## 2024년 한국곤충학회

# 추계학술대회 및 정기총회

## Urban Entomology

일정 | 2024년 11월 28일(목) ~ 30일(토)

장소 | 국립생물자원관 생생채움동

주최 | 사단법인 한국곤충학회
The Entomological Society of Korea

주관 | 국립생물자원관

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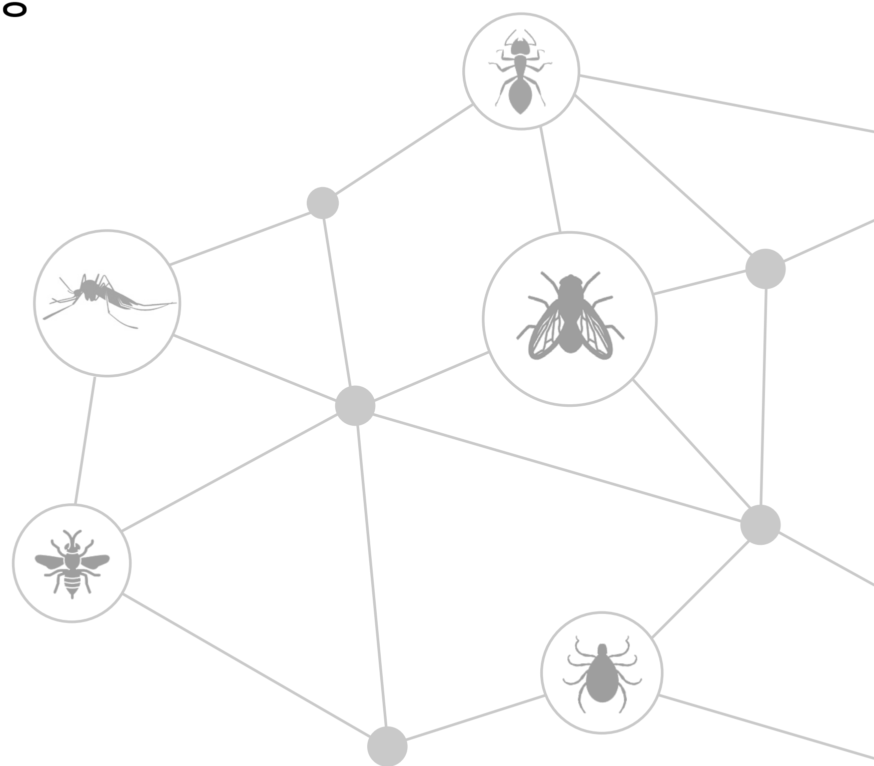

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# 2024년 한국곤충학회 추계학술대회 및 정기총회

## - Urban Entomology -

일정: 2024년 11월 28일(목) 13:30 ~ 30일(토) 11:00 / 장소: 국립생물자원관

| 11월 28일(목) | 행사 및 장소 | | |
|---|---|---|---|
| 12:30~13:30 | 접수(로비) | | |
| 13:30~13:45 | 개회사 및 축사(대강당)<br>진행: 장호암 총무<br>개회사: 한국곤충학회 이용석 회장<br>축 사: 국립생물자원관 서민환 관장 | | |
| 13:45~14:00 | 전체 기념사진촬영 | | |
| | **Session I (대강당)**<br>좌장: 조용훈(순천향대학교) | | |
| 14:00~14:40 | **기조강연 1**<br>Why does insecticide resistance rarely occur in *Anopheles* mosquitoes in the GMS region?<br>Theeraphap CHAREONVIRIYAPHAP (Kasetsart University, Thailand) | | |
| 14:40~15:20 | **기조강연 2**<br>Global perspective of bed bug management and its challenges<br>CHOW-YANG LEE (University of California, USA) | | |
| 15:20~15:30 | **Break** | | |
| | **Session II (대강당)**<br>좌장: 조영호(국립생태원) | **심포지엄 I (세미나실)**<br>좌장: 안능호(국립생물자원관) | |
| 15:30~16:00 | **특별강연 1**<br>Emerging threats: Urban entomology and the rise of invasive species in South Korea<br>김대윤(Kasetsart University, Thailand) | 15:30~17:30 | **석주명 선생 표본 귀환 기념 심포지엄**<br>- 한국 초기 곤충 연구의 선구자, 석주명 선생 - |
| 16:00~16:30 | **특별강연 2**<br>Ecological study of *Ephemera orientalis* mass emergence in the Hangang River<br>김동건(삼육대학교) | | |
| 16:30~17:00 | **특별강연 3**<br>Evolution and adaptive capacity of aquatic insects in urban environments<br>강지현(고려대학교) | | |
| | **평의원회 및 정기총회(대강당)** | | |
| 17:30~17:45 | 평의원회 | | |
| 17:45~18:00 | 정기총회 | | |
| 18:30 | 간친회 | | |

| 11월 29일(금) | 행사 및 장소 | | |
|---|---|---|---|
| 9:30~10:00 | 접수 | | |
| | **신진과학자 강연(대강당)**<br>좌장: 김명철(SOKN생태보전연구소) | **심포지엄 II (세미나실)**<br>좌장: 최문보(경북대학교) | |
| 10:00~10:30 | Historical review of Acentropinae (Crambidae, Lepidoptera) from Korea<br>이탁기(이화여자대학교) | 10:00~11:30 | 사회성 곤충 심포지엄 I |
| 10:30~11:00 | Taxonomic studies on Korean Miridae and future research prospects<br>오민석(서울대학교) | | |
| 11:00~11:30 | DNA barcoding of chironomid larvae (Diptera: Chironomidae) from large rivers in South Korea to facilitate freshwater biomonitoring and public health surveillance<br>강효정(삼육대학교) | | |
| 11:30~12:30 | **점심 / Break** | | |
| 12:30~13:30 | **포스터발표** | | |
| | **일반구두발표(대강당)**<br>좌장: 최진경(대구교육대학교) | **심포지엄 III (세미나실)**<br>좌장: 최문보(경북대학교) | |
| 13:30~14:45 | 일반구두발표 | 13:30~15:00 | 사회성 곤충 심포지엄 II |
| | **학생구두발표(대강당)**<br>좌장: 정종철(곤충생태환경연구소) | | |
| 14:45~17:00 | 학생구두발표 | | |
| | **조복성 퀴즈 및 시상식(대강당)** | | |
| 17:00~17:15 | 조복성 퀴즈 | | |
| 17:15~17:30 | 우수상시상식 | | |
| **11월 30일(토)** | **행사 및 장소** | | |
| 10:00~10:50 | 한국곤충학회 운영위원회 회의 | | |
| 10:50~11:00 | 폐회식 | | |

## 11월 28일(목) Session Ⅰ 기조강연(대강당) 좌장: 조용훈(순천향대학교)

## 11월 28일(목) Session Ⅱ 특별강연(대강당) 좌장: 조영호(국립생태원)

## 11월 29일(금) 신진과학자 발표(대강당) 좌장: 김명철(SOKN생태보전연구소)

**11월 28일(목)** | **심포지엄 Ⅰ (세미나실)** | **좌장: 안능호(국립생물자원관)**

**- 석주명 선생 표본 귀환 기념 심포지엄 -**

**11월 29일(금)** | **심포지엄 Ⅱ (세미나실)** | **좌장: 최문보(경북대학교)**

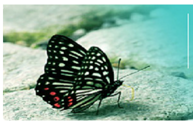
**- 사회성 곤충 심포지엄 Ⅰ -**

**11월 29일(금)** | **심포지엄 Ⅲ (세미나실)** | **좌장: 최문보(경북대학교)**

**- 사회성 곤충 심포지엄 Ⅱ -**

## 11월 29일(금) 일반구두발표(대강당) 좌장: 최진경(대구교육대학교)

**11월 29일(금)** **학생구두발표(대강당)** **좌장: 정종철(곤충생태환경연구소)**



## ◈ 분야별 포스터 학술연구발표

### 【 분 류 】

## 【 생 태 】

## 【 형 태 】

## 【 생 리 】

## 【 분자생물 】

【 방 제 】

【 식용곤충 】

## 【 기 타 】

# 기조강연

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 28일(목) 14:00 ~ 15:20

Session Ⅰ (대강당)

**<기조강연 1>**

# Why does insecticide resistance rarely occur in *Anopheles* mosquitoes in the GMS region?

Theeraphap CHAREONVIRIYAPHAP[1,2]

*[1]Department of Entomology, Faculty of Agriculture, Kasetsart University, Bangkok, Thailand*
*[2]Research and Lifelong Learning Center for Urban and Environmental Entomology, Kasetsart University, Kasetsart University Institute for Advanced Studies, Bangkok, Thailand*

Chemical pesticides are still commonly used in Thailand and other GMS countries for the control of agricultural pests and disease vectors. Organophosphates, carbamates, and synthetic pyrethroids are commonly used for agricultural purposes, whereas synthetic pyrethroids have become more popular and predominate for public health use. The genetic selection of insecticide resistance (physiological) in pests and disease vectors has been extensively reported, especially with two dengue vectors, *Aedes aegypti* and *Aedes albopictus*. Most surprisingly, however, there have been few reported cases of pyrethroid resistance in anopheline mosquito populations in this region. The precise reasons for this are not fully understood, but behavioral avoidance of insecticides may play a key role by reducing selection pressure, which in turn limits the development and spread of resistance. Additionally, primary malaria vectors in this region tend to breed and rest in forested or forest-edge habitats where insecticide use is minimal. Further investigation into physiological resistance to insecticides in *Anopheles* mosquitoes is warranted to better understand and address potential resistance issues.

**Keywords:** Insecticide, Resistance, Behavioral, Malaria vector, GMS

**<기조강연 2>**

# Global perspective of bed bug management and its challenges

CHOW-YANG LEE

*Department of Entomology, University of California, Riverside, CA 92521, USA*

Bed bugs have become an important group of urban insect pests in many parts of the world. Approximately US$1 billion is estimated to be spent yearly on bed bug management in the US alone. Bed bug infestations have been reported in residential and public accommodations, buses, trains, airplanes, etc. Over the last 20 years, the pest management industry worldwide has seen a drastic increase in the bed bug market segments. Two bed bug species are important globally – the common bed bug (*Cimex lectularius*) and the tropical bed bug (*Cimex hemipterus*). *C. lectularius* is generally distributed in the temperate and subtropical regions, while *C. hemipterus* is found in the tropics. The worldwide resurgence of both bed bug species has been mainly due to insecticide resistance. To date, bed bugs have been reported to become resistant to all the major classes of insecticides. The mechanisms involved include penetration resistance, metabolic resistance (cytochrome P450, esterase, glutathione S-transferase, and ABC transporters, target-site resistance (*kdr* and altered acetylcholinesterase), and behavioral resistance. The strategies used in resistance management against bed bugs are to prevent or delay insecticide resistance development. There are many chemical control formulations for bed bug control such as liquid spray, pressurized aerosol, dust, fumigants, insecticide-impregnated fabric, repellent, and total release foggers. Many contain pyrethroids and are ineffective against pyrethroid-resistant bed bugs. Insecticide rotation is a resistance management strategy that rotates insecticides of a different mode of action in sequence (e.g., once every quarter). However, with extensive pyrethroid resistance now, there are limited options available for rotation. Another resistance management strategy is to use an insecticide mixture. This single insecticide formulation contains two or more toxicants of different modes of action (e.g., pyrethroid + neonicotinoid). However, bed bugs have recently been resistant to mixture formulations. Other control approaches against resistant bed bugs include using entomopathogenic fungi, botanical insecticides, fumigants), heat treatment, physical removal using vacuuming, and inorganic and mineral compounds such as diatomaceous earth or silica gel. Some modern approaches that are presently being investigated are (1) RNA interference (*RNAi*), which silences vital genes (2) bed bug bait, which incorporates phagostimulants such as ATP with a toxicant; and (3) antibiotics to kill bed bug symbionts. The biggest challenge for all these methods is developing a feasible, low-cost, low-maintenance, oral delivery system for bed bugs. Low-income housing probably remains the reservoir for bed bug infestation. In most situations (when the control of bed bugs is not effectively carried out), the infestation in low-income houses will become massive and serve as an insecticide-resistant bed bug reservoir for spreading throughout the community.

# 특별강연

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 28일(목) 15:30 ~ 17:00

Session Ⅱ (대강당)

**<특별강연 1>**

# Emerging threats: Urban entomology and the rise of invasive species in South Korea

Daeyun Kim[1,2]

[1] *Research and Lifelong Learning Center for Urban and Environmental Entomology (RESCUE);*
[2] *Department of Entomology, Faculty of Agriculture, Kasetsart University, Bangkok, Thailand*

This talk will provide an overview of urban and medical entomology in Southeast Asia, drawing on my decade-long experience in Malaysia and Thailand. The recent emergence of invasive species, such as termites, bed bugs, and ants, in South Korea has heightened public concern regarding the adaptation of tropical insects to changing climates. Increased international trade is a significant pathway for these invasions. For instance, the first case of Red Imported Fire Ant (RIFA) was reported in 2017 within international cargo yards, with infestations spreading to both construction and residential areas. Additionally, three termite species have recently been identified in Korea for the first time, raising concerns about their ability to overwinter in southern regions and indoors in northern areas. The influx of tourists post-pandemic has facilitated the spread of another indoor species like tropical bed bugs, with increased travel leading to wider dissemination throughout the country. Furthermore, a potential dengue outbreak looms as cases surge in Southeast Asia. To combat these invasive species and diseases, proactive detection through effective monitoring and systematic surveillance programs is essential. Community involvement and local expertise in tropical species will be crucial for achieving sustainable pest management and mitigating future invasions.

**Keywords**: Urban entomology, medical entomology, invasive species, Southeast Asia, Community engagement

**<특별강연 2>**

# Ecological study of *Ephemera orientalis* mass emergence in the Hangang River

Dong Gun KIM

*Smith College of Liberal Arts, Sahmyook University, Seoul 01795*

To understand the ecological characteristics of the recurring mass emergence of *Ephemera orientalis* in the Hangang River, a comprehensive field study was conducted from April to October 2024. This study focused on analyzing the density of *E. orientalis* larvae in relation to physical habitat features such as water depth and substrate composition, aiming to identify key habitats within various zones of the Hangang River, including central and riparian areas. By examining larval density across these locations, we were able to compare habitat preferences and understand how physical characteristics influence larval distribution. Additionally, preliminary experiments were conducted to explore the use of light as a potential control method for reducing *E. orientalis* density. These trials yielded significant results, indicating that light-based interventions could be effective in managing larval populations. This study provides valuable insights into the substrate and depth preferences of *E. orientalis* larvae and suggests that light may serve as a viable tool for outbreak management. These findings offer a foundation for developing effective management strategies for *E. orientalis* in the future.

**<특별강연 3>**

# Evolution and adaptive capacity of aquatic insects in urban environments

Ji Hyoun Kang[p1] and Yeon Jae Bae[c1,2]

[1]*Korean Entomological Institute, Korea University, Seoul 02841;*
[2]*Division of Environmental Science and Ecological Engineering, Graduate School, Korea University, Seoul 02841*

Urban environments are novel and challenging conditions that differ substantially from natural ecosystems to most animal taxa. Urban stressors, such as artificial structures, pollution, light, and noise, can be unique environmental pressures that diverse taxa have not encountered throughout their long evolutionary histories. Some organisms have developed specific strategies to adapt and evolve under these conditions. Aquatic insects, which represent 60% of freshwater biodiversity, are particularly suitable model systems for studying adaptive capacity in urban aquatic habitat due to their short life cycles, dual aquatic-terrestrial life stages, and resilience to environmental stress. Case studies on the genetic diversity and population structures of urban aquatic insects, such as mayflies, mosquitoes, and giant water bugs, will show how they respond to and adapt to specific urban stressors. Understanding the adaptive capacity of aquatic insects in urban environments through genetic analysis offers valuable insights into the resilience of species facing human-driven environmental changes.

* This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MIST) (2020R1C1C1007098, RS-2024-00350469).

# 신진과학자 발표

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 29일(금) 10:00 ~ 11:30

(대강당)

**<신진과학자 1>**

# Historical review of Acentropinae (Crambidae, Lepidoptera) from Korea

Tak-Gi Lee[p1,2], Jae Ho Jin[3], and Neung-Ho Ahn[c2]

[1]*Research Institute of EcoScience, Ewha Womans University, Seoul 03760;*
[2]*National Institute of Biological Resources, Incheon 22689;*
[3]*Cheomdan Elementary School, Incheon 21986*

In Korea, the study of the aquatic moths, Acentropinae, began with Leech (1889)'s record of moths in the Wonsan (Gensan) region of North Korea. Most of the early studies were conducted by foreign scholars, including those from Japan, and research by Korean researchers began after the 1950s. However, since the research lineage was not continuous, there are many errors that occur due to the omission of past records depending on the scholar. In particular, there were important changes in the classification system, such as the consolidation of three subfamilies, so it is important to determine whether the related information was properly applied to Korea. This study examined the research history of Korean Acentropinae to clarify how each species was recorded and to determine whether the changes made by foreign research were properly applied in Korea. As a result, this study confirmed that the synonym relationship of one species and the promotion of one subspecies to species were not applied, and provides information on the complexly intertwined factual relationships of Acentropinae inhabiting Korea.

* This work was supported by a grant from the NIBR (National Institute of Biological Resources), funded by the Ministry of Environment (MOE) of the Republic of Korea (2024 Training postdoctoral experts for unexplored taxa; NIBR202402108).

**<신진과학자 2>**

# Taxonomic studies on Korean Miridae and future research prospects

Min Suk Oh[p1,2] and Seunghwan Lee[c1,2]

*[1]Laboratory of Insect Biosystematics, Department of Agricultural Biotechnology,*
*Seoul National University, Seoul 08826;*
*[2]Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826*

Miridae comprises a significant portion of heteropteran diversity, and they dwell on wide range of environments. Based on a comprehensive review of species records and recent publications, Miridae encompasses approximately 11,700 species across seven subfamilies. In Korea, taxonomic study on mirids began in the early 20th century, primarily by Japanese researchers. Korean researchers subsequently joined these efforts in the mid-1940s, partly collaborate with several european taxonomists. Since the 21st century, domestic researchers have taken the lead in taxonomic studies on Miridae, and describes numerous species and report novel distribution records actively. In addition, the integration of molecular information into phylogenetic analysis and species classification has widened the possibility for exploring the evolutionary history and internal relationships within this large family. This presentation will provide a brief overview of the research history of Korean Miridae fauna and outline prospects of research.

* This work was supported by NIBR, NRF and SNUR&D grant

**<신진과학자 3>**

# DNA barcoding of chironomid larvae (Diptera: Chironomidae) from large rivers in South Korea to facilitate freshwater biomonitoring and public health surveillance

Hyo Jeong Kang[p,c]

*Institute of Environmental Ecology, Sahmyook University, Seoul 01795*

The benthic macroinvertebrates are essential members of freshwater ecosystems, adapted to various habitats due to their diversity in richness and abundance. There are about seven thousand known species of Chironomidae worldwide. Larvae are often used to assess water quality because they respond to both short- and long-term changes in water conditions. However, most species remain identified only to the genus or family level due to the lack of species-level identification keys.

Since the 1970s, massive outbreaks of chironomid larvae in tap water have been reported in countries such as England, the USA, and Israel. Recently, similar outbreaks have been reported in several regions of Korea, including Incheon, Seoul, Busan, and Jeju, raising nationwide concerns about water safety. Additionally, adult midges are recognized as nuisance pests for humans. In response to this public health issue, a rapid and comprehensive study of Korean chironomids, including genetic characterization and ecological analysis, is needed to gain a clearer understanding of the species involved in this problem. However, the morphological classification of Korean chironomid larvae remains confusing and is still at a preliminary stage.

Therefore, this study aims to identify the Chironomidae adults inhabiting rivers using morphological and DNA-based approaches in four major rivers in Korea, which are critical as water intake sources. Additionally, this study proposes a new DNA barcode library for Chironomidae, which can be applied to larvae at different developmental stages. As a result, a total of 40 species were recorded at the study sites, including three newly recorded species and one taxonomically unassociated species. Compared to previous records, this study has added 17 new species to the Korean chironomid fauna and expanded its barcode library.

# 심포지엄 I

# 석주명 선생 표본 귀환 기념 심포지엄

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 28일(목) 15:30 ~ 17:30

(세미나실)

**<강연 1>**

# 일본 규슈대로부터 기증받은 석주명 선생의 표본에 대하여

김창무[P], 안능호

*환경부 국립생물자원관 생물다양성연구부 생물종다양성연구과, 인천 22689*

석주명(1908~1950)은 한국 나비류의 분류학에 큰 공헌을 한 초기 곤충학자이다. 그는 평생 약 75만 개체의 나비 표본을 수집했던 것으로 알려져 있으나 표본의 대부분은 소실되었고 그의 누이인 석주선이 전쟁 때 피난하면서 가져온 32점의 나비 표본만이 남아있다. 이 표본은 국가등록문화재 610호로 지정되어 단국대 석주선 기념박물관에 소장되어 있다.

한편, 국립생물자원관이 2010년부터 지금까지 일본의 규슈대학교 곤충학연구실을 수차례 방문하여 한반도의 표본 현황을 조사한 결과, 1931년부터 1942년까지 석주명이 채집한 곤충 건조표본 35종 129개체가 처음으로 확인되었고 표본은 대부분 매우 양호한 상태로 보관되어 있었다.

표본의 대부분은 석주명이 당시 개성에 위치한 송도고등보통학교에서 교사로 근무했던 1933년~1937년에 채집된 것이다. 확인된 석주명의 표본은 메뚜기목 5종, 노린재목 7종, 풀잠자리목 5종, 뱀잠자리목 1종, 밑들이목 1종, 날도래목 4종, 나비목 10종, 벌목 2종이다.

국립생물자원관은 규슈대로부터 석주명의 표본을 기증받아 지난 9월에 국내로 인수하였으며 현재 국립생물자원관 곤충건조표본 수장고에 보관되어 있다.

이번 기증을 계기로 앞으로 한일 연구자 간 학술 교류 등 긴밀한 관계를 유지하고 공동조사 등 후속 연구를 지속할 계획이다.

**<강연 2>**

# Japanese entomologists related to D. M. Seok in the 1920-40s

Toshiya Hirowatari[d1], Neung-Ho Ahn[2], Toshiharu Mita[1], Wanggyu Kim[2], and Jinwhoa Yum[2]

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D. M. Seok was the first Korean entomologist who made significant contributions to the taxonomy of butterflies of Korea. During his lifetime, he classified Korean butterflies into 248 species (Seok, 1973) and collected 750,000 butterfly specimens.

His teacher, Ginji Okajima, established the three laboratories of Zoology, Entomology, and Silkworm Science at Kyushu University between 1921 and 1922 and built the foundation by organizing the literature related to entomology before the currently recognized first professor of the Entomological laboratory, Teiso Esaki, took up the position. Ginji Okajima's name is also associated with the species names "*Neptis okajimai*" and "*Zephyrus ginzii*," which were named after him by Seok (Seok, 1936). Currently, the former is treated as a synonym of *Neptis philyra*and the latter as *Protantigius surepance ginzi* (Joo et al., 2021).

Atsuhiro Sibatani, who studied Seok's work, had direct contact with him. Sibatani received materials from Seok from the Korean Peninsula while publishing a book on Lepidopteran genitalia.Seok also had been in contact with Iwahiko Sugitani, a famous entomologist and mathematics teacher at Kyoto Sanko High School at the time, who visited the Korean Peninsula many times and built up a valuable collection.

Seok dedicated the species named *Clossiana selene sugitanii*to Sugitani (Seok, 1939, 1947). Sugitani's collection of 36,000 butterflies and moths is currently preserved at Kyushu University and was also utilized in the taxonomic revision of the genus *Maculinea* conducted by Sibatani et al. (1993), contributing to the understanding of lepidopteran fauna of the Korean Peninsula.

* This work was supported by grants from the NIBR (NIBR202402108).

**<강연 3>**

# 한국 과학사로 본 석주명의 연구 활동

**문만용**[d]

*전북대학교 한국과학문명학연구소, 전주 54932*

일제 강점기 과학기술 중 가장 활발한 모습을 보였던 분야는 생물학이었으며, 생물학자로 가장 왕성하게 활동했던 인물은 전문학교 졸업 후 중등학교 박물교사를 지내면서 연구를 병행했던 석주명이었다. 그는 일제 강점기 한국인 과학자로서는 유일한 영문 단행본을 펴냈다. 석주명은 한국의 나비분류학을, 1기: '학명으로 기록되기 이전의 시대'(~1881), 2기: '서양인이 기록한 시대'(1882~1901), 3기: '주로 일본인(本邦人)이 기록한 시대' (1905~29), 4기: '內外人이 추록(追錄)한 시대'(1924~39), 5기: '정리의 시대'(1940~50)로 구분했는데, 바로 정리의 시대는 그가 펴낸 *A Synonymic List of Butterflies of Korea* (1939) 이후를 의미했다. 나비분류학을 넘어 서지학자로서의 면모를 보여준 *A Synonymic List*는 석주명이 한국산 나비 연구에 집중하면서도 이를 위해 국제적인 교류를 비롯한 트랜스내셔날한 접근을 적극적으로 취했음을 보여준다. 해방 이후 석주명은 국립과학박물관(이후 국립과학관)의 동물학부장으로 활동하면서 다수의 '국토구명사업'을 통해 한반도 자연조사 활동을 이끌었고, 그 결과는 국립과학박물관에서 발표되었다. 과학박물관에는 곤충학자였던 관장 조복성을 비롯해 식물학자 정태현 등 한국의 동식물을 연구하는 연구자가 다수 활동하고 있었고, 그 덕분에 자연사박물관으로서의 기능을 추진할 수 있었다. 이는 현재 한국의 국립과학관이 자연사박물관 역할을 겸하고 있는 상황의 기원이라 할 수 있다. 비록 한국전쟁 과정에서 갑작스러운 죽음으로 인해 석주명의 활동은 중단되었지만, 그의 연구가 한국 과학사에 남긴 발자취는 분명 선명했다.

**<강연 4>**

# 한국의 르네상스인 석주명

윤용택[d]

*제주대학교 철학과, 제주 63243*

석주명 선생(1908~1950)은 나비 채집을 위해 전국을 여행하는 과정에서 자연환경이 달라지면 동식물 분포뿐만 아니라 인간의 삶의 방식도 달라지는 것을 알았다. 그는 우리나라의 옛 모습을 알기 위해 제주의 언어, 문화, 사회, 자연 등을 연구하여 6권의 제주도총서를 남겼다. 그래서 우리는 그를 제주학의 선구자라 부른다. 그는 8.15해방 이후 당대 지식인으로서 자연과학 분야에서 국학운동을 펼쳤고, 우리 민족이 세계시민국가의 당당한 일원이 될 수 있도록 국민들끼리는 한국어로, 외국인과는 세계 공통어인 에스페란토로 소통을 주장한 에스페란토 초기 운동가였다. 그는 자신의 전문인 나비 분야에서 대가가 되었을 뿐만 아니라, 자연과 인문사회 분야까지도 두루 능통한 폭넓은 학문세계를 구축하였고, 지역주의, 민족주의, 세계주의 어느 한쪽에 매몰되지 않고 잘 조화를 이뤘다. 그는 다양한 분야에서 전문성과 보편성을 발휘한 한국의 르네상스인이었다. 그러한 그의 학문 태도는 학문 융복합의 시대이자 지역과 세계를 아우르며 살아가야 하는 오늘날 우리에게 많은 메시지를 던져준다.

# 심포지엄 II
# 사회성 곤충 심포지엄 I

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 29일(금) 10:00 ~ 11:30

(세미나실)

**<강연 1>**

# Ecological consequences of Argentine ant invasion: Homogenization of native ant populations

Sang-Hyun Park

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The Argentine ant (*Linepithema humile* (Mayr, 1868)), a highly invasive species, disrupts ecological balance across diverse habitats, reducing native ant diversity and homogenizing ant communities through aggressive competition. This study systematically examines the ecological impacts of Argentine ant invasions, with a focus on biodiversity loss, shifts in community structure, and declines in ecosystem functions, such as seed dispersal, resulting from reduced functional diversity. Findings reveal that Argentine ants form extensive supercolonies in invaded regions, monopolizing resources and habitats by outcompeting native ants, including *Formica japonica*. This supercolony expansion not only suppresses local biodiversity but also weakens ecological interactions, substantially impairing the resilience of invaded ecosystems. Consequently, implementing integrated management strategies to limit supercolony proliferation and support native ant resilience is essential for preserving ecosystem integrity. This study proposes a novel approach to managing Argentine ants by emphasizing supercolony containment and the conservation of native biodiversity, offering foundational data for invasive species management and biodiversity conservation efforts.

**<강연 2>**

# Got Argentine ants? - An alliance to improve their management in California

Dong-Hwan Choe

*Department of Entomology, University of California, Riverside, CA*

Ants are one of the major pests around structures in many urban environments. In urban residential areas of California, the Argentine ant, *Linepithema humile* (Mayr), is the most common nuisance ant species treated by pest management professionals (PMPs). Contact and residual insecticide sprays are commonly used for outdoor Argentine ant control due to their ease of application and cost-effectiveness. Some of insecticide active ingredients used in the spray products are frequently detected in urban surface waters at levels that are deleterious to sensitive aquatic species. In an effort to minimize the environmental contamination by the insecticides, various reduced-risk strategies have been developed. However, it remains important for the reduced-risk strategies to maintain an acceptable level of control efficacy. The primary goal of pest management alliance project was the implementation and promotion of low-impact strategies to effectively manage pest ants in urban environments. The project aimed to reduce PMPs' reliance on repeated use of insecticide sprays by incorporating two biorational approaches: (1) pheromone adjuvant for initial spray, and (2) baiting for maintenance visits. A mini study provided a useful piece of information for strategic placement of the baits. Future development in bait delivery method will also help to increase the use of baits rather than repeated use of insecticide sprays.

**<강연 3>**

# Evolution of the ant waist: From locomotion to morphology

Minsoo Dong[p1,2] and Brendon E. Boudinot[c2]

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Micro-computed tomography (μ-CT) technology, widely adopted in modern biological research, has facilitated three-dimensional modeling of organisms' internal and external structures, opening new frontiers in morphological studies. Combined with phylogenetics and genomics, μ-CT produces phenome-scale data, enabling unprecedented quantitative inference for evolutionary research. However, despite the principal importance of function for morphological form, research examining the evolutionary relationship between locomotion and morphology remain scarce. Our study focuses on the morphology of petiole of Hymenoptera, particularly in ants (Formicidae), which is believed to have contributed to their explosive species diversification. Although petiole morphology serves as a crucial taxonomic character in ants, the underlying factors driving its morphological diversity and evolutionary patterns remain poorly understood. Using micro-CT data primarily obtained from synchrotron radiation, this study investigates how differences in locomotion patterns have influenced the skeletomuscular system of ants. Using phylogeny as a guide, we compared the skeletomuscular structures between groups that notably elevate their gaster and those that do not. Additionally, we explore methodologies for analyzing the relationship between locomotion and morphology through in-silico simulations in computational environments.

**<강연 4>**

# Interceptions and establishments of invasive termites: Are we ready to battle?

Sang-Bin Lee[d1], Yong-Seok Choi[2], and Si-Hyun Kim[3]

*[1]Division of Agriculture and Natural Resources, University of California, Fairfield, CA, USA;*
*[2]Wood Engineering Division, National Institute of Forest Science, Seoul, Republic of Korea;*
*[3]Restoration Technology Division, National Research Institute of Cultural Heritage,*
*Daejeon, Republic of Korea*

Once termites are found in urbanized areas, they are no longer regarded as ecosystem engineers but as economically important pests. Historically, subterranean termites in the genus *Reticulitermes* have been known to inhabit Korea. Recent studies, however, have reported interceptions of *Coptotermes*, infestations of *Cryptotermes domesticus*, and establishments of *Incisitermes minor* in Korea. These invasive termites are more significant pests compared to native subterranean termites and therefore require greater attention in prevention and management programs. This presentation provides an overview of invasive termites in Korea, and the management programs will be discussed.

# 심포지엄 III
# 사회성 곤충 심포지엄 II

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 29일(금) 13:30 ~ 15:00

(세미나실)

**<강연 5>**

# Distribution and rising risks of social wasps in urban environments: A case study of Seoul

Hyeonsuk An[p1,3], Moon Bo Choi[1,2], and Ohseok Kwon[c1]

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The population of social wasps in South Korea has recently surged, resulting in a significant rise in wasp nest removal requests and sting-related incidents. Historically, native social wasps in South Korea primarily inhabited mountainous regions, but they are now increasingly observed in urban areas due to climate change and habitat destruction. Furthermore, the invasive hornet species *Vespa velutina* has been thriving predominantly in urban environments. This study aimed to assess the distribution of social wasps and the frequency of sting incidents in Seoul, the largest city in South Korea.

The results indicated that, in 2023, there were a total of 14,344 reports of wasp nest removals, marking a 20-fold increase compared to 706 cases in 2000. Over the past five years, there have been 2,163 cases of wasp stings, with 1,389 cases (74%) occurring between July and September, and the highest number of incidents reported in August. A total of 1,849 wasp specimens representing 13 species were collected: 1,003 individuals from 12 species in forested areas, 620 individuals from 11 species in urban parks, and 226 individuals from 10 species in urban areas. These findings indicate that social wasps are widely distributed across Seoul, with *V. velutina* present at all surveyed locations. As wasp populations increase, various social challenges may arise. Therefore, research on urban-dwelling wasps is essential to develop safe and effective control strategies for wasp populations in densely populated urban areas.

**Keywords:** Vespinae, social wasps, urban, Seoul

**<강연 6>**

# First record of six predators of the invasive hornet, *Vespa velutina nigrithorax*, in Korea

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*Kyungpook National University, Daegu, Korea;*
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*Daegu, Republic of Korea*

*Vespa velutina nigrithorax* (VVN, Yellow-legged hornet) is recognized as a serious invasive species due to its remarkable capacity for spreading and its negative impact on pollination services. VVN is primarily known for establishing and expanding nests in high locations and producing colonies with the largest number of workers among species of the same genus. Observing whether various insectivores of social wasps can target VVN colonies could serve as an indicator of this invasive species' potential for ecological adaptation in new environments. In the Western Palearctic realm, bee-eaters (*Merops apiaster*) and European honey buzzards (*Pernis apivorus*) have been reported to attack the nests of VVN, while in South Korea, only yellow-throated martens (*Martes flavigula*) have been observed doing so.

This report aims to introduce Korean predators capable of attacking colonies of VVN. We observed that Asian giant hornets (*Vespa mandarinia*), brown-eared bulbuls (*Hypsipetes amaurotis*), great spotted woodpeckers (*Dendrocopos major*), grey-headed woodpeckers (*Picus canus*), and crested honey buzzards (*Pernis ptilorhynchus*) preyed upon nest contents. Additionally, numerous remains of VVN were found in badger (*Meles leucurus*) feces, confirming these six species as predators of VVN. This suggests that various insectivorous animals in Korea may recognize VVN colonies as a food source. Further research is required to determine whether these animals, based on their predatory behaviors and ecological characteristics, could exert a significant impact on the population of VVN.

**<강연 7>**

# Exploring gut microbiota diversity in *Vespa velutina*: Implications for invasion success in South Korea

Woong-Bae Park[P] and Yuno Do[C]

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Invasive hornet species, especially *Vespa velutina*, present significant ecological, economic, and health risks in South Korea. This study explores how gut microbial communities and stable isotope analyses (carbon and nitrogen) contribute to *V. velutina*'s adaptability and invasion success. Across five *Vespa* species, gut bacteria were primarily Proteobacteria, along with Firmicutes and Bacteroidetes. Notably, *V. velutina* and *V. mandarinia* exhibited higher levels of Firmicutes, which aid in digesting complex carbohydrates and producing short-chain fatty acids, potentially giving them an advantage in non-native habitats. Although nitrogen and carbon isotope values across species indicate similar food sources, *V. velutina* showed a greater number of unique bacterial OTUs, hinting at a specialized gut microbiome that may enhance adaptability. Furthermore, positive correlations between bacterial diversity and $\delta 15N$ values suggest that gut microbiota diversity might broaden dietary options. Our findings indicate that gut microbiota likely play a crucial role in supporting *V. velutina*'s survival and adaptability, providing valuable insights for managing invasive species through targeted control strategies. Expanded studies across larger regions and sample sizes are needed to further investigate the role of gut microbiota in *Vespa* invasions.

**<강연 8>**

# 등검은말벌 침입 21년, 그동안의 확산과 피해 및 방제에 대한 평가

최문보

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2003년 부산 지역에서 처음 침입이 확인된 등검은말벌(*Vespa velutina nigrithorax*)은 이후 빠르게 확산되어, 21년이 지난 현재 제주도, 울릉도 및 일부 섬 지역을 제외한 전국에 퍼져 있다. 이 외래종은 다른 외래종과 비교할 수 없을 정도로 사회경제적 피해가 크지만, 효과적인 방제법은 여전히 개발되지 않았다. 등검은말벌은 현재 유럽에서도 확산 중이며, 최근에는 북미 지역에도 침입했다.

국내에서는 2019년에 이 종이 생태계 교란종으로 지정되었으나, 국가 차원의 생태 연구는 대부분 분포 확인에 그치고 있다. 반면, 유럽은 생태적 연구를 기반으로 다양한 방제법을 개발 중이다. 국내에서는 주로 유인트랩과 살충제를 이용한 전통적인 방제 방법이 활용되며, 연구 또한 이들의 기능 향상에 초점을 맞추고 있다. 최근 AI, 딥러닝, 드론 기술을 접목한 방제법이 개발되고 있으나, 부족한 생태적 지식으로 인해 명확한 한계가 드러나고 있다. 반면, 유럽에서는 생태적 특성을 분석한 뒤 친환경적이고 최신 기술을 활용한 비교적 효율적인 방제법을 적용하고 있다.

본 연구는 이러한 특성들을 비교하여 향후 등검은말벌 연구의 새로운 방향성을 제시하고자 한다.

# 일반구두발표

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 29일(금) 13:30 ~ 14:45

(대강당)

**<구두발표 1>**

# Identification of tick-borne pathogens in ticks infesting cattle and sheep from Kyrgyzstan, using next-generation sequencing

Ji Ye Seo[p1], Jin Seo Park[1], Bekbolsun Aknazarov[2], and Hee Il Lee[c1]

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*[2]Kyrgyz National Agrarian University, Kyrgyz Republic Bishkek 68 Mederov st., 720005*

The Korea Disease Control and Prevention Agency (KDCA) has been cooperating with Kyrgyz National Agrarian University (KANU) for national tick surveillance since 2020. This study collected 546 ticks infesting cattle and sheep across Kyrgyzstan in 2022. Using next-generation sequencing (NGS) along with confirmatory PCR and sanger sequencing, we aimed to characterize the tick-borne bacterial pathogens present in two families, five genera, and twelve species ticks (*Dermacentor* spp. 30.2%, *Hyalomma marginatum* 17.2%, and *H. scupense* 13.4%, etc.). Our results revealed an overall infection rate of 11.7% for pathogens. *Rickettsia* spp. were the most frequently detected at 8.6%, including confirmed species of *R. raoultii*, *R. aeschlimannii*, *R. slovaca*, *R. conorii*, *R. rickettsii*, and *R. sibirica*. *Anaplasma* and *Ehrlichia* spp. were detected at 2.7% and 0.2%, respectively, identified as *A. ovis*, *A. bovis*, *A. capra*, *Anaplasma* sp., and *Ehrlichia* sp. Additionally, *Bartonella* species were identified to *B. bovis.* This is the first nationwide study investigating tick-borne bacterial pathogens in ticks collected from cattle and sheep in Kyrgyzstan. Our findings contribute to a better understanding of the epidemiology and emergence of tick-borne diseases in the country.

**<구두발표 2>**

# Expression of recombinant parasite excretory/secretory proteins using baculovirus-insect cell expression system and its regulatory effect on bladder urothelial barrier dysfunction

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Anti-inflammatory proteins (AIP)-1 and AIP-2, identified as parasite excretory/secretory (ES) proteins, play a vital role in promoting parasite survival and evading the host immune response. These proteins inhibit inflammatory reactions, induce apoptosis in effector cells, and influence immune response phenotypes. Many parasite-derived proteins have shown promise as therapeutic targets for inflammatory and allergic diseases, though the precise biological roles and molecular characteristics of many remain unclear. In this study, hookworm AIP-1 and AIP-2 proteins were produced using the baculovirus-insect cell expression system (BEVS). Insect cell-derived AIP-1 and AIP-2 exhibited inhibitory effects against human matrix metalloproteinases (MMPs). This study explored the impact of AIP-1 derived from baculovirus-infected insect cells on the expression of PANX1 and Cx43 in TCCSUP and HBdSMC cells. Insect cell-derived AIP-1 was downregulated the expression of proteins associated with the Cx43/Erk/AP-1 signaling pathway in HBdSMC cells during inflammation induced by PDGF-BB, including the nuclear translocation of the transcription factor AP-1, the expression of these pathway proteins in vivo using a CYP-induced IC animal model, and assessed the severity of inflammation through pathophysiological analyses. This study demonstrated that the insect cell-derived AIP-1 and AIP-2 have potential as therapeutic proteins for diseases related to the MMP-TIMP axis and elucidated the molecular mechanisms underlying changes in PANX1 and Cx43 expression caused by AIP-1 from baculovirus-infected insect cells, thereby suggesting new strategies for treating IC/BPS.

* This work was supported by a National Research Foundation of Korea grant funded by the Korean Government (MEST) (NRF-2023R1A2C100473512).

**<구두발표 3>**

# Ectoparasite loads in small mammals of the Republic of Korea: Effects of season, host sex and body mass

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Various factors potentially influence the abundance and distribution of ectoparasites on host animals. This study investigated the effects of season, host sex, and body mass on ectoparasite distribution among small mammal species in the Republic of Korea. A total of 49,953 ectoparasites were collected from 513 individual hosts, representing eight small mammal species, through a nationwide survey. *Apodemus agrarius* (85.24%) was the dominant species, followed by *Crocidura lasiura*, *Craseomys regulus*, and others. Chigger mites constituted the majority of ectoparasites collected (91.40%), followed by ticks (6.25%) and other ectoparasites. Host preferences were observed, with chigger mites showing a higher preference to *C. regulus* than to *A. agrarius*, while ticks were most prevalent on *A. agrarius*. Ectoparasite loads varied across species, with *A. agrarius* harboring the highest loads. While the average ectoparasite load per individual small mammal was greater in autumn than in spring, seasonal differences in chigger mite burden were not observed in *A. agrarius*. A comparative analysis of chigger mite and tick burdens between male and female *A. agrarius* showed that males were more heavily infested with both ectoparasites than females. This discrepancy was attributed to differences in host body mass rather than host sex for chigger mites. In contrast, tick abundance exhibited minimal evidence of sex bias, potentially due to the questing tick distribution and behavioral differences between host sexes. These findings underscore the importance of understanding seasonal and host-specific factors that influence ectoparasite loads and their potential link to zoonotic disease risks.

**<구두발표 4>**

# 럼피스킨(LSD) 매개체 침집파리(*Stomoxys calcitrans*)의 유전자형 분석

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주로 소에 발생하는 1종 가축전염병인 럼피스킨(LSD)는 흡혈곤충에 의해 기계적 전파가 이루어지며, 대표적인 매개체는 침집파리(*Stomoxys calcitrans*)로 알려져 있다. 우리나라는 2023년 10월에 충남 서산에서 럼피스킨이 최초로 발생했으며, 4주만에 전국적으로 확산하였고, 올해도 지속적으로 발병하여 축산업에 비상이 걸린 상황이다. 우리는 2024년 5월부터 10월까지 럼피스킨 매개충 예찰을 통해 총 20개 지점에서 채집된 개체들의 COI 전반부 염기서열 658 bp를 분석하였다. COI 유전자염기서열의 Pairwise comparison 결과, 한국 서부해안을 중심으로 채집된 침집파리는 1.7%에서 2.7%의 서열 차이를 보이면서 크게 2개의 그룹으로 분지되었다. Haplotype 분석 결과, 침집파리는 총 34개의 Haplotype이 확인되었고, 이 중 H1 (18개체)과 H2 (136개체)가 우점하는 것으로 나타났다. MJ network 분석에서는 앞선 2가지 분석 결과를 반영하면서 크게 2개의 주요 Haplotype (H1, H2)을 중심으로 network를 형성하였으며, 이 두 Haplotype 간의 mutation point는 최소 15번 이상으로 나타났다. 이 결과는 COI 유전자상에서 우리나라에 분포하는 침집파리는 크게 2개의 주요 유전자형이 존재하며, 두 유전자형의 유전적 형질 차이가 큰 것으로 확인되어 국외로부터 개체의 유입이나 이동이 있었을 것으로 추론된다. 우리는 추가로 침집파리의 유입경로 분석 및 역학조사 기법 개발의 일환으로 NGS 분석을 이용하여 집단유전학적 판별을 위한 유용 염기서열 정보를 구축하고 microsatellite 마커 개발을 추진하고 있다.

**<구두발표 5>**

# Population genetic structure analysis of *Anopheles kleini* in Korea based on the mitochondrial *CO I* gene

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*Anopheles kleini* is a competent vector that is only observed in the northern malaria-risk areas of Korea. We analyzed the population genetic structure of *An. kleini* using the mitochondrial cytochrome *c* oxidase subunit I (*COI*) marker in the first nationwide survey of Korea. Network analysis identified 140 haplotypes organized into three clusters. Cluster II was related with *An. kleini* from eastern Russia and northwestern China. The pairwise genetic distance ($F_{ST}$) values among the populations showed regional genetic differences between Gangwon-do and Gyeonggi-do. Analysis of molecular variance (AMOVA) analysis indicated that individual mosquitoes within the population had a significant influence on the total variation. The neutrality test indicated that all values were negative. Through this information we identified that *An. kleini* is expanding population. The spatial population structure is crucial in understanding the characteristics of *An. kleini* population in Korea.

# 학생구두발표

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 29일(금) 14:45 ~ 17:00

(대강당)

**<학생구두발표 1>**

# Vapor toxicity effects of transfluthrin liquid vaporizer on susceptible *Aedes aegypti* in experimental huts

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*Aedes aegypti* pose a significant role in indoor arbovirus transmission. Household insecticide products like liquid vaporizers (LV), utilizing volatile pyrethroids like transfluthrin (TFT) could be a potential intervention tool to address biting problems. Transfluthrin-Liquid Vaporizers (TFT-LV) has been available nationwide in Thailand. However, its efficacy in field setting is still not evaluated. The objective of this study was to evaluate the effects of TFT-LVs' on susceptible *Ae. aegypti* in field setting and generate sublethal doses of TFT-LV. The study was conducted at a field station in Kanchanaburi, Thailand, using experimental huts. Three huts served as treatment groups, while one acted as the control, and was rotated following a 4 × 4 Latin-square design totaling 12 replications per concentration. Each hut contained four mesh cages, each holding 25 TFT-susceptible, nulliparous *Ae. aegypti* mosquitoes. Knockdown rates (%KD) were recorded during a continuous 6-hour exposure and mortality at 24-hour post-exposure. Probit analysis was used to generate knockdown time (KT) in minutes using SPSS program. The mean %KD for TFT concentrations of 1.5%, 3%, and 6% showed a substantial effect within the first two hours reaching 68–76% and ultimately achieving 98–100% total knockdown. The mean %KD and mortality was found directly proportional TFT concentrations. While the KT value was found inversely proportional to TFT concentration. High and low concentrations of TFT-LVs demonstrated actual effectiveness against TFT-susceptible, nulliparous *Ae. aegypti* in the field. TFT 0.75% and 1% exhibited sublethal effects and will be used in further experiments against TFT-resistant population of *Ae. aegypti*.

**Keywords:** *Aedes aegypti*, Caged bioassay, Experimental hut, Liquid vaporizer, Transfluthrin

**<학생구두발표 2>**

# Developmental substaging of *Musca domestica* larvae (Diptera: Muscidae) using morphological analysis of posterior spiracles for estimation of minimum postmortem interval

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In forensic entomology, the estimation of postmortem interval (PMI) based on the developmental stages of flies has been extensively validated and applied in forensic casework. Numerous studies have focused on rearing different species of flies to establish quantitative relationships between larval morphological changes and the time required for their development under controlled conditions. *Musca domestica* (Diptera: Muscidae), due to its wide distribution and its close ecological overlap with human habitats, holds significant forensic importance.

With studies that already divide *M. domestica* larvae into three instars (1st, 2nd, and 3rd), this study aimed to further classify the 3rd instar into five substages (S1, S2, SAG1, SAG2, and SAG3) based on morphological changes of the posterior spiracles. The larvae were reared under seven different constant temperatures ranging from 16°C to 34°C, with five replicates per temperature. Data were collected on developmental duration, accumulated degree hours (ADH), and larval length at each substage, providing a more detailed characterization of *M. domestica* larval development under varying thermal conditions for use in PMI estimations.

**Keywords:** Forensic entomology, *Musca domestica*, larval substaging, PMI estimation

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**<학생구두발표 3>**

# Study on antimicrobial responses of JNK kinase, *Tm*MAPKK, in JNK signaling pathway against microbial infection in *Tenebrio molitor*

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Antimicrobial peptides (AMPs) are crucial antimicrobial substances in the immune response of insects. The c-Jun N-terminal Kinase (JNK) signaling pathway is also reported to be involved in AMP production. The JNK kinase, mitogen-activated protein kinase kinase (MAPKK), in vertebrates has been studied in cell proliferation, cell death and apoptosis. Whereas in invertebrates, MAPKK is known to participate in immune responses through antimicrobial peptides, apoptosis, and autophagy. We investigated the immunological function of MAPKK in *Tenebrio molitor*. First, we identified the ORF sequence of *T. molitor MAPKK* (*TmMAPKK*), and performed phylogenetic analysis of deduced amino acid sequence of *Tm*MAPKK with its orthologs. And, we investigated the expression patterns of *TmMAPKK* in developmental and tissues. Following injections of microorganisms~~,~~ including *E. coli*, *S. aureus*, and *C. albicans*, we examined the expression patterns of *TmMAPKK* were investigated at 3-, 6-, 9-, 12-, and 24-h post-injection, resulting that the highest induction confirmed at 6 hours post-injection. Using RNAi, *TmMAPKK* was silenced to analyze mortality and expression patterns of AMP genes following microbial infection. In ds*TmMAPKK* treated group, the larval mortality against *E. coli* infection was increased, and the expression of AMP genes against *E. coli* infection was also suppressed in whole body. In addition, a CFU assay was conducted to know the antimicrobial activity with ds*TmMAPKK*-treated larvae. This study may provides an important insight of the JNK pathway in AMP production in *T. molitor*.

**<학생구두발표 4>**

# Comparative behavioral responses of β-caryophyllene against four *Anopheles* mosquito species, potential vectors of malaria in Thailand

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Insecticides are commonly used as a primary tool for mosquito control. However, their environmental impact and the potential for mosquitoes to develop physiological resistance raise significant concerns. As an eco-friendly alternative, chemicals like β-caryophyllene, a non-toxic compound, have gained attention for their potential in mosquito control. While β-caryophyllene has shown promise, its chemical interactions with *Anopheles* mosquitoes remain largely unexamined. This study evaluated β-caryophyllene's repellency effects on four *Anopheles* species using an excito-repellency test system. Among the tested species, *Anopheles minimus* exhibited the highest escape rates, with 100% escape at a 2.5% concentration in contact trials and at 5% in non-contact trials. *Anopheles harrisoni* also showed strong repellency, with a 72.73% escape rate at a 7.5% concentration. In contrast, *An. dirus* and *An. epiroticus* had comparatively lower escape rates. Comparative analysis indicated no significant difference between contact and non-contact trials for most species, except for *An. minimus* and *An. harrisoni*, which displayed higher escape rates in contact trials. No knockdown or mortality was observed across species. Survival curves demonstrated quicker escape rates in contact trials, particularly for *An. minimus*. Log-rank analysis showed significant differences in escape responses at various concentrations, with higher concentrations being more effective in repelling *An. minimus*, *An. harrisoni*, and *An. dirus*. In conclusion, β-caryophyllene presents potential as an effective repellent for *Anopheles* mosquitoes, especially *An. minimus* and *An. harrisoni*.

**Keywords:** *Anopheles*, behavioral response, excito-repellency, β-caryophyllene, chemical actions

**<학생구두발표 5>**

# Applying model-agnostic meta-learning for bioacoustic classification on mosquitoes' wingbeat frequencies and flight duration patterns

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Mosquitoes, as vectors of numerous pathogens, pose significant global health threats. Traditional monitoring and control methods often rely on visual cues or chemical attractants, but recent advances in bioacoustics and meta learning algorithms founded on artificial intelligence offer new opportunities to enhance mosquito monitoring and management. As such, experiments regarding mosquito flight behaviors within an experimental monitoring device in a laboratory setting and utilization of deep learning for identification of mosquitoes based on their wingbeat frequency and recorded spectrogram patterns were conducted. For this study, a total of 20 hours of mosquito flight audio recordings have been labeled from four mosquito species (*Aedes albopictus*, *Ae. togoi*, *Culex pipiens, Cx. tritaeniorhynchus*) using Audacity and were placed as training sets for the model-agnostic meta-learning (MAML) algorithm to process. The wingbeat frequencies were calculated using the baseline F0 harmonic frequency whereas the overall flight durations were measured using the labeled spectrograms in Audacity. The results show that wingbeat frequencies, harmonics and the flight durations differ significantly between the four species placed under similar conditions, with species identification precision rate of 97%, 90.5%, 92%, 89% for *Ae. albopictus, Ae. togoi, Cx. pipiens, Cx. tritaeniorhynchus*, respectively. The study would serve as preliminary data for structuring future data collection and monitoring methods.

**Keywords:** *Aedes*, *Culex*, artificial intelligence, biocoustics, mosquitoes, wingbeat frequency

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**<학생구두발표 6>**

# Urbanization disproportionately impact on aboveground and belowground insect community

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Urbanization, resulting from human activities, leads to biodiversity loss, which has significant implications for ecosystem services. The impact of urbanization may vary between aboveground and belowground insect communities; however, the differences remain unclear to date. Our study analyzed the correlation patterns between urbanization factors, such as increased impervious surface area, building density, and changes in vegetation cover, and both species richness and abundance of aboveground and belowground insects. While overall insect species richness and abundance showed relatively little variation across different levels of urbanization, a distinct trend emerged when comparing aboveground and belowground communities. Aboveground insect abundance displayed a positive correlation with urbanization, whereas belowground communities showed a negative correlation in both species richness and abundance. In particular, predatory belowground insects appeared to be more negatively impacted by urbanization. This study highlights the disproportionate effect of urbanization on aboveground and belowground insect communities, offering valuable insights for developing strategies to conserve both types of insect diversity within urban planning initiatives.

**<학생구두발표 7>**

# The intracellular kinase of Toll pathway, Pelle, plays an important role in *E. coli* infection in *Tenebrio molitor* hemocytes

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The Toll pathway is involved in antimicrobial peptides (AMPs) production and the dorsal/ventral formation. Pelle, an intracellular kinase of the Toll pathway, is known to phosphorylate the Cactus in *Drosophila* embryos, regulating the expression of AMP genes. However, the function of Pelle in *Tenebrio molitor* has not been elucidated. In this study, we identified the sequence of *T. molitor* Pelle (*Tm*Pelle) and conducted *in silico* analysis. We also investigated the developmental and tissue-specific expression patterns of *TmPelle*. After pathogenic injection to the larvae, we assessed the expression levels of *TmPelle* at 3, 6, 9, 12, and 24 hours post-injection. To understand the immunological role of *Tm*Pelle during pathogenic infection, we injected pathogens to the *Pelle* knockdown group, and investigated the larval mortality and expression of AMP genes in whole body and tissues. Additionally, we investigated the antimicrobial activity with hemolymph isolated from the *TmPelle*-silenced larvae infected by pathogens using CFU assay. The results indicated that the larval mortality against *E. coli* was dramatically increased in the *TmPelle*-silenced group. Furthermore, the expression levels of the AMP genes were significantly decreased in hemocytes. Through this study, we hypothesize that *Tm*Pelle responds specifically to *E. coli* infection in hemocytes.

**<학생구두발표 8>**

# Distribution, genetic structure, and biology of *Toxorhynchites christophi* (Portschinsky) (Diptera: Culicidae) in South Korea

Junyoung Lee[P] and Yeon Jae Bae[C]

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*Toxorhynchites christophi* (Portschinsky, 1884) is a non-hematophagous mosquito preying on other mosquito larvae, in forest areas. Despite its ecological importance as key predator and potential biological agent of mosquitoes, general biology of *Tx. christophi* is poorly understood. Our field surveys conducted from 2022 to 2024 as well as literature and citizen science data compiled distribution of *Tx. christophi* extending to southern Korean Peninsula with new distributional records, Chungcheongbuk-do and Gyeongsangbuk-do. Also, population structures based on the *mt-CO1* gene sequence were analyzed, along with morphological variations (e.g. absence of pale band on proboscis) in each regional population. Lastly, we present updated ecological information including habitat environment, co-occurring vector species and adult male behavior.

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**<학생구두발표 9>**

# 멸종위기야생생물 Ⅱ급 은줄팔랑나비(*Leptalina unicolor*) 인공 증식을 위한 사육 조건 확립에 관한 연구

이 혁p[1,2], 정준양[2,3], 홍찬의[1,2], 신현준[1,2], 이경원[1,2], 상민규[2,3], 박지은[2,3], 송대권[2,3], 이용석c[1,2,3]

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은줄팔랑나비(*Leptalina unicolor*)는 한국, 일본, 중국 그리고 러시아에 분포하는 것으로 알려진 팔랑나비과에 속하는 소형 나비로, 국내에서는 개체수와 서식지 감소로 인해 2017년 환경부에 의해 멸종위기 야생생물 II급으로 지정되었다. 이 연구는 멸종위기종인 은줄팔랑나비의 인공 증식을 통해 향후 종 보존을 위한 기초 자료를 마련하고자 수행되었다. 연구에 사용된 개체는 금강유역환경청의 허가를 받아 채집하였으며, 실내 사육 조건을 확립하기 위해 선행 연구를 참조하여 초기 사육 환경을 설계하였다. 무인자동기상관측장비(AWS)에 기록된 2021년 7월부터 2023년 7월까지의 서식지 평균 기온을 바탕으로 실내 온도는 24±3℃로 유지하여 사육을 진행하였다. 기주식물로는 선행연구에서 보고된 참억새(*Miscanthus sinensis*)를 사용하였다. 이번 연구의 결과를 통해, 은줄팔랑나비의 안정적인 실내 사육 가능성을 확인하였으며, 향후 다양한 온도 조건에서의 사육 실험을 통해 최적의 사육 조건을 확립하여 은줄팔랑나비의 안정적인 인공 증식을 위한 기초 자료로 활용할 수 있을 것으로 기대된다.

# 포스터 발표

사단법인 한국곤충학회 THE ENTOMOLOGICAL SOCIETY OF KOREA

11월 29일(금) 12:30 ~ 13:30

【 분 류 】

A-01

# *Actidium* Matthews and *Actinopteryx* Matthews (Coleoptera: Ptiliidae: Ptiliini) new to Korea: First records of the halophilous ptiliid species

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The genus *Actidium* Matthews comprises 40 species and known to inhabit areas close to fresh or salt water, such as sand, dried mud, mosses or plant waste. The genus *Actinopteryx* Matthews is also halophilious and comprises seven species. In Northeast Asia, a single *Actidium* species has been reported from the Russian Far East, and a single *Actinopteryx* species, *Actinopteryx parallela* Britten, has been reported from Japan and the Russian Far East. In this study, we report two halophilous ptiliids, *Actidium* sp. and *Actinopteryx parallela*, from the southern regions of the Korean Peninsula. Illustrations of habitus, diagnostic characters, and genital structures, and a distribution map are provided.

* This work was supported by grants from the National Institute of Biological Resources, funded by the Ministry of Environment of the Republic of Korea (NIBRE202406).

A-02

# Taxonomic overview of the Pyralini (Lepidoptera: Pyralidae: Pyralinae) from Korea

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The tribe Pyralini was established by Latreille in 1809, with type genus *Pyralis* Linnaeus, 1758. Pyralini belongs to the subfamily Pyralinae within the family Pyralidae. This tribe includes mostly medium-sized moths, and approximately 30 genera have been described worldwide (Nuss *et al*., 2024). Each genus has unique ecological traits and plant associations, with some closely linked to specific plant groups, such as landscape trees, crops, oak trees etc. In this study, a total of 19 species of Korean Pyralini are listed to date. Illustrations of adults are provided.

A-03

# Checklist of *Olethreutes* group (Lepidoptera: Tortricidae: Olethreutinae) in Korea

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According to Diakonoff (1973), the subtribe Olethreutina is classified into a total of 27 genera and three genera groups: *Olethreutes* group, *Hedya* group, *Apotomis* group.

Up to date, 39 species from 5 genera within the *Olethreutes* group have been reported in Korea. In this study, we provide a checklist of *Olethreutes* group along with illustrations of adult and genitalia.

A-04

# Insect biodiversity in Indochina: Survey and collection in Cleopatra's Needle critical habitat, Palawan, Philippines

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The biodiversity of SE Asia is generally considered to be one of the most diverse regions on Earth, with its main biogeographic units comprising Sundaland, Wallacea, Indochina, and the Philippines (Myers, 2000). The survey area is known as the Philippine's "last ecological frontier" endowed with rich natural resources and highly diverse flora and fauna.

In this study, we have reviewed the insect fauna based on the expeditions in the Philippines from 2022 to 2024, with a focus on Lepidoptera fauna. Results of the survey identified approximately 320 species of 120 genera in 58 families belonging to eight orders are identified, including some new and newly recorded species. Of these, 200 species from 82 genera of 24 families were lepidopterans. However, many specimens need further examination to verify their species identity.

A-05

# Snouted tiger moth (Noctuoidea, Erebidae, Aganainae) in Korea a connection with Lepidopterism

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The subfamily Aganainae belonging to the family Erebidae, includes 109 described species in 11 genera worldwide (Fibiger and Lafontaine 2005; Zahiri *et al*. 2012), excluding genus *Mecodina* Guenée, 1852. Korean Aganainae fauna has been studied by Kim *et al*. (2016) (Agananinae misspl.), Kim *et al*. (2016), Lee *et al*. (2021), and Bayarsaikhan *et al*. (2024), identifying seven species in two genera, *Mecodina subviolacea* (Butler)*, M. cineracea* (Butler), *M. nubiferalis* (Leech), and *M. subcostalis* (Walker), *Asota egens* (Walker), *A. caricae* (Fabricius), and *A. plaginota* (Cramer). The genus *Asota,* one of the largest in subfamily Aganainae, is primarily distributed in Oriental and African regions. Known for secreting toxic substances, such as histamines and peptides, *Asota* species can trigger allergic reactions during their life cycle transitions (Wills *et al.* 2016; Ubaidulla *et al.* 2022). In Kerala, India, *A. caricae* caused fever symptoms initially misdiagnosed as chikungunya or dengue, which were later attributed to Lepidopterism (Wills *et al*. 2016).

With increasing *Asot*a populations, particularly *A. caricae* and *A. plaginota*, recently reported on Jeju and Ulleung Islands, public health risks may be significant. *Asota*-induced Lepidopterism can result from skin contact or inhalation and could impact tourism and health. Given *A. caricae*'s history of causing mass allergic outbreaks in India, proactive population management is essential to prevent similar issues locally.

* This work was supported by by the Ministry of Education (2020R1A6A1A03041954).

A-06

# Mitogenome-based phylogenetic analysis of two ball-rolling dung beetles, *Gymnopleurus mopsus* and *Gymnopleurus geoffroyi* (Coleoptera: Scarabaeidae: Scarabaeinae), with notes on the phylogenetic relationships of Scarabaeinae

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The tribe Gymnopleurini is a well-known group within Scarabaeinae, characterized by its diurnal ball rolling behavior. While mitochondrial genomes have been reported for numerous Scarabaeinae species, those of Gymnopleurini remain unexplored. Here, we document for the first time the mitochondrial genome sequences of two dung beetles, *Gymnopleurus mopsus* (Pallas, 1781) and *Gymnopleurus geoffroyi* (Fuessly, 1775), and infer the tribe's position within Scarabaeinae. The mitochondrial genomes of the two species are 15,591 bp and 15,460 bp in size, respectively, and consist of 37 genes, with an identical gene order in Scarabaeinae. Mitochondrial phylogeny, based on the sequences of 13 protein-coding genes (PCGs) from 72 Scarabaeinae species, recovered monophyly of Scarabaeinae and a sister relationship between *Gymnopleurus* (Gymnopleurini) and *Sarophorus*. Notably, the monophyly of the Onthophagini + Oniticellini lineage was supported, reflecting its biogeographic history and highlighting the need for a taxonomic revision of this species-rich and cosmopolitan group, incorporating additional suprageneric groups. Our results not only helps fill the gap in the missing mitochondrial genome data for the Gymnopleurini tribe but also contributes to future conservation efforts by providing insights into the genomic diversity and population structure of these two threatened species.

* This research was supported by the Core Research Institute Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2021R1A6A1A10045235).

A-07

# Two new species of Baetidae (Insecta: Ephemeroptera) from Korea

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The family Baetidae, comprising over 900 species across nearly 100 genera, represents the most diverse taxon within the order Ephemeroptera, with a global distribution across all biogeographic regions. The nymphs of this family inhabit a wide range of freshwater microhabitats, displaying notable adaptability. Due to limited morphological key characters in adults, species identification within Baetidae primarily relies on nymphal characteristics. Between 2022 and 2024, we conducted extensive surveys in Korean streams to identify unrecorded Baetidae species. We extracted mitochondrial *COI* barcode sequences from nymphal specimens and compared them with those in the NCBI database. Our findings revealed that some groups of specimens within the genera *Baetis* and *Alainites* formed distinct clades with significant genetic divergence from other Northeast Asian species. Detailed morphological examinations of the mouthparts and abdominal segments provided diagnostic traits distinguishing these new species from other related species. This discovery helps to improve our understanding of Baetidae distribution in Northeast Asia.

**Keywords:** Baetidae, DNA barcode, Korea, New Species, Reverse 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 (NIBR202402202).

A-08

# Two new records in Orfeliini fungus gnats (Diptera: Keroplatidae) from Korea

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The family Keroplatidae, commonly known as fungus gnats, is one of the most diverse groups within the superfamily Sciaroidea. Globally, around 100 genera and 1,000 species of Keroplatidae have been documented, yet no research has been conducted on this family in Korea. Keroplatidae comprises six extant subfamilies - Arachnocampinae, Keroplatinae, Lygistorrhininae, Macrocerinae, Platyurinae, and Sciarokeroplatinae - as well as one fossil subfamily, Adamacrocerinae. This study focuses on the tribe Orfeliini within the subfamily Keroplatinae, reporting on two species, *Neoplatyura flava* (Macquart, 1826) and *Rutylapa ruficornis* (Zetterstedt, 1851). All specimens were collected at Mt. Gyeryong in Gongju-si, Chungcheongnam-do, in 2022 by Malaise trap. This is the first report of the family Keroplatidae in 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-09

# New Records of the genus *Mycetophila* Meigen (Diptera: Mycetophilidae) from Ulleung Island, Republic of Korea

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Sung Hwan Park, and Yeon Jae Bae[C]

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Ulleung Island, characterized by its distinctive geological traits, has a unique array of fauna and flora. Although studies have been conducted on insect fauna of this island, but the Mycetophilidae had not previously been documented. Therefore, we conducted field investigations at three sampling locations on Ulleung Island from 2021 to 2024, utilizing sweeping and Malaise traps. The Mycetophilidae family represents one of the largest groups within the infraorder Bibionomorpha in Diptera, encompassing eight subfamilies, 230 genera, and nearly 4,500 species that have been described globally. They have a mycophagous larval stage, and adults act as pollinators in nature. The adults are typically found in moist environments, such as under tree roots and on rocks covered in mosses near aquatic systems. As a result, we document five new country records of the genus *Mycetophila* (*M. devioides* Bechev 1988*, M. rudis* Winnertz 1864*, M. sigillata* Dziedzicki 1884*, M. stolida* Walker 1856 and *M. trinotata* Staeger 1840) from this Island. Diagnosis, photographs of morphological characters, and habitat information are provided.

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A-10

# New records of the genus *Janus* Stephen, 1829 (Hymenoptera: Cephoidea: Cephidae: Cephinae) from South Korea

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The genus *Janus* belongs the subfamily Cephinae into family Cephidae. The family Cephidae is slow-flying sawflies and generally having dark coloured body, long and cylindrical body shape, and fore tibia with one apical spur (Benson, 1946). The genus Janus includes 28 species worldwide, only one species, *Janus piri* Okamoto & Muramatsu, 1925, which was already reported from South Korea. In this study, a total of five species are recognized from South Korea. Among them, three new species, *Janus* sp. nov. 1, *J.* sp. nov. 2, *J.* sp. nov. 3, are described, moreover two species, *Janus hakusanus* and *J. micromaculatus*, are reported for the first time from South Korea.

**Keywords:** Cephidae, Korea, new species, Symphyta, sawfly

A-11

# First record of *Phyllocecus etorofensis* (Takeuchi, 1955) (Hymenoptera: Cephoidea: Cephidae: Cephinae) from Korea

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The species *Phylloecus etorofensis* (Takeuchi, 1955) belongs the subfamily Cephinae. In 1955, Takeuchi reported this species from Etorofu Island, southern Kuriles. This species having a mainly black body color and with yellow marks on the lower inner orbit, mandible, and each apical corner of the metasomal tergites 3 and 4 (Hara et al., 2021). In this study, description and photographs of key characters are provided.

**Keywords:** Cephidae, Korea, *Phyllocecus,* Symphyta, sawfly

A-12

# Discovery of two new species and two new record of spring stoneflies (Plecoptera: Perlodidae) in Korea

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The diversity of stoneflies has been extensively studied in remote areas over recent decades, revealing an increasing catalog of approximately 4,000 species worldwide. Among these, the family Perlodidae comprises at least 60 genera and over 380 species. Within the subfamily Perlodinae, primarily distributed across the Holarctic region, a few species extend into the northern Oriental Realm. A recent paper documented twelve Perlodinae species on the Korean Peninsula. These twelve species belong to eight genera: *Arcynopteryx* Klapálek, 1904; *Habaek* Murányi and Hwang, 2023; *Levanidovia* Teslenko & Zhiltzova, 1989; *Megaperlodes* Yokoyama, Isobe & Yamamoto, 1990; *Megarcys* Klapálek, 1912; *Perlodes* Banks, 1903; *Pictetiella* Illies, 1966; and *Stavsolus* Ricker, 1952. Recent Malaise trap surveys in South Korea yielded an unexpectedly rich collection of Perlodinae specimens. This study introduces two new species from South Korea and two species recorded for the first time on the Korean Peninsula: *Kogotus* n. sp., *Megarcys* n. sp., *Skwala compacta* (McLachlan, 1872), and *Stavsolus shihu* Zhang, Li & Li 2024. Materials, distributional data, descriptions of new species, and diagnoses for four species are provided.

**Keywords:** Plecoptera, stonefly diversity, new species, new Korean records, Korean peninsula

A-13

# Notes on the Korean *Anclyopus* species (Coleoptera: Endomychidae) with a newly recorded species

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Two species in the genus *Ancylopus* Costa, 1850 of the family Endomychidae have been known to Korean fauna. The first one species, *Anchylopus pictus asiaticus* Stromhecker, 1972 is well known and most common in Korean penninsula. But, the second one spcies, *A. phungi* Pic, 1926 was recently known to the Korean fauna in 2017 by Japanese Taxonomists, Sogoh and Yoshitomi with a specimen collected from Daejeon. These two species have quite similar external characters and are usually confused in many papers and faunal reports. But they can be easily distinguished from each other by the shape of dorsal sulcus on pronotum, blackish marking on elyta, shape of tibiae and the color of basal part of femora. In this research, we reviewed the Korean species of the genus *Ancylopus* and add one newly recorded species, *Anchylopus borealior* Stroheker, 1972 to Korean Fauna.

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A-14

# New host plant records of Korean sawflies (Hymenoptera: Symphyta)

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Suborder Symphyta, except for the family Orussidae, feeds on plants that are economically important to humans. Adult sawflies can generally be distinguished from the suborder Apocrita by their abdomen, which is broadly joined to the thorax, wings with numerous veins (except for Orussidae), legs with two trochanters, and the presence of cenchrus (except in Cephidae). Most sawfly larvae resemble caterpillars, a unique feature among Hymenoptera, and are often confused with lepidopteran larvae. Sawflies comprise about 8,900 species worldwide, with 418 species recorded in Korea. Despite active research on sawflies in other countries, little is known about the host plants of Symphyta in Korea. This study presents the first records of host plants for five species in Korea: *Neurotoma coreana* on *Quercus acutissima*, *Arge captiva* on *Zelkova serrata*, *Allantus nigritibialis* on *Rosa multiflora*, *Macrophya sibirica* on *Sambucus nigra*, and *Rhogogaster convergens* on *Spiraea prunifolia* var. *simpliciflora*.

A-15

# Larvae of genus *Apethymus* Benson (Hymenoptera, Tenthredinidae) associated with oak trees in South Korea

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The egg-overwintering sawfly genus *Apethymus* is commonly distributed in the Oriental and Palaearctic regions, with 23 species reported worldwide. This genus is known for its unusual biology. Adults fly in late summer and fall, and after overwintering as eggs, the next generation of larvae hatches in spring. The larvae feed on deciduous trees and shrubs, particularly those in the families Fagaceae and Rosaceae. In Korea, larvae of the genus *Apethymus* have been reported for only one species, *A. kunugi* Togashi. Here, we report the discovery of larvae from two additional species of *Apethymus*, *A. kolthoffi* (Forsius) and *A. sidorenkoi* Sundukov. Furthermore, we record a new host plant for *A. kolthoffi*, *Quercus mongolica* (Fagaceae), for the first time.

* This work was supported by a grant from the National R&D Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2020R1A6A3A01095736).

A-16

# First record of the genus *Filixungulia* Wei (Hymenoptera: Tenthredinidae) from Korea with description of complete mitochondrial genome sequence

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*Filixungulia*, a small genus within the subfamily Allantinae (Symphyta: Tenthredinidae), consists of three species that are distributed only in Northern China. It is closely related to *Asiemphytus* Malaise and *Macremphytus* MacGillivray, but can be distinguished by the following characteristics: simple, very slender claws; absence of the basal lobe and inner tooth. To date, *Filixungulia* has not been recorded outside of China. As a result of the present study, the genus *Filixungulia* is newly reported from Korea, with *F. alboclypea* Wei, 1997. In addition, the complete mitochondrial genome of this species is reported for the first time, with a length of 16,727 bp. The genome includes 37 typical mitochondrial genes, comprising 13 protein-coding genes (PCGs), two rRNAs, 22 tRNAs, and one A+T-rich region. This discovery extends the known distribution of the genus *Filixungulia*, which was previously considered endemic to China.

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A-17

# First record of *Janus micromaculatus* (Hymenoptera: Cephidae) from Korea

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The Cephidae are a small family of Hymenoptera, classified into three subfamilies: Cephinae, Athetocephinae, and Australcephinae. The latter two subfamilies are represented by only four species and restricted to the Afrotropical and Australasian regions, whereas the Cephinae contains about 165 described species in the Holarctic and Oriental regions. The suprageneric classification of the Cephinae remains as proposed by Benson (1946), who divided into three tribes, Cephini, Hartigiini and Pachycephini based both on morphology and host utilization. During an ongoing survey of Korean Hymenoptera, we discovered *Janus micromaculatus* Sato, in Korea, a species previously known to be endemic to Japan. Until now, only one species, *Janus piri* Okamoto & Muramatsu, has been recorded from Korea. The genus comprises 33 described species, which can be further divided into four species groups: *bimaculatus* group, characterized by fore wing with distinct spots and a body primarily black (five species); *cephoides* group with a slender body, long antenna, and a narrow and long second abdominal segment (eight species); *compressus* group, which has short antenna and body, and very short and high second abdominal segment (19 species); and *megamaculatus* group, with the large body and mainly yellowish-brown coloration (one 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 (NIBR202304203).

A-18

# Re-classification of the microleafhopper tribe Empoascini distant from Korea (Hemiptera: Cicadellidae: Typhlocybinae)

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Korean taxa of the tribe Empoascini is revised herein, adopting recent alternation and re-definition of *Empoasca* and allied genera. The previously known genus *Empoasca* (s.str.) from old world including Palaearctic region has been treated as an errorneous application, and should be excluded or substituted with other allied genera, as the former genus is distributed restrictively in new world. As the current alternation, a total of 17 genera in this tribe are recognized, including 3 newly recorded genera in Korean fauna. All together, a sum of 60 species belonging to this tribe from Korea are described, among these 4 species are new to science and further 8 species are newly recorded from Korean fauna. Keys, descriptions and illustrations of morphological features of the Korean taxa are provided respectively.

**Keywords:** Homoptera, Auchenorrhyncha, Cicadellidae, Typhlocybinae, taxonomy, new species

A-19

# Classification of the microleafhopper genus *Alnetoidia* Dlabola from Korea (Hemiptera: Cicadellidae: Typhlocybinae)

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Hitherto, 7 species with 2 subgenera of the typhlocybine microleafhopper genus *Alnetoidia* Dlabola, 1958 have been listed in the inventory of the Cicadellidae from Korean fauna, since our previous revision (Hossain *et al*., 2020). As a continuous taxonomic survey on the subfamily Typhlocybinae in Korea, the authors have found further 2 species, enumerating one new to science: *A. hastata* sp. nov. and the other one newly recorded in Korea: *A. lutescens* Anufriev, 1971 rec. nov. Descriptions, illustrations of morphological features and keys to 9 Korean species all together are provided respectively.

**Keywords:** Homoptera, Auchenorrhyncha, Typhlocybinae, taxonomy, identification, new species

A-20

# Taxonomic revision of the microleafhopper genus *Arboridia* Zachvatkin from Korea (Hemiptera: Cicadellidae: Typhlocybinae)

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Currently, a total of 10 species of the typhlocybine microleafhopper genus *Arboridia* Zachvatkin, 1946 have been listed in the inventory of the Cicadellidae from Korean fauna. Some of them are treated as sporadic pests injurious to viniculture in Asia. As a continuous taxonomic survey on the subfamily Typhlocybinae in Korea, the authors have found further 4 species new to science: *Arboridia balwangsana* sp. nov., *A. deokgasana* sp. nov. *A. hambaeksana* sp. nov., and *A. kisui* sp. nov. which named after Dr. Kisu Ahn, former Director of the Institute of Entomology, Agricultural Technology Center, Chungcheongbuk-do Province, Korea. Additionally, *A. yanonis* (Matsumura, 1932) is newly recorded from Korea. Descriptions and illustrations of morphological features of the present new taxa and keys to 15 Korean species are provided respectively.

**Keywords:** Hemiptera, Auchenorrhyncha, Typhlocybinae, taxonomy, identification, new species

A-21

# Classification of the microleafhopper tribe Dikraneurini McAtee from Korea (Hemiptera: Cicadellidae: Typhlocybinae)

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So far as the authors know, a total of 14 species belonging to 8 genera of the typhlocybine microleafhopper tribe Dikraneurini McAtee, 1926 have been listed in the inventory of the Cicadellidae from Korean fauna, since our previous contribution in the present taxa (Hossain *et al*., 2019, 2021). As a continuous taxonomic survey on the subfamily Typhlocybinae in Korea, the authors have found further 2 genera newly discovered from Korea as: *Micantulina* and *Vilbasteana,* both established by Anufriev in 1970. A new subgenus and 3 new species are described here as new to science all together: *Naratettix* (*Neonaratettix*) subgen. nov., *N.* (s. str.) *gamcheonus* sp. nov., *N.* (s. str.) *goheonsanus* sp. nov., and *N.* (s. str.) *jirisanus* sp. nov. A newly recorded species is added to the Korean fauna, too: *Micantulina pseudomicantula* (Knight, 1965). Descriptions and illustrations of morphological features of the present new taxa and keys to 18 Korean species are provided respectively.

**Keywords:** Homoptera, Auchenorrhyncha, Typhlocybinae, taxonomy, identification, new species

A-22

# A new species of the dancefly genus *Hybos* Meigen from Korea (Dptera: Empidoidea: Hybotidae)

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So far, two species belonging to the dancefly genus *Hybos* Meigen, 1820, the nominate genus of the family Hybotidae, has been recorded in the inventory of Korean Empidoidea made by Kwon *et al*. (2022). During the taxonomic survey on the danceflies in Korean peninsula, the authors have found the third species new to science: *Hybos hambaeksanus* sp. nov. The present new species is allied to *Hybos crassipess* (Linnaeus, 1758), but the former can be easily recognized by having the characteristc structure in male genitalia. Description, illustration of morphological features and key to the three Korean species are provided respectively.

**Keywords:** Diptera, Empidoidea, Hybotidae, *Hybos*, dancefly, taxonomy, new species

A-23

# 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 *Thecophora fulvipes* (Robineau-Desvoidy, 1830). Morphological diagnoses and illustrations of these species are presented. Additionally, a key to all species of Conopidae from Korea is also provided.

**Keywords:** *Conops ceriaeformis ussuriensis*, *Physocephala pielina*, *Thecophora fulvipes*

A-24

# PCR-Based species identification method using unique genetic markers for invasive termites (*Glyptotermes nakajimai, Coptotermes formosanus, Coptotermes gestroi,* and *Incisitermes minor*)

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This study introduces an efficient diagnostic system for rapid identification of four economically significant termite species (*Glyptotermes nakajimai, Coptotermes formosanus, Coptotermes gestroi,* and *Incisitermes minor*) using species-specific genetic markers developed through an automated de novo whole genome sequencing (WGS) pipeline. Our methodology incorporates multi-layered quality control processes, including dual de novo assembly using ABySS and MEGAHIT, coverage analysis through BWA and Samtools, and repetitive sequence elimination via RepeatMasker, followed by species specificity validation through DIAMOND BLASTX and BLAST analyses.

The resulting PCR-based diagnostic system enables species identification within three hours, providing a practical tool for quarantine procedures and timber industry inspections. Beyond immediate practical applications, our study provides the first complete WGS datasets for these termite species, establishing a foundation for future research in termite genetics and pest control strategies. This comprehensive approach not only enhances the efficiency of pest management protocols but also offers a cost-effective solution for early detection and prevention of termite invasions, contributing to both ecological conservation and economic protection in the construction and timber industries.

## 【 생 태 】

B-01

# 매미나방의 국내 분포와 난괴 기생벌류 검토

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매미나방은 태극나방과 독나방아과에 속하는 곤충으로 연 1회 발생한다. 섭식 가능한 기주식물의 범위가 매우 넓어 대 발생할 경우 큰 피해를 일으키는 산림해충이다. 최근 국내에서는 2021년 강원, 경기 등 북부 지방을 중심으로 대발생하였으나, 2022년 이후 개체수가 크게 감소하였다. 본 연구에서는 2024년 산란 난괴 채집을 통해 매미나방의 현재 국내 분포에 대해 조사하였으며, 더불어 개체수 감소에 대해 추측되는 여러 원인 중, 난괴에 발생하는 기생벌류에 대해 검토하였다.

B-02

# 한국 남부지역에서 채집된 등에모기 발생 양상 분석(2023~2024)

**류지훈**p1,2,3, **전지승**1,2,3, **안승박**1,2,3, **최광식**c1,2,3

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등에모기(Genus *Culicoides*)는 사람과 반추류를 포함한 척추동물에 흡혈성을 가지며, 블루텅, 아프리카마역, 아카바네 등 여러 질병을 매개하는 것으로 알려져 있다. 본 연구는 한국 남부지역(경남, 전남, 제주)에서 이들의 발생 양상과 분포를 조사하기 위해 2023년과 2024년 5월부터 10월까지 월 2회씩 소와 염소 축사에서 black light trap을 이용해 채집을 실시하였다. 그 결과, 총 16종 220,853마리의 *Culicoides*가 채집되었으며, 두 해의 데이터 비교를 통해 *Culicoides*의 발생량이 2023년에 비해 2024년에 약 22.6% 감소한 것을 확인하였다. 2024년에 한국 미기록종으로 새롭게 채집된 *C. asiana*와 *C. palawanensis*를 제외한 14종에 대하여 기후 변수 데이터를 바탕으로 분석한 결과, 기온 관련 변수 및 채집일 이전 한 달간 누적 강수량 변수가 채집량에 큰 영향을 미치는 것으로 나타났다. 본 연구 결과는 한국 남부지역에서의 *Culicoides* 발생 양상 및 분포에 대한 구체적 데이터를 제공하며, 향후 질병 매개체 및 방제 연구에 중요한 자료가 될 것으로 판단된다.

B-03

# 왕피천 수생태계 내 저서성 대형무척추동물의 군집분석 및 생물학적 수질평가

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왕피천 수생태계 내 저서성 대형무척추동물의 군집구조 분석을 위해 총 5개 지점에서 2024년 총 2회(4월, 8월) 조사를 실시하였다. 조사기간 중 저서성 대형무척추동물은 총 4문 6강 17목 60과 118종, 9,993.7개체/$m^2$가 출현하였다. 수환경 변화에 민감한 E.P.T. 분류군은 74종(62.71%)이 출현하였다. 섭식기능군(FFGs) 분석결과, 주워먹는 무리(Gathering collector: GC)가 33종(27.97%), 5,520.4개체/$m^2$(55.24%)로 가장 높은 종수 및 개체수가 출현하였다. 서식기능군(FHGs) 분석결과, 붙는 무리(Clinger: CL)가 60종(50.85%), 6,922.7개체/$m^2$(69.27%)로 우점하는 경향을 보였다. 군집지수 분석결과, 우점도지수(DI) 0.41, 다양도지수(H′) 3.59, 풍부도지수(R1) 4.6, 균등도지수(J′) 0.77로 나타났다. 저서동물지수(BMI)의 경우, 평균 93.07(1차 : 95.61, 2차 : 90.53)로 ‘매우 좋음’으로 평가되었다. 저서성 대형무척추동물 평균생태점수(AESB)의 경우, 평균 3.37(1차 : 3.49, 2차 : 3.26)로 나타나 “양호”로 평가되었다.

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

B-04

# A study on the ecological characteristics of major infectious disease-borne mosquito species

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In this study, eggs, larvae, and adults were collected from each habitat in urban and rural Chungcheongbuk-do to investigate ecological characteristics according to the specificity of the major mediated mosquito species and to utilize them for effective mosquito control. Due to the high heat island phenomenon and high population density, the city center has an overwhelming number of *Culex pipiens* that overwinter as adults and spawn in organic-rich places, and few are found in rivers. Mosquito control in the city center requires intensive control of larvae in winter or spring in order to remove winter mosquitoes in warm indoor areas. In rural areas, *Culex orientalis, Culex tritaeniorhynchus*, and *Anopheles* spp., which have the characteristics of spawning from clean and wide sources, were mainly found, and their populations increased from August to September except during periods of heavy rain. In order to control rural mosquitoes, it is necessary to remove water holes that occur after rain and block a wide range of sources such as wetlands, reservoirs, and rice paddy irrigation channels.

B-05

# Ectoparasite loads in small mammals of the Republic of Korea: Effects of season, host sex and body mass

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Various factors potentially influence the abundance and distribution of ectoparasites on host animals. This study investigated the effects of season, host sex, and body mass on ectoparasite distribution among small mammal species in the Republic of Korea. A total of 49,953 ectoparasites were collected from 513 individual hosts, representing eight small mammal species, through a nationwide survey. *Apodemus agrarius* (85.24%) was the dominant species, followed by *Crocidura lasiura*, *Craseomys regulus*, and others. Chigger mites constituted the majority of ectoparasites collected (91.40%), followed by ticks (6.25%) and other ectoparasites. Host preferences were observed, with chigger mites showing a higher preference to *C. regulus* than to *A. agrarius*, while ticks were most prevalent on *A. agrarius*. Ectoparasite loads varied across species, with *A. agrarius* harboring the highest loads. While the average ectoparasite load per individual small mammal was greater in autumn than in spring, seasonal differences in chigger mite burden were not observed in *A. agrarius*. A comparative analysis of chigger mite and tick burdens between male and female *A. agrarius* showed that males were more heavily infested with both ectoparasites than females. This discrepancy was attributed to differences in host body mass rather than host sex for chigger mites. In contrast, tick abundance exhibited minimal evidence of sex bias, potentially due to the questing tick distribution and behavioral differences between host sexes. These findings underscore the importance of understanding seasonal and host-specific factors that influence ectoparasite loads and their potential link to zoonotic disease risks.

B-06

# Patterns of *Limax maximus* distribution and establishment in Korea

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The leopard slug (*Limax maximus* Linnaeus, 1758) is an alien species newly identified in Gyeonggi-do Suwon-si in 2023. The current study was conducted to provide basic data for alien species management by investigating the settlement and dispersal potential of leopard slugs. As a result of the range survey, 1,060 leopard slugs were identified in an area of about 2.3 square kilometers within a 1 kilometer radius of Bambat Green Frog Park, a stronghold site. The body lengths of 160 and 549 individuals in March and August, respectively, were found to be smaller in March than in August, with a mean of 27.9 mm in March and 73.3 mm in August, with a p-value of less than 0.99 and a t-statistic of -31.34. The nucleotide diversity of the 27 leopard slugs collected around the outbreak site was 0.00271, indicating no diversity, and the haplotype was the same as that of leopard slugs collected in the UK and Switzerland. The life cycle of the leopard slug was consistent with its native habitat in Europe and other invasive areas, so we concluded that it has a high potential for establishment. The low genetic diversity and lack of a wide range suggest that it is in the early stages of invasion and that a small number of individuals or the same genetic population were introduced during the initial introduction. However, the area of Bambat Green Frog Park where leopard frog occurs in high density has a location characterized by logistics and human movement, such as Uiwang ICD, Yeongdong Expressway, Osong Station, and Uiwang Station, which are inland container bases within a radius of 5 km, and it is highly likely to spread nationwide through unintentional spread due to its ecological characteristics of feeding and resting in food waste and domestic and agricultural waste, so rapid management of this species is necessary.

* This study was supported by National Institute of Ecology (NIE-A-2024-08)

B-07

# Monitoring of pathogen-transmitting mosquito populations in Chungcheongnam-do, Korea from 2017 to 2020

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As vector-borne diseases are increasing due to climate change, we conducted four years of mosquito outbreak surveillance at research sites in Cheonan and Geumsan counties, Daejeon and Chungcheongnam-do, and used real-time PCR to investigate the incidence of flaviviruses in female mosquitoes from 2017 to 2020. A total of 12,706 mosquitoes were collected during the surveillance period, of which only 39 *Culex tritaeniorhnchus,* the main vector of Japanese encephalitis, were collected and no pathogens were detected. Flavivirus detection in 711 pools of 11,119 mosquitoes, excluding Anopheles spp, resulted in two positive cases in 2018, identified as Chaoyang virus and Culex virus, respectively.

* This work was supported by KDCA grant

B-08

# Four-year surveillance study of the vector of tsutsugamushi, chigger mites, in Boryeong-si, Chungcheongnam-do, South Korea

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Tsutsugamushi disease is a serious public health problem worldwide because it can be fatal and is difficult to diagnose and treat. Tsutsugamushi is a disease transmitted by chigger mites, and chigger mites use rodents as intermediate hosts. Therefore, this study monitored the occurrence of chigger mites and investigated the prevalence of infection through rodent collections in Chungcheongnam-do Province from 2020 to 2023. A total of 94 rodents were collected during the study, and the infection rate of Tsutsugamushi was calculated using 2,106 mites, half of the total of 4,191 ticks. Among them, a total of two positive pools of Boryeong type were identified from 2020 to 2023.

* This work was supported by KDCA grant.

B-09

# Comparative analysis of benthic macroinvertebrates in Gucheon Stream, 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. The individual ratio of E.P.T. Group were 57.04% in Ephemeroptera, 18.07% in Plecoptera and 11.66% in Trichoptera. 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 result of the similarity analysis, highest at 82.2% at the adjacent points, St.5 and St.6. Average annual community indices analysis, DI 0.38(±0.05), H′ 3.48(±0.19), R′ 3.23(±0.41), and J′ 0.85(±0.04) in 2018, and DI 0.55(±0.09), H′ 2.98(±0.31), R′ 2.91(±0.65), and J′ 0.70(±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(±2.84) in 2018 and 96.99 (±1.13) in 2021.

B-10

# Assessment of potential effects on the diversity of non-target insects against GM turfgrass varieties

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The experiment assessed the potential impacts of GM turfgrass cultivation on pest outbreaks, insect populations, and other insect species using two transgenic GM turfgrass varieties (JG21 and JG21-MS1) and the non-GM parental species, Zoysiagrass (*Zoysia japonica* Steud.). This study was conducted in isolated living modified organism (LMO) fields in Jeonju, Jeollabuk-do, and Seogwipo, Jeju-do, South Korea, in 2022. Multivariate analysis revealed that the abundance and diversity of plant-dwelling pests were similar across all treatments, with no significant differences ($P < 0.05$). Overall, the results suggest that the GM turfgrass varieties did not negatively affect the community of non-target plant-dwelling pests and arachnids.

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B-11

# 기후변화 대비 곤충상 모니터링을 위한 거점 수목원 및 모니터링 대상 식물종의 선정

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최근 전 세계적으로 대두되고 있는 기후변화로 인해 다양한 분야에서 이를 예측하고 대응하기 위한 연구가 진행 중에 있다. 기후변화로 인해 발생되는 이상고온현상 및 저온현상, 한파, 겨울철 평균기온의 상승 등은 생태계에 영향을 미치며 특히 식물과 동물의 생존에 영향을 미칠 것으로 사료되므로 기후변화를 대비한 동·식물의 지속적인 모니터링은 매우 중요한 부분이다. 이러한 관점에서 모니터링 거점 지역 및 대상 생물종을 정하는 것은 추후 기후변화로 인해 발생되는 동·식물의 변화양상을 보다 명확하게 예측·분석하는 데 중요한 기준 자료가 될 것이다. 본 연구는 곤충을 대상으로 기후변화에 대비한 지속적인 모니터링을 위하여 위도, 곤충과 식물의 종다양성 등의 요인을 고려한 모니터링 거점지역을 선정하였으며, 개화시기, 시기별 곤충의 이용 빈도 등을 고려한 모니터링 대상 식물종을 선정하였다.

* 본 연구는 국립수목원 기후변화 대응 전시원 산림생물다양성 증진 및 관리기반 구축 연구(KNA3-1-10,21-4)의 지원을 통해 얻어진 결과입니다.

B-12

# Observation of caste-specific activity seasons of hornets collected at an apiary in Daegu and the effectiveness of the pesticide-coated hornet release method

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Hornet (Genus *Vespa*) colonies are annual, and the new life cycle, comprising six periods, always begins in the spring with a single fertilized queen. The timing of each period may vary due to factors such as geographic location and differences in the condition of individual colonies. Our aim was to observe the transition from the pre-nesting, solitary, and cooperative periods to the polyethic period for five major *Vespa* species found in the southern region of South Korea under the same geographic conditions. We set up traps near an apiary in Daegu and conducted periodic observations. For *V. analis, V. mandarinia, V. velutina nigrithorax*, and *V. crabro*, new queens were captured until mid-June, and workers were captured from mid-July. However, *V. ducalis* showed a high proportion of queens, along with some workers, still present until July 12.

Additionally, many personal apiaries have recently adopted a hornet control method in which insecticide dust is applied to the bodies of *V. velutina* workers, which are then released to return to their nests. In the apiary where our study was conducted, this control method was implemented starting in late July, when the number of *V. velutina* workers increased, and we observed a noticeable decline in the number of *V. velutina* workers captured in traps within three weeks of the control's implementation.

In future studies, it will be necessary to gather more diverse and meaningful information, such as the timing of the transition to the reproductive period, through investigations conducted over a longer period and in more locations.

B-13

# 단감 착과향상을 위한 화분매개곤충 적정 투입 시기

이주영, 최덕수, 오상아, 권혜영, 김선암, 이유범, 김지수, 임윤지, 주경천

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국내 화분매개곤충 이용작목은 2011년 19개 작목에서 2020년 26개 작목으로 빠르게 증가하고 있으며 이와 관련하여 현장 적용 기술 확립 및 표준화가 필요한 실정이다.

단감의 화분매개곤충 사용률은 10.4%로 꿀벌이 99% 차지하고 있으나 현장에서 투입 시기는 아직 설정되지 않아 단감(부유)의 개화 조사로 투입 시기를 구명하고자 하였다.

단감(부유)의 개화 시기는 지역에 따라 차이를 보이긴 하나 5월 중하순이며 개화 15일 전 기온의 영향을 크게 받는데 이 기간이 따뜻할수록 개화가 빨라진다고 알려져 있다.

단감의 주요 품종은 부유, 차량이며, 수분수 품종으로는 서촌조생, 태추, 선사환이 주로 이용되는데 수분수의 개화 시기는 암꽃보다 7일 빠르며 개화 후 2일이 되면 수술에서 화분 나오게 된다. 단감의 암술은 개화 직후 백색에 가깝지만 2~3일 후 갈색으로 변하며 수분 능력을 잃게 된다. 따라서 화분매개곤충 투입시기는 5월 평균기온이 15℃보다 높은 날이 10일 지속되고, 암꽃 꽃받침이 완전히 열리고 꽃봉우리가 90% 형성될 때가 적기이다. 벌통의 출입구는 해가 오래 비출 수 있도록 동·남쪽 방향으로 설치하고 출입문 출구가 노출되도록 완전히 열어 1일 안정화시켜야 한다.

## 【 형 태 】

C-01

# Microstructure of web spiral scaffold silk in the golden orb-web spider, *Trichonephila clavata*

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In this study, we investigated the structural and functional characteristics of scaffold silk used by *Trichonephila clavata* during web construction. Scaffold silk, typically produced by the minor ampullate gland, serves as a temporary framework for supporting spiral adhesive silk during web formation. However, unlike other orb-weaving spiders, *T. clavata* retains this minor ampullate silk as a permanent web component. Utilizing optical microscopy and field emission scanning electron microscopy (FESEM), we analyzed the microstructural properties of dragline, spiral, and minor ampullate silk, as well as the role of minor ampullate silk in enhancing web stability. Our results indicate that the retained scaffold forms loose transverse structures, with 4~8 spiral silk threads wrapping around the minor ampullate silk in a musical stave-like arrangement. This scaffold and radial silk structure creates approximately 1,800 web sections, which prevent extensive web damage when some sections are compromised by struggling prey. Additionally, comparisons between sticky flagelliform silk and minor ampullate silk reveal significant differences in droplet size and adhesive properties, with the minor silk exhibiting a smooth, glycoprotein-free surface. These findings suggest that the unique retention of minor ampullate silk not only reinforces web structure but also enhances web durability and prey capture efficiency.

**Keywords:** microstructure, spider, minor ampullate silk, web

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

C-02

# Morphological analysis of the eggcase surface on the wolf spider, *Paradosa astigera*

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The wolf spider, *Paradosa astigera* is a wandering predator that directly hunts its prey rather than setting traps (web). Nevertheless, its silk glands have not degenerated and instead produce silk used for offspring protection. Following oviposition, the female constructs an eggcase to cover the eggmass, which she attached to her abdomen. This study investigates the structural differences between the inner and outer silk layers of the eggcase and the surface granules of the egg chorion. Internally, the eggcase comprises a dense yet flexible silk wall, with curled silk bundles arranged randomly. Each bundle consists of multiple silk fibers approximately 500 nm in diameter, with substrate materials, likely chorionic microspheres, filling the spaces between the fibers to form a durable inner wall. In contrast, the outer surface is densely packed with foreign particles, exhibits a rough texture, with occasional porous regions showing a polygonal silk network. This outer silk mesh ranges from 10 to 500 nm in diameter, sharply contrasting with the robust, linear bundles of the inner wall. Additionally, the eggs adhere to each other, forming a single mass covered with a monolayer of chorionic microspheres ranging from 20 nm to 2 μm in diameter. These observations support the hypothesis that granules and eggcase silk perform complementary offsprings protective functions.

**Keywords:** microstructure, wandering spider, eggcase, silk

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## 【 생 리 】

D-01

# Impact of ethanol on maggot development: Implications for accurate post-mortem interval estimation

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Estimating the post-mortem interval (PMI) through analysis of maggot growth rates is a fundamental practice in forensic entomology. However, maggot growth can be influenced by drugs and toxins, potentially leading to inaccuracies in PMI estimations. Ethanol, a substance of social and forensic relevance, is a primary component of alcoholic beverages. This study investigates the effects of ethanol on the fat body, a tissue essential for maggot growth. Under controlled conditions of 25°C and 70% relative humidity, 140 *Sarcophaga peregrina* maggots were reared on rabbit carcasses treated intravenously with either a median lethal dose of ethanol or 0.9% NaCl as a control. Each treatment group included seventy maggots. Post-feeding stage maggots were preserved as permanent specimens, and fat body tissue was analyzed, showing a statistically significant reduction in fat body development in maggots feeding on ethanol-treated carcasses. This suggests that ethanol inhibits fat body development and may impact overall maggot growth. These physiological changes underscore the importance of considering ethanol exposure in PMI estimations to improve forensic accuracy, particularly in cases of alcohol exposure.

## 【 분자생물 】

E-01

# Insect cell-derived human CD200-Fc increases ZO-1 tight junction protein in urothelial carcinoma cells

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CD200 is a ligand for interaction to the CD200R1, having anti-inflammatory effects. It inhibits the NF-κB pathway, attenuating the inflammatory response and maintaining barrier function. In this study, human CD200 was fused with the human IgG Fc to generate recombinant CD200-Fc fusion protein and produced in insect cells using BEVS. CD200-Fc$^{I}$ inhibited proliferation of TCCSUP cells, bladder epithelial cancer cell. The mRNA and protein levels of ZO-1, tight junction protein for barrier protection in epithelial tissues increased in TCCSUP cells treated with CD200-Fc$^{I}$. These results suggest that CD200-Fc$^{I}$ could alter the ZO-1 expression in a bladder epithelial cancer cell, enhancing the cell barrier protein function, which could inhibit cancer metastasis. Taken together, the BEVS can be applied to express anti-tumor therapeutic CD200-Fc for bladder cancer.

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E-02

# A study on the expression and immmunogenicity of bladder cancer vaccine candidate A

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Cancer-testis antigens (CTAs) are expressed in various types of cancers but their expression in normal tissues is restricted to germ cells which are immune privileged. So, they are an ideal candidate for cancer immunotherapy or vaccination in tumors. Candidate A belongs to CTAs and we designed the human IgG Fc fusion A (A-Fc) using baculovirus expression vector systems to study the development of bladder cancer vaccine candidate. The expressed A-Fc was injected into mice and then blood sampling to obtain serum. To confirm the presence of A-Fc antibodies in serum, it was analyzed through ELISA using bladder cancer cell line and human recombinant A. As a result, we confirmed that serum had binding activity. In conclusion, we successfully produced A-Fc and had the potential to develop immunogenicity. We will study the anti-cancer effect in the future.

**Keywords:** Cancer-testis antigen, bladder cancer, Fc fusion protein

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E-03

# Comparative analysis of *Tm*Tube in response to microbial infection in *Tenebrio molitor*: Systemic versus oral infection pathways

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Toll pathway is a major signaling pathway to regulate antimicrobial peptides (AMPs) production against pathogenic infection. Tube, intracellular components of Toll pathway, forms a complex with Pelle and MyD88 through Death domain and activates NF-κB in *Drosophila melanogaster*. In contrast, immunological function of Tube in *Tenebrio molitor* is insufficient. Here, we identified the *TmTube* gene and performed a domain and phylogenetic analyses using the amino acid sequences of its orthologs. In addition, the induction patterns of *TmTube* were investigated at 3, 6, 9, 12, and 24 hours-post injection of pathogens into 10th to 12th instar larvae. To understand the immunological function of *Tm*Tube, we investigated the effects of *TmTube* RNAi on larval mortality against pathogenic infection. It is known that the systemic infection is directly injected the pathogens into the host's hemocoel which is the experimental model for the study of the insect immune, however, in nature, most pathogens were orally infected into the hosts. These two different routes of infection are expected to express different patterns of immune factors. In the further study, we plan to compare the immunological function of *Tm*Tube in between oral infection and systemic infection.

E-04

# Molecular characterization of c-Jun N-terminal Kinase, *Tm*JNK, against microbial infection in *Tenebrio molitor*

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Insects have an strong innate immunity without adaptive immunity. Producing antimicrobial peptides (AMPs) is an important response against infectious microbes. It is well known that the JNK signaling pathway also involved in stress-related response, cell death, apoptosis, autophagy and AMP production. c-Jun N-terminal Kinase (JNK) is activated by the phosphorylation of serine/threonine residues by upstream factors. We identified the ORF sequence of *JNK* from *Tenebrio molitor* (*TmJNK*) and conducted phylogenetic analysis of deduced amino acid sequence of *Tm*JNK with its orthologs. We performed qRT-PCR to investigate expression patterns of *TmJNK* in developmental stages and tissues. To understand immunological function of *TmJNK*, early larvae were injected with microorganisms including *E. coli*, *S. aureus*, and *C. albicans*. and investigated the induction patterns of *TmJNK* at 3-, 6-, 9-, 12-, and ⁻24-h post-injection. To further investigate the immunological function of *Tm*JNK, the larval mortality and expression patterns of AMP genes wiil be examined after microbial injection into ds*TmJNK*-treated larvae. Our study may contribute to understanding the antimicrobial function of *Tm*JNK.

E-05

# The preliminary study of trained immunity in *Tenebrio molitor*

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Immunological memory is the ability of the immune system to respond more rapidly and effectively against re-exposure than previously encountered pathogens, mainly observed in the adaptive immunity of vertebrates. Recent studies have discovered evidence that innate immunity also forms immunological memory. Immune priming refers to the process through which the host experiences a primary infection with pathogens, become immune-primed. Trained immunity is the whole process by which a host forms a memory and responds more strongly to secondary infection. Trained immunity is known to be regulated by epigenetic modifications and metabolic reprogramming of cells. Antimicrobial peptides are representative molecules of innate immune response that produced against pathogenic infections. To investigate trained immunity in *Tenebrio molitor*, we infected larvae with the Gram-negative bacteria, *Escherichia coli*. We first investigated larval mortality against *E. coli* and PBS to determine the appropriate lethal concentration. To confirm the priming effects, we investigated the mortality following secondary infection 10 days after the primary infection. We also investigated the expression patterns of antimicrobial peptides after both primary and secondary infection. In the further study, we will explain the phenomenon of trained immunity through an epigenetic approach.

E-06

# Functional study of *Tm*Pellino in response to microbial infection in *Tenebrio molitor*

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In insects, the Toll pathway is one of the main innate immune processes that produce antimicrobial peptides (AMPs) in response to fungi and Gram-positive bacteria. Pellino, is a highly conserved E3 ubiquitin ligase in the Toll pathway. In *Drosophila*, two possibilities have been proposed for Pellino, either acting as a positive regulator of innate immunity through interaction with Pelle or acting as a negative regulator of the Toll pathway by targeting MyD88 to mediate K48-linked ubiquitination. However, the molecular mechanisms of Pellino in innate immune responses have been poorly studied. Therefore, we aimed to characterize the immunological functions of *Tenebrio molitor* Pellino (*Tm*Pellino). In this study, to understand the immunological function of *Tm*Pellino, we screened the expression patterns of *TmPellino*. In addition, we injected the pathogens into ds*TmPellino* treated *T. molitor* larvae and investigated the larval mortality. In the future, to know the effects of *Pellino* RNAi on AMPs production, we plan to investigate the expression patterns of AMP genes after pathogen injection into *TmPellino*-silenced *T. molitor* larvae. This study may provide basic information to understand how *Tm*Pellino regulates AMPs production in *T. molitor*.

E-07

# Identification and expression analysis of *TmTab2* in *Tenebrio molitor*

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The immune deficiency (Imd) pathway, a widely conserved immune signaling pathway in invertebrates, regulates the production of antimicrobial peptides. It is known that multiple key components are involved in the Imd pathway. TAK1-associated binding protein (TAB2), an intracellular signaling component of this pathway, is essential for regulating the Imd pathway. The TAK1/TAB2 complex simultaneously activates two downstream components known as JNK and Relish. To investigate TAB2 in *T. molitor*, we identified the *TmTab2* genes from *T. molitor* EST and RNA sequencing data. Furthermore, we examined the mRNA expression of each gene at different developmental stages and in various tissues from both late instar larvae and 5-day-old adults of *T. molitor*. Tissue-specific induction levels of *TmTab2* were assessed at 3, 6, 9, 12, and 24 hours post-infection with *Escherichia coli*, *Staphylococcus aureus*, *Listeria monocytogenes*, and *Candida albicans*. These data provide insight into the role of *TmTab2* in the Imd pathway.

E-08

# Identification and functional characterization of *TmIAP2* in the innate immune response of *Tenebrio molitor*

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In insects, inhibitor of apoptosis protein 2 (IAP2) functions as a critical regulator of the immune deficiency (Imd) pathway. Studies in *Drosophila melanogaster* have shown that DIAP2 promotes K63-linked ubiquitination, facilitating the nuclear translocation of the NF-κB protein Relish. In *Tenebrio molitor*, the expression pattern of IAP2 (TmIAP2) varies across developmental stages and tissues. The highest expression level was observed during the P1 developmental stage (day 1 of pupae), while in young larvae, expression peaked in the gut, indicating a potential role in local immune responses or gut homeostasis at this stage. In this study, to investigate the role of TmIAP2 in AMP production, dsRNA specific to TmIAP2 was synthesized and used to knock down TmIAP2 via RNA interference (RNAi). Following knockdown, *Escherichia coli*, *Listeria monocytogenes*, and *Candida albicans* were injected into *T. molitor* to facilitate the analysis of the expression levels of 15 AMP genes. These levels were then compared with those in a control group injected with dsEGFP. Among the AMP genes examined, six showed decreased expression in the TmIAP2-knockdown group compared to the control, while four showed increased expression. The remaining AMP genes did not show significant changes in expression. Therefore, this study suggests that TmIAP2 may play a key role in regulating the Imd pathway in *T. molitor*.

E-09

# Identifiaction and functional characterization of *TmDorX1* in the yellow mealworm, *Tenebrio molitor*

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Antimicrobial peptides (AMPs) in *Tenebrio molitor* are produced through the Spätzle-Toll signaling cascade, with the transcription factor Dorsal, a member of the nuclear factor-kappa B (NF-κB) family, playing a key role in this process. In a previous study, we identified and reported the characterization of *TmDorX2*. In this study, we aimed to identify and explore the immunological function of another dorsal gene, *T. molitor TmDorX1*. We found that *TmDorX1* is expressed throughout all developmental stages, with the highest gene expression observed in young larvae. Spatial analysis revealed that *TmDorX1* mRNA expression was highest in the larval gut. To investigate the role of *TmDorX1* in AMP production, we compared the expression levels of 15 AMP genes between the *TmDorX1*-silenced group and the control group following microbial infection. Upon *Listeria monocytogenes* infection, AMP gene mRNA expression was significantly reduced in the whole body, fat body, and Malpighian tubules compared to the control. These findings confirm that *TmDorX1* plays a crucial role in AMP production in response to *L. monocytogenes* infection and has a significant impact on AMP expression.

**Keywords:** Toll pathway, Dorsal1, *Tenebrio molitor*, RNAi, antimicrobial peptides

E-10

# *Tribolium castaneum* TcCPAP1-C cuticular protein is required for the integrity of internal tendon cuticle and limb movement

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Structural cuticular proteins (CPs) and the polysaccharide chitin are the primary components of insect cuticle/exoskeleton. A large number of *CP* genes have been identified in insect genomes and classified into several distinct families defined by the presence of specific amino acid sequence motifs. Cuticular Protein Analogous to Peritrophins (CPAPs) composed of one (CPAP1s) or three (CPAP3s) chitin-binding domain comprise one of CP families. In this work, we report a novel role for TcCPAP1-C in limb movement and locomotion of *Tribolium castaneum* adults. RNAi for *TcCPAP1-C* had no effect on any types of molt, growth or development. However, the resulting adults exhibited a defect in movement of legs, particularly femur-tibia joints. In the legs dissected from TcCPAP1-C-deficient pharate pupae, the internal tendon cuticle was ruptured near the femur-tibia joint. There was no obvious defect on morphology of exoskeletal cuticle, muscles, microtubule arrays and hemiadherens junction, all of which are also important for insect limb movement. These results indicate functional specialization of TcCPAP1-C in the structural integrity of the internal tendon cuticle, and loss of function of TcCPAP1-C caused internal tendon cuticle breakage, resulting in impaired leg movement and defective locomotion.

E-11

# Functions of groups I and II chitinases, TcCHT5 and TcCHT10, in turnover of chitinous serosal cuticle during embryogenesis in *Tribolium castaneum*

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Chitinases (CHT) comprise a large gene family in insects and have been classified into at least eleven subgroups. Many studies involving RNA interference (RNAi) have demonstrated that loss of function of group I (CHT5s) and group II (CHT10s) CHTs causes lethal molting arrest in many insect species including the red flour beetle, *Tribolium castaneum*. TEM analysis revealed a failure in turnover of the endocuticular layer of the old cuticle, indicating that both group I and group II chitinases are required for degradation of chitin in the old cuticle, which is critical for insect molting. In this study we further investigated the functional importance of *TcCHT5* and *TcCHT10* in eggshell turnover during embryonic development of *T. castaneum*. Real-time qPCR analysis revealed that expression of *TcCHT10* occurred prior to that of *TcCHT5* during embryonic development as has been observed at post-embryonic molting periods in several other insect species. With immunogold-labeling TEM analysis using an FITC-conjugated chitin-binding domain protein (FITC-CBD) probe, chitin was detected in the serosal cuticle but not in any other regions of the eggshell including the chorion and vitelline membrane layers. Injection of double-stranded RNA (dsRNA) for *TcCHT5* (ds*TcCHT5*) or *TcCHT10* (ds*TcCHT10*) into mature adult females had no effect on their fecundity and the resulting embryos developed normally inside the egg. There were no obvious differences in the morphology of the outer chorion, inner chorion and vitelline membrane among eggs from these dsRNA-treated females. However, ds*TcCHT10* eggs failed in turnover of the serosal cuticle in which the horizontal chitinous laminae remained intact, resulting in lethal embryo hatching defects. In ds*TcCHT5* eggs, digestion of the serosal cuticle was not complete but it is apparently sufficient for embryos to hatch. Group I lytic polysaccharide monooxygenase (TcLPMO15-1) catalyzes oxidative cleavage of cuticular chitin, which is also required for the old cuticle turnover during post-embryonic molting in *T. castaneum*. The functional importance of TcLPMO15-1 in the serosal cuticle digestion is also discussed.

E-12

# Structural protein CPAP1-H functions in organization of cuticular extracellular matrix in a beetle

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The two different structural biopolymers, cuticular proteins (CPs) and chitin, are major components of insect cuticle, which play critical roles in protecting them from several environmental stresses and pathogens. Insect *cuticular protein analogous to peritrophins* (*CPAPs*) genes comprise one of the major *CP* gene families, and its products have been classified into two subfamilies, CPAP1 and CPAP3, with respectively one or three copies of a CBM14 chitin-binding domain. In this work we investigated the physiological functions of TcCPAP1-H, belonging to the CPAP1 subfamily in *Tribolium castaneum*. RNAi of *TcCPAP1-H* at young instar larval stages resulted in lethal developmental arrest where the larvae exhibited a rough and crumpled cuticle. Injection of dsRNA for *TcCPAP1-H* (ds*TcCPAP1-H*) into last instar larvae had no effect on the subsequent larval-pupal molt. However, the resulting pupae failed abdominal contraction, wing expansion or tightening of head and appendages. Those pupae eventually died entrapped their pupal exuviae during adult eclosion. TEM analysis revealed that TcCPAP1-H is required for proper organization of chitinous horizontal laminae and vertical pore canal in the cuticle of adult *T. castaneum*.

E-13

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

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Lytic polysaccharide monooxygenases (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 *Psacothea 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-14

# 산호랑나비(*Papilio machaon*) 미토콘드리아 유전체 assembly 및 annotation

**정준양**p1,2, **홍찬의**1,3, **신현준**1,3, **이 혁**1,3, **이경원**1,3, **상민규**1,2, **박지은**1,2,
**송대권**1,2, **정헌천**1, **이용석**c1,2,3

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산호랑나비(*Papilio machaon*)는 한반도 전역에 분포하며 주로 산지 및 초지에서 서식하는 종이다. 산호랑나비는 현재까지 38종의 아종이 보고된 것으로 알려져 있으나, 야생에서의 잡종 발생 빈도, 형태학적 특성, 생태적 선호도 등의 차이에 따라 그 분류학적 위치에 대한 논의가 활발히 이루어지고 있다. 이 연구는 산호랑나비의 미토콘드리아 유전체 분석을 통해 해당 종의 주요 유전자와 기능적 요소를 확인하고, 이를 통해 대사 및 진화적 관계를 이해하기 위한 기초 자료를 제공하는 것을 목표로 하였다. 단일 개체의 *P. machaon*에서 Whole genomic DNA를 추출한 뒤 Illumina Hiseq 2500 플랫폼을 이용하여 sequencing을 수행하였다. 이후, MitoZ를 사용하여 WGS 데이터를 assembly 한 후 미토콘드리아 유전체를 선별하여 annotation 및 분석을 진행하였다. 추가적으로, 미토콘드리아 유전체 내 tRNA 유전자의 위치와 구조를 확인하기 위하여 tRNAscan-SE v.2.0을 사용하여 분석을 진행하였다. 분석 결과, 유전체 길이는 약 15,352 bp로 확인되었으며, 13개의 단백질 코딩 유전자, 22개의 tRNA, 그리고 12S 및 16S rRNA를 포함하는 것으로 확인되었다. 또한, tRNAscan-SE v.2.0 분석을 통해 총 10개의 tRNA의 유전자가 예측되었다. 이 연구는 *P. machaon*의 미토콘드리아 유전체에 대한 기초 데이터를 제공하며, 해당 유전체의 assembly와 annotation을 통해 주요 유전자와 기능적 요소들을 확인하였다. 이 데이터는 *Papilio* 속 나비들의 미토콘드리아 유전체 구조 및 기능을 이해하고 아종 간 또는 종간의 진화적 관계 연구에 중요한 기초 자료로 활용될 수 있을 것으로 사료된다.

【 방 제 】

F-01

# Bed bug outbreaks in South Korea: Implications for urban entomology and effective pest management

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Urban entomology is a recognized discipline that focuses on the study of household and structural pests, emphasizing their emotional and medical significance in urban environments. The financial burden of managing pests such as ants, cockroaches, bed bugs, and termites is substantial. Within this context, the genus *Cimex*, belonging to the subfamily Cimicinae, consists of hematophagous and cosmopolitan insects. This genus includes 23 described species categorized into four species groups based on DNA analyses: *C. hemipterus, C. lectularius, C. pilosellus*, and *C. pipistrelli*. Additionally, they can be classified by their trophic preferences into bird bugs, bat bugs, and human bugs, with *C. lectularius* and *C. hemipterus* being the primary human-associated species. Other members, such as *C. columbarius* and *C. pipistrelli*, have also been reported to occasionally feed on humans. Currently, South Korea is experiencing a bed bug outbreak, prompting the launch of various initiatives aimed at managing this growing issue. This study highlights the need for effective pest control strategies to mitigate the public health impacts associated with *Cimex* species.

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**【 식용곤충 】**

G-01

# 사육 환경조건이 갈색거저리(*Tenebrio molitor* L.) 노숙유충의 용화에 미치는 영향

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갈색거저리(*Tenebrio molitor* L.)는 실내 인공사육을 하면서부터 온도와 습도, 광주기 조건, 밀기울 대체 먹이원 등에 대한 연구는 국내외에서 많이 이루어져 있으며, 국외는 대부분 기업농으로 공장형 자동화 대량사육 시스템이 개발되어 사용되고 있다. 그러나 국내 갈색거저리 사육농가는 소규모 영세농이 대부분이라 생산과 가공 과정에서 많은 노동력이 소요되는 문제들이 대두되고 있다. 따라서, 본 연구는 갈색거저리 생산과정에서 노동력 절감을 위해 유충이 동시에 번데기가 될 수 있는 사육환경 조건들을 조사하였다. 유충 동시용화 유도 실험은 멀티인큐베이터를 이용하였으며, 사육환경 중 온도는 대조구로 25℃와 16, 32℃, 그리고 먹이공급 유무 조합으로 용화율과 생존율을 확인하였다. 온도에 따른 유충 동시용화율은 25℃와 32℃에서 52.6±2.9%, 44.3±2.1%였으며, 16℃에서는 대조구보다 18.8배 낮았다. 먹이공급 유무는 동시용화 유도에 유의차가 없었고, 용무게와 생존율도 온도와 먹이공급 유무에서 차이가 없었다. 광주기 조건에서는 24명:0암, 18명:6암, 0명:24암과 14명:10암을 대조군으로 용화율을 확인한 결과, 대조구보다 24명:0암과 18명:6암은 각각 1.8배, 1.3배 증가하였다. 용무게와 우화율에서는 대조구와 차이가 없었으며, 우화하는 데 걸리는 일수에서는 24명:0암에서 7.3±0.1일로 8.1±0.2일인 대조구와 약간의 차이를 보였다. 이상의 결과 온도와 광주기 조절로 동시용화를 유도함으로써 사육농가의 노동력 소요시간을 줄일 수 있을 것으로 사료된다.

G-02

# 펠렛사료 크기에 따른 갈색거저리(*Tenebrio molitor* L.) 유충 생육특성 비교

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국내 갈색거저리 사육 농가는 대부분 소규모 영세농으로 노동에 의존하여 곤충을 사육하기 때문에 인건비 비중이 높아 생산물 가격이 높게 형성되거나 먹이원인 밀기울의 분진 날림으로 건강상의 이유 등 문제가 대두되고 있다. 본 연구는 갈색거저리 사육에서 노동력 절감 및 사료 급이 편리성을 위해 밀기울을 펠렛 직경별(2, 4, 6, 8 mm)로 제조하였고, 이를 급이하였을 때 사료 직경이 갈색거저리 유충 생육에 미치는 영향에 대해 밀기울 분말을 급이한 대조구와 비교하였다. 제조한 펠렛의 특성을 알아보기 위해 물성과 수분공급 형태에 따라 풀어지는 정도를 조사하였다. 풀어지는 정도는 채소 급이시 풀어지지 않았으며, 젤리 급이에서는 펠렛 직경 2, 4 mm는 1시간 만에 풀어졌으며, 6 mm 이상은 2시간 이상 소요되었다. 펠렛 직경별 급이시 갈색거저리 유충 무게는 생육 60일에는 대조구가 2 mm 펠렛사료 급이보다 16.6% 무거웠으나, 생육 90일일 때 4, 6, 8 mm 펠렛사료 처리구가 대조구와 차이가 없음을 확인하였다. 먹이소화율도 대조구는 30.6±5.4%, 8 mm 펠렛사료 처리구 31.7±2.3%와 같이 유의차가 없었으며, 생존율에서도 대조구와 펠렛사료 처리구에 차이가 없었다. 다만, 번데기(용)의 발생에서 대조구가 8 mm 펠렛사료 처리구보다 2.8배 많이 발생하였다. 이를 통해 갈색거저리 유충 사육에 펠렛형 사료 사용이 가능한 것으로 판단되며, 추후에는 펠렛형 사료가 자동화 사육장비에도 적용할 수 있는지에 대한 연구를 진행할 계획이다.

G-03

# 흰점박이꽃무지 사육 농가별 배지원과 유충 산물의 영양성분 상관분석

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흰점박이꽃무지(*Protaetia brevitarsis*) 먹이원은 주원료 참나무톱밥에 미생물과 첨가물을 혼합하여 부숙 후 사용하기 때문에 농가별로 상이하다. 본연구는 식용 곤충종인 흰점박이꽃무지의 선도 사육농가 5개소를 대상으로 먹이원 제조 방법과 먹이원, 수확 유충의 영양성분 함량을 비교 분석하였다.

일반성분의 경우 건량 기준으로 먹이원의 조단백질은 농가간에 8.5% 차이가 있었으나 유충에서는 2.1% 차이를 보여 먹이원에 포함된 조단백질 함량이 유충 발육에 필요한 단백질 형성에 크게 영향을 미치지 않은 것으로 보인다. 조지방은 강진농가에서 21.4%로 타 농가에 비해 10.4~13.7% 차이를 보였는데, 그 이유는 사육 온도가 2령까지는 30℃, 3령 25℃, 종령 유충 20℃로 변온 사육을 하며 사육기간이 길어지고 이 시기 지방이 축적된 것으로 사료된다. 조회분은 농가별로 먹이원 제조시 첨가물에 따라 차이를 보였지만 유충에서는 차이를 보이지 않았다.

무기물은 무안농가에서 칼슘 함량이 유충과 배지에서 높게 나타났는데 이는 먹이원 제조 시 버섯폐배지를 넣어 만드는 농가로 버섯배지 제조 시 첨가되는 석회성분이 영향을 준 것으로 사료된다. 그 외 인(P), 칼륨(K), 마그네슘(Mg)의 함량은 배지와 유충간 유의미한 차이는 보이지 않았으며, 유해물질의 분석결과 농가별로 카드뮴(Cd), 비소(As), 납(Pb) 모두 불검출되었다.

G-04

# pH 조건별 갈색거저리(*Tenebrio molitor* L.) 추출 단백질 함량 및 품질조사

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식용곤충을 활용한 제품개발은 대부분이 곤충 건조, 탈지 및 분말화와 같은 1차 적인 가공형태로 이루어져 있다. 본 연구의 목적은 식용곤충의 식품 소재로서의 저장성과 성분 함량, 품질개선 등 활용도를 높이고, 곤충에 대한 소비자의 인식 및 거부감을 줄이기 위해 알칼리 추출법을 이용하여 곤충분리단백질을 제조함에 있다. 먼저 단백질 추출을 위해 절식, 세척, 건조, 탈지, 분쇄 단계를 거친 갈색거저리 유충에 1N NaOH를 이용하여 pH 8, 9, 10, 11 및 12의 조건에서 1시간 동안 추출한 후 추출액의 pH를 2, 4, 6으로 조정하여 침전시켰다. 갈색거저리 분말과 위 시험에서 제조된 갈색거저리 추출 단백질(이하 갈색거저리 분리단백질)의 단백질 함량, 수율, 색도를 비교하였다. 그 결과 갈색거저리 분말의 조단백 함량은 53%인 반면 갈색거저리 분리단백질은 pH 12 추출과 pH 4 침전 조건에서 가장 높은 함량인 76%를 나타냈다. 수율 또한 pH 12 추출조건에서 20.45%로 가장 높게 나타났다. 위 실험 결과를 토대로 pH 12 조건에서 추출 효율이 가장 높았던 등전점을 pH 4, 4.5, 5, 세분화하여 추가 실험을 진행하였다. 그 결과 pH 4.5~5 조건에서 선행 실험보다 더 높은 81% 단백질 함량을 나타냈다. 색도는 갈색거저리 탈지분말을 대조구로 하여 시료간 색상 차이를 수치화하여 $\Delta E$ 값으로 나타내었다. 결과 값은 pH 12 추출 범위에서 가장 낮았으며, pH 11에서 추출한 단백질은 등전점이 높아질수록 값 차이가 컸고 육안으로도 짙게 갈변된 것을 확인할 수 있었다. 결과적으로 갈색거저리 단백질은 pH 12의 추출 조건과 pH 4.5~5 침전 조건에서 가장 추출 효율과 순도가 높은 것을 확인하였다.

## 【 기 타 】

H-01

# 비의도적으로 유입된 외래 흰개미(*Coptotermes gestroi*) 발견 및 차단 사례 보고

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침입외래종의 빠른 발견 및 대응을 위해 환경부·국립생태원은 2019년부터 외래생물 신고센터를 운영하고 있다. 외래 흰개미류 의심 신고는 2023년 5월부터 접수가 급증하였다. 2024년 4월 서울특별시 금천구에 위치한 산업용 기계 및 장비 도매업을 하는 수입 회사의 창고에서 외래 흰개미 발견 신고가 접수되었다. 외래 흰개미 의심 개체가 발견된 물품의 경우 2024년 4월 23일 항공편으로 싱가포르에서 인천으로 이동하였으며, 2024년 4월 24일 해당 수입 회사 창고로 물품이 인도되었다. 현장 조사 결과 목재 파렛트 및 종이상자에서 이동과 가해 흔적이 확인되었으며, 흰개미(일개미, 병정개미) 약 1,000여 마리를 발견하였다. 유전자 분석 결과 *Coptotermes gestroi*로 확인되었다. 이에 앞서 2024년 3월에도 수입물품을 통해 *C. formosanus*의 비 의도적 유입을 확인하였으며, 외래생물 신고를 통해 빠른 대응으로 확산을 차단하였다.

* 이 연구는 NIE-수탁연구-2024-32의 지원을 받아 수행하였습니다.

H-02

# 비의도적으로 편승 유입된 외래 개미(*Tetraponera rufonigra*) 발견 보고

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국가 간 인적 물적 교류 증가로 수입 물품은 매년 증가하고 있다. 2024년 5월 외래생물신고센터를 통해 경기도 이천시의 물류센터에서 외래 개미류 의심 신고가 접수되었고, 현장 조사 결과 외래 개미 *Tetraponera rufonigra* 1개체를 확인하였다. *T. rufonigra*는 인도가 원산으로 추정되고 동남아시아, 중국, 아프리카 등에 분포하고 있으며, 이 종은 침을 가지고 있어 침에 쏘이게 되면 알러지 반응을 일으킨다는 사례가 있다. 본 연구에서는 채집된 개미의 형태와 유전자 정보를 통해 대상종을 확인하였고, 향후 해당 종의 관리를 위한 기초자료를 제공하고자 한다.

* 이 연구는 NIE-수탁연구-2024-32의 지원을 받아 수행되었습니다.

H-03

# 인공증식 물장군의 2023년도와 2024년도의 부화율과 생존율 비교

고민희[p], 장은비, 윤원종, 박지권[c]

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물장군은 멸종위기 야생생물 Ⅱ급의 노린재목에 속하는 수서곤충으로 다른 곤충이나 개구리 유생을 잡아먹는 포식성 곤충이다. 제주테크노파크 생물종다양성연구소는 환경부 지정 서식지외보전기관으로 멸종위기인 물장군을 인공증식하여 제주도 내 습지에 방사하는 역할을 수행하고 있다. 2023년 물장군의 인공증식 시 부화율은 76.4%이며 부화한 개체의 생존율은 51.2%였다. 2024년 물장군의 인공증식 시 부화율은 51.7%였으며 부화한 개체의 생존율은 22.1%였다. 부화율과 생존율이 낮아진 원인은 제주도의 이른 장마로 인한 높은 습도와 최고 기간을 기록한 폭염과 같은 전국적인 이상기후 때문으로 보인다. 2025년에도 이상기후가 예상되고 있어 인공증식 방법에 대한 개선이 필요할 것으로 보인다.

* 본 연구는 환경부 서식지외보전기관 운영사업의 지원을 받아 수행되었습니다.

H-04

# Seasonal and regional distribution of blowflies (Diptera: Calliphoridae) in southern South Korea: Forensic implications

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Blowflies (Diptera: Calliphoridae) are among the earliest insects to colonize decomposing remains, providing essential information for forensic investigations. This study examined the monthly and spatial distribution of blowflies in southern South Korea, specifically in Changnyeong, Jeju, Pohang, and Yeosu, to evaluate their ecological distribution and potential as seasonal indicators. Over the study period, 3,934 adults representing 14 species across five genera were collected. Nine species, including *Calliphora calliphoroides*, were consistently observed across regions, while *Chrysomya megacephala* was absent only in Jeju during winter, suggesting its potential as an indicator in early decomposition stages. Species such as *C. calliphoroides*, *Calliphora grahami*, and *Calliphora nigribarbis*, which were not found outside Jeju in the summer, may serve as seasonal markers. This study provides foundational data on the ecological distribution of blowflies in southern South Korea, emphasizing seasonal and environmental patterns that can enhance decomposition assessments and account for seasonal variations in forensic casework.

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H-05

# 떠돌이쉬파리(*Sarcophaga peregrina*)의 성장단계와 온도에 따른 누적 유효온도(Accumulated Degree Hours, ADH)를 활용한 사후경과시간(PMI) 추정 연구

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이 연구는 떠돌이쉬파리(*Sarcophaga peregrina* (Robineau-Desvoidy, 1830))의 성장단계와 온도 조건에 따른 누적 유효온도(Accumulated Degree Hours, ADH) 데이터를 통해 사체의 사후경과시간(Postmorterm interval)을 추정하고자 하였다. 야외에서 채집된 떠돌이쉬파리의 F2 세대 구더기를 16°C, 19°C, 22°C, 25°C, 28°C, 31°C, 34°C의 온도 조건에서 사육하였으며, 각 온도에서 구더기와 성충이 발생하기까지 걸리는 시간을 기록하였다. 12시간 간격으로 총 13,230마리의 샘플을 채집하여 분석하였으며, 성장단계별 온도 조건에 따라 누적된 ADH 값을 산출하였다. 이를 통해 기저온도 10.87°C를 확인하고, 온도별 ADH 회귀식을 도출하였다. 이 회귀식을 통해 사후경과시간을 더욱 정밀하게 추정할 수 있는 가능성을 제시하였으며, 이 연구 결과는 한국 내 법의곤충학적 PMI 추정의 정확도 향상에 중요한 기초자료로 기여할 것으로 기대된다.

H-06

# Effects of concealment on insect succession and PMImin estiamtion in forensic entomology

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In forensic investigations, estimating the minimum postmortem interval (PMImin) often relies on analyzing decomposition and insect colonization on carcasses exposed to insects. However, bodies in real homicide cases are often concealed, delaying insect colonization and altering decomposition, which can skew PMImin estimates. This study examined how concealment affects decomposition and insect succession by comparing two pig carcasses in a wooded area in Yeondong-ri, Iksan, South Korea, from June 21 to June 28, 2024. One carcass was concealed in a suitcase, while the other remained exposed. In total, 40 insect species across six orders and 19 families were collected. On the exposed carcass, *Lucilia caesar* and *Chrysomya pinguis* arrived on day one, with oviposition on day two. In contrast, these species appeared on the concealed carcass on day four, with oviposition on day five. By day seven, the exposed carcass reached the dry stage, while the concealed carcass was still in the decay stage. These findings highlight that concealment delays insect colonization, and if unaccounted for, can cause errors in PMImin estimates. Accurate forensic analysis must consider concealment effects when estimating PMImin for concealed bodies.

H-07

# 충남 아산 지역의 Flavivirus 매개 모기 감시 현황(2020~2024)

이경원p[1,2], 정준양[2,3], 홍찬의[1,2], 신현준[1,2], 이 혁[1,2], 상민규[2,3], 박지은[2,3], 송대권[2,3], 이용석c[1,2,3]

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지구온난화로 인한 한반도의 기후변화와 온도 상승은 환경변화에 영향을 받는 질병 매개 곤충의 분포 및 밀도 증가에 영향을 미칠 수 있는 것으로 알려져 있다. 이에 따라 충남 아산 권역에서 발생 및 유입되는 모기의 개체수와 Flavivirus의 감염률을 확인하기 위해 5년에 걸쳐 순천향대학교와 주변 도심에서 DMS (Digital Mosquito Monitoring System) 및 BG-sentinel trap, LED trap을 사용하여 3~11월간 월 4회 수행하였다. 그 결과 5년간 채집된 모기는 총 19,514 마리로, 7속 12종을 확인하였다. 그중 빨간집모기(*Culex pipiens*)는 10,258 마리로 가장 높은 우점도를 나타냈으며, 흰줄숲모기(*Aedes albopictus*) 3,659 마리, 금빛숲모기(*A. vexans*) 1,457 마리로 나타났다. 본 연구진은 Flavivirus 감염 여부를 확인하기 위해 RNA를 추출한 후 RT-qPCR을 통해 바이러스 검출 유무를 확인하였으나, 모든 검체에서 음성으로 확인되었다. 이 연구 결과는 기후 변화에 따라 변화하는 감염병 매개 모기 및 매개 질환의 모니터링과 발생 예측을 위한 기초자료로써 활용될 수 있을 것으로 사료된다.

H-08

# 충남 당진 지역의 중증열성혈소판감소증후군(SFTS) 매개 참진드기 감시 현황(2018~2024)

**신현준**p[1,2], 정준양[2,3], 홍찬의[1,2], 이 혁[1,2], 이경원[1,2], 상민규[2,3], 박지은[2,3], 송대권[2,3], 이용석c[1,2,3]

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중증열성혈소판감소증후군(Severe Fever with Thrombocytopenia Syndrome, SFTS)과 라임병(Lyme Disease)은 참진드기과(Ixodidae)에 속한 진드기를 매개로 전파되는 인수공통감염병으로, 고열, 근육통, 다발성 장기 부전 등의 증상을 유발할 수 있다. 이러한 곤충 매개 전파 질병은 기후 변화 및 지역적 요인에 따라서 영향을 받을 수 있기 때문에 활동 시기에 따른 감염병 매개체의 발생 밀도와 병원체 보유 현황을 지속적으로 모니터링하는 것이 중요하다. 이에 우리 연구진은 충청남도 당진시에서 2018년부터 2024년까지 총 7년간 매년 4월에서 11월 사이, 월 1회씩 4가지 환경(무덤, 산길, 잡목림, 초지)에서 드라이아이스 트랩을 사용하여 참진드기의 발생 밀도 및 병원체 감염 여부를 조사하였다. 그 결과, 2018년 16,996 마리, 2019년 21,668 마리, 2020년 9,086 마리, 2021년 8,774 마리, 2022년 12,659 마리, 2023년 5,654 마리, 2024년 5,309 마리가 채집되어 총 80,146 마리가 채집되었으며, 초지에서 가장 높은 밀도가 관찰되었다. 확인된 참진드기는 2속 3종으로, 작은소피참진드기(*Haemaphysalis longicornis*), 개피참진드기(*H. flava*), 일본참진드기(*Ixodes nipponensis*) 순으로 많이 채집되었으며, 그중 작은소피참진드기(*H. longicornis*)가 78,191 마리(97.56%)로 가장 높은 우점도를 나타냈다. 병원체 감염 여부를 확인하기 위해 RNA virus 추출법을 사용해 검사를 수행하였으나, 양성 검체는 발견되지 않았다. 이 연구 결과는 당진시 내 참진드기 매개 질병 관리 전략 수립 및 발생 양상 파악에 중요한 기초자료로 활용될 수 있을 것으로 사료된다.

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