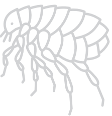
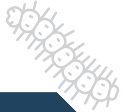
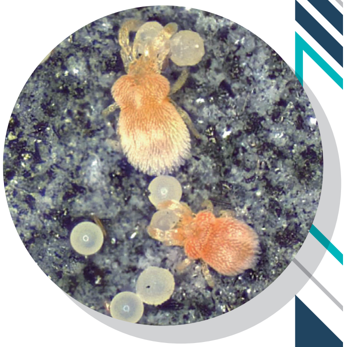




2024 Spring Conference of KSAE & ESK





Korean Society of Applied Entomology &
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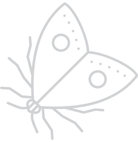
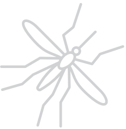
자료집 보기

THREAT TO INSECT BIODIVERSITY BY HUMANS & THREAT TO HUMAN HEALTH BY INSECTS

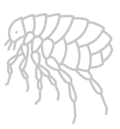
25(Thu)-26(Fri) April 2024
Grand Plaza Cheongju Hotel



주최 (사)한국응용곤충학회 Korean Society of Applied Entomology
(사)한국곤충학회 The Entomological Society of Korea

후원 농촌진흥청
충청북도 CHUNGCHEONGBUK-DO
충북문화재단 Chungbuk Cultural Foundation



2024 Spring Conference of KSAE & ESK

Korean Society of Applied Entomology &
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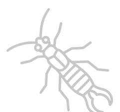

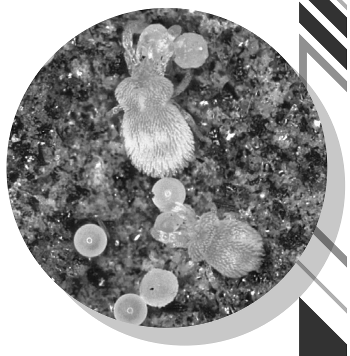

자료집 보기

THREAT TO INSECT BIODIVERSITY BY HUMANS & THREAT TO HUMAN HEALTH BY INSECTS

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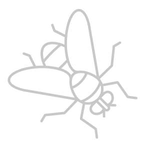

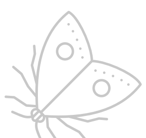

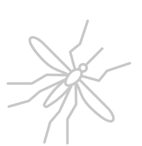

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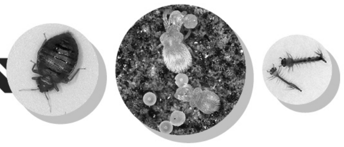


인사말

존경하는 한국곤충학회 및 한국응용곤충학회 회원 여러분

안녕하셨습니까?

2023년에 이어 올해도 한국곤충학회와 공동으로 춘계 학술발표대회를 개최하게 되어 무척 기쁘게 생각합니다. 공동 개최를 통하여 더 넓고 다양한 분야까지 상호 정보를 교환 할 수 있게 되어 매우 감동적이고 미래 대한민국 곤충학 분야의 발전이 눈부실 것으로 기대가 됩니다. 덧붙여 연속 공동 개최를 위한 새로운 의미로 MOU 체결 행사로 더욱 양 학회 관계를 공공히 하고자 합니다.

우리는 미래에 자라나는 젊은 곤충학자들을 위해 다양한 분야의 다양한 경험을 할 수 있는 기회를 주어야 하고 이끌어 가야 할 의무가 있다고 생각합니다. 이것이 우리 기성세대의 역할이고 오늘 같은 공동 학회 개최를 통하여 단독 학회 개최시 경험할 수 없었던 부분이 있을 것으로 생각합니다.

당연히 공동학회 개최를 위해서는 상호 불편한 여러 가지 상황이나 느낌들이 발생 될 수 있습니다. 그럼에도 불구하고 이용석 학회장님을 중심으로 한국곤충학회 임원진 분들의 노력과 수고에 깊이 감사드립니다. 아울러 한국응용곤충학회의 임언택 학술위원장님을 비롯하여 여러 수고하신 위원님들에게도 감사의 말씀을 드립니다.

멀고 어렵고, 여러 가지 애로사항이 있을 수 있지만 지속적인 양 학회의 공동 개최 뿐 만 아니라 양봉, 양잠, 산업 곤충, 농약과학회, 방역관련 학회 및 협외 관련 학회와도 공동 개최가 이루어진다면 많은 시너지 효과가 있을 것으로 생각됩니다.

오늘 공동 학술행사가 성공리에 이루어져 곤충학 발전에 큰 획이 될 것으로 믿으며, 다시한번 본 행사를 위해 수고하신 여러분들에게 깊이 감사드리고 항상 건강하시고 양 학회 회원 여러분 가정에 행운이 가득하시길 기원합니다.

2024년 4월 25일
한국응용곤충학회장 **박 종 균**

인사말

존경하는 한국응용곤충학회 및 한국곤충학회 회원 여러분

작년 2023년 약 20년 만에 다시 시작된 공동학술대회를 성공적으로 잘 치루기 위해 노력했던 기억이 엊그제 같은데 벌써 일 년이 지나 다시 공동학술대회를 개최하게 되어 너무나 즐거운 마음이 벅차오릅니다.

무엇보다도 이번 공동학술대회를 주최할 수 있도록 도와주신 한국응용곤충학회 박종균 회장님과 임언택 학술운영위원장님 그리고 김주일 사무총장님 또한 한국곤충학회 조용훈 학술위원장님, 총무 장호암 박사님께 진심어린 감사의 말씀을 올립니다. 또한 물심양면으로 도와주신 두 학회의 사무국 책임자 김선숙, 안현숙 선생님께도 감사의 말씀을 전합니다.

코로나19 이후 4차산업혁명 기술의 눈부신 발전 그리고 급속한 기후변화 등 곤충관련 연구는 첨단 최신 학문들과 융합되어 도약하고 있습니다.

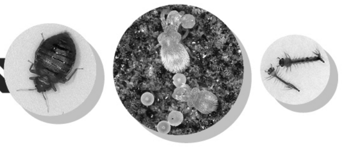
하지만 곤충관련 기초연구를 할 새로운 신진인력이 점차 줄어들고 있습니다.

장기적으로 최신학문의 기술들을 겸비한 곤충 분류학자, 생태학자들이 많이 양성될 수 있도록 한국응용곤충학회와 한국곤충학회는 힘을 모아야 할 때라고 생각합니다. 그러한 노력의 일환으로 박종균 회장님께서 제안하셨던 양봉, 양잠, 산업곤충 관련 학회들과의 공동학술대회 개최를 위한 시작을 해야 할 듯 합니다. 두 학회의 임원진들과 회원들 모두의 염원이 대한민국 곤충학의 새로운 미래를 만들어 갈 수 있도록 노력하였으면 좋겠습니다.

이번 공동학술대회에서는 “자랑스러운 대한민국 곤충인 상”이 새롭게 만들어 졌습니다. 1회 수상자로는 양 학회 모든 회원들의 존경을 담아, 대전대학교 총장이신 남상호 교수님께서 추대 되셨습니다. 지면을 통해서 다시 한번 축하의 말씀 전합니다.

마지막으로 2024년 한국응용곤충학회, 한국곤충학회 춘계 공동학술대회에 참여 해 주신 모든 곤충학자님들께 감사의 말씀을 올리며, 양 학회 회원 모든 분들의 가정에 행복과 기쁨이 가득하시길 기원합니다. 감사합니다.

2024년 4월 25일
한국곤충학회장 **이 용 석**



Program

■ 2024 Spring Conference of KSAE & ESK ■

"THREAT TO INSECT BIODIVERSITY BY HUMANS & THREAT TO HUMAN HEALTH BY INSECTS"

25(Thu)-26(Fri) April 2024 Grand Plaza Cheongju Hotel

25 April (Thu)

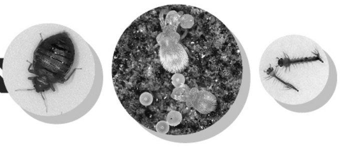
Time	Section		Room
11:00~12:00	Registration		Desk
12:00~12:20	Opening Ceremony & Photography		Grand Ballroom A+B 3F
Plenary Lecture			
12:20~12:50	Current Status and Future Projections on Mosquito Borne Diseases and their Vectors in Korea Dong-Kyu Lee (Kosin University)		Grand Ballroom A+B 3F
12:50~13:20	Pterostichine Carabid Beetles and Why Fundamental Taxonomic Science is Critical to Modern Conservation Efforts Kipling Will (University of California, Berkeley)		
17:20~17:50	Mechanisms, Diagnosis and Management of Pesticide Resistance: Current Status and Future Prospects Si Hyeock Lee (Seoul National University)		Grand Ballroom A+B+C 3F
Oral Presentation			
13:20~16:00	Generals	All subjects	Grand Ballroom A+B 3F
	Graduates	Ecology / Pest Control / Medical Entomology I	Grand Ballroom C 3F
		Ecology / Pest Control / Medical Entomology II	Uam Hall 3F
		Physiology / Molecular Biology / Industrial Entomology / Forensic Entomology	Jikji Hall A 3F
		Taxonomy / Phylogeny / Morphology	Jikji Hall B 3F
	Generals	All subjects	Hwarang Room 2F
	Graduates	Taxonomy / Phylogeny	
16:00~16:10	**Coffee Break**		
Poster Presentation			
16:10~17:10	In-person Presentation (Competition & Non Competition)		Jusung Hall 3F
17:10~17:20	**Coffee Break**		

25 April (Thu)

Time	Section	Room
KSAE/ESK Meeting		
17:20~18:00	Grand Ballroom A+B+C	Uam Hall
	General Meeting & Special Lectures of the Winner for Korean Entomologist Award Ceremony (KSAE)	General meeting (ESK)
18:00~18:20	**Coffee Break**	
18:20~20:00	Proud Korean Entomologist Award & Banquet	Grand Ballroom A+B+C 3F
Small Group Meeting		
20:00~21:00	Academic Committee Meeting (KSAE) Un Taek Lim (Andong National University) Donghun Kim (Kyungpook National University)	Mars 2F
	Industrialization of dsRNA Biopesticides (KSAE) Youggyun Kim (Andong National University) June-Sun Yoon (Jeonbuk National University)	Hwarang Room 2F
	Current Status of Pollinating Insect Research in Korea Il-Kwon Kim (Korea National Arboretum)	Jikji Hall A 3F
	Editorial Board Meeting (ENR) Ohseok Kwon (Kyungpook National University)	Uam Hall 3F
	ICE2024 Meeting (ESK) Yong Hun Jo (Soonchunhyang University)	Jikji Hall B 3F

26 April (Fri)

Time	Section	Room
Symposia		
09:00~11:30	Part Ⅰ: Threat to Insect Biodiversity by Humans Ilgoo Kang (Kyungpook National University) Part Ⅱ: Threat to Human Health by Insects Yeon Soo Han (Chonnam National University)	Grand Ballroom A+B 3F
	Insect Chemical Ecology in Korea, 7th: The Road to Practical Application Junheon Kim (National Institute of Forest Science) Gwang Hyun Roh (Gyeongsang National University)	Grand Ballroom C 3F
	Insect-Microbe Immunity and Interaction June-Sun Yoon (Jeonbuk National University) Se Jin Lee (Sunchon National University)	Uam Hall 3F
	Vector Surveillance and Control Hee Il Lee (Korea Disease Control and Prevention Agency)	Jikji Hall A 3F
	Modern Approaches to Artificial Intelligence (AI) in Entomology Ho Am Jang (Soonchunhyang University)	Jikji Hall B 3F
11:30~11:40	**Coffee Break**	
11:40~	**Closing Ceremony** Awards of Competition and Raffle Tickets, Presidential Address Gwanjung Bok-Sung Cho Quiz	Grand Ballroom A+B 3F



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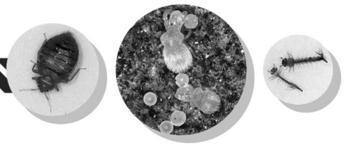
S1. Threat to Insect Biodiversity by Humans & Threats to Human Health by Insects

4. 26. Fri | Grand Ballroom A+B (3F) ESK | **Organizer :** Yeon Soo Han (Chonnam National University)

S2. Insect Chemical Ecology in Korea, 7th: The Road to Practical Application

4. 26. Fri | Grand Ballroom C (3F) | **Organizer :** Junheon Kim (National Institute of Forest Science)
Gwang Hyun Roh (Gyeongsang National University)



S3. Insect-Microbe Immunity and interaction

4. 26. Fri Uam Hall (3F) **Organizer :** June-Sun Yoon (Jeonbuk National University)
Se Jin Lee (Sunchon National University)

S4. Vector Surveillance and Control

4. 26. Fri Jikji Hall A (3F) **Organizer :** Hee Il Lee (Korea Disease Control and Prevention Agency)

S5. Modern Approaches to Artificial Intelligence (AI) in Entomology

4. 26. Fri | Jikji Hall B (3F) | **Organizer :** Ho Am Jang (Soonchunhyang University)

Oral Presentation

1. Competition - Generals_All subjects

4. 25. Thu | Grand Ballroom A+B (3F) KSAE | **Moderator :** Iksoo Kim (Chonnam National University)
Heungsik Lee (Animal and Plant Quaratine Agency)

4. 25. Thu | Grand Ballroom A+B (3F) | **ESK**

Moderator : Jin-Kyung Choi (Daegu National University of Education)

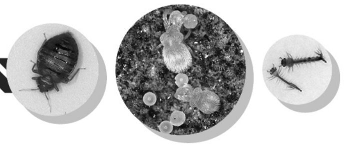
2. Competition - Graduates_Ecology, Pest Control, Medical Entomology I

4. 25. Thu | Grand Ballroom C (3F) | **KSAE**

Moderator : Keon Mook Seong (Chungnam National University)
Kyungjae Andrew Yoon (Seoul National University)

3. Competition - Graduates_Ecology, Pest Control, Medical Entomology II

4. 25. Thu	Uam Hall (3F) KSAE	**Moderator :** In-hong Jeong (National Institute of Agricultural Sciences) Young Su Lee (Gyeonggi Agricultural Research and Extension Services)



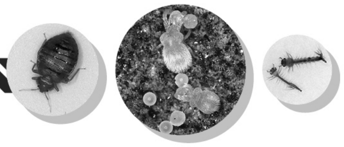
4. 25. Thu | Uam Hall (3F) ESK | **Moderator :** In-hong Jeong (National Institute of Agricultural Sciences)
Young Su Lee (Gyeonggi Agricultural Research and Extension Services)

4. Competition - Graduates_Physiology, Molecular Biology, Industrial Entomology

4. 25. Thu | Jikji Hall A (3F) KSAE | **Moderator :** Junheon Kim (National Institute of Forest Science)
Donghun Kim (Kyungpook National University)

5. Competition - Forensic Entomology

4. 25. Thu	Jikji Hall A (3F) ESK	**Moderator :** Myeoung Cheol Kim (SOKN)



6. Competition - Graduates_Taxonomy, Phylogeny, Morphology

4. 25. Thu
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KSAE
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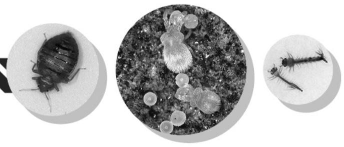
7. Non-Competition - Generals_All subjects

4. 25. Thu Hwarang Room (2F) KSAE
Moderator : Juil Kim (Kangwon National University)
Myung Suk Rho (Seoul National University)

8. Competition - Taxonomy, Phylogeny

4. 25. Thu Hwarang Room (2F) ESK
Moderator : Jong Chul Jeong (Wild Bugs Eco-Environment institute)

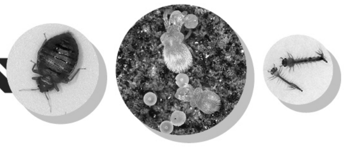


Poster Presentation - Competition

1. Graduate - Taxonomy, Phylogeny

Moderator : Deuk-Soo Choi (Quarantine Techonology Institute Inc.)
Dong June Lee (Animal Research Division, Honam National Institute of Biological Resources)

Moderator : Jong-Seok Park (Chungbuk National University)
Hee-A Lee (Gyeonggi-do Agricultural Research and Extension Services)



2. Graduate - Ecology, Pest Control

Moderator : Changku Kang (Seoul National University)
Young-gyun Park (Purdue University)

3. Graduate - Medical Entomology, Physiology, Molecular Biology

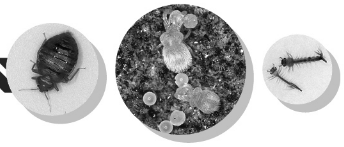
Moderator : Se Jin Lee (Sunchon National University)
Tae Young Shin (Jeonbuk National University)

4. Graduate - Applied Entomology

Moderator : Kyeong Yong Lee (National Institute of Agricultural Sciences)
Bo-Sun Park (National Institute of Agricultural Sciences)

5. General - Taxonomy , Phylogeny

Moderator : Il-Kwon Kim (Korea National Arboretum)
Sora Kim (Jeonbuk National University)

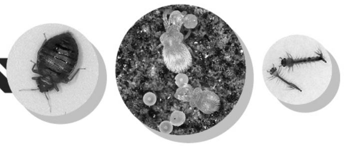


6. General - Ecology, Pest Control

Moderator : Youngjin Park (Andong National University)
Jong-Hoon Kim (Pukyong National University)

7. General - Medical Entomology, Physiology , Molecular Biology

Moderator : Gwang Hyun Roh (Gyeongsang National University)
Jong-Kook Jung (Kangwon National University)

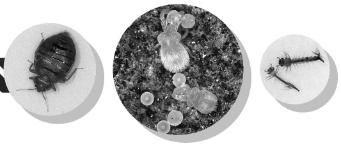


8. General - Applied Entomology

Moderator : Gwang Hyun Roh (Gyeongsang National University)
Jong-Kook Jung (Kangwon National University)

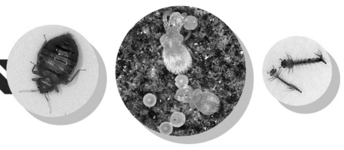
Poster Presentation - Non-Competition

9. Taxonomy



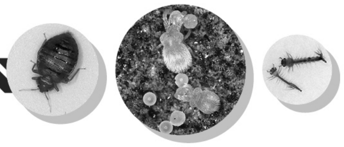
10. Ecology

11. Pest Control



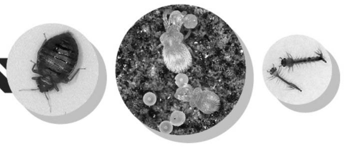
12. Medical Entomology_Physiology

13. Applied Entomology

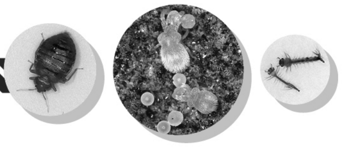


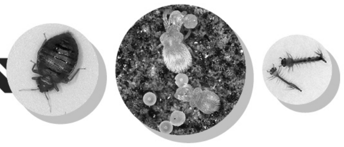
Poster Presentation - ESK

14. A - 분류



15. B - 생태

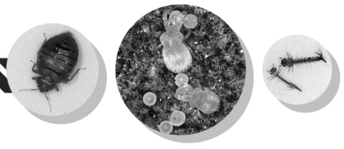




16. C - 형태

17. D - 생리

18. E - 분자생물



19. F - 방제

20. G - 식용곤충

21. H - 기타

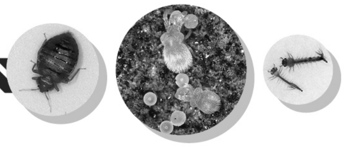
Small Group Meeting

1. Academic Committee Meeting

4. 25. Thu	Mars (2F) KSAE	**Organizer :** Un Taek Lim (Andong National University) Donghun Kim (Kyungpook National University)

2. Industrialization of dsRNA Biopesticides

4. 25. Thu	Hwarang Room (2F) KSAE	**Organizer :** Youggyun Kim (Andong National University) June-Sun Yoon (Jeonbuk National University)



3. Current Status of Pollinating Insect Research in Korea

4. 25. Thu Jikji Hall A (3F) KSAE **Organizer :** Il-Kwon Kim (Korea National Arboretum)

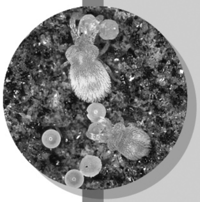
4. Editorial Board Meeting (ENR)

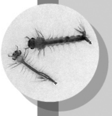
4. 25. Thu Uam Hall (3F) **Organizer :** Ohseok Kwon (Kyungpook National University)

5. ICE2024 Meeting

4. 25. Thu Jikji Hall B (3F) ESK **Organizer :** Yong Hun Jo (Soonchunhyang University)

Plenary Lecture





Plenary Lecture I

Current status and future projections on mosquito-borne diseases and their vectors in Korea

Dong-Kyu Lee
Department of Public Health and Environment, Kosin University

In light of global climate change, Korea faces significant challenges with indigenous mosquito-borne diseases, notably malaria and Japanese encephalitis. Moreover, there is a growing incidence of imported arboviral diseases attributable to the increasing number of international travelers. Dengue fever emerges as the predominant mosquito-borne ailment among Korean travelers, while cases of Japanese encephalitis and chikungunya are also seeing an upward trend. Many countries have witnessed arboviral infections transmitted by pathogens-carrying mosquitoes, primarily due to the introduction of viruses by travelers. Additionally, the ongoing processes of global warming and urbanization are creating increasingly favorable environments for mosquitoes and the proliferation of mosquito-borne pathogens. This underscores the urgency of assessing both the current status and future projections of mosquito-borne diseases in Korea.

Key words: vector, mosquito, mosquito-borne disease, Korea

Plenary Lecture II

Pterostichine carabid beetles and why fundamental taxonomic science is critical to modern conservation efforts

Kipling Will
Department of Environmental Science, Policy, and Management, University of California, Berkeley, USA

The hyperdiverse beetle family Carabidae is one of the largest families of Coleoptera. Nearly 10% of described carabid species are classified in the tribe Pterostichini or tribes historically closely associated with Pterostichini. Beetles in these groups are found worldwide and in habitats from ocean beaches to high-elevation glacial edges. Pterostichines are often abundant and local species richness can be exceptionally high. I will present an overview of the diversity, biogeography, and current phylogenetic arrangement of the included taxa. I will discuss some of the many amazing aspects of the group's natural history including cases of mate marking during copulation, secondary sexual characters, mate guarding, burrow construction, maternal care for eggs and larvae, and apparent stridulatory structures. I will introduce the Australian trichosternus group and discuss the conservation status of these imperiled beetles and how fundamental taxonomic science led to gaining protection for some species. I will make the case that taxonomy has a unique role among the life sciences to explore, describe, classify, and provide an understanding of the diversity of life, at and above the species level, focusing on individual characters, and within the context of evolutionary history.

Key words: Gtound beetle, Carabidae, Coleoptera, phylogeny, evolution

Plenary Lecture III

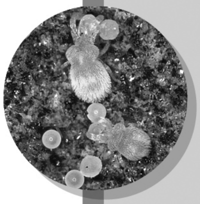
Mechanisms, diagnosis and management of pesticide resistance: Current status and future prospects

Si Hyeock Lee
Department of Agricultural Biotechnology, Seoul National University

전 세계적으로 농업해충의 약제 저항성 발달에 따른 방제 효율 저하는 농약의 과다 사용을 초래하여 농업의 생산성 저하 및 환경 파괴 문제 등을 야기하고 있다. 뿐만 아니라 위생해충의 경우에도 약제 저항성 발달이 심각한 수준으로 나타남에 따라 인류 보건에 큰 위협이 되고 있다. 해충의 약제 저항성은 자연계에 존재하는 극히 낮은 빈도의 저항성 형질이 반복적인 약제 사용에 따라 선발되는 과정을 통해 발달 되는데, 해충 약제 저항성의 효과적 관리를 위해서는 저항성 발달 기작의 규명과 신속·정확한 진단법의 확립이 필수적이다. 현재까지의 저항성 관리는 저항성 발달 후 대응적(reactive)으로 이루어져 왔으나, 미래에는 보다 다양한 분자 마커를 활용하여 저항성 형질 빈도를 관리 가능한 수준에서 유지하는 선제적(proactive) 저항성 관리도 가능할 것으로 예상하고 있다. 본 발표에서는 해충 약제 저항성 연구의 현재 상황과 미래 전망에 대해 소개하고자 한다.

검색어: Pesticide resistance, Mechanism, Diagnosis, Management

Symposium



S1-1

Insect population dynamics according to environmental change: Prediction of forest pest distribution

Yang-Seop Bae[1], **Young-Seuk Park**[2], **Tae-Soo Chon**[3], **Bong-Kyu Byun**[4],
Seunghwan Lee[5], **Jong Kyun Park**[6] **and Tak-Gi Lee**[7]
[1]Incheon National University, Republic of Korea
[2]Kyung Hee University, Republic of Korea
[3]Pusan National University, Republic of Korea
[4]Hannam University, Republic of Korea
[5]Seoul National University, Republic of Korea
[6]Kyungpook National University, Republic of Korea
[7]Iwha Womans University, Republic of Korea

Global warming and changes in ecosystems are either causing a rapid decline in insect diversity on earth or, on the other hand, are increasing the likelihood of unexpected insect pests emerging. This study summarizes and reports the followings: Introduction to the Insects of Red Data Book of Korea and Nationally Protected species, the establishment of monitoring strategy for exotic insects by the investigation of species distribution range through field surveys and others, the dispersal of exotic insects, and with the expansion of exotic insects and development of ecosystem impact prediction model.

Key words: biodiversity, extinct, exotic forest pests, dispersal, prediction

S1-2

Diversity and future of Hymenoptera in South Korea

Jin-Kyung Choi[1,2]
[1]Department of Science Education, Daegu National University of Education
[2]Insect Inquiry · Education Institute, Daegu National University of Education

곤충 생물다양성의 파괴는 결국 인류의 몰락을 가져올 정도로 심각하지만, 생물다양성을 지키는 것이 그리 간단하지만은 않은 것 같다. 벌목의 곤충은 잎을 섭식하는 식식성부터 숙주의 개체수를 조절해주는 기생성과 집단으로 생활하며 먹이를 공급받는 사회성에 이르기까지 다양한 습성을 갖는 분류군이다. 뿐만아니라 나비목, 딱정벌레목, 파리목, 노린재목과 같이 다양성이 매우 높은 5대 분류군 중 하나이다. 2021년 발간된 한국곤충명집에 따르면 현재 우리나라 벌목의 곤충은 67과 1,137속 4,223종으로 알려져 있다. 국내 분류학 전문가들의 꾸준한 연구 노력의 결과 우리나라 벌목 뿐만아니라 곤충의 분포 정보는 해마다 늘어가고 있으나, 생물다양성의 손실은 세계 곳곳에서 가시화되고 있다. 국내에 서식하는 다양한 벌목 곤충들이 앞으로도 이곳을 떠나지 않고 우리와 함께 하기를 바라며 이번 심포지움이 국내 곤충다양성 유지를 위한 작은 움직임이 되길 바란다.

검색어: 기생벌, 벌목, 사회성, 생물다양성, 식식성, 해충

S1-3

Current status and biodiversity of aquatic insects in Korea

Sang Woo Jung
DASARI Research Institute of BioResources, Daejeon, 35203, Korea

수서곤충은 일반적으로 하루살이목, 날도래목, 강도래목, 잠자리목, 노린재목, 딱정벌레목, 뱀잠자리목, 파리목의 8개의 목(Order)에 속하며, 물을 기반으로 서식하는 곤충들을 의미한다. 국내 수서곤충의 연구는 도입기(40-50년대), 형성기(60년대), 발전기(70-80년대), 도약기(90-2010년대)를 거쳐 왔다. 물을 기반으로 수질을 평가하기 위해 수서곤충은 생태학적 연구가 먼저 시작되었으며, 이후 분류학적 연구가 시행되고 현재는 유전학적 및 응용학적 연구로 다양성을 증명하고 있다. 하지만, 물을 기반으로 하는 수서곤충의 서식처는 도시화로 인한 다양한 개발과 교란으로 감소하고 사라지고 있다. 서식처뿐만 아니라 수서곤충을 연구하는 학자들과 학생들도 정체기와 쇠퇴기를 거치고 있다. 국내 수서곤충의 다양성 종 목록은 1999년 처음으로 학술논단에서 491종이 정리되었으며, 이후 약 10년 만에 개정목록이 2011년에 988종으로 수정되었다. 이후 지속적인 국가생물다양성 확보 및 보전 전략에 따라 미발굴된 수서 파리류들이 대거 기록되면서 2018년에는 처음 기록보다 3배 이상 증가하여 1,567종이 보고되었다. 이처럼 표면적으로는 수서곤충의 연구가 활성화되어 다양성은 늘어가고 있는 것처럼 보이지만 다양한 문제점들이 나타나고 있다. 수서곤충은 성충보다는 유충을 주로 연구하는 학문으로 많은 연구자가 어려움을 겪고 있다. 단기간의 다양성 증진보다는 심도 있는 다양한 주제로 접근하는 방법이 필요할 것으로 보이며, 수서곤충의 다양성과 함께 서식처 회복 및 복원 방안도 함께 마련되어야 할 것으로 판단된다. 본 발표에서는 국내 수서곤충의 다양한 연구주제와 피해 상황 및 활용방안을 소개하여 미래의 수서곤충의 방향성과 연구방향을 심도 있게 논의하고자 한다.

검색어: 수서곤충, 다양성, 분류, 생태, 한국

S1-4

Human fatalities caused by social wasp in Korea

Moon Bo Choi
Institute of Agricultural Science and Technology, Kyungpook National University

전국적으로 매년 말벌 벌집 신고수는 약 20만건이 넘으며 부상자는 1-2만명, 사망자도 10-15명씩 나타나고 있다. 이에 따라 매년 소방청에서는 여름과 가을에 벌 쏘임 사고 '주의보'를 발령하고, 벌 쏘임 사고 예방에 대한 주의를 요하고 있다. 이처럼 말벌은 강력한 독침을 가진 사회성 곤충으로 외부 천적으로부터 그들의 군집을 지키기 위한 방어행동이 매우 잘 발달되어 있다. 말벌은 외부의 인위적인 자극에 대해 천적의 침입으로 인식하고 집단 공격을 하는데 주로 검은색과 같은 짙은색의 긴털을 가진 대상에 대해 강한 공격성을 보였으며, 초록색, 노란색과 같은 자연색에는 크게 반응하지 않았다. 집단 공격시 약 10-15m 정도까지 추적하면서 공격을 하였고 천적이 벌집으로부터 약 3m 이내에 들어오면 경계 비행 후 공격하였다. 따라서 말벌 위험 지역에서는 이러한 특성을 잘 파악하여 행동하는 것이 말벌의 피해를 줄이는 방법이다. 또한 말벌의 독성 강도는 장수말벌의 독이 가장 강했으며 그 뒤로 꿀벌, 좀말벌, 털보말벌, 등검은말벌, 말벌, 왕바다리 순으로 나타났다.

검색어: 말벌, 쏘임 피해, 방어행동, 검은색, 독성강도

S1-5

Ecological understanding of Q fever diseases transmission among rodents, ticks, and cow

Sungwon Hong[1], Young Ho Kim[2] and Kyoung-Seong Choi[1]
[1]Department of Animal Science and Biotechnology, Kyoungpook National University
[2]Department of Vector Entomology, Kyoungpook National University

Q fever is a highly infectious tick-borne zoonotic disease caused by *Coxiella burnetii*, a major pathogen that can cause reproductive disorders in ruminants such as cattle. Being one of the livestock infectious diseases with uncelar causative factors and transmission routes, there is a high possibility of transmission between wildlife, disease vectors, and livestock. Despite extensive research due to its high infectivity and significant economic losses, much of the focus has been on aspects such as pathogen detection, immunodiagnosis, and veterinary medicine. However, understanding the ecological interaction between the vector (ticks) and reservoir hosts (rodents) is crucial for elucidation the transmission dynamics to livestock. In this presentation, we aim to discuss genetic variation analysis approaches and ecological co-occcurrence analysis to understand the transmission pathways between rodents, ticks, and cow.

Key words: Disease Ecology, Spatio-Temporal Dynimcs, Transmission Mechanism, Urbanization, Climate change

S2-1

Study on the application of repellents from natural products for the control of two-spotted spider mites in greenhouse

Ji Hye Oh[1], Dong Hee Kim[1], Ryeo Eun Kim[1], Hyeon Gu Kim[1], Eun Su Jang[1], Sung Youn Jo[1],
Seo Yeon Park[1], Da Hyeon Yu[1] and Gwang Hyun Roh[1,2]
[1]Department of Plant Medicine, Gyeongsang National University, Jinju
[2]Institute of Agriculture and Life Science, Gyeongsang National University, Jinju

The series compounds from natural products are an effective repellent and deterrent against various kinds of pests. In this study, we evaluated the spatial repellency of fifteen compounds from natural products on the two-spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae), in the laboratory and field by using two-choice and no-choice bioassays. In laboratory two-choice tests, six compounds displayed active spatial repellency against female adult mites at a 2mg dose. The repellency of each compound was also as effective as the 6-compound blend. Three of the six compounds showed the predominant repellent activity (over 90%) that lasted for at least 3 days in laboratory no-choice tests. In a field test, we found that the number of *T. urticae* was fewer in strawberry seeding treated lure with 2mg of these compounds than in strawberry seeding treated lure with solvent control. Given that the findings are efficacious, economical, and natural products, they can be used in the sustainable management of *T. urticae* in greenhouse.

Key words: *Tetranychus urticae*, natural product, spatial repellency, choice test

S2-2

Seasonal occurrence of bark and woodboring Coleoptera in stands of *Pinus densiflora* (Pinales: Pinaceae) and *Larix kaempferi* (Pinales: Pinaceae) and monitoring method using multi-funnel traps baited with pine volatiles

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This study investigated the seasonal occurrence of bark and wood-boring Coleoptera in *Pinus densiflora* (Siebold & Zucc.) (Pinales: Pinaceae), and *Larix kaempferi* (Lamb.) (Pinales: Pinaceae) stands using multi-funnel traps baited with pine volatiles in Korea. The number and species of bark and woodboring beetles caught in traps baited with ethanol, *α*-pinene, and ethanol+*α*-pinene were compared to determine the effective attractants. In addition, the effects of other pine volatiles, such as (-)-*β*-pinene, *β*-caryophyllene, (±)-limonene, *β*-myrcene, and 3-carene, were investigated. A total of 13,134 wood-boring beetles from 150 species were collected from pine and larch stands from 2019 to 2020. *Tomicus minor* (Hartig) (Coleoptera: Curculionidae) adults were more attracted to traps baited with *α*-pinene, whereas *Xyleborinus saxesenii* (Ratzeburg) (Coleoptera: Curculionidae), *Cyclorhipidion pelliculosum* (Eichhoff) (Coleoptera: Curculionidae), and *Phloeosinus pulchellus* (Blandford) (Coleoptera: Curculionidae) adults were more attracted to traps baited with ethanol. *Hylurgops interstitialis* (Chapuis) (Coleoptera: Curculionidae), Shirahoshizo genus group, *Rhagium inquisitor* (Linne) (Coleoptera: Cerambycidae) and *Rhadinomerus maebarai* (Voss & Chûjô) (Coleoptera: Curculionidae) were more frequently attracted to traps baited with ethanol+*α*-pinene than to traps baited with other attractants. The addition of 3-carene to ethanol+*α*-pinene enhanced the capture of *H. interstitialis*, *R. inquisitor,* and *Hylobius (Callirus) haroldi* (Faust) (Coleoptera: Curculionidae).

Key words: pine, larch, pine volatiles, bark and woodboring beetle, seasonal occurrence, monitoring

S2-3

Field Application of a combination treatment of pheromone and kairomone against Citrus Longhorned Beetle, *Anoplophora chinensis*

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최근 친환경 블루베리 및 감귤 과원을 중심으로 알락하늘소 피해가 증가하고 있지만 효과적인 예찰 수단이 부족한 실정이다. 본 연구에서는 알락하늘소의 예찰 효율 증진을 위하여 페로몬과 기주식물 휘발성 물질(카이로몬)을 조합하여 복합유인제를 구성하였고, 알락하늘소가 다발생한 친환경 과원에 유인제와 트랩을 설치하여 성충 유인효과를 확인하였다. 포장 실험 결과, caryophyllene과 limonen을 페로몬과 조합하여 유인제를 구성한 경우 성충이 대량으로 유인되는 것을 확인할 수 있었다. 이는 알락하늘소가 종내 신호물질을 인지할 때 서식지로서 적합한지 판단의 기준으로 기주식물의 존재여부를 동시에 확인하기 때문인 것으로 판단된다. 향후 알락하늘소에 대한 복합유인제 현장적용 연구를 통하여 효과적인 알락하늘소 예찰도구로 활용될 수 있을 것으로 판단된다.

검색어: 날락하늘소, 카이로몬, 방출기, 페로몬

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S2-4

Development and effectiveness testing of *Conogethes punctiferalis* mating disruptor emitter and treatment method

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밤나무 과원에서 복숭아명나방을 대상으로 친환경 성페로몬 교미교란 실험을 진행하였다. 충북 충주 소재 유기농 밤과원과 관행농 밤과원에서 처리 방법을 달리하여 교미교란 효과를 검증하였다. 기준 처리량은 OECD Series on Pesticide number 12에 기록된 미국 EPA 기준, 50g AI/ha를 적용(한 시즌 동안 교미교란 효과가 발현할 수 있는 최소량)하였다. 처리량은 산지 지형을 생각하여 기준량의 두 배를 적용하였으며, 처리 방법은 1회 처리 방법과 2회 처리 방법을 선택하였다. 1회 처리는 기준량의 두 배를 한 번에 처리한 방법이고, 2회 처리는 기준량을 2회에 걸쳐 처리한 방법이다. 교미교란제 첫 번째 처리는 1회, 2회 모두 6월 15일에 진행하였고, 두 번째 처리는 2회 처리 방법만 8월 9일에 실시하였다. 실험 결과 유기농 밤과원 1회 처리 교미억제율은 87.8%였고, 교미교란 효과는 72.5%(무처리 대비 방제가)였다. 2회 처리 교미억제율은 94.9%였고, 교미교란 효과는 82%였다. 관행농 밤과원에서는 1회 처리 교미억제율은 89.6%였으며, 교미교란 효과는 66.9%였다. 2회 처리 결과 교미억제율은 95%였고 교미교란 효과는 74%였다. 관행농보다 유기농에서 더 높은 효과를 보였는데, 두 과원의 지형적 차이로 보인다. 아울러, 2회 처리 방법이 밤과원에서 복숭아명나방을 대상으로 더 효과적인 처리 방법이라 판단한다.

검색어: 복숭아명나방, 교미교란제, 성페로몬, 친환경, 밤나무

S2-5

Approaches of urban forest pest management using pheromone-based mating disruption

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최근 가로수, 공원 등에 수목이 많이 식재되어 우리 생활 주변에 녹지가 조성되고 있었고, 이를 생활권 수목 또는 도시숲으로 불리다. 이러한 생활권 수목의 증가로 따른 현상으로, 대상 수목을 가해하는 해충 또한 증가하였다. 생활권 해충에 대한 방제 수단으로는 농약 살포, 나무 주사 등의 화학적 방제법이 있으나, 생활권 주변이라는 특성으로 인하여 농약 살포나 나무주사 등은 바람직한 방제 수단으로 여기기 어렵다. 이에, 친환경적인 방제 방법중의 하나인 페로몬을 이용한 교미교란제법이 하나의 대안으로 판단되어 수목 해충 중 나비목 해충에 대한 교미교란제의 적용해 보았다. 대상 수목과 해충으로는 무궁화-큰붉은잎밤나방, 동백나무-차독나방, 왕벚나무-복숭아유리나방으로, 잎을 가해하는 해충 2종과, 천공성 해충 1종을 선택하였다. 큰붉은잎밤나방은 무궁화의 가장 큰 식엽성 해충이다. 차독나방은 남부지역 동백나무에 발생하는 식엽성 해충으로, 접촉시 피부염을 일으켜 일부 관광지에서 문제가 되고 있다. 복숭아유리나방은 줄기를 가해하는 천공성 해충으로, 화학방제가 어려운 해충이다. 본 발표에서는 큰붉은잎밤나방, 차독나방, 복숭아유리나방의 교미교란제를 이용한 방제 효과와 방제 효과 평가법에 대하여 발표하고자 한다.

검색어: 페로몬, 교미교란제, 생활권 수목, 화학 방제 대체

S2-6

Technical aspects of sensory electrophysiology in insect chemical communication studies: EAG, GCEAD and SSR

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Sensory electrophysiological recording techniques such as EAG (electroantennogram), GCEAD (coupled gas chromatograph-electroantennogram detection) and SSR (single sensillum recording) have been useful in the chemical ecology studies of insects and plants. Numerous pheromones and other semiochemicals have been identified through GCEAD analysis, and the response profiles of antennae and individual olfactory receptor neurons have been characterized by using EAG and SSR techniques. In this talk, the practical aspects of these techniques are presented in detail. Standard setup and procedure of each electrophysiological recording technique, and important parameters and proper data analysis methods will be introduced as well as its applications. Common mistakes and limitations of these techniques will also be discussed.

Key words: chemical ecology, EAG, electroantennogram, electrophysiological recording technique, GC-EAD, olfaction, single sensillum recording, SSR

S2-7

Chemical communication system of three *Spodoptera* moth species for pheromones and plant volatiles

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Spodoptera 속의 담배거세미나방, 열대거세미나방 및 파밤나방은 여러 나라에 분포하는 광식성 해충으로, 본 연구에서는 이들의 페로몬 및 식물냄새물질과 관련한 화학통신시스템에 대해 이해하기 위해 냄새감각기의 종류와 분포, 냄새활성물질 동정 및 야외행동 반응에 대한 연구를 진행하였다. 주사전자현미경 관찰을 통해, 세 종 나방의 암, 수컷 촉각에 여러 종류의 냄새감각기가 존재하며, 형태적으로 구분되는 종특이적 또는 성특이적 냄새감각기들이 존재한다는 것을 확인하였다. GC-EAD 실험을 통해 세 종 나방에 냄새활성을 나타내는 식물 냄새물질과 페로몬 관련 물질들을 동정하고, 이들을 개별 또는 조합하여 야외 트랩실험을 통해 행동활성을 검정한 결과, 이 중 여러 물질이 담배거세미나방과 파밤나방의 성페로몬에 대한 유인행동 반응을 저해하는 것을 알 수 있었다. 열대거세미나방은 발생이 저조하여 야외에서의 행동반응을 확인할 수 없었다.

검색어: *Spodoptera*, 담배거세미나방, 열대거세미나방, 파밤나방, 주사전자현미경, GC-EAD, 야외행동검정

S3-1

Insect gut microbiome as a novel source for synthetic plastic biodegradation

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Over the last decade, there has been growing interest in the plastic degradation capabilities of insect because herbivorous insects may be a valuable resource for microorganisms that can break down synthetic plastics. Insects that can digest plastics using their gut microbiota are gaining interest for use in bioremediation, although their environmental benefits remain unknown. However, most plastics biodegraded by insect gut microbes are polyethylene, polystyrene with little knowledge available on the gut microbiome of insects capable of degrading other synthetic plastics. Therefore, there is an urgent need to secure microbial resources based on insect-microbiome interactions and promote end-of-life solutions for synthetic plastics.

Key words: Insect-gut symbionts, plastic biodegradation, plastic waste management, bio-upcycling

S3-2

EpOMEs act as immune resolvins in insects

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Upon immune challenge, recognition signals trigger insect immunity to remove the pathogens through cellular and humoral responses. Various immune mediators propagate the immune signals to nearby tissues, in which polyunsaturated fatty acid (PUFA) derivatives play crucial roles. However, little was known on how the insects terminate the activated immune responses after pathogen neutralization. Interestingly, C20 PUFA was detected at the early infection stage and later C18 PUFAs were induced in a lepidopteran insect, *Spodoptera exigua*. This study showed the role of epoxyoctadecamonoenoic acids (EpOMEs) in the immune resolution at the late infection stage to quench the excessive and unnecessary immune responses. In contrast, dihydroxy-octadecamonoenoates (DiHOMEs) were the hydrolyzed and inactive forms of EpOMEs. The hydrolysis is catalyzed by soluble epoxide hydrolase (sEH). Inhibitors specific to sEH mimicked the immunosuppression induced by EpOMEs. Furthermore, the inhibitor treatments significantly enhanced the bacterial virulence of *Bacillus thuringiensis* against *S. exigua*. This study proposes a negative control of the immune responses using EpOME/DiHOME in insects.

Key words: Innate immunity; Insect; Oxylipin; EpOME; DiHOME; Resolution

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S3-3

Insect host-pathogen interaction: Signaling pathway for antimicrobial peptides production

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It is well known that invertebrates do not have adaptive immunity because of their short life cycle. Especially, insects have a strong innate immune system, including antimicrobial peptides (AMPs) production, to protect themselves from a wide range of pathogens. Previously, we identified over 60 genes related to AMP production, including Toll and Imd pathways, and characterized their immunological role in response to pathogenic infection through target gene-specific RNAi. This resulted in decreased expression levels of most AMPs in the larvae which were injected with target gene-specific dsRNA and microbes. Currently, we are focusing on studying the regulation of AMP production through epigenesis. It may help us understand how to regulate the innate immune system induced by pathogenic infection.

Key words: antimicrobial peptides, host-pathogen interaction, signaling pathway, epigenetic regulation

S3-4

Introduction of BRL: Insect-microbe interaction Lab

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Climate change has led to increased insect pests and pest distribution changes. Traditionally, chemical control using synthetic pesticides has been the main method for pest management, but the emergence of pesticide-resistant pests has become a problem. There is a need to develop new pest control agents to overcome these issues. Entomopathogenic fungi used in pest management have minimal environmental side effects and possess a mechanism of action distinct from that of synthetic pesticides. However, there is a need for the development of technologies to maximize the insecticidal effects of fungi against pests, and expressing and releasing dsRNA within the fungi can preemptively knock out the activation of the insect's defense system, thereby enhancing the insecticidal effect. Controlling insect defense genes and using entomopathogenic fungi as bio-carriers forms a new pest management strategy. This approach, described as a "microbial insecticide agents development strategy of cassette concept, " can versatilely modify genes and microbes. It is expected to overcome the limitations of synthetic pesticides.

Key words: BRL, dsRNA, entomopathogenic fungi, microbial insecticides, pest management

S4-1

Importance of vector surveillance in the era of climate change

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IPCC가 발간한 "지구온난화 1.5℃ 특별보고서에서는 전 지구적인 경제피해, 생태계, 종다양성에대한 피해를 언급하고 있다. 우리나라를 기준으로 보았을 때 평균 기온이 상승하는 경우 가장 우려되는 현상 중 한가지는 매개체들의 서식범위가 북쪽으로 확대되어지고 이에 따라 매개체가 옮기는 질병들에 대한 우려가 매우 크다. 특히 국내에 서식하지 않던 매개체들의 유입 위험이 증가되고 있다. 이에 질병관리청은 16개의 매개체감시거점 센터를 운영하고 있다. 하지만 최근 5년간 매개체 관련 과제 숫자는 감소하고 있어 매개체 감시의 중요성이 대두 되어질 필요가 있다.

검색어: Climate Change, Vector, RVSC (Regional Vector Survelliance Center)

S4-2

Development of Smart Aerial Net Trap (SANT) for monitoring of migrating pests

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The brown planthopper (BPH) and white-backed planthopper (WBPH), significant rice pests, cannot overwinter in Korea and primarily originate and migrate from Southeast Asia and China, where they cause considerable damage. These planthoppers, along with other pests, annually migrate to the Korean Peninsula. Monitoring their migration is essential for controlling their populations and maintaining agricultural productivity. Traditional monitoring methods often struggle with timeliness due to time and manpower constraints. To address this, we developed the Smart Aerial Net Traps (SANT) for immediate tracking of pests. The SANT system is installed in 43 locations across the country and has been used for over 10 years to track migrating insects. Our research shows that SANT is a more effective method for monitoring migratory pests compared to traditional methods. SANT enables real-time tracking of various migratory pests and can also be utilized in different areas, such as analyzing pest population changes and determining pest origins through the study of air currents.

Key words: pests, monitoring, migrating pest, brown planthopper, SANT

S4-3

National mornitioring of mosquito populations in the Republic of Korea in 2023

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About 1 billion cases of vector-borne infectious diseases occur every year, of which more than 1 million is dead in worldwide. Japanese encephalitis and malaria continue to occur, and infectious diseases such as dengue fever being imported aborad have been increasing significantly due to the increasing number of overseas travelers in Korea. The Korea Disease Control and Prevention Agency has established local centers to monitor pathogen vector population density related to chimate change at 16 locations. We collected 59,389 mosquitoes in traps at 36 collection sites in 30 urban regions and migratory bird habitats in 2023. The trap index was 34.6, and the predominant mosquito species were the *Culex pipiens* complex, *Aedes albopictus*, *Armigeres subalbatus*, *Aedes vexans*, and *Ochlerotatus Koreacus*. The mosquitoes were pooled into 4,371 pools to monitor flavivirus infection. In flavivirus dietection, no virus was detected.

Key words: mosquito, flavivirus, Japanese encephalities

S4-4

Surveillance of vectors for arthropod-borne animal diseases

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2023년 10월 국내 소 럼피스킨이 최초 유입이 확인된 이래, 4주만에 전국적으로 확산됨에 따라, 국가 인접국의 유입 가능한 가축질병 전파 매개체의 감시·예찰을 확대하고 강화할 필요성이 높아지고 있다. 농림축산검역본부(이후, 검역본부)는 해외 유입 가능한 가축전염병 전파 매개체와 가축에 대한 매개체성 질병 모니터링을 수행하고 있다. 매개체 감시 사업은 ‘07년부터 전국 공항만을 중심으로 시작 후, ’17년부터는 가축농장으로 확대하여, 현재는 전국 공항만(계류장) 4개 지점와 가축 농장 32개 지점에서 모기와 등에모기 대상으로 수행 중에 있다. ‘17~’23년까지 모기는 6속 15종 236,752마리, *Culex pipiens*(25.8%), *Aedes vexans*(25.5%), *Anpheles spp.*(24.6%), *Culex tritaeniorhynchus*(12.0%)가 우점종으로 확인되었다. 등에모기는 20종 127,267마리, 우점종은 *Culicoides(C.) puntctatus*(40.0%), *C. arakawae*(37.5%)였다. *C. tainanus* 등 3개 종에서 블루텅바이러스(1종 가축전염병)가 검출되고, ‘23년 럼피스킨 양성농장(7개소)의 채집된 침파리에서 원인체가 확인됨에 따라, 가축(동물)에 대한 매개체의 감시·예찰를 강화하기 위해 민-관 협력 지역별 가축질병 매개체 감시 센터 구축, 방제기술 개발 등 기후변화 대응 가축질병 연구개발에 박차를 가할 예정이다.

검색어: 럼피스킨, 블루텅, 등에모기, 모기, 침파리

S4-5

AI-IoT based automated imaging trap system for monitoring vector mosquito population

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Due to climate change and the rise in international transportation, there is an emerging potential for outbreaks of mosquito-borne diseases such as malaria, dengue, and chikungunya. Consequently, the rapid detection of vector mosquito species, including those in the *Aedes*, *Anopheles*, and *Culex* genera, is crucial for effective vector control. Currently, mosquito population monitoring is manually conducted by experts, consuming significant time and labor, especially during peak seasons where it can take at least seven days. To address this challenge, we introduce an automated mosquito monitoring system designed for wild environments. Our method is threefold: It includes an imaging trap device for the automatic collection of mosquito data, the training of deep-learning models for mosquito identification, and an integrated management system to oversee multiple trap devices situated in various locations. Using the well-known Faster-RCNN detector with a ResNet50 backbone, we’ve achieved mAP (@IoU=0.50) of up to 81.63% in detecting *Aedes albopictus*, *Anopheles* spp., and *Culex pipiens*. As we continue our research, our goal is to gather more data from diverse regions. This not only aims to improve our model’s ability to detect different species but also to enhance environmental monitoring capabilities by incorporating gas sensors.

Key words: Artificial Intelligence, Insect Monitoring, Internet of Things, Mosquito Trap, Vector Control

S4-6

Paradigm shift to control strategy based on mosquito surveillance data

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In the Republic of Korea, public health centers conduct vector mosquito control in accordance with infectious disease prevention laws. However, most public health centers have traditionally conducted periodic, uniform vector control across their respective regions without considering specific information on vector occurrence. In 2021, The Korea Diseases Control and Prevention Agency(KDCA) launched a control project to shift the paradigm toward mosquito control strategy based on mosquito surveillance data. In 2024, 18 local public health centers will participate in this project, which will progressively expanding so that it can be used countrywide. Local public health centers evaluate mosquito monitoring data using data gathered from Daily Mosquito Monitoring System(DMS), which enables them to pinpoint the best times and locations for vector control. Vector control activities carried out by local public health centers are computerized utilizing Vector Control Geographic Information System(VCGIS). Using the new control strategy with mosquito surveillance, the number of mosquito occurrences, number of control activities, and amount of insecticides have decreased compared to the periodic control activities. Based on mosquito surveillance data, it is anticipated that evidence-based mosquito vector control will offer a more efficient and effective means of mosquito control.

Key words: mosquito control, surveillance data, Daily Mosquito monitoring System(DMS), Vector Control Geographic Information System(VCGIS)

S4-7

Differences in insecticide resistance profiles among medical insects: Status and patterns

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[2]Department of Agricultural Biotechnology, Seoul National University

Medically significant indoor/ectoparasitic insect populations, including bed bugs and head lice, have developed considerable resistance to insecticides due to limited introduction of new genetic traits and the absence of an overwintering barrier. In contrast, outdoor pests like *Anopheles* and *Culex* mosquitoes exhibit fluctuating resistance patterns, likely influenced by factors such as overwintering barriers and relatively wider open habitats. Mosquitoes also face selection pressure from diverse sources beyond public health insecticides unlike bed bugs or head lice. Understanding different factors driving resistance among pests is essential for effective resistance management.

Key words: Medical insect, bed bug, head louse, mosquito, resistance, insecticide

S5-1

Beyond visuals: unveiling the multifaceted applications of AI in entomology

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This presentation explores the application of Artificial Intelligence (AI) in entomology beyond traditional image analysis. It highlights AI's potential in auditory and olfactory analysis, areas less explored in entomological research. Utilizing machine learning, AI enhances insect classification and ecosystem assessment through improved analysis of existing data. The discussion includes AI's capability in developing indices for habitat evaluation using insects as bioindicators, emphasizing its versatility across different research areas within entomology. This approach aims to broaden the scope of AI applications, promoting a deeper understanding of ecological dynamics through entomological studies.

Key words: machine learning, acoustic analysis, habitat index, olfactory analysis

S5-2

Construction of an insect protein 3D structure prediction system using AlphaFold2

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단백질의 구조 예측은 생명 과학 및 의약학 분야의 핵심적인 연구 주제 중 하나로, 단백질의 기능 및 상호작용을 이해하기 위한 주요 정보를 제공할 수 있어 다양한 연구가 수행되고 있다. 이러한 연구의 일환으로 최근 Google DeepMind의 AlphaFold2가 등장하였으며, 단백질 구조 예측 성능을 대폭 향상시켜 CASP(Critical Assessment of Protein Structure Prediction)에서 뛰어난 평가점수를 받아 단백질 구조 예측 분야의 최신 기술을 크게 향상시켰다. 이러한 컴퓨터 기반의 단백질의 구조 예측 방법은, 고전적인 방법을 사용하여 직접 단백질 구조를 결정하는 방법에 비해 매우 정확하고 빠르며 경제적인 비용으로 수행될 수 있어 단백질 구조 예측 및 생리학 연구를 수행하는 연구자들에게 유용한 방법론이 될 것으로 사료된다. 따라서 본 연구소에서는 곤충을 포함한 무척추 자생동물을 연구하는 연구자들을 위해 단백질 구조 예측을 수행할 수 있도록 64Core/128Threads의 CPU, 256GB의 RAM과 6장의 GeForce RTX 3090으로 이루어진 GPU(Graphical Processing Unit) 고성능 컴퓨터 시스템에 AlphaFold2 program을 구축하였다. 최근 인간을 대상으로 한 단백질 구조 예측 연구는 상당한 진전을 보이고 있지만, 곤충을 포함한 자연계의 동물을 대상으로 한 연구는 여전히 미비한 상황이다. 이러한 자생동물자원연구의 확대를 위해 본 연구소에서 구축한 GPU 시스템 및 생물정보학적 분석 방법이 많이 활용되어야 하며, 이를 위해서는 연구자들의 협력과 참여가 필요하다.

검색어: Alphafold2, Protein 3D Prediction

S5-3

Advances in artificial intelligence for vector identification and monitoring

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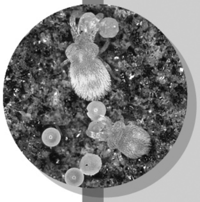
Recent advances in artificial intelligence and machine learning, such as the use of convolutional neural networks (CNNs) for image recognition, have emerged as a promising modality with the capability to visually differentiate between mosquito species. Here we present the first performance metrics of IDX, Vectech's system for AI mosquito identification, as part of Maryland's mosquito control program in the USA. Specimens were collected over fourteen weeks from twelve CDC gravid trap collection sites, identified morphologically by an entomologist, and imaged using the IDX system. By comparing entomologist identification to the algorithm output by IDX, we are able to calculate the accuracy of the system across species. Over the study period, 2,591 specimens were collected and imaged representing 14 species, 10 of which were available in the identification algorithm on the device during the study period. The micro average accuracy was 94.9%. Of these 10 species, 7 species consisted of less than 30 samples. The macro average accuracy when including these species was 79%, while the macro average when excluding these species was 93%. In the next iteration of this technology, Vectech is translating the vector identification capabilities of IDX into systems capable of processing greater numbers of specimens at large public health facilities, and remote sensing systems that will allow public health organizations to monitor vector abundance and diversity from the office. These advances demonstrate the utility of artificial intelligence in entomology and its potential to support vector surveillance and control programs around the world.

Key words: artificial intelligence, machine learning, mosquito, tick, vector identification

Oral Presentation



01

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

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

검색어: 마이크로파, 침투가열, 인삼뿌리썩음병균, 선충, 저항성

02

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

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

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

03

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

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

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

04

Energy flux in soil ecosystem in the threats to biodiversity

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

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

05

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

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

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

06

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

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

Key words: Jewel beetle, saproxyic, nondistructive inspection. life history

07

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

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

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

O8

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

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[2]Washington State Department of Agriculture, Tumwater Washington, USA
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[4]Pacific Lutheran University, Tacoma, Washington, USA
[5]Genomics Core lab, Washington State University, Pullman, WA, USA

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

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

09

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

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

Key words: scrub typhus, *Orientia*, chigger

010

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

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

검색어: 굼벵이 유충, 유기성 폐자원, 곤충 선발

011

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

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

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

O12

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

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

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

O13

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

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

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

014

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

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

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

O15

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

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

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

016

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

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The box tree moth (BTM, *Cydalima perspectalis* Walker) is a pest that infests various plants within the *Buxus* genus. Although a specific parasitoid wasp species associated with the BTM has been observed in the Republic of Korea, no research on this species has been published. Here we describe the fundamental biological and morphological characteristics of this parasitoid. We placed the wasp under the genus *Eriborus* (Hymenoptera: Ichneumonidae: Campopleginae). *Eriborus* sp. parasitizes within the living host body, with one wasp emerging from each host. The parasitism rate in collected BTM populations was 33.1%. The emergence rate was 87.1%, with all emerging adults being females, resulting in a sex ratio of 0. The pupal period averaged 9.5 days, and the adult lifespan averaged 10.5 days. *Eriborus* sp. parasitized BTM larvae from the first to the fourth instar and reproduced by parthenogenesis. *Eriborus* sp. exhibited morphological differences compared with previously reported *Eriborus* species in Korea, particularly in the length of the ovipositor sheath. In addition, the proportion of the highest similarity in nucleotide sequences of mitochondrial cytochrome oxidase I DNA was only 94.53%, rendering species identification using GenBank's mt cytochrome c oxidase 1 DNA sequences unfeasible. These data suggest *Eriborus* sp. could be used as a biological control agent for managing BTM infestations.

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

O17

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

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Five insecticides (Acrinathrin, Dinotefuran, Emamectin benzoate, Chlorfenapyr and fluxametamide) approved for tomato cultivation were evaluated in *Frankliniella occidentalis* populations collected from Chungcheong province (Cheongyang, Chungju and Gongju). Leaf dip bioassay was used to evaluate resistance levels (LC_{50}). Bioassays on Acrinathrin demonstrated higher LC_{50} concentration in evaluated populations. In particular, the Chungju population was 745.61 times the recommended concentration of the insecticide. Other remarkable resistance levels were recorded for the Dinotefuran with 435.06 times and 196.29 times the recommended concentrations for the populations from Chungju and Gongju, respectively. Bioassays for Emamectin benzoate, Chlorfenapyr and Fluxametamide showed low resistance to insecticides in the evaluated populations.

Key words: Bioassay, Emamectin benzoate, *Frankliniella occidentalis*, LC_{50}, pest

O18

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

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

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

O19

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

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

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

O20

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

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

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

O21

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

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

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

O22

Canceled by Author

O23

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

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

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

O24

Frankliniella occidentalis monitoring using deep learning algorithms

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

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

O25

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

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

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

O26

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

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

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

O27

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

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담배가루이는 전세계의 온대 및 아열대 지방에 넓게 분포하고 있으며, 한국에서는 시설재배작물의 주요 해충이다. 1998년 충북 친천군 장미재배지에서 처음 확인되었으며, 이후 전국적으로 확산된 것으로 추정된다. 담배가루이는 고추, 토마토, 오이 등 300종이 넘는 넓은 기주범위를 가지며, 식물체를 흡즙하여 작물의 생산성을 저하시키고 토마토황화잎말림바이러스(tomato yellow leaf curl virus, TYLCV) 등 100여종이 넘는 바이러스를 매개한다. 담배가루이는 주로 살충제를 이용한 방제가 이루어진다. 하지만 살충제를 이용한 방제법은 살충제 저항성 개체를 발생시킨다. 살충제 저항성 개체가 발생하게 되면 방제 효율이 급감하여 농가에 추가적인 경제적 피해를 야기한다. 본 연구는 국내 지역별 담배가루이를 대상으로 약제별 살충제 저항성의 발생 현황을 조사하여, 지역별 효과적인 약제를 탐색하고 향후 방제 전략 수립에 기여하고자 한다. 담배가루이는 전국 15지역(파주, 양평, 화성, 양구, 횡성, 평창, 당진, 천안, 공주, 예천, 구미, 사천, 남원, 나주, 고흥)에서 채집되었다. 살충제는 작용기작 별 사용량이 많은 8종을 선정하였으며, 엽침지법을 사용하여 살충률을 확인하였다. 곤충생장조절제(insect growth regulators, IGR) 피리프록시펜계 약제는 알을 대상으로, 그 외 7개 약제는 2령약충을 대상으로 살충률을 확인하였다. 모든 지역에서 높은 살충력을 보인 약제는 아버멕틴과 밀베마이신계, 스피노신계, METI살충제, 디아마이드계 약제이다. 특히 아버멕틴과 밀베마이신계 약제는 살충제 권장사용농도(10ppm)보다 낮은 8.9ppm이하의 LC_{90}값을 보여 감수성으로 추정되며, 예외적으로 천안 지역의 25.6ppm으로 상대적으로 높은 LC_{90}값을 보였다. 낮은 살충력을 보인 약제는 네오니코티노이드계, 설폭시민계, 피리프록시펜계, 테트론산 및 테트람산 유도체 약제이다 특히 네오니코티노이드계 약제는 모든 지역에서 살충제 권장사용농도(50ppm)보다 높은 715ppm이상의 LC_{90}값을 보여, 모든 지역에서 살충제 저항성이 발생한 것으로 추정된다. 실험결과를 통해 살충제 별 살충력의 차이와 지역별 살충제 저항성을 검정하였다. 연구결과를 통해 지역별/약제별 저항성관리 및 대응전략을 수립하여 농업 생산성을 향상시키는 것에 도움이 되고자 한다.

검색어: 담배가루이, 생물검정, 살충제, 고추, 약제저항성

O28

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

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

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

O29

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

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

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

O30

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

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Major pests of greenhouse strawberry include *Tetranychus kanzawai* (Acari: Tetranychidae) and *Bemisia tabaci* (Hemiptera: Aleyrodidae) causing significant damage in both yield and quality. We compared control efficacy of two entomopathogenic fungus strains of *Beauveria bassiana*, AAD16 and GHA, against *T. kanzawai* and *B. tabaci.* Both fungus were applied as a foliar spray targeting the undersides of leaves. In preliminary studies in the laboratory, adult *T. kanzawai* and *B. tabaci* showed lower LT_{50} values when treated with AAD16 strain compared to GHA. In the greenhouse, the densities of the both mites (adult and nymph) and whiteflies (adult) were significantly reduced with the application of the two fungus strains compared to the control. The mycosis rate was 88-94% in *T. kanzawai* and 48-59% in *B. tabaci* on collected leaves. These findings suggest that *Beauveria bassiana* AAD16 can be an effective mycoinsecticide against both *T. kanzawai* and *B. tabaci*.

Key words: Biological control, Entomopathogenic fungus, Mycosis rate

O31

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

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식물에 전기장을 처리하면 식물의 생장속도가 빨라지거나 영양학적으로 긍정적인 변화가 생긴다고 알려져 있다. 최근 음이온 처리 시 식물에 전기장을 처리한 것과 유사한 효과가 나타난다고 보고되었고 본 연구에서는 이러한 음이온을 온실해충인 점박이응애와 목화진딧물에 처리하여 방제효과 여부를 확인하였다. 그 결과 음이온 처리 시 점박이응애와 목화진딧물에서 살충효과와 기피효과가 나타났다. 또한, 점박이응애 알에서도 음이온 처리가 부화율에 영향을 주는 것을 확인할 수 있었다. 이러한 시험 결과를 바탕으로 온실에서 밀도실험 결과, 700,000 ion/cm^3 농도에서 무처리구에 비해 밀도가 감소함을 확인할 수 있었다. 따라서, 본 연구는 음이온 처리 시, 부가적인 효과로 온실해충(점박이응애, 목화진딧물)에 대해 친환경적 방제 가능성을 보여준다.

검색어: 점박이응애, 목화진딧물, 친환경 방제, 음이온

O32

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

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

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

O33

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

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

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

O34

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

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

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

035

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

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

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

036

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

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*Xenorhabdus*와 *Photorhabdus* 속은 각각 곤충병원성 선충인 *Steinernema*와 *Heterorhabditis*에 공생하는 공생세균이다. 감염성 선충의 유충은 공생세균을 표적 곤충의 혈강에 전달하고, 여기서 세균이 증식하여 숙주 선충의 발달을 돕는다. 이러한 선충과 세균 복합체의 성공적 공생관계는 세균의 이차대사산물을 통한 숙주의 면역억제에 달려져 있다고 알려져 있다. 본 연구에서는 서로 다른 살충력을 보이는 6종의 *Xenorhabdus*를 확보하고 이러한 차이가 세균의 성장속도와 NRPS (Non ribosomal peptide synthease)에 의해 생성되는 세균의 이차대사산물 발현에서 기원한다는 것을 확인하였다. 서로 다른 균주들은 콩명나방 (*Tenebrio molitor*)에 대한 살충력에 차이를 가지고 있었다. 이러한 세균들은 TSB 배지에서는 세균 성장 속도에 차이가 존재하지 않았지만 콩명나방 혈강 내에서는 세균의 성장 속도에 차이가 존재하는 것으로 나타났다. 또한 각 세균의 이차대사산물 추출물을 통한 곤충의 면역억제 실험 결과 PLA$_2$ 활성 억제, 세포독성 능력들이 살충력과 상관관계가 있는 것으로 나타났다. 이러한 이차대사산물의 경우 많은 물질이NRPS (Non ribosomal peptide synthease)에 의해 생성되므로 각 세균 별 NRPS의 유전자 발현을 보았을 때 흥미롭게도 살충력이 더 높은 스트레인의 세균이 일부 NRPS 유전자의 발현이 더 높은 것으로 나타났다. NRPS에 의해 합성되는 물질을 포함한 세균의 이차대사산물의 차이를 서로 비교하기 위하여 이차대사산물 추출액을 GC-MS/MS를 이용하여 분석하였다. 본 연구를 통해 곤충병원세균에 살충력의 기원이 NRPS를 통해 합성되는 이차대사산물에 있다는 것을 확인하였으며 이를 이용한 다양한 NRPS 유래 물질 연구는 신규 살충 물질 개발에 들어가는 비용과 시간을 획기적으로 줄일 수 있을 것으로 기대된다.

검색어: 곤충병원세균, *Xenorhabdus*, 살충력, NRPS

037

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

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

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

038

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

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전 세계적으로 RNA 간섭(RNA interference, RNAi)을 활용한 해충방제제 연구가 활발히 진행되고 있다. 대표적으로 Monsanto의 서부 옥수수 뿌리벌레(*Diabrotica virgifera virgifera*) 특이적 방제용 dsRNA (DvSNF7)를 발현하는 옥수수 종자가 상용화 되었고, 2016년 이 종자가 국내 사료 및 식품용으로 수입이 승인 되었다. 본 연구는 국내에 서식하는 좁은가슴잎벌레(*Phaedon brassicae*)를 Non-target 곤충으로 사용하여, 옥수수 종자에 사용된 DvSNF7 dsRNA의 잠재적 위해성을 평가했다. *P. brassicae*의 SNF7 유전자와 DvSNF7 dsRNA 간 Sequence유사성을 확인했다. 다음으로 *P. brassicae*가 DvSNF7 dsRNA를 섭식할 수 있는 환경을 조성하여, 치사 효과 실험과 Sequence특이적인 Knockdown효과를 확인하였다. 그 결과, DvSNF7 dsRNA는 *P. brassicae*생존에 영향을 미치지 않았으며, *P. brassicae*의 SNF7유전자를 Knockdown시키지 않음을 확인했다. 이번 연구를 통해 *D. virgifera virgifera*와 같은 과인 *P. brassicae* 는 SNF7유전자 간 Sequence유사성이 있지만, Sequence특이성이 부족하여 생존과 유전자 발현에 영향을 주지 않음으로써 위해성이 낮음을 확인했다.

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

039

First outbreaks of cricket disease in South Korea

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

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

040

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

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

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

041

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

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

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

042

History and current state of Korean forensic entomology

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

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

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043

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

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

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

044

Influence of micro-environmental factors on decomposition and insect colonization

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

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

O45

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

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

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

046

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

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

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

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047

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

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

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

048

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

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

Key words: Glyphipterigidae, Acrolepiinae, Glyphipteriginae, new record, Korea

049

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

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

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

O50

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

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

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

O51

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

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Scathophagidae, commonly known as dung flies, is a small dipteran family of Muscoidea and is the sister group of Anthomyiidae. Currently, there are 373 described species distributed across 47 genera worldwide. Scathophagidae is subdivided into two subfamilies, Scathophaginae and Delininae. Notably, Delininae is characterized by tergite 6 short, bare, and firmly fused with syntergosternite 7+8. Delininae includes five genera and one uncertain genus with around 26 species described to date. Taxonomic instability within Delininae has been raised by notable inconsistencies, particularly evident in the classification of genera of *Americina* Malloch, 1923, *Parallelomma* Becker, 1894, and *Leptopa* Zetterstedt, 1838. These disparities necessitate a systematic reevaluation to rectify taxonomic uncertainties, acknowledging the nuanced variations introduced by different taxonomists. To address these taxonomic conundrums within Delininae, molecular approaches were employed, using three mitochondrial genes (16S, Cytb, COIb) and three nuclear genes (28S, Ef1a, Pol II). Phylogenetic analysis was conducted by maximum likelihood and Bayesian methods to elucidate the comprehensive phylogenetic relationships within Delininae. Particularly, this study includes previously unexplored genera, namely *Neochirosia* Malloch, 1917 and *Micropselapha* Becker, 1894, and uncertain genus *Synchysa* Vockeroth, 1987, encompassing all genera in Delininae. The incorporation of all taxa contributes to a more thorough understanding of the evolutionary history within Scathophagidae, shedding light on previously overlooked aspects of its phylogenetic landscape.

Key words: Delininae, Multigene phylogeny, Scathophagidae

O52

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

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

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

O53

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

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

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

054

Spelaeochthonius - past, present, and future of pseudoscorpions

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

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

055

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

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

Key words: Stathmopodidae, wing venation, 3D model

056

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

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

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

057

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

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

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

O58

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

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

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

O59

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

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

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

060

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

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동물의 종 유지에 있어서 교미행동은 매우 중요한 위치를 차지함. 교미과정에서 수컷의 경우 모든 암컷에 대해 성행동을 보이는반면, 암컷은 가장 적절한 교미의 시기를 정하며, 적절한 수컷을 선택하고 교미행동을 보이기 때문에 암컷의 교미행동을 유도하는 과정은 생물학에서 매우 중요한 의미를 지님. 본 연구에서는 초파리 (*Drosophila melanogaster*) 전자현미경자료와 총신경망분석 (Connectomics)을 이용하여 초파리 뇌에서 암컷의 교미행동을 조절하는 것으로 알려진 pC1신경의 하부신경 pC1b,c가 성적 성숙과정에서 교미를 하고자 하는 욕구 (sexual drive)를 증가시키는 기능을 하는 것을 처음으로 밝힘. 본 연구에서는 처음으로 pC1b,c 신경 내의 cAMP 수준이 교미의 욕구변화를 보여주는 중요한 물질이라는 것을 밝혔고 cAMP의 수준이 오르기 위해서는 신경펩티드인 Dh44와 그 수용체 GPCR인 Dh44R1과 Dh44R2가 필요하다는 것을 확인함. 또한 cAMP의 변화는 신경내의 CREBB를 통하여 하위 유전자인 pyx (pyrexia)의 발현을 유도한다는 것을 밝힘. 본 연구로 종 유지 메커니즘을 좀 더 이해할 수 있음.

검색어: 초파리, 교미행동, GPCR, pC1

061

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

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

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

062

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

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

검색어: 쌍별귀뚜라미, 볼보바이러스, 유전체 분석, 유병률 조사

063

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

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

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

064

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

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

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

065

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

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

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

066

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

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

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

067

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

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

Key words: ground beetle, Pterostichini, phylogeography

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068

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

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

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

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069

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

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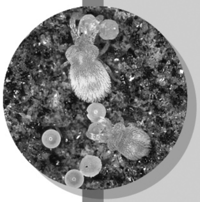
The genus *Vespa* consists of 22 species worldwide, and their phylogenetic relationships are well established through adult morphology and molecular analyses. However, taxonomic studies of larvae are lacking. In this study, we provided descriptions and taxonomic keys for eight species of Korean *Vespa*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

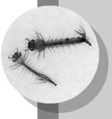
Key words: Vespidae, Vespa, larvae, taxonomic key

Poster Presentation – KSAE

Competition

Non-Competition





P1

One newly recorded *Paragabara* species (Lepidoptera, Erebidae, Boletobiinae) from Korea

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The genus *Paragabara* is recognized as a member of the subfamily Boletobiinae, with six species in the Eastern Palaearctic. In Korea, three species of this genus are known. Konoenko et al. (2010) designated a lectotype for *P. flavomacula* (Oberthür, 1880) and described a new species, *P. curvicornuta*. In this study, the misidentification of the Korean *P. flavomacula* as *P. curvicornuta* has been corrected. Additionally, one newly recorded species, *P. curvicornuta*, is reported from Korea. In total, four *Paragabara* species are recognized in Korea. All available information, images of adults, a checklist, and male and female genitalia, etc., are provided.

Key words: Boletobiinae, *Paragabara*, newly recorded, reidentification, Korea

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P2

Review of the genus *Cephennodes* Reitter (Coleoptera: Staphylinidae: Scydmaeninae) in Korea with a new record

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The genus *Cephennodes* Reitter (Coleoptera: Staphylinidae: Scydmaeninae) comprises approximately 220 species worldwide within three subgenera (*Cephennodes*, *Aculeodes*, *Fusionodes*). In Korea, two species are recorded: *C.* (s. str) *japonicus* (Sharp) and *C.* (*Fusionodes*) *graeseri*Reitter. The two subgenera, *Cephennodes* and *Fusionodes*, can be distinguished by the form of the parameres in relation to the median lobe, whether fused or divided. In this study, we redescribed two species: *C.* (s. str) *japonicus* and *C.* (*Fusionodes*) *graeseri*. Additionally, *Cephennodes* (*Fusionodes*) *ussuricus* (Kurbatov) is recorded first time in Korea. Images of habitus, aedeagus, and a distribution map are provided.

Key words: *Cephennodes*, redescription, new record, Korea, taxonomy

P3

Taxonomic study of the genus *Spilonota* Stephens (Lepidoptera: Tortricidae: Olethreutinae: Eucosmini) with descriptions of two new species in Korea

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A taxonomic study was conducted on *Spilonota* Stephens, 1834 in Korea. As a result of the research based on materials from Incheon National University two new species; *S. samseong* Choi, Bae & Nasu, and *S. laticucullusa* Choi, Bae & Nasu from Korea. This study provides a brief description of the new *Spilonota* species in Korea, as well as comparisons with similar species and illustrations of adult and genital morphology.

Key words: leaf roller moth, distribution, new record, taxonomy

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P4

3D Description of Stathmopodidae Type Species using Micro-CT

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Stathmopodidae, in the superfamily Gelechioidea, was first described by Edward Meyrick in 1913. This family has various characteristics, such as feeding on crops, moss, spores of fern, aphids, etc., but there is a lot of difficulty in identification due to morphological similarities between species. Therefore, it is necessary to understand the genitalia structure through dissection, but this process necessarily involves damage to the type specimen. To solve these problems, Micro-CT(Computed Tomography) which allows observation of internal structures without damage, was utilized to create a 3D model of the genitalia. In this study, the genitalia structure of *Stathmopoda pedella* (Linnaeus, 1761), the type species of Stathmopodidae, was imaged using Micro-CT under a resolution of 4 um conditions, providing a 3D description.

Key words: Stathmopodidae, genitalia, Micro-CT, 3D model

P5

First Record of genus *Dyseriocrania* Spuler, 1910 (Lepidoptera: Eriocraniidae), a Leaf Miner from Korea

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Eriocraniidae is a microleidopteran family (Lepidoptera: Eriocraniidae) that includes six genera and distributed to the Holarctic region. The larvae of this family are known leaf miners, typically infesting *Betula* and *Ouercus*. Herein. the first reord of the genus *Dyeriocrania* Spuler, 1910 in Korea is presented, including the previously undscribed species. Adult and female genitalia are provided based on illustrations.

Key words: Leaf miner, New record, *Dyseriocrania*, Korea, Taxonomy.

P6

A New Record of a Forest Lepidopteran Pest of genus *Acronicta* Ochsenheimer, 1816 (Lepidoptera: Noctuidae) from Korea with Molecular data

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[2]Lab. of Insect phylogenetics & evolution, Department of Plant Protection & Quarantine, Jeonbuk National University

The genus *Acronicta* Ochsenheimer, 1816 is known as a forest pest. The acronictine species is widely distributed across the Afrotropical, Oriental, Australian, and Neartic regions. This study presents a new record of an acronictine species from Korea, including descriptions, illustrations, and diagnostic characteristics. Additionally, the CO1 barcode data of the newly recorded species is compared with the global barcode reference at the species level. New data on the recently recorded species has been obtained from this study. This information will aid in the prompt identification and preparation for potential pest outbreaks.

Key words: Forestry pest, *Acronicta*, Noctuidae, Taxonomy, COI gene, DNA barcoding

P7

Species diversity comparisons of subtropical and tropical Lepidoptera in Vietnam: Noctuoidea fauna and flora

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Vietnam is a country in Southeast Asia, long from north to south, with temperate, subtropical, and tropical climates in different parts of the country. Based on the results of two years of insect surveys in the subtropical and tropical regions of Vietnam, we conducted a comparative analysis of the species diversity of the Noctuoidea (Insecta: Lepidoptera) in the two survey areas, Bach Ma National Park and Protected Forest in the Vạn Xuân region. In addition, the host flora of the identified moths were analysed to determine the differences in host communities.

검색어: fauna, flora, hostplant, Noctuoidea, Vietnam

P8

A new species of the genus *Altenia* (Lepidoptera: Gelechiidae) from Korea

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The family Gelechiidae (Lepidoptera: Gelechioidea) is known as one of the largest families in Microlepidoptera, encompassing about 600 genera and more than 5,000 described species worldwide. However, the genus *Altenia* Sattler, 1960 has been poorly studied in Korea, with only one known species. Here we introduce a new species, *Altenia parascriptella* sp. nov., from Korea, providing photos of adults and genitalia for both sexes, along with diagnostic characteristics.

Key words: Gelechiids, tribe Litini, new record, Korean peninsula

P9

Literature Review of Insect Pests on *Citrullus lanatus* in Korea

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전북특별자치도 수박(*Citrullus lanatus* (Thumb.) Matsum. et Nakai) 재배면적은 2,235ha이며, 익산과 정읍은 주요 수박 재배 지역이다. 본 연구는 수박에서 발생하는 해충 목록 작성을 위한 기초자료 구축을 목적으로 최근 20년간 보고된 문헌자료를 조사하였다. 문헌조사에 따르면, 수박에서 발생하는 주요 해충은 총 7목, 11과, 22종으로 정리되었다. 이 중 점박이응애(*Tetranychus urticae* Koch), 목화진딧물(*Aphis gossypii* Glover), 아메리카잎굴파리(*Liriomyza trifolii* Burgess) 등이 우점해충으로 다수의 문헌을 통해 확인되었다. 그 외 파밤나방(*Spodoptera exigua* Hübner), 꽃노랑총채벌레(*Frankliniella occidentalis* Pergande), 목화바둑명나방(*Diaphania indica* Saunder)등의 해충들이 최근 연구로부터 추가되었다. 본 연구 결과를 기반으로 앞으로 수박 해충에 대한 현장 조사 계획을 수립하고, 적합한 방제 전략을 세우고자 한다.

검색어: 수박, 해충, 분류, 문헌조사

P10

Revision of Genus *Addyme* Walker, 1863 (Phycitinae: Pyralidae: Lepidoptera) and its allied genera

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The family Pyralidae comprises over 6,000 species, and is composed of five subfamilies. Among those, the subfamily Phycitinae includes 3 genera, *Addyme* Walker, 1863, *Calguia* Walker, 1863, and *Coleothrix* Ragonot, 1888, with more than 3,300 species worldwide. However, several species of the genera have been erroneously stated and identified due to confusions caused by high morphological similarities. Therefore, we correct those errors through re-examinations of most of the type specimens, along with a diagnosis and table exhibiting the history of those genera. Additionally, we introduce two misidentified Korean pyralids belonging to the genus *Addyme*.

Key words: reinstatment, synonym, Malaysia, NHMUK

P11

A New record of *Hemipsocus chloroticus* (Hagen, 1858) (Psocodea: Hemipsocidae) in South Korea

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Hemipsocus chloroticus (Hagen, 1858) is a leaf litter barklice and has been recorded in Japan, China, Taiwan, South-East Asia, Sri Lanka, and North America. We collected *H. chloroticus* on Jinju-si, Sanchung-gun, Seoguipo-si, and Ulsan-si from 2022 to 2023. In this study, *H. chloroticus* is reported for the first time in Korea, and illustrations of diagonistic characters are provided.

Key words: Psocodea, new record, Hemipsocidae, *Hemipsocus chloroticus*, South Korea

P12

The first record of *Greenidea nigra* Maki, 1917 (Hemiptera: Aphididae: Greenideinae) from South Korea

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The Genus *Greenidea* includes 66 species worldwide. Only two species have been recorded in Korea: *G.kuwanai* and *G.nipponica*. We collected *Greenidea nigra* Maki, 1917 on *Quercus glauca* in Jeju. This species has been recorded in Japan and Taiwan. In this study, we report this species for the first time in South Korea, and describe morphological features of apterous viviparous females.

Key words: Aphids, Greenidea, *Quercus glauca*, South Korea

P13

Comparison of Male Genitalia of the *Coptolabrus smaragdinus* (Coleoptera: Carabidae) from South Korea

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Currently, 12 subspecies of *Coptolabrus smaragdinus* have been recorded in Korea, of which 7 subspecies are listed in South Korea. *C. smaragdinus* has limited movement due to degenerated hindwings, resulting in high intraspecific diversity due to geographic isolation. Previous studies have been mainly classified based on external characters or genitalia structure, but the differences between subspecies are very ambiguous. In this study, we aimed to more clearly distinguish at the subspecific classification level, by examining the male aedeagal and inflated endophallus. Additionally, we provide photos of adult, endophallus and the process of endophallus inflation.

Key words: Carabidae, Coleoptera, *Coptolabrus smaragdinus*, male genitalia, aedeagal, endophallus, South Korea

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P14

Review of the subgenus *Plataphus* (Bembidiini: Bembidiina: *Bembidion*) of Korea

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The genus *Bembidion* is a prominent terrestrial group found in various regions around the world, encompassing a large number of species. Species of this genus have a reduced apical palpomere, as do all members of the tribe Bembidiini. This study reviews four species belonging to the subgenus *Plataphus*, which is included within the genus *Bembidion*. Descriptions and photos of adults are provided.

Key words: *Bembidion, Plataphus,* taxonomy

P15

A new record of the crane fly, *Dolichopeza* (*Oropeza*) *satsuma* (Alexander, 1918) (Diptera: Tipulidae), from South Korea

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The subgenus *Oropeza* Needham, 1908 (Diptera: Tipulidae: *Dolichopeza*) comprises 27 described species distributed across the Holarctic region. Certain *Oropeza* species have been reported in neighboring countries of the Korean Peninsula—6 species in Japan, 3 species in China, and 4 species in Russia. Some researchers, such as Byers (1961) and Savchenko (1983), suggested that the distribution of *Oropeza* cover the East-Palearctic regions, including the entirety of the Korean Peninsula. However, previous records of *Oropeza* from the Korean Peninsula have not been accepted because of the lack of comprehensive species-level investigations in this region. In this study, we present a new record of the species *Dolichopeza* (*Oropeza*) *satsuma* (Alexander, 1918) in South Korea, with redescription and photographs: general habitus, wing veins, and male genitalia. This finding marks the rediscovery of the subgenus *Oropeza* in the Korean Peninsula.

Key words: Diptera, Tipulidae, *Dolichopeza*, *Oropeza*, new record, taxonomy, South Korea

P16

A new species of *Plecoptera* Guenée 1852 (Lepidoptera: Erebidae) from Korea

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The family Erebidae (Lepidoptera: Noctuoidea) is known as one of the largest families in Lepidoptera, comprising about 1,760 genera and more than 24,569 described species worldwide. Within this family, the genus *Plecoptera* Guenée, 1852, belonging to the subfamily Anobinae, has been documented across the Palaearctic, Oriental, and Afrotropical regions. Here, we introduce the subfamily and genus for the first time in Korea, along with a new species. The diagnosis, description and photographs of adult and genitalia are provided here.

Key words: Macrolepidoptera, *Plecoptera* cf. *reflexa*, Korean fauna, Korean Peninsula.

P17

Expansion of Korean records for the family Coleophoridae (Lepidoptera, Gelechioidea): Four newly recorded species and two overlooked additions

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This study reports the first records of four coleophorids, namely *Coleophora kamchatica* (Anikin, 1999), *C. lativittella* Erschoff, 1877, *C. levantis* Baldizzone & Oku, 1988, and *C. citrarga* Meyrick, 1934, in Korea. Additionally, the presence of two species, *C. montaniella* Oku & Kusunoki, 2018, and *C. artemisicolella* Bruand, 1855, in Korea has been overlooked in the previous checklist of the family Coleophoridae in Korea, despite there being evidence of their existence. Consequently, with these additions, the total number of known species in Korea has been confirmed to be 42, expanding from the previously identified 36 species. Diagnostic characteristics and photographs of adults and genitalia for the four newly recorded species are provided, along with evidence supporting the presence of the two overlooked species in Korea.

Key words: Microlepidoptera, Gelechioidea, casebearers, new record, Korean fauna, Korean Peninsula

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P18

Molecular epidemiological investigation of the invasive pest Drywood termite (*Cryptotermes domesticus* Haviland) in South Korea, 2023

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Drywood termite (*Cryptotermes domesticus*), native to South East Asia, is distributed in India, China, Taiwan, Australia and so on. In China, it is considered an economically important pest causing damage to wood. It lives in dry wood environments such as furniture, buildings, and structural timber. It is difficult to find drywood termite within a structure but it can be detected by the presence of alate flight and small egg-like pellets of excreta. It was found in a house in Seoul, Korea in July 2023 and was investigated joint by APQA, National Institute of Ecology, National Institute Biological Resources, National Institute of Forest Science, Cultural Heritage Administration and Gyeongsang National University. The *COII* barcode region was analized with PCR method and compared with the sequences of all *C. domesticus* registered in NCBI 557bp of base sequence. Genetic difference ranged from a minimum of 0.0072 to a maximum of 0.0557. Among these, the individual with the minimum genetic distance was from Guangdong Province, China.

Key words: drywood termite, barcode, population, invsion, *COII*

P19

Molecular epidemiological investigation of the invasive pest Western drywood termite (*Incisitermes minor* (Hagen)) in South Korea, 2023

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Western drywood termite, Incisitermes minor, is distributed southwestern USA and northern Mexico. Invasions had been reported to Canada, China, Hawaii and Japan. Incisitermes minor may be introduced through wooden structures. In California and Arizona, it caused economic damage of about $250 million. In September 2023, it was discovered in a house in Changwon-city, Korea and a joint investigation was conducted by APQA and other government agencies. The 16S rRNA sequence was used in the molecular epidemiological investigation to trace the origin of the invasion. Five individuals found in Changwon and 18 foreign sequences collected by NCBI were compared. A total of 462bp of base sequences were compared, and the genetic distance was observed to range from a minimum of 0.000 to a maximum of 0.1791. They were most genetically similar to the California individual in the United States.

Key words: western, termite, barcode, population, invsion, 16S rRNA

P20

Not Presented

P21

Reconciling the molecular phylogeny and fossil records by total evidence tip-dating in cave crickets (Rhaphidophoridae: Orthoptera)

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Rhaphidophoridae (Orthoptera: Ensifera), commonly known as cave crickets, are a wingless family and considered the most ancient lineage within Tettigoniidea. However, previous molecular phylogenetic studies and morphological hypotheses have shown inconsistencies. Although their fossils have been found in Baltic amber, their systematic placement remains unrevealed. This study reconstructed a comprehensive phylogeny integrating both extant and fossil lineages. Initially, we revealed relationships within extant lineages through molecular phylogenetics including all extant subfamilies for the first time. Subsequently, using a cladistic approach based on morphology, we confirmed the systematic position of fossil taxa †Protroglophilinae with a report of a new species. Integrating molecular and morphological phylogeney by total evidence tip-dating, we present the comprehensive phylogeny of Rhaphidophoridae considering both extant and fossil groups.

Key words: Orthoptera ,Bayesian, tip-dating, fossil, Biogeography

P22

To fly, or not to fly—that is the question: Wings in Melanoplinae

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Despite having enabled insects to become the most abundant and successful group on Earth, wings have been lost in numerous insect lineages, including Orthoptera. Melanoplinae, a subfamily that includes over 100 genera and more than 800 species in Acrididae, exhibits various wing-types and dispersal abilities. Some species possess extensive flight capabilities with long wings, while many groups that inhabit alpine environments tend to reduce their wings and dispersal ability. In order to infer the evolutionary history of Melanoplinae and their wings, we conducted molecular phylogenetic research. We established the phylogeny using seven mitochondrial (Cox1, Cox2, CytB, Nad2, Nad5, 12S and 16S) and two nuclear genes (H3 and Wg) for 139 taxa. By investigating the wing types in Melanoplinae, we estimated the ancestral state of the wings and traced their evolutionary history. Our results present that loss and recovery of wings occurred multiple times within Melanoplinae, showing distinct histories across inner taxa within the subfamily.

Key words: Orthoptera, Acrididae, Melanoplinae, Ancestral reconstruction, Wing

P23

Complete mitochondrial genome of the *Vespa binghami* (Hymenoptera: Vespidae) and comparison to other species in *Vespa*

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Vespa binghami (Hymenoptera: Vespidae) is one of the 10 species in the genus *Vespa* distributed in South Korea and is the only nocturnal wasp. In this study, we sequenced complete mitochondrial genome (mitogenome) of the species using the Sanger method and using *Vespa*-specific 30 primer sets. The length of *V. binghami* was 15,957 bp and the total A/T content was 80.6%. The A+T-rich region of *V. binghami* was 152 bp, and other *Vespa* species ranged from 39 bp (*V. velutina*) to 2,230 bp (*V. v. auraria*). Compared to the majority of insects, the gene arrangement of *V. binghami* had differences as followings: *trnY-trnI-trnM-trnQ*, *trnN-trnE-trnS*$_1$*-trnF*, and *trnS*$_2$*-trnL*$_1$. However, all species in the genus *Vespa* registered in GenBank to date were composed of the same arrangement. Phylogenetic analysis using 13 PCGs and 2 rRNA genes showed the sister relationship between *V. binghami* and *V. orientalis* with the higher nodal supports.

Key words: mitochondrial genome, *Vespa binghami*, gene arrangement, phylogeny

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P24

Complete mitochondrial genome of *Tropilaelaps mercedesae* Anderson and Morgan, 2007 (Acari: Laelapidae)

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Tropilaelaps mercedesae Anderson and Morgan, 2007 (Acari: Laelapidae) is a serious ectoparasite of the brood of several honey bee species. Among the four recognized species of *Tropilaelaps*, Korean population was renamed as *T. mercedesae* from *T. clareae* on the basis of morphological evidences and genetic data. In this study, we report the complete mitochondrial genome (mitogenome) sequence of *T. mercedesae*. The 15,119-bp long mitogenome has an identical gene arrangement to that of Chinese sample reported previously. Comparison of two geographic samples showed *COII, ND5*, *ND4*, *ND6*, *CytB,* and *ND1* to have higher number of variable sites than *COI*, which is often used for population-level study, suggesting these genes to have potential usefulness for population genetic study. The mitogenome sequence of *T. mercedesae* from Korea could be useful for species identification for geographic samples, trace of the origin of local populations, and illustration of evolutionary distinction among *Tropilaelaps* species either using part of or whole genome.

Key words: *Tropilaelaps mercedesae,* Mitochondrial genome, Laelapidae.

P25

Morphological identification of subfamily Plusiinae (Lepidoptera: Noctuidae) using the patterns of forewings based on multivariate analysis

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본 연구는 검거세미밤나방(*Agrotis ipsilon*) 성페로몬 트랩에 혼재하여 유살되는 은무늬밤나방아과 형태적 분류와 동정법 수립을 위해, 날개 무늬의 형태계측학 분석을 실시하였다. 은무늬밤나방아과 개체는 2023년 11월부터 12월까지 제주도 애월읍 일대에서 채집되었으며, 콩 해충으로 알려진 콩은무늬밤나방(*Ctenoplusia agnata*)을 비롯하여, 다양한 농작물을 가해하는 것으로 알려진 붉은금무늬밤나방(*Chrysodeixis eriosoma*)의 수컷 성충이 포획되었다. 앞날개의 형태 및 무늬를 가지고 현장에서 쉽게 동정할 수 있는 형태적 특징을 도출하기 위하여, 각 성충 개체의 앞날개를 잘라 현미경 카메라로 촬영하고, 앞날개의 내횡선, 아외연선, 반점 크기 등 15개의 형질을 측정하였다. 또한 각 형질 간의 상관관계를 분석하였으며 빈도분포를 통하여 두 종간 분리되는 형질을 파악하였다. 최종적으로 다변량 분석법을 적용하여 두 집단이 어떻게 군집을 이루는지 분석하고, 날개형태만으로 붉은금무늬밤나방과 콩은무늬밤나방을 구분할 수 있는 방안을 제시하였다.

검색어: 밤나방과, 성페로몬 트랩, 형태적 동정, 형태계측학 분석, 다변량 분석

P26

Host preferences of *Spodoptera frugiperda* by corn varieties and nutrient composition by corn cultivar

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Fall armyworm (FAW, *Spodoptera frugiperda*) is a major pest worldwide, and since its first domestic invasion was confirmed in 2019, its damage has been steadily increasing in crops such as corn until recently. In order to provide basic data for the management of FAW, we conducted a comparison of host preference and nutritional composition analysis of corn varieties. A total of 12 varieties of corn were selected for the experiment. To investigate the preference among the varieties, we examined the host preferences at the population level and the individual level, and found no statistically significant differences. In the population-level experiment, the highest damage rate was observed for Saekso 4 and the lowest for Heukgeom 2. In the individual-level experiment, the highest damage rate was found for Kangilok and the lowest for Oryun 2 when using leaves, and the highest for Saekso 1 and the lowest for Dreamok when using stems. As a result, the population-level and individual-level results were not consistent, suggesting that FAW's corn variety preference is not clear and may vary depending on various conditions such as corn tissue. Composition analysis of the 12 varieties showed no correlation between composition and FAW preference among the varieties, and considering the feeding behavior of FAW, which are highly polyphagous, it is recommended to control FAW as early as possible to improve control effectiveness.

Key words: *Spodoptera frugiperda*, host preference, corn variety, composition, control

P27

Studies on some biological characteristics and summer diapause of the *Euonymus* defoliator moth, *Pryeria sinica* Moore (Lepidoptera: Zygaenidae) in Seoul, Korea

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The *Euonymus* defoliator moth, *Pryeria sinica* Moore (Lepidoptera: Zygaenidae), is a pest that causes considerable damage to the *Euonymus* genus, especially *Euonymus alatus* and *Euonymus japonicus*. The biological characteristics of *P. sinica* have been studied in China, Japan, Taiwan, and the United States, but there has been no research conducted on this species in Korea. Also, *P. sinica* has two dormant phases in each generation, one as eggs in winter and the other as pupae in summer. Our purposes are to study the biological characteristics of Korean populations of *P. sinica* and to examine the effects of temperature and photoperiod on summer diapause. The biological characteristics were investigated in laboratory conditions (25 ± 1 °C, 65 ± 1% R.H., 16L:8D) and the number of eggs in an egg mass, developmental periods and mortality rate in each larvae stage, and adults' life span were determined. The results showed that 190.7 ± 31.64 eggs were contained in one egg mass and it took 25.57 ± 0.61 days from 1st larval stage to the pre-pupal stage. *P. sinica* has 4 larval stages and each stage took 4.28 ± 0.21, 6.2 ± 0.55, 6.02 ± 0.68, and 8.93 ± 0.88 days. The mortality rate of larvae peaked at 22.5% in 3rd larval stage. The adults' life span was 4.67 ± 0.97 days in males and 4.61 ± 1.82 days in females. To study summer diapause, we divided pupae into 4 groups. Both low temperature and short daytime were effective in shortening the pupal stage. The pupal stage was the shortest in group D (122.12 ± 1.24 days), in which the initial condition was 25 °C-16L:8D and the altered condition was 16 °C -12L:12D, and the longest in group A (161.92 ± 3.15 days, 25 °C-16L:8D). These data could be utilized to propose the optimal timing for controlling the population of *P. sinica*.

Key words: *Euonymus* defoliator moth, *Pryeria sinica* Moore, biological characteristics, summer diapause

P28

Survey on the diversity of visiting and pollinating insects in major gardens at Sejong national arboretum

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현재 기후변화 및 산업화 등으로 생물다양성 감소, 환경오염에 대한 위기가 확산되고 있어 지속가능한 미래설계에 대한 관심이 높아지고 있다. 이에 따라, 본 연구에서는 대표 도시숲인 국립세종수목원에 조성된 총 16개 전시원을 대상으로 총 6차례에 걸쳐 방문곤충과 화분매개곤충 다양성을 조사하였다. 조사시기별 분석결과로 2차(‘23.7.31) 조사 시기에 가장 다양한 종을 확인할 수 있었으며(총 80종), 전시원별 분석결과 숲정원에서 가장 다양한 종을 확인할 수 있었다(총 59종). 또한 주요 식물 6종(배롱나무, 나무수국, 무궁화, 좀개미취, 범부채, 부처꽃)에 7~10월 기간 중 양봉꿀벌, 애황나나니, 호박벌, 네발나비, 호랑나비, 흰점박이꽃무지, 호리꽃등에, 배짧은꽃등에가 화분매개 행동을 하는 것을 확인하였다. 본 발표에서는 2023년 국립세종수목원 전시원 내 방문곤충 및 화분매개곤충 다양성 연구의 구체적인 결과를 제시하고, 곤충의 보전 필요성, 도시숲 내 체계적인 방문곤충 및 화분매개곤충 조사의 중요성에 대하여 논하고자 한다.

검색어: 국립세종수목원, 도시생물다양성, 도시숲, 방문곤충, 수분매개곤충

P29

Seasonal occurrence of forest insect pests (Scolytinae, Cerambycidae) on the border of South and North Korea

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최근 국제적인 기후변화로 인해 다양한 산림해충들이 새로운 국가 또는 인접한 지역으로의 분포 확대가 증가하고 있는 추세이다. 국내외의 대표적인 산림해충 분류군인 나무좀아과와 하늘소과에는 넓은 기주식물 범위를 가지고 있어 산림 생태계에 직간접적으로 피해를 야기하는 종들이 다수 포함되어 있다. 본 연구에서는 2023년 5월부터 10월까지 남북 접경지(강원 철원군, 양구군, 고성군) 내 혼합림에서 린드그렌 퍼넬 트랩(Lindgren funnel trap)을 활용하여 4가지 유인제(Ipsenol, Ipsedienol, Alpha-pinene, Monochamol) 조건별 나무좀류와 하늘소류의 유인효과와 시기별 발생 양상을 조사하였다. 연구 결과, 나무좀아과는 총 26속 45종 7,743개체, 하늘소과는 총 35속 42종 649개체를 확인하였다. 본 발표에서는 남북 접경지에서의 시기별, 지역별 나무좀류와 하늘소류 발생 양상과 4가지 유인제별 효과에 대한 결과를 보고한다.

Key words: Scolytinae, Cerambycidae, wood-boring insect pests, Korean Peninsula

P30

Insect fauna of Gotjawal Provincial Park and Seonheulgot Dongbaek-Dongsan in Jeju, Korea

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본 조사는 2023년 국가생물다양성 기관연합 공동조사의 일환으로 제주도 곶자왈도립공원 및 선흘곶 동백동산 일대의 곤충류 분포현황을 파악하고, 자연자원의 발굴 및 관리에 대한 기초자료를 확보하고자 수행되었다. 곤충류 현지조사는 주요 곤충류가 출현하는 시기인 2023년 5월 22~26일 및 8월 28일~9월 1일 총 2회에 걸쳐 채집조사가 수행되었다. 조사방법으로는 조사지 주변에 깔때기 트랩을 설치하여 조사 마지막날 수거하였으며, 주간에는 포충망을 이용하여 채어잡기, 쓸어잡기, 털어잡기, 직접찾기 및 사진촬영 등을 수행하였다. 야간에는 조사시 식생이 양호한 지역을 선정하여 일몰 전에 유아등을 설치한 후 자정 이전까지 야간조사도 병행하였다. 현지조사를 통하여 채집된 곤충은 연구실로 가져온 후 건조표본 및 액침표본으로 제작되었으며, 각 분류군별 도감을 참고하여 종 수준까지 분류 및 동정 작업을 수행하였다. 조사결과 총 10목 69과 264종의 곤충류가 조사되어 비교적 다양한 분류군이 출현하는 것으로 확인되었다. 또한 금번조사 결과 멸종위기야생생물 II급에 해당되는 애기뿔소똥구리 1종이 확인되었으며, 국외반출 승인대상종 46종, 유용곤충 17종, 분포특이종 12종, 해충 9종, 고유종 5종 등을 포함하여 총 70종의 특정종이 확인되었다.

검색어: 제주도, 곶자왈도립공원, 선흘곶 동백동산, 곤충상

P31

Assessing the effectiveness of combined application of *Beauveria bassiana* (Balsamo) Vuillemin AAD16 and azadirachtin against *Plodia interpunctella* Hubner larvae in laboratory

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Indian meal moth, *Plodia interpunctella* (Lepidoptera: Pyralidae), is a serious pest of stored products. We assessed the efficacy of combined application of *Beauveria bassiana* AAD16 and azadirachtin against *P. interpunctella* under laboratory conditions by using filter paper dipping method. *P. interpunctella* larvae showed lowest LT_{50} in combined application of AAD16 and azadirachtin compared to the application of only azadirachtin. The mycosis rate of *P. interpunctella* larvae was 100% after 14 days of the combined application while AAD16 only application showed 93%. These findings suggest that *B. bassiana* AAD16 and azadirachtin combined solution can be an effective controlling technique against *P. interpunctella* larvae.

Key words: *Beauveria bassiana* AAD16, Azadirachtin, Mortality, Mycosis rate.

P32

Confirmation of the mycological characteristics and insecticidal activity of *Metarhizium pemphigi*

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Aphids are well-known insect pests that, due to their feeding habits, affect various crops' productivity and marketability. Additionally, they cause significant damage worldwide as vectors of viruses. Chemical pesticides are widely used to control these agricultural pests. However, due to resistance to various chemical pesticides, pest control is becoming difficult in agricultural environments. Entomopathogenic fungi such as the genus *Metarhizium* and *Beauveria* are being extensively researched as alternatives to these chemical pesticides. In this study, the mycological properties of isolated from soil *Metarhizium pemphigi* IPBL-H and the insecticidal activity of this strain against *Myzus persicae* and *Aphis gossypii* were evaluated for potential of development as a biopesticide.

Key words: Aphid, Entomopathogenic fungi , *Metarhizium pemphigi*

P33

A comparison of biological characteristics between *Metarhizium anisopliae* strains

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Entomopathogenic fungi have been studied to control insect pests as an alternative to chemical insecticides. However, all fungi haven't a high virulence against pests. In this study, we compared the biological characteristics of *Metarhizium anisopliae* strains. First, we selected four *M. anisopliae* strains and compared the thermotolerance, conidial productivity, and virulence. For the thermotolerance test, conidial suspensions were exposed to 0, 30, 60, and 90 min at 45 °C. As a result, the conidial germination rates were over 95% when exposed for 0 min but, were 64, 37.7, 6, and 3% when exposed for 30 min at 45°C, respectively. To compare conidial productivity, 200g of millet were used and inoculated with a conidial suspension of 1 ml (1×107 conidia/ml). Conidial productivity was investigated after 14 days. As a result of conducting a virulence test against mealworms using a spray method, differences in virulence between strains were confirmed.

Key words: conidial productivity, *Metarhizium anisopliae* strains, themotolerance, virulence

P34

Investigating the interaction between mosquitoes and fungi through transcriptome analysis

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Entomopathogenic fungi serve as eco-friendly alternatives to chemical pesticides. In this study, we investigate the interactions between mosquitoes and *Metarhizium anisopliae* JEF-157, which showed high insecticidal activity against mosquitoes, by RNA-seq analysis. RNA from mosquitoes was extracted at the median lethal time to identify changes in gene expression. The results showed 580 genes were up-regulated, while 336 genes were down-regulated in fungal treated mosquitoes. Up-regulated genes were related to metabolic and cellular processes such as cytochrome P450, DNA replication, and apoptosis. Down-regulated genes were involved in metabolism pathways such as lysosome, starch and sucrose metabolism, and fatty acid biosynthesis. These results are crucial for elucidating the mechanisms of fungal invasion and interaction in insects, providing insights for future pest management strategies.

Key words: mechanism, *Metarhizium anisopliae*, mosquitoes, transcriptome analysis

P35

Spatial repellent and oviposition deterring activities of series compounds from ester-containing natural products against *Tetranychus urticae* Koch (Acari: Tetranychidae)

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The two-spotted spider mite, *Tetranychus urticae* Koch, is one of the economically important agricultural pests globally, as it attacks a wide range of vegetable and horticultural crops. In this study, we evaluated spatial repellent and oviposition deterrent activities of *T.urticae* in response to fifteen compounds derived from ester-containing natural products. To evaluate the tests, we used bridge two-choice test and host two-choice test in laboratory conditions. Among the eight compounds showed spatial repellent and oviposition deterrent activities against *T. urticae* at the 20 mg dose and some compounds had the activities at lower dose. We also conducted two-choice test with a blend and single compounds to determine which showed stronger spatial repellent and oviposition deterrent activities. In host two-choice test, we evaluate repellence between distance of compounds. This study concluded that series compounds from ester-containing natural products have the potential to be used managing *T. urticae* in the field.

Key words: two-spotted spider mite, two-choice test, blend, host choice

P36

Development and assessment of microencapsulation-based formulation of Autographa californica multiple nucleopolyhedrovirus

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Spodoptera exigua is one of the worldwide distributed agricultural pest insects and has been known to show high resistance to conventional chemical insecticides. *Autographa california* multiple nucleopolyhedrovirus (AcMNPV) has been used as eco-friendly biological control agent for *S. exigu*a, as it exhibits high level of host specificity, stability and safety. In this study, for formulation of AcMNPV, the optimal conditions for mass-production of AcMNPV polyhedra was established using *S. exigua* larvae. Mass-produced AcMNPV polyhedra was formulated as wettable powder using microencapsulation method and its control efficacy against *S. exigua* was evaluated both in laboratory and semi-field experiment. Chinese cabbage treated with the AcMNPV formulation showed significantly reduced damage rates, suggesting that the AcMNPV formulation in this study could be useful for control of *S. exigua*

Key words: *Spodoptera exigua*, AcMNPV, mass-production, formulation

P37

Mass-production and Formulation of *Bacillus thuringiensis* IMBL-B9 Strain

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Bacillus thuringiensis (Bt) is widely used as an environmentally friendly insecticide compared to chemical insecticides. However, challenges such as difficulty in direct practical application, limited efficacy duration, and stability have been identified. To solve these issues, formulation-based research is being extensively conducted. In this study, the high insecticidal activity strain Bt IMBL-B9, identified in previous research, was subjected to large-scale cultivation using a fermentor. Subsequently, various formulations were developed through formulation processes. and characteristics such as their wettability, suspensibility and particle size were assessed to select the optimized formulation.

Key words: *Bacillus thuringiensis*, biopesticide, formulation

P38

Investigation of the insect pests and natural enemies of *Cnidium officinale* Makino in Korea

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천궁(*Cnidium officinale* Makino, COM)은 산형과(Umbelliferae)에 속하는 산림약용자원 중 하나로 뿌리나 지하부를 건조한 후 약용으로 사용하는 여러해살이 산림약초 중 하나이다. 천궁(COM)은 고혈압, 진통 및 진정 등에 효과가 있다고 알려져 있어, 산림약용자원으로서 재배되는 품목 중 하나이지만 해충의 피해가 심각하여 방제에 어려움이 많이 있다. 천궁은 뿌리가 약재로 사용되지만 종근에 피해를 가하는 응애류 및 파리류 해충은 지하부에 활동하는 생태특성을 가지고 있어 피해초기에 발견하기 어려울 뿐만 아니라 방제가 어려운 실정이다. 천궁(COM)은 연작이 되지 않은 작물 중에 하나이므로 재배포장을 매년 바꿔가면서 재배되고 있는 실정이다. 수확시기는 가을이므로 재배하는 동안에는 정확한 병해충조사가 쉽지 않을 뿐만 아니라 정확한 발생시기 및 피해정도를 확인하는 것이 어려운 실정이다. 본 연구의 목적은 천궁의 해충 및 천적곤충에 대해 조사하여 천궁의 해충종류 및 발생에 대해 이해하고 이를 기반으로 친환경 방제를 위한 천적류의 정보수집 및 분석 등을 위한 기초자료로 제공하고자 한다.

검색어: 천궁, 해충, 천적, 예찰, 생물적방제

P39

Report on Mosquito Monitoring Results through a smart high-altitude insect net

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모기류는 흡혈을 통해 원충, 바이러스, 사상충 등 다양한 병원체를 보유하며 말라리아, 일본뇌염, 웨스트나일열, 뎅기열 등을 사람에게 매개하는 위해성이 있는 위생해충이다. 이번 연구에서는 해외유입 모기류 감시를 위해 경남 고성지역에 설치한 스마트 고공포집기를 이용하여 2022년부터 2023년까지 모기류들을 모니터링하였다. 조사기간 동안, 총 3속 5종 43개체가 채집되었으며, 이중 삼일열 말라리아를 매개하는 *Anopheles belenrae*를 경남지역에서 처음으로 발생함을 확인하였다. 본 연구는 해외유입 모기류에 대한 감시망 구축의 최초 시도로서, 고공포집기를 활용하여 모기류 감시가 가능함을 확인하였다.

검색어: 모기류, 위생해충, 스마트 고공포집기, 해외유입, 모니터링

P40

Exploring host-parasite interactions between human and the body louse via miRNA

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Parasites have co-evolved with their host for a long period of time, resulting in unique parasitic systems tailored to each host species. This makes them suitable for research on physiological function control through cross-species molecules like miRNA. The body louse, a vector of bacterial pathogens, is particularly valuable as a model insect due to their frequent feeding on human blood, which results in the continuous ingestion of human-derived miRNA and injection of salivary gland-derived miRNA into the human body. In this study, we conducted miRNA sequencing on body lice with mixed stages and identified 105 miRNAs, including 50 novel miRNAs. Sequence analysis of human miRNAs remaining in body lice and the functional analysis of these miRNAs are in progress.

Key words: body louse, miRNA, cross-species interactions, parasite

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P41

Development of Molecular Diagnostic Protocols for Simultaneous Identification between Common Bed Bugs and Tropical Bed Bugs

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The recent increase in the occurrence of common bed bug and tropical bed bug in shared areas highlights the need for rapid species identification at infestation sites, which is crucial for implementing targeted control measures due to differences in genetic and physiological traits. In this study, molecular diagnostic methods were developed using species-specific *ITS2* sequences. Both multiplex PCR and loop-mediated isothermal amplification (LAMP) protocols with a DNA release method successfully distinguished between the two bed bug species regardless of developmental stages in 0.5~2.5 hours, even with dead specimens. Especially, LAMP's simplicity and speed make it applicable for rapid and accurate bed bug diagnosis at infestation sites.

Key words: Bed bug, multiplex PCR, LAMP, molecular diagnosis, on-site diagnosis

P42

Genome Analysis of *Anopheles kleini* and *Anopheles pullus*, Vectors of Vivax Malaria in South Korea

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This study focused on the genomic analysis of *Anopheles kleini* and *Anopheles pullus*, both vectors of vivax malaria within the *Anopheles* Hyrcanus group. Using Illumina NovaSeq600 and Oxford Nanopore platforms, we identified 126 and 116 contigs, along with 40,420 and 32,749 genes from *An. kleini* and *An. pullus*, respectively. The assembled genome sizes were 282 Mb for *An. kleini* and 247 Mb for *An. pullus*, which are within a similar range to the sizes previously estimated by digital PCR (249 Mb and 226 Mb). We are currently also estimating the genome sizes of other *Anopheles* spp. and manually curating key genes determining vectorial capacity.

Key words: *Anopheles* Hyrcanus group, Genome analysis, Genome size estimation, digital PCR, vectorial capacity

P43

Development of a Point-of-Care Testing (POCT) Kit for Scabies Diagnosis

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Scabies, caused by an infestation of the skin with the itch mite (*Sarcoptes scabiei*), is highly contagious and classified as a prevalent neglected tropical diseases. The current diagnostic approach relies solely on clinical judgment based on symptoms, history, and microscopic observation by an experienced dermatologist. To enhance sensitivity and specificity, we developed an alternative method based on mite-derived DNA. Our method involves a quick DNA release from skin scraping samples and Loop-Mediated Isothermal Amplification (LAMP) targeting the scabies mite-specific DNA sequences, enabling diagnosis within 30 minutes. Importantly, no cross-reactivity was observed when the sample was contaminated by two house dust mite species, and false positives were barely detected. Currently, we are in the process of developing a Point-of-Care Testing (POCT) kit for a scabies survey targeting school-age children in Timor-Leste as a global health project.

Key words: Scabies, LAMP, POCT, Neglected Tropical Disease

P44

Negative effect of exposure to four pesticides on homing ability and expression of genes associated with 'learning and memory' in honey bee, *Apis mellifera*

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Honey bee plays an important role in pollinating plants. Recently, however, declines in honey bee populations have been reported in many countries, and pesticides have been pointed out as one of the factors contributing to honey bee loss. To determine the effects of pesticides on honey bee behavior, we investigated the homing ability of honey bee exposed to four pesticides (acetamiprid, imidacloprid, fenitrothion, and carbaryl). In addition, the changes in expression levels of genes associated with 'learning and memory' (*cGMP-dependent protein kinase foraging*, *Kruppel homolog 1*, *Adenlyate cyclase 3*, *Early growth response protein 1*, *Hormone receptor 38*) were examined after pesticide treatment in forager bee. The four pesticides tested in this study generally reduced the homing ability of foragers. In the examination of gene expression, learning and memory-related genes were induced by the exposure to acetamiprid, imidacloprid, and carbaryl, whereas fenitrothion decreased the expression of these genes in honey bee. Although further studies are needed, this suggests that pesticides may have negative effects on honey bee behavior and behavior-related gene expression.

Key words: Honey bee, Forager bee, Pesticide, Homing ability, Learning and memory

P45

Expression of genes associated with putative pathway for chemical tolerance in *Drosophila melanogaster*

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The habitat of *Drosophila melanogaster* is the environment of fruit decay/fermentation which emits high concentrations of chemicals. Our recent studies revealed that *D. melanogaster* has been evolutionarily adapted to its habitat through tolerance to chemicals and induction of antimicrobial peptides (AMPs) plays an important role for chemical tolerance. To determine the correlation between AMPs and the chemical tolerance pathway, we hypothesized that expression of AMPs is induced by tissue damages or ROS caused by chemical exposure and AMPs activate antioxidant enzymes, thereby inducing chemical tolerance in *D. melanogaster*. Therefore, in this study, we investigated the induction levels of genes associated with necrosis (*EGR* and *BSK*), apoptosis (*Dronc*, *Dcp1*, and *Drice*), antioxidant physiology (*SOD1*, *SOD2*, *CAT*, *Trxr1*, *GstD2*, and *GstD5*), and SAM metabolism (*Gnmt* and *Foxo*) in *D. melanogaster* exposed to three chemicals, 2-phenylethanol, ethanol, and acetic acid. As a result, above genes were induced in chemical-exposed fly, and this supports our hypothesis of chemical tolerance pathway in *D. melanogaster*.

Key words: *Drosophila*, environmental chemicals, tolerance, antimicribial peptide, pathway analysis

P46

Transcriptome profiling reveals differential gene expression of detoxification and mitochondrial-related enzymes in *Tribolium castaneum* responding to carbonyl sulfide

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A new fumigant, carbonyl sulfide (COS), has potential for use as a replacement for methyl bromide, yet its mechanism of toxicity to insects remains poorly understood. In this study, transcriptome analysis was performed on *Tribolium castaneum* malpighian tubules and fat bodies, which are known to play an essential role in energy storage and utilization in insect species. In total, upon exposure to COS, 3,034 and 2,973 genes were differentially expressed in the *T. castaneum* malpighian tubules and fat body, respectively. These differentially expressed genes comprise a significant number of detoxification-related genes, including 105 P450s, 18 glutathione S-transferases (GSTs), 82 ABC transporters, 25 UDP-glucosyltransferases and 42 carboxylesterases and mitochondrial–related genes, including 9 complex I genes, 2 complex II genes, 1 complex III gene, 9 complex IV genes, 8 complex V genes from both malpighian tubules and fat body tissues. Moreover, KEGG analysis demonstrated that the upregulated genes were enriched in xenobiotic metabolism by ABC transporters and drug metabolism by other enzymes. We also investigated the role of carbonic anhydrases (CAs) in toxicity of COS using dsRNA treatment in *T. castaneum*. These results show that CA genes have a key role in toxicity of the COS. Furthermore, the results of transcriptomic analysis provide new insights into the insecticidal mechanism of COS fumigation against *T. castaneum* and eventually contribute to the management of this important stored grain pests.

Key words: red flour beetle, carbonyl sulfide, mode of action, carbonic anhydrase

P47

A chromosome-scale and annotated reference genome assembly of *Plecia longiforceps* (Diptera: Bibionidae)

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Urbanization is a driving force of global biodiversity changes, and species that successfully adapt to city environments can become pests with the assistance of human factors. Here we present the first genomic data of *Plecia longiforceps*, an invasive pest exhibiting intensive outbreaks in the Seoul Metropolitan Area of Korea. HiFi and Pore-C sequencing data were used to construct a highly continuous genome assembly with a total size of 707 Mb and 8 major pseudochromosomes. Gene annotation using transcriptome data and *ab initio* predictions revealed significant numbers of genes related to detoxification and heat tolerance. Comparison to the *Bibio marci* genome showed high levels of synteny with some regions of chromosomal rearrangement. Our data will serve as an essential resource for population and functional genomic studies on dispersal and outbreaks of *P. longiforceps*, and facilitate research on eco-evolutionary processes of dipterans in urbanizing habitats.

Key words: invasive species, lovebug, march fly, Pore-C, urban pest

P48

MicroRNA expression profiling of *Spodoptera frugiperda* under Chlorantraniliprole, Indoxacarb and Thiamethoxam exposure

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The fall armyworm, *Spodoptera frugiperda*, has developed extremely high levels of resistance to chlorantraniliprole and other classes of insecticides in the field. As microRNAs (miRNAs) play important roles in various biological processes through gene regulation. we examined the miRNA profile of *S. frugiperda* in response to Chlorantraniliprole, Indoxacarb and Thiamethoxam. Transcriptome analysis showed significant changes in the abundance of some miRNAs after treatment of *S. frugiperda* larvae with LC_{20} concentrations of three insecticides. A total of 197 miRNAs were systematically identified from *S. frugiperda*, and 16, 9, 2 miRNAs were differentially expressed after treatments of three insecticides. Importantly, three miRNAs were significantly downregulated and three were upregulated by RT-qPCR after treatment the LC_{50} of three insecticides with *S. frugiperda* larvae. Microinjection of agomirs of these six miRNAs into *S. frugiperda* larvae resulted in significant changes in mortality rates when exposed to three insecticides. Additionally, we also screened potential target genes for some of differentially expressed miRNAs, which may play important roles in insecticide resistance development. These findings provide valuable insights into the molecular mechanisms of insecticide resistance and underscore the potential of miRNAs as targets for the development of novel pest control strategies in *S. frugiperda*.

Key words: *Spodoptera frugiperda*, miRNA, Chlorantraniliprole, Indoxacarb, Thiamethoxam

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Gryllus bimaculatus densovirus suppression using RNAi in two-spotted cricket (*Gryllus bimaculatus*)

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쌍별귀뚜라미는 국내에서 식용 및 파충류의 먹이로 사용되는 중요한 산업곤충으로 알려져있다. 2023년 국내 쌍별귀뚜라미 농가에서 쌍별귀뚜라미 덴소바이러스 감염이 확인되었으며 바이러스 억제제가 요구되는 실정이다. RNA 간섭(RNAi)은 dsRNA를 이용해 목적 유전자의 발현을 억제할 수 있는 작용기작을 가지며, 바이러스 특이적 시퀀스를 이용한다면 효과적으로 타겟 바이러스의 증식을 저해할 수 있다. 본 연구에서는 덴소바이러스에 감염된 귀뚜라미에 덴소바이러스 특이적 dsRNA를 제작하여 주입(injection)하고, 바이러스 발현 저해 효과를 관찰했다. 바이러스 감염 수준은 qPCR로 평가하였으며 dsRNA를 접종한 결과 체내 바이러스양이 감소함을 확인했다. 이 연구는 향후 RNAi를 이용한 쌍별귀뚜라미 덴소바이러스 억제제 개발에 도움이 될 것으로 기대된다.

검색어: RNAi, 쌍별귀뚜라미, 덴소바이러스, qPCR

P50

Evaluation of Next Generation Sequencing assembly software for the genome of Oryctes rhinoceros nudivirus

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차세대 염기서열 분석(Next Generation Sequencing, NGS)은 대량의 병렬 데이터 생산으로 유전체의 염기서열을 고속으로 분석하는 기술이며, 이 기술은 바이러스 유전체 분석에도 광범위하게 사용되고 있다. 하지만, 바이러스의 전장 유전체가 100kb를 넘을 경우, 동일한 raw data라도 분석 방법 및 소프트웨어 그리고 매개변수(parameter)에 따라 유전체의 크기와 구조가 다르게 결정된다. 따라서 유전체가 큰 바이러스 분석 시, 최적화된 NGS 분석 방법을 선택하는 것이 중요하다. 본 연구는 장수풍뎅이 누디바이러스(Oryctes rhinocerous nudivirus, 120kb) 유전체를 기반으로, 다양한 Assembly 소프트웨어(metaviralSPAdes, metaSPAdes, velvet, shovill, Geneious, megahit)를 사용하여, 최적화된 NGS 분석 방법을 고안하였다. Assembly 소프트웨어에 따라 바이러스 유전체 크기와 특징(Single Nucleotide Polymorphism, Insertion&Deletion, repetitive genomic variants)의 차이를 확인하였다. Assembly 소프트웨어 간의 차이가 있는 염기서열은 Sanger sequencing을 통해 재확인하여, 참조 유전체(reference sequence)를 구축하였다. 이 참조 유전체를 기반으로 가장 정확한 Assembly 소프트웨어와 parameter를 평가하였다. 본 연구는 분석 방법에 따라 달라지는 유전체의 특성을 이해하고, 바이러스 유전체를 정확하게 구축하는 분석 파이프라인을 제공할 것으로 기대된다.

Key words: Next-generation sequencing, Nudivirus, Genome, Bioinformatics

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Prevalence of virus in the Ascomycota and Zygomycota fungus in Korea

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마이코바이러스는 곰팡이를 감염시키는 바이러스로 자낭균류, 담자균류 및 난균류에서 주로 발견되며 일부의 경우 곰팡이의 표현형에 영향을 끼치는 것으로 알려져 있다. 이번 연구에서는 대한민국 토양 샘플에서 분리된 65개의 자낭균류 및 접합균류 균주의 전체 핵산을 추출하고, 전기영동을 통해 바이러스 특이적 밴드를 스크리닝하였다. 스크리닝 결과 65개의 균주 중에서 *Tolypocladium* spp. 균주 2개와 *Marquandomyces marquandii* 균주 1개에서 바이러스 특이적 밴드를 발견하였다. 그 후, Cellulose Chromatography를 이용하여 double-stranded RNA를 분리하고 DNase I 및 S1 Nuclease 처리를 통해 DNA와 single-stranded RNA를 제거하여, *Tolypocladium* sp. 균주 1개와 *Marquandomyces marquandii* 균주에서 발견한 특이적 밴드가 dsRNA임을 확인하였다. 추후 virus-free isogenic line을 확보하여 virus 유무에 따른 표현형 변화를 확인하고, 마이코바이러스와 곰팡이 간의 상호작용에 관해 연구할 계획이다.

검색어: 마이코바이러스, dsRNA, *Tolypocladium* spp., *Marquandomyces marquandii*

P52

Molecular characterization of virus in the entomopathogenic fungus *Metarhizium pinghaense*

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Mycoviruses are a group of viruses that infect filamentous fungi. While most hosts infected with mycoviruses do not show any symptoms. In some cases, mycoviruses induce various phenotypic changes include alterations in morphology, drug resistance, pathogenicity, virulence, sporulation, and growth. Entomopathogenic fungi are one of the integrated pest management agents as an alternative to conventional insecticides. Mycoviruses have the potential as supportive agents, enhancing the efficiency of the insecticidal activity of the fungi. Studies about mycoviruses themselves and their interaction with their hosts, especially entomopathogenic fungi, are needed to realize their full potential. In this work, the sequence of the dsRNA element isolated from the entomopathogenic fungus *Metarhizium pinghaense* 4-2 strain was determined. Through this study, we report the sequence of a dsRNA virus isolated from the *Metarhizium pinghaense* for the first time. In further studies, the ORF of the mycovirus that induces a phenotype change in the host will be researched.

Key words: RLM-RACE,

P53

Differences in immune response between *Aphis gossypii* adults and nymphs against entomopathogenic fungal infection

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Aphis gossypii is a representative pest that transmits plant viral diseases. It is difficult to control with chemical pesticides alone due to their high pesticide resistance. Entomopathogenic fungi are biological control agents that can replace chemical pesticides and have characteristics of high host specificity and safety to humans. Therefore, we investigated the immune pathways of aphids against initial infection by entomopathogenic fungus. We treated aphids with the *Beauveria bassiana* JEF 544 strain and examined the immune response in early infection by qPCR. furthermore, we also studied changes the molting time of nymphs and changes in adult nymphal production caused by entomopathogenic fungi.

Key words: *Aphis gossypii*, entomopathogenic fungi

P54

Profiling of destruxins, the toxin from entomopathogenic fungi *Metarhizium* against *Aphis gossypii*

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*Metarhizium*은 대표적인 곤충병원성 진균 중 하나로, 종에 따라 매우 다양한 곤충에게 병원성을 일으키는 폭 넓은 기주범위를 형성한다. 이들이 주로 생성하는 것으로 알려진 destruxins (DTXs)이라는 2차 대사산물은 살충 활성 뿐만 아니라 항바이러스, 항증식, 항암 등 다양한 분야에서 효능이 연구되고 있어, 해당 물질에 대한 관심이 집중되고 있다. 살충 물질로서의 DTXs는 여러 곤충에 있어 병원성을 나타내는 것이 확인되었으나, 해충으로서 전 세계적으로 심각한 경제적 피해를 일으킴과 동시에, 화학 살충제 저항성 문제가 야기되고 있는 목화진딧물에 대해서는 아직 DTXs의 역할이 연구되지 않고 있는 실정이다. 본 연구에서는 목화진딧물에 대해 곤충병원성 진균 *Metarhizium* spp.의 병원성 발현에 DTXs가 미치는 역할을 간접적으로 확인하기 위해, qPCR을 활용하여 진균 처리 후 목화진딧물 사망 시간과 관련하여 충체 내 DTX 합성효소의 발현을 비교 분석하였다.

검색어: *Metarhizium*, Destruxin, *Aphis gossypii*, qPCR

P55

Construction of optimal expression forms for efficient production of hand, foot, and mouth disease virus like particles

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Hand, foot, and mouth disease (HFMD) is a highly contagious disease with no specific treatment. Since it is common in immunocompromised children under the age of 5, there is a need to develop a safe vaccine. Virus-like particles (VLPs) are similar structures to viruses with the lack of genetic material which makes them impossible to replicate and infect, and therefore have a high level of biological safety and are considered to have high value as vaccines. In this study, the insect virus expression system that is widely used for vaccine and drug production due to its high post-translational modification efficiency, was used to produce VLPs for Coxsackievirus type A6 and A10, which are recently reported to be the main causes of HFMD. For this purpose, the selection of promoters that can control the timing and intensity of expression of 3CD protein, which is essential for VLPs assembly but has been reported to be cytotoxic, was conducted to construct an optimal expression form for HFMD-VLP.

Key words: Hand, foot, and mouth disease, Virus-like particles, Insect virus expression system

P56

Increasing the efficiency of target protein production by regulating VLF-1 in insect cell expression system

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The baculovirus expression system (BES) utilize the *p10* or *polyhedrin* promoter, a very late promoter that exhibits strong transcriptional activity primarily at the end of viral infection, to produce useful recombinant proteins. The burst sequence of the very late promoter is essential for strong transcription, and VLF-1 is a transcription factor that binds specifically to the burst sequence, and it has been reported that it can regulate the amount and timing of expression of protein by the very late promoter. Recently, a VLF-1 constitutively expressing cell line was constructed to increase the production of the target protein, but the effect was minimal. In this study, to find the optimal VLF-1 expression conditions to increase target protein production efficiency, we controlled the expression of VLF-1 through various promoters and evaluated the target protein expression efficiency by the *p10* promoter accordingly.

Key words: BES, VLF-1, *p10* promoter, burst sequence

P57

Biological potential of Bacteria 'Ch-1' isolated from Chinese Tiger Beetle (*Cicindela chinensis*) against Fungi and Antibiotics

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우리는 길앞잡이(*Cicindela chinensis*)의 장에서 다양한 공생 미생물들을 분리하였다. 그중 다양한 곰팡이 성장을 억제하는 세균을 동정하였고 "Ch-1"이라 명명하였다. 우리는 Ch-1 균주를 사용하여 10종의 식물 병원성 곰팡이와 2종 곤충 병원성 곰팡이의 생장 억제를 확인하였다. 또한 8종의 항생제에 대한 저항성을 확인하였다. 동시에, 본 균주의 genomic sequence를 수행하였고 유전적, 생화학적, 생리적 특성을 조사하였다. Ch-1균주는 특허등록과 친환경 미생물제제로 등록하였고 향후 생물학적 방제제로써 활용될 수 있을 것으로 판단한다.

검색어: 길앞잡이, 장내 미생물, 길항작용, 항생제, 생물학적 방제

P58

Biochemical characterization and IAA activation test of potential plant growth promoting bacteria *Enterobacter roggenkampii* isolated from *Monochamus alternatus* gut

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우리는 솔수염하늘소(*Monochamus alternatus*) 장에 존재하는 공생미생물들을 분리하였다. 그중 다양한 식물들을 대상으로 성장 촉진 효과가 보고된 세균을 단일배양 분리하였다. 이 세균은 16S rRNA sequencing을 통하여 *Enterobacter roggenkampii*로 동정되었다. 우리는 분리된 *E. roggenkampii*에 대하여 genomic sequencing을 수행하였고 유전학적 특성을 확인하였다. 우리는 *E. roggenkampii*가 식물의 성장을 촉진할 수 있는 다양한 유전자들을 가지고 있는 것을 확인하였고 그 중 IAA-Asp hydrolase 유전자를 가지고 있음을 알 수 있었다. 동시에, 분리된 *E. roggenkampii*와 같은 속의 세균을 대상으로 다양한 API kit와 기질 첨가 배지를 이용하여 생화학적 특성을 비교하였다. 향후 IAA-Asp 가수분해효소를 생산하는 잠재적인 식물 생장 촉진 비료 미생물로 등록하여 다양한 작물을 대상으로 생장 촉진 효과를 확인할 것이다.

검색어: 곤충 장내 미생물, 생화학, 식물 생장 촉진

P59

Taxonomic review of the genus *Nycteola* Hübner (Lepidoptera, Nolidae) in Korea

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Here we review the genus *Nycteola* of the Nolidae (Lepidoptera). As the result of this study, we recognized already synonymized species *N. costalis* Sugi, 1959 of *N. coreana* (Leech, 1900) and newly recorded species *N. dufayi* Sugi, 1982. Whlie the number of Korean *Nycteola* species remain unchanged, the composition has been changed.

Key words: endemic species, Japan, hostplant, synonym, Palearctic region

P60

First report of the western drywood termite *Incisitermes minor* (Hagen, 1858), a new invasive alien species in South Korea

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서부마른나무흰개미(신칭)는(*Incisitermes minor*) 미국 서부와 멕시코 북부를 포함하여 북미 서부가 원산인 종이며 주택을 포함한 목조 구조물에 치명적인 해충이다. 국내에선 2023년 9월 외래생물신고센터를 통해 경남 창원시 진해구의 한 가정집에서 흰개미 유시충이 발견되었다는 민원 신고로 처음 확인되었다. 그 이후 주변 지역 조사 결과 민원인 주택 주변에서 군집비행하는 흰개미 유시충 및 목재 피해 흔적을 통해 군체를 발견 확인하였다. 또한, 최초발견지에서 약 1km 떨어진 한 아파트 단지의 정자 및 그 일대에서 추가 군체가 확인되었다. 본 연구에서는 채집된 흰개미의 형태와 유전자 정보를 통해 대상종을 확인하였고, 발견 및 피해 상황 정보를 통해 향후 해당 종의 관리를 위한 기초자료를 제공하고자 한다.

검색어: 서부마른나무흰개미, *Incisitermes minor*, 외래생물

P61

A report of two provisional micro-lepidopteran pests from Jeju island

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Jeju Island has been facing to threat of high-risk invasive pests from tropical areas. To protect domestic agriculture from those invasive pests, APQA has conducted a regular monitoring program on Jeju Island. We collected especially phototactic heteroceran pests by light bucket trap and identified them using their superficial appearances, and also mitochondria COI gene. As a result, a total of 24 families, 136 genera, 193 species, and 819 individuals were collected from around Jeju Island in 2023. Among them, two unidentified epidopteran pests, *Palpita* sp. (Crambidae) and *Xyrosaris* sp. (Yponomeutidae) were collected.

In the present study, we report two unidentified micro-lepidopteran pests using superficial characteristics and mitochondria COI gene.

Key words: COI, jeju, micro-lepidoptera, plant quarantine

P62

Two species of the genus *Grapholita* (Lepidoptera: Tortricidae) new to Korea

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The genus *Grapholita*, belonging to the tribe Grapholitini under the family Tortricidae, which is small to medium-sized moths ranging from 7mm to 16mm. It is a relatively diverse group in Grapholitini, comprising more than 150 species worldwide. This group is generally distributed throughout the world, with the majority of its species occurring in the Holarctic region. Some species in the genus *Grapholita* are known worldwide as serious pests that feed on leaves, roots, fruits and other plant parts. In Korea, the genus is known to have 8 described species up to date.

In this study, we report two newly recorded species of the genus *Grapholita* from Korea, including a brief description and illustrations of adult and genitalia. Additionally, all available information including distribution, host plants and a taxonomic key to Korean *Grapholita* species is provided.

Key words: Lepidoptera, Tortricidae, Olethreutinae, Grapholitini, *Grapholita*, new record, taxonomy, pest

P63

First records of *Acerocnema* Becker, 1894 (Diptera: Scathophagidae) from South Korea

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This study reports the first Korean records of the genus *Acerocnema* Becker, 1894, with one new species, *Acerocnema saurischia* sp. nov., and one newly recorded species, *A. flavifrons.* A key to the Korean Scathophagidae is provided with morphological diagnosis and images of habitus and male genitalia structures. To assist in species identification, mitochondrial cytochrome c oxidase subunit I (COI) gene sequences were obtained from all specimens to conduct DNA barcoding.

Key words: *Acerocnema*, new species, Scathophagidae, COI barcoding, South Korea

P64

A new species of *Pararhabdepyris* Gorbatovsky (Hymenoptera, Bethylidae) from the Korean Peninsula with an updated key to the world species

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Pararhabdepyris Gorbatovsky, 1995, is a small genus in Bethylidae (Hymenoptera, Chrysidoidea), currently comprising only six valid species worldwide. A new species is described and illustrated from South Korea. *Pararhabdepyris* sp. nov., which appears closely related to *P. paradoxus*, is characterized by the combination of the following characters: the basal two-thirds of the scape are dark castaneous, coxa and femora are dark castaneous, the median and submedian metapectal-propodeal disc is rugulose, and the transverse posterior carina is straight. Images of diagnostic characteristics and an updated key to the seven world species of the genus are presented.

Key words: Classification, flat wasp, Old World, Palaearctic region, Scleroderminae

P65

Three newly recorded species of the genus *Argyresthia* Hübner (Lepidoptera: Argyresthiidae) from Korea

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The genus *Argyresthia* Hübner, [1825] of the family Argyresthiidae is known to comprise over 150 species worldwide. Among them, more than 70 species are recognized in the Palearctic region. The Korean fauna of the genus *Argyresthia* includes 11 described species to date.

In this study, we report three species of the genus *Argyresthia* for the first time in Korea: *A. brockeella* (Hübner, [1813]), *A. longalbella* Liu, Wang & Li, 2017, and *A. mala* Liu, Wang & Li, 2017. All available information, images of adults and genitalia for species are provided.

Key words: Lepidoptera, Yponomeutoidea, Argyresthiidae, *Argyresthia*, new record, Korea

P66

Complete mitochondrial genome of the clearwing moth, *Synanthedon bicingulata* (Lepidoptera: Cossoidea: Sesiidae)

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The clearwing moth, *Synanthedon bicingulata* (Staudinger, 1887), is a pest that infests various species of cherry trees. However, genetic information regarding the genus *Synanthedon* including *S. bicingulata*, is limited. In this study, we sequenced a complete mitochondrial genome (mitogenome) of the species. The 16,255 bp of *S. bicingulata* mitogenome differs from the typical gene arrangement formed in Lepidoptera: *trnQ*-*trnS*$_2$-*trnM*-*trnI* arrangement between the A+T-rich region and the *ND2* junction. Moreover, the genome has untranslated repetitive sequences in the intergenic space between *lrRNA* and *trnV*, as well as the CGA start codon in *COI* and the TTG start codon in *ATP8*. Similar observations are noted in species belonging to the tribe Synanthedonini within the genus *Synanthedon*.

Key words: *Synanthedon bicingulata*, clearwing moth, mitochondrial genome, gene arrangement

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P67

Integrative species delimitation and mitochondrial heteroplasmy of the East Asian genus *Aphaenomurus* Yosii (Tomoceridae, Collembola)

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To assess the accuracy of species delimitation in the genus *Aphaenomurus* Yosii, we conducted a comparative micro-morphological study and molecular analysis using two mitochondrial (COI, 16S) and two nuclear genes (18S, 28S) on 118 specimens from 24 localities. The results showed that the morphological characters of *A. vicinus* and *A. interpositus*, as presented in the original description, were intermixed in phylogenetic lineages within the genus and did not form independent lineages. Furthermore, there were enough differences among *Aphaenomurus* individuals to be considered as morphologically distinct species (Th. III is 1+1 or 2+2, Abd. I is 2+2 or 3+3, Abd. II is 2+2 or 3+3), but they do not form an independent lineage. Molecular and morphological analyses have determined that *A. vicinus* and *A. interpositus* are the same species, exhibiting morphological variation in dental spines formula, claws, chaetotaxy, and other features. Additionally, the genus *Aphaenomurus* forms a monophyletic clade, which is further divided into several lineages within the genus. No morphological differences were observed to distinguish these lineages. This cladistic divergence is attributed to heteroplasmy, which is supported by previous studies that have suggested the possibility and problems of heteroplasmy in Collembola, and by the high genetic distances between individuals in the mitochondrial genes of *Aphaenomurus*.

Key words: *Aphaenomurus*, morphologcial variation, species delimitation, heteroplasmy

P68

Preliminary research on fruit fly (Diptera: Tephritidae) larvae

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우리는 식물검역 과정에서 검출되는 파리목 유충을 효과적으로 동정하기 위하여 대화형 검색표를 제작하고 있다. 파리목은 농업 분야와 식물검역 분야에서 매우 중요한 해충이며, 특히 과실파리과는 다양한 식물에 피해를 주는 대표적인 분류군이다. 과실파리과는 예전부터 형태, 생태, 분자, 분류, 모니터링, 방제 등 다양한 주제로 연구가 이루어져 왔으며, 현재까지 다양한 연구가 이루어지고 있다. 본 연구에서는 과실파리과를 연구하는데 중요한 기초자료로 활용될 수 있도록 1)과실파리과 유충의 형태학적 특징을 포함하여 2)과실파리과의 일반적인 특징과 3)생태학적 특징 등 관련 정보를 수집하고 분석하여 결과를 종합정리하였다.

검색어: 과실파리, 유충, 형태적 특징, 생태적 특징

P69

Investigation of insect diversity on the golf course using light traps

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The effective management of insect pests requires decisions based on monitoring information. In this study, we aimed to monitor insect species diversity and monthly occurrence patterns on the golf course using light traps. Sampling was conducted at Anyang Country Club, Korea, from May to October 2023. A total of 5,149 individuals were collected, with Lepidoptera and Coleoptera being the most abundant orders. Among them, there were six species (*Agrotis ipsilon*, *Blitopertha orientalis*, *Heptophylla picea*, *Maladera orientalis*, *Parapediasia teterrella*, and *Spodoptera depravata*) of insect pests that caused serious damage to the turfgrass. The results of this study could be used as data to establish efficient management strategies for turfgrass insect pests.

Key words: golf course, turfgrass insect pests, insect diversity, light trap

P70

Impacts of arsenate on the size and fecundity of *Myzus persicae* across generations

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Herbivorous insects can be exposed to soil contaminants via trophic transfer. To assess the effect of accumulated arsenate (As(V)) in host plants on aphids across generations, *Myzus persicae* were reared for several generations on pepper (*Capsicum annuum*) grown in soil treated with 0, 2, 4, and 6 mg of As(V) per kg. In the first generation, the body length of *M. persicae* significantly ($p < 0.05$) increased on As(V)-treated plants ($\mu = 1.29$ mm) compared to untreated plants ($\mu = 1.21$ mm). Aphids showed higher fecundity on plants treated with 2mg/kg of As(V) (15.3) compared to untreated ones (10.6), but it decreased again under the 4mg/kg (11.4) and 6mg/kg (11.2) treatments. When newborns were transferred to untreated plants after being reared on each treatment for two previous generations, they exhibited higher fecundity as their parents were treated with higher levels of As(V). While more research is needed to understand the unexpected beneficial effects, this study highlights the complex impacts of soil As(V) on aphid dynamics which span multiple generations.

Key words: green peach aphid, heavy metal, trophic transfer, ecotoxicology

P71

Computational behavior applied to spatio-temporal movement of individuals and groups in insects

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Group movements of insects are bases for unravelling origin of social behavior of animals and are important in both theoretical (e.g., evolution) and practical (monitoriing) aspects. Automatic recognition and effective computational methods were developed for characterizing multi-individual interactions in laboratory conditions. Movements of *Drosophila* species in different genetic strains were continuously observed across days. Characteristic behaviors are objectively expressed based on parameter extraction and data structure visualization. Group activities, including aggregation, inter-individual interactions and arena positioning were objectively characterized in different photo- and scoto-phases according to machine-learning and spatio-termporal patterning techniques. Individual-group relationships are presented regarding how individual movements would contribute to formulating group activities. Usefulness of automatic monitoring of insect group movement is further discussed for a basis for genetic functioning in behavioral aspect.

Key words: Drosophila, automatic movement detection, Geo-SOM, crowding, computational behavior

P72

Field monitoring and genetic diversity of the large copper butterfly *Lycaena dispar* (Lepidoptera: Lycaenidae), a near-threatened species in South Korea

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The large copper butterfly *Lycaena dispar* (Haworth, 1803; Lepidoptera: Lycaenidae) has been categorized as a near-threatened species (NT) in South Korea from 2012 mainly due to limited distribution. In this study, we visited 36 sites spread across all South Korean provinces to verify the distributional range of the species and sequenced mitochondrial COI for 53 individuals from nine sites. We observed *L. dispar* at 15 sites in six provinces, including the two previously known provinces, indicating a southward range expansion. The in-field monitoring and genetic data collectively suggested that *L. dispar* does not have a limited distribution nor is it isolated, indicating that it should be reclassified as less vulnerable. Our study demonstrates that the combination of field and genetic data can provide a more reliable assessment of the stability of a species.

Key words: *Lycaena dispar*, near-threatened species, range expansion, genetic diversity, field monitoring

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P73

Characteristics Investigation of *Apis cerana* RX Genotype in JEONBUK STATE

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본 연구는 우수한 꿀벌 신품종 육성을 위해 국립농업과학원에서 육성된 재래꿀벌 RX계통을 분양받아 ’23~’24년까지 부안군 변산면에 위치한 전북농업기술원 잠사곤충시험장 양봉사에서 꿀벌세력, 수밀력, 질병저항성, 온순성, 질병발생, 월동능력을 한라벌 품종과 비교하여 조사하였다. 8~11월 RX계통의 꿀벌세력 감소는 3.9%로 한라벌 39.8% 대비 상대적으로 낮았고, 수밀력, 청소능력, 온순성은 유의적 차이가 없었다. 낭충봉아부패병 등 질병은 전북동물위생시험소에서 병성검정한 결과, 두 시험군 모두 항원이 검출되었으나 임상증상은 없었다. 그리고 월동 중 한라벌 품종은 폐사한 반면, RX계통은 모든 시험군이 월동에 성공하였고, 또한 월동전·후 먹이감소량이 적어 월동능력이 우수한 것으로 판단하였다. 본 연구는 국립농업과학원 공동연구사업(PJ01504205)의 지원을 받아 수행하였다.

검색어: 꿀벌, 동양종꿀벌, 신품종, 재래꿀벌, 전북특별자치도, 지역적응시험

P74

Comparison of biomass of herbivores using macromoths in two forest characteristics

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대표적인 초식곤충인 나방은 기주식물 특이성을 갖고 있어 기주식물 분포에 따른 식생구조나 서식지 유형을 이해하는데 사용이 가능한 분류군이다. 나방은 종 다양성이 높고 분류학적으로 잘 알려져 있어 조사가 많이 이루어져 풍부한 데이터가 존재하여 이들의 공간적, 시간적 규모의 생물량 변화 추세를 확인할 수 있다. 본 연구에서는 공간적인 유형에 따라 나방의 생물량을 비교하고자 하였다. 생물량을 추정하기 위해 이용된 분류군은 자나방과, 밤나방과, 태극나방과로 이들 분류군의 앞날개 길이를 기준으로 종별로 계산을 하였다. 공간적인 유형은 숲의 위치(연속된 숲, 파편화된 숲)와 숲의 구성(침엽수림, 활엽수림, 혼효림)을 사용하였다. 그 결과 숲의 위치에 따라 생물량은 차이가 존재했지만($F = 16.76, P < 0.001$), 숲의 구성($F = 1.54, P = 0.22$)과 숲 위치와 구성의 상호작용은($F = 0.34, P = 0.71$) 생물량의 차이를 확인하지 못하였다. 숲 구성에 따라 차이가 나타날 것으로 예상하였지만 나타나지 않은 데에는 추후 분류군을 더 늘려 확인하는 것이 필요하다. 또한 식물 생물량 추정을 통한 곤충과 먹이자원의 가용 관계를 파악하는 연구도 필요할 것으로 예상한다.

검색어: 나방, 생물량, 초식, 공간수준, 상호작용

P75

Injury symptoms and diagnosis result caused by *Cuphodes diospyrosella* Issiki of Persimmon in Gyeongsangbuk-do Province

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2023년 경상북도 상주시 떫은감 과수원에서 잎 표피아래 굴을 파고 들어가면서 원형 또는 부정형의 식흔자국을 남기는 증상을 관찰하였다. 해충의 유충은 녹색에서 적색으로 변하며 번데기 단계를 거쳐 성충(길이 3㎜, 갈색)이 되어 탈출하였다. 본 해충에 대해 잎에서의 피해증상과 실험실에서 유전분석 결과 Genbank(GU816671,486bp DNA liner, 2016)에 등재되어 있는 감잎가는나방(*Cuphodes diospyrosella*)으로 동정되었다. 일본에서 1957년 최초 보고 후 우리나라에서는 주로 경남 창원과 진주의 농약 무살포 및 유기농 단감원에서 발생하였으나, 이번 경북지역에 처음 발견되어 떫은감 재배 농업인과 현장지도원의 감잎가는나방에 대한 피해증상 진단에 활용할 수 있을 것으로 생각된다.

검색어: 해충, 피해증상, 감잎가는나방, 감, 경북지역

P76

Ecological characteristics and control of three invasive termites (*C. domesticus, C. gestroi, I. minor*) and potential risk species in South Korea

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2023년에 국내에서 보고된 적이 없던 외래흰개미 3종이 각각 인천, 서울, 창원에서 발견되었다. 종 동정 결과, 인천에서 출현한 종(*Coptotermes gestroi*)은 Subterranean termite로 밝혀졌으며, 서울과 창원에서 출현한 종(*Cryptotermes domesticus, Incisitermes minor*)은 Drywood termite로 밝혀졌다. 본래 우리나라에는 Subterranean termite 흰개미가 2종이 분포하고 있다고 보고되어 있었으나, 새로운 과 또는 속의 외래흰개미가 발견되면서 국민들의 우려가 커지고 있다. 국내에서는 일부 외래흰개미를 법적으로 지정(유입주의 생물 2종, 관리병해충 15종)하여 관리하고 있는데, 해당 흰개미와 그 외의 신규 흰개미의 출현으로 인한 피해가 우려되는 상황이다. 본 연구에서는 '23년 유입된 3종 및 기존 법정관리 외래흰개미, 그리고 국내 유입과 위해가 우려되는 외래흰개미 5과(Archotermopsidae, Kalotermitidae, Rhinotermitidae, Termitidae, Termopsidae)를 조사하였으며, 이들의 생태적 특징과 외국의 사례를 통해 외래흰개미 대비 방법에 대하여 고찰하였다.

검색어: 외래생물, 외래흰개미, 유입주의 생물, 관리병해충

P77

Attraction test method for effective Codling moth (*Cydia pomonella*) pheromone trap

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코드린나방은 사과, 배, 복숭아 등 과실류를 비롯한 다양한 작물에 피해를 주는 해충으로써, 대한민국 식물방역법상 금지해충에 속해있다. 검역실적으로는 2016년 6월에 1건, 2018년 6월에 2건이 모두 인천공항으로 수입된 우즈베키스탄산 양벚에서 검출되었다. 코드린나방은 국내 침입이 매우 우려되는 해충 중의 한 종으로써 한국, 일본, 대만을 제외한 거의 모든 온대지역에 분포하고 있다. 따라서 우리나라는 본 해충에 대한 정밀하고 지속적인 표적 예찰이 필수 불가결이다. 효과적인 예찰을 위한 페로몬 트랩 개발을 위해 다음 사항들을 고려할 수 있다. 우선 페로몬 성분비에 따른 유인력의 차이를 검정해 효과적인 성분비를 찾는 것이 중요한데, 그 방법으로는 GC-MS/MS 분석법을 통해 루어의 페로몬 구성비율을 분석한다. 이후 적합한 실험환경을 설정하고 페로몬 혼합물을 적용한 여과지를 케이지에 달아 일정 시간 동안 여과지에 접촉한 횟수를 기록 후 통계분석을 통한 유의성 검정을 실시한다. 이어서 페로몬을 루어에 주입, 흡착시킨 후 페로몬 트랩을 현장에 설치해 포획된 수컷 성충 수를 조사해 효과적인 약량 및 루어형태 등을 선별하게 된다. 이를 통해 효과적인 코드린나방 트랩 개발을 위한 기초연구를 수행하고자 하며, 우리나라의 농업과 자연환경 보호에 기여하고자 한다.

검색어: 코드린나방, 유인제, 금지해충

P78

A comprehensive analysis of global measures implemented to control the spread of the Khapra beetle during quarantine

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In countries without strong biosecurity systems, Khapra beetle, *Trogoderma granarium* poses a continuing threat to agriculture. Even when quarantine laws exist, the risk is greater if one of the world's most serious pests becomes introduced to imported stored grain. The rate of Khapra beetles introduced is rising sharply with increased transport, trade, travel, and tourism between countries and continents. Species identification is usually the key to success in Khapra beetle control programs. Countries that export/import grains, such as Australia, Canada, Russia, Korea and USA, must ensure that their ports, grain storage facilities, and transportation systems are free of khapra beetle. Researchers so far developed effective quarantine treatments and eradication strategies to deal with khapra beetle infestations that occur upon import at inland port. Khapra beetle introductions are likely to be impacted by a variety of factors, including trade flow and quarantine laws. In this study, we provide an overview of the current global quarantine laws, invasions of khapra beetle, and its control strategies.

Key words: Quarantine pests, Genetic control, World economy, Stored products

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P79

Genetic techniques for controlling stored food products insects

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Numerous Dermestidae insects are considered significant pests because of their capacity to inflict substantial economic harm on stored food items. Trogoderma and Attagenus genera members are commonly discovered in imported grain and other food products. Usually, infestations of these species consist of various species that reproduce quickly and spread effortlessly. The small size of Attagenus and Trogoderma stored-product stages makes it extremely challenging to identify them based on their morphological characteristics. Hence, it is imperative to have precise identification techniques in place to ensure the safety and dependability of the grain industry, as well as to streamline efficient plant quarantine measures. Various molecular methods have been employed for insect species identification, such as restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD), single-strand conformation polymorphism (SSCP), DNA sequence analysis, and species-specific primer PCR (SS-PCR) techniques. Despite the considerable focus on quickly identifying these species in stored products in recent years, there is a notable absence of systematic molecular identification. This research highlights the use of genetic techniques to differentiate between Trogoderma and Attagenus species.

Key words: Quarantine pests, pest control, stored products

P80

Managing early invasion of alien species in Korea: a perspective from the differential grasshopper, *Melanoplus differentialis* (Orthoptera: Acrididae)

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Melanoplus differentialis (Thomas, 1865) is a widely distributed Orthopteran species in North America, including the United States and Mexico. Known for causing damage to various crops such as vegetables and grains throughout its lifecycle. In South Korea, it has been observed concentratedly in the vicinity of the Onsan National Industrial Park in Ulsan and was designated as "Ecosystem Disturbing Species" by Ministy of Environment in 2020. This study aims to present foundational data on pest management strategies for *Melanoplus differentialis* identified within the Onsan National Industrial Park. Through collaborative efforts between the National Institute of Ecology, related agencies, and tenant private companies from 2020 to 2023, we will demonstrate the reduction in habitat area as a result of proactive pest control measures.

Key words: Invasive alien species, *Melanoplus differentialis*, Alien species Management

P81

Survey of scrub typhus vectors at epidemic season in Honam region, Korea 2023

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A surveillance of chigger mites was performed to monitor the incidence of scrub typhus vectors at four environmental collection points in two locations (Sunchang and Haenam) in the Honam region of Korea from August to December 2023. During the surveillance period, 4,174 chigger mites were collected and the predominant species were *Leptotrombidium scutellare* (94.3%). The density of chigger mites had the peaked at 44 week (10.26~11.1), while the density of patients peaked at 45 week (11.2~11.8) respectively. A positive correlation (r=0.69) observed between scrub typhus patients and vectors. This result suggests that this vector surveillance method will be useful for alarm system of tsutsugamushi disease. However, the relationship between scrub typhus cases and chigger mite density will be studied through long-term periodic surveillance.

Key words: scrub typhus, chigger mites, *Leptotrombidium scutellare*, correlation, alarm system

P82

Reporting on molecular authentication and counterfeit distribution cases of animal-derived medicine 'O-gong,' the centipedes through DNA barcode analysis

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국내에서 유통되는 한약재 오공(蜈蚣)의 정·위품 유통 현황 파악과 유전자 감별법 개발을 위해 서로 다른 6개 유통사에서 오공으로 판매중인 전형약재를 구매하여 각 약재 포장 단위별 크기, 색깔, 무늬 등 형태적으로 차이가 있는 개체를 분류하여 국내에서 채집된 왕지네 표본 2개체를 포함 총 30개 시료를 대상으로 DNA 바코드 분석을 실시하였다. 확보한 미토콘드리아 COI 염기서열 정보와 기 등재된 NCBI GenBank 염기서열 정보를 이용하여 계통 분석을 실시한 결과, 28개 약재 시료 중 국산 및 중국산 전형약재 유통품 13 개체는 모두 대한민국약전외한약(생약)규격집에 정품 기원종으로 수재된 *Scolopendra subspinipes mutilans*로 확인되었으며, 이들은 국내 채집 왕지네 개체들과 함께 하나의 단계통군을 형성하였다. 하지만 인도네시아산 전형약재 유통품 15 개체의 경우 4개의 그룹으로 구분되었는데, 그 중 3개 그룹은 *S. dehaani*, *S. subspinipes*, 그리고 명확한 종을 알 수 없는 *Scolopendra* sp.로 *Scolopendra* 속으로 확인되었고 나머지 그룹을 형성하는 한 개체는 *Scolopendra* 속에 속하지 않고 *Rhysida singaporiensis*와 89%의 유사도를 보였다. COI 바코드 분석을 통해 국내 유통되는 오공은 원산지가 한국 또는 중국인 경우 모두 정품 기원종으로 확인되었으며, 원산지가 인도네시아인 경우에는 모두 위품인 것으로 확인되었다. 또한 위품으로 확인된 유통약재는 총 4개의 종으로 분류되었고, 대부분은 정품인 *Scolopendra*속의 분류군이었으며 *Rhysida*속과 가까운 분류군도 오공으로 수입되어 유통되고 있는 것으로 확인되었다.

검색어: 오공, *Scolopendra*, 유전자 감별, COI, DNA 바코드

P83

The effect of rapid cold hardening followed by low temperature treatment on the expression of glycerol kinase gene in fall armyworm, *Spodoptera frugiperda*

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겨울과 같은 환경에서 곤충은 생존과 번성을 위해 생리학적, 생화학적 및 행동적 메커니즘을 이용하고 있다. 대부분의 곤충은 생리학적 적응가운데 급속내한성(Rapid cold hardiness, RCH) 유기를 통해 기온이 급격히 낮아지는 외부 환경에 대해 빠르게 적응하고 저온조건에서 생존율을 높인다. 열대거세미나방의 경우 행동적 메커니즘을 통해 따뜻한 곳을 찾아 장거리 비행을 하며, 생존에 유리한 환경으로 이동한다. 본 연구에서는 열대거세미나방의 생리적 월동능력과 RCH 능력에 관해 조사하였다. 그 결과, RCH에 의해 혈중 글리세롤의 농도가 증가와 체내빙결점이 하강하는 것을 확인할 수 있었다. 또한, RCH(-10℃, 1h)에 노출된 2령 유충기를 대상으로 4령과 5령 유충기에 단기저온(5℃, 30min)에 노출 시 글리세롤 생합성에 관여하는 유전자(glycerol kinase 1, 2)의 발현이 RCH에 노출되지 않은 대조구와 비교하여 빠르게 발현되었다. 이는, 열대거세미나방의 유전자 수준에서 저온에 대한 단기기억이 존재하는 것을 제시한다.

검색어: 열대거세미나방, 급속내한성, 글리세롤 키나제, 단기기억, 유전자

P84

Computational movement analysis of behavioral modulation by cGMP-dependent protein kinase of the western flower thrips, *Frankliniella occidentalis*

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Behavioral modulation by genetic changes garners a special attention nowadays as an effective means of revealing genetic function on the one hand and broadening the scope of *in situ* monitoring on the other hand. The cGMP-dependent protein kinase was treated to the western flower thrips, *Frankliniella occidentalis*. Automatic recognition techniques and computational methods were utilized to investigate behavioral changes across photo- and scoto-phases. Movement behaviors are objectively expressed according to parameter extraction and data structure visualization in different light phases. By comapring with the individuals without treatment, activities of treated thrips were changed including decrease in circadian rhythm. Usefulness of automatic monitoring of insect movement in different genetic strains is further discussed for providing useful information on monitoring and diagnosing natural and unntatural genetic disturbances.

Key words: Behavior detection, machine learning, circadian rhythm, movement parameter, monitoring

P85

Groups I and II chitinases, TcCHT5 and TcCHT10, function in turnover of chitinous cuticle during embryo hatching and post-embryonic molting in the red flour beetle, *Tribolium castaneum*

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Insect cuticular extracellular matrices (ECM) including the eggshell and exoskeleton play vital roles in protecting them from natural environmental stresses. However, these chitinous ECMs must be degraded at least in part during embryonic and post-embyonic molting periods to accommodate continuous growth all the way to the adult stage. In this study we investigated the functions of groups I and II chitinases, TcCHT5 and TcCHT10, in turnover of the eggshell and cuticle in *Tribolium castaneum*. RNAi and TEM analyses revealed that TcCHT10 is required for digestion of chitin in the serosal cuticle for embryo hatching as well as in the old cuticle during post-embryonic molts including larval-pupal and pupal-adult metamorphosis. However, although TcCHT5 is apparently involved in these vital physiological events, TcCHT10 could substitute for TcCHT5 except during the pupal-adult molting when both enzymes are indispensable to degrade chitin in the old pupal cuticle.

P86

Development of genetic database for detected quarantine pests

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With the increasing indroduction and spread of invasive quarantine pests, accurate diagnosis of pests detected in quarantine sites has become crucial. DNA barcoding, a standardized method that complements morphological analysis for rapid and precise species identification, is actively researched worldwide. In this study, we established a molecular biological identification system for major pests encountered during the import and export of agricultural and forestry products. By analyzing the DNA barcode sequences of pests collected domestically and those detected in quarantine inspections, we compiled genetic information for 1,292 individuals representing 472 species, 108 families across 11 insect orders. Among these, order Lepidoptera had the highest diversity, with 251 species across 27 families. We also secured barcodes for 52 species, 24 families in order Hemiptera, and 70 species, 20 families in order Coleoptera. By constructing a comprehensive biological foundation and database for various pests detected in quarantine sites, we aim to enhance the quarantine system by enabling rapid and accurate identification of invasive pests, thereby blocking early.

Key words: plant quarantine, DNA barcod, invasive pests, molecular biological identification

P87

Study on the breeding satisfaction survey of Orthoptera breeding kits

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The purpose of this study is to select various insect species for healing resources and develop a healing program in order to use insect as a healing agriculture. In this study, there are two kinds of breeding kit were developed, one for Gryllus bimaculatus and the other for Oxya chinensis sinuosa. Using these insect breeding kits, we conducted a survey of 60 children and the elderly. In the case of children, the results of the insect breeding satisfaction showed that 30.6% said that the sound of crickets was very good, and 11.1% said that it was good. In addition, the higher the child's awareness of insects, the higher the proportion of children who wanted to raise insects in the future. As a result of a survey of seniors, 45.2% do not like insects and 51.6% are not interested, meaning that most seniors are not very interested in insects. However, the emotions after breeding insects showed positive results, with 45.2% saying their personality became brighter, 48.4% reducing their anger, 48.4% relieving their irritation, 54.8% relieving loneliness, 58.1% feeling more responsible, and 51.6% developing intimacy.

Key words: Emotional insects, Insect Healing Program, Mass rearing of the insect

P88

Addition of agricultural byproducts to feeding substrate affects growth performance and nutritional value of mealworms, *Tenebrio molitor* (Coleoptera: Tenebrionidae)

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갈색거저리 유충의 사료인 밀기울은 대부분 수입에 의존하고 있는데 일부 국가의 식량 수출 중단 조치 등에 따른 국제 곡물가격 상승으로 밀기울 가격은 인상되고, 식용곤충 판매가격이 하락하면서 생산비 절감을 위한 사료 개발이 요구되고 있다. 농업부산물 3종을 50% 이상 급이하게 되면 유충 생육이 저하되었기 때문에 본 연구는 적정한 배합비율을 선정하기 위해 첨가사료 20, 30% 함량으로 밀기울과 혼합하여 사료를 급이하였을 때 갈색거저리 유충의 생육 특성과 영양성분 변화에 대해 밀기울만 제공한 대조구와 비교하였다. 부산물 A와 B, C를 각각 30% 함유한 처리구에서 갈색거저리 유충 무게는 대조구와 차이가 없음을 확인하였다. 먹이소화율은 부산물B를 20% 함유한 처리구가 80.5%로 대조구에 비해 높았고, 부산물C 30% 처리구에서 72.6%로 가장 낮았다. 갈색거저리 유충의 생육일수 100일 기준으로 부산물B 30% 처리구에서 용화율이 76.1%로 대조구보다 1.6배 높았으며, 부산물A 20% 처리구는 29.2%로 용화율이 가장 낮았다. 갈색거저리 유충의 조단백질 함량은 부산물 C 30% 처리구에서 대조구보다 10.3% 증가하여 아미노산 분석을 진행한 결과 sarcosine과 ornithine이 2.5배 이상 증가하였다. 이를 통해 부산물 B나 C를 30% 함유한 사료를 급이하였을 때 사육 원가를 절감하여 유충을 생산할 수 있을 것으로 사료된다.

검색어: 갈색거저리, 사료, 생육특성, 영양성분

P89

Trend of ants (Hymenoptera: Formicidae) at quarantine and surveillance sites in South Korea

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We analyzed trends of ants intercepted on imported plants and lumber over the past 30 years, using data extracted from the Pest Information System (PIS). There were 1,629 cases of about 112 species (5 subfamilies, 45 genera) from planting plants such as *Asparagales*, *Alismatales*, and *Saxifragales*, and 2,217 cases of about 86 species (7 subfamilies, 42 genera) from lumbers such as square lumber, pellets, and solid wood. For intercepted trends by continent, Asia was the most frequently detected at 91%, followed by Europe at 1% and North America at nearly 1%. Among Asian countries, Malaysia (27%) represented the highest number of interceptions, followed closely by Indonesia at 26%.

Key words: invasive species, identification manual, pest, PIS, quarantine

P90

Management of Storage Pests in grain exporting countries and Detection status of Stored Grain Pests at Quarantine Sites

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The current inspection count for imported grains is 37,072. The scientific management of stored grain, which includes methodical pest identification and control procedures, is highly prioritized in the nations that export these grains. International documents on stored grain pests include a thorough description of all life phases, including mites and larvae, as well as methodical treatment techniques. They are more valuable than domestic manuals because of their comprehensive coverage and methodical management strategies. There is lack of genetic resources and photographs since the identification of stored grain pests in the domestic have been based on data from before 2017.

During the course of 13 years(2010-2022) 1,469 incidences of stored grain pests were detected. Of these, 7 orders 34 families and 81 species had cases where the identification was confirmed down to the species level, for a total of 963 cases. This number shows that about 18% of the domestic quarantine site's stored grain pests are not species-identified. Objectives in this study are to present genetic barcode data, high-resolution photoes for classification and identification, and information on international stored grain pest management techniques. Building on this, a new identification manuals for stored grain pests might be created, which would improve the site's taxonomic identification levels.

Key words: identification, interception, genetic barcode, taxonomic key

P91

Unrecorded genus *Psectra* and *Psectra diptera* (Neuroptera: Hemerobiidae) new to Korea

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The Genus *Psectra* is a small group of Hemerobiidae, and *Psectra diptera* is one of the rare and attractive species in this group because of hindwing variation. They are well known to have their hindwing reduced, similar to flies, depending on their habitat environment. We report Genus *Psectra* and *Psectra diptera*, new records from Korea. We provide brief descriptions and photos of adults and genitalia.

Key words: Neuroptera, Hemerobiidae, brown lacewing, *Psectra*, *Psectra diptera*

P92

New record of genus *Necyla* (Neuroptera: Mantispidae: Mantispinae) from Korea

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Mantidflies or Mantid lacewing (Mantispidae) is a morphologically interesting group of Neuroptera. This group is a general predator of arthropods and is equipped with raptorial forelegs similar to praying mantis. In Korea, only three species, *Climaciella quadrituberculata*, *Mantispa harmandi*, and *Mantispilla japonica*, are recorded until now. Here we report Genus *Necyla* and *Necyla formosana*, new records in Korea. We provide diagnostic character and photos of adult and genitalia.

Key words: Neuroptera, Mantispidae, *Necyla*, *Necyla formosana*

P93

Taxonomic study of *Trichophysetis* (Crambidae, Lepidoptera) in Korea

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The genus *Trichophysetis* is one of the taxa that has recently undergone frequent changes in its taxonomic position. Only four species have been recorded in Korea, including synonymized Hendecasis species. Recent studies on the taxonomic classification of *Trichophysetis* have not addressed any species inhabiting Korea. Therefore, it is necessary to conduct a renewed morphological analysis of Korean species. In this study, we compare and analyze four Korean *Trichophysetis* species with one newly recorded species.

Key words: Glaphyriinae, morphology, wings, key, Amur

P94

Native insect Bio-scan project for Korean islands

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Islands often have relatively well-preserved ecosystem and an abundance of bioresources with a high conservation value, with unrecorded species continuing to be reported (Hong, 2011).

Approximately 1,000,000 species of insect known worldwide (Costello et al., 2012), and 20,710 species are known in Korea (NIBR, 2023). Among these, there are 6,117 species in Korean islands (HNIBR, 2022).

Native insect Bio-scan project for Korean islands is to estimate the number of insect species on Korean islands. We attempted to estimate the number of insect species on Korean islands using Barcode Index Number (BIN), and also found unrecorded species. The samples were collected four times from April to July at five locations in the Amtedo, an island located in Shinan-gun Jeollanam-do. We tried to obtain a minimum of one to usually a maximum of four samples per morphospecies to enable DNA barcoding.

Key words: Bio-scan, Korean islands, insect fauna, Lepidoptera

P95

A first record of invasive species, *Lepisiota frauenfeldi* (Mayr, 1855) (Hymenoptera: Forcmicidae) from Korea

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Native to southern Europe, *Lepisiota frauenfeldi* (Mayr, 1855) is an invasive species that has been introduced worldwide through cross-border trade. It has been documented to be distributed in the Mediterranean, Middle East, Africa, and Indo-Malaya. This species, also known as Browsing ant, was first found around a warehouse in Gwangyang, Jeollanam-do, South Korea, and was probably introduced into the country via cargo. The external morphology and gene sequences were checked for taxonomic identification, and it was identified as *Lepisiota frauenfeldi* based on comparative analysis of the morphological classification key and NCBI data. This study is the first report of a newly invasive alien ant and provides basic data on the species, including external morphological and ecological features and sequencing results.

Key words: Hymenoptera, *Lepisiota frauenfeldi*, Invasive Alien Species, Browsing ant

P96

New species of the genus *Olethreutes* (Lepidoptera: Tortricidae: Olethreutinae) in Korea

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The genus *Olethreutes,* established by Hübner in 1822, is based on the type species *Phalaena arcuella* Clerk, 1759. *Olethreutes* is one of the largest group within the family Tortricidae, with more than 130 species worldwide. As of now, about 31 species of the genus *Olethreutes* have been reported in the Korean peninsula. The proposes of this study is to describe one new species, with three similar species form Korea.

Key words: Tortricoidea, Palearctic Region, taxonony, new species

P97

Taxonomic notes on the genus *Hypsopygia* Hübner, 1825 (Lepidoptera, Pyralidae, Pyralinae) in Korea

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The genus *Hypsopygia* was established by Hübner, 1825, with type species *Phalaena costalis* Fabricius, 1775. *Hypsopygia* is characterized by the elongated uncus and valva, and pointed saccus in the male genitalia. It consists of 105 described species (Nuss *et al.*, 2003–2024) in the world, and 11 species have been recorded in Korea (Kim & Paek, 2020; Shin *et al.*, 2023). In this study, we reported one newly recorded species in Korea. Illustrations of adults provided, with information of host plants of all examined species.

Key words: Lepidoptera, Pyraloidea, taxonomy, new record, host plants.

P98

Taxonomy of the Subfamily Miltogramminae (Diptera: Sarcophagidae) in Korea

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The Miltogramminae (Diptera: Sarcophagidae) includes 600 species divided into more than 40 genera. The biological feature of the miltogrammine species is being kleptoparasites in the nests of solitary wasps and bees, but insect parasitoids and termite inquilines have been also recorded. In Korea, only three species in two genera have been recorded.

In this study, five unrecorded species (*Amobia oculata*, *Metopia inermis*, *Metopia nudibasis*, *Miltogramma angustifrons* and *Phylloteles formosana*) are reported for the first time in Korea. The diagnosis, photographs and checklists are provided herein.

Key words: Taxonomy, Diptera, Sarcophagidae, Miltogramminae

P99

New record of the genus *Megastylus* Schiødte, 1838 (Hymenoptera, Ichneumonidae, Orthocentrinae) from South Korea

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The genus *Megastylus* is a moderate group of the subfamily Orthocentrinae, comprising 38 species in two subgenera from worldwide. The subfamily Orthocentrinae is a high proportion of the genera are cosmopolitan in distribution. Orthocentrines are known as almost solitary koinobiont endoparasitoids. We report this genus for the first time from South Korea. In this study, descriptions of some new species, photographs of diagnostic characterists are provided.

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

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P100

eDNA analysis of some terrestrial insects in Korea

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eDNA(enviromental DNA)는 물, 토양, 대기 등 다양한 환경에서 채취한 생명체의 유전자 또는 그 유전자를 채취·분석하는 기술로 생물을 직접적으로 관찰하지 않아도 생물이 남긴 흔적을 통해 종의 동정이 가능하다는 장점이 있다. 따라서, 야외에서 해충의 예찰조사, 외래종 감시 및 멸종위기종 모니터링 등 다양한 목적으로 활용될 수 있는 장점이 있다. 최근, 국제적으로 미생물, 수생태계 및 육상곤충 등 다양한 방면으로 eDNA가 연구되고 있으나 국내에서는 eDNA 연구가 수생태계, 미생물 등 일부 분야에서만 진행 중이며 육상곤충의 eDNA 연구는 미비한 실정이다.

따라서, 금번 연구에서 육상곤충에 활용할 수 있는 eDNA 실험방법 확립을 위해 기존문헌 참고 및 곤충분야에 접목하여 활용 가능한 육상곤충 샘플링 방법을 탐색 및 정리하였으며, 추후 eDNA 연구에 기반을 마련하고자 한다.

검색어: eDNA, 육상곤충, 분류학, 동정, 분자진단

P101

Morphological characteristics of the reproductive system and DNA barcoding for the classification of the Herminiinae (Lepidoptera, Erebidae) in Korea

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줄수염나방아과는 나비목 중에서 가장 큰 분류군 중 하나인 밤나방과에 속한다. 분류군 내에서 날개무늬가 비슷한 경우가 있어 동정에 어려움이 많은 그룹 중 하나이다. 또한, 이 들은 산림 지역, 초지 및 물가 등 다양한 환경에 서식하며, 생활 습성에 따라 일부는 임업 및 농업에 피해가 큰 해충으로 알려져 있는 중요한 경제곤충 그룹이라 할 수 있다. 본 연구는 이와 같이 분류동정이 어려운 줄수염나방아과 곤충을 대상으로 야외채집조사, 표본제작, 생식기 해부검경 및 DNA 바코드 등을 수행하여 최종적으로 분류학적 동정지침서를 작성하고자 수행되었다. 연구결과 19속 63종으로 정리되었다. 본 연구를 통해 확보된 DNA바코드 데이터는 정확한 바코드를 활용한 진단 및 동정 연구 등에 활용되고, 이들의 분포정보 구축, 형태적 특징 및 분자분석 연구의 기초데이터 확보를 통한 관련 분야 활성화 등에도 기여할 수 있을 것으로 기대된다.

검색어: DNA barcode, reproductive system, Herminiinae, Erebidae, Korea

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P102

First record of the coprophagous beetle genus *Stenotothorax* Schmidt (Scarabaeidae: Aphodiinae) in Korea

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The genus *Stenotothorax* is reported for the first time in the Korean Peninsula. While working on Korean Aphodiinae, we identified *Stenotothorax hibernalis* (Nakane & Tsukamoto) from the Goseong-gun, Gangwon Province. This species was found in the northern region of South Korea. A key to Aphodiini genera in Korea, habitus photographs, and illustrations of diagnostic characters are provided to facilitate identification.

Key words: *Stenotothorax*, Aphodiinae, coprophagous beetle, taxonomy

P103

Lepidopterous insect fauna of Chungju and Eumseong, Chungcheongbuk-do, Korea

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본 조사는 제5차 전국자연환경조사의 일환으로 육상곤충류의 분포현황을 알아보기 위해 수행되었다. 조사도엽은 충북 음성군(장호원, 생극 도엽) 및 충주시(동량, 앙성 도엽) 등지에서 각각 2개 도엽씩 구분하여 최소 2계절 이상 포함되도록 2023년 4월부터 7월까지 총 24회(도엽당 4회)의 채집·조사를 실시하였다. 조사방법으로는 포충망을 이용한 쓸어잡기, 채어잡기 및 현장확인 등을 통해 기본조사를 수행하였으며, 트랩 조사방법으로는 버킷라이트트랩을 사용하였다. 현지조사를 통해 채집된 곤충은 건조표본으로 제작하여 종 수준까지 분류 및 동정 작업을 수행하여 총 157과 932종 5,235개체의 육상곤충류가 채집·조사되었다. 2017년 수행된 선행조사에서는 62과 235종의 육상곤충류가 확인되었으며 선행 조사 결과와 금번 현지 조사종을 종합하면, 충청북도 음성군 및 충주시의 나비목은 총 44과 984종으로 정리되었다. 이 중 91과 697종이 금번 현지조사에서 새롭게 확인된 종이었다.

검색어: 2023년 전국자연환경조사, 육상곤충류, 버킷라이트트랩

P104

Monitoring of the genus *Grapholita* (Lepidoptera: Tortricidae) in Korea

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The genus *Grapholita* Treitschke, 1829 is a complex group belonging to the tribe Grapholitini of the subfamiliy Olethreutinae, due to their similar characteristics among the species. The genus comprises about 150 described species worldwide. The majority of described species occur in the Holarctic region. To date, eight species of *Grapholita* have been reported from Korea. The genus contains several notorious pests such as *G. dimorpha* Komai and *G. molesta* (Busck). Among them, *G. inopinata* has been doubtful in distribution.

This study aim to optimize species specific sex pheromone composition/amount and establish the distribution of the pest species of the genus *Grapholita* in Korea.

Key words: Lepidoptera, distribution, *Grapholita*, Korea

P105

Taxonomic study of *Trichophysetis* (Crambidae, Lepidoptera) in Korea

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[2]National Institute of Biological Resources, Incheon

The genus *Trichophysetis* is one of the taxa that has recently undergone frequent changes in its taxonomic position. Only four species have been recorded in Korea, including synonymized Hendecasis species. Recent studies on the taxonomic classification of *Trichophysetis* have not addressed any species inhabiting Korea. Therefore, it is necessary to conduct a renewed morphological analysis of Korean species. In this study, we compare and analyze four Korean *Trichophysetis* species with one newly recorded species.

Key words: Glaphyriinae, morphology, wings, key, Amur

P106

The sugarcane looper, collected from Byeonsanbando National Park, Korea

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Mocis frugalis (Fabricius, 1775), the sugarcane looper, was collected in Byeonsanbando National Park in South Korea for the first time. This species is known as a major crop pest, especially to sugarcane at tropical and subtropical regions. Due to climate change and the subtropicalization of the southern part of the Korean Peninsula, some tropical and subtropical crops are cultivated in Korea, including sugarcane. Besides, *Oryza sativa* L. and *Zea mays* L., which of main crops in Korea, are known as host plants of *M. frugalis* in the Oriental region. Even if unclear of domestic settlement, precision monitoring will be necessary.

Key words: sugarcane looper, insect pest, invasion, Jeollabuk-do

P107

A new silkworm variety, NuriGeumJam, producing yellow sericin cocoons

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연구에서는 '누리금잠'이라 명명된 새로운 누에 신품종을 개발하였으며, 이는 황색 고치와 세리신 고치를 생산하는 두 개의 기존 계통, 잠311과 D751의 교배를 통해 육성되었습니다. 이 신품종은 첫 교배 실험을 거친 2019년 봄부터 2021년 봄까지 총 4차례의 생산력 평가를 진행했으며, 이어진 2022년 봄부터 2023년 가을까지 4차례에 걸친 지역 적응성 평가를 통해 2023년 가을에 새로운 품종으로 공식 인정받았습니다. '누리금잠'은 봄과 가을 시즌에 각각 평균 부화율 86.9%, 89.6%를 기록하였고, 유충의 평균 성장 기간은 봄에는 21일과 12시간, 가을에는 19일과 22시간으로 나타났습니다. 세리신 고치의 평균 생산성은 봄에 79.17%, 가을에 74.9%였으며, 수확된 세리신의 평균 중량은 누에고치 250개를 기준으로 봄에 6g, 가을에는 7.7g으로 측정되었습니다.

이와 같은 결과는 '누리금잠'이 높은 부화율과 우수한 세리신 생산성을 갖추고 있음을 시사합니다. 이는 세리신 기반 제품의 생산 효율성을 증가시킬 뿐만 아니라, 양잠산업의 경제적 가치를 상승시키는 데 기여할 수 있을 것으로 생각됩니다.

검색어: 누에, 세리신, 색견, 신품종

P108

A tentative mechanism for the pupal chamber construction of the Japanese pine sawyer, *Monochamus alternatus* Hope (Coleoptera: Cerambycidae) in pine trees

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The Japanese pine sawyer (JPS), *Monochamus alternatus* Hope, is an important vector of the pine wood nematode, *Bursaphelenchus xylophilus* (Steiner and Buhrer), which causes pine wilt disease. JPS selects a characteristic life cycle of a four- or five-instar pathway, which indicates the number of instars before pupation. In this study, we investigated the potential presence of a three-instar pathway and sought to determine the minimum larval age required for JPS to construct a pupal chamber. The results showed that no third instars made pupal chambers, suggesting that there is no three-instar pathway. The initiation time of digging the tunnel to make the pupal chamber ranged widely from Julian date 274 (30 September) to 332 (27 November). This timing became an average age stage of 4.8 instar, which equals an 80% completion of the fourth instar. Thus, the minimum larval age at which JPS constructs the tunnel to pupate the next year is estimated to be late in the fourth larval instar. Further, we discuss the diapause ecology in relation to the larval development of JPS in different thermal environments. Tentatively, we suggest that the regulation of diapause induction in JPS involves a dual process of reaching a critical developmental stage and stimulus (tentatively a cold temperature). This hypothesis will be helpful for future studies of diapause mechanisms and the selection of the instar-pathway in JPS and related species.

Key words: Vector of pine wilt disease, Diapause ecology, Entrance hole, Mandible length, Life cycle

P109

A prediction model for the adult emergence of *Delia antiqua* (Diptera: Anthomyiidae) from overwintered pupae and its field validation

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고자리꽃파리는 양파 및 마늘 등 백합과 *Allium* 속에 속하는 농작물에 중요한 해충으로 전 세계적으로 온대지역에서 경제적 해충으로 취급하고 있다. 본 연구에서는 기존 자료를 바탕으로 월동번데기의 성충으로 우화모델를 작성하고 포장 실측자료와 비교하여 평가하였다. 월동번데기 발육모형으로 선형과 비선형모형을 작성하고 발육기간 분포모형과 결합하여 예찰모형을 작성하였다. 비선형발육모형 작성시 3-매개변수 락틴모형 적용뿐만 아니라 4-매개변수 모형의 마지막 변수 값을 선형모형의 절편값으로 대체하여 저온에서 선형성이 강화도록 변형시켰다. 성충우화 50% 예측에서 일일평균온도를 이용하는 경우 적산온도 모형을 비롯하여 발육률 적산모형(선형식 및 비선형식) 모두 실측치와 큰 차이가 있었다. 시간별온도를 입력값으로 한 경우 3-매개변수 모형을 제외한 사인곡선 적산온도 모형, 선형 발육률 적산모형, 4-매개변수 비선형 발육률 적산모형의 평균편차는 3일과 차이가 없었다. 최종적으로 선형모형 및 4-매개변수 비선형모형을 바탕으로 시간별온도자료를 이용한 발육률 적산모형은 선발하였다. 그 결과 선형 발육률 적산모형이 두 포장적합 집단(1984, 1987)에서 실측일과 편차가 3일과 차이가 없었다. 비선형 발육률 적산모형은 1984년 적합은 0.8일 편차로 정확하였으나 1987년 집단에서 평균편차가 6.5일로 다소 증가하였다.

검색어: 고자리꽃파리, 발생예측모형, 적산온도, 우화모형, 시간별온도

P110

Growth period by temperature of *Rhopalosiphum nymphaeae* (Hemiptera: Aphididae) occurring on medicinal crop *Alisma plantago-aquatica* L. subsp. *orientale* (Sam.) Juz.

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질경이택사(*Alisma plantago-aquatica* L. subsp. *orientale* (Sam.) Juz.)는 습지에서 자라는 여러해살이 풀로 질경이택사는 덩이줄기를 약용으로 사용하며, 이뇨작용, 고혈압, 고지혈증 등에 효과가 있다. 국내에서는 전남 순천에서 주로 재배되고 있으며, 8월 중・하순에 벼를 수확하고 같은 논에 후작으로 육묘한 택사를 이모작으로 심어 소득을 올리고 있다. 2022년 8월 전남 순천에서 재배중인 질경이택사에 진딧물이 발생하였으며 수생식물에 주로 발생하는 연테두리진딧물로 확인되었다. 연테두리진딧물(*Rhopalosiphum nymphaeae*)은 노린재목 진딧물과에 속하는 곤충으로 몸체는 황색, 황갈색 또는 적갈색을 띄고, 알로 월동하고, 질경이택사, 연꽃, 수련 등의 수생식물로 이주하여 흡즙가해한다. 연테두리진딧물을 5개 온도(15.0, 20.0, 25.0, 30.0, 35.0℃), 65±5%, 16L:8D의 조건에서 발육기간을 조사하였다. 약충의 발육기간은 각각 10.8, 8.2, 5.5, 4.7일이었고, 35℃에서는 발육하지 못하였다. 성충의 생존기간은 각각 29.2, 28.2, 17.2, 8.6일이었고, 35℃에서는 발육하지 못하였다.

Key words: *Rhopalosiphum nymphaeae*, *Alisma plantago-aquuatica*, Growth period, Survival period

P111

Potential distribution in South Korea of three quarantine mealybug species (Hemiptera: Pseudococcidae): here’s what CLIMEX says

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Dysmicoccus brevipes (Cockerell), *Dysmicoccus neobrevipes* Beardsley and *Pseudococcus longispinus* (Targioni-Tozzetti) are widely-distributed pests that feeds on many economically important hosts, particularly tropical fruits and ornamentals. The potential distribution of these mealybug pests into South Korea remains a primary concern because of their high incidence in interceptions screened during inspection. Hence, these species prompted a modelling effort to assess their potential risk of introduction. Potential risk maps were developed for these pests with the CLIMEX model based on occurrence records under environmental data. The potential distribution of these pests in South Korea in the 2020s, 2050s and 2090s was projected based on the RCP 8.5 climate change scenario. Results show that *D. brevipes*, *D. neobrevipes* and *P. longispinus* have little potential for invasion in the exterior environment of South Korea due to high cold stress in the 2020s. However, for *D. brevipes* and *P. longispinus*, 3 and 86 locations in Jejudo, were predicted to be marginally suitable for this pest under future climate factors, respectively. In that respect, the results of these model predictions could be used to prepare a risk-based surveying program that improves the probability of detecting early *D. brevipe*, *D. neobrevipes* and *P. longispinus* populations.

Key words: Climate change, pink pineapple mealybug, grey pineapple mealybug, long-tailed mealybug, risk prediction

P112

Report on the Survey Results of Terrestrial Insects in Muju-gun, Jeollabuk-do

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Insects, constituting a classification group with exceptionally high diversity, account for over half of all known species on Earth and over 80% of the animal kingdom, holding potential for diverse genetic resources. Therefore, this study aimed to assess the distribution of terrestrial insects in major surveyed areas, focusing on firefly habitats in Muju-gun and key locations such as Ilsadae, Pahoe, Sushimdae, and Naedori Riverside Park in Muju-gun, to acquire fundamental data for the exploration and management of natural resources.

As result of survey, Total 12 order, 104 family, 314 species of insect has been confirmed.

Key words: Muju-gun, terrestrial insects, biodiversity.

P113

Seasonal adult occurrence of three pest moths in Iksan, Korea

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최근들어 평균 온도가 평년보다 높게 경과함에 따라 노지 작물에 발생이 많은 파밤나방, 담배거세미나방, 담배나방의 발생소장을 2023년 전북 익산의 노지 고추포장에서 성페로몬트랩을 이용하여 조사하였다. 파밤나방은 4월 중순부터 채집되기 시작하였으나 채집량은 적었고 6월 중순, 7월 중순, 9월 상순, 9월 하순에 발생최성기를 보였다. 담배거세미나방은 5월 중순부터 채집되기 시작하여 6월 상순, 7월 상순, 8월 상순, 9월 상순, 11월 상순에 발생최성기를 보였으며 8월 하순이후 발생량이 많은 경향이었다. 담배나방은 5월 상순부터 발생하기 시작하여 6월 중순, 8월 상순, 9월 상순에 발생최성기를 보였으며 10월부터는 채집량이 적은 경향이었다.

검색어: 성페로몬트랩, 파밤나방, 담배거세미나방, 담배나방, 발생소장

P114

Effect of temperature on the development of *Autographa nigrisigna* (Lepidoptera: Nictuidae)

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상추는 수요가 연중 지속됨에 따라 재배면적과 생산량이 증가하고 있는데, 주로 생식으로 이용되며 수확간격이 짧아 해충 다발생시 약제방제가 어려운 작물이다. 최근 검은무늬밤나방이 약제방제가 소홀한 포장에서 잎을 광포식하여 빠른 시간내에 직접적인 피해를 주고 있다. 본 연구에서는 검은무늬밤나방의 온도별 발육특성을 구명하여 방제를 위한 기초자료로 이용하고자 한다. 검은무늬밤나방은 시설재배 상추에 발생한 유충을 채집하여 실내 사육 후 항온조건(15, 20, 25, 30℃)에서 발육단계별 발육기간을 조사하였다. 온도가 높아짐에 따라 각 태별 발육기간은 짧아지는 경향이었으며, 유충은 보통 4회 탈피하였다. 25℃에서 알기간은 2.5일, 유충기간 10.0일, 전용기간 1.0일, 번데기기간 7.0일로 알에서 성충까지의 발육기간은 20.5일 이었다.

검색어: 상추, 검은무늬밤나방, 온도, 발육기간

P115

Estimate occurrence period of the brown planthopper, *Nilaparvata lugens* using a temperature-dependent developmental model

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최근 이상기후 및 기후변화로 인해 농작물 병해충 발생이 증가하고 발생양상 또한 다양해지고 있으며, 국제무역 및 해외 여행객 증가로 인한 외래 병해충 유입 위험성이 높아지고 있는 추세이다. 특히 대표적인 비래해충 중의 하나인 벼멸구(*Nilaparvata lugens* Stål, 1854)의 발생 범위, 출현율 및 빈도수가 꾸준히 증가하여 피해를 호소하는 농가들이 많아진 반면, 이들에 대한 대응책은 피해발생의 불규칙성, 이전 자료의 부족 및 불명확성으로 인해 미비한 실정이다. 본 연구에서는 이러한 문제를 대비해 벼멸구의 온도발육모형을 이용하여, 기상자료, NCPMS와 더불어 연발생 횟수와 분포 가능 범위 및 발생 시기를 예측하였다. 또한, 벼멸구의 발생량이 많았던 충남 예산, 경남 사천, 진주의 최초발생일, 최초비래일, 최고발생일, 발생최성일 기준으로 각각 발육영점온도 및 유효적산온도를 적용하여 세대별 발생시기를 예측하였다. 최초발생일과 최초비래일은 예산 7월 9일, 7월 16일, 사천 7월 2일, 7월 19일, 진주 7월 26일, 7월 26일로 나타났으며, 최초발생일과 최초비래일 사이를 초발생일로 적용하면 다음세대 발생이 실제 조사한 지역별 최고발생일인 예산 9월 7일, 사천 8월 9일, 진주 8월 8일과 근접한 시기로 추정되어 효과적임을 알 수 있었다.

검색어: 벼멸구, 비래해충, 온도발육모형, 유효적산온도, 초발생일

P116

Occurrence of three Noctuid moths in July and September (2020-2023)

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국내 농작물에 크게 피해를 주고 있는 파밤나방, 담배거세미나방과 담배나방에 대하여 2020년부터 4년 동안 7월과 9월에 전국 7개 지역의 발생 추이를 조사하였다. 조사지역은 경기도 안성, 충청북도 청주, 강원도 횡성, 경상북도 김천과 안동, 경상남도 창녕, 전라북도 김제를 포함하고 있다. 각 해충의 포획 마릿수는 2021년과 2022년도에 크게 다르지 않았으며, 지역 간 해충 발생 수준도 비슷하였다. 2021년도와 2022년도와 비교해서 2023년도에 담배거세미나방과 파밤나방은 각각 119% 및 70% 증가했지만, 담배나방은 23% 감소하였다. 전체적으로 지역별 발생 시기 및 발생량이 매년 차이를 보이는 것은 기후 등 환경변화의 영향이 가장 큰 것으로 사료 된다. 전체 해충 포획수는 파밤나방이 가장 많고, 담배나방의 수가 가장 적었다. 전년 대비 담배거세미나방과 파밤나방의 경우 중부지역이 남부에 비해 더 많이 발생하였다. 9월에 더 많이 포획되어 전년과 유사한 경향을 보였으며, 최근 3년 동안 9월 발생 밀도가 가장 높았다. 담배나방은 전년에 비해 발생량이 급감하였으며, 안성지역을 제외한 대부분 지역에서 감소하였다.

검색어: 파밤나방, 담배나방, 담배거세미 나방, 모니터링

P117

Effects of fluctuating temperature on the population parameters and growth of *Myzus persicae* (Sulzer) (Hemiptera: Aphididae)

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We investigated the effects of fluctuating temperature on development and fertility of *M. persicae* at different temperature conditions, 10, 15, 20, 25, 28, and 30±5°C, respectively. In this study, we collected detailed data on development periods, and fertility of *M. persicae* at six different temperatures. We analyzed the life table parameters of *M. persicae* using age-stage, two-sex life table program. The intrinsic and finite rate of increase were the highest at 25±5°C. The fertiltiy was the highest at 20±5°C.

Key words: *Myzus persicae,* Life table parameter, Population growth, Temperature

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P118

Community structure and Biodiversity of Rice field spiders in Korea

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Spiders play an important role in regulating insect pests in the agricultural ecosystem. The community structure and biodiversity of rice field spiders were surveyed in 5 areas (Anseong, Nonsan, Imsil, Namwon, and Gurye) from 20 May to 30 September, 2021. A total of 5,525 spiders collected were identified as 64 species of 17 families. Species richness and abundance were high in Lycosidae, Tetragnathidae and Linyphiidae. The similarity of rice field spider communities among regions was about 72% and was divided into three groups: the middle inland area, the southern mountainous area, and the southern inland area. Species diversity averaged as 2.55±0.06. On the seasonaliy of The boidiversity tended to increase toward the latter half of cultivation.

Key words: biodiversity, community, rice field, seasonality, spiders

P119

Population dynamics of Soybean insect pests in climate change scenario

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The moth species and bugs are highly polyphagous that feed on a wide range of field and vegetables crops, including soybean in Korea. The monitoring study was conducted in soybean fields in Southern area Miryang from 2021-2023. Commercial funnel and rocket traps housing species-specific baiting with pheromone were used for monitoring of moth species *(Spodoptera frugiperda, Spodoptera litura, Agrotis ipsilon, Helicoverpa armigera, Ostrinia furncalis*, *Spodoptera exigua*, and *Mythimna separata*) and bean bugs (*Riptortus pedestris*), respectively. The higher number of Spodoptera species (*S. litura* and *S. exigua*) were captured in August to September with several seasonal population peaks. The higher number of *R. pedestris* was captured in July to September. Climatic components were found as critical and influential factors in the population dynamics of moth species and bean bug. The population information of this study can be used to understand the spring emergence along with number of generations, and integrated into management programs of moths and bugs.

Key words: Monitoring, seasonal peaks, spring emergence, generations, management

P120

Selection of pine sawyer, *Monochamus salturius* aerial sparying control agent with low honeybee toxicity

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Gyeonggido Forestry Enviroment Research Center

최근 소나무재선충병 항공방제를 위해 살포한 네오니코티노이드계 농약이 꿀벌 폐사에 영향을 미친다는 우려와 이슈가 제기됨에 따라 산림청은 소나무재선충병 항공방제를 중지하고 해당 약제들을 방제용 약종 결정에서 제외시켰다. 본 연구에서는 북방수염하늘소의 항공방제를 위해 꿀벌 독성이 낮은 살충제를 선발하여 살충효과를 조사하고 향후 방제 약제로 활용하고자 한다.

꿀벌 독성이 낮은 살충제를 선발하기 위해 The Pestcide Manual Nineteenth Edition(BCPC)에서 살충제 원제 231종을 대상으로 꿀벌에 대한 접촉독성이 100*μg*/bee 이상인 원제 중에서 테트라닐리프롤 액상수화제, 아피도피로펜 미탁제, 플로니카미드 입상수용제, 플루벤디아마이드 액상수화제, 피메트로진 입상수화제 5개의 약종을 선발하였다. 선발한 약제 5종을 소나무재선충병의 매개충인 북방수염하늘소에 직접 분무하고 시간경과별 살충효과를 조사한 결과, 피메트로진 입상수화제에서 분무 후 1일차에 약 53.3%의 가장 높은 방제율을 나타냈으며, 3일차에는 86.7%, 5일차에는 100%로 매우 효과적인 살충효과를 나타냈다.

검색어: 소나무재선충병 방제, 살충제, 북방수염하늘소, 꿀벌 독성

P121

Regional release effect of *Neodryinus typhlocybae* (Hymenoptera: Dryinidae) for controlling *Metcalfa pruinosa* (Hemiptera: Flatidae)

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M. pruinosa has been found on 98 families and 345 species of plants, indicating a wide host range. Since its first report in a persimmon orchard in Gimhae in 2009, it had spread to 126 municipalities over 12,429 ha. Because of powerful dispersal ability, it's difficult to control with insecticides. Therefore, it is necessary to reduce the population density through the release of *M. pruinosa*'s natural enemy, *N. typhlocybae*. *N. typhlocybae* females prey on or externally parasitize the nymphs of *M. pruinosa*. This natural enemy was introduced from Italy in 2017 through an international cooperative project between National Institute of Agricultural Sciences and University of Padova for controlling the sporadic pest, *Metcalfa pruinosa*. This study reported the results of mass rearing *N. typhlocybae* indoors and releasing them outdoors from 2020 to 2023 in 21 regions nationwide, showing an average parasitism rate of 27.3% and an average production of 7.9 cocoons per host, suggesting the possibility of their establishment in Korea.

Key words: *Neodryinus typhlocybae, Metcalfa pruinosa*, Natural enemy, Regional release

P122

Parasitic fly species(Diptera: Tachinidae) on the third generation of *Hyphantria cunea* and the difference in parasitic rates by disturbance

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본 연구는 서식 환경에 따라 구분된 3화기 미국흰불나방(*Hyphantria cunea* Drury)을 숙주로 하는 기생파리의 종과 기생률의 차이를 확인했다. 조사 기간은 2023년 10월 24일부터 29일까지로, 방제를 실시한 서천군 국립생태원과 방제를 실시하지 않은 군산시 근린공원에서 숙주인 미국흰불나방의 유충을 채집하였다. 유충은 기주식물인 수국을 급여하여 실내 개별 사육하였다. 각 조사지에서 미국흰불나방의 기주식물은 국립생태원에서 8종, 근린공원에서 6종이 확인되었다. 총 숙주 380마리 중 기생파리는 106개체로 총 27.9%의 기생률을 보였고(유충 92개체, 미동정 알 14개체), 기생률은 근린공원이(39.6%) 국립생태원(12.5%)보다 더 높았다. 성충의 우화율은 63.0%로, 동정 결과 4속 92개체가 나타났다. 전체 종과 가장 많은 개체가 확인된 *Exorista japonica* (Townsend, 1909)의 조사지에 따른 유충 생존율과 성충 우화율은 모두 근린공원이 더 높은 것으로 확인 되었다. 조사결과 E. japonica가 미국흰불나방의 생물적 방제제로 유효할 것이라 판단되며, 근린공원에서의 더 높은 기생파리 유충 생존율과 성충 우화율을 통해 인간에 의한 교란이 적은 환경에서 기생파리를 이용한 미국흰불나방 방제가 더 효과적일 것이라고 고려된다. 또한 숙주의 생존율과 기생파리의 우화율을 비교한 결과 해충 방제가 이뤄지지 않는 환경에서 천적 개체군이 유지될 가능성이 더 높다고 사료 된다.

검색어: 미국흰불나방, 기생파리, 기생, 화학적 방제, 기생률

P123

Detection and frequency of nematode infestations in Chinese Ginger during quarantine

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식물기생선충은 식물에 기생하여 식물의 생장을 저하시키거나 심할 경우 식물의 고사를 일으키는 주요 병원체의 하나이다. 이들 선충은 수입 식물을 통해 국내로 유입될 수 있으며, 이로 인해 식물의 생장이 저하되거나 식물이 죽는 등의 실제적 피해를 야기할 수 있다. 생강은 한국의 대표 음식인 김치를 비롯한 다양한 요리와 음료, 전통약재 등에 사용되는 중요한 식약재료이며, 그 가치와 수요가 매우 높다. 최근 10년(2014-2023년) 동안 종구로써 사용되는 재식용 생강의 수입량은 총 31,740톤이었는데, 수입 생강 원산지의 대부분은 중국으로써 최근 10년간 수입량의 99.99%를 차지했다. 동기간 검역처분 내역은 합격 수량이 1,090건(27,637톤), 폐기 수량은 222건(4,102톤)이었다. 폐기 처분을 받는 주용 원인을 분석해보면, 관리급 선충 검출이 139건, 종구에 흙이 부착된 경우가 26건 등이었다. 앞으로도 농림축산검역본부는 수입 재식용 생강에 대한 실험실정밀검역을 통해 우리나라의 농업과 자연환경에 위해를 가할 수 있는 식물기생선충의 차단을 위해 최선의 노력을 다하고자 한다.

검색어: 식물검역, 관리해충, 폐기

P124

Control effect of *Frankliniella occidentalis* using eco-friendly agricultural materials package in a pepper greenhouse

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To control western flower thrips (*Frankliniella occidentalis*), a significant pest of peppers, the control effects of eco-friendly agricultural materials were tested when treated alone and in combination. The control effects of yellow sticky roll traps installed on the stem, predatory natural enemy (*Hypoaspis miles*) inoculated on the stem, and plant extracts (50% custard apple seed oil + 10% cinnamon extract) sprayed on the foliage were 45.3%, 36.6%, and 50.2%, respectively, when treated individually. Meanwhile, when three eco-friendly agricultural materials were comprehensively applied, the control effect was maintained between 62.4% and 80.9% compared to untreated conditions during the pepper harvesting season. These methods can be utilized for the eco-friendly control of western flower thrips in pepper greenhouses.

Key words: Pepper, western flower thrips, natural enemy, sticky roll trap, plant extract

P125

Ovicidal effect of plant extract mixture against seven major insect pests

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The ovicidal effect of plant extract mixture (5% cinnamon extract + 10% citronella oil + 30% citrus oil + 10% derris extract + 20% neem extract + 25% penetrating surfactant) against several major insect pests was tested using the spraying method. In the case of stink bugs, eggs tended to die during hatching. When treated with a plant extract mixture (500-times solution), mortality for *Halyomorpha halys*, *Riptortus clavatus*, *Eurydema dominulus*, *Trialeurodes vaprarorium*, *Bemisia tabaci*, *Spodoptera exigua*, and *Agrotis ipsilon* reached as high as 100%. Therefore, it is believed that industrialization will be feasible in the future.

Key words: plant extract mixture, ovicidal effect, stink bug, whitefly, moth

P126

Impact of release densities on parasitism efficiency of larval parasitoids, *Exorista japonica* and *Meteorus pulchricornis*

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노지 나방류 해충인 담배거세미나방 방제를 위한 유충기생성 천적 2종인 긴등기생파리와 예쁜가는배고치벌의 방사조건을 확립하고자 콩 재배포장에서 방사거리 및 방사밀도별 기생율을 조사하였다. 긴등기생파리는 방사 후 24시간 이내 방사지점으로부터 10m까지 이동하여 나방류 유충을 기생하였으며, 예쁜가는배고치벌도 방사지점으로부터 15m에서도 기주유충에 산란하여 고치가 형성된 것이 확인되었다. 긴등기생파리는 면적당 방사밀도가 높아질수록 기생율이 증가했으며, ㎡당 0.15마리(천적:해충=1:5) 방사했을 때 평균기생율 63.1%로 나타났다. 예쁜가는배고치벌은 긴등기생파리와 같은 방사밀도에서 평균기생율 47.8%로 확인되었으나, 방사밀도에 따른 기생율 차이는 없었다.

Key words: 적정방사밀도, 방사비율, 방사간격

P127

Establishment of soybean banker plant system for aphid parasitoid, *Binodoxys communis* (Hymenoptera, Braconidae)

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We established a soybean banker plant system and evaluated the biological control effects of aphid control in bell pepper greenhouses. The soybean banker plant was *B.communis* breeding system and developed as an alternative aphid control agent to the most common Barley banker(Barley-Colemani). After inoculating approximately 50 soybean aphids(*Aphis glycines*, aphid starter population) on 2 week old soybean seedling pot after sowing and then releasing aphid parasitoids, an average of 348.7 parasitic wasps per a soybean banker plant could be produced without additional host aphid inoculation. Common recommendation for installation in the greenhouses are about 2 soybean banker plants per 330㎡ before or immediately after planting. If the number of aphids per stem is fewer than three on 2 weeks after installation of the banker plant, additional supplementation of 20~30 aphids is necessary to maintain this system for one month. When one soybean banker plant was installed per 120㎡, the aphid control effect was about 60% on the 21st day after installation.

Key words: Aphid parasitoid, Soybean aphid, Cotton aphid

P128

Orientation bioassay for chemical synthesis aggregation pheromone of Scotinophara lurida using 4 choice olfactometer

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먹노린재 합성집합페로몬 후보물질 12종에 대한 유인력을 평가하였다. 페로몬 방출기는 4구 후각계(Olfacomter)를 사용하였고 4개의 진공관에 각각 후보물질을 투입 후 진공 유압 방식으로 방출하여 포집기에 유인되는 먹노린재의 개채수를 측정하는 방법으로 검정하였다. 4구 후각계 페로몬 평가 방법은 기존 Y-관 후각계의 문제점인 양방향 선택성과 공간 한정성을 개선하여 평가의 정확성을 향상시켰다. 유인력 평가 결과 12종의 유인제 후보물질 중 Trans-2-Decenal이 먹노린재 실험개체에 대하여 100% 유인력을 보였다. 또한, 선별된 Trans-2-Decenal의 먹노린재 유인력에 대한 유효농도 시험을 진행 한 결과, 50%의 농도에서 유인력이 가장 높았다. 본 연구를 통해서 선별된 Trans-2 Decenal은 기존의 노린재과에 대한 페로몬 트랩에 비해 먹노린재에 대한 유인 효과가 높을 것으로 사료되었다. 이에 따라, Trans-2 Decenal을 기반으로 한 페로몬 트랩이 상용화된다면 추후의 먹노린재 방제 효과가 높아질 것으로 기대된다.

검색어: 먹노린재, 집합페로몬, 4 Choice Olfactometer, Trans-2-Decenal

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P129

Control effect of several insecticides on adults of the black rice bug, *Scotinophara lurida* (Hemiptera: Pentatomidae)

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효과적인 먹노린재 방제 방법을 제시하고자 벼에 등록되어 있는 살충제 10종에 대해 접촉독성과 잔효독성 특성을 충체분무법과 기주분무법으로 각각 실내에서 검정하였다. 그리고 논의 담수 여부에 따른 방제 효과는 작용기작이 다른 4종의 약제를 이용하여 실내 벼 포트 망사검정과 야외 논 포장 망사검정을 통해 비교하였다. 그 결과, 5종의 살충제는 충체분무법과 기주분무법 모두 살충률 100%의 높은 살충활성을 보였으나, 일부 살충제는 충체분무법 대비 기주분무법에서 살충률이 다소 낮았다. 한편, 약제 살포 5일 후 담수한 벼 포트의 살충률은 93.3% 이상, 배수한 포트는 96.7% 이상으로 높은 방제 효과를 나타냈으며, 논 포장에서도 약제 살포 7일 후 담수 시 97.8%이상, 배수 시 98.9% 이상으로 나타났다. 이러한 결과로부터 대부분의 먹노린재 방제용 살충제는 높은 접촉독성과 잔효독성을 모두 갖고 있으나 일부는 잔효독성이 낮아 충체에 충분히 묻어야 높은 방제 효과가 기대되었다. 또한 살충제 살포 시 논의 담수 여부는 방제 효과에 크게 영향이 없을 것으로 보였다.

검색어: 먹노린재, 살충제, 접촉독성, 잔효독성, 담수, 방제 효과

P130

Initial Exploration of Nematicide-Based Control for Plant-Parasitic Nematodes

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This study evaluates the efficacy of two nematicides in controlling plant-parasitic nematodes, surrogate of the exotic invasive species(EIS) *Pratylenchus penetrans*, to mitigate the introduction and spread of EIS. The indoor bioassay experiments involved immersing *Syngonium podophyllum* and *Philodendron spp*. in nematicides at concentrations of 0.4 and 5.0 ml/L for periods of 10 minutes and 1 hour. The results indicated no phytotoxic effects on the host plants at any tested concentration or duration, and a 100% mortality rate of *P. penetrans* was achieved under the specified conditions. Future research should build on these findings by focusing on plants infested with *P. penetrans.*

Key words: *Pratylenchus penetrans*, immersion, nematicides, *Syngonium podophyllum, Philodendron spp.*

P131

Efficacy of phosphine and low temperature treatment on *Drosophila suzukii*

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Drosophila suzukii (Matsumura) (Diptera: Drosophilidae) is found in many regions, including Asia and Europe. Unlike other vinegar flies, *D. suzukii* uses its serrated ovipositor to pierce the pericarp of healthy fruits and lay eggs, causing severe damage. In order to develop a disinfect method of *D. suzukii* during the quarantine process, low-temperature and phosphine(PH_3) fumigation treatment at five different concentration conditions were performed. In the experiment, eggs, early larvae, late larvae, and pupae were used. As a result of low temperature treatment, eggs, early larvae, and late larvae were 100% controlled on the 4th day, and pupae were at 6th day. As a result of PH_3 treatment, in order to achieve 100% mortality rate, eggs needed to be treated at 0.5mg/L, early larvae at 0.4mg/L, late larvae at 0.3mg/L, and pupae were not controlled even when treated at 0.5mg/L, the highest concentration of the experiment. Although additional experiments are required for PH_3 treatment of pupae, it is believed that it can be used to design the combined treatment method of low-temperature and PH_3 fumigation under the same experimental conditions.

Key words: *Drosophila suzukii,* PH_3, low temperature

P132

Mortality of *Ceratitis capitata* (Diptera:Tephritidae) and phytotoxicity of dragon fruits by combined treatment of ethyl formate, phosphine and low-temperature

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Mediterranean fruit fly(Ceratitis capitata) is an important plant quarantine pest globally. Although C. capitata is not existed in Korea, securing a proper treatment method is important to prepare the fruit fly invasion. In this study, mortality of C. capitata and phytotoxicity of dragon fruits by combined treatment of ethyl formate, phosphine and low-temperature have been evaluated as a preliminary study to establish a treatment standard of C. capitata. As a result, 3rd instar larva of C. capitata was the most tolerant growth stage to low temperature and fumigants. For phytotoxicity test, treatment dosage was set to EF 15mg/L+ PH3 0.7 mg/L, which showed 100% mortality to 3rd instar larva of C. capitata. After treatment of EF+PH3+low temperature to dragon fruit, phytotoxicity was not observed, however, quality of fruit was rapidly decreased as storage time was elongated. To maintain the fruit quality, decrease of low temperature storage period is required.

Key words: Medieterranean fruit fly, dragon fruit, fumigant, low temperature

P133

Investigation of phosphine resistance of stored-product insects collected from Rice Processing Complex (RPC) in Korea, 2021-2023

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Phosphine is a common pesticide used to control grain pests in Rice Processing Complex(RPC). However, increasing use of aluminum phosphide caused the occurrence of phosphine resistance pests. In this study, phosphine resistance pests collected at RPC in 2021-2023 was investigated with FAO No. 16 test and Dihydrolipomaide dehydrogenase(DLD) test the occurrence of phosphine resistance in Korea. Test pests were collected in investigated the 42 region. As a result of the FAO No. 16 test, all sample were phosphine sensitive, and Jincheon had the lowest mortality rate of 48%. In the DLD test, 18 regions showed weak resistance, with Eumseong being the most resistant at 30%. It is required to inspect the RPC and other grain storage continuously to inhibit the widespread of resistant pest.

Key words: Phosphine, Resistance, Rice processing complex, Fumigant

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P134

Insect repellent effects of multilayer films with adhesives containing natural plant extracted anti-insect materials

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가공식품 비닐포장을 천공하여 소비자 클레임을 유발하는 저장해충 피해를 저감화하는 허들방충포장 개발을 위해 천공성 저장해충(화랑곡나방, 수시렁이 유충)을 대상으로 천공을 방해하는 점착제와 유인을 억제하는 천연식물 추출 방충물질을 적용한 다층필름을 제작하여 방충효과를 검증하였다. 연구에 사용된 다층필름은 기존 열 경화성 접착제, 수용성 점착제, 천연식물 추출 방충물질을 혼합한 점착제, 탄닌을 혼합한 점착제를 1급지(OPP 20μ) 필름과 2급지(LLDP 50μ) 필름 사이에 도포하여 제작 후 각 다층필름으로 파우치포장을 제작하여 NO CHOICE TEST를 수행하여 방충 효과를 분석하였다. 천연식물 추출 방충물질 함유 점착제 적용 다층필름으로 제작된 파우치 포장은 모든 부위에서 화랑곡나방, 수시렁이 유충의 유인을 통계적으로 유의하게 억제하는 것으로 분석되었고 다층필름 제작시 사용한 점착제는 천공성 해충의 천공행동을 억제할 수 있을 것으로 판단되어 식품 유형에 따라 천공성 해충 오염이 우려되는 제품의 포장에는 적합할 것으로 조사되었다.

검색어: 허들방충포장, 다층필름, 천공성 저장해충, 소비자클레임, 천연방충성분

P135

Improved model for the time of upward-movement to reset the control period of overwintered *Cacopsylla jukyungi* in southern region of Korea

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Cacopsylla jukyungi, a significant pest affecting pear trees, typically overwinters beneath the rough bark of pear trees before ascending to laying eggs in February. The optimal time for control is between overwintered adults climb trees and laying eggs. Analyzed temperature data from 2009 to 2013 and 2021 to 2022, the predicted period of upward-movement using the basic model was compared with the date when actual upward-movement was observed. As a result, in the southern region, the actual upward-movement date was faster than the predicted time of the basic model, and the egg laying period was same or faster than the actual upward-movement date in 2021 to 2022. Improved models were proposed through comparative analysis of the accumulated daily maximum temperature and the cumulative number of days for each daily maximum temperature. In addition, taking into account the earlier spawning season, it is proposed that the optimal control period be improved.

Key words: pear pest, *C. jukyung*i, improved model

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Investigation the Role of Flies as Vector in the Spread of Lumpy Skin Disease Virus During Outbreak in the Republic of Korea

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전 세계적으로 가축의 경제적·사회적 피해가 큰 럼피스킨은 매개체(흡혈곤충: 침파리, 모기, 진드기 등)에 의한 기계적 전파가 된다고 알려져 있다. 본 연구는 2023년 10월 국내 최초로 발생한 럼피스킨의 전파 매개체의 역할을 조사하고자 하였다. 럼피스킨 의심 또는 확진 농장에서 채집된 매개체를 대상으로 형태학적, 분자 유전학적 검사를 실시하였고, 매개체 종 동정, 럼피스킨 바이러스 검출 유무와 유전학적 특징을 조사하였다. 그 결과 럼피스킨 바이러스가 검출된 매개체는 집파리와 침파리였으며, 럼피스킨 바이러스의 계통학적 분류를 통해 주변국에서 유행하는 백신유래 야외주와 유사함을 확인하였다. 백신유래 야외주는 중국, 러시아, 몽골 등에 다발하는 럼피스킨 바이러스로 인접국에 주로 발생되었다. 국내 럼피스킨은 역학적으로 주변 발생국의 매개체에 의해 국내 유입되었을 가능성이 크며, 국내 전파는 물류·인적 이동 등에 의한 확산일 것으로 추정되었다. 결과적으로, 국내 럼피스킨은 파리가 농장간 전파의 주요 요인이었을 가능성이 높다. 향후, 국내 럼피스킨 재발생과 전파를 효과적으로 차단하여 농가 피해를 최소화하기 위해 지속적인 매개체 분포·서식 조사와 더불어 방제, 매체 전파능 연구를 강화해야 할 것이다.

검색어: 럼피스킨, 럼피스킨 바이러스, 침파리, 집파리

P137

Plasticity in ovariole number is mediated by complex interactions between temperature and nutrient balance in *Drosophila melanogaster*

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The number of ovariole is an important fitness-related trait in *Drosophila melanogaster* flies, because it determines the number of eggs that can be potentially produced by females. Ovariole number is also a highly plastic trait, which is profoundly affected by a number of environmental factors, such as temperature and nutrition, experienced during larval development. While multiple studies have examined the separate effects of rearing temperature and nutrition on ovariole numbers in *D. melanogaster*, few studies have explored how the combination of these two environmental factors affects the phenotypic expression of this plastic trait. In this study, we recorded ovariole number and its correlated life-history traits from *D. melanogaster* flies reared under one of nine larval rearing conditions where three temperatures (18, 23, 28°C) were fully combined with three dietary protein:carbohydrate ratios (P:C= 1:8, 1:2, 2:1). Preadult survivorship was reduced at the lowest P:C ratio (1:8), but was unaffected by temperature. *D. melanogaster* flies reared in cooler environments developed into larger individuals. The extent of such temperature effect on body size was consistent across diet, as indicated by non-significant interaction between temperature and diet. In manner opposite to body size, the number of ovarioles tend to decrease in response to decreasing temperature. Importantly, as evidenced by a significant interaction between temperature and diet for this trait, this negative effect of rearing temperature on ovariole number was observed in *D. melanogaster* flies reared at two low P:C ratios (1:16 and 1:2) but not at high P:C ratio (2:1). If reared on a protein-enriched diet (P:C=2:1), *D. melanogaster* flies attained a high number of ovarioles (35−40) that was not statistically distinguishable across the temperature regime. Our results indicate that high protein intake can buffer the negative effect of cool temperature on ovariole development.

Key words: Development, Nutrition, Ovariole, Temperature, *Drosophila melanogaster*

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Not Presented

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Effects of macronutrient balance on larval life-history traits in the two sibling species of *Drosophila*: *D. melanogaster* and *D. simulans*

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The two sibling species of fruit fly, *Drosophila melanogaster* and *D. simulans* (Diptera: Drosophilidae), have long been used as the key model organisms in ecological and evolutionary research. While numerous studies have investigated the thermal responses of these two species, no study has yet systematically compared their response to dietary macronutrient balance. To fill this knowledge gap, we compared how various life-history traits expressed during larval development would response to an array of dietary ratio of protein to carbohydrate (P:C ratio) in these two sibling species. Largely consistent with previous studies, *D. melanogaster* took longer to complete their larval development and were much larger at adult emergence than *D. simulans*. For both species, an increase in dietary P:C ratio resulted in improved larval survivorship and faster development. However, the two species showed qualitatively different response to dietary P:C ratio when body mass at adult eclosion was concerned. The body mass of *D. melanogaster* peaked at an optimal P:C ratio of 1:4, but decreased as the P:C ratio either increased or decreased from this optimum. In marked contrast, the body mass of *D. simulans* was insensitive to dietary P:C ratio.

Key words: Carbohydrate, *Drosophila*, Life-history trait, Nutrient, Protein, Sibling species

P140

Geographical characteristics of *Culex tritaeniorhynchus* and *Culex orientalis* microbiome in Korea

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Mosquitoes, the primary vectors of arboviruses, harbor a diverse microbiome that plays a crucial role in their development, immunity, and vector competence, tThe composition of the mosquito microbiome is heavily influenced by the environment and habitats, Therefore, identifying the relationship between the habitat and the mosquito's microbial community can improve the overall understanding of mosquito biology, However, the microbiome profiles of *Culex tritaeniorhynchus* and *Culex orientalis*, known as transmission vectors of the Japanese encephalitis virus, are poorly understood. Using 16s rRNA Illumina sequencing, we hereby investigated the microbial profiles in these two mosquito species collected in several areas in Korea. Thirty-six prevalent bacterial familes were identified from these mosquito species. the microbial composition variation were primarily influenced by the mosquito collecting sites. Moreover, species biomakers were identified by utilizing the regional specificity of the mosquito microbiome. Based on the microbiome profiles representing high similarity, *Culex orientalis* may share an ecological niche with *Culex tritaeniorhynchus*.

Key words: mosquito, microbiome, *Culex tritaeniorhynchus, Culex orientalis*

P141

miRNA-Target mRNA Interactions Reveal Novel Insights into Detoxification Mechanisms in *Spodoptera frugiperda*

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Spodoptera frugiperda, commonly known as the fall armyworm (FAW), is a major pest across the globe due to its broad host range and distribution worldwide. We investigated the function of microRNAs (miRNAs) in the detoxification of insecticides, with a specific focus on its susceptibility to chlorantraniliprole which is widely utilized insecticide for its management. miRNAs are small non-coding RNA molecules, crucial for post-transcriptional regulation of gene expression. This study aims to elucidate the impact of these miRNAs on the expression of cytochrome P450 genes, which play a significant role in conferring insecticide resistance. We identified notable changes in the abundance of two specific miRNAs, sfr-miR-10465-5p and sfr-miR-10476-5p through RNA sequencing, after chlorantraniliprole exposure. These miRNAs exhibited significantly high expression in the fat body tissue, while showing relatively lower expression in the head, midgut, and malpighian tubules. Further analysis suggested that these miRNAs might target specific cytochrome P450 genes, like CYP4C1 and CYP4C21, which are known to play a role in insecticide resistance development. Experimentation with miRNA mimics through microinjection revealed a notable increase in the survival rates of *S. frugiperda* larvae when subjected to chlorantraniliprole exposure, with a significant reduction in CYP4C1 and CYP4C21 gene expression levels. This suggests a direct connection between the miRNAs and the increased tolerance of *Spodoptera* larvae to the insecticide. Our research presents the complex function of miRNAs in gene expression regulation related to insecticide resistance, offering valuable insights into the molecular mechanisms of chlorantraniliprole resistance in *S. frugiperda*. These findings pave the way for further investigations into miRNA roles and their potential in managing pesticide resistance in agricultural pests.

Key words: miRNAs, *Spodoptera frugiperda*, chlorantraniliprole, cytochrome P450, insecticide resistance

P142

Mitochondrial COI-based population genetic analysis of the cicada, *Cryptotympana atrata* (Cicadidae: Hemiptera), which is a climate-sensitive indicator species in South Korea

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The blackish cicada, *Cryptotympana atrata* Fabricius, 1775 (Hemiptera: Cicadidae) was originally distributed mainly in the southernmost remote island, Jeju and rarely throughout low lands in South Korea, but has been explosively increased at the urban areas, where annual temperature is higher. In this study, we sequenced a partial mitochondrial COI from a total of 171 individuals collected throughout 12 localities in South Korea. The haplotype found with the highest frequency in Jeju island shares only with two inland localities in southern region with a low frequency, whereas the haplotype found with the highest frequency throughout inland localities was not found in Jeju island. These results showed that Jeju population, southern region, and other inland populations form somewhat different genetic groups.

Key words: blackish cicada, climate sensitive species, climate change, COI, Korean peninsula

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Expression profiles and phylogenetic properties of venom gland-specific viruses in some Aculeate bees and wasps

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To identify viruses and compare their abundance levels in the venom glands of hymenopteran species, we conducted venom gland-specific transcriptome assemblies and analyses of 22 Aculeate bees and wasps and identified the RNA genomes of picornaviruses. Additionally, we investigated the expression patterns of viruses in the venom glands over time following capture. Honeybee-infecting viruses, including black queen cell virus (BQCV), deformed wing virus (DWV), and Israeli acute paralysis virus (IAPV), were highly expressed in the venom glands of Apis mellifera and social wasps. This finding suggests that the venoms of bees and wasps likely contain these viruses, which can be transmitted horizontally between species through their stinger usage. A. mellifera exhibited an increasing pattern of abundance levels for BQCV, DWV, IAPV, and Triatovirus, while the social wasp *Vespa crabro* showed increasing abundance levels of IAPV and Triatovirus over different capture periods. This suggests that the venom glands of honeybees and wasps may provide suitable conditions for active viral replication and may be an organ for virus accumulation and transmission. Some viral sequences clearly reflected the phylogeny of Aculeate species, implying host-specific virus evolution. On the other hand, other viruses exhibited unique evolutionary patterns of phylogeny, possibly caused by specific ecological interactions. Our study provides insights into the composition and evolutionary properties of viral genes in the venom glands of certain Aculeate bees and wasps, as well as the potential horizontal transmission of these viruses among bee and wasp species.

Key words: bee virus, aculeata, solitary hunting wasp, social wasp, honeybee, bumblebee

P144

Pollination activities of *Apis mellifera* and *Apis cerana* in strawberry greenhouse

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시설재배 딸기의 화분매개에 꿀벌 사용이 보편화되어있지만 동양종(*A. cerana*) 꿀벌의 화분매개효과 연구는 미비한 실정이다. 따라서 본 연구는 딸기에서 동양종 꿀벌의 화분매개자로 가능성을 평가하기 위하여 비닐하우스 딸기에서 서양종 꿀벌과 화분매개행동 특성을 비교하였다. 향후 봉군 수명과 착과된 딸기의 기형과율품질을 평가 할 예정이다. 서양종과 동양종 꿀벌은 10시 이후부터 활동량이 증가하고, 13시에 방화활동이 가장 활발하였으며 이후부터 감소하는 일주행동 패턴을 보였다. 서양종과 동양종 꿀벌 활동성은 모두 온도, 조도, 자외선과 정의 상관관계를 나타냈으며 상대습도와는 부의 상관을 보였다. 특히 서양종 꿀벌은 온도, 조도, 자외선이 같은 수준의 상관($r=0.7$)을 보이는 것에 반해, 동양종 꿀벌의 경우 온도와 습도보다 광조건(조도, 자외선)에서 더 높은 상관계수($r > 0.9$)가 나타났다. 서양종과 동양종 꿀벌의 방화특성을 조사한 결과 꽃에 머무는 시간은 서양종 꿀벌이 평균 6.9초, 동양종 꿀벌이 7.0초로 같은 수준이었으나($p>0.05$), 꽃 간 이동시간은 동양종 꿀벌이 2.4초로 서양종꿀벌(3.1초)보다 20% 유의미하게 짧은 것으로 나타났다($p=0.011$). 따라서 같은 시간에 동양종 꿀벌이 서양종 꿀벌보다 더 많은 꽃을 방문 할 수 있을 것으로 생각된다.

검색어: 화분매개벌, 동양종 꿀벌, 서양종 꿀벌, 일주행동 패턴, 시설재배 딸기

P145

Comparative analysis of reporting status about the Invasive Alien Species Report Center in 2022 and 2023

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외래생물 유입에 대응하기 위해 (환경부)국립생태원에서는 2019년부터 외래생물 신고센터를 운영하고 있으며, 민원 신고에 대한 신속한 대응과 국민 행동요령을 안내하고 있다. 외래생물 전체 신고 건수는 2022년 140건 중 곤충 88건, 2023년 645건 중 곤충 530건으로, 1년 만에 외래생물 전체 신고 건수는 505건, 곤충 신고 건수는 442건이 증가하였다. 2022년 전체 신고 중 붉은불개미(*Solenopsis lnvlcta*) 의심 신고 건수가 78건로 가장 많았으며, 그 중 노랑밑드리개미 12건 등 개미과가 49건으로 확인되었다. 2023년은 전체 민원 신고 중 외래흰개미류 의심 신고가 418건으로 가장 많았고, 붉은불개미 66건 순으로 많았다. 외래흰개미류 의심 신고의 경우 대부분이 국내에서 서식하는 흰개미(*Reticulitermes speratus kyushuensis*)로 190건, 붉은불개미의 경우 밑드리개미류(10건), 주름개미(8건), 권련침벌(8건) 등으로 확인되었다.

검색어: 외래생물, 외래곤충, 외래흰개미, *Reticulitermes speratus kyushuensis,* 신고센터

P146

Long-term storage and growth control of the yellow mealworm, *Tenebrio molitor* Linnaeus

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We introduce a method for preserving yellow mealwom (*Tenebrio molitor*) larvae for an extended period and show that a high percentage of larvae can survive in good health under low-temperature storage conditions combined with specific diapause termination conditions. When storing larvae for 140 days, the storage temperature can be varied based on our goals, giving us control over yellow mealworm production to meet specific demands. To produce adult beetles, storing larvae at 15 °C with wheat bran and ending diapause at 30 °C resulted in 90% pupation rate, with 60% becoming adults in 21 days. If our aim is larvae production, storing them at 10–12 °C with wheat bran and ending diapause at 25–30 °C allows the larvae to reach a suitable weight for processing. This approach ensures long-term storage of yellow mealworm larvae and provides a practical way to control their development, allowing efficient mass production tailored to market demands.

Key words: *Tenebrio molitor*, low-temperature storage, diapause termination temperature

P147

2023 IRA reports and case study for avocado fruit from Philippines

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Division of the risk management, APQA(Animal and Plant Quarantine Agency) is conducting the IRA(Import Risk Assessment) to prevent the introduction of pests when importing foreign agricultural products. In the 2023 IRA, 55 cases of 19 items from 23 countries was analyzed, and fresh avocado(variety: HASS) from the Philippines was concluded in September 2023 and can be imported in accordance with appropriate phytosanitary measures. The main issue in the IRA of fresh avocado fruits from the Philippines was whether HASS variety avocados were host plants of *Bactrocera dorsalis*. As a result of the risk analysis, *B. dorsalis* were included in the pest list that needs to be managed by special risk management. As a risk management for *B. dorsalis*, one trap using methyl-eugenol is installed per 20 ha once a week. After surveying, if the population is more than 2/trap/day, control measures such as adding traps and spraying pesticides are necessary. As equivalence, regionalization, and transparency have been strengthened with the recent entry into force of the mega FTA, a higher level of scientific basis is required. Accordingly, division of the risk management, APQA is working harder to improve its expertise, and we need your cooperation and attention of the IRAs.

Key words: Import risk assessment, quarantine, avocado, fruitfly

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Research on data collection and utilization for smart rearing of edible insects

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식용곤충은 미래식량 자원으로써 우수한 가치를 지니고 있어 해외에서는 사육자동화, IoT 및 AI 기술적용, 수직재배시스템 구축 등 많은 연구가 진행되고 있지만 국내에서는 대규모 사육농가나 곤충스마트팜 기술개발이 부족하여 이를 위한 AI/빅데이터 인프라 구축이 시급한 실정이다. 학습용 인공지능 데이터는 식용곤충으로 활용되고 있는 장수풍뎅이, 흰점박이꽃무지, 갈색거저리, 백강잠, 메뚜기, 풀무치의 생애 주기별 총 6종의 RGB 사진데이터와 분광이미지 데이터 408,000장을 구축하였으며 온도, 습도, CO,, 암모니아, 조도, 수분 등 환경 데이터 200,000세트를 수집하였다. 수집된 데이터는 원시데이터 수집, 원천데이터 가공, 라벨링 데이터 결합, 가공데이터 검수 등을 통해 만들어졌으며 관련 데이터는 AI Hub(www.aihub.or.kr)에서 다운받을 수 있다. 확보된 식용곤충 6종의 데이터는 곤충 종별 성장단계, 환경 변수에 따른 최적의 사육환경 조성, 생산시기 예측, 스마트대량사육 시스템 개발, 제품 가공시 추적이력제 도입, 식용곤충 스마트팜 기술 개발 및 연구 등 다양한 분야에 활용될 수 있을 것으로 예상된다.

검색어: 식용곤충, 기후변화, 질병, 스마트, 데이터

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Investigating the viability of silkworm seeds post extended low-temperature preservation

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누에씨는 매년 계대사육을 통해 자원을 보존하지만, 이 과정에서 잠종의 소실 및 혼합사고 등의 위험이 있어, 누에 유전자원의 효율적이고 안전한 장기보존법 개발이 필요한 상황이다. 본 연구에서는 2년 동안 저온에 보관된 누에 보급품종(백옥잠, 대황잠, 백황잠)과 누에 유전자원(n29, sa2, yang2)의 누에씨를 봄과 가을 사육기에 맞추어 점진법을 사용하여 부화를 유도하였다. 부화된 누에씨의 부화비율과 함께 전령 경과기간, 화용비율, 전견중 등의 사육 성적을 조사하였다. 2년간 저온 보관된 누에씨의 부화비율은 보급품종에서 87~88%, 유전자원에서는 71~75%로 나타났다. 화용비율은 보급품종에서 79~89%, 유전자원에서는 71~79%로 조사되었다. 품종 지정 시 사육 성적과 비교해 볼 때, 부화비율, 화용비율, 번데기 무게, 고치무게 모두 감소하는 경향을 보였다. 또한, 2년 동안 저온에 보관된 후의 누에씨 부화기간은 1년 동안 저온에 보관된 누에씨보다 1~2일 더 길었다.

검색어: 누에, 누에씨, 저온보존

P150

Effects of a sound insect-based animal assisted therapy program on depression in the elderly

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본 연구는 소리곤충을 활용한 동물매개치료 프로그램이 노인의 우울에 어떠한 영향을 미치는지 살펴보고자 하였다. 연구대상은 I시에 위치한 I치매안심센터에서 추천을 받은 우울 척도 검사에서 5점 이상을 받은 노인 20명이며, 실험집단과 통제집단 각 10명을 선정하였다. 프로그램은 2023년 6월부터 8월까지 주 1회, 회기당 50분씩 총 12회기를 실시하였다. 효과 검증을 위해 SPSS v.26을 활용하여 집단 간 동질성 검증(Mann-Whitney U test)을 하여 동질성이 입증이 된 후 각 집단의 사전과 사후에 노인 우울 척도 측정을 실시하고 비모수 윌콕슨 부호 순위 검정(Wilcoxon signed-rank test)으로 분석하였다. 그 결과, 실험집단의 우울 전체의 사전ㆍ사후에 유의미한 차이가 나타났다($Z=-3.53$, $p<.05$). 그러나 통제집단의 우울 전체의 사전ㆍ사후에는 유의미한 차이가 나타나지 않았다($Z=-1.06$, $p>.05$). 따라서 본 연구는 소리곤충을 활용한 동물매개치료 프로그램이 노인의 우울에 긍정적인 영향을 준 것으로 확인이 되었다. 이번 연구결과는 소리곤충을 활용한 정서 및 심리 치료에 대한 과학적 근거를 제시하여 관련 분야 활성화에 기여할 수 있을 것으로 기대된다.

검색어: 소리곤충, 노인, 우울

본 연구는 농촌진흥청 지역특화작목 기술개발(과제 번호 : PJ016956) 지원에 의하여 연구가 수행되었습니다.

P151

Effects of a sound insect counseling program on emotional expression in the elderly

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본 연구는 소리곤충 상담 프로그램이 노인의 정서표현에 도움을 주는지를 확인하고자 하였다. 연구대상은 남녀 구분 없이 만 65세 이상이며 정서표현 척도 검사에서 51점 이하, 의사소통에 문제가 없는 자로 실험집단 10명 통제집단 10명을 선정하였다. 프로그램은 2023년 7월부터 8월까지 주 2회, 회기당 50분씩 총 12회기를 실시하였다. 효과 검증을 위해 SPSS/WIN 26.0을 활용하여 집단 간 동질성 검증을 하고 입증이 된 후 실험집단과 통제집단의 사전과 사후에 노인 정서표현 척도 측정을 실시하고 분석하였다. 그 결과, 실험집단의 정서표현 전체의 사전 평균 56.25에서 사후평균 66.38로 유의미한 차이가 나타났다($Z=-3.41$, $p<.05$). 그러나 통제집단의 정서표현 전체의 사전평균 58.15에서 사후 평균 58.92로 유의미한 차이가 나타나지 않았다($Z=-0.43$, $p>.05$). 향후 본 연구결과를 기반으로 소리곤충을 활용한 노인의 정서표현 향상에 이점을 유도하는 소리곤충 활용 상담 프로그램으로 확대 적용할 수 있을 것으로 기대된다.

검색어: 소리곤충, 노인, 정서표현

본 연구는 농촌진흥청 지역특화작목 기술개발(과제 번호 : PJ016956) 지원에 의하여 연구가 수행되었습니다.

P152

Flight patterns of *Apis mellifera* and *Bombus terrestris* near their hives for image deep learning

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Bee traffic at the hive entrance can be used as an important indicator of foraging activity. We investigated patterns of honeybees and bumblebees near their hives as a basis for calculating bee traffic using the image deep learning. The flight pattern near the hive differed significantly according to bee at entering and leaving the hive. Honeybees mainly showed flight that changed flight direction more than once (69.5%), whereas bumblebees mainly performed straight flight (48.7%) or had a single turn (36.5%) in flight. When bees entered the hive, honeybees primarily showed one-turn or two-turn flight patterns(88.5%), and bumblebees showed a one-turn flight pattern (48.0%). In contrast, when leaving the hive, honeybees primarily showed a straight flight pattern (63.0%), and bumblebees primarily showed a straight or one-turn pattern (90.5%). There was a significant difference in flight speed according to the flight pattern. The speed of straight flight (0.89±0.47 m/s) was 1.5 to 2.1 times faster than flight where direction changed. Therefore, our results can help determine the capturing and recognizing the flying image of bees when calculating bee traffic by image deep learning.

Key words: Flight speed, deep leaening, *Apis mellifera*, *Bombus terrestris*

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The field application and test of insect pollinators in 5 fruit and vegetable crops

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국내 원예작물에서 화분매개곤충의 의존도는 해마다 증가하고 있다. 우리는 사과, 딸기 등 화분매개곤충의 의존도가 높은 주요 과수와 시설작물에 대하여 화분매개곤충의 사용기술을 개발하고 이를 현장에 적용하는 연구를 수행하고 있다. 2021년부터 2022년까지 딸기, 키위 등 5가지 주요 농작물에서 화분매개벌을 적용한 결과, 딸기에서 뒤영벌의 적용결과 기존 꿀벌과 통계적으로 같은 수준의 화분매개효과를 나타내었으며, 하우스에서 농약적용시 하우스 밖으로 벌통을 위치시키는 것이 방치보다 벌의 소실을 20% 더 감소시킬 수 있었다. 인공수분에 의존하고 있는 씨없는 수박에서 수분수 식재와 꿀벌을 이용함으로 기존 벌 방사보다 16% 착과율을 향상시킬 수 있었다. 시설고추에서 꿀벌과 뒤영벌의 혼합사용시 기존 꿀벌 방사보다 고추 수량이 10% 향상되었고, 토마토에서 660㎡당 뒤영벌의 봉군량을 1.5배 증가시 토마토 수량은 4.4% 향상되었다. 키위는 꿀벌로 기존의 인공수분을 충분히 대체할 수 있었고, 인건비가 60%이상 절감되었다. 또한 현재 시판중인 30종의 살충제와 27종의 살균제에 대하여 24시간내 반수치사를 보인 농약은 각각 살충제 6종와 살균제 4종 이었다. 이어서 2023년부터 참외, 멜론, 사과, 단감에 대한 현장적용연구가 진행되고 있다.

검색어: 화분매개, 꿀벌, 뒤영벌, 딸기, 수박, 키위

P154

Research on smart beekeeping data collection and utilization

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최근 기후변화 등으로 인한 꿀벌의 폐사가 증가하고 있으나 관련 데이터가 부족하여 이에 대한 연구가 어려움을 겪고 있어 학습용 인공지능 데이터를 구축하여 양봉 산업 발전에 기여하고자 한다. 학습용 데이터로 생애주기별 5단계(알, 애벌레, 번데기, 숫벌, 여왕벌), 종봉별 4가지(이탈리안, 카니올란, 한봉, 호박벌), 발생질병 1종(백묵병) 총 10가지 클래스를 데이터 수집장소 6곳(장성, 포천, 칠곡, 완주, 의령, 장흥)에서 학습용 데이터를 274,206장 구축하였다. 수집된 데이터는 원시데이터, 원천데이터 가공, 라벨링 데이터 결합, 가공데이터 검수 등을 통해 만들어졌으며 관측지에서 온습도, CO, CH_4, NH_3 등 환경데이터를 200,000건 확보하여 데이터 라벨링을 수행하였다. 데이터는 AI Hub(www.aihub.or.kr)에서 다운받을 수 있다. 확보된 데이터는 꿀벌의 생애 단계별, 종별, 건강 상태별 이미지 데이터로 구성되어 있어 양봉 관리 자동화, 꿀벌 질병 예측, 양봉 기술 개발 및 연구 등 다양한 분야에 활용될 수 있을 것으로 예상된다.

검색어: 양봉, 기후변화, 질병, 스마트, 데이터

P155

Biological control of entomopathogenic nematode *Heterorhabditis megidis* (Rhabditida: Heterorhabditidae) GJ1-2 from Korea

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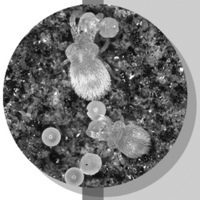
곤충병원성 선충인 *Heterorhabditis. megidis*(큰형광병원선충)는 참나무 군락지(광주광역시 소재) 사양토에서 분리 동정되었고, 곤충병원성을 가지는 공생세균은 *Photorhabdus temperata*로 분리 동정되어 각각 GJ1-2로 명명하였다. *H. megidis* GJ1-2는 고구마(주황미) 큰 검정풍뎅이 *Holotrichia parallela*에 대한 방제 효과는 평택시(경기도 소재)와 논산시(충청북도 소재)의 노지 재배 사양토에서 관주처리 30일 후 각가 81.1%, 78.9%로 나타났으며, 인삼(재래종) 거세미나방 *Agrotis segetum*에 대한 방제 효과는 이천시(경기도 소재)와 청주시(충청북도 소재)의 비가림 재배(차광막 설치) 사양토에서 관주처리 14일 후 방제가는 각각 79.9%, 80,2%로 나타났다. *H. megidis* GJ1-2는 고구마(주황미)와 인삼(재래종)에서 약제 처리 후 3, 7, 14일 후 외관상 약해는 나타나지 않았다.

검색어: 곤충병원성 선충, 큰형광병원선충, 공생세균, 고구마 큰 검정풍뎅이, 인삼 거세미나방, 방제 효과

Poster Presentation – ESK



A-01

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

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

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

A-02

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

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

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

A-03

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

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

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

A-04

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

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

A-05

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

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

Key words: new record, parasitoids, Perilissini, wasps

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

A-06

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

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

Key words: new record, Orthocentrinae, parasitoids, wasps

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

A-07

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

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

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

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

A-08

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

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

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

A-09

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

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

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

A-10

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

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

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

A-11

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

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

A-12

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

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

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

A-13

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

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

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

A-14

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

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

Key words: biodiversity, morphology, new species, taxonomy

A-15

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

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

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

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

A-16

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

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

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

A-17

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

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

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

A-18

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

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

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

A-19

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

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

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

A-20

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

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

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

A-21

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

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

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

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A-22

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

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

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

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

A-23

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

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

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

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A-24

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

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

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

A-25

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

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

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

A-26

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

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

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

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A-27

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

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

Key words: Dolichopodinae, intertidal zone, identification key

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A-28

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

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

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

A-29

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

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

Key words: Phaoniinae, Dichaetomyiini, unrecorded species

A-30

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

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

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

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B-01

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

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

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

B-02

Benthic Macroinvertebrates monitoring in the weirs of Han River

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

검색어: 한강, 보, 저서성 대형무척추동물, 군집분석

B-03

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

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

검색어: 흰줄숲모기, 도시열섬, 기후변화, AWS, 부화율

B-04

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

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

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

B-05

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

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

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

B-06

Seasonal community fluctuation of benthic macroinvertebrates in Gonyangcheon Estuarine Wetland

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

Key words: Gonyangcheon, Estuarine wetland, Benthic Macroinvertebrates

B-07

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

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In the Gucheon stream of Deogyusan National Park, a survey was conducted at three sites (six sites in total) in 2018 and 2021. A total of benthic macroinvertebrates of 107 taxa 46 families 13 orders in 6 classes of 5 phyla were found. According to the analysis of the appearance by year, a total of 87 species were surveyed in 2018, and a total of 89 species were surveyed in 2021. As a results to the functional feeding group analysis, Gathering-Collector (GC) accounted for a high species share (2018: 29.89%, 2021: 25.84%). In the functional habitat group analysis, Clinger (CL) accounted for a high species share (2018: 56.32%, 2021: 57.30%). Average annual community indices analysis, DI 0.38(±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.

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

B-08

Community structure of benthic macroinvertebrates in Wangpicheon water system

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왕피천 수계 내 저서성 대형무척추동물의 군집구조 분석을 위해 총 5개 지점에서 2023년 총 4회(4월, 6월, 8월 11월) 조사를 실시하였다. 조사기간 중 저서성 대형무척추동물은 총 5문 7강 17목 77과 156종 17,179.1개체/㎡가 채집되었다. 수환경 변화에 민감한 E.P.T. 분류군은 전체 156종 중 91종이 출현하여, 전체 출현종의 58.3%를 차지하였다. 섭식기능군(FFGs) 분석결과, 종 출현 양상은 육식성 포식자(Predator: P)가 51종(32.69%)으로, 개체 출현 양상은 주워먹는 무리(Gathering-collector: GC)가 6,867.2개체/㎡(39.97%)로 높은 비율로 출현하였다. 서식기능군(FHGs) 분석결과, 붙는 무리(Clinger: CL)가 70종(44.87%), 12,720.6개체/㎡(74.04%)로 가장 높은 비율로 출현하였다. 군집지수 분석결과, 우점도지수(DI) 0.43, 다양도지수(H′) 3.51, 풍부도지수(R1) 4.59 균등도지수(J′) 0.77로 나타났다. 생물학적 수질 판정 지수(BMI) 분석결과, 평균 92.36(±0.83)으로 모든 지점에서 “매우 좋음”으로 판정되었다.

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

B-09

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

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

Key words: 광릉 숲, 나비상, 기후변화, 지구온난화

B-10

Distribution of hymenoptera insects in Korean national parks

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

Key words: Korea National Park, Hemiptera, Species diversity

B-11

Biodiversity assessment of insect population in Ilgwang, Busan

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

Key words: Biodiversity, Community analysis, insect, Policy, Least Cocern

B-12

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

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

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

B-13

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

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

B-14

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

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

B-15

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

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

B-16

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

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

모델 예측 정확도(AUC)는 0.983으로 출현지점을 정확하게 예측하는 비율이 매우 높다고 할 수 있다. 모델 예측 정확도의 증감에 영향을 주는 환경변수 중 먹이식물의 기여도가 70%를 상회하는 것으로 나타났다. 현재 75% 이상 분포 가능지역은 전라남도 진도군 일대와 경상북도 포항시 일대로 나타났으나 2050년에는 서해안을 따라 태안군까지 동해안을 따라 북한의 고성군까지 분포가 가능한 것으로 나타났다. 또한 75% 이상 분포 가능 면적은 현재 423㎢에서 2050년에는 9,270㎢로 약 대한민국 면적의 1/10 정도 확산될 것으로 예측된다.

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

B-17

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

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[4]Trackers School

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

검색어: 등검은말벌, 외래종, 오소리, 직박구리, 천적

B-18

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

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

검색어: 등검은말벌, 외래종, 양봉장, 둥지밀도, 의성, 안동

B-19

Quantitative study of wild bees diversity in Seocheon Maeul-soop

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

검색어: 야생벌, 다양성, 수분매개, 베인트랩, 마을숲

B-20

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

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

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

B-21

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

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

검색어: 곱슬털쉬파리, 법의곤충학, 사후경과시간, 발육 성장 속도

B-22

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

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

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

B-23

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

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

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

B-24

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

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

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

B-25

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

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

검색어: 연두금파리, 법의곤충학, 사후경과시간, 사육 실험

B-26

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

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서식반경이 좁고 개체수가 감소하는 경향을 보이고 있어 멸종위기 종으로 지정된 뚱보주름메뚜기(*Haplotropis brunneriana* Saussure 1888)를 대상으로 개체군 추이와 적절한 모니터링 방법을 확인하기 위해 방형구법과 선조사법을 이용하여 밀도 조사를 수행하였다. 뚱보주름메뚜기에 대한 조사 자료가 부족하여 먼저 방형구법을 이용하여 2021년 3월부터 6월까지 월 1회 서식지 내 개체군 밀도를 확인한 결과 6개체/100㎡(3월), 2개체/100㎡(5, 6월)로 각각 영월과 제천에서 가장 많은 개체가 확인되었고, 지역 간에 유의한 차이는 나타나지 않았다($p > 0.05$). 선조사법을 이용하여 2022년 3월부터 6월까지 월 3회 개체군 밀도를 확인한 결과 1.5(±0.79)개체/100㎡, 0.76(±0.11)개체/100㎡로 각각 영월과 제천에서 4월에 가장 많은 개체가 확인되었고, 지역 간에 유의한 차이는 나타나지 않았다($p > 0.05$). 조사 방법에 따라 시기와 면적에 차이가 있어 이 두 방법을 정확히 비교할 수 없으나, 공통 적으로 3, 4월 약충 시기에 많은 개체가 확인되는 것을 알 수 있었다.

검색어: 뚱보주름메뚜기, 개체군 모니터링, 선조사법, 방형구법

B-27

Effects of removal of artificial structures in valleys on benthic macroinvertebrates

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

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

Key words: 저서성대형무척추동물, 인공구조물, 복원

B-28

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

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

검색어: 털진드기, Trombiculidae, 발생감시, 쯔쯔가무시증

B-29

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

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

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

B-30

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

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

검색어: 참진드기, 진드기매개질환, SFTS

C-01

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

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

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

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C-02

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

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

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

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

C-03

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

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

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

C-04

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

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

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

C-05

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

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

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

D-01

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

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

검색어: 장수풍뎅이, 가수분해물, 항비만, 지방세포, 지질축적

D-02

Anticoagulant properties and therapeutic potentials of wasp venom

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

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

E-01

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

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

Key words: Athaliidae, mitogenome, phylogenetic status, Symphyta

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E-02

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

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

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

E-03

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

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

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

E-04

Functional importance of group I lytic polysaccharide 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-05

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

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

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

E-06

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

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

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

E-07

Study on immunological role of *Tm*Pelle in *Tenebrio molitor*

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

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

E-08

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

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

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

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E-09

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

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

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

E-10

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

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

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

E-11

Enhancement of Antimicrobial peptides production by epigenetic regulation

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

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

E-12

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

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

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

E-13

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

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

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

E-14

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

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

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

검색어: *Haemaphysalis longicornis*, microbiome

E-15

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

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

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

E-16

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

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

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

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

E-17

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

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

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

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

E-18

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

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

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

검색어: *Polyphylla laticollis manchurica*, transcriptome analysis

E-19

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

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

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

E-20

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

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

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

F-01

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

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

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

F-02

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

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

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

G-01

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

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

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

H-01

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

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

Key words: *Sarcophaga peregrina*, Forensic entomology, Post-mortem interval (PMI_min), Decomposition, Temperature-dependent development

H-02

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

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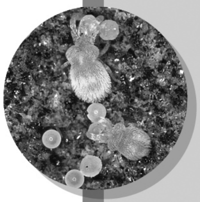
Ecdysteroids were first discovered in silkworm larvae in 1954 and are known to act as molting hormones in insects. Recently, biologically active phytoecdysone has gained increasing interest as it affects many physiological functions in mammals and has been reported to have a wide range of pharmacological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

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

Small Group Meeting



SG1-1

dsRNA pesticides from laboratory to industry

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과거 약 50년간 국내에서는 화학농약 기반의 병해충 방제가 지속적으로 농업 생산량을 안정적으로 유지시켜왔다. 그러나 무분별한 화학 농약 사용은 병해충의 약제저항성 발달을 유발하였으며, 이는 기존의 방제효과를 얻기 위해 고농도 살포가 불가피하였으며, 또한 막대한 개발 비용이 필요한 신규 작용점 살충제 개발로 고비용의 방제기술로 전락하게 되었다. 여기에 대부분의 살충제가 신경계에 작용하여 인축 및 비표적 생물계에 영향을 주어 광범위한 사용에 제한을 받게 되었다. 대체 방제기술로 천적과 미생물에 의존하는 생물농약은 방제효율에서 대부분 화학약제의 수준을 따르지 못해 농민의 절대적 호응을 받지 못하였다. 이 가운데 새로운 패러다임의 생물농약으로 살포용 dsRNA 농약이 화학농약의 방제 효과와 버금가는 시험 농가 반응으로 2023년 12월에 미국 EPA 등록을 받게 되었다. 향후 살포용 dsRNA는 살충제는 물론이고 살균제 및 제초제에 이르기까지 작물보호제 시장 전체에 영향을 미치게 된다. 이에 국내에서도 dsRNA를 실험실 단계에서 산업계 적용 기술 개발 단계로 전환하여야 할 시점에 이르게 되었다.

검색어: 생물농약, dsRNA, 살충제, 살균, 제초제

SG1-2

Laboratory Research: Development of dsRNA as a Sustainable Bioinsecticide

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RNAi (RNA interference, RNA 간섭)은 타겟 유전자의 mRNA 시퀀스와 상동한 이중 가닥 RNA (double-stranded RNA)에 의해 일어난다는 사실이 밝혀진 이후, 유전자의 기능을 파악하는 연구 도구로 활용되다가, 2018년에 비로소 사람의 유전자 치료제로 상용화가 되었다. 지금은 더 많은 질병들의 유전자 치료제를 만들기 위해 다양한 회사들이 임상을 진행하고 있다. 농업의 분야에서는 곤충의 '생존 필수 유전자'를 타겟함으로써 해충 방제제로 개발되어 서부 옥수수 뿌리벌레(Western corn rootworm)를 RNAi로 방제하기 위한 제품이 종자 형식으로 상용화 되었고, 최근에는 심각한 농약저항성을 가진 콜로라도 감자벌레(Colorado potato beetle)를 RNAi로 방제하기 위해 '스프레이 방식의 뿌리는 dsRNA'가 상용화되었다. 추후에 더 많은 해충을 타겟으로 하는 제품이 개발될 예정이다. 본 발표에서는 위에 언급한 상용화된 dsRNA 시퀀스의 환경안전성평가와 관련된 연구, off-target effect, siRNA 활용, nanoparticle 등 RNAi 기술을 보다 안전하고 유용하게 농업적으로 사용할 수 있는 방법에 대한 '실험실의 역할'이 무엇인지 알아보고자 한다.

검색어: RNA interference, Gene siliencing, biopesticide, 환경안전성, dsRNA

SG1-3

Industrial aspects: Development of dsRNA as a Sustainable Biopesticide

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Since the gene expression interference induced by dsRNA was discovered, dsRNA has been considered as an antiviral agent and pesticide to protect beneficial insects and crops, respectively. Recently, dsRNA was classified as IRAC mode of action group 35, and the first dsRNA pesticide, Calatha of GreenLight Bioscience, has been approved by EPA. Also an animal drug for Asian honeybee, HoneyGuard-R of Genolution is about to be approved by APQA. During the last two decades, hundreds of papers already had demonstrated the application and capability of dsRNA for agriculture, however, we have just a few commercialized products at hand at this moment. It is time to understand the processes, hurdles and limitations on the industry side that are indispensable for the development, registration and commercialization of dsRNA-based products.

Key words: dsRNA, RNAi, pesticide, animal drug, registration

SG1-4

Study on institutionalizing pesticide registration standards for industrialization of dsRNA

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국내외적으로 기후변화, 이상기상 등 다양한 요인이 新문제 병해충의 발생을 가속화하고 있으나, 반대로 국제기구에서 2030년까지 화학농약의 사용 및 위해도를 50%로 낮출 것을 요구하고 있다(생물다양성협약 COP15. 2022.12). 따라서 화학농약을 줄이면서 효과적으로 병해충을 방제할 수 있는 대안을 찾아야 한다.

화학농약의 대안으로 생명과학에 공학적 기술개념을 도입하여 인공적으로 생명체의 구성요소·시스템을 설계·제작·합성하는 학문분야로 합성생물학이 주목받고 있다. 코로나19 백신개발과정에 합성생물학을 활용하여 개발기간을 단축한 사례(mRNA 백신)도 있다. 미국 농업분야에서는 dsRNA를 이용한 천연식물보호제(생물농약)의 개발은 이미 상용화 단계로 넘어서고 있다. 이에 우리나라도 합성생물학을 활용한 농약의 개발과 상용화를 지원할 수 있는 제도적 기반을 마련할 시점이다. 본 발표에서는 합성생물학 기술을 이용한 新천연식물보호제의 개발과 상용화에 필요한 등록기준 마련 필요성과 고려할 사항에 대해 다각적으로 논의하고자 한다.

현재 우리나라에서 농약은 「농약관리법」 에 따라 관리되며, 유효성분으로 쓰이는 원료의 종류에 따라 화학농약과 천연식물보호제로 구분되고 있다. 화학농약은 “화학적으로 합성한 유효성분으로 제조한 것”을 말하며, 천연식물보호제는 “살아있는 미생물 또는 자연계에서 생성된 유기화합물 및 무기화합물”을 유효성분으로 제조한 것“을 말한다. dsRNA 농약 등록을 위해서는 dsRNA 등 합성생물학 기술을 이용한 농약이 “자연계에서 생성된 유기화학물”로 분류될 수 있는 지에 대한 검토가 필요하며, dsRNA를 활용한 농약의 등록 기준이 마련되어야 한다. 기준을 마련하기 위해서는 합성생물학 기술에 대한 정확한 이해가 선행되어야 하고, 안전성에 대한 다각적인 검토는 물론, 사회적 합의와 공감대 형성이 이루어져야 할 것이다.

우선 가장 중요한 이슈는 역시 유전자변형생물체(이하 ”LMO“) 문제이다. 국내에서는 LMO 작물의 재배 자체에 대한 논란이 많은 상황이라는 점과 LMO일 경우 농약으로 등록시 기준 적용에 차이가 크기 때문이다. 천연식물보호제는 화학농약보다는 등록시 요구되는 자료가 많이 간소화되어 있지만, LMO에 해당되면 그렇지 않다. 실제 미국에서 등록된 dsRNA 농약에는 LMO에 해당되는 것과 해당되지 않는 것이 있다. 따라서 국내에서 천연식물보호제로 등록하기 위해서는 먼저 dsRNA를 활용한 기술이 LMO에 해당되는 지 여부가 먼저 정립되어야 하고, 해당 dsRNA 원제(Technical) 또는 해당 dsRNA 제품(Item)이 LMO 기술이 적용되지 않았음을 입증할 수 있는 체계의 정립이 필요할 것이다.

또한 국제기준과 조화의 문제를 고려해야 한다. OECD 발간 문서(ENV/CBC/MONO(2023)26, ENV/JM/MONO(2020)26)에 따르면 dsRNA 농약은 dsRNA의 변이가 인체, 환경은 물론, 표적/비표적 유기체에 어떠한 영향을 미칠수 있는지에 대한 시험이 필요하고 이는 각 국가별 규제요건에 따라 달라질 수 있다고 밝히고 있다. 국내 기준을 마련하기 위해서는 외국 사례를 정밀하게 조사분석한 후 국내 여건에 맞도록 기준을 정립해야 할 것이다.

마지막으로 새로운 기술은 항상 부작용에 대한 우려가 따르기 마련이므로 전문가에 의해 과학적 근거에 기반한 기준안이 마련함은 물론, 해당 기준안에 대한 대국민 소통/공감을 형성하는 과정도 필요하다.

dsRNA농약은 우리나라에 새로운 도전이자 기회가 일 수 있다. 농약원제 개발에 뒤처져 수입에 의존하는 산업에서 벗어나, 세계를 선도하며 수출하는 농약산업으로 바꿔야 할 시점인 것 같다.

SG2-1

Climate change and insect pollination relative to ecosystem service

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Pollination is an important ecosystem service mostly provided by diversity of pollinating insects and other animals. As in the anthropocene biodiversity crisis with the climate change, pollination systems are experiencing strongly challenged such as pollinator diversity and abundance decline, pollinator health weakness, pollinator-plant network instability as well as the crop-pollinator habitat fragmentation and insuitability. Here we present some research progress conducted from our group in the last decade. As the pollination dependence of Korean agriculture increases, pollination contribute ap. one forth of national agricultural production, and is responsible substantial portion of vitamin and mineral provisioning. Pollinator diversity is declining in various crop systems and network connectivity is decreasing. Still in agricultural landscape, honeybee (Apis spp) is the main pollinator, accounting ap. 70% of bees, and showed the possible resource partitioning between the native, A. cerana and the introduced, A. mellifera. Simulation of crop-pollinating insect distribution suitability showed up and down directional responses, but more on the negative Further research area for better understanding and stabilizing the plant-pollinator system was proposed.

Key words: diversity, network, landscape, suitability, stability

SG2-2

Hymenoptera, especially Bees as Important Pollinators

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Hymenoptera is one of the most important pollinators for many crops and wild plants in Korea. Many species visit in flowers for acquirement energy source of adults, and especially bees need pollen for rearing larvae. So, bees forage on flowers more than other insects. In 2023, specice number of bees in Korea is 308 species under 6 families, 38genera. However, many bees as like bumblebees are reduced rapidly because of climate change to warm, habitat destruction as like urbanization and pestcide abuse as like Neonicotinate. For example, in Gwangreung forests there were 6 species records : *Bombus ignitus, B. ardens, B. koreanus, B. ussuriensis, B. atripes* and *B. opulantus*. But, in 2023 we could find only two species *Bombus ignitus* and *B. ardens*. Bees need protection of Habitat, healthe, and food plants by human.

Key words: bee, pollination, bumblebee, Hymenoptera

SG2-3

Development of pollinator inventory: Dipteran pollinators

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국립수목원 산림생물다양성연구과는 2023년부터 산림생태계 보전을 위한 화분매개곤충 특성연구 사업을 추진하면서 그 첫 번째 단계로 화분매개곤충 인벤토리 구축을 위한 연구를 수행하고 있다. 수목원 4개소(강원도립화목원, 경상남도수목원, 국립수목원, 대구수목원)에서 9종의 식물(국수나무, 미선나무, 산수유, 산철쭉, 생강나무, 수수꽃다리, 아까시나무, 진달래, 히어리)을 대상으로 각 식물에 어떤 곤충들이 방문하는지 쓸어잡기 방법을 이용하여 확인하였다. 조사된 곤충 중에서 가장 많은 개체수를 차지하고 있는 곤충은 파리목(1,407개체)이었으며, 26과의 다양한 파리목 곤충들을 확인할 수 있었다. 그중에서도 가장 많은 개체수를 차지하고 있는 과는 재니등에과(4속, 5종, 651개체), 꽃등에과(24속, 34종, 302개체), 기생파리과(8속, 9종, 111개체)로 집계되었으며 이 중에서도 꽃등에과의 종다양성이 가장 높게 나타났다. 조사한 식물 중에서 가장 많은 파리목 곤충이 모인 식물은 수수꽃다리와 미선나무였고, 각각 314, 308개체 이상의 파리목 곤충을 확인하였다. 반면 파리목 곤충의 방문이 가장 저조한 식물은 국수나무와 아까시나무였으며 확인된 개체수는 각각 38, 45개체였다. 우리는 화분매개곤충에 대한 인벤토리 구축을 통해 화분매개곤충에 대한 다양한 분류학 및 생태학적 데이터의 지속적인 확보를 위해 노력하고 있으며, 본 소모임에서 이에 대한 발전방안 및 축적된 데이터의 활용방안에 대해 모색하고자 한다.

검색어: 화분매개곤충, 파리목, 재니등에과, 꽃등에과, 기생파리과

SG2-4

Review of pollinating Nitidulidae (Coleoptera: Cucujoidea) in Korea

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The family Nitidulidae, the largest group in Cucujoidea, comprises approximately 350 genera and nearly 4,500 recorded species across ten subfamilies. In Korea, 86 species of Nitidulidae have been recorded. They are well-known for their diverse feeding habits. Anthophagy is a common habit, with certain species from the Epuraeinae, Carpophilinae, and Meligethinae recognized as pollinators. Despite their ecological significance, these groups rarely studied in Korea, due to their small size and morphological similarities. Our study reviews Korean species in three subfamilies, identifying 14 unrecorded species and 2 newly described species, and describes their ecological habits.

Key words: Coleoptera, Nitidulidae, Epuraeinae, Meligethinae, pollinator

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**THREAT TO INSECT BIODIVERSITY BY HUMANS &
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