치는 상대방의 영향이 강도에 따른 공격 행동의 종류마다 다를 수 있다는 것을 시사한다.

O30

Comparative analysis of cold tolerance of two flower thrips (*Frankliniella occidentalis and F. intonsa*) and prediction of their overwintering sites in hot pepper fields

Chul-Young Kim, Du-Yeol Choi, Dong-Hyun Lee and Yong Kyun Kim
Department of Plant Medicals, Andong National University

시설 재배지 고추에 주요 총채벌레는 꽃노랑총채벌레(*Frankliniella occidentalis*)과 대만총채벌레(*F. intonsa*)이다. 본 연구는 이들 총채벌레의 월동 생리를 분석하는 데 목적을 두었다. 두 총채벌레는 동결감수성 곤충으로 낮은 온도(-15～-25℃)에서 체내빙결점을 보였다. 그러나 이 체내빙결점은 두 곤충 종 사이에 그리고 발육시기에 따라 상이하였다. 꽃노랑총채벌레의 경우 성충 –25.7±0.5℃, 번데기 –17.2±0.3℃, 유충 –15.0±0.4℃를 각각 나타냈고, 대만총채벌레는 성충 –24.0±1.0℃, 번데기 –26.9±0.5℃, 유충 –17.2±0.8℃을 각각 기록하였다. 그러나 실제로 저온 피해는 체내빙결점 보다 높은 온도에서 일어났다. 저온 노출 실험에서 처리온도가 내려갈수록 그리고 노출시간이 증가할수록 저온 피해가 증가하였다. 대만총채벌레에 비해 꽃노랑총채벌레가 저온에 대해서 높은 내한성을 보였으며 발육시기별로는 유충 보다는 성충이 높은 내한성을 나타냈다. 동계 기간 야외 조사는 시설재배지에서 진행되었다. 동계기간 동안 꽃노랑총채벌레 성충이 황색점착트랩, 잡초 그리고 토양에서 발견되었다. 고추에 일명 칼라병을 유발하는 TSWV 바이러스는 동계기간 일부 잡초에서 양성으로 나왔으나, 월동하는 꽃노랑총채벌레에서는 검출되지 않았다. 이상의 결과는 꽃노랑총채벌레가 시설재배지의 잡초 주변에서 월동이 가능하다는 것을 제시하며, 대만총채벌레의 경우는 번데기 휴면으로 월동할 것으로 추정된다.

검색어: 꽃노랑총채벌레, 대만총채벌레, 월동, 휴면, 체내빙결점

O31

Liquid culture for improving thermotolerance of *Beauveria bassiana* JEF-350 blastospores

Yu-jin Jeong[1], So-eun Park[1], Ye-ram Im[1], Insoo Jeon[1], Yu-lim Park[1], Ki-jung Kim[1], Ga-hyeon Song[1], Jong-cheol Kim[1] and Jae Su Kim[1, 2*]

[1]Department of Agricultural Biology, Jeonbuk National University, Korea
[2]Department of Agricultural Convergence Technology, Jeonbuk National University, Korea

Compared to solid culture, liquid culture reduces production time. However, blastospores are generally unstable to heat. In this study, *Beauveria bassiana* JEF-350 produced in different media were investigated to produce heat-resistant propagules. After liquid cultures of JEF-350 at SDB, SSYP, and YPG media for seven days, the productivity and thermotolerance were investigated. The blastospore productivity of JEF-350 was the highest in SSYP media. As a result of heat exposure to 45°C for 60 minutes, blastospores produced in SSYP-liquid medium showed the highest germination rate (22.6%). From a virulence test against *Thrips palmi*, the mortality of *T. palmi* on all treatments showed more than 95% in day 7 after fungal treatment. SSYP-liquid medium was considered as an excellent substrate to culture JEF-350.

Key words: *Beauveria bassiana*, culture media, thermotolrance, productivity, virulence

O32

Effect of repellency light on the *Grapholita molesta* (Busck)

Yong Ju Jang[1], Young Ha Woo[1] and Un Teak Lim[2]

[1]Agricultural corporation, Agricultural Management
[2]Department of Plant Medicals, Andong National University

환경독성을 유발하는 농약사용을 줄이기 위한 친환경 해충방제법의 하나로 횃불에서부터 LED까지 해충을 유살하기 위한 광원들이 개발되어 왔다. 일본에서는 여러 실험을 통해 야행성 곤충이 청색과 황색광 모두에서 명반응시간이 짧아져 방제에 효과적이라는 연구 결과가 보고되었고, 그 중에서 주로 590 nm파장의 황색광이 주로 사용되었다. 본 연구에서는 일본에서 개발된 황색광을 국내 과수원에서 적용하고자 실내외 평가를 실시하였다. 실내에서 복숭아순나방의 산란수가 황색광 처리구에서 48시간 후에 대조구에 비해 50%로 감소했다. 실외 사과과원에서는 복숭아순나방 피해가 유의하게 감소하는 것을 확인하였다, 따라서 황색등이 야행성 나방류 명적응 행동에 영향을 주어 해충유인성을 낮추는 방충등으로 적합하다고 판단하였다.

Key words: Repellent light, Oriental fruit moth, Aapple, 590nm

O33

Identification of entomopathogenic fungus *Metarhizium rileyi* and evaluation of its pathogenicity on fall armyworm, *Spodoptera frugiperda* larvae in Korea

Rajendra Acharya[1,2], Matabaro Joseph Malekera[1], Seung-Yeol Lee[1] and Kyeong-Yeoll Lee[1,3]
[1]Department of Applied Biosciences, Kyungpook National Ubiversity, Daegu, Korea
[2]Department of Entomology, HICAST, Purbanchal University, Nepal
[3]Institute of Plant Medicine, Kyungpook National University, Daegu, Korea

The fall armyworm (FAW), *Spodoptera frugiperda* is one of the important invasive pest in Africa and Asia. The chemical control of this pest is unsuccessful due to the development of resistant and harmful effects on the environment. In this study, the native strain of *Metarhizium rileyi* was identified using morphological and molecular characterization which was collected from the cornfield at Yeongcheon, Korea during August 2021. Susceptibility of fourth instar larvae of FAW to this native strain *M. rileyi* was examined in the laboratory. The results showed that the Korean strain of *M. rileyi* was highly pathogenic to FAW larvae, causing 89% mortality after 7 days post-treatment. Therefore, *M. rileyi* strain identified in this study could be used for biological control of FAW in the fields.

Key words: Fall armyworm, invasive pest, *Metarhizium rileyi*, mortality, biological control

O34

The potential of methyl benzoate as an insecticide: A critical evaluation against a variety of target arthropod pests

Md Munir Mostafiz[1], Ji-Youn Lee[2] and Kyeong-Yeoll Lee[1,2]
[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea
[2]Department of Agricultural management, Chilgok Agricultural Technology Center, Chilgok 39851, Korea
[2]Sustainable Agriculture Research Center, Kyungpook National University, Gunwi 39061, Korea

Biopesticides are biorational pesticides as they are less harmful to human health and the environment than synthetic pesticides. Methyl benzoate (MBe) is a relatively new botanical insecticide that occurs naturally as a metabolite in plants. In this study, we evaluated the insecticidal activity of MBe against a variety of insect pests. According to our laboratory findings, MBe has significant contact toxicity against cotton aphid and two-spotted spider mites, with an LC50 range of 1800 ppm to 3800 ppm. However, the LC50 values of MBe for *Aedes* and *Culex* mosquito species were found to be 61 and 185 ppm, respectively. Furthermore, MBe demonstrated strong fumigation toxicity against Indian meal moth and flat grain beetle with an LC50 value of 0.1 μL/L and 0.76 μL/1.5 L air, respectively. Additionally, MBe also has the ability to suppress acetylcholinesterase enzyme activity. Overall, MBe seems to be a highly promising candidate for the development of green insecticides that are more efficient, safe, and environmentally-friendly.

Key words: contact toxicity, fumigation toxicity, mode of action, naturally occurring compound, sustainable agriculture

O35

Inference of direct and indirect selection pressures for insecticide resistance development in *Anopheles* and *Culex* mosquitoes

Do Eun Lee[1], Ju Hyeon Kim[2] and Si Hyeock Lee[1,3]
[1]Department of Agricultural Biotechnology, Seoul National University
[2]Department of Tropical Medicine and Parasitology, Seoul National University
[3]Research Institute of Agriculture and Life Sciences, Seoul National University

Extensive use of synthetic insecticides, such as DDT, pyrethroids (PYRs), and organophosphates (OPs) for the control of medical pests, has resulted in high levels of resistance. Although only PYRs and some OPs are currently permitted as public health insecticides in South Korea, high levels of cyclodiene and OP resistance mutations have been observed in the field and thus it remains to be elucidated whether non-public health insecticides drive selection pressure against mosquito species. In this study, to test the hypothesis that agricultural insecticides can play a critical role in selection depending on mosquitoe's ecological habitat, resistance profiles to three insecticide groups (cyclodienes, PYRs and OPs) in two representative mosquito species (*Anopheles sinensis* and *Culex pipiens*) were investigated by analyzing the resistance allele frequencies of *rdl, kdr* and acetylcholinesterase 1 (*ace1*) G119S, respectively. After that, the correlation between the resistance allele frequency and the landuse status of 3-km radius of collection sites was analyzed. The *kdr* and *rdl* frequencies in *An. sinensis* showed negative correlation with forest area (r=-0.47 and r=-0.47 respectively), as forest is less likely to be exposed to insecticides. In the case of *Cx. pipiens*, the *kdr*, *rdl* and *ace1* mutations showed positive correlation with residential space (r=0.53), rice paddy (r=0.59) and field (r=0.87), respectively. Therefore, it can be inferred that PYRs used for public health function as the main direct resistance selection pressure, whereas agricultural insecticides such as fipronil and carbamates may work as indirect minor selection pressure.

Key words: *Anopheles sinensis*, *Culex pipens*, insecticide resistance, indirect selection, agricultural insecticides

O36

Use of entomopathogenic fungi to suppress *Spodoptera frugiperda* population

Insoo Jeon[1], So-Eun Park[1], Yeram Im[1], Yujin Jung[1], Yulim Park[1], Kijung Kim[1], Gahyeon Song[1], Jong Cheol Kim[1] and Jae Su Kim[1,2]
[1]Department of Agricultural Biology, Jeonbuk National University, Korea
[2]Department of Agricultural Convergence Technology, Jeonbuk National University, Korea

Fall armyworm, Spodoptera frugiperda is an invasive polyphagous pest derived from America. This pest has developed resistance to insecticides, such as pyrethroid, organophosphorus, and oxadiazine. Entomophatogenic fungi are alternative methods to control fall armyworm. Herein, virulence of entomophathogenic fungi against fall armyworm was screened. The productivity and thermotolerance of conidia were evaluated to figure out the potential for field application. Of the isolates, two isolates showed high virulence to pupae at soil treatment. Another two-isolate caused high mortality of larvae. These high virulence isolates would be promising biological control agents for the management of fall armyworm.

Key words: biological control, entomopathogenic fungi, Spodoptera frugiperda,

O37

Morphological and biological characteristics of *Lepgtoglossus occidentalis* Heidemann (Heteroptera: Coreidae) in Korea

Jae-Woo Lee[1], Minjung Huh[1], Il Nam[1], Ji-Hong Park[1], Dongho Lee[1], Minwoo Lee[1], Kyungjoo Hwang[1], Soungbin Cho[1] and Il-Kwon Park[1,2]

[1]Department of Agriculture, Forestry and Bioresources, Seoul National University
[2]Research Institute of Agriculture and Life Sciences, Seoul National University

The western conifer seed bug (WCSB), *Leptoglossus occidentalis* Heidemann is one of the most devastating pests in various conifers, which has caused significant decreases in seed production of seed orchards and pine nut plantations globally, especially *Pinus koraiensis* Siebold & Zucc. in central Korea since 2010. Herein, we investigated the morphological and biological characteristics of Korean WCSB population. The population showed relatively identical morphology with overseas populations. Body lengths of adult males and females were 17.2 and 19.05 mm, respectively, while pronotum widths were 4.85 and 5.55 mm, respectively. Body weights were 111.27 and 169.89 mg, respectively. Body lengths of the first to fifth instar nymphs were 3.07, 4.76, 8.77, 13.56, and 15.53 mm, respectively. Developmental duration of the eggs and nymphal instar stages were 8.63, 3.69, 7.63, 5.82, 5.83, and 9.15 days, respectively. Nymphal mortality was shown as 47.5%. Life expectancy of adult males and females were 58.2 and 63.9 days. A single Korean WCSB adult female laid averagely 68.6 eggs during the lifetime. Our results may contribute to understanding WCSB ecology and damage aspects in Korea.

Key words: *Leptoglossus occidentalis*, morphological characteristic, biological characteristics

O38

Response of fat body from Japanese pine sawyer beetle, *Monochamus alternatus* to the entomopathogenic fungus, *Beauveria bassiana* ERL836

Yulim Park[1], Soeun Park[1], Yeram Im[1], Insoo Jeon[1], Yujin Jeong[1], Kijung Kim[1], Gahyeon Song[1], Jong-Cheol Kim[1] and Jae Su Kim[1,2]

[1]Department of Agricultural Biology, Jeonbuk National University, Korea;
[2]Department of Agricultural Convergence Technology, Jeonbuk National University, Korea

Japanese pine sawyer beetle, *Monochamus alternatus*, is a vector of pine wilt nematode causing pine wilt disease. In this study, *Beauveria bassiana* ERL836, which showed high virulence against *M. alternatus* and the highest conidial thermostability was used to control *M. alternatus*. To investigate the response of fat body, we performed RNA-seq analysis of RNA samples obtained from fat body of *M. alternatus* in 2 and 4 days after ERL836 treatment. On day 2 and 4, genes involved in muscle contraction were upregulated, however, genes involved in defense response were downregulated.

검색어: *Monochamus alternatus*, transcriptome analysis, *Beauveria bassiana*, RNA-seq, biological control

O39

Selection of grain media for *Beauveria bassiana* 331R strain showing high acaricidal activity against *Tetranychus urticae*

Jin Yong Lee, Ra mi Woo, Thida Win, Hyun Soo Kim and Soo Dong Woo
Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheougju 28644, Korea

점박이응애는 200여개의 과수와 채소, 관상식물들을 가해하는 주요 해충으로 무분별한 살충제 사용에 따른 천적제거와 빠른 저항성발달로 방제가 어려운 실정이다. 이를 방제하기 위해 높은 살비력을 보이는 곤충병원성 곰팡이 *Beauveria bassiana* 331을 대량생산 할 수 있는 배지를 선발하고자 하였다. 각 곡물에서 생산된 conidia의 살비력, 포자생산량, 환경안정성을 평가한 결과 기장과 쌀에서 높은 살충활성과 생산효율을 보였으며, 특히 쌀 배지에서 상대적으로 높은 열과 UV-B에 대한 안정성이 확인되었다. 쌀 배지가 *B. bassiana* 331R균주에 최적배지로 결정되었고, 추후 제제화 후 활성에 대한 연구를 진행하고자 한다.

검색어: 곤충병원성곰팡이, *Beauveria bassiana*, 점박이응애, 곡물배지

O40

Bioassay and genotyping based Diamide resistant status of Korean populations of *Spodoptera exigua* (Lepidoptera: Noctuidae)

Chang Hee Han[1], Hwa Yeun Nam[2] and Juil Kim[1,2]
[1]Program of Applied Biology, Division of Bio-resource Sciences, CALS, Kangwon National University
[2]Agriculture and Life Science Research Institute, Kangwon National University

Beet armyworm, *Spodoptera exigua*, is one of the most destructive polyphagous lepidopteran pests worldwide including in Korea. To control *S. exigua*, diamides have been widely used for more than a decade. Since 2017, a high level of diamide resistance has been reported up to now. Bioassay-based diamide resistance was tested field populations of *S. exigua* for some years. The level of diamide resistance varied with tested year and region. Known three point mutations such as Y4701, I4790, and G4946 in RyR which target site of diamide was surveyed. Among them, only I4790 mutation was detected in most field populations. Moreover, insecticide-resistant population-specific intronic InDels and SNPs were also identified. This genetic diversity possibly generates different levels of diamide resistance in Korea. Therefore, population genetics-based insecticide resistance management (IRM) strategy has to prepare for diamide resistant population of *S. exigua*. A genetic marker-based diagnostic tool such as LAMP was developed and applied in the IRM of *S. exigua*.

Key words: *Spodoptera exigua*, diamide, I4760 mutation, InDel