

01

Research on controlling harmful diseases and pests in soil using microwave penetration heating effect

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특정작물의 연작재배가 만연한 국내 경작지 중, 특히 인삼재배지는 인삼뿌리썩음병균, 시설재배지는 선충에 의한 연작피해가 매우 심각하며, 주로 화학·생물학 약제로 방제하지만 효과가 낮고 토양오염과 약제저항성 등의 부작용을 유발하고 있음. 모든 살아 있는 병해충은 고온에 저항성이 없는 장점에 착안하여 마이크로파(915MHz) 전력밀도 균일화 응용으로 경작지 토양 30cm 이상 깊이까지 100°C 이상 침투 가열하는 마이크로파 방제장치 및 방제기술을 개발하여 토양 속에 존재하는 선충, 개미, 인삼뿌리썩음병균에 적용한 결과, 선충은 60°C, 개미는 50°C에서 완전사멸 되었으며, 인삼뿌리썩음병균은 80°C에서 연작 가능한 수치까지 떨어지는 방제 효과를 나타냄에 따라 농약을 대체하는 방제기술로 평가된다.

검색어: 마이크로파, 침투가열, 인삼뿌리썩음병균, 선충, 저항성

02

Remote sensing to predict insect vector migration and plant virus outbreaks: An example from California

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Climate change has made outbreaks of insect-transmitted plant viruses increasingly unpredictable. Understanding spatio-temporal dynamics of insect vector migration can help forecast virus outbreaks, but the relationship is often poorly characterized. The incidence of *Beet curly top virus* (BCTV) was examined in 2,196 tomato fields in California from 2013-2022. In addition, we experimentally showed dispersal of the beet leafhopper, the only known vector of BCTV is negatively correlated with plant greenness, and we estimated spring migration timing using a vegetation greenness-based model. Potential environmental factors and spring migration time of beet leafhoppers were associated with BCTV incidence. We found BCTV incidence is strongly associated with spring migration timing rather than environmental factors themselves. In addition, the vegetation greenness-based model was able to accurately predict the severe BCTV outbreaks in 2013 and 2021 in California. The predictive model for spring migration time was implemented into a web-based mapping system, serving as a decision support tool for management purposes.

Key words: *Circulifer tenellus*, beet curly top virus, migration modeling

03

Seasonal occurrence of insect pests from endangered coniferous trees in subalpine forests of Korea

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The Korea Forest Service has designated seven alpine tree species—*Abies koreana*, *A. nephrolepis*, *Juniperus chinensis*, *Picea jezoensis*, *Pinus pumila*, *Taxus cuspidata*, and *Thuja koraiensis*—as threatened with extinction in Korea. In 2023, we conducted a study on the seasonal occurrence of insect pests, focusing mainly on two coleopteran taxa (Cerambycidae and Scolytinae) and two hemipteran taxa (Aphrophoridae and Cicadellidae) in subalpine forests dominated by *A. koreana*, *A. nephrolepis*, *Picea jezoensis*, *Thuja koraiensis*, and *Taxus cuspidata*. We utilized three types of traps—Malaise trap, Lindgren funnel trap, and window trap—in eight investigation locations in Korea. In this presentation, we present the study results and discuss the effects of insect pests on alpine coniferous trees in Korea.

Key words: Coniferous, extinction, insect pest, Korea, subalpine

04

Energy flux in soil ecosystem in the threats to biodiversity

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Ecosystems provide various ecosystem services based on biodiversity. However, biodiversity is facing crises due to anthropogenic factors such as pollution, land use change, and climate change. Threats to biodiversity can significantly impact the provision and stability of ecosystem services, extending beyond simple species decline. To address threats to biodiversity, it is crucial to evaluate how anthropogenic factors affect not only biodiversity but also ecosystem services. This study aims to investigate the energy flux in a post-mining area based on the biodiversity of soil ecosystems and assess its suitability as an evaluation metric. It was observed that as the concentration of the primary pollutant, arsenic, increased, both the biomass of soil organisms and energy flux decreased. Furthermore, soil ecosystem multifunctionality may be negatively affected by pollution. These findings contribute to understanding the impact of pollution on soil ecosystem biodiversity and energy flux in post-mining areas and provide important information for more effective conservation and management of ecosystem services.

Key words: ecosystem service, multifunctionality, food web, heavy metal, pollution

05

Development of binomial sampling plan of *Bemisia tabaci* in greenhouse tomato

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Density survey should be carried out for applying integrated pest management strategies, but it is labor-intensive, time- and cost-consuming. Therefore, binomial sampling plans are developed for estimating and classifying the population density of whiteflies late larvae based on the relationship between the mean density per sample unit (7 leaflets) and the proportion of leaflets infested with less than T whiteflies (P_T). In this study, models were examined using tally thresholds ranging from 1 to 5 late larvae per 7 leaflets. Regardless of tally thresholds, increasing the sample size had little effect on the precision of the binomial sampling plan. Based on the precision of the model, $T=3$ was the best tally threshold for estimating the densities of late larvae. Models developed using $T=3$ validated by Resampling Validation for Sampling Plan program. Above all, the binomial model with $T=3$ performed well in estimating the mean density of whiteflies in greenhouse tomato.

Key words: IPM, *Bemisia tabaci*, tomato, binomial sampling plan, tally threshold, precision

06

Experimental investigation of the life history of *Chrysochroa coreana* (Coleoptera: Buprestidae) via nondestructive computed tomography method

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The biggest jewel beetle in Korea, *Chrysochroa coreana*, has been nominated as the Natural Monument No. 496 and also classified as Category I of Endangered Species by the Red Data Book. Due to the invisible feature of a saproxylic larval hood inside the host tree for years, the whole life history was hitherto been unknown to the academic world. In order to clarify the period of larval-hood and record images of the process of the final stage of emergence, we obtained sample eggs from two mated couples of adults that emerged from a dead tree of *Celtis sinensis* on Wando Island, which is well-known as the habitat of *C. coreana*. Larvae were hatched on four pieces of timber (*Celtis aurantiaca*) in July 2018 and kept in a growth chamber under the conditions of 25°C, 65% humidity, and in a 12-hour light/dark cycle. The development of larvae was monitored via the non-destructive C/T method every month. Six adults were emerged between February and March 2024. As a result, we obtained the fact that the larval period of *C. coreana* is minimum 66 months (5.5 years) under lab conditions.

Key words: Jewel beetle, saproxylic, nondestructive inspection. life history

**Ecological integration of *Vespa velutina* lepeletier, 1836 in South Korea:
A comprehensive study of Co-occurrence and interaction patterns with native social
wasps**

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Over four years (2020–2023), 305 traps were strategically placed across South Korea to collect data on Vespidae species. Our findings showed that *Vespula flaviceps*, *Vespa crabro*, and *Vespula koreensis* were the most frequently encountered species. *Vespa velutina* was also widespread, suggesting its successful integration into local ecosystems. The ARL analysis, using the “apriori” algorithm, identified significant co-occurrence patterns and potential interactions. The rules generated indicated both competitive and coexistent relationships with varying levels of association strength across different regions. Clustering analyses, including hierarchical and k-means clustering, grouped species based on their occurrence similarities. The distinct clusters formed in the analysis highlighted the unique ecological roles and interactions of *V. velutina* and other Vespidae species in South Korean ecosystems.

Key words: Invasive species, association rule learning, Vespidae, ecological interactions, species distribution

Fecal metabarcoding and prey pellets reveal differences in prey breadth of *Vespa mandarinia* in native and novel ecosystems

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Vespa mandarinia (Vespidae: Hymenoptera) is one of the two largest true hornets known to science. The species is a noted predator of social Hymenoptera and a significant pest of managed honey bees in its native range, but is also known to feed on a wide variety of other species when available. Most of the prey records for *V. mandarinia* are derived from visual observations in Japan, with sparse observations from other parts of its native range. A population of *V. mandarinia* was detected in North America in 2019 and five nests were removed between 2019 and 2021. We extracted DNA from larval meconia from four nests collected in Washington State, USA, and amplified the CO1 region to determine the potential prey base. We compared these with sequences generated from three nests in the Republic of Korea, and with prey pellets collected from foraging hornets at several locations in Korea. Results indicate that the prey base was much wider in the ROK than the USA, although social Hymenoptera were the most abundant and common prey items in both regions. Prey range seems to be bound by an intersection of organism size and local biodiversity, with little evidence to suggest that the latter is a limiting factor in colony success.

Key words: *Vespa mandarinia*, larval meconia, CO1, prey pellet, USA, Korea

Detection of *Orientia* spp. from chiggers (Acari: Trombiculidae) in the Republic of Korea, 2022

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Scrub typhus is a zoonotic bacterial disease caused by *Orientia tsutsugamushi* (Rickettsiales: Rickettsiaceae) and trombiculid mite larvae, also known as chigger, are known vector. Until recently, *O. tsutsugamushi* is the only species of the genus. However, two new species *Candidatus O. chuto* and *Candidatus O. chilensis* that causes scrub typhus were reported recently in the Middle East, southern Chile, and Africa. In addition, *Orientia* spp. bacteria detected from field collected free-living *Eutrombicula* chigger mites in the United States. Despite these trends, research on new species is insufficient in the Republic of Korea. Therefore, we focused on finding the presence of novel species or strains from chiggers. Specimen chiggers harvested from rodents collected in 16 regions in October 2022 collaborating with the Regional Center for Vector Surveillance against Climate Change were selected. A total of 1,249 specimen belonging 4 genera and 14 species were identified by using a fluorescence microscope and 266 pools were produced by pooling up to 10 individuals per species chiggers. To detect *Orientia* spp., we screened by using a real-time PCR targeting the 16S rRNA gene. Overall minimum infection rate was 0.56% (7 pools/1,249 tested specimen). After screening, conventional nested-PCR for targeting 47-kDa *htrA* gene was conducted to obtain sequences, and four of the positive pools were amplified. Through phylogenetic analysis, three pools were clustered with *O. tsutsugamushi* Gilliam and UT221 strain, and the other pool was formed a clade that was distinct from *O. tsutsugamushi*. These results suggest that novel species of *Orientia* may exist in the Republic of Korea.

Key words: scrub typhus, *Orientia*, chigger

010

Decomposition ability of organic waste by *Protaetia brevitarsis seulensis* larval instar stages

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우리나라의 “곤충산업의 육성 및 지원에 관한 법률”은 곤충산업에 대한 직면한 문제 등 다양한 관점에서 다루고 있다는 점을 시사한다. 이는 곤충에 대한 연구를 인간과 함께 할 수 있는 식용화, 약리활성 접근법을 통해 변화를 가져야 한다는 것을 의미하기도 한다. 최근의 시사점은 곤충을 식용화하여 곤충산업을 활성화 하는 것이 최우선 과제로 이 역시 곤충에 대한 혐오가 가장 큰 문제였다. 예를 들면, 곤충은 생리활성물질을 포함하고 있어 기능성 식품으로 개발되었지만 곤충에 대한 인식전환의 문제점을 내포하고 있다. 곤충을 활용할 때 가장 큰 장점은 유기성 폐자원을 분해할 수 있기 때문에 우수한 곤충자원을 확보하는 하는 것이 우리의 연구에서 매우 중요하다. 따라서 본 연구에서는 대표적인 곤충인 굽벱이 유충을 성장단계에 따라 유기성 폐자원을 분해할 수 있는지를 평가했다. 우리의 연구에서 굽벱이 유충은환경정화곤충으로서의 가치는 감소가 되었다. 또한 이 결과는 곤충농가의 활용 측면에서 기초적 정보를 제공하는데 있다.

검색어: 굽벱이 유충, 유기성 폐자원, 곤충 선발

011

Evidence against Thayer’s hypothesis: Distractive markings hinder camouflage in moth-like targets

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Distractive marking, as conceptualized by Abbott H. Thayer, refers to diminutive patterns of contrasting colors on an animal’s body. Thayer hypothesized that these patterns augment camouflage by diverting predatory focus from the outline of the prey, however, the evidence was insufficient. In this study, we verified the hypothesis that the presence of distractive markings confers a survival advantage under specific conditions. Specifically, the experiment aimed to ascertain whether the existence of lichens on trees hinders the visual detection of prey, given that lichens resemble distractive markings. The experimental design involved human subjects as predators and artificial moth images on a monitor as prey. The survival of moths with and without distractive markings was compared, also considering the influence of the presence of lichens in the background. As an analysis result, the survival likelihood of moths was statistically significantly hindered when the distractive marking was present. This result contradicts Thayer’s hypothesis and implies the presence of a function distinct other than the enhancement of camouflage.

Key words: distractive marking, moth, camouflage, survival analysis, crypsis

012

From Decay to Diversity: Ecological relationships of environmental variables and saproxylic beetles in dead wood

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Our study examined a total of 60 dead wood samples (*Quercus* spp.), collecting 30 samples each in summer and winter, and measured various environmental variables in the field. These samples were classified into three decay classes: fresh, intermediate, well-decayed. We sampled saproxylic beetles within the collected dead wood using emergence traps. Conducted a cluster analysis to explore their relationships of saproxylic beetle and environmental variables. Our results revealed that season and decay class were significant environmental variables affecting saproxylic beetle communities. These results highlight the sensitivity of saproxylic beetles to fluctuations of environment and climate. In summary, our study highlights the intricate relationships between environmental variables and saproxylic beetles and suggests that different types of dead wood should be maintained in forests.

Key words: beetles, dead wood, emergence trap, environmental variables, saproxylic

013

A sheep in wolf's clothing: A microlepidopteran species mimics jumping spiders

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깡충거미과의 모습을 의태하여 시각적 포식자인 깡충거미로부터 자신을 보호하는 전략은 여러 나비목 곤충에서 진화하였다. 하지만 나비목 곤충이 깡충거미 간의 의사소통 신호를 의태한다는 가설은 제안된 바 없다. 본 연구에서는 깡충거미과의 구애/영역성 행동을 의태하는 것으로 추정되는 붉은꼬마꼭지나방(*Atkinsonia ignipicta*)의 빗살 모양 더듬이와 추켜 올린 다리가 포식을 단념시키는 의태 신호로 작동하는지 실험적으로 검증하였다. 깡충거미 의태라 추측되는 붉은꼬마꼭지나방의 형태적 및 행동적 특성들을 단계적으로 제외한 뒤 포식자(흰눈썹깡충거미, *Evarcha albaria*)와의 조우 시 생존을 비교하였다. 연구 결과, 붉은꼬마꼭지나방은 비슷한 크기의 바-의태 나방에 비해 포식자의 공격을 덜 받았으며, 더듬이나 다리 중 하나라도 결여되었을 때 흰눈썹깡충거미의 공격이 증가하였다. 이는 붉은꼬마꼭지나방의 더듬이와 다리 모두가 시각적 방어에 중요한 신호로 작동한다는 것을 시사한다. 하지만 흰눈썹깡충거미가 붉은꼬마꼭지나방을 향해 구애/영역성 행동을 보이지 않았다는 점에서 깡충거미의 낮은 공격 빈도가 같은 깡충거미 종류로 오인해서인지 다른 이유에서인지는 불투명하다. 그러나 사충깡충거미(*Marpissa pulla*)는 붉은꼬마꼭지나방을 상대로 영역성 행동을 잦은 빈도로 보였으며, 이는 붉은꼬마꼭지나방의 형태가 깡충거미 의태 효과를 가진다는 것을 보여준다.

검색어: Batesian mimicry, predator-prey interaction, protective mimicry, visual signals

014

Dissecting the molecular underpinnings of an ancient mutualism: An integrative study of fig-wasp symbiotic evolution

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This research explores the complex interdependencies and dynamic interactions governing the adaptation of species co-evolving within the framework of Eco-Evo-Neuro-Devo, using the fascinating fig-wasp mutualism as a model system. Figs, which have many flowers blooming inside the fruit, are completely dependent on fig wasps as pollinators. The fig-wasp mutualism is a symbiotic relationship where fig trees provide a habitat and food source for specific wasp species, while the wasps, in turn, facilitate pollination and seed dispersal for the fig tree. The fig wasp is born and grows inside the fig fruit and becomes an adult. After mating, the female fig wasp is covered with pollen and enters another fruit, pollinates it and lays eggs there. In addition to the fig-wasp mutualism, additional interactions among hyperparasitic wasps, called non-pollinating fig wasp (NPFW), and flies, nematodes are frequently observed, shaping the co-evolution of the symbionts in the fig community. This study aims to identify the symbionts that make up the symbiotic system, their ecological interactions and genome evolution, and build a model to explore the mechanisms of symbiotic evolution at the molecular level. Sampling and identifying figs and fig-related insects through fieldwork in Korea, various techniques including GC-MS, in situ staining, electrophysiology, and diverse omics tools including WGS, RNA-seq will be implemented to investigate how chemical ecologies of the fig community shape the chemosensory systems of species. Additionally, we will build a cross-platform with *Drosophila* to narrow the distance between model species and non-model species, facilitating comparative studies across different model organism systems.

Key words: Fig-wasp, Ecological interaction, Symbiosis, Coevolution, Sensory system evolution, *Drosophila*

O15

Evaluation of insecticidal activity in western flower thrips, *Frankliniella occidentalis*, occurring from greenhouse peppers in Gyeonggi-do

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Yellow flower thrips (WFT), *Frankliniella occidentalis* is mainly controlled using chemical control methods. But the continuous use of chemical pesticides in greenhouse may contribute to development of insecticide resistance. Therefore, in this study, we evaluated the insecticidal activity of eleven insecticides against the WFT occurring in greenhouse pepper cultivation in the Gyeonggi province. The results showed no resistance in treatments with emamectin benzoate, fluxametamide, and flometoquin while high levels of resistance were recorded in treatments with acrinathrin, acetamiprid, and dinotefuran. The Anseong and Yeosu population was more resistant against spinetoram and chlorfluazuron, respectively, than populations from other regions.

Key words: insecticidal activity, red pepper, resistance, yellow flower thrips

O16

Biological and morphological characteristics of *Eriborus* sp. (Hymenoptera: Ichneumonidae), a parasitoid wasp of the box tree moth, *Cydalima perspectalis* Walker (Lepidoptera: Crambidae)

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The box tree moth (BTM, *Cydalima perspectalis* Walker) is a pest that infests various plants within the *Buxus* genus. Although a specific parasitoid wasp species associated with the BTM has been observed in the Republic of Korea, no research on this species has been published. Here we describe the fundamental biological and morphological characteristics of this parasitoid. We placed the wasp under the genus *Eriborus* (Hymenoptera: Ichneumonidae: Campopleginae). *Eriborus* sp. parasitizes within the living host body, with one wasp emerging from each host. The parasitism rate in collected BTM populations was 33.1%. The emergence rate was 87.1%, with all emerging adults being females, resulting in a sex ratio of 0. The pupal period averaged 9.5 days, and the adult lifespan averaged 10.5 days. *Eriborus* sp. parasitized BTM larvae from the first to the fourth instar and reproduced by parthenogenesis. *Eriborus* sp. exhibited morphological differences compared with previously reported *Eriborus* species in Korea, particularly in the length of the ovipositor sheath. In addition, the proportion of the highest similarity in nucleotide sequences of mitochondrial cytochrome oxidase I DNA was only 94.53%, rendering species identification using GenBank's mt cytochrome c oxidase I DNA sequences unfeasible. These data suggest *Eriborus* sp. could be used as a biological control agent for managing BTM infestations.

Key words: box tree moth, parasitoid, biological characteristics, morphological characteristics

017

Evaluation of insecticide resistance in *Frankliniella occidentalis* from tomato greenhouses in Chungcheong-do, Cheongyang, Chungju and Gongju

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Five insecticides (Acrinathrin, Dinotefuran, Emamectin benzoate, Chlorfenapyr and fluxametamide) approved for tomato cultivation were evaluated in *Frankliniella occidentalis* populations collected from Chungcheong province (Cheongyang, Chungju and Gongju). Leaf dip bioassay was used to evaluate resistance levels (LC₅₀). Bioassays on Acrinathrin demonstrated higher LC₅₀ concentration in evaluated populations. In particular, the Chungju population was 745.61 times the recommended concentration of the insecticide. Other remarkable resistance levels were recorded for the Dinotefuran with 435.06 times and 196.29 times the recommended concentrations for the populations from Chungju and Gongju, respectively. Bioassays for Emamectin benzoate, Chlorfenapyr and Fluxametamide showed low resistance to insecticides in the evaluated populations.

Key words: Bioassay, Emamectin benzoate, *Frankliniella occidentalis*, LC₅₀, pest

018

Development of LAMP assay for rapid identification of *Spodoptera eridania* and *S. ornithogalli* (Lepidoptera: Noctuidae) using species-specific whole genome sequences

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Spodoptera eridania and *S. ornithogalli* (Lepidoptera: Noctuidae), which are polyphagous pests that damage various crops such as tomatoes and beans are regulated quarantine species that are highly likely to invade South Korea. Therefore, it is crucial to promptly and accurately identify the presence of *S. eridania* and *S. ornithogalli* in crop fields to effectively eradicate as a regulated quarantine species. In this study, we developed a loop-mediated isothermal amplification (LAMP) assay, which allows for rapid in-field identification. To develop the LAMP assay, we selected target species-specific genomic regions from the whole-genome sequences of one target and 13 other lepidopteran species. We validated each five and six primer sets that consistently produced positive reactions in *S. eridania* and *S. ornithogalli*, respectively. To test the sensitivity of the each locus, LAMP reactions were performed using various reaction times using crude DNA, which was extracted from various types of adult tissues. All sensitivity tests were also successful.

Key words: *Spodoptera eridania*, *Spodoptera ornithogalli*, LAMP, Whole genome, diagnosis method

019

Trade-off between reproduction and defense in *Akanthomyces attenuatus* JEF-147-infected two-spotted spider mite

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Two-spotted spider mite (*Tetranychus urticae* Koch; TSSM) is an agriculturally serious pest that has acquired strong resistance against acaricide. Alternatively, mite-pathogenic fungi could be used to control the mites. The spider mite has symbiotic microorganisms which could be involved in the physiological and ecological adaptation to biotic stress. In this study, mite-pathogenic fungi were used to control female adults, and the change of microbiome in the fungus-infected mites was analyzed. The acaricidal activity of fungal isolates was tested, and *Akanthomyces attenuatus* JEF-147 with the highest acaricidal activity was determined, followed by semi-field assay. Microbiome in the female adults which was infected by *A. attenuatus* JEF-147 was analyzed, and composition of microorganism was changed by fungal treatment. In bacteria abundance, the arthropod defense-related *Rickettsia* increased, but reproduction-associated *Wolbachia* decreased. The change in major bacterial abundance in the infected mites could be explained by the trade-off between reproduction and immunity. This work describes that a possible trade-off in arthropods against fungal pathogens could be predicted by the microbiome analysis.

Key words: Arthropod-pathogenic fungi, microbiome, *Tetranychus urticae*, *Rickettsia*, *Wolbachia*

O20

Antennal olfactory receptor neurons for plant volatiles in harlequin ladybird, *Harmonia axyridis* (Pallas, 1773) (Coleoptera: Coccinellidae)

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Harlequin ladybird (*Harmonia axyridis* (Pallas, 1773)) is an invasive species originating from Asia, posing a potential threat to the ecosystem and the wine industry in New Zealand due to wine taint, although it can also be a useful biocontrol agent. In this study, the response profiles of antennal olfactory receptor neurons (ORNs) to 32 plant volatiles were examined in male and female *H. axyridis*, using the single sensillum recording technique. Various types of ORNs were identified from four types of olfactory sensilla in both male and female *H. axyridis*, with no sexual dimorphism. The most abundant type of sensilla contained two ORNs exhibiting highly specialized responses to methyl benzoate and β -caryophyllene, respectively. Another type of sensilla also contained two specialized ORNs, one responsive to geranyl acetate and the other to some aromatic compounds such as 2-phenylethanol, benzyl acetate, methyl benzoate, and methyl phenylacetate. In contrast, two other types of sensilla contained broadly tuned ORNs, one containing ORN(s) responsive to six-carbon alcohols such as (*Z*)-3-hexen-1-ol, 1-hexanol, and isomers of 2-hexen-1-ol as well as some other non-alcohol green leaf volatiles, and the other containing ORN(s) exhibiting responses to β -myrcene, geraniol, linalool, nerol, benzyl acetate, and methyl phenylacetate. This study suggests that *H. axyridis* possesses a set of ORNs specialized for specific plant volatiles, providing insights into the olfactory communication system of this species and potential volatiles to be used for trapping this insect.

Key words: *Harmonia axyridis*, plant volatiles, single sensillum recording

O21

Invasion risk of *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae) in Korea under climate change: Predictions based on MaxEnt modeling with elevation and land cover

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As climate changes and global trade volume increases, the spread of invasive alien species accelerates. Early prevention before occurrence is crucial for invasive pest control. Therefore, this study modeled the current and future potential distribution of the tomato leafminer (*Tuta absoluta*) (Meyrick) (Lepidoptera: Gelechiidae), the most significant pest affecting tomatoes, in Korea. This pest primarily feeds on Solanaceae crops and can cause extensive damage, resulting in 50-100% loss of crops in greenhouses or fields. While previously unreported in Korea, it invaded China in 2017, indicating a potential threat to Korea. The potential distribution of the tomato leafminer in Korea under current and three future climate scenarios (SSP1-26, SSP3-70, SSP5-85) was predicted using the MaxEnt model. Additionally, elevation and land cover were incorporated as abiotic factors considering the ecological characteristics of the pest.

Key words: *Tuta absoluta*, MaxEnt model, Tomato leafminer

O22

Canceled by Author

O23

Effects of symbiotic bacteria, *Caballeronia insecticola*, on behaviors and fitness parameters of female *Riptortus pedestris* (Hemiptera: Alydidae)

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Riptortus pedestris is known to acquire their symbiotic bacteria, *Caballeronia insecticola*, from soil environments in every generation. The symbionts have been demonstrated to affect behavioral and physiological traits of the host insect such as the enhancement of development. In particular, symbiotic effects on female adults could directly entail changes in their population growth. Therefore, we investigated a suite of symbiotic effects of *C. insecticola* on behaviors and fitness-related parameters of female *R. pedestris*. Overall, symbiotic females showed an behavioral enhancement in both feeding efficacy and movement capacity including walking and flight. In addition, the survival rates under exposure to overwintering conditions and insecticide resistance level were significantly higher in symbiotic females than the apo-symbiotic. Finally, although symbiotic females exhibited shorter longevity, their fecundity was found higher compared to the apo-symbiotic.

Key words: bean bug, insect-microbe interaction, gut symbiosis, environmental determination

O24

Frankliniella occidentalis monitoring using deep learning algorithms

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In agricultural ecosystems, the relationship between insect pests and hosts is important, as insect pests can invade hosts, increasing insect pest density that threatens the hosts' health. Insect pests and hosts are negatively correlated and affect the environment around them. i.e., host health, environment, and insect pest density are causally related, and the environment affects insect pest density. Deep learning is method of machine learning based on neural network theory. This approach enables handling uncertain environmental factors that simultaneously impact the density of *F. occidentalis*. Environmental factors affecting the density fluctuation of *F. occidentalis* selected atmosphere factors, soil factors, and host factors. This study aims to *F. occidentalis* monitoring using deep learning models inputting environmental factors.

Key words: *Frankliniella occidentalis*, environmental factors, deep learning algorithm

025

Development of a metal detector system for tracking soil-dwelling insects

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To overcome the challenges in tracking insects underground, a detection method consisting of a metal detector and aluminum tag was developed for tracking a dung beetle, *Copris ochus* (Coleoptera: Scarabaeidae). First, detection rate was evaluated for varying volumes of aluminum tags varying orientations of the tags under soil. Then, the detection efficacy was evaluated in the field at varying depths of hidden tags in two types of vegetation. Finally, the effect of aluminum-tagging on the survivorship, burrowing depth, and horizontal movement of *C. ochus* adults were assessed. Generally, an increase in tag volume resulted in a greater detection depth with maximum depth of 17 cm. Orientation, however, did not affect detection rate except when tag was placed perpendicular to the soil surface. In the field, metal detectors could detect aluminum-tagged models with success rates $\geq 85\%$ up to 10 cm and 45–60% at 20 cm under soil. Finally, no significant effect of tagging on survivorship and behaviors of *C. ochus* was observed.

Key words: insect behavior, dispersal, monitoring, dung beetle

026

The effect of temperature on rice stripe virus (RSV) acquisition and transmission of the small brown planthopper, *Laodelphax striatellus*

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The small brown planthopper (SBPH), *Laodelphax striatellus*, is a major insect pest for the rice plants. SBPH is also a known vector of rice stripe virus (RSV), which causes severe yield losses in rice crops throughout the East Asia. RSV is persistently transmitted by SBPH and can also be transmitted to offspring through transovarial transmission. SBPH is known to migrate from China to the west coast of the Republic of Korea (ROK). The study investigated the impact of temperature on the acquisition and transmission of RSV by SBPH in ROK, which is expected to experience increased migration and emergence of SBPH due to climate change. The results revealed that the acquisition and transmission rates of RSV were higher at 27°C compared to 24°C, with rates of 100% and 78.3%, respectively. However, at 30°C, the acquisition and transmission rates of RSV was decreased. The results suggests that temperature can impact the transmission of RSV by SBPH. To investigate this further, SBPH adults were fed on RSV-infected plants and infection rates were compared across various tissues, including the head, salivary glands, midgut, Malpighian tubules, ovary, and hindgut. Results showed that at 36 hours post-infection, RSV was highly detected in the Malpighian tubules, ovary, and hindgut. At 48 hours post-infection, RSV was also detected in the thorax. These results suggest that the transmission rates of RSV in SBPH increase with temperature between 24-27°C, but decrease at 30°C, indicating that the vectorial capacity of SBPH for RSV decreases above a certain threshold.

Key words: *Laodelphax striatellus*, Rice stripe virus, climate change, virus acquisition, virus transmission

Comparative monitoring of insecticide resistance of *Bemisia tabaci* collected from greenhouse peppers in the Republic of Korea

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담배가루이는 전세계의 온대 및 아열대 지방에 넓게 분포하고 있으며, 한국에서는 시설재배작물의 주요 해충이다. 1998년 충북 친천군 장미재배지에서 처음 확인되었으며, 이후 전국적으로 확산된 것으로 추정된다. 담배가루이는 고추, 토마토, 오이 등 300종이 넘는 넓은 기주범위를 가지며, 식물체를 흡즙하여 작물의 생산성을 저하시키고 토마토황화잎말림바이러스(tomato yellow leaf curl virus, TYLCV) 등 100여종이 넘는 바이러스를 매개한다. 담배가루이는 주로 살충제를 이용한 방제가 이루어진다. 하지만 살충제를 이용한 방제법은 살충제 저항성 개체를 발생시킨다. 살충제 저항성 개체가 발생하게 되면 방제 효율이 급감하여 농가에 추가적인 경제적 피해를 야기한다. 본 연구는 국내 지역별 담배가루이를 대상으로 약제별 살충제 저항성의 발생 현황을 조사하여, 지역별 효과적인 약제를 탐색하고 향후 방제 전략 수립에 기여하고자 한다. 담배가루이는 전국 15지역(파주, 양평, 화성, 양구, 횡성, 평창, 당진, 천안, 공주, 예천, 구미, 사천, 남원, 나주, 고흥)에서 채집되었다. 살충제는 작용기작 별 사용량이 많은 8종을 선정하였으며, 엽침지법을 사용하여 살충물을 확인하였다. 곤충생장조절제(insect growth regulators, IGR) 피리프록시펜계 약제는 알을 대상으로, 그 외 7개 약제는 2령약충을 대상으로 살충률을 확인하였다. 모든 지역에서 높은 살충력을 보인 약제는 아버멕틴과 밀베마이신계, 스피노신계, METI살충제, 디아마이드계 약제이다. 특히 아버멕틴과 밀베마이신계 약제는 살충제 권장사용농도(10ppm)보다 낮은 8.9ppm이하의 LC₉₀ 값을 보여 감수성으로 추정되며, 예외적으로 천안 지역의 25.6ppm으로 상대적으로 높은 LC₉₀ 값을 보였다. 낮은 살충력을 보인 약제는 네오니코티노이드계, 설폭시민계, 피리프록시펜계, 테트론산 및 테트람산 유도체 약제이다. 특히 네오니코티노이드계 약제는 모든 지역에서 살충제 권장사용농도(50ppm)보다 높은 715ppm이상의 LC₉₀ 값을 보여, 모든 지역에서 살충제 저항성이 발생한 것으로 추정된다. 실험결과를 통해 살충제 별 살충력의 차이와 지역별 살충제 저항성을 검정하였다. 연구결과를 통해 지역별/약제별 저항성관리 및 대응전략을 수립하여 농업 생산성을 향상시키는 것에 도움이 되고자 한다.

검색어: 담배가루이, 생물검정, 살충제, 고추, 약제저항성

028

Insecticide resistance tests of *Bemisia tabaci* (Hemiptera: Aleyrodidae) collected from greenhouse cucumbers in Korea

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The continuous use of pesticides with the same mode of action has led to the development of insecticide resistance in the target pests. Establishing pesticide resistance management methods and effective control strategies for these pests has become an important target. *Bemisia tabaci*, a representative pest of greenhouse, directly affects the growth of crops at all stages of its development except eggs. It also causes indirect damage by secreting honeydew that eventually promotes sooty mold in leaves and fruits. In this study, eight insecticides with different mechanisms of action (Flonicamid, Fluxametamide, Spinetoram, Cyantraniliprole, Dinotefuran, Pyridaben, Milbemectin and Pyriproxyfen), and registered for use against cucumber *B. tabaci* were selected and tested for insecticide resistance. The tested populations of *B. tabaci* were collected from greenhouse cucumber cultivations in 12 domestic regions. The results were presented as RR (Resistance ratios), and CEI (Control efficacy index) values.

Key words: Pesticide, Insecticide, *Bemisia tabaci*, RR, CEI, Greenhouse, Cucumber

029

Co-evolutionary patterns between false heads and associated traits in lycaenid butterflies

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Hindwings of many lycaenid butterflies have a unique tail-like wing structure referred to as a false head, which actually mimics the antennae. False heads increase butterfly survival by directing predatory attacks towards the false heads thereby enhancing the chance of escape. In this study, using discrete character evolution models of European and American butterflies, we examined the co-evolutionary patterns between false head structures and two associated traits: a highly contrasting color patch neighboring the false head, and hindwing rubbing behaviors. The former is considered a eye-mimicking structure that enhances the effectiveness of false head, and latter generates the movement of false heads which likely increases the success of false head deception. Our findings demonstrate that false heads are ancestral states for both European and American lycaenids. Both contrasting colors and hindwing rubbing behaviors follow correlated evolution models, suggesting that these traits co-evolved in lycaenid butterflies. However, specific evolutionray patterns differed between the two continents.

Key words: Lycaenidae, false head, co-evolution, ancestral state reconstruction

O30

***Beauveria bassiana* (Balsamo) Vuillemin AAD16 control *Tetranychus kanzawai* Kishida and *Bemisia tabaci* Gennadius on greenhouse strawberry**

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Major pests of greenhouse strawberry include *Tetranychus kanzawai* (Acari: Tetranychidae) and *Bemisia tabaci* (Hemiptera: Aleyrodidae) causing significant damage in both yield and quality. We compared control efficacy of two entomopathogenic fungus strains of *Beauveria bassiana*, AAD16 and GHA, against *T. kanzawai* and *B. tabaci*. Both fungus were applied as a foliar spray targeting the undersides of leaves. In preliminary studies in the laboratory, adult *T. kanzawai* and *B. tabaci* showed lower LT₅₀ values when treated with AAD16 strain compared to GHA. In the greenhouse, the densities of the both mites (adult and nymph) and whiteflies (adult) were significantly reduced with the application of the two fungus strains compared to the control. The mycosis rate was 88-94% in *T. kanzawai* and 48-59% in *B. tabaci* on collected leaves. These findings suggest that *Beauveria bassiana* AAD16 can be an effective mycoinsecticide against both *T. kanzawai* and *B. tabaci*.

Key words: Biological control, Entomopathogenic fungus, Mycosis rate

O31

Control effect of anion on *Tetranychus urticae* and *Aphis gossypii*

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식물에 전기장을 처리하면 식물의 성장속도가 빨라지거나 영양학적으로 긍정적인 변화가 생긴다고 알려져 있다. 최근 음이온 처리 시 식물에 전기장을 처리한 것과 유사한 효과가 나타난다고 보고되었고 본 연구에서는 이러한 음이온을 온실해충인 점박이응애와 목화진딧물에 처리하여 방제효과 여부를 확인하였다. 그 결과 음이온 처리 시 점박이응애와 목화진딧물에서 살충효과와 기피효과가 나타났다. 또한, 점박이응애 알에서도 음이온 처리가 부화율에 영향을 주는 것을 확인할 수 있었다. 이러한 시험 결과를 바탕으로 온실에서 밀도실험 결과, 700,000 ion/cm³ 농도에서 무처리구에 비해 밀도가 감소함을 확인할 수 있었다. 따라서, 본 연구는 음이온 처리 시, 부가적인 효과로 온실해충(점박이응애, 목화진딧물)에 대해 친환경적 방제 가능성을 보여준다.

검색어: 점박이응애, 목화진딧물, 친환경 방제, 음이온

032

Occurrences of *Orientia tsutsugamushi* infection rates of chigger mites (Acari: Trombiculidae) captured in Yesan, Chungcheongnam-do (2018-2023)

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Orientia tsutsugamushi 에 의해 발생하는 쯤쯤가무시증은 제3급 법정감염병으로 관리되고 있으며, 설치류에 기생한 털진드기 유충에 의해 주로 매개되는 것으로 알려져 있다. 원인균인 *O. tsutsugamushi* 는 Gilliam, Karp, Kato와 같은 표준 혈청형 외에도 유행하는 국가에 따라 30종 이상의 다양한 혈청형이 존재하는 것으로 알려져 있어, 각 지역에 대한 지속적인 조사가 필요하다. 우리 연구진은 야생 설치류에 기생하는 털진드기의 *O. tsutsugamushi* 감염 여부를 확인하기 위해 충남 예산에서 2018년부터 2023년까지 3-4월, 10-11월에 걸쳐 수행하였다. 총 142마리의 설치류가 포획되었으며, Hanging method로 설치류에서 분리된 털진드기는 총 18,347마리였다. 수거된 털진드기의 샘플 중 1/2은 질병관리청으로 이관하였으며, 나머지 절반을 이용하여 *O. tsutsugamushi* 감염 여부를 확인한 결과 2018년 5건, 2019년 2건, 2020년 0건, 2021년 9건, 2022년 0건, 2023년 36건이 확인되었으며, 혈청형 분석 결과 Je-cheon 28건, Young-worl 3건, Boryoung 9건, Koto Akita 1건, Gilliam 2건, Karp 9건으로 확인되었다. 이번 연구를 통해 예산 지역 내 다양한 *O. tsutsugamushi* 혈청형이 있음을 확인하였으며, 이러한 결과는 향후 지역에 따른 혈청형 차이가 반영된 공중보건학적 전략 수립을 위한 기초자료로 활용될 수 있을 것으로 사료된다.

검색어: 설치류, 털진드기, 쯤쯤가무시, *Orientia tsutsugamushi*, 발생 감시

033

Pharyngeal gustatory receptors: Gatekeepers of salt intake in *Drosophila*

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Salt is crucial for survival, yet excessive intake of sodium chloride can have adverse effects. In the fruit fly, *Drosophila melanogaster*, internal taste organs located in the pharynx play a pivotal role in determining whether to accept or reject food. However, our understanding of how pharyngeal gustatory receptor neurons (GRNs) perceive high salt levels is still limited. In this study, we discovered that a specific member of the ionotropic receptor family, *Ir60b*, is selectively expressed in a pair of GRNs that respond to high salt concentrations. Through a two-way choice assay (DrosoX) to measure ingestion volume, we established that IR60b, along with two coreceptors, IR25a and IR76b, is necessary to deter excessive salt consumption. Interestingly, mutants lacking external taste organs but retaining internal taste organs in the pharynx showed significantly higher salt avoidance compared to flies missing all three IRs while still possessing all taste organs. These findings underscore the crucial role of IRs in pharyngeal GRNs in regulating the intake of high salt levels.

Key words: salt, taste, *Drosophila melanogaster*, pharyngeal gustatory receptor neurons, ionotropic receptors

034

Effects of several amino acid residues forming the back door on molecular properties of *Apis mellifera* acetylcholinesterase 1

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Acetylcholinesterase (AChE) is a key enzyme that terminates impulse transmission by rapidly hydrolyzing the neurotransmitter acetylcholine at cholinergic synapses. Previous studies have discovered a transiently opening channel referred to as the “back door” in *Torpedo californica* AChE. Previously, we observed that substituting the Tyr391 residue with a Phe residue significantly decreased the catalytic efficiency of recombinant *Apis mellifera* AChE1 (AmAChE1), while the reverse substitution restored it. Interestingly, substitution of the Tyr391 residue with a Phe residue in AmAChE1 disrupted the formation of the backdoor, while the reverse substitution restored it. This finding suggests that the Tyr-to-Phe substitution impairs backdoor formation, thereby leading to a significant reduction in the catalytic activity of AmAChE1. This serves as one of the driving forces for the functional transition from AmAChE1 to AmAChE2. In this experiment, we also confirmed the gradual restoration and increase in AChE activity by substituting Phe391 in AmAChE1 with Ser, Trp, Thr, Ile, Asn, and Tyr residues through kinetic assay and molecular dynamics simulation.

Key words: acetylcholinesterase, back door, *Apis mellifera*, kinetic assay, molecular dynamics

Detection of *kdr* mutations in local populations of the German cockroach and cloning of sodium channel genes from other cockroach species

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Pyrethroid resistance in cockroach populations has been a public health challenge since the 1950s. The pyrethroid resistance in the German cockroach, *Blattella germanica*, is primarily attributed to knockdown resistance (*kdr*) mutations (E434K, C764R, and L993F) in the voltage-sensitive sodium channel gene (*vssc*). In this study, the pyrethroid resistance state of the German cockroach in the Republic of Korea (ROK) was assessed by analyzing the frequencies of *kdr* mutations using one-step PCR with total RNA. The results revealed that among the 25 populations examined, 14 populations exhibited the L993F *kdr* mutation, while no other mutations were detected. Since other cockroach species are also commonly found in human dwellings in ROK, the *vssc* genes were cloned from four other species, including *Blattella nipponica*, *Periplaneta americana*, *Periplaneta japonica*, and *Periplaneta fuliginosa*. Based on the genomic DNA (gDNA) sequences obtained from the *vssc* cloning, primer sets were designed to amplify the *vssc* fragment spanning the L993F mutation for each species and used to monitor the development of pyrethroid resistance in cockroach populations in the ROK. The study will facilitate the implementation of a nationwide monitoring program to assess cockroach resistance and select suitable alternatives.

Key words: cockroach, *Blattella germanica*, indoor pesticide, pesticide resistance development, pyrethroids, *kdr* mutation

Comparative analysis of genome composition of non-ribosomal peptide synthetases and insecticidal virulence in six *Xenorhabdus* bacterial species

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*Xenorhabdus*와 *Photorhabdus* 속은 각각 곤충병원성 선충인 *Steinernema*와 *Heterorhabditis*에 공생하는 공생세균이다. 감염성 선충의 유충은 공생세균을 표적 곤충의 혈강에 전달하고, 여기서 세균이 증식하여 숙주 선충의 발달을 돕는다. 이러한 선충과 세균 복합체의 성공적 공생관계는 세균의 이차대사산물을 통한 숙주의 면역억제에 달려져 있다고 알려져 있다. 본 연구에서는 서로 다른 살충력을 보이는 6종의 *Xenorhabdus*를 확보하고 이러한 차이가 세균의 성장속도와 NRPS (Non ribosomal peptide synthetase)에 의해 생성되는 세균의 이차대사산물 발현에서 기원한다는 것을 확인하였다. 서로 다른 균주들은 콩명나방 (*Tenebrio molitor*)에 대한 살충력에 차이를 가지고 있었다. 이러한 세균들은 TSB 배지에서는 세균 성장 속도에 차이가 존재하지 않았지만 콩명나방 혈강 내에서는 세균의 성장 속도에 차이가 존재하는 것으로 나타났다. 또한 각 세균의 이차대사산물 추출물을 통한 곤충의 면역억제 실험 결과 PLA₂ 활성 억제, 세포독성 능력들이 살충력과 상관관계가 있는 것으로 나타났다. 이러한 이차대사산물의 경우 많은 물질이 NRPS (Non ribosomal peptide synthetase)에 의해 생성되므로 각 세균 별 NRPS의 유전자 발현을 보았을 때 흥미롭게도 살충력이 더 높은 스트레인의 세균이 일부 NRPS 유전자의 발현이 더 높은 것으로 나타났다. NRPS에 의해 합성되는 물질을 포함한 세균의 이차대사산물의 차이를 서로 비교하기 위하여 이차대사산물 추출액을 GC-MS/MS를 이용하여 분석하였다. 본 연구를 통해 곤충병원세균에 살충력의 기원이 NRPS를 통해 합성되는 이차대사산물에 있다는 것을 확인하였으며 이를 이용한 다양한 NRPS 유래 물질 연구는 신규 살충 물질 개발에 들어가는 비용과 시간을 획기적으로 줄일 수 있을 것으로 기대된다.

검색어: 곤충병원세균, *Xenorhabdus*, 살충력, NRPS

037

An insect with ADHD?: Diet-mediated transgenerational effect on hyperactivity, impulsivity, and diffuse attention in *Riptortus pedestris* (Hemiptera: Alydidae)

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In vertebrates, it is well documented that the parental consumption of high-fat diet increases the risk of Attention-Deficit Hyperactivity Disorder (ADHD) in offspring. While insects have long been used as popular study organisms in various biological research, few studies have explored how the nutritional quality of parental diet affects offspring behavioral phenotypes associated with ADHD in insects. Here we used the bean bug, *Riptortus pedestris* (Hemiptera: Alydidae), as a study organism to test the effect of parental high-fat diet on offspring hyperactivity, impulsivity, and diffuse attention, which are widely held as the three core symptoms of ADHD in vertebrates. Peanut was used as the high-fat diet while soybean was the control. Parental high-fat diet consumption induced hyperactivity in *R. pedestris* offspring. Compared to the controls, the hyperactive offspring of parents fed on high-fat diet were behaviorally more impulsive and less attentive, as they were found to be highly attracted to visual stimuli but losing attention easily. Collectively, these results provide the experimental evidence that the parental consumption of high-fat diet results in increased hyperactivity, impulsivity, and diffuse attention in an insect. This study implies that the well-known association between parental high-fat diet and offspring ADHD is conserved across the tree of life and opens up the new horizons that insects can arise as novel and feasible models for studying the mechanism and evolution of this common neurodevelopmental disorder in humans.

Key words: Parental effect, High-fat diet, Diet quality, Bean bug, Attention-Deficit/Hyperactivity Disorder

038

Environmental risk assessment of DvSNF7 dsRNA in transgenic corn using domestic non-target insect

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전 세계적으로 RNA 간섭(RNA interference, RNAi)을 활용한 해충방제 연구가 활발히 진행되고 있다. 대표적으로 Monsanto의 서부 옥수수 뿌리벌레(*Diabrotica virgifera virgifera*) 특이적 방제용 dsRNA (DvSNF7)를 발현하는 옥수수 종자가 상용화 되었고, 2016년 이 종자가 국내 사료 및 식품용으로 수입이 승인 되었다. 본 연구는 국내에 서식하는 좁은가슴잎벌레(*Phaedon brassicae*)를 Non-target 곤충으로 사용하여, 옥수수 종자에 사용된 DvSNF7 dsRNA의 잠재적 위해성을 평가했다. *P. brassicae*의 SNF7 유전자와 DvSNF7 dsRNA 간 Sequence 유사성을 확인했다. 다음으로 *P. brassicae*가 DvSNF7 dsRNA를 섭식할 수 있는 환경을 조성하여, 치사 효과 실험과 Sequence 특이적인 Knockdown 효과를 확인하였다. 그 결과, DvSNF7 dsRNA는 *P. brassicae* 생존에 영향을 미치지 않았으며, *P. brassicae*의 SNF7 유전자를 Knockdown시키지 않음을 확인했다. 이번 연구를 통해 *D. virgifera virgifera*와 같은 과인 *P. brassicae*는 SNF7 유전자 간 Sequence 유사성이 있지만, Sequence 특이성이 부족하여 생존과 유전자 발현에 영향을 주지 않으므로써 위해성이 낮음을 확인했다.

검색어: 환경안전성평가, RNA interference, dsRNA, DvSNF7, *Phaedon brassicae*

039

First outbreaks of cricket disease in South Korea

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귀뚜라미는 단백질 함량이 높고 필수아미노산이 풍부하여 세계적으로 식용과 사료용 곤충으로서 가치가 높다. 국내에서 쌍별귀뚜라미(*Gryllus bimaculatus*)는 사육이 용이하다는 장점이 있고 주로 파충류, 물고기 등의 사료로 대량 소비되고 있기 때문에 매우 중요한 산업곤충으로 자리매김하고 있다. 그러나 최근 쌍별귀뚜라미의 활동성이 저하되고 다리가 마비되는 등 이상 증상이 발생하여 대량 폐사된 농가가 급증하였다. 이에 대한 원인을 규명하기 위해 질병 발생 농가로부터 귀뚜라미 시료를 수집하여 RNA를 추출하고 metatranscriptomic analysis를 수행하였다. 그 결과, 신규한 덴소바이러스(Densovirus)가 대량 폐사의 원인임을 밝혀내었고, 이 바이러스를 *Gryllus bimaculatus* densovirus (GbDV)로 명명하였다. 또한, GbDV의 유전체 분석 결과, genome size는 5,643 bp로 5개의 ORFs(Open Reading Frames)을 포함하며, 왼쪽에는 세 개의 Non-structural proteins을 포함하는 유전자(NS1, NS2, NS3)가 존재했고 오른쪽에는 두 개의 Structural proteins을 포함하는 유전자(VP1, VP2)가 존재했다. 본 연구는 알 수 없는 곤충 질병의 원인을 밝혀내어 해당 질병에 대한 모니터링을 가능케 함으로써 산업곤충 질병의 예찰하고 확산을 방지하는 데 기여할 것으로 사료된다.

검색어: 귀뚜라미, 쌍별귀뚜라미, Densovirus, *Gryllus bimaculatus* densovirus, GbDV

040

Development of Thrips-cide dsRNA and its application to hot peppers

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RNA interference (RNAi) has been applied to control insect pests using gene silencing machinery in which small interfering RNA derived from dsRNA specifically degrades target mRNA. This study optimized dsRNA insecticide specific to thrips infecting hot peppers. Among potent candidate target genes, *vATPase B* was chosen because its RNAi was highly efficient as much as *Snf7*, a well-known RNAi target gene. Although RNAi specific *vATPase B* is lethal to *Frankliniella occidentalis*, it was not much effective to control other thrips species such as *F. intonsa* and *Thrips tabaci*. To expand its target spectrum, we devised a mixture treatment of dsRNA specific to individual species. As expected, each dsRNA was highly efficient in a species-specific manner. This supported the hypothesis of 21mer identity for the efficient RNAi. However, the dsRNA mixture efficiently killed the three thrips species in a crop field. To further expand its spectrum to the whitefly, *Bemisia tabaci*, we applied virus-induced gene silencing (VIGS) to produce dsRNA in the hot peppers using Tobacco Rattle Virus. VIGS successfully suppressed control gene. dsRNA produced by VIGS gave significant mortality to *B. tabaci* in addition to the thrips. These results suggest a technique to expand dsRNA insecticide spectrum using a mixture treatment and VIGS in insect pest control.

Key words: dsRNA insecticide, Thrips species, *vATPase B*, VIGS, *Snf7*.

O41

Effect of a commensal bacterium, *Bacillus subtilis*, on insect immune priming

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Although insects lack the adaptive immunity characteristic of vertebrates, certain species exhibit enhanced subsequent immune responses upon re-encountering a pathogen, a phenomenon known as immune priming. The underlying mechanism of this phenomenon is still elusive. This study evaluated the immune priming of the diamondback moth, *Plutella xylostella*, induced by a nonpathogenic and commensal bacterium, *Bacillus subtilis*. Prior exposure of *P. xylostella* to *B. subtilis* significantly increased survival against a pathogenic bacterium, *Bacillus thuringiensis*, compared to larvae without pre-exposure. To extend the effect of the microbial commensals, two antibiotics, ampicillin and kanamycin, were treated to suppress their populations. In the axenic-like condition in the gut, cellular and humoral immune responses were significantly suppressed. An addition of *B. subtilis* to the diet of *P. xylostella* significantly enhanced the immune responses. Apolipoprotein D, known as a lipid carrier, acts like a vertebrate lipocalin in the immune priming of the other insect, *Spodoptera exigua*. The ortholog of this gene has been identified in *P. xylostella*, and its expression was induced upon *B. subtilis* treatment. This study sheds light on the potential role of commensal gut microbes, including *B. subtilis*, in the immune priming of these insects.

Key words: Immune priming, *Bacillus subtilis*, *Plutella xylostella*, nodulation, antimicrobial peptide

O42

History and current state of Korean forensic entomology

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법곤충학은 곤충과 관련된 법적 문제를 해결하는 학문으로써, 미국, 유럽, 한국 등 다양한 국가에서 범죄 수사, 사후경과시간 추정 등에 활용되고 있다. 한국은 최근, 법곤충감정실(경찰청) 개소하여 전국의 법곤충 사건을 감정하고 있다. 한국은 짧은 연구역사를 가짐에도 불구하고, 중앙행정기관 산하의 법곤충감정실을 설립, 운영할 수 있는 것은, 그 특이적인 연구역사에서 기인했다. 한국 법곤충 연구는 2004년경부터 시작되었으나, 중앙행정기관(경찰청, 국립과학수사연구소, 농림축산검역본부)의 투자로 연구개발이 진행되었다. 특히, 한국의 경찰청은 2016-2020년과 2022-2026년, 10년간의 연구과제 발주를 통해 현장 중심의 법곤충 감정 시스템 구축, 비전문가를 위한 형태 및 분자 유전학적 종 동정 기법 개발, 한국형 DB 확보 등을 진행하고 있으며, 법곤충 감정기법의 세계적인 선도를 목표로 하고 있다.

검색어: 법곤충학, 범죄 수사, 사후경과시간 추정, 법곤충감정실, 법곤충 감정기법

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Seasonal and habitat impacts on biodiversity of forensically important blowflies (Diptera: Calliphoridae) in Gyeongsangnam-do, South Korea

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The study of blowfly (Diptera, Calliphoridae) biodiversity and distribution is crucial for forensic investigations involving cadavers. Abiotic and biotic factors, such as seasonality and habitat type, have significant impacts on blowfly populations. However, few forensic entomology studies have been conducted in South Korea, particularly the Gyeongsangnam-do region. To address this, in this study, an extensive year-long survey was conducted to analyze the compositions, habitat preferences, distribution, and seasonal abundance of forensically relevant blowflies in urban and forested habitats in Gyeongsangnam-do, utilizing mouse carcass-baited traps set for 48 h each month. A total of 3,478 adult blowflies were recorded, encompassing six genera and 14 species, with a noted absence of specimens during the winter months. The predominant species was *Lucilia porphyrina*, accounting for 37.1% of the total sample, followed by *Chrysomya pinguis* (27.5%), *Lucilia sericata* (7.6%), and *Lucilia illustris* (7.1%). The species composition was consistent across all surveyed regions; however, seasonal variation in species diversity was evident, with a peak in spring and decline in summer. Notably, certain species exhibited clear preferences for either urban (*Calliphora calliphoroides* and *L. sericata*) or forested habitats (*L. porphyrina* and *Ch. pinguis*). This pioneering study elucidates the diverse blowfly communities in Gyeongsangnam-do, highlighting significant seasonal and habitat-dependent variations.

Key words: forensic entomology, Calliphoridae, season, habitat, bait trap, community composition

O44

Influence of micro-environmental factors on decomposition and insect colonization

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This study explores the significant influence of micro-environmental factors on carcass decomposition and insect colonization, with a particular emphasis on detailed insect community analysis. The research employed an innovative approach by placing two pig carcasses in contrasting environments that one in a sunlit open field and the other in a shaded forest. The findings revealed dynamic shifts in insect diversity in the sunlit area, characterized by a rapid increase followed by a decrease, in contrast to the more steady, gradual changes observed in the shaded area. This contrast highlights the sensitivity of insect communities to even minor changes in environmental conditions like sunlight and temperature. It unveils the nuanced ways in which such factors shape the composition and dynamics of insect communities. These insights are crucial for the field of forensic entomology, enhancing the accuracy of post-mortem interval estimations. By providing a clearer understanding of how different micro-environmental conditions influence insect activity and decomposition processes, this study significantly contributes to the refinement of forensic methodologies.

Key words: forensic entomology, insect community dynamics, micro-environmental factors, post-mortem interval estimation

045

Forensic entomology in South Korea: Cataloging insect species for legal investigations

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This study aims to identify insect species relevant to medicolegal entomology in South Korea, to develop valuable forensic indicators for addressing legal challenges. We conducted carcass experiments with animals from 2015 to 2023 and analyzed domestic medicolegal literature. Species with uncertain taxonomic status or those recorded only once in experiments or literature were excluded. Our dataset includes observations from 185 carcasses, 24 criminal cases, and 468 autopsies. We identified a total of 254 carcass-associated species across 67 families and 8 orders. Of these species, 32 species consistently found on both human corpses and animal carcasses, suggesting their significance in forensic contexts. The order Diptera, comprising 53.13% of these taxa, was predominantly represented by the families Calliphoridae (70.59%), Muscidae (17.65%), and Sarcophagidae (11.76%). Coleoptera constituted 46.87% of the identified taxa, with the families Silphidae (53.33%), Dermestidae (26.67%), Cleridae (6.67%), Scarabaeidae (6.67%), and Staphylinidae (6.67%) being most significant. *Lucilia sericata* was the most frequently found species in autopsies of corpses found indoors (51.95%) and outdoors (14.77%), followed by *Phormia regina*, *Chrysomya megacephala*, *Chrysomya pinguis* and *Lucilia illustris*, highlighting their potential as forensic markers. This comprehensive study provides crucial baseline data for medicolegal entomologists in South Korea, identifying key insect species as forensic indicators.

Key words: Forensic Entomology, Medicolegal Investigation, Autopsy, Diptera, *Lucilia sericata*

046

Taxonomic review of the family Ptiliidae (Coleoptera: Staphylinoidea): The smallest known beetles in Korea

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The family Ptiliidae, also called featherwing beetle because of their remarkable feather-like hind wings, is group of the smallest beetles, with their body size generally about 1 mm long. Although more than 1,000 valid ptiliids within approximately 100 genera are distributed worldwide, this family remains one of the least understood beetle groups in Korea. In this study, we introduce 13 known Korean ptiliids species within seven genera and additional some unknown species. All available information about Korean ptiliids, including their natural histories, distributional data, and diagnostic characters are provided.

Key words: taxonomy, featherwing beetles, soil insects, Korean Peninsula

047

Taxonomic review of the genus *Bucculatrix* Zeller, 1839 (Lepidoptera: Bucculatricidae) in Korea

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This study was conducted to review the genus *Bucculatrix* Zeller, 1839 belonging the family Bucculatricidae. In Korea, only three species have been reported to date (Park, 2013; Lee and Jeun, 2022; 2023). A total nine species were identified in Korea in this study. Among them, two species, *Bucculatrix* sp. nov.1 and *B. sp. nov.2* was described as new to science. Also four species: *B. duanwuia* Liu, 2020, *B. tsurubamella* Kobayashi, Hirowatari & Kuroko, 2010, *B. demaryella* (Duponchel, 1840) and *B. comporabile* Seksjaeva, 1989 are reported for the first time from Korea. These species were identified by visiting Osaka Metropolitan University and comparing the specimens. Available information, host plants, images of adults and genitalic structures, and DNA barcode for the species are provided.

Key words: Bucculatricidae, *Bucculatrix*, leafminer, taxonomy, Korea

048

Review of the family glyhipterigidae (Lepidoptera: Yponomeutoidea) in Korea

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The family Glyhipterigidae comprises more than 500 described species worldwide. In Korea, only 11 species of 4 genera under 2 subfamilies recorded. In this study, a total of 16 species were discovered, including 5 new recorded species. The new recorded species discovered are as follows; *Glyhipterix euleucotoma* Diakonoff & Arita, 1976, *G. gamma* Moriuti & Saito, 1964, *G. gemmula* Diakonoff, 1976, *G. mikadonis* Arita & Owada, 2006 and *G. semiflavana* Issiki, 1930. All available information, adults and genital images structures are provided.

Key words: Glyhipterigidae, Acrolepiinae, Glyhipteriginae, new record, Korea

049

Taxonomic notes of genus *Pidonia* Mulsant (Coleoptera: Cerambycidae: Lepturinae) from Korea with a new record

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A total of 187 species are involved in the genus *Pidonia* Mulsant (Coleoptera: Cerambycidae: Lepturinae) worldwide, of which 174 species are distributed in Eurasia. Since Bates recorded *P. (P.) gibbicollis* in 1888, a total of 17 species have been recorded in Korea. After An & Kwon's study on Korean *Pidonia* in 1991, no taxonomic study has been carried out for almost 30 years, making it difficult to identify the species due to their mutations. In this presentation, we provide an update on the taxonomic study of Korean *Pidonia* and report a newly recorded species, *P. (P.) obscurior hakusana*, in Korea.

Key words: Cerambycidae, Coleoptera, Korea, new record, *Pidonia*

050

Two new records of Chalcididae (Hymenoptera, Chalcidoidea) from Korea

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The Chalcididae belong to a medium-sized family of parasitoids in the superfamily Chalcidoidea (Hymenoptera). Chalcidids can be recognized by the swollen hind femur, the indistinct prepectus, the sharp occipital carina bordering the gena posteriorly, and the strong punctation of the mesosoma. They have been recorded parasitizing six insect orders, and several species are facultative or obligate hyperparasitoids. More than 1,500 species in 90 genera have been recorded worldwide, of which 12 species in six genera have been recorded in South Korea. As a result of taxonomic and faunal studies on Korean Chalcididae, we have found two newly recorded species, *Haltichella nipponensis* Habu and *Dirhinus anthracia* Walker, in Korea. These species were discovered using Malaise traps, Lindgren funnel traps, and observation with the naked eye in Jeonbuk, Gangwon province, and Sejong city in 2023. The genus *Haltichella* Spinola, 1811, is recorded in Korea for the first time. In this presentation, we provide morphological and ecological information on these species.

Key words: Chalcid wasp, *Haltichella*, *Dirhinus*, new record, South Korea, taxonomy

051

First complete molecular phylogeny of the subfamily Delininae (Diptera: Scathophagidae)

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Scathophagidae, commonly known as dung flies, is a small dipteran family of Muscoidea and is the sister group of Anthomyiidae. Currently, there are 373 described species distributed across 47 genera worldwide. Scathophagidae is subdivided into two subfamilies, Scathophaginae and Delininae. Notably, Delininae is characterized by tergite 6 short, bare, and firmly fused with syntergosternite 7+8. Delininae includes five genera and one uncertain genus with around 26 species described to date. Taxonomic instability within Delininae has been raised by notable inconsistencies, particularly evident in the classification of genera of *Americina* Malloch, 1923, *Parallelomma* Becker, 1894, and *Leptopa* Zetterstedt, 1838. These disparities necessitate a systematic reevaluation to rectify taxonomic uncertainties, acknowledging the nuanced variations introduced by different taxonomists. To address these taxonomic conundrums within Delininae, molecular approaches were employed, using three mitochondrial genes (16S, Cytb, COIb) and three nuclear genes (28S, Efla, Pol II). Phylogenetic analysis was conducted by maximum likelihood and Bayesian methods to elucidate the comprehensive phylogenetic relationships within Delininae. Particularly, this study includes previously unexplored genera, namely *Neochirosia* Malloch, 1917 and *Micropselapha* Becker, 1894, and uncertain genus *Synchysa* Vockeroth, 1987, encompassing all genera in Delininae. The incorporation of all taxa contributes to a more thorough understanding of the evolutionary history within Scathophagidae, shedding light on previously overlooked aspects of its phylogenetic landscape.

Key words: Delininae, Multigene phylogeny, Scathophagidae

052

Phylogeographic relationships of the wild silkworm, *Bombyx mandarina* (Lepidoptera: Bombycidae), inferred from mitochondrial genome sequences

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Bombyx mandarina (Lepidoptera: Bombycidae), the presumed ancestor of the domesticated silkworm *B. mori*, has long been a subject of study to illustrate the geographic relationships in connection with origin of *B. mori*. We sequenced 100 mitochondrial genomes of *B. mandarina* collected from South Korea and Japan and these were combined with public data. Phylogenetic and population genetic analyses showed that all individuals collected in South Korea, except one individual from Inje, formed a strong group together with northern China and some individuals of southern China. This group was placed as the sister group to *B. mori* strains, suggesting that this group could have been served as an immediate progenitor for *B. mori*. For further robust inference more analysis is underway.

Key words: mitochondrial genome, *Bombyx mandarina*, wild silkworm, phylogeny, population structure, biogeographic

053

Comparative population genetics of the oriental fruit fly, *Bactrocera dorsalis*, using mitochondrial molecular markers

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The oriental fruit fly, *Bactrocera dorsalis*, is highly polyphagous pest that damages over 400 plant species, including commercially grown crops and fruits. It was first described in Taiwan and has since invaded Japan and China. In 2021, *B. dorsalis* was reported on Jeju Island in the Republic of Korea (ROK). To investigate its origin and understand its colonization pathway in ROK, the genetic characteristics were analyzed by using mitochondrial genes. The study analyzed the haplotypes and genetic differences among populations oriental fruit flies collected from Southeast Asia, including Thailand, Taiwan, and Vietnam. The mitochondrial genes cytochrome oxidase subunit I (COI) and cytochrome B (CytB) were used for the analysis. The results showed that *B. dorsalis* had high levels of haplotype diversity among species. No major haplotype was found among populations. The present study enhances our understanding of the haplotype diversity of *B. dorsalis* in neighboring countries of ROK. This will expand our knowledge of the source of origin and invasive pathway for *B. dorsalis*.

Key words: *Bactrocera dorsalis*, population genetics, mitochondrial gene

054

Spelaeochthonius - past, present, and future of pseudoscorpions

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Spelaeochthonius Morikawa, 1954, which comprises 11 species, is a genus in the family Pseudotyranchochthoniidae Beier, 1932. Members of this group can be represented by troglitic characteristics and narrow-range endemism. Three species are documented on the Korean Peninsula: *Spelaeochthonius cheonsooi* You, Yoo, Harms and Harvey, 2022; *S. dentifer* Morikawa, 1970; *S. seungsookae* You, Yoo, Harms & Harvey, 2022. In this study we utilize ten species, including three recorded Korean species, two Japanese species, and five new species, for molecular analysis. We employ four genes (COI, H3, 18S, 28S) commonly used in pseudoscorpions studies. This study aims to (i) identify the most specific gene for species identification in pseudoscorpions, (ii) demonstrate the narrow-range endemism of *Spelaeochthonius*, and (iii) explore the speciation pathway of this genus. Consequently, our understanding of biodiversity and necessity of species conservation.

Key words: biodiversity, biogeography, conservation, false scorpion, phylogeny

055

Beyond morphology: 3D modeling approach to species diversity in Stathmopodidae

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Over 350 species of Stathmopodidae have been reported worldwide, but due to their morphological similarities, there are many difficulties in species identification. To address these issues, various methods including larval, behavioral ecology, molecular techniques, and others have been utilized. In this study, we compared the resistance to pressure based on wing venation, which has not been extensively covered before, to further elucidate the differences between species. Type species, and one species from the genus reported in Korea, this study utilized Fusion 360 to create 3D models and visually represented resistance under the same pressure with colors. Colors derived from simulation results are extracted for trend analysis using PCA (Principal Component Analysis), and differences between groups formed through K-means clustering are analyzed.

Key words: Stathmopodidae, wing venation, 3D model

056

Revisiting Šípek *et al.* (2016): evolutionary analysis for flower chafers and its current status of phylogenetic study (Coleoptera: Scarabaeidae: Cetoniinae)

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Flower chafers (Coleoptera: Scarabaeidae: Cetoniinae) are globally distributed, comprising approximately 4,000 described species. They primarily feed on nectar and sap of deciduous trees. The larvae exhibit the unique characteristic of crawling on their backs, distinguishing them from other scarabs. Additionally, the majority of flower chafers fly with their elytra closed, unlike other scarabs that fly with fully opened wings. Šípek *et al.* (2016) conducted the first molecular phylogenetic study to investigate their phylogenetic relationships and characters of elytra related to the flight mode. Building upon this study, we infer the diversification times and rates of Cetoniinae and its subgroups, and reconstruct the evolutionary process of flight mode transformation. Furthermore, we discuss the current limitations and future directions of this topic.

Key words: flower chafer, Cetoniinae, phylogenetics, phylogenetic comparative methods, macroevolution

057

Revision of subfamily Calonecrinae (Coleoptera: Cucujoidea: Nitidulidae), systematics and natural history of a mysterious group

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Calonecrinae represent a unique but small subfamily of Nitidulidae that is endemic to South Asia. Their habitats, the South Asian lowland forests, are under the imminent threat of degradation, posing a risk of rapid extinction for these species in their specific locales. Despite the looming threat to their existence, our understanding of this enigmatic group remains limited. We conducted an examination of museum and newly collected specimens, alongside a review of the literature, leading to the discovery of a new species, *Calonecrus mindanaoensis*, from Mindanao, Philippines. For the first time, the morphology of all immature stages of the Calonecrinae was described, with detailed photographs including SEM images. Additionally, their natural history was uncovered for the first time, revealing that all life stages are uniquely adapted to spending their entire life cycle within sticky resin. We re-evaluated the phylogenetic placement of the Calonecrinae by constructing a phylogenetic tree based on the mitochondrial genome. Calonecrinae are positioned within the Epuraeinae clade and show significant affinity with the genus *Trimenus*. Consequently, this study proposes reclassifying Calonecrinae as Calonecrini stat nov, an extremely modified tribe within the Epuraeinae.

Key words: Coleoptera, Nitidulidae, Calonecrinae, phylogeny, immature stage

O58

Updated genome assembly of *Diadegma fenestrata* (Hymenoptera: Ichneumonidae), and its symbiotic virus DfIV

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Chromosomal level of Korean *Diadegma fenestrata* (Jeju strain, JK-2023a) of genome assembly was achieved through a combined approach utilizing Nanopore long-read sequencing and Illumina NovaSeq short-read sequencing (approximately 217.2× coverage). The assembled genome spans 221.1 Mb, comprises 68 scaffolds, with most of the genome contained within 11 chromosomal level scaffolds. The completeness of the assembly is reflected in BUSCO assessment, with values reaching 99.6%. Scaffold N50 was 17.4 Mb, and GC % was 40%. RNAseq was performed using RNA extracted from larvae, pupae, and adults at various developmental stages (trimmed RNA-Seq data, 11.3 Gb), and a total of 13,544 genes were predicted by synthesizing the transcriptome information with the annotation information of five closely related species such as, *Campoletis sonorensis* (GCA_013761285.1), *Venturia canescens* (GCF_019457755.1), and *Nasonia vitripennis* (GCF_000002325.3, and GCF_009193385.2). Of these, 13,498 genes were identified by BLAST and are being further analyzed. Although the frequency of DfIV genome integration into the host's 11 chromosomes varies from 0 to 32%, it was confirmed that all 62 DfIV genome fragments were inserted into the Hymenopteran host genome.

Key words: polydnavirus, koinobiont, Campopleginae, coevolution, host adaptation

O59

Tunnel specialization in termites: why do they never switch tasks during tunneling?

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This study investigates the phenomenon of task specialization in subterranean termites, focusing on their tunneling behavior. Termites, known for their complex social structure, allocate specific individuals for tunnel construction, rarely switching tasks. To explore this behavior, we developed a simulation model comparing termite groups with and without task shifts. While tunnel orientation showed no significant difference between the two tunnel pattern groups, the absence of task shifts resulted in larger tunnels, indicating enhanced foraging efficiency. This suggests that maintaining a consistent division of labor without task rotation benefits termite foraging. This study sheds light on the ecological advantages of task specialization in social insects, highlighting its role in foraging success and colony survival.

Key words: termite, labor division, tunnel pattern, individual-based model

O60

Neuropeptide modulation of female sexual drive through pC1 neurons and pyrexia TRP channel in *Drosophila melanogaster*

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동물의 종 유지에 있어서 교미행동은 매우 중요한 위치를 차지함. 교미과정에서 수컷의 경우 모든 암컷에 대해 성행동을 보이는 반면, 암컷은 가장 적절한 교미의 시기를 정하며, 적절한 수컷을 선택하고 교미행동을 보이기 때문에 암컷의 교미행동을 유도하는 과정은 생물학에서 매우 중요한 의미를 지님. 본 연구에서는 초파리 (*Drosophila melanogaster*) 전자현미경자료와 총신경망분석 (Connectomics)을 이용하여 초파리 뇌에서 암컷의 교미행동을 조절하는 것으로 알려진 pC1 신경의 하부신경 pC1b,c가 성적 성숙과정에서 교미를 하고자 하는 욕구 (sexual drive)를 증가시키는 기능을 하는 것을 처음으로 밝힘. 본 연구에서는 처음으로 pC1b,c 신경 내의 cAMP 수준이 교미의 욕구변화를 보여주는 중요한 물질이라는 것을 밝혔고 cAMP의 수준이 오르기 위해서는 신경펩티드인 Dh44와 그 수용체 GPCR인 Dh44R1과 Dh44R2가 필요하다는 것을 확인함. 또한 cAMP의 변화는 신경내의 CREBB를 통하여 하위 유전자인 pyx (pyrexia)의 발현을 유도한다는 것을 밝힘. 본 연구로 종 유지 메커니즘을 좀 더 이해할 수 있음.

검색어: 초파리, 교미행동, GPCR, pC1

O61

The central brain neurons play a role in the quicker removal of male ejaculate by *Drosophila* females in response to male pheromones

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From invertebrate to vertebrate, females uptake sperm for a specific duration post-copulation known as the ejaculate holding period (EHP) before expelling un-stored sperm and the mating plug through sperm ejection. Our study uncovered that encountering males or mated females after mating substantially shortens EHP, a phenomenon we term ‘male-induced EHP shortening (MIES)’. MIES requires Or47b⁺ olfactory and ppk23⁺ gustatory neurons, activated by 2-methyltetracosane and 7-tricosene, respectively. These odorants raise cAMP levels in pC1b and c neurons, which are responsible for processing male courtship and regulating female receptivity. Elevated cAMP levels in pC1b and c reduce EHP and reinstate their responsiveness to male courtship cues, promoting re-mating with faster sperm ejection. This study establishes MIES as a genetically tractable model of sexual plasticity with a conserved neural mechanism.

Key words: sperm ejection, cAMP, pC1, Or47b, ppk23, 2-methyltetracosane, 7-tricosene

062

Genome analysis of volvovirus isolated from *Gryllus bimaculatus* in South Korea

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한국 귀뚜라미 산업은 최근 큰 성장을 보였으며, 수직농장을 이용한 대량생산과 기술발전으로 사육수와 판매량이 늘어나는 추세다. 그러나 귀뚜라미 사육시스템은 농가 간의 교류 및 밀집 사육으로 인해 곤충병원체에 의한 전염병에 매우 취약한 구조를 가진다. 사육 곤충의 질병을 이해하는 것이 중요함에도 곤충병원성 미생물에 대한 연구가 부족한 실정이다. 본 연구는 국내 쌍별귀뚜라미 농가에서 발견된 볼보바이러스를 식별하였으며, *Gryllus bimaculatus* volvovirus (GbVVV-KR)의 계놈 특성을 분석하였다. GbVVV-KR의 전체 계놈 서열은 Sanger 시퀀싱을 통해 얻어졌으며, 계놈 크기가 2,515개 뉴클레오티드인 원형 단일가닥 DNA 바이러스임을 밝혔다. 단일 핵산 염기 다형현상 분석(Single nucleotide polymorphism, SNP)으로 정지코돈 돌연변이로 인한 ORF3 영역이 다른 귀뚜라미 volvovirus 들에 비해 큰 변화를 확인하였다. 또한, 전국 11개 농장에서 수집한 귀뚜라미를 대상으로 PCR/qPCR을 실시하여 GbVVV-KR의 감염 정도를 확인하였다. 이러한 결과는 GbVVV-KR의 계놈 구조와 유전적 특성, 계통발생 및 유병률에 대한 귀중한 통찰력을 제공하고 귀뚜라미 바이러스에 대한 이해를 도울 것으로 기대한다.

검색어: 쌍별귀뚜라미, 볼보바이러스, 유전체 분석, 유병률 조사

063

Ecological predictions using AI in the era of big data to advance pest management

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As new AI techniques are developed and various types of big data accumulated, new approaches for pest management are also being attempted. Various spatio-temporal scale big data are being accumulated, and attempts are being made to utilize them to classify target objects and analyze their characteristics. Remote sensing data is widely used across various fields, and is being measured, stored, and shared in diverse formats. Hyperspectral imaging and satellite data are ecologically relevant big data, with distinct formats and potential applications. We will introduce real-world AI examples of utilizing hyperspectral image analysis, as well as estimating pest population density using satellite data.

Key words: remote sensing, hyperspectral image analysis, satellite data, machine learning

O64

Differences in seasonal dynamics and pyrethroid resistance development among *Anopheles* Hyrcanus Group species

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Six mosquito species in the *Anopheles* Hyrcanus group are known as vectors responsible for transmitting vivax malaria in South Korea. In this study, seasonal dynamics of *Anopheles* Hyrcanus group species and knockdown resistance (*kdr*) mutations in malaria-endemic sites, Paju and Gimpo, were monitored over two years. In August 2023, all six species were observed simultaneously in one of the Paju collecting sites, and *kdr* mutations were newly identified in all species except *Anopheles kleini*. Although *Anopheles pullus* was revealed as a relatively resistant species among five species populations without *kdr* mutation via bioassays, there were no critical differences in the voltage-sensitive sodium channel sequence. These findings suggest variability in pyrethroid resistance mechanisms among *Anopheles* Hyrcanus Group species.

Key words: *Anopheles* Hyrcanus Group, pyrethroid resistance, *kdr* mutation, seasonal dynamics

O65

The effects of protein and carbohydrate intake on lifespan and reproduction in the yellow mealworm beetle, *Tenebrio molitor*

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The yellow mealworm beetle, *Tenebrio molitor* L. (Coleoptera: Tenebrionidae), has long been used as a key study organism in many fundamental researches, including biochemistry, physiology, and behavior. Lifespan and reproduction are two of the most important components of fitness in all insects, but it remains largely unexplored how these two traits are influenced by macronutrient intake in this beetle. In this study, we used the nutritional geometry framework to analyze the complex and interactive effects of dietary protein and carbohydrate intake on lifespan and reproductive performance in *T. molitor* beetle. Lifespan and the number of eggs laid throughout the lifetime were quantified from more than 2,000 individual beetles provided with one of 35 chemically defined diets representing a full combination of seven protein-to-carbohydrate ratios (P:C= 0:1, 1:5, 1:2, 1:1, 2:1, 5:1, or 1:0) and five protein plus carbohydrate concentrations (P+C=25.2, 33.6, 42, 50.4, or 58.8 %, dry mass). All measures of lifespan and egg production were expressed highly at high caloric intake, but they differed in the optimal P:C ratio where traits peaked. While lifespan was the longest at a moderately carbohydrate-biased P:C ratio of 1:1.36, the rate of egg production was maximized at a protein-biased P:C ratio of 1.75:1, suggesting a possible nutrient-mediated trade-off between lifespan and daily reproductive efforts in *T. molitor* beetles. Lifetime egg production was maximized at a P:C ratio of 1.31:1, which was still protein-biased but lower than that maximized egg production rate. Reproductive lifespan was the longest at a P:C ratio of 1:1.06. When given a food choice, *T. molitor* beetles preferred a P:C ratio of 1:1, which is closest to the ratio that enables *T. molitor* beetles to stay reproductively active as long as possible.

Key words: Fecundity, Longevity, Macronutrient, Nutritional geometry, *Tenebrio molitor*

O66

Revision of the monotypic New Zealand genus *Adalmus* Reitter (Staphylinidae: Pselaphinae) with six new species

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Six new species are described that are members of the New Zealand endemic genus *Adalmus* Reitter (Staphylinidae: Pselaphinae: Euplectitae: Trichonychini: Panaphantina): *A. bullerensis* **sp. nov.**, *A. kanierensis* **sp. nov.**, *A. karekarensis* **sp. nov.**, *A. mangamukaensis* **sp. nov.**, *A. puberilumbus* **sp. nov.**, and *A. serrilumbus* **sp. nov.** In addition, *Dalmisus* Sharp is placed as a junior synonym of *Adalmus* (gen. syn.) and the species *Dalmisus batrisodes* Sharp, 1886, *Plectomorpha longiceps* Broun, 1913 and *P. longipes* Broun, 1912 are placed as junior synonyms of *A. velutinus* Reitter, 1885 **spp. syn.** Also, *P. rugiceps* Broun, 1921 is transferred to the genus *Adalmus*, **comb. nov.** *Adalmus* now holds eight species.

Key words: taxonomy, ant-loving beetles, Trichonychini, Panaphantina, new synonymies, new combination.

O67

Molecular phylogenetics and biogeographic studies of the subgenus *Nialoe* s. lat. (Coleoptera: Carabidae: *Pterostichus*)

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Nialoe Tanaka, 1958 is a subgenus of the ground beetle genus *Pterostichus* (Coleoptera: Carabidae), endemic to East Asia. In a wide sense of *Nialoe*, it consists of more than 200 species, which has reduced hindwing and possibly diversified by geographical isolation due to poor dispersal ability. To understand this vast group, phylogenetic studies have been conducted, showing that *Nialoe* s. lat. comprises of five subgenera: *Nialoe* s. str., *Sphodroferonia*, *Koreonialoe*, and two unnamed subgenera. However, there is little knowledge regarding their origin and dispersal. In this study, we examine phylogenetic relationships among the five subgenera of *Nialoe* s. lat. based on 28S rRNA, wingless, COI, and 16S rRNA. The molecular clock and S-DIVA analyses are devised to investigate the biogeographical history of the group in East Asia. This study may give insight into the biogeographical dispersal and diversification of East Asian carabids.

Key words: ground beetle, Pterostichini, phylogeography

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Molecular systematics of Bythinini Raffray of Korea with two new species (Coleoptera: Staphylinidae: Pselaphinae)

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The tribe Bythinini Raffray is species-rich pselaphine group including over 600 species distributed worldwide. Despite its diversity, only one genus, *Bryaxis* Kugelann, has been reported in Korea. In this study, we newly describe *Bryaxis* sp. n. mainly based on the male antennal modification. We also report a new species of the genus *Tychobythinus* Ganglbauer from Korea. Members of these two bythinine genera are commonly characterized by the traits of maxillary palpi: elongated second palpomere, shortened penultimate, and enlarged last one. In addition, we conducted phylogenetic analyses to demonstrate the relevance between antennal modification and evolutionary relationship of *Bryaxis*. To perform the phylogenetic construction, we assembled three mitochondrial genes (*cox1*, *cox2*, and *16S*) and three nuclear genes (*18S*, *28S*, and *wingless*) into a dataset. Eleven species of *Bryaxis* and two *Tychobythinus* species are included, the latter genus of which are used to root the consensus trees.

Key words: new species, new record, phylogeny, Goniaceritae, Korea

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Taxonomic study on eight species of mature larvae of Genus *Vespa* (Hymenoptera: Vespidae) from South Korea

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The genus *Vespa* consists of 22 species worldwide, and their phylogenetic relationships are well established through adult morphology and molecular analyses. However, taxonomic studies of larvae are lacking. In this study, we provided descriptions and taxonomic keys for eight species of Korean *Vespa* larvae.

Key words: Vespidae, *Vespa*, larvae, taxonomic key