

A-01

## **New species of *Asphalmus* (Curculionidae: Entiminae) from Gangwon Province, Korea**

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Weevils are known as economic and agricultural pests. Additionally, many entimine beetles are also known to cause harm in agriculture. On the other hand, soil-dwelling entimine beetles are known as detritivores, feeding on leaf litter and contributing to soil decomposition. The subfamily Entiminae is the largest group among the family Curculionidae. The genus *Asphalmus* Sharp comprises 45 species, with only two species [*Asphalmus japonicus* Sharp and *Asphalmus kostali* Borovec] recorded in Korea, while the rest are found in Japan. All these species are known as inhabiting leaf and soil litter. While examining of entimine specimens, we distinguished 20 specimens that do not share diagnostic characters with existing *Asphalmus* species. New species can be identified by the following characters: Reddish-brown body color, elongated body form, absence of teeth on all femora, and the form of male genitalia and female spermatheca.

**Key words:** broad-nosed weevil, Entiminae, new species, Gangwon province

A-02

## **A taxonomic review of the genus *Caenoscelis* C. G. Thomson (Coleoptera: Cucujoidea: Cryptophagidae) in Korea with description of a new species**

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The genus *Caenoscelis* C. G. Thomson (Coleoptera: Cryptophagidae: Cryptophaginae) comprises approximately 30 species in the world, primarily distributed in the Holarctic region. Although 15 *Caenoscelis* species occur in the Palearctic region, only a single species, *Caenoscelis sibirica* Reitter, has been documented in Korea. In this study, *Caenoscelis koreanus* sp. nov. is described, and *Caenoscelis ferruginea* (C. R. Sahlberg) is reported for the first time in Korea. The new species can be distinguished from other *Caenoscelis* species by their subquadrate antennomere 10, fully developed hind wings, and male genitalia with subacute parameres and indistinctly separated lateral lobes. Illustrations of habitus, diagnostic characters, and a distribution map of Korean *Caenoscelis* species are provided.

**Key words:** Asia, new records, Palearctic, silken fungus beetle, taxonomy

A-03

### Seven species of the family Cryptophagidae (Coleoptera: Cucujoidea) new to Korea

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The family Cryptophagidae Kirby (Coleoptera: Cucujoidea) comprises minute beetles, with approximately 800 described species within about 50 genera worldwide. Most members of this family are found in moldy environments and feed on fungal spores and hyphae. The Korean cryptophagid fauna is poorly known, consisting of 22 species belonging to 8 genera. In this study, seven species of Cryptophagidae reported for the first time in Korea: *Atomaroides ussurica* (Lyubarsky), *Cryptophagus micaceus* Rey, *Cryptophagus pumilus* Reitter, *Cryptophagus zonatus* Lyubarsky, *Henoticus pilifer* Reitter, *Micrambe (Micrambinus) bimaculata* (Panzer), and *Serratomaria vulgaris* Sasaji. Illustrations of habitus, male genitalia, and collection localities of these seven species are provided.

**Key words:** Asia, new records, Palearctic, silken fungus beetle, taxonomy

A-04

### An additional jewel beetle species of *Trachys* (Coleoptera: Buprestidae), new to Korea, with ecological and distributional information

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The jewel beetle, *Trachy dilaticeps* Gebhardt, 1928 has been known to occur in Japan, China, Taiwan, and Vietnam hitherto. This species is typically distributed in Oriental region. In the case of Palearctic region, it has only been documented in Japan (Kyushu). In this study, we report *T. dilaticeps* for the first time from Korea, along with its diagnostic characters. Ecological and distributional information is also provided herein.

A-05

**Taxonomic study of the genus *Priopoda* Holmgren, 1856(Hymenoptera, Ichneumonidae, Ctenopelmatinae) from South Korea**

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The genus *Priopoda* is a small group of the subfamily Ctenopelmatinae, comprising 22 species from worldwide, 10 species from the Eastern Palaearctic and 13 species from the Oriental region. This species and genus are report for the first time from South Korea. The Ctenopelmatinae comprises one of the two major radiations of parasitoids of sawflies. The approximately 1,350 species have been reported in 105 genera and nine tribes. In this study, diagnoses and photos of four unrecorded species from South Korea are provided.

**Key words:** new record, parasitoids, Perilissini, wasps

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government(MSIT) (NRF-2021R1F1A1052395)

A-06

**Taxonomy of the genus *Helictes* Haliday, 1837(Hymenoptera, Ichneumonidae, Orthocentrinae) from South Korea**

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The genus *Helictes* is a small group of the subfamily Orthocentrinae, comprising 11 species from worldwide, most species from the Palaearctic region, four species from the Nearctic, and two species from the Neotropical region. This subfamily is wide morphological variation between genera but most are readily recognizable as orthocentrines. They are generally small sized, clypeus strongly convex and malar space long. Among them, this genus is reported for the first time from South Korea. In this study, description, photographs of diagnostic characterists are provided.

**Key words:** new record, Orthocentrinae, parasitoids, wasps

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government(MSIT) (NRF-2021R1F1A1052395)

A-07

## New additions to the Korean fauna based on the tenthredinid sawflies housed in the Hungarian Natural History Museum (Hymenoptera)

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The North Korean sawflies housed in the Hymenoptera Collection of the Hungarian Natural History Museum are studied, with a focus on the subfamilies Athaliinae and Allantinae. Five genera and ten species of the two subfamilies are identified. *Athalia indiana* Benson is reported for the first time from East Asia (North Korea), and further eight species and one subspecies are discovered in the new country of North Korea: *Allantus helanshanicus* Wei, Li and Xiao, *Apethymus kolthoffi* (Forsius), *A. sidorenkoi* Sundukov, *Athalia japonica* (Klug), *A. proxima* (Klug), *A. rosae ruficornis* Jakowlew, *Beleses satonis* (Takeuchi), *Taxonus carbonarius* Takeuchi, and *T. montanus* Togashi. Additionally, *Athalia infumata* (Marlatt) syn. nov. is considered a junior subjective synonym of *A. proxima* (Klug). Diagnoses and photographs of the newly recorded species are provided, as well as new distributional records and brief notes on the new synonymy.

**Key words:** *Athalia indiana*, new record, North Korea, Symphyta, Tenthredinidae

This work was supported by the National R&D Program through the National Research Foundation of Korea (NRF) funded by Ministry of Science and ICT under Grant number 2020R1A6A3A01095736.

A-08

## Taxonomic note on three species of the genus *Trixagus* Kugelann (Coleoptera: Throscidae) in Korea with a new species

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The genus *Trixagus* Kugelann is one of the most diverse genera in the family Throscidae Laporte, which comprises about 80 species. Only a single species of this genus has been reported in Korea throughout the entire family. In this study, three additional species, *Trixagus* sp., *Trixagus leseigneuri* Muona, and *Trixagus turgidus* Hisamatsu are reported for the first time in Korea. Similar to that of the species illustrated in Kovalev, males of *Trixagus leseigneuri* Muona and *Trixagus turgidus* Hisamatsu possess sexual modification on mesotarsus. *Trixagus* sp. and *Trixagus turgidus* Hisamatsu exhibit characters that are unusual for this genus, including the unincised eye, a blade-like structure on the protibia, and others. Illustrations of habitus and diagnostic characters of each species are provided.

**Key words:** biodiversity, morphology, new species, taxonomy, redescription.

A-09

## **New distribution record of genus *Neomyrhessus* Minkina (Coleoptera, Scarabaeidae, Aphodiinae) from South Korea**

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*Neomyrhessus* Minkina, 2024, is a rare genus comprising six species, recently erected from *Myrhessus* Balthasar, 1955 for *N. nanjingensis*. To date, all six species have been reported in East Asia, with five from Japan and one from China. In this study, the genus *Neomyrhessus* is recorded for the first time in South Korea, with the discovery of a new species *Neomyrhessus coreanus* sp. nov. Description, illustrations of morphological characters, and habitat information for a new species are provided.

**Key words:** dung beetle, *Myrhessus*, Psammodiini, Rhysselina, taxonomy

A-10

## **Review of distribution of *Bactrocera dorsalis* (Diptera: Tephritidae)**

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Oriental fruit flies (*Bactrocera dorsalis*) are one of the most important pests in horticulture worldwide. The distribution information of this species is not easy to be found as it is scattered in many forms of publications such as books, journals, and research reports. The study was conducted by collecting data from various resources, analyzing the information, and interpreting the results. As a result, *B. dorsalis* was confirmed to be distributed in a total of 82 countries, and the distribution status of each country is presented by dividing it into present (widespread, localized, few occurrences, under eradication) and absent (eradicated, confirmed by survey, intercepted only, invalid presence record). This review is very useful for biologists, entomologists, as well as practitioners of plant protection.

**Key words:** Oriental fruit flies, *Bactrocera dorsalis*, distribution, plant protection

A-11

**PCR-based species identification method using unique genetic markers for invasive drywood termites (*Cryptotermes domesticus*), domestic termites (*Reticulitermes speratus*), and kanmon termites (*Reticulitermes kanmonensis*)**

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This study focuses on developing diagnostic compositions, kits, and information provision methods for identifying species-specific genes in domestically residing *Reticulitermes speratus* and *Reticulitermes kanmonensis*, as well as the recently introduced *Cryptotermes domesticus*. The core innovation of this invention lies in the utilization of species-specific genetic markers to facilitate rapid and accurate species identification using a PCR (polymerase chain reaction)-based diagnostic technique. This approach enables swift identification of termites at quarantine stages, contributing to efficient management of imported goods and minimizing ecological and economic damages caused by termites. Through genome analysis of termites, this research has identified candidate species-specific genetic markers, developed diagnostic compositions and kits based on these markers, and proposed a rapid diagnostic method capable of determining termite species within a day, optimally within three hours. This invention provides a groundbreaking tool for termite management and research, significantly contributing to pest control and biodiversity conservation efforts.

A-12

## Taxonomic review of the genus *Campylomyza* Meigen (Diptera: Cecidomyiidae) in Korea with description of seven new species

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The genus *Campylomyza* Meigen, 1818, from the Micromyinae subfamily of the Cecidomyiidae, includes 40 known species globally. The genus *Campylomyza* has been primarily studied within the Palearctic region, with 39 species, 2 from the Nearctic region, and 1 from the Oriental region. As of now, four species have been documented in Korea: *Campylomyza appendiculata*, *C. flavipes*, *C. furva*, and *C. spinata*. Our research from 2017 to 2020 uncovered five previously unreported species in Korea (*C. abjecta*, *C. aborigena*, *C. cornuta*, *C. cavitata*, and *C. cingulata*) and introduces seven new species (*C. angusta* sp. nov., *C. ambulata* sp. nov., *C. convexa* sp. nov., *C. cornigera* sp. nov., *C. hori* sp. nov., *C. odae* sp. nov., and *C. yeongyangensis* sp. nov.). These findings are based on morphological evidence and DNA analysis. We present comprehensive data, including the mitochondrial COI sequences, diagnoses, detailed descriptions, and identification keys for these species. This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea.

**Key words:** *Campylomyza*, Cecidomyiidae, DNA barcodes, New distributional data, New species

A-13

## New finding of the Subfamily Catotrichinae (Diptera: Cecidomyiidae) from South Korea with DNA barcode

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This research introduces the subfamily Catotrichinae to the South Korean fauna for the first time. Within the globally recognized 6,651 Cecidomyiidae species, only ten are categorized under the Catotrichinae subfamily. Notably, this subfamily, which ingests fungi during larval development, is among the most primordial lineages of the Cecidomyiidae, both in morphological and molecular terms. The species *Catoricha nipponensis* of Catotrichinae was newly observed in Yeongwol, Gangwon-do, in October 2021. It was recorded for the first time in Korea, with its holotype initially collected in Honshu, Japan, in November 1923. This study provides the diagnosis, photographs of distinguishing characteristics, and the DNA barcode sequences for *Catoricha nipponensis*. This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea.

**Key words:** Catotrichinae, *Catoricha nipponensis*, DNA barcode, New distributional data, South Korea

A-14

## Taxonomic note on the family Anamorphidae Strohecker (Coleoptera: Coccinelloidea) in Korea

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The family Anamorphidae Strohecker is a beetle family that comprises about 170 species worldwide. This family was traditionally considered as a subfamily of the family Endomychidae Leach because of their similar appearance, but a phylogenetic study revealed it is a separate family. The adults of this family can be distinguished from endomychid species by possessing a tentorium with corpotentorium and separated anterior arms, mesocoxal cavities being broadly closed by meso- and metaventrites, and others. Although more than 20 species have been reported in East Asia, this family has never been reported in Korea. In this study, the family Anamorphidae Strohecker and its 5 species of 3 genera, *Bystodes kidoi* Sasaji, *Bystodes* sp.1, *Bystodes* sp.2, *Dexialia hiranoi* Narukawa, *Idiophyes* sp., are reported for the first time in Korea. Illustrations of habitus and diagnostic characters of each species are provided.

**Key words:** biodiversity, morphology, new species, taxonomy



A-15

## New species of the spiny crawler mayfly *Drunella* Needham (Ephemeroptera: Ephemerellidae) from South Korea

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The mayfly genus *Drunella* is the most diverse genera in the family Ephemerellidae, and is found in lotic streams throughout East Asia and North America. The species *D. ishiyamana* is found widely throughout East Asia and their species concept has not been properly defined until recently. The *D. ishiyamana* species group was examined, and morphological and molecular evidence of a new species were uncovered. In this study *Drunella punctata* sp. nov. is formally described, mainly distinguished from *D. ishiyamana* by the lack of a notch in their median clypeal tubercle in their larval stage. Photographs, diagnosis, and descriptions of *D. punctata* are provided.

**Key words:** *Drunella punctata*, *Drunella ishiyamana*, Ephemerellidae, Ephemeroptera, South Korea

\*This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR202402202).

A-16

## First report of the genus *Anaclasiger* Raffray (Coleoptera, Staphylinidae, Pselaphinae) from South Korea

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The genus *Anaclasiger* which is one of the myrmecophilous beetle (Clavigeritae) was described by Raffray in 1890 with the type species, *A. sinuaticollis*. Since then, only one species, *A. zhudiae*, had been added in this genus. The former species has known to distribute in Singapore (type locality), Taiwan (Raffray, 1914), Malaysia (Nomura & Idris, 2005), Thailand and Japan (Nomura et al., 2006), and the latter has been reported only in China (Yin et al., 2012). During specimens research of Korea National Arboretum, we were recognized one species, *A. sinuaticollis*, collected by pitfall trap in Mt. Geombong. Therefore, we are going to report this unrecorded genus and species for the first time from Korea. Both the information of the species including diagnosis, habitus and male genitalia, and that of the genus distribution on the map are going to be provided.

**Key words:** Clavigeritae, Myrmecophilous beetle, *Anaclasiger*, Taxonomy

A-17

### First record of *Dolichovespula kuami* from Jilin Province, China

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Since *Dolichovespula kuami* Kim & Yoon was first recorded in Korea in 1996, there has been ongoing debate over its valid specific status. However, through recent analysis of the male genitalia structure and DNA barcode, it has been proven that it is a different species from *D. flora* Archer, which live in China. *D. kuami* is an endemic species that mainly lives in forest areas in the central and northern parts of South Korea. It is a hornet species that is relatively rare due to low nest density. Therefore, little is known about their ecological characteristics. However, as numerous wasps of *D. kuami* were recently collected in the Jilin Province of China, their distribution records have been confirmed to be beyond the Korean Peninsula to China. Therefore, this study aims to record the distribution of *D. kuami* in China for the first time.

**Key words:** *Dolichovespula kuami*, distribution, Jilin, China

A-18

### The complete mitochondrial genome of a burying beetle, *Nicrophorus quadraticollis* Portevin, 1903 (Coleoptera: Staphylinidae: Silphinae)

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*Nicrophorus* Fabricius, 1775, commonly known as necrophagous beetle, is associated with vertebrate carrion. Up to date, the genus consists of 72 species worldwide. In recent years, various phylogenetic studies explored on the evolution and relationship of the species in the genus. However, morphological and molecular phylogenetic studies produced conflicting results, continuing the problem over whether *Nicrophorus quadraticollis* is monotypic or not. The present study is to report the complete mitochondrial genome (mitogenome) of *N. quadraticollis* that was sequenced in prior to a systematic research of Silphinae. It was 17,747bp in length and comprised 12 protein-coding genes (PCGs), 2 rRNA Genes, 22 tRNA Genes and one non-coding region. The nucleotide composition is 40.9% for A, 36.7% for T, 9.0% for G and 13.4% for C.

**Key words:** *Nicrophorus*, Mitochondrial genome, Silphinae, Phylogeny

A-19

**A newly recognized species, *Nemophora ochsenheimerella* Hoffmannsegg, 1798, of Adelidae (Lepidoptera) from South Korea**

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*Nemophora* Hoffmannsegg, 1798 is a relatively large group in Adelidae, including about 350 species worldwide. Only 13 species are known to Korean insect fauna up to date. The present study is to report *N. ochsenheimerella*, which is new to Korea. *N. ochsenheimerella* is externally similar to *N. wakayamensis* but can be distinguished by having characters in male genitalia as follows: cucullus longer than *N. wakayamensis* and *N. ochsenheimerella* has two rows of curnus consisting of numerous minute spines.

**Key words:** Taxonomy, Lepidoptera, Adelidae, *Nemophora*

A-20

**A new species of the genus *Valgus* Kolbe, 1909 (Coleoptera: Scarabaeidae: Cetoniinae) from South Korea**

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*Valgus* Kolbe, 1909 is a small genus of Cetoniinae, with 20 described species worldwide. In Korea, only one species, *Valgus koreanus* Sawada, have been recorded. Species of this genus have been known that they are commonly associated with termite colonies. They feed on the wall of termite burrows in logs or standing dead trees. In this study, we report a new species of this genus, *Valgus gwangneungensis* sp. nov.. We provide a key to the species of *Valgus*, description of the new species and photographs of habitus and male aedeagus.

**Key words:** Coleoptera, Cetoniinae, *Valgus*, New species, Taxonomy

A-21

### Three minute orb weavers (Araneae: Theridiosomatidae and Mysmenidae) new to Korea

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Three species belonging to two families of minute-sized spiders, viz, *Theridiosoma fulvum* (Araneae: Theridiosomatidae), *Microdipoena ogatai* and *Microdipoena shenyang* (Araneae: Mysmenidae), were discovered for the first time in Korea. Previously *T. fulvum* and *M. ogatai* were known to distribute only in Japan, *M. shenyang* only in China. All former records of *Microdipoena jobi* from Korea are misidentifications of *M. shenyang*. Detailed descriptions and photographs of three species are provided.

**Key words:** *Microdipoena*, misidentification, taxonomy, *Theridiosoma*, unrecorded species

\*This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR202304105).

A-22

### A taxonomic study on the genus *Peromitra* (Diptera: Phoridae) from South Korea

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The genus *Peromitra* Enderlein is a small group of phorid flies, including two European parasitic species known to parasitize larval bibionid flies. In this study, specimens of the *Peromitra* species collected from South Korea are examined morphologically on the basis of characteristics on ocellar region, leg chaetotaxy and hypopygium. As a result, four species are described new to science and two species, viz. *P. fimbriata* and *P. multisetalis* are newly recorded from South Korea. Photographs of diagnostic characters and a key to males of South Korean species are provided.

**Key words:** Korea, new species, *Peromitra*, scuttle fly, taxonomy

\*This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR202203201).

A-23

### Three moth fly genera (Diptera: Psychodidae) newly recorded from Korea and one more...?

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Moth flies (Diptera: Psychodidae) are small fuzzy flies found in diverse habitats from mountains to urban areas, even in your house. Approximately 3,000 species among 6 subfamilies are recorded worldwide. However, in Korea, only 10 species from 3 genera of the subfamily Psychodinae have been recorded, including 8 species from North Korea. A preliminary study on moth flies in Korea was conducted using specimens collected via malaise traps and by hands from various locations in South Korea. As a result, *Brunettia lungjingensis*, *Thornburghiella decoricornis*, *Philosepedon monstruosus* and our friendly but unrecorded, *Clogmia albipunctata* are newly described in Korea. Brief descriptions, photographs, and illustrations of these four species are provided.

**Key words:** Psychodidae, Moth flies, Korea, New record, Taxonomy

A-24

### Automatic detection of intraspecific variation in *Stenaptinus occipitalis* (Coleoptera: Carabidae: Brachininae) using machine learning

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The integration of machine learning for species identification is becoming increasingly important in entomological research. However, automatic species identification faces significant challenges such as low resolution, sample discoloration, and small dataset sizes, which impede the reliability of traditional machine learning methods. Building upon the previous research on quantification of the color patterns of *Stenaptinus occipitalis jessoensis* using R-based analysis, this study demonstrates how to overcome these challenges in training machine learning for species identification. This approach allowed us to successfully classify geographic variations of *S. occipitalis*. Our results demonstrate the model's ability to identify these variations, despite the small size of the image datasets. This advancement shed some light on the potential of machine learning to identify morphological variation in highly polymorphic species.

**Key words:** Machine learning, Pattern recognition, Species identification, *Stenaptinus*

A-25

**A newly recognized gall midge, *Schizomyia castanopsisae*, inducing inflorescence galls on *Castanopsis sieboldii* from southern areas of South Korea**

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An unrecorded gall midge was discovered from inflorescence galls on *Castanopsis sieboldii* (Makino) Hatus. ex T.Yamaz. & Mashiba, which is one of major components in evergreen forests on the Korean Peninsula. The galls occurred on 20 trees out of 230 on Yokiji Island. The gall midge was identified as *Schizomyia castanopsisae* Elsayed & Tokuda, 2018 (Diptera: Cecidomyiidae), using morphological characters and mitochondrial DNA cytochrome oxidase subunit 1 (COI) region sequences of gall midge's larvae. The Barcode sequences of 40 samples collected from Yokji Island were identical, and the individuals from Yokji Island formed a clade with the individuals from Kyushu, with robust bootstrap support in a maximum likelihood tree. This result suggests the gall midges may have migrated from Kyushu, Japan to Yokji Island, South Korea. However, it is too early to determine if the gall midge is truly invasive or not at present due to paucity of distribution data in the country.

**Key words:** *Castanopsis sieboldii*, Fagaceae, inflorescence gall, *Schizomyia castanopsisae*, Cecidomyiidae

A-26

***Baetis spinoculis* sp. nov., a new mayfly from Korea (Ephemeroptera: Baetidae)**

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The family Baetidae is known to be the most species-rich family in the order Ephemeroptera. The genus *Baetis* contains up to 160 species, but members of the genus in East Asia are still poorly investigated. In this paper, *Baetis spinoculis* sp. nov., is described based on larval specimens collected in a stream of the Chiaksan mountain in Korea. While four species in the genus have been described in Korea: *Baetis fuscatus* (Linnaeus), *B. silvaticus* Kluge, *B. pseudothermicus* Kluge, and *B. ursinus* Kazlauskas, this new species is distinguished from other Korean baetid species by both genetic and morphological characteristics. *B. spinoculis* can be separated from the related *B. pseudothermicus* group by the *COI* genetic distant. The cuticle structures on paraproct plates and abdominal pigment patterns also distinguish *B. spinoculis* from *B. pseudothermicus* and other related species.

**Key words:** *Baetis spinoculis*, mayfly, *COI*, Korea, description

\*This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR202402202).

A-27

## Taxonomy of the genus *Muscidideicus* Becker (Diptera: Dolichopodidae) with three new species

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The genus *Muscidideicus* Becker, 1917 is comprised of only one species, *M. praetextatus* (Haliday, 1855) reported in west Palearctic region. The adults were typically found on sandy beach within the intertidal zone. In the survey of Korean fauna, authors found three new to science species of this genus on the west sea side of Korean Peninsula and Jeju Island. Descriptions and figures of external features of new to science species and key to species of the world are provided here.

**Key words:** Dolichopodinae, intertidal zone, identification key

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A-28

## Three newly recorded species of the family Conopidae (Diptera: Conopoidea) from Korea

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Hitherto, 37 species in 10 genera under 4 subfamilies have been known from the Korean Peninsula. In this study, three newly recorded species are reported for the first time from Korea: *Conops ceriaeformis ussuriensis* Zimina, 1974, *Physocephala pielina* Chen, 1939, and *Myopa picta* Panzer, 1797. Morphological diagnoses and illustrations of these species are presented. Additionally, a key to all species of Conopidae from Korea is also provided.

**Key words:** *Conops ceriaeformis ussuriensis*, *Physocephala pielina*, *Thecophora fulvipes*.

A-29

### Taxonomic revision of the genus *Dichaetomyia* (Diptera: Muscidae) from Korea

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Until now, only two species of *Dichaetomyia* Malloch have been recorded in the Korean fauna. In this study, we report two unrecorded species for the first time in Korea. External photographs, key to Korean species and taxonomic information are presented herein.

**Key words:** Phaoniinae, Dichaetomyiini, unrecorded species

A-30

### First record of the genus *Hyadina* Haliday (Diptera: Ephydriidae) from Korea

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The genus *Hyadina* Haliday, 1830 is reported for the first time from Korean fauna along with two nominate species: *Hyadina fukuharai* Miyagi, 1977, and *H. pulchella* Miyagi, 1977. Their diagnoses, external feature, and a key of these species are provided here.

**Key words:** Ilytheinae, Hyadinini, *Hyadina fukuharai*, *Hyadina pulchella*

\*This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBRE202401).



B-01

## Surveillance of Wild rodents and chigger mites in southern part of Gyeongsangbuk-do, Korea in 2022 and 2023

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Seon Min Kim<sup>2</sup>, Dong Yeol Lee<sup>2</sup> and Kwang Shik Choi<sup>1,2,3,4</sup>

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쯔쯔가무시증은 급성 발열성 질환으로 *Orientia tsutsugamushi*을 보유한 털진드기 유충이 숙주를 흡혈할 때 전파된다고 알려져 있다. 국내에서는 한국전쟁 중에 첫 감염사례가 확인되었고 이후 지속적으로 보고되고 있다. 털진드기 유충이 성장하기 위해선 반드시 동물의 체액을 필요로 하기 때문에, 일시적으로 야생 설치류 등에 기생하는데 봄철과 가을철에 주로 발생한다. 이처럼 인간에게 피해를 주는 털진드기의 분포와 병원체 유무를 조사하기 위해, 2022년부터 2023년까지 경상북도 김천시에서 3월, 4월과 10월, 11월 5가지 환경(논, 밭, 수로, 야산, 저수지)에서 Sherman trap을 이용하여 설치류 채집을 진행하였다. 2022년에는 총 18마리의 설치류가 채집되었고, *Apodemus agrarius*가 14마리(77.8%)로 가장 많이 채집되었다. 2023년에는 총 25마리의 설치류가 채집되었고, *Apodemus agrarius*가 19마리(76.0%)로 역시 가장 많이 채집되었다. 채집된 설치류의 개체수는 2022년 대비 2023년에 약 39% 증가하였다. 설치류에서 채집된 털진드기의 개체수를 조사한 결과, 2022년에는 총 1,862마리, 2023년에는 3,243마리가 채집되어 전년 대비 약 74% 증가하였다. Chigger index 값을 살펴보았을 때 2022년에는 *Apodemus agrarius*에서 122.2, 2023년에는 *Apodemus agrarius*에서 169.7로 가장 높았다. 설치류에서 채집된 털진드기의 반수에 대한 병원체 보유 여부를 확인하기 위해 최대 30마리씩 pooling하여 실험한 결과, 모두 음성으로 확인된 2022년과 달리 2023년 10월 3개, 11월 1개의 pool에서 쯔쯔가무시 양성 확인되었다. 확인된 양성 샘플은 모두 저수지에서 채집된 개체로 해당 지역에 대한 지속적인 감시가 필요할 것으로 생각된다.

**검색어:** 털진드기, 쯔쯔가무시증, 설치류, *Apodemus agrarius*

B-02

## Benthic Macroinvertebrates monitoring in the weirs of Han River

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한강 3개 보 구간 수변부 11개 지점을 대상으로 2023년 총 2회 채집된 저서성 대형무척추동물은 총 100종 평균 426.0 개체/m<sup>2</sup>였다. 여주보에서 64종으로 가장 많이 출현하였고, 강천보에서 59종, 이포보에서 54종, 한강보상류에서 41종, 한강보하류에서 32종이 확인되었다. 전체 평균 개체밀도는 강천보에서 944.1 개체/m<sup>2</sup>로 가장 많았고, 한강보상류에서 282.7 개체/m<sup>2</sup>, 여주보에서 251.9 개체/m<sup>2</sup>, 이포보에서 180.6 개체/m<sup>2</sup>, 한강보하류에서 172.9 개체/m<sup>2</sup> 순으로 확인되었다. 한강 보 구간에서는 플라나리아류, 실지렁이, 깔따구류 등이 우점함. 보구간의 특성상 상대적으로 단순한 하상 및 깊은 수심에 적응성이 높은 실지렁이, 깔따구류의 우점은 일반적인 특성으로 볼 수 있으며 일시적으로 수변부에서 밀집된 플라나리아류의 채집이 이뤄져 우점된 결과를 보인 것으로 보임. 한강 보 구간 수변부 및 중앙부 조사지점별 군집분석을 실시한 결과 한강보 하류는 3개 보에 비해 우점도가 높고 다양도와 풍부도가 낮았으며 전반적으로 상류부에 위치한 한강보상류 등의 지점에서 군집안정성이 확보되고 있는 것으로 보이며 이러한 점은 상대적으로 다양한 미소서식환경에 기인한 것으로 판단된다.

**검색어:** 한강, 보, 저서성 대형무척추동물, 군집분석

B-03

## The effects of urban heat island-induced temperature differences on the hatching rates of *Aedes albopictus*

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흰줄숲모기(*Aedes albopictus*)는 국내보다 해외에서 주요 질병들의 매개체로 인식되고 있으며, 도시 환경에 잘 적응하는 특징을 가지고 있다. 최근 기후변화에 따른 도심 지역의 환경 변화로 인해 모기의 부화율에도 영향을 미칠 수 있을 것으로 예상되어 관련 연구를 위해 서울시 내 25개의 기상청 자동관측장비(AWS)를 통해 수집된 기후데이터를 분석하였으며, 이 가운데 열섬 현상이 강한 도심 지역과 약한 교외 지역을 선정하였다. 이를 통해 임의의 사이 구간을 생성하여 총 9개의 열섬 조건에서 흰줄숲모기의 부화율을 분석하였다. 분석 결과, 열섬 현상이 강할수록 부화율이 증가하였으며, 회귀분석을 통하여 열섬 강도가 강해질수록 이러한 추세가 더욱 빨라질 수 있음을 확인하였다. 본 연구의 결과는 도시열섬 현상에 따른 기온 변화가 흰줄숲모기의 부화율에 중요한 영향을 미칠 수 있음을 시사한다.

**검색어:** 흰줄숲모기, 도시열섬, 기후변화, AWS, 부화율

B-04

## Urban webs: analyzing spider diversity and ecological dynamics in urban habitats

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This study investigated the distribution and diversity of spider communities living in natural and semi-natural environments located in Gongju, Chungcheongnam-do, South Korea, and thereby emphasizes the importance of urban planning and biodiversity conservation. In this study, we documented 128 spider species through pit-fall trapping, sweeping, and manual collection methods and analyzed their alpha and beta diversity, nestedness, and interactions. As a result, natural habitats (forests) showed higher biodiversity and more complex species interactions. Despite anthropogenic impacts, such as human activities, urban habitats have shown notable biodiversity. Nestedness analysis and association rule learning reveal diverse community structures in multiple habitats and intricate interspecies relationships. This study highlights the importance of habitat heterogeneity in supporting biodiversity and the importance of considering multiple ecological factors in urban planning.

**Key words:** urban habitat, natural habitat, habitat heterogeneity, spider diversity, urban biodiversity

B-05

## Analysis of brown trout living downstream of Soyang River Dam and benthic macroinvertebrates used as a food resource

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본 연구는 소양강댐 하류에서 서식하는 생태계교란 생물 종인 브라운송어와 그 먹이원으로 이용되는 저서성 대형무척추동물에 대한 파악을 위해 2022년부터 2023년까지 총 8회에 걸쳐 소양강댐 하류(St.1~St.3)와 지류(St.4)에 대해 브라운송어와 공서종, 브라운송어의 위 내용물, 저서성 대형무척추동물의 종조성 및 기능군 분석을 실시하였다. 저서성 대형무척추동물의 경우, 하루살이목에서 가장 많은 분류군이 확인되었으며(27.1%), 그 중 붙는 무리(CL)와 헤엄치는 무리(SW)가 높은 비율을 차지하는 것으로 확인되었다. 브라운송어 채집 결과, 전장은 26~246mm까지 총 105개체가 채집되었으며, 전장-체중 관계의 매개변수 b값이 3을 초과하여 안정적인 성장이 이루어지는 것으로 확인되었다. 브라운송어의 위 내용물에 대한 먹이원 분석 결과, 빙어(0.2%, TL: 246mm)와 육상곤충(2.7%, TL: 154mm, 183~185mm)을 섭식한 개체는 매우 적었으며 상대적으로 전장이 큰 개체에서 확인되었다. 대부분 수서곤충(73.8%)과 물 속에서 서식하는 비곤충류(23.3%)를 섭식하는 것으로 나타났다. 브라운송어의 전장에 따른 먹이 섭식 패턴을 파악하기 위해 위 내용물에서 확인된 종들과 상관분석을 실시한 결과, 브라운송어의 먹이원 중 유수성 환경 선호 종들의 경우 전장과 양의 상관관계( $p < 0.05$ )를 나타낸 반면, 모래 기질 이하의 흐름이 적은 서식처를 선호하는 종들의 경우 전장과 음의 상관관계( $p < 0.05$ )를 나타냈다.

**검색어:** 저서성 대형무척추동물, 브라운송어, 생태계교란 생물, 소양강댐, 먹이원

B-06

## Seasonal community fluctuation of benthic macroinvertebrates in Gonyangcheon Estuarine Wetland

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This investigation was conducted three times (April, August, and October) from 2023 at five surveyed sites in Gonyangcheon estuarine wetland. A total of benthic macroinvertebrates belonging to 59 taxa 44 families 21 orders in 8 classes of 4 phyla were collected. The numbers of benthic macroinvertebrates species in each surveyed site were from 10 (St.1) to 41 (St.2). As a community indices analysis, the average DI is 0.78 ( $\pm 0.12$ ), H' is 1.6 ( $\pm 0.68$ ), R' is 0.96 ( $\pm 0.39$ ), and J' is 0.61 ( $\pm 0.24$ ). Community indices tended to decrease as the diversity and abundance decreased downstream. Total ecological score of benthic macroinvertebrates community (TESB), an average score of 35.47 ( $\pm 15.86$ ). The Habitat of *Clithon retropictum* and *Ellobium chinense* belonging to endangered species II, were identified at st.3~st.5.

**Key words:** Gonyangcheon, Estuarine wetland, Benthic Macroinvertebrates

B-07

## Functional Feeding Groups (FFGs) of benthic macroinvertebrates in Gucheon stream of Deogyusan National Park

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In the Gucheon stream of Deogyusan National Park, a survey was conducted at three sites (six sites in total) in 2018 and 2021. A total of benthic macroinvertebrates of 107 taxa 46 families 13 orders in 6 classes of 5 phyla were found. According to the analysis of the appearance by year, a total of 87 species were surveyed in 2018, and a total of 89 species were surveyed in 2021. As a results to the functional feeding group analysis, Gathering-Collector (GC) accounted for a high species share (2018: 29.89%, 2021: 25.84%). In the functional habitat group analysis, Clinger (CL) accounted for a high species share (2018: 56.32%, 2021: 57.30%). Average annual community indices analysis, DI 0.38( $\pm 0.05$ ), H' 3.48( $\pm 0.19$ ), R' 3.23( $\pm 0.41$ ), and J' 0.85( $\pm 0.04$ ) in 2018, and DI 0.55( $\pm 0.09$ ), H' 2.98( $\pm 0.31$ ), R' 2.91( $\pm 0.65$ ), and J' 0.70( $\pm 0.05$ ) in 2021. As a results of the benthic macroinvertebrates index (BMI) analysis, indicating that all sites were classified as "very good," with average BMI values of 95.24( $\pm 2.84$ ) in 2018 and 96.99( $\pm 1.13$ ) in 2021.

**Key words:** Deogyusan National Park, Benthic Macroinvertebrates, Functional Feeding Groups (FFGs)

B-08

## Community structure of benthic macroinvertebrates in Wangpicheon water system

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왕피천 수계 내 저서성 대형무척추동물의 군집구조 분석을 위해 총 5개 지점에서 2023년 총 4회(4월, 6월, 8월 11월) 조사를 실시하였다. 조사기간 중 저서성 대형무척추동물은 총 5문 7강 17목 77과 156종 17,179.1개체/m<sup>2</sup>가 채집되었다. 수환경 변화에 민감한 E.P.T. 분류군은 전체 156종 중 91종이 출현하여, 전체 출현종의 58.3%를 차지하였다. 섭식기능군(FFGs) 분석결과, 종 출현 양상은 육식성 포식자(Predator: P)가 51종(32.69%)으로, 개체 출현 양상은 주워먹는 무리(Gathering-collector: GC)가 6,867.2개체/m<sup>2</sup>(39.97%)로 높은 비율로 출현하였다. 서식기능군(FHG) 분석결과, 붙는 무리(Clinger: CL)가 70종(44.87%), 12,720.6개체/m<sup>2</sup>(74.04%)로 가장 높은 비율로 출현하였다. 군집지수 분석결과, 우점도지수(DI) 0.43, 다양도지수(H') 3.51, 풍부도지수(R1) 4.59 균등도지수(J') 0.77로 나타났다. 생물학적 수질 판정 지수(BMI) 분석결과, 평균 92.36(±0.83)으로 모든 지점에서 “매우 좋음”으로 판정되었다.

**검색어:** 왕피천, 저서성 대형무척추동물, 섭식기능군, 서식기능군, E.P.T., BMI

B-09

## 26 year-monitoring reveals changes on the spring occurrence of butterflies in the Gwangneung Forest, South Korea

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광릉 숲의 곤충상 조사는 1932년으로 거슬러 올라간다. 광릉 숲의 경로조사법에 의한 나비상 모니터링 연구는 1998년부터 2023년까지 지속되었다. 26년 동안 총 223회 조사를 실시한 결과 118종, 20,181개체가 확인되었다. 봄철 출현하는 나비종 8종(노랑나비, 대만흰나비, 먹부전나비, 멧팔랑나비, 쇠빛부전나비, 애호랑나비, 큰줄흰나비, 흰줄표범나비)은 첫 출현일이 빨라지는 경향을 보였으며, 평균 5.2일 빨라졌다. 조사된 나비종에서 큰줄흰나비, 뿔나비, 남방부전나비 순서로 많은 개체수가 확인되었으며, 연 출현 빈도는 큰줄흰나비가 26회로 가장 많았다. 확인된 나비의 분포, 서식지, 식성에 따라 분류한 결과 분포는 북방계 27%, 남방계 14%이며, 서식지는 산림 경계 36%, 산림 내부 33%, 초지 30% 그리고 식성은 다식성 8%, 단식성 42%, 협식성 51%로 이루어진 것이 확인되었다. 또한, 기후변화 따른 나비류 생활주기 변화 여부를 검토하여 지구온난화 지표 자료로 활용할 계획이다.

**Key words:** 광릉 숲, 나비상, 기후변화, 지구온난화

B-10

## Distribution of hymenoptera insects in Korean national parks

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Field surveys were conducted to collect and refine "Natural resource survey" and ecosystem research data of 23 National parks in South Korea, including Hallasan on Jeju Island and Palgongsan newly designated as national park in 2023. Among the collected data, a total of 1,538 species from 54 families of Hymenoptera insects were recorded. Within these families, the largest number of species was recorded in the family Ichneumonidae with 514 species, followed by Formicidae (118 species), Braconidae (112 species), and Tenthredinidae (135 species), exhibiting relatively high species diversity. Among the National parks, Jirisan, the first designated National park in South Korea with a relatively large area compared to other parks, recorded the highest species diversity with 618 species, while Taebaeksan recorded relatively low species diversity with 77 species. Correlation analysis between the number of Hymenoptera species and other factors revealed a statistically significant and relatively strong positive correlation ( $P > 0.005$ ,  $R = 0.864$ ) with the total number of insects, and a statistically significant but relatively weak positive correlation ( $P > 0.005$ ,  $R = 0.615$ ) with the park's area.

**Key words:** Korea National Park, Hemiptera, Species diversity

B-11

## **Biodiversity assessment of insect population in Ilgwang, Busan**

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This study aimed to collect foundational data essential for devising a natural environment conservation plan and implementing relevant policies. It underscores the significance of understanding the current state of the natural environment. Our research concentrated on surveying the biodiversity and distribution of key natural habitats within Busan Metropolitan City, with the goal of gathering crucial data to guide the development of conservation and management strategies. The focus of our investigation was on the insect populations in Ilgwang, covering two primary habitats: mountains and wetlands. The survey, conducted from July to September 2023, utilized various collection methods, including pitfall traps, fly traps, sweeping nets, and aspirators. Our findings documented the presence of 109 species across 88 genera, 50 families, and 9 orders. Specifically, the study identified two species from the order Odonata, two from Blattodea, one from Mantodea, six from Orthoptera, eleven from Hemiptera, twenty-nine from Coleoptera, twelve from Diptera, ten from Lepidoptera, and thirty-five from Hymenoptera. Through community analysis, biodiversity indices were calculated, revealing a Shannon-Wiener index ( $H'$ ) of 4.07 for mountain habitats and 3.92 for wetlands. The Margalef richness index ( $R$ ) displayed values of 13.92 for mountains and 14.78 for wetlands, while the Pielou evenness index indicated values of 0.96 and 0.91, respectively. Among the identified species, one was classified as endangered, and thirteen were designated as of Least Concern, according to legal protection statuses.

**Key words:** Biodiversity, Community analysis, insect, Policy, Least Concern

B-12

**Sex-dependent variations in the gut bacterial communities of *Monochamus alternatus* in response to *Bursaphelenchus xylophilus* infection**

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This study investigates the impact of *Bursaphelenchus xylophilus* infection on the gut bacterial communities of the pine sawyer beetle, *Monochamus alternatus*, with a distinction between male and female individuals. Utilizing specific primers, we determined the infection status and analyzed the bacterial composition across different taxonomic levels. Regardless of infection status or sex, Proteobacteria and Firmicutes were found to dominate the phylum level, with significant contributions from Actinobacteria and Bacteroidetes. At the class level, Bacilli, Gammaproteobacteria, Alphaproteobacteria, and Actinobacteria emerged as prevalent groups. Meanwhile, the genus level was characterized by a high abundance of *Lactobacillus*, *Rickettsia*, *Bacillus*, and *Rahnella*. Our analysis of alpha diversity metrics, including Observed Species, Shannon Index, Inverse Simpson Index, and Phylogenetic Diversity, revealed no significant differences attributable to *B. xylophilus* infection; however, notable variations were observed between sexes. Principal Coordinates Analysis and Non-metric Multidimensional Scaling further underscored that the differences in gut bacterial communities were more pronounced between male and female beetles than between infected and uninfected individuals. These findings highlight the influence of host sex over infection status in shaping the gut microbiome of *Monochamus alternatus*, providing new insights into the complex interactions between host biology, gut microbiota, and pathogen infection.

**Key words:** gut bacteria, host-microbe interactions, pine wood nematode, sakhalin pine longicorn beetle



B-13

### Seasonal prevalence of mosquitoes collected with mosquito traps in Gyeongsangnam-do Province, Republic of Korea, 2023

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The vector mosquito surveillance is important when recommending prevention and control measures. The surveillance of the vectors were conducted at a total of 7 locations with light emitting diode (LED traps) and BG-Sentinel traps from March to November, 2023 in Gyeongnam province. In the surveillance, a total of 13 species belonging to seven genera were collected in a total of 6,537 females and 51.9/trap/night (Trap Index; TI) in 2023. Among the collection sites, Gangseo-gu at the pigsty in Busan with a LED trap recorded the highest TI 60.6 (Species Ratio; SR 65.6%) for *Culex tritaeniorhynchus* females in 2023. Each one of *Cx. tritaeniorhynchus* female was firstly collected for 2023 at Eulsukdo in Busan at 22th March. In the results of isolation of viral RNA, *Flavivirus* were positive in one pool (Chaoyang virus; 30 individuals) of *Aedes vexans* and negative in 341 pools (4,152 individuals) of 12 mosquito species including *Cx. tritaeniorhynchus*, *Cx. pipiens*, *Aedes vexans*, *Ae. albopictus*, and *Ochlerotatus togoi* in 2023.

B-14

### Surveillance of hard ticks (Acarina: Ixodidae), the Vector of Severe Fever with Thrombocytopenia Syndrome (SFTS) in Gyeongsangnam-do, Republic of Korea, 2023

Chang-Jun Lee<sup>1</sup>, Jae-Soon Park<sup>1</sup>, Hye-Rim Ju<sup>1</sup>, Suvin Cho<sup>1</sup>, Hyunji Shin<sup>1</sup>, Sun Ho Jung<sup>1</sup>,  
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A tick survey was conducted to monitor ticks using tick traps attached dry ice method at each four sites in Ulju and Gimhae counties, Gyeongsangnam-do from April to November, 2023. Two species belonging to one genera were collected with tick traps. A total of 1,064 ticks were collected as *Haemaphysalis longicornis* (Trap Index; TI 11.0), *Haemaphysalis flava* (TI <0.1) in Ulju and A total of 843 ticks were collected as *Haemaphysalis longicornis* (Trap Index; TI 8.7), *Haemaphysalis flava* (TI 0.1) in Gimhae 2023. *Haemaphysalis longicornis* was the most frequently collected, representing 99.2% in Ulju, 98.9% in Gimhae. In the collection environments, a total number of 685, 268, 64, and 47 ticks were collected from a glassland, a copse, a mountain path, and a grave of Ulju a total number of 469, 216, 83, and 75 ticks were collected from a glassland, a copse, a Grave, and a mountain path of Gimhae respectively. In the results of the isolation of Severe Fever with Thrombocytopenia Syndrome (SFTS) from the ticks, no pathogens were detected from RNA of 101 pools (Ulju), 98 pools (Gimhae) of the ticks using a Polymerase Chain Reaction method in 2023.

B-15

## Seasonal prevalence of chigger mites from wild rodents in Gyeongsangnam-do Province, Republic of Korea, 2023

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A seasonal chigger-borne disease surveillance program was established at Geoje in March, April, October, and November, 2023. Three species of 45 wild rodents were collected by using Sherman traps, including *Apodemus agrarius* (Species Ratio; SR 88.9%), *Crocidura* spp. (SR 8.9%), *Micromys minutus* (SR 2.2%) in Geoje, 2023. A total of 2,597 chiggers were collected from three species of the rodents in Geoje. The chigger mites were collected from *A. agrarius* (Chigger Index; CI 64.9) and *C. spp.* (CI 0.3) for Geoje. In the collection environments, a total number of 734, 659, 172, 520, and 512 chiggers were collected from a reservoir, a ditch, a rice paddy, a field, and a hill, respectively. In the results of the isolation of *Orientia tsutsugamushi* from the chigger mites, no pathogens were detected from the DNA of the 62 pools of the mites using a Polymerase Chain Reaction method in 2023.

B-16

## Predicting the potential distribution of an invasive species, *Anoplophora horsfieldii* (Coleoptera: Cerambycidae), under climate change using species distribution model

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세계 100대 악성 침입외래종인 유리알락하늘소(*Anoplophora glabripennis*)와 근연종인 노랑알락하늘소(가칭, *Anoplophora horsfieldii* (Hope, 1843))가 2019년 제주도에서 처음 발견된 후 2023년까지 지속적으로 확인되었다. 본 연구는 MaxEnt 알고리즘을 기반으로 하는 생물종 분포 모델을 이용하여 19개의 기후변화 변수에 노랑알락하늘소(가칭) 먹이식물 5종(차나무, 팽나무, 멸구슬나무, 종가시나무, 비술나무)의 변수를 추가하여 외래해충인 노랑알락하늘소(가칭)의 현재·미래의 분포 가능지역에 대한 공간적 분포 특성을 규명하고 국가적 확산을 대응하고자 한다.

모델 예측 정확도(AUC)는 0.983으로 출현지점을 정확하게 예측하는 비율이 매우 높다고 할 수 있다. 모델 예측 정확도의 증감에 영향을 주는 환경변수 중 먹이식물의 기여도가 70%를 상회하는 것으로 나타났다. 현재 75% 이상 분포 가능지역은 전라남도 진도군 일대와 경상북도 포항시 일대로 나타났으나 2050년에는 서해안을 따라 태안군까지 동해안을 따라 북한의 고성군까지 분포가 가능한 것으로 나타났다. 또한 75% 이상 분포 가능 면적은 현재 423km<sup>2</sup>에서 2050년에는 9,270km<sup>2</sup>로 약 대한민국 면적의 1/10 정도 확산될 것으로 예측된다.

**검색어:** 침입외래종, 기후변화, 종분포모델, 노랑알락하늘소(가칭), *Anoplophora horsfieldii*

B-17

**First record of two predators of the invasive alien hornet, *Vespa velutina nigrithorax***

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2003년 국내에 침입한 외래종 등검은말벌(*Vespa velutina nigrithorax*)은 현재 남한 전체에 확산된 상태이며 이들로 인한 사회 경제적 피해는 지속적으로 증가하고 있다. 따라서 이들을 방제하기 위한 다양한 방법이 시도되고 있으나 그 효과는 대부분 미미한 상황이다. 그러나 최근 생물학적 방제에 대한 관심이 집중되는 상황에서 외래종 등검은말벌에 대한 새로운 포식자 2종이 발견되어 이를 보고하고자 한다. 2023년 8월 11일 전북 무주군 적상면 일대에서 오소리 배설물 조사 중 배설물 속에 다량의 말벌 사체가 발견되었고 분석 결과 10여개체의 등검은말벌로 나타났다. 이는 일반적으로 땅벌류를 주로 포식하는 오소리가 대형 말벌류를 포식하는 첫 기록이다. 또한 2023년 12월 10일 안동 일대에서 등검은말벌 벌집 조사를 하던 중 벌집에 10여 마리의 직박구리가 벌집 외피를 깨고 내부에 있는 애벌레와 성충들을 포식하는 장면이 관찰되면서 벌매에 이어 새로운 조류 포식자를 기록한다.

**검색어:** 등검은말벌, 외래종, 오소리, 직박구리, 천적

B-18

**Survey of nest density of the invasive alien hornet, *Vespa velutina nigrithorax*, in apiaries in Uiseong and Andong, Gyeongsangbuk-do**

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외래종 등검은말벌은 양봉농가에 막대한 경제적 피해를 입히는 대표적인 양봉 해충으로 알려져 있다. 본 연구에서는 경북 의성 및 안동 일대에서 양봉장 주변 2km 지점 내에 발생하는 등검은말벌의 벌집 밀도에 대해 조사하였다. 조사기간은 2023년 12월 1-20일까지 조사되었으며 육안, 망원경 및 드론을 통해 가능한 한 모든 지점을 조사하였다. 이번 조사에서 발견된 총 등검은말벌 벌집 수는 133개로 조사되었다. 그 중 의성에 위치한 5곳의 양봉장에서는 총 67개로 평균 13.4개, 안동에 위치한 5곳의 양봉장에서는 총 66개로 평균 13.2개로 나타나 두 지역이 거의 유사한 경향을 나타내었다. 10개의 양봉장 중 안동 안기동 일대 양봉장에서 최대 26개의 등검은말벌 벌집이 발견되었으며 의성 단촌 일대 양봉장에서는 4개만이 발견되어 큰 격차를 보였다. 양봉장에 피해를 주는 등검은말벌의 출현 비율은 주변 벌집 밀도에 영향을 직접적으로 받고 있기 때문에 정확한 밀도 및 거리 등을 토대로 적절한 방제 전략이 필요할 것으로 보인다.

**검색어:** 등검은말벌, 외래종, 양봉장, 등지밀도, 의성, 안동

B-19

## Quantitative study of wild bees diversity in Seocheon Maeul-soop

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생태계내에서 중요한 수분매개체인 야생벌을 보전하기 위해서는 풍부도와 다양성을 모니터링 하는 것이 중요하다. 충청남도 서천군의 마을숲에서 야생벌을 2년간 조사한 결과 총 9과 57종 3,258개체를 채집하였다. 우점종은 애꽃벌과의 꼬마애꽃벌이 가장 많았으며, 다음으로 양봉꿀벌, 수염줄벌, 구리꼬마꽃벌이었다. 종수는 2월부터 증가하다가 8월에 가장 많았으며, 개체수는 4월에 가장 많고 이후 줄어들었다. 야생벌의 종 목록 살펴보면, 꿀벌과가 16종으로 가장 많았으며, 애꽃벌과의 꼬마애꽃벌은 1종이지만 개체수는 2,084개체로 본 연구에서 가장 많이 나타났다. 본 연구에서 조사된 결과는 향후 기후변화로 인한 수분매개 곤충의 영향을 파악하는데 유용하게 쓰일 것이다.

**검색어:** 야생벌, 다양성, 수분매개, 베인트랩, 마을숲

B-20

## Occurrence of stylopization by *Xenos* in invasive alien hornet, *Vespa velutina*, in South Korea

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In *Vespa velutina*, although no parasites or parasitoids have been found as natural enemies, strepsipteran parasites were first discovered in 11 workers in Andong in 2020. Identification using the DNA barcode method along with the morphological characters, identified them as *Xenos moutoni* and *X. oxyodontes*. These were all males (except for one parasite whose appearance was not identified), and consisted of four larvae and seven pupae. This is the first recorded strepsipteran parasites in Korea, Japan, and Europe, invaded by *V. velutina*. A Strepsipteran parasite is prevalent in *Vespa* species, but reports on the host is lacking in Korea. Although it was not possible to determine the exact infection rate of the strepsipteran parasites in this study, it seems that the parasite of *V. velutina* has already progressed in the southern region due to the geographical characteristics of Andong, located in the central region of Korea. In particular, stylopized workers do not work in the nest, which negatively affects nest development, and reproductive individuals (male and new queen) do not mate, which negatively affects the formation of new colonies in the following year. Nevertheless, the control effect is likely to be minor due to the high reproductive rate and compensatory effect of social wasps.

**Key words:** Strepsiptera, *Vespa velutina*, invasive species, DNA barcodes, *Xenos moutoni*, *X. oxyodontes*

B-21

## Measurement of the growth rate of *Parasarcophaga similis*, one of the major necrophagous flies for forensic entomological applications

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기존의 사후경과시간(PMI) 추정 방법은 대략적인 사후경과시간의 추정, 사후 48~72시간 경과 또는 부패 시 추정 불가능이라는 문제가 발생하여 최근에는 법의곤충학(Medicolegal entomology)을 통한 최소 사후 경과시간(PMImin) 추정이 더욱 강조되고 있다. 이로 인해 시식성파리의 발육 성장속도 파악은 시체의 최소 사후 경과시간 추정에 있어 효과적인 도구로 활용될 수 있다. 본 연구에서는 곱슬털쉬파리(*Parasarcophaga. similis*)를 사육대상 종으로 선정하였다. *P. similis*는 부패한 시체를 섭식하는 시식성파리 중 하나로서, 발육 성장 속도에 따른 법의곤충학(Forensic entomology) 최소 사후 경과시간을 추정하는 데 중요한 지표가 된다. 실험에 사용된 대상종의 경우, 경북 칠곡군 지천면 일대에서 6~9월경 야외쉬파리 채집하였고, 종 동정, 사육 및 증식, 예비 실험을 거친 후 본 실험을 진행하였다. 본 실험은 산란 집단 케이지 내에서 산란 유도 후 12시간 간격으로 6개체를 샘플링하였고, 이를 Leica M125 Microscope (Leica Microsystems, Germany), EG-2HDNL(이지테크, Korea)로 이미지와 측정치를 확보하였다. *P. similis*를 16~34°C 사이 7개의 온도 조건에서 성장 속도 측정을 3회 반복 실험하였으며, 곱슬털쉬파리의 최초 출현시점, 특정 온도 조건 별 발육 성장 속도 측정, 유충 몸길이 데이터, 이미지 자료, 표본 등을 확보하였다. 16, 19, 22, 25, 28, 31, and 34°C에서 *P. similis*의 알에서 성충까지의 발달 기간은 각각 822.0±5.9, 605.0±12.2, 442.3±9.4, 339.3±6.1, 289.3±7.5, 253.0±8.0, and 248.7±3.4h이 경과함을 확인하였다. 본 연구의 결과는 *P. similis*의 성장과정 데이터와 PMImin 추정을 위한 지표로서 활용가능한 데이터를 제공한다.

**검색어:** 곱슬털쉬파리, 법의곤충학, 사후경과시간, 발육 성장 속도

B-22

## Investing insect diversity in coastal habitats of East Busan: Implications for conservation and policy

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This study aims to systematically investigate the insect diversity within the distinct coastal grassland and mountain habitats of East Busan, Busan Metropolitan City. The objective is to gather foundational data that will inform natural environment conservation plans and contribute to policy formulation. Employing a comprehensive collection approach, we utilized trapping nets, pitfall traps, and flying insect traps to capture a broad spectrum of insect species. The investigation identified a rich diversity of 132 species across 9 orders and 52 families. Coleoptera emerged as the most prevalent order with 13 families and 41 species, followed by Diptera with 8 families and 24 species, and Lepidoptera with 9 families and 21 species. To assess the biodiversity and structure of these communities by habitat type, we applied several biodiversity indices: the Shannon-Wiener index ( $H'$ ), Margalef index ( $R$ ), and Pielou evenness index. Coastal grasslands exhibited an  $H'$  of 3.153,  $R$  of 11.08, and a Pielou evenness of 0.371; coastal mountains showed an  $H'$  of 2.922,  $R$  of 13.02, and a Pielou evenness of 0.202. These metrics reveal no significant differences in diversity and evenness between the two habitats. The endangered *Copris tripartitus* was notably observed in coastal grasslands, alongside 20 species classified as Least Concern (LC) in the National Red List across both habitats. The comparative analysis of biodiversity and evenness levels across coastal grassland and mountain areas highlights the ecological significance of both habitats in supporting a diverse insect fauna. The detection of endangered and LC species within these areas emphasizes the critical need for ongoing monitoring and the development of effective conservation strategies tailored to protect Busan's coastal ecosystems. The findings underscore the necessity of conducting periodic surveys to monitor faunal changes and inform conservation efforts actively. By ensuring the continued protection of insect diversity, these efforts will play a pivotal role in maintaining the ecological integrity of coastal areas, thereby supporting broader environmental conservation objectives.

**Key words:** East Busan, coastal area, insect fauna, diversity index, endangered

B-23

## Monitoring of mosquito populations in Chungnam Province during the period of 2017 to 2020

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This study presents the results of mosquito surveillance monitoring in Chungnam Province from 2017 to 2020. A total of 130,750 mosquitoes were collected, and we analyze variations of mosquito populations with emphasis on the most abundant species. We also provide the field survey data based on the different habitats in Chungnam Province.

**Key words:** *Aedes vexans nipponii*, climate data, monitoring, surveillance

B-24

## Analysis of spatial and seasonal variations of *Haemaphysalis longicornis* population based on field survey collected under different habitats and years

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In the study, a variation of *Haemaphysalis longicornis*, a major vector of fever-causing conditions, was statistically analyzed to identify the spatial and climatic factors affecting the time-dependent variations of its population. The survey occurred in different habitats in South Korea. In addition, we developed a predictive model by using a probability function to find the peak occurrence time annually. As a result, the numbers of adults and nymphs were found to be related to temperature and relative humidity and their population peaked at the end of May in all habitats except deciduous forests. This study is expected to provide information on habitat types, times, and climate patterns that require attention to help control *H. longicornis* populations.

**Key words:** Asian longhorned tick, climate variables, habitat type, seasonal phenology, statistical analysis

B-25

Measurement of the growth rate of *Lucilia illustris* at constant temperatures

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최소 사후 경과 시간(PMImin) 측정에 필수적으로 이용되는 것 중 하나가 시식성 곤충의 발육 속도를 정확히 측정할 수 있는 데이터이다. 법의곤충학(Medicolegal entomology)을 이용한 최소 사후 경과 시간 측정 방법은 과거에 비해 빠르게 발전하고 있지만, 보다 정확한 데이터를 얻기 위해서는 추가적인 기초 데이터 확보가 필요하다. 이에 본 연구에서는 가장 대표적인 시식성 곤충 중 하나인 연두금파리(*Lucilia illustris*)를 대상으로 온도에 따른 성장 속도를 측정하였다. 흔히 blow fly 또는 green bottle fly라고도 불리는 연두금파리는 사체에 가장 먼저 나타나는 시식성 파리 중 하나이기 때문에, 해당 종의 유충 성장 속도를 측정하면 최소 사후 경과 시간을 비교적 정확하게 추정하는 것이 가능하다. 실험에 사용된 연두금파리는 5~9월경 대전 유성구 일대에서 성충을 채집하여 종 동정, 사육 및 증식, 예비 실험을 거친 후 본 실험을 진행하였다. 본 실험은 성충 사육 케이지 내에서 교미 및 산란 유도 후 산란된 알을 돼지 생간에 접종하여 유충 사육 전용 챔버에 넣고, 12시간 간격으로 6개체 샘플링하고 추가로 각 령기 변화 시점에 샘플링을 진행하였다. 샘플링된 유충은 길이 측정 및 이미지 촬영을 진행하였다. 16°C, 19°C, 22°C, 25°C, 28°C, 31°C, 34°C 7개 온도 조건에서 연두금파리의 성장 속도 측정 실험을 3회 반복하였으며, 산란으로부터 부화 및 우화까지 시간 등을 포함한 전체 성장 시간 데이터와 유충 몸길이 데이터, 이미지 자료, 샘플링한 유충 액침표본 등을 확보하였다. 16°C, 19°C, 22°C, 25°C, 28°C, 31°C에서 연두금파리의 전체 성장 시간은 각각 792.7±70.2, 441.0±53.3, 366.7±15.1, 288.0±7.2, 255.7±4.0, 260.3±13.2로 측정되었으며, 34°C에서는 3령 이후 성장하지 못하고 폐사함을 확인하였다. 본 연구의 결과는 연두금파리의 성장 과정 데이터와 최소 사후 경과 시간 추정을 위한 지표로서 활용 가능한 데이터를 제공한다.

**검색어:** 연두금파리, 법의곤충학, 사후경과시간, 사육 실험



B-26

## A survey to confirm the population trends and monitoring methods for *Haplotropis brunneriana* (Orthoptera: pamphagidae)

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서식반경이 좁고 개체수가 감소하는 경향을 보이고 있어 멸종위기 종으로 지정된 뚱보주름메뚜기(*Haplotropis brunneriana* Saussure 1888)를 대상으로 개체군 추이와 적절한 모니터링 방법을 확인하기 위해 방형구법과 선조사법을 이용하여 밀도 조사를 수행하였다. 뚱보주름메뚜기에 대한 조사 자료가 부족하여 먼저 방형구법을 이용하여 2021년 3월부터 6월까지 월 1회 서식지 내 개체군 밀도를 확인한 결과 6개체/100m<sup>2</sup>(3월), 2개체/100m<sup>2</sup>(5, 6월)로 각각 영월과 제천에서 가장 많은 개체가 확인되었고, 지역 간에 유의한 차이는 나타나지 않았다( $p > 0.05$ ). 선조사법을 이용하여 2022년 3월부터 6월까지 월 3회 개체군 밀도를 확인한 결과 1.5(±0.79)개체/100m<sup>2</sup>, 0.76(±0.11)개체/100m<sup>2</sup>로 각각 영월과 제천에서 4월에 가장 많은 개체가 확인되었고, 지역 간에 유의한 차이는 나타나지 않았다( $p > 0.05$ ). 조사 방법에 따라 시기와 면적에 차이가 있어 이 두 방법을 정확히 비교할 수 없으나, 공통 적으로 3, 4월 약충 시기에 많은 개체가 확인되는 것을 알 수 있었다.

**검색어:** 뚱보주름메뚜기, 개체군 모니터링, 선조사법, 방형구법

B-27

## Effects of removal of artificial structures in valleys on benthic macroinvertebrates

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최근 하천 환경 개선을 위한 노력과 연속성확보의 일환으로 인공구조물에 대한 철거 정책이 시행되고 있으나, 인공구조물 철거가 하천 환경에 미치는 장기적인 영향에 대해서는 명확하게 알려지지 않았다. 이에 본 연구는 하천 내 인공구조물 철거의 장기적인 영향을 분석하고, 지속 가능한 하천 관리 방안을 모색하기 위해 수행되었다.

설악산에 위치한 가는고래골의 인공구조물을 대상으로 2021년 8월부터 2023년 10월까지 8회에 걸쳐 조사한 결과, 조사기간동안 총 3문 3강 8목 11과 85종이 출현하였다. 총 출현종수는 보의 철거 전(총 44종)과 비교하여 철거직후(43종) 다소 감소하였으나, 이후 점진적으로 증가(2022년 56종, 2023년 64종)하였으며, 특히 절지동물문에 해당하는 분류군의 증가가 확인되었다. 인공구조물과의 거리에 따른 출현종수는 구조물과 가까울수록 종수가 현저히 감소하였으며, 이격될수록 종수가 증가하였다. 장기적인 조사결과 인공구조물과 이격되어 있는 정점부터 점진적인 종수의 안정화가 확인되었으며, 인공구조물 철거지점과 가까운 지점에서는 지속적인 하상 변화가 관찰되고 회복이 느렸다. 이에 인공구조물 철거 후, 빠른 회복을 위해서는 초기 주변환경을 고려한 서식환경의 조성 및 관리에 관한 추가적인 연구가 필요할 것으로 보인다.

**Key words:** 저서성대형무척추동물, 인공구조물, 복원

B-28

**Surveillance the occurrence of chigger mites (Acari: Trombiculidae)  
in Yesan, Chungcheongnam-do (2017-2023)**

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털진드기 유충 (Acari: Trombiculidae)은 쯤쯤가무시증을 전파하는 주요 매개체이다. 털진드기 유충의 발생량은 가을철에 증가하는 것으로 알려져 있지만, 환경 및 시기에 따라 발생 패턴이 다르게 나타날 수 있어 각 지역에 대한 조사가 필요하다. 이 연구는 충남 예산의 털진드기 발생 양상을 확인하기 위해 2017년부터 2023년까지 36-51주차(9-12월)에 걸쳐 현장 조사를 수행하였다. 논, 밭, 수로, 초지에 5m 간격으로 털진드기 트랩을 환경별로 5개씩 설치하여 채집하였다. 그 결과 총 3,257개체로 2017년 1,104마리, 2018년 785마리, 2019년 650마리, 2020년 160마리, 2021년 139마리, 2022년 233마리, 2023년 186마리 채집되었다. 동정 결과 5속 12종이 확인되었으며 둥근혀털진드기(*Neotrombicula tamiyai*)가 1,882개체(57.78%)로 우점도가 가장 높게 나타났다. 이러한 발생 양상에 관한 연구는 매개 질환의 예방 및 관리 전략 수립에 있어 중요한 기초 자료로 활용될 수 있으므로 지속적인 연구와 모니터링이 필요할 것으로 사료된다.

**검색어:** 털진드기, Trombiculidae, 발생감시, 쯤쯤가무시증

B-29

## Occurrence of Flavi-virus infection rate in mosquito collected in sanctuary of migratory birds (Dangjin, Chungcheongnam-do) (2021-2023)

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국립기상연구소의 보고에 의하면 최근 한반도의 기온 상승으로 인해 온대내륙성 기후형에 속했던 지점은 온대해양성 기후형으로, 온대해양성 기후형은 아열대습윤 기후형으로 변화하고 있다. 이러한 한반도의 기후 변화는 환경 변인에 민감한 질병 매개 곤충의 분포와 밀도 변화에 영향을 미칠 수 있어 지속적인 모니터링이 중요하다. 이 연구는 철새도래지 내 발생 및 유입될 수 있는 모기와 관련 바이러스 감염률을 확인하기 위해 충남 당진의 철새도래지에서 BG-sentinel trap 및 LED trap을 사용하여 2021년부터 2023년까지 4-11월간 월 2회 수행하였다. 채집된 모기는 총 3,723마리로, 4속 16종을 확인하였다. 그 중 금빛숲모기 (*Aedes (Aedimorphus) vexans nipponii*) 가 1,711마리(45.96%)로 가장 높은 우점도를 나타냈으며, 흰줄숲모기 (*A. (Stegomyia) albopictus*) 와 큰검정들모기 (*Armigeres (Armigeres) subalbatus*) 각각 588마리(15.79%), 빨간집모기 (*Culex (Culex) pipiens pallens*) 269마리(7.23%)로 나타났다. 채집된 모기의 Flavi-virus 감염 여부를 확인하기 위해 RNA 추출 및 RT-PCR을 통해 확인하였으나, 모두 음성으로 확인되었다. 이러한 연구 결과들은 기후변화에 맞추어 변화하는 감염병 매개 모기의 발생 현황을 감시·예측하는데 유의한 자료로 활용될 수 있으며, 향후 모기 매개 질환 발생을 예측하기 위한 기초 자료로 활용될 수 있을 것으로 사료된다.

**검색어:** 해외 유입성 모기, 모기 매개 감염병, Flavi-virus

B-30

## Occurrence of SFTS infection rate in hard ticks collected in Dangjin, Chungcheongnam-do (2018-2023)

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지속적인 기후변화로 인해 매개 곤충을 통한 다양한 신종감염병이 국제적으로 확산되고 있으며, 발생빈도 또한 증가하는 추세이다. 이러한 매개질병을 관리하기 위해서는 질병을 매개하는 매개체에 대한 정보와 지속적인 모니터링이 필요하다. 이 연구는 제3급 법정 감염병으로 지정된 중증열성혈소판감소증후군(Severe Fever with Thrombocytopenia Syndrome, SFTS) 및 라임병(Lyme disease) 등의 매개체로 알려져 있는 참진드기를 대상으로 충남 당진 일대에서 2018년부터 2023년까지 총 6년, 4월-11월의 기간동안 월 1회 4개의 환경(무덤, 산길, 잡목림, 초지)에서 드라이아이스 유인트랩을 사용하여 발생밀도를 조사하였다. 그 결과 2018년 16,996마리, 2019년 16,698마리, 2020년 6,417마리, 2021년 7,380마리, 2022년 3,451마리, 2023년 3,465마리로, 총 54,407마리가 채집되었으며, 초지에서 가장 많이 채집되었다. 채집된 참진드기는 2속 3종으로 작은소피참진드기(*Haemaphysalis longicornis*), 개피참진드기(*H. flava*), 일본참진드기(*Ixodes nipponensis*)이며, 작은소피참진드기 (*H. longicornis*)가 42,489마리(78.09%)로 높은 우점도를 보였으며, SFTS 보유 여부를 확인하기 위해 RNA 추출 및 Nested RT-PCR 단계를 걸쳐 전기영동을 수행하였으나 양성 검체는 0건으로 확인되었다. 이러한 연구 결과는 SFTS의 주요 매개체인 참진드기 발생 양상 파악 및 매개 질병 관리 전략 수립에 기초 자료로서 활용될 수 있을 것으로 사료된다.

**검색어:** 참진드기, 진드기매개질환, SFTS

C-01

## Functional morphology of stabilimentum in the Garden Spider, *Argiope bruennichi*

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The genus *Argiope* are known to decorate their webs with various patterns. The purpose of these web decorations, referred to as stabilimenta, is still a subject of debate. They are believed to serve either as lures to attract prey insects or as a means of providing protection to the spider by enhancing the web's visibility to deter potential predators. In this study, we observed spider orientation with respect to the direction of the sun in a controlled laboratory environment. To assess the orientation preference of the spider, the frame was repositioned daily by reversing its direction. Over a period of 21 days, the orientation of the spider was meticulously recorded, distinguishing between the illuminated side (open side) and the shaded side (closed side). field emission scanning electron microscopy (FESEM) visualization were used to investigate the microstructural characterization of stabilimenta in both juvenile and adult spiders. Our results represent that the decorative structure of stabilimentum shows diverse microstructural features according to the maturation level of the spider. In addition, it has been confirmed that spiders tend to prefer the open side direction when stabilimentum is present.

**Key words:** microstructure, spider, stabilimentum, *Argiope bruennichi*

**Acknowledgement:** This research was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. 2019R1I1A3A01062105).

C-02

**Microstructural observation of non-woven silk fabric in the golden orb web spider, *Trichonephila clavata***

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Spider silk, which combines strength and lightness, emerges as an ideal candidate for non-woven fabric production. Unlike synthetic polymeric materials, silk are nontoxic and biocompatible and cause no allergic reaction. In particular, the dragline silk produced by the golden orb-web spider, *Trichoephila clavata*, is renowned for its superior strength and exceptional mechanical properties compared to other spider silks. Non-woven fabrics have found extensive applications in diverse industrial sectors, owing to their advantageous qualities such as breathability, durability, and lightweight characteristics. Natural dragline silk was extracted from the orb-weaving spider and subsequently randomly arranged. Compressing into a sheet-plane form, in addition to inducing the formation of water-resistant, stable  $\beta$ -sheet structures through ethanol vapor treatment or direct treatment, preserved the morphology of the silk fibers. The resulting non-woven sheets were analyzed with an field emission scanning electron microscope (FESEM) to observe their fine structures and mesh size were measured through image analysis.

**Key words:** FESEM, fine structure, *Trichonephila clavata*, non-woven silk, scaffold

**Acknowledgement:** This research was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. 2019R111A3A01062105).

C-03

**Microstructure of the *Trichonephila clavata* orb-web spider's cardiac muscle cells**

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Transmission electron microscopy was used to examine the microscopic structural features and myofibril organization of cardiac muscle cells in the orb-web spider *T. clavata*. There are many myofibrils, many mitochondria, a large sarcoplasmic reticulum, and transverse tubules (T-tubules) in the muscle fibers, even if the myofibril striations may not be as noticeable as in skeletal muscles. Because of their consistent striations, sarcomeres are characterized by Z-lines that are 2.0  $\mu\text{m}$  on average in length and do not clearly distinguish between the A- and I-bands. A single T-tubule paired with a terminal cisterna of the sarcoplasmic reticulum constitutes a dyadic junction, which is primarily located at the A-I level of sarcomeres. Cells are joined by intercalated discs, which create several linkages via specialized junctions such as desmosomes, gap junctions, and fascia adherens—all of which are essential for heart function. Our results with transmission electron microscopy (TEM) clearly show that the contraction of the spider's heart muscle is neurogenically controlled, since each fiber is innervated by a motor neuron branch via neuromuscular junctions. These results highlight the neurogenic process controlling spiders' cardiac muscle contractions and advance our knowledge of the peculiar cardiac muscle structure of these animals.

**Key words:** microstructure, cardiac muscle, sarcomere, spider, *Trichonephila clavate*

C-04

### Microstructural characteristic of the silk-based hydrogel scaffolds derived from *Trichonephila clavata*

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Silk fibroin (SF) from silkworms has special qualities, and these qualities have drawn a lot of interest lately in SF-based hydrogels for a range of biological applications. However, because there is a dearth of naïve silk materials to collect and prepare, research on the SF-based hydrogels isolated from spider silks has been rather limited. Thus, this study compared the microstructural properties of silk fibroin (SF) hydrogel scaffold, which was taken from the cocoon of the insect silkworm *Bombyx mori*, with those of hydrogel scaffolds derived from two types of woven silk glands in the orb-web spider *Trichonephila clavata*: the major ampullate gland (MAG) and the tubuliform gland (TG). The SF hydrogel, which is stabilized by connected SF fibers, has a loose top structure, high porosity, and translucency, according to our FESEM investigation. While the TG hydrogel showed greater porosity, ridge-like or wall-like structures, and stable biocapacity generated by physical cross-linking, the MAG hydrogel showed even higher porosity, elongated fibrous structures, and superior mechanical properties. It is anticipated that the unique microstructural properties of MAG and TG hydrogels will be advantageous when choosing customized substrates to support particular cell types for tissue engineering and regenerative medicine applications.

**Key words:** microstructure, hydrogel, scaffold, silk, spider

C-05

### Differences in the microstructure of silk-based film scaffolds derived from spider cocoons (*Trichonephila clavata*) and silkworm (*Bombyx mori*)

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In contrast to conventional silk fibroin, spider silk's potential as a scaffold material for tissue engineering is examined in this work. The remarkable qualities of spider silk are being researched for use in making films for tissue regeneration. In comparison to silk fibroin films, the study's analysis of orb-web spider *Trichonephila clavata* films highlights their improved cell adhesion and nanofibrous network structure. Tests for solubility substantiate the durability of spider silk films, while in vitro investigations demonstrate low cytotoxicity and enhance cellular viability. The conclusion highlights the exceptional properties of spider silk, which make it a viable option for tissue engineering applications and a step forward for in vitro cell culture and regenerative bioengineering.

**Key words:** silk, spider, silkworm, cell culture, scaffold

D-01

## Anti-obesity efficacy of Japanese Rhinoceros Beetle (*Allomyrina dichotoma*) larvae Flavourzyme and Protana Prime hydrolyzate

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본 연구는 장수풍뎅이(*Allomyrina dichotoma*) 유충을 가수분해한 후 발생한 가수분해물 시료의 항비만 효능에 관한 결과이다. 먼저 3T3-L1 세포에 대한 시료의 독성을 테스트하였다. 시료 F10, P10, P30은 세포에 62.5ug/ml 처리 시 세포 생존율은 ~87.5% 정도로 나타났으며 F30의 경우 세포가 모두 건강하게 성장하는 것을 알 수 있었다. 다음으로 지질합성 관여 단백질인 SREBP-1과 FAS에 대한 발현 억제 실험을 진행하였다. 시료 F10과 F30을 처리 하였을 때 SREBP-1과 FAS의 발현을 가장 잘 억제한다는 것을 알 수 있었다. 3T3-L1 지방세포 분화 과정을 Oil Red O staining 방법으로 염색 후 관찰을 진행하였다. 컨트롤과 비교하여 시료 F10, F30, P10과 P30을 처리한 지방 세포들은 모두 세포 분화 억제가 관찰되었으며 특히, 시료 F10에서 지방세포 분화 억제가 활발히 발생한다는 것을 알 수 있었다. 위 결과를 종합해 보면, 시료 F10과 F30을 혼합하여 사용한다면 반려동물에 대하여 효과 있는 항비만 사료를 개발할 수 있으리라 판단된다.

**검색어:** 장수풍뎅이, 가수분해물, 항비만, 지방세포, 지질축적

D-02

## Anticoagulant properties and therapeutic potentials of wasp venom

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Wasp venom is rich in bioactive substances, such as proteins, peptides, and small molecules. The venom significantly affects the mammalian cardiovascular, nervous, and immune systems, causing mild to severe symptoms following stings. It exhibits both procoagulant and anticoagulant activities, and significant research has identified its ability to modulate the mammalian coagulation system. Active substances that inhibit clotting were identified and purified through patient case reports and experimental studies. The study reviewed the findings on how wasp venom interacts with platelets and coagulation factors, such as fibrinogen and prothrombin, and demonstrated its dual influence on the coagulation cascade. This highlights the potential of the venom in therapeutic applications, especially as an anticoagulant, as evidenced by the inhibition of coagulation factors and prolonged clotting times after envenomation, suggesting its utility in developing novel anticoagulant therapies. This review focuses on the anticoagulant effects of social wasp venom, which is prevalent in sting incidents, summarizing the research and observations on its therapeutic potential. This emphasizes the significance of further studies to identify and utilize venom components as innovative anticoagulant treatments.

**Key words:** Wasp venom, anticoagulant, coagulation factors, therapeutic application, thrombosis



E-01

## Complete mitochondrial genome sequence of the Korean turnip sawfly *Athalia japonica* (Klug) (Hymenoptera: Tenthredinoidea)

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*Athalia japonica* (Klug, 1815) is a significant insect pest of turnips in Korea. The complete mitochondrial genome of this species isolated in Korea is reported in this study, which is the first attempt to study Korean *Athalia* species. The circular genome is 15,662 bp in length and consists of 13 protein-coding genes, two rRNA genes, 22 tRNA genes, and an A+T-rich region. Consistent with most members of the genus *Athalia*, five of the tRNA genes are rearranged from the typical ground pattern of ancestral insect gene order. Phylogenetic analyses inferred from the nucleotide sequences of 25 mitochondrial genomes indicate that the Korean *A. japonica* is a distinct member of the genus *Athalia*. This study accumulates mitochondrial genome data of *A. japonica* from various countries, providing useful information on mitochondrial genetic differences across geographical distances in the East Asian region.

**Key words:** Athaliidae, mitogenome, phylogenetic status, Symphyta

This work was supported by the National R&D Program through the National Research Foundation of Korea (NRF) funded by Ministry of Science and ICT under Grant number 2020R1A6A3A01095736.

E-02

**Development and Characterization of novel microsatellite markers for *Nemoura geei*  
(Plecoptera: Nemouridae)**

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Stoneflies (Plecoptera) are known for being sensitive to water pollution and are used as bioindicators for evaluating water quality. Among them, Nemouridae, especially the genus *Nemoura*, which are commonly referred to as winter stoneflies, can be found around streams even during the cold winter months. *Nemoura geei* Wu, 1929, among them, was originally described from Beijing and is widely distributed in Korea, China, Japan, and the Russian Far East. Here, we report the development and characterization of new functional microsatellite markers of *N. geei* using high-throughput sequencing technology. A total of 80,661 microsatellite loci were identified with a total length of 1,801,591 bp. The average length was 22.34 bp, and microsatellites occupied 0.42% of the entire sequence. The novel 20 microsatellite markers developed in this study can be usefully applied to the population genetics analyses as important genetic resources for understanding the ecological and evolutionary characteristics of a stonefly species at the population level in Korea.

**Key words:** stonefly, high-throughput sequencing, Microsatellite, population genetics

E-03

## Identification of SFTS virus infected *Haemaphysalis longicornis* ticks using immune response gene-based screening approach

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The major innate immune pathways in Asian longhorned ticks, *Haemaphysalis longicornis*, include Toll, IMD, and JAK/STAT. In the field, *H. longicornis* can be infected with various pathogens including Severe Fever with Thrombocytopenia Syndrome Virus (SFTS virus), *Rickettsia*, *Babesia* and *Anaplasma* species. One approach to identify whether ticks are infected with pathogens is by examining the expression levels of immune response genes. To evaluate whether upregulation of immune genes from *H. longicornis* can serve as an indicator for pathogen infection in ticks, we first designed primer sets for Dorsal, STAT, and Relish from the *H. longicornis* genome. We then conducted quantitative reverse transcription PCR (qRT-PCR) on cDNA of field-collected *H. longicornis* and identified individuals with high expression levels in immune response genes. Subsequently, we performed digital PCR assays to determine whether selected ticks were infected with SFTS virus. Using this approach, we evaluated correlation between pathogen infection and upregulation of immune response genes in ticks. Although more experiments are needed to draw conclusions, this study suggests immune response gene-based screening methods for pathogen infected ticks from the field.

**Key words:** *Haemaphysalis longicornis*, Severe fever with thrombocytopenia syndrome virus, Innate immunity

E-04

**Functional importance of group I lytic polysaccharide monoxygenase  
in turnover of chitinous cuticle in two longhorn beetle species,  
*Monochamus alternatus* and *Psacotheta hilaris***

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Lytic polysaccharide monoxygenases (LPMOs) catalyze the oxidative cleavage of glycosidic bonds in crystalline polysaccharides including chitin and cellulose. The recent discovery of LPMO family proteins in many insect species suggests that they presumably play a role in chitin degradation in the cuticle/exoskeleton, tracheae and peritrophic matrix during insect development. Insect LPMOs belong to auxiliary activity family 15 (AA15/LPMO15) and have been classified into at least four groups based on phylogenetic analysis. In this study, we identified and investigated the physiological functions of group I LPMO15 (MaLPMO15-1 and PhLPMO15-1) in two longhorn beetle species, *Monochamus alternatus* and *Psacotheta hilaris*. In both species, depletion of *LPMO15-1* transcripts by RNAi resulted in a lethal pupal-adult molting defect. The insects were unable to shed their old pupal cuticle and died entrapped in their exuviae. Furthermore, TEM analysis revealed a failure of degradation of the chitinous procuticle layer of their old cuticle, retaining intact horizontal laminae and vertical pore canals containing perpendicularly oriented chitin fibers (pore canal fiber, PCF) in their core. These results indicate that MaLPMO15-1 and PhLPMO15-1 are required for turnover of the chitinous old cuticle, which is critical for insect molting.

E-05

**JNK Kinase, *hep*, regulating AMP production in *Tenebrio molitor***

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It is well known that the JNK pathway regulates AMP production against pathogenic infection in both vertebrates and invertebrates. *Tenebrio molitor hep* (*Tmhep*) is an homolog of MAP kinase kinase in mammals. Here, we investigate the immunological function of *Tmhep* in responses in microbial infection using RNA interference technology. The results showed that silencing of *Tmhep* increased the larval mortality against microbial challenge, as well as reduced AMP production compared to the control group (*dsEGFP*-treated group). Conclusively, *Tmhep* plays an critical role in antimicrobial defense in *T. molitor* larvae.

**Key words:** *Tenebrio molitor*, *Tmhep*, JNK pathway, innate immunity, microbial challenge, RNAi

E-06

### ***In silico* identification and expression analysis of glutathione S-transferase in *Tenebrio molitor***

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In insects, the glutathione S-transferase is initiated in both the detoxification process and the protection of cellular membranes against oxidative damage. In this study, we identified the open reading frame (ORF) sequence of *GST-iso1* and 2 from *Tenebrio molitor* (*TmGST-iso1* and 2). To investigate the expression patterns of *TmGST-iso1* and 2 in response to herbicide, 0.06, 0.6, and 6  $\mu\text{g}/\mu\text{l}$  of butachlor (FarmHannong, Seoul, South Korea) was challenged into *T. molitor* larvae, resulting that the *TmGST-iso1* were highly induced at 3 and 24 h-post injection. Whereas, the highest expression of *TmGST-iso2* was detected at 24 h after treatment. This study may contribute to basic information about the detoxifying activities of *T. molitor*.

**Key words:** *Tenebrio molitor*, Detoxification, Herbicide, Developmental stages, Tissue specificity

E-07

### **Study on immunological role of *TmPelle* in *Tenebrio molitor***

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Pelle, a serine/threonine kinase, is an intracellular component of the Toll pathway and is involved in antimicrobial peptides (AMPs) production due to pathogenic infection. It is known that the Pelle phosphorylates Cactus and activates the NF- $\kappa$ B signaling pathway in *Drosophila*, but it is not studied in *Tenebrio molitor*. In this study we investigated the tissue-specific expression patterns of the *Pelle* following pathogenic infection at 3, 6, 9, 12, and 24 hours. Additionally, larval mortality and AMP expression against microbial injection were investigated in ds*Pelle*-treated *T. molitor* larvae. Our results may help to understand the antimicrobial function of *TmPelle*.

**Key words:** *Tenebrio molitor*, Toll pathway, Pathogen infection, qRT-PCR, RNAi

E-08

### Study on antimicrobial function of *Tm*TRAF in *Tenebrio molitor*

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Tumor necrosis factor receptor-associated factor (TRAF) is known to regulate antimicrobial peptides (AMPs) production in mammals. Here, to understand the immunological function of *Tm*TRAF against microbial challenge, the induction patterns of *Tm*TRAF against microbial infection was investigated by qRT-PCR in the whole-body and tissue of young larvae. In addition, the effects of *Tm*TRAF RNAi on larval mortality and expression of 15 AMP genes in response to microbial infection were investigated. Our studies may help to understand the basic role of AMP production.

**Key words:** *Tenebrio molitor*, *Tm*TRAF, Antimicrobial peptide, Microbial infection, qRT-PCR, RNAi

E-09

### Functional study of *Tm*Tube on AMPs production against microbial infection

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Tube, an intracellular protein of the Toll-pathway, forms a complex with Pelle and MyD88, and regulates a signal transduction to activate NF- $\kappa$ B in *Drosophila*. To understand the antimicrobial function of *Tm*Tube, the induction patterns of *Tm*Tube were investigated at 3, 6, 9, 12, and 24 h-post injection of pathogens into 10<sup>th</sup> to 12<sup>th</sup> instar larvae. In addition, we investigated the effects of *Tm*Tube RNAi on larval mortality and tissue specific AMP expression in response to microbial challenge. Our results will provide a basic information to elucidate the immunological function of *Tm*Tube

**Key words:** *Tenebrio molitor*, Toll pathway, *Tm*Tube, RNAi, antimicrobial peptides, larval mortality

E-10

### Effects of *TmPellino* silencing on larval mortality and AMPs production

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Pellino, a highly conserved E3 ubiquitin ligase, is known to mediate ubiquitination of phosphorylated Interleukin-1 receptor-related kinase (IRAK) homologs in Toll signaling pathway. To understand the immunological function of *TmPellino*, we screened the knockdown efficiency of *TmPellino* by injecting *TmPellino*-specific dsRNA into *T. molitor* larvae. Subsequently, we investigated the larval mortality and the tissue-specific expression patterns of antimicrobial peptide (AMP) genes against microbial challenges. Interestingly, the results indicate that the expression of many AMP genes was upregulated in the Malpighian tubules of *TmPellino*-silenced *T. molitor* larvae. This study may provide basic information to understand how *TmPellino* regulates AMPs production in *T. molitor*.

**Key words:** *T. molitor*, Toll pathway, *TmPellino*, pathogenic infection, qRT-PCR, RNAi

E-11

### Enhancement of Antimicrobial peptides production by epigenetic regulation

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Recently, it is demonstrate that the invertebrates have a immune memory, called Immune priming (IP). It was partially studied that the IP is mainly regulated by epigenetic modification. Here, to understand the IP on antimicrobial peptides (AMPs) production, we investigated larval mortality and time-dependent expression patterns of AMP genes in *T. molitor* larvae challenged with *E. coli* (two-times injection with a one-month interval). Interestingly, the results indicate that the higher and faster expression levels of most AMP genes were detected compared to the non-primed *T. molitor* larvae. Our results may used to improve the understanding of mechanisms of invertebrate immune memory.

**Key words:** Immune priming, *Tenebrio molitor*, Pathgen injection, Antimicrobial peptides, qRT-PCR

E-12

## Transcriptomic analysis of RNA expression in mice treated with insect-derived chitin and chitosan

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Chitin and chitosan, abundant biopolymers from shellfish, crustaceans, and fungal hyphae, have diverse applications in food, biomedical, and industrial sectors. Also, insects offer a one of the chitin and chitosan source, yet research into the biological processes of chitin and chitosan within insects remains inadequate. To investigate the safety and benefits of insect-derived chitin and chitosan, we orally administered crab-derived and insect-derived chitin and chitosan to mice and compared RNA expression. NGS derived sequences were obtained and DEG and GO analyses were performed. This study displays a chance to progress the application of edible insects.

**Key words:** Transcriptome, DEG, insect-derived chitin, insect-derived chitosan



## Transcriptome analysis and identification of SSR markers in *Haemaphysalis flava* females using Illumina HiSeq 4000

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참진드기과(Ixodidae) 속하는 개피참진드기(*Haemaphysalis flava*)는 동남아시아에서 남아시아에 걸쳐 분포하며, 다양한 질병을 매개하는 것으로 알려져 있다. 특히 중국, 일본, 한국에서 개피참진드기의 주요 매개 질병인 중증열성혈소판감소증후군(SFTS)의 감염 사례가 지속적으로 증가하는 것으로 보고되고 있다. 이 연구는 Illumina HiSeq 4000 시퀀싱을 통해 raw 데이터를 획득하고, Trinity를 기반으로 *de novo* assembly를 수행하여 unigene을 확보하였다. 이 결과, 총 69,822개의 unigene이 생성되었으며, 이 중 46,175개의 unigene이 PANM-DB에 annotation 되었다. 또한 KOG, GO 및 KEGG 분석을 통해 30,000개, 19,074개, 9,333개의 unigene이 annotation 되었으며, InterProScan 결과를 통해 protein kinase, zinc finger (C2H2-type), reverse transcriptase, RNA recognition motif domain 등과 같은 세포 조절 메커니즘과 관련된 유전자가 확인되었다. RepeatMasker(v4.0.6)와 MISA(v1.0)를 사용하여 unigene에서 SSR 마커를 확인한 결과, 총 3,480개의 SSR 마커가 확인되었으며 이 중 trinucleotide 반복이 1,907개, dinucleotide 반복이 1,274개로 확인되었다. 이러한 연구 결과는 *H. flava* 암컷의 유전자 및 유전자 조절 메커니즘을 이해하는데 기초 자료로서 활용 가능하며, 질병 전파 감수성에 대한 후속 연구에 유용한 정보를 제공할 것으로 사료된다.

**검색어:** Tick, *Haemaphysalis flava*, Vector, Transcriptome, SSR markers

E-14

## Characterization of *Haemaphysalis longicornis* microbiome collected from different regions of Korean Peninsula

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*Haemaphysalis longicornis*는 사람과 동물에게 여러 심각한 병원체를 전달하는 주요 매개체로, 한반도에 널리 분포하고 있다. *H. longicornis*는 *Rickettsia* spp., *Borrelia* spp., *Francisella* spp., *Coxiella* spp., 그리고 중증열성혈소판 감소증후군 바이러스 (SFTS virus) 등을 매개하는 것으로 알려져 있다. 국내에 서식하는 *H. longicornis*의 미생물 군집과 관련된 연구는 많이 진행되지 않은 것으로 확인되었다. 이 연구는 한반도 내 다양한 지역에서 채집된 *H. longicornis*의 미생물군집 다양성을 지역별, 성장 단계 및 성별에 따라 분석하였다.

2019년 6월부터 7월까지 질병관리청 권역별기후변화매개체감시거점센터 16개 지역에서 채집한 *H. longicornis*의 16S rRNA 유전자 V3-V4 영역을 PCR로 증폭 후 Illumina MiSeq 플랫폼으로 시퀀싱하였다. Qiime2를 활용한 미생물 다양성 분석을 통해 총 46개의 샘플에서 1,754,418개의 non-chimeric reads를 얻었으며, 평균 126개의 operating taxonomic unit (OTU)을 식별하여 총 1,398개의 OTU를 확인하였다. 대부분의 지역에서 *Coxiella* spp.가 우점종으로 나타났으며, 특히 *Coxiella endosymbiont*는 가장 높은 우점도를 보이며, *Coxiella burnetii*와 계통 발생학적으로 유사한 것으로 확인되었다. 이 연구를 통해 분석된 결과는 각 지역의 *H. longicornis* 미생물군집 데이터 베이스 구축에 활용되었으며, 이를 통해 지역별 미생물군집의 특이성을 식별할 수 있게 하였다. 이는 한반도의 *H. longicornis*에 의한 질병 전파 연구와 이를 통한 공중보건 개선에 기여할 것으로 기대된다.

**검색어:** *Haemaphysalis longicornis*, microbiome

E-15

## Comparison of microbial communities of *Vespa mandarinia* according to sequencing platforms (Illumina MiSeq and PacBio HiFi)

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장내 미생물 군집은 소화 과정, 면역 시스템, 질병 발생 등 숙주의 다양한 면에 광범위한 영향을 주는 것으로 알려져 있으며, 주요 장내 미생물 종은 숙주의 생리 기능에 핵심적인 역할을 수행한다고 발표된 바 있다. 곤충의 장내 미생물 군집에 관한 연구가 최근 활발히 이루어지고 있으며, 이들 연구는 주로 장내 미생물 군집과 기생충, 병원체 간의 상호작용, 종간의 신호 전달 네트워크, 먹이의 소화 과정 등을 중심으로 이루어지고 있다. 이러한 연구들은 대부분 Illumina MiSeq을 활용하여 16S rRNA 유전자의 V1부터 V9 영역 중 선택된 특정 부분을 대상으로 짧은 서열 정보를 대상으로 진행되었다. 그러나, 최근에는 PacBio HiFi 기술이 상용화되면서 16S rRNA의 전장 분석이 가능할 수 있게 되었다. 이번 연구는 장수말벌(*Vespa mandarinia*)의 해부를 통해 gut과 carcass 부분을 분리한 뒤, 각 샘플을 Illumina MiSeq과 PacBio HiFi 기술을 활용하여 미생물 군집 간의 차이점을 확인하기 위하여 수행되었다.

**검색어:** *Vespa mandarinia*, Illumina MiSeq, PacBio HiFi, microbiome

**Whole transcriptome analysis of *Haemaphysalis longicornis* with Phlebovirus contamination in Korea**

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작은소피참진드기(*Haemaphysalis longicornis*)는 중증열성혈소판감소증후군 (SFTS)을 전파하는 주요 매개체로 알려져 있으며, 대한민국 전역에 분포하고 있다. SFTS는 2013년 첫 환자 보고 이후 SFTS의 보고 사례가 꾸준히 증가하고 있으며 이에 해당 질병을 전파하는 주요 매개체인 작은소피참진드기를 대상으로 한 연구의 중요성이 증가하고 있다.

전사체 분석은 Illumina HiSeq 4000 platform을 활용하여 진행하였다. Illumina HiSeq 4000에서 확보된 전사체 데이터를 Trinity 프로그램을 활용하여 *de novo* assembly를 진행하였으며, 이후 TGICL 프로그램을 통해 unigenes을 확보하였다. 이후 확보된 unigenes는 전사체의 기능을 추정 및 식별하기 위해 Swiss-Prot, KOG, GO, KEGG, PANMDB를 기반으로 한 BLASTx를 수행하였다. 또한 Phlebovirus의 존재 여부를 확인하기 위해 NCBI에 등록된 Phlebovirus 유전자원을 수집하여 데이터베이스를 구축하였으며, 구축된 데이터베이스에서 BLASTx를 진행하여 바이러스 전사체의 존재 여부를 분석하였다. 확보된 28,078개의 unigenes 중 19,414개의 unigene이 PANMDB에 annotation 되었으며, Swiss-Prot, KOG, GO, KEGG에서는 각각 13,117개, 13,002개, 8,588개, 1,651개의 unigene이 annotation 되었다. Phlebovirus 전사체 존재 여부 분석 결과, BLASTX를 통해 작은소피참진드기로부터 SFTS RNA polymerase와 유사성을 보이는 3개의 unigene의 존재를 확인하였다. 이번 연구 결과는 국내 작은소피참진드기 및 SFTS 바이러스 감시와 전염병 예방·통제에 있어 기초 자료로써 활용될 수 있을 것으로 사료된다.

**검색어:** *Haemaphysalis longicornis*, transcriptome, Phlebovirus, SFTS

**Transcriptome analysis of the endangered dung beetle *Copris tripartitus* (Coleoptera: Scarabaeidae) and characterization of genes associated to immunity, growth and reproduction**

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애기뿔소똥구리(*Copris tripartitus*)는 배설물 분해를 통해 환경정화와 생태계 균형에 기여하는 것으로 알려져 있다. 그러나 무분별한 농약 사용과 서식지 파괴로 인해 개체수가 감소되고 있어 2017년 환경부에서 애기뿔소똥구리를 멸종위기 야생생물 II급으로 지정하였다. 애기뿔소똥구리의 미토콘드리아 유전자를 활용한 선행연구가 발표되었지만 유전자원 확보는 여전히 미비한 실정이다.

이번 연구는 애기뿔소똥구리의 성장, 면역 및 생식과 관련된 유전 정보를 확보하기 위해 Illumina HiSeq 4000 platform을 활용하여 전사체 분석을 실시하였다. Illumina HiSeq 4000을 통해 확보된 전사체 데이터를 Trinity 프로그램을 통해 *de novo assembly*를 진행하여 contigs를 생성하였다. 생성된 contigs를 TGICL 프로그램을 통해 clustering 하여 unigenes을 확보하였다. 이후 확보된 unigenes는 PANMDB 및 Swiss-Prot, KOG, InterProScan, GO, KEGG를 기반으로 한 BLASTx를 사용하여 annotation을 진행하였다. 25,106개의 unigene 중에서 23,289개가 PANMDB에 annotation 되었으며, Swiss-Prot, InterProScan에서는 각각 19,660개, 13,545개의 unigene이 annotation 되었다. KOG 분석에서는 ‘general function prediction only’ 범주에서 높은 비율로 나타났으며, GO 분석에서는 ‘Molecular Function’ 카테고리에서 가장 많이 annotation 되었다. KEGG 분석을 통해서도 ‘Environmental information processing’ 항목이 높은 발현을 보였다. 이번 연구를 통해 확보된 기능적 데이터는 야생에서의 보존 계획을 수립하는 데 있어 기초 자료로써 활용될 수 있을 것으로 사료된다.

**검색어:** *Copris tripartitus*, Transcriptome, Illumina sequencing, Immunity-related genes, Simple sequence repeats, Informed conservation planning

E-18

## Transcriptome analysis of *Polyphylla laticollis manchurica* for discovering characteristics of endangered species

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수염풍뎅이(*Polyphylla laticollis manchurica*)는 과거에는 흔히 발견되었으나, 1970년대 이후 한반도 내 개체수가 급격히 감소하여 2005년 환경부에 의해 멸종위기 야생생물 I급으로 지정되었다. 또한 해당종의 분자생물학적 연구는 멸종위기종이라는 특성으로 인해 제한적으로 진행되었다. 그로 인해 NCBI 등 공공 데이터베이스에서 제공되는 서열정보들 또한 부족한 실정이다. 이 연구는 이러한 한계를 극복하고 수염풍뎅이의 유전적 특성을 규명하기 위해 생물정보학적 기술을 활용하여 전사체 분석을 진행하였다.

Illumina HiSeq 2500 플랫폼을 사용하여 53,433,048개의 RNA reads를 얻었으며, Trinity와 TGICL을 이용한 *De novo* 어셈블리 분석을 통해 18,172개의 unigenes를 생성하였다. 생성된 unigenes는 GO, KOG, KEGG, PANMDB를 활용하여 annotation을 진행하였다. 그 결과, GO 분석에서는 ‘binding and catalytic activities’와 관련된 항목이 높은 발현을 보였으며, KOG 분석의 경우 ‘Cellular Processes and Signals’ 범주가 높은 비율을 나타내었다. KEGG 분석을 통해 2,118개의 unigenes가 metabolic 카테고리 annotation된 것을 확인하였다. SSR 모티프 분석에서는 AT/AT (42.90%) 모티프, AAT/ATT (13.13%) 모티프 순으로 많이 나타나는 것을 확인하였다. 이 연구를 통해 분석한 결과들을 이용하여 유전자원 및 종 정보를 실시간 제공 및 정보 공유가 가능하도록 Database 및 web-interface를 구축하였으며, 이러한 자료들은 국내 멸종위기종인 수염풍뎅이의 고유한 유전적 특성을 발굴 및 확보할 수 있는 기반자료로써 활용될 수 있을 것으로 사료된다.

**검색어:** *Polyphylla laticollis manchurica*, transcriptome analysis

E-19

### Investigating the effects of *TmTak1* silencing on AMP production as an Imd pathway component in *Tenebrio molitor*

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*Tenebrio molitor* (*T. molitor*) is gaining attention as a sustainable food source with high nutrient content. Understanding their immune system, particularly the role of Tak1 in the Imd pathway, is essential for mass breeding. This study investigates *TmTak1* function in *T. molitor*. We investigated the immune function of *TmTak1*, followed by systemic infection using *E. coli*, *S. aureus*, and *C. albicans*. As a result, silencing *TmTak1* significantly affects expression levels of AMPs in the whole body, fat bodies, and integuments. These results showed lower expression levels of AMP compared to the control group during *E. coli* injection.

**Key words:** *Tenebrio molitor*, Imd pathway, *TmTak1*

E-20

### Molecular characterization of *FADD* gene in *T. molitor* and its requirement for survivability against *E. coli* infection

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Fas-associated death domain protein (FADD) functions as an apoptotic adapter in mammals, recruiting caspases for death-inducing signaling complexes, while in lower animals, it interacts with IMD and DREDD to initiate antimicrobial responses. In this study, we examined the *T. molitor* FADD sequence (*TmFADD*) using molecular informatics methods to understand its involvement in the host's immune response against microorganisms. Knocking down *TmFADD* transcripts resulted in increased susceptibility of *T. molitor* larvae to *E. coli*, underscoring the significance of FADD in insect defense mechanisms and providing valuable insights into insect immunity.

**Key words:** IMD pathway, FADD, *Tenebrio molitor*, RNAi

F-01

## Insecticide resistance mutations in *Anopheles sinensis* from Republic of Korea

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말라리아는 *Anopheles* 모기들에 의해 전파되며, 대한민국에서는 코로나 팬데믹 기간 동안(2020~2022) 약 200~300명대의 말라리아 환자가 발생하였으나, 지난 2023년에는 그 수가 폭증해 약 800명의 환자가 발생하였다. 현재까지 모기를 방제하기 위한 가장 효율적인 수단은 살충제를 사용한 방제이나, 지속적으로 이러한 화학물에 노출된 모기 개체군은 살충제에 저항성을 갖게 되는 것으로 알려져 있다. 이에 본 연구에서는 대한민국의 주요 말라리아 발생 지역인 비무장지대 부근 및 이외 지역인 용산, 평택, 오산에서 채집을 진행하였으며, 채집된 *An. sinensis*에 대해서 살충제 저항성과 관련되어 있다고 알려진 유전자인 acetylcholinesterase-1(*ace-1*)와 voltage-gated sodium channel(*vgsc*) 영역에 대한 저항성 돌연변이 보유 여부를 각각 확인하였다. 실험 결과 채집된 모든 지역에서 G119S(*ace-1*), L1014F,C(*vgsc*) 돌연변이가 발견되었으며, 그 빈도는 계절과 장소에 따라 차이를 나타내었다. 본 실험 결과는 향후 말라리아 감염 억제를 위한 매개체 연구에 활용될 수 있을 것으로 기대된다.

**검색어:** Insecticide resistance, Voltage-gated sodium channel, Acetylcholinesterase, *Anopheles sinensis*



F-02

**Phyto-metabolites 3-hydroxy-1,2-dimethyl-4(1H)-pyridone and Tyrosol from coral jasmine (*Nyctanthes arbor-tristis*) flower extracts toxicity and enzyme inhibitory actions on agricultural pest and beneficial earthworm**

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Green pesticides, derived from natural sources, have gained wider attention as an alternative approach to synthetic pesticides in managing polyphagous pests like *Spodoptera litura*. In this study, the methanolic flower extract of *Nyctanthes arbor-tristis* (Mx-Na-t) was subjected to chemical screening, and major peak area derivatives 3-Hydroxy-1,2-dimethyl-4(1H)-pyridone (3H-dp) and Tyrosol (Ty-ol) were identified. The toxicity against *S. litura* larvae of Mx-Na-t (at 500 ppm) was highest in third instars (96.4%), and for 3H-dp and Ty-ol (at 5 ppm) in II instars (76.5% and 81.4%, respectively). The growth and development of *S. litura* larvae and pupae were significantly reduced by all three extract and phytochemical treatments. Fecundity rates also declined with the treatments, from 1,020 eggs (control) to 540 eggs (Mx-Na-t), 741 eggs (3H-dp), and 721 eggs (Ty-ol). The extract and its active constituents decreased adult emergence and slowed total larval development in a dosedependent manner. The major gut enzymes of *S. litura* decreased in young larvae (II instar) exposed to Mx-Na-t, 3H-dp, and Ty-ol. Fourth instar midgut tissues were severely damaged by Mx-Na-t (250 ppm), 3H-dp, and Ty-ol (2.5 ppm) treatments, which induced structural damage to the epithelial cells and gut lumen. The earthworm *Eisenia foetida* was used to test for non-target toxicity. Crude Mx-Na-t at 500 ppm (13% and 3%) and 3H-dp (9.3% and 2.1%) and Ty-ol (10.2% and 1.5%) at 5 ppm produced lower mortality than the synthetic chemical cypermethrin at 1.0 ppm (27% and 18%) in filter paper and artificial soil assays, respectively. In addition, there was no significant change in earthworm weights under all three phytochemical treatments compared to controls. Additionally, the in-silico predictions of BeeTox and ProTox II indicated little or no toxicity toward honey bees and other nontargets associated with 3H-dp and Ty-ol. Overall these phyto-chemicals offer an effective pest management strategy.

**Key words:** Plant Toxin; Tyrosol; 3-Hydroxy-1,2-dimethyl-4(1H)-pyridone; Lepidopteran pests; Enzyme Inhibition; Earthworm toxicity

G-01

## Effects of density, feed material, and container on development of *Protaetia brevitarsis* larvae

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*Protaetia brevitarsis* larvae have been widely used for traditional medicine and food in East Asia. This research comprised two experiments. The first experiment compared the growth in densities (10, 20, 30 larvae), substrates (commercial, self-made), and containers (Tyvek, zipper bags). In the second experiment, different numbers of air holes (16, 32, 48 holes) in zipper bags experiment is ongoing. The results indicated that the larvae development rate was 72.6%, 69.98%, and 55.33% in 10, 20, and 30 larvae densities, respectively. However, there was no significant difference in larvae survival rate and weight. In the different feed material experiments, the average larvae weight of commercial feed was 1.09g and for self-made, it was 2.85g. The survival rate was 86% and 96% in commercial and self-made feed, respectively. Lastly, while 96% of larvae survived in Tyvek bags, none of the larvae survived in the zipper bags.

**Key words:** *Protaetia brevitarsis*, edible insect, density, tyvek bag, feed material

H-01

## Temperature effect on *Sarcophaga peregrina* (Diptera: Sarcophagidae) for PMI estimation in South Korea

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*Sarcophaga peregrina* (Robineau-Desvoidy, 1830) play a pivotal role in forensic entomology, particularly in the context of decomposing corpses in South Korea, with its prevalence most notable from May to October. This study aims to leverage the growth metrics of *S. peregrina* to refine estimates of the minimum post-mortem interval (PMI<sub>min</sub>), thereby providing a more localized and accurate measure of the time elapsed since death. By cultivating specimens across a range of temperatures (22°C, 25°C, 28°C, and 34°C), we documented the corresponding larval and pupal development rates, observing significant variances in development times across temperatures: 475.1 hours at 22°C, 347.0 hours at 25°C, 326.0 hours at 28°C, and 247.3 hours at 34°C. Our findings highlight a temperature-dependent acceleration in life cycle progression of research emphasizes the importance of considering environmental factors, particularly temperature, to enhance the accuracy of forensic investigation.

**Key words:** *Sarcophaga peregrina*, Forensic entomology, Post-mortem interval (PMI<sub>min</sub>), Decomposition, Temperature-dependent development

H-02

## Content of 20-Hydroxyecdysone in *Achyranthes japonica* (roots) and *Protoetia brevitarsis* (larvae)

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Ecdysteroids were first discovered in silkworm larvae in 1954 and are known to act as molting hormones in insects. Recently, biologically active phytoecdysone has gained increasing interest as it affects many physiological functions in mammals and has been reported to have a wide range of pharmacological properties such as protein synthesis and anticancer. 20-Hydroxyecdysone is a class of ecdysteroids commonly found in plants and animals and is known to stimulate antibody formation in humans, reduce cholesterol levels, and exert anabolic and blood sugar-lowering effects. In order to determine the content of 20-Hydroxyecdysone in *Achyranthes japonica* (roots) and *Protoetia brevitarsis* (larvae), which are known to have related benefits, we wanted to confirm their value as medicinal ingredients. The results of the analysis showed 0.0389 ug/g for *Protoetia brevitarsis* and 4.36 ug/g for *Achyranthes japonica*. These results confirm that plants secrete high concentrations of ecdysteroids to prevent insect damage, and are expected to be used as a basis for future research on the extraction of 20-Hydroxyecdysone for biological control and pharmacological use.

**Key words:** 20-Hydroxyecdysone, *Achyranthes japonica*, *Protoetia brevitarsis*