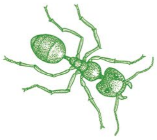
자료집 보기



ESG in Entomology

2025년
한국곤충학회 · 한국응용곤충학회 공동
춘계학술대회

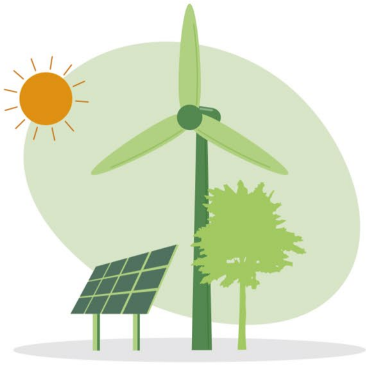
일 정 | 2025년 4월 24일(목) ~ 25일(금), 1박 2일

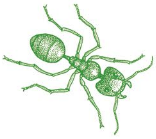
장 소 | 소노캄 비발디파크

주 최 | (사)한국곤충학회, (사)한국응용곤충학회

주 관 | (사)한국곤충학회, (사)한국응용곤충학회, 국립농업과학원

후 원 | 강원관광재단





ESG
in Entomology

2025년
한국곤충학회·한국응용곤충학회 공동
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주관 | (사)한국곤충학회, (사)한국응용곤충학회, 국립농업과학원

후원 | 강원관광재단

인사말

존경하는 한국곤충학회 및 한국응용곤충학회 회원 여러분

2025년 한국곤충학회와 한국응용곤충학회가 공동으로 주최하는 3번째 춘계학술대회에 참석해 주신 모든 분들께 진심으로 환영의 인사를 드립니다. 이 자리를 통해 곤충학자님들과 다시 만나 학문적 성과를 나누고, 미래를 함께 논의할 수 있게 되어 매우 뜻깊게 생각합니다.

이번 학술대회는 “ESG 시대, 곤충과 함께 여는 지속가능한 미래”를 주제로, 곤충학이 환경(Environment), 사회(Social), 지배구조(Governance)라는 시대적 요구에 어떻게 기여할 수 있을지를 다각도로 조망하고자 합니다. ESG는 단순한 트렌드를 넘어, 연구와 산업, 정책의 전반에 걸쳐 요구되는 핵심 가치로 자리잡았습니다. 이러한 변화 속에서 곤충학은 생물다양성 보전, 친환경 방제기술, 대체단백질 자원화, 바이오소재 개발 등 다양한 응용 가능성을 바탕으로 그 역할이 점점 확대되고 있습니다.

학술대회에서 발표될 다채로운 연구들은 곤충학의 학문적 깊이를 더할 뿐만 아니라, 실질적 사회기여를 위한 기반이 될 것입니다. 특히 이번 학술대회는 과학기술정책, 산업화 등 학제 간 융합적 논의가 함께 이루어지는 중요한 장이 될 것으로 기대됩니다.

오늘날 우리에게 주어진 과제는 단지 연구성과를 축적하는 데 그치지 않습니다. 기초연구에서 출발한 지식이 어떻게 사회적 가치로 확장될 수 있을지, 그리고 그 과정에서 곤충학이 어떤 방향성을 갖추어야 할지를 고민해야 할 시점입니다. ESG라는 프레임은 이러한 고민에 실천적 기준을 제시하며, 학문과 사회의 간극을 좁히는 가교 역할을 해줄 것입니다.

이번 학술대회를 위해 헌신적으로 준비해 주신 양 학회의 학술위원장님과 사무국장님 총무간사님, 학회 임원진 여러분께 깊이 감사드리며, 바쁜 일정 속에서도 발표와 토론에 적극적으로 참여해 주신 모든 곤충학자 여러분께도 진심으로 감사의 말씀을 전합니다. 특히, 미래 곤충학을 이끌어갈 신진 연구자들과 대학원생 여러분의 열정과 참여가 이 자리를 더욱 빛내주고 있습니다.

이번 대회를 통해 여러분 모두가 학문적 교류의 기쁨을 나누고, 지속 가능한 곤충학의 미래를 함께 그려나가시기를 바랍니다. 뜻깊고 유익한 시간이 되시기를 기원합니다.

감사합니다.

2025년 4월 24일
(사)한국곤충학회 회장 **이용석**

인사말

곤충학에서의 ESG - 지속 가능성과 사회적 책임을 향한 새로운 접근 -

안녕하십니까?

이번 춘계학술대회는"ESG in Entomology"를 주제로 한국곤충학회와 한국응용곤충학회가 공동으로 개최하고 있습니다. 먼저 학회를 준비하는데 모든 노력을 다하신 양학회 학술위원회 위원님들께 깊이 감사를 드리며, 이 자리를 빛내주시고 계신 모든 회원님들께도 감사를 드립니다.

이 기회를 통하여 ESG 즉 "사회가치경영"속에서 곤충학과 응용곤충학의 지평을 짚어 보고자 합니다. 최근 농업과 생명과학 분야 전반에서도 ESG의 개념이 자리잡고 있습니다. ESG는 단순한 경영 지표를 넘어, 환경 보호, 사회적 가치 실현, 투명한 거버넌스를 아우르는 지속 가능한 발전 프레임워크로 자리 잡고 있으며, 이러한 흐름은 곤충학 분야에서 곤충과 인간, 생태계 간의 복잡한 관계를 보다 윤리적이고 지속 가능한 방식으로 재구성할 필요성이 있음을 말해주고 있습니다.

첫째, 환경(Environmental) 측면에서 생물다양성 보전, 자연 생태계 내 곤충의 기능적 가치 이해, 그리고 친환경 해충관리 전략(IPM, biological control 등)의 확산은 ESG의 환경 요소와 직결된다고 할 수 있습니다. 특히 곤충은 생태계의 기능을 유지하는 핵심 그룹으로서, 화분매개, 분해, 먹이망의 유지 등 다양한 역할을 수행합니다. 따라서 곤충 다양성의 감소는 생태계 회복탄력성 저하와 직결되며, 이는 응용곤충학 연구의 환경적 책무를 더욱 강화시킵니다.

둘째, 사회적 가치(Social) 영역에서 곤충학은 다양한 방식으로 사회적 가치를 창출할 수 있습니다. 최근에는 곤충 단백질을 활용한 식용곤충 산업, 해충 발생정보의 디지털화 및 공유를 통한 농업 현장의 정보격차 해소, 지역 사회와 협력하는 시민과학(Citizen Science) 프로젝트 등이 그 예라고 봅니다. 이러한 접근은 과학의 사회적 신뢰를 높이고, 학문이 공동체 발전에 기여할 수 있는 통로를 제시한다고 생각합니다.

셋째, 지배구조(Governance) 측면에서는 곤충학 연구와 실천의 윤리성, 투명성, 협치(거버넌스) 강화가 요구됩니다. 특히 생물자원의 활용과 보존, 연구 자료의 공유 및 접근성(open data), 정책 결정에의 과학적 근거 제공 등은 거버넌스 원칙에 부합하는 곤충학의 실천 영역이 될 것입니다. 또한, 농업 방제 정책이나 생물다양성 관련 법안의 설계에 있어 편협되지 않은 곤충학자의 과학적 소통과 책임 있는 참여가 강조될 수 있습니다.

결국, 곤충학에서의 ESG는 단순히 기존 연구에 ESG 개념을 덧씌우는 것이 아니라, 오히려 곤충이라는 생물적 대상을 통해 인간-자연-사회 간의 지속 가능한 상호작용 모델을 탐색하는 창구가 될 수 있다고 봅니다. 향후 곤충학은 생태 중심을 넘어서, 환경과 사회, 윤리를 통합하는 다학제적 과학으로 진화해 나갈 필요가 있을 것입니다.

오늘 학회를 준비하는 데 노고를 아끼지 않은 사무국과 관련 위원님들께 깊은 감사를 다시 한번 드리며, 이번 학술대회의 참여를 통하여 곤충학에서 ESG의 가치가 실현되기를 기원합니다. 감사합니다.

2025년 4월 24일

(사)한국응용곤충학회 회장 **김 동 순**

2025년 한국곤충학회 • 한국응용곤충학회 공동 춘계학술대회

ESG in Entomology

일시: 2025년 4월 24일(목) 11:00 ~ 25일(금) 12:00 / 장소: 소노캄 비발디파크

Program

24 April (Thursday)

Time	Contents		Room
11:00~12:00	Registration		DESK (2F)
12:00~12:20	Opening ceremony & Photography		GRAND BALLROOM I (3F)
Keynote Address			
12:20~12:50	**Keynote I** Advancing from Climate Response Strategies to Innovation Challenges: Envisioning the Future of Entomology through the ESG Paradigm Woo-Jin Lee (Science & Technology Policy Coordination Division Director, Ministry of Science and ICT)		GRAND BALLROOM I (3F)
12:50~13:20	**Keynote II** The Role of Insect Chemical Ecology in ESG: Sustainable Solutions for a Better Future Il-Kwon Park (Seoul National University)		GRAND BALLROOM I (3F)
17:20~17:50	**Keynote III** Beetle Diversity: From the Field to the Lab Seunghyun Lee (Seoul National University)		GRAND BALLROOM I (3F)
13:20~13:30	**Coffee Break**		
Oral Presentation			
13:30~16:00	**Non-Competition**	All subjects	GRAND BALLROOM I (3F)
		All subjects	GRAND BALLROOM II (3F)
	Competition	Taxonomy / Phylogeny	EMERALD (3F)
		Taxonomy / Morphology	SAPPHIER I (2F)
		Ecology	SAPPHIER II (2F)
		Molecular Biology / Pest Control	SAPPHIER III (2F)
		Physiology / Medical Entomology	RUBY I (2F)

24 April (Thursday)

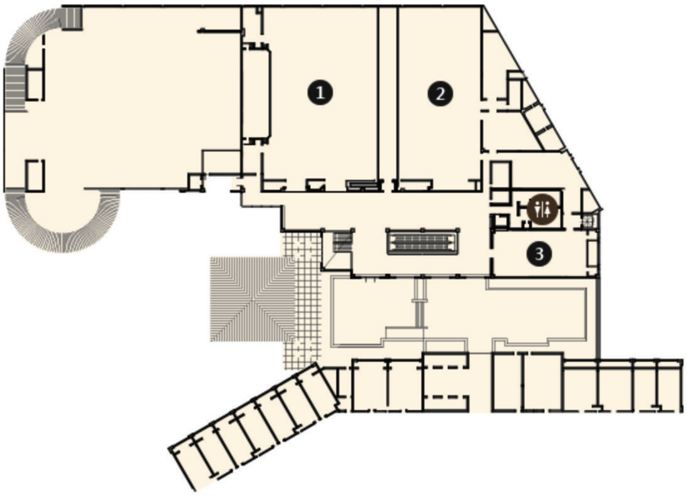
Time	Contents	Room
	Poster Presentation	
16:10~17:10	**Poster Presentation (Competition)**	DIAMOND (2F)
	Poster Presentation (Non-Competition)	
17:10~17:20	**Coffee Break**	
	KSAE/ESK Meeting	
17:20~18:00	**GRAND BALLROOM I (3F)**	**EMERALD (3F)**
	General Meeting & Awards of the Songjeong (Il-Kwon Park) and Young Entomologist (Seunghyun Lee) (KSAE)	General Meeting (ESK)
18:00~18:20	**Coffee Break**	
18:20~20:00	**Proud Korean Entomologist Award (Kyu-Tek Park) & Banquet**	GRAND BALLROOM I, II (3F)
	Small Group Meeting	
20:00~21:00	**Group I (ESK)** Issues on Forest Insect Pests and Future Research Jong-Kook Jung (Kangwon National University)	EMERALD (3F)
	Group II (ESK) Modeling Insect Ecology Using Machine Learning Dong Gun KIM (Sahmyook University)	SAPPHIER I (2F)
	Group III (KSAE) Academic Committee Meeting Dong Woon Lee (Kyungpook National University) Donghun Kim (Kyungpook National University)	RUBY I (2F)
	Group IV (KSAE) Research on Pesticide Resistance Bioassays Dong Woon Lee (Kyungpook National University)	RUBY II (2F)
	Group V (KSAE) Sustainable Agriculture through dsRNA Technology: Reality and Future June-Sun Yoon (Jeonbuk National University)	SAPPHIER II (2F)
	Group VI (KSAE) Research on Automatic Trap and Digital Pest Control Kyungsan Choi (BySTo)	SAPPHIER III (2F)

25 April (Friday)

Time	Contents	Room
	Symposia	
09:00~11:30	**Symposium Ⅰ (ESK+KSAE)** ESG in Entomology Yong Hun Jo (Soonchunhyang University) Dong Woon Lee (Kyungpook National University)	Grand Ballroom Ⅰ (3F)
	Symposium Ⅱ (KSAE) Development of Tomato Leafminer Control Technology - Research Status and Strategy Kwang-Ho Kim (National Institute of Agricultural Sciences) Jong Ho Park (National Institute of Agricultural Sciences)	Grand Ballroom Ⅱ (3F)
	Symposium Ⅲ (ESK) An Integrated Understanding of Vector-Borne Infections Jong Chul Jeong (Wild Bugs Eco-Environment institute)	RUBY Ⅰ (2F)
	Symposium Ⅳ (KSAE) Expanding Our Horizons with Ecological Entomology Doo-Hyung Lee (Gachon University) Yun-sik Lee (Pusan National University)	SAPPHIER Ⅰ (2F)
	Symposium Ⅴ (ESK) **Current Research Trends in Entomology** Jin-Kyung Choi (Daegu National University of Education)	SAPPHIER Ⅱ (2F)
	Symposium Ⅵ (KSAE) Bridging Disciplines and Borders in Insect Biodiversity Research Seunghwan Lee (Seoul National University) Seunghyun Lee (Seoul National University)	EMERALD (3F)
11:30~11:40	**Coffee Break**	
11:40~	**Closing Ceremony** Gwanjung Bok-Sung Cho Quiz, Awards of Competition and Raffle Tickets, Presidential Address	Grand Ballroom Ⅰ, Ⅱ (3F)

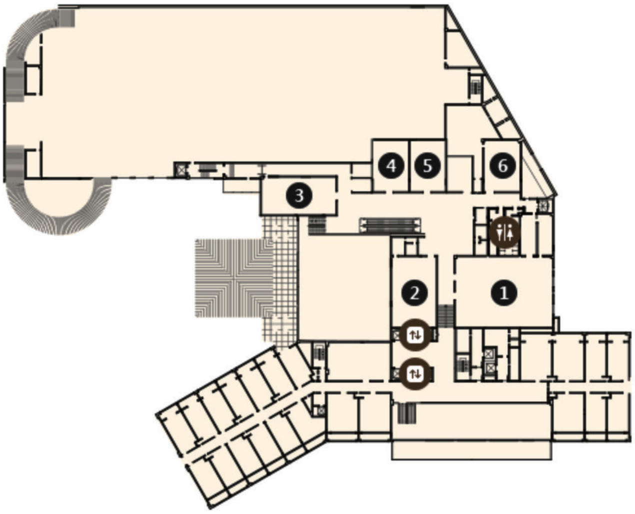
학회장 안내도

3F



- ❶ 그랜드볼룸 I
- ❷ 그랜드볼룸 II
- ❸ 에메랄드

2F



- ❶ 다이아몬드
- ❷ 루비 I
- ❸ 루비 II
- ❹ 사파이어 I
- ❺ 사파이어 II
- ❻ 사파이어 III

Contents

Keynote Address

4. 24. Thu **GRAND BALLROOM I (3F)** **Organizer:** Yong Hun Jo (Soonchunhyang University)
Dong Woon Lee (Kyungpook National University)

GRAND BALLROOM I (3F) **Organizer:** Jong-Seok Park (Chungbuk National University)

Symposia

S1. ESG in Entomology

4. 25. Fri **GRAND BALLROOM I (3F)** **Organizer:** Yong Hun Jo (Soonchunhyang University)
Dong Woon Lee (Kyungpook National University)

S2. Development of Tomato Leafminer Control Technology - Research Status and Strategy

4. 25. Fri **GRAND BALLROOM II (3F)** **Organizer:** Kwang-Ho Kim (National Institute of Agricultural Sciences)
Jong Ho Park (National Institute of Agricultural Sciences)

S3. An Integrated Understanding of Vector-Borne Infections

4. 25. Fri **RUBY I (2F)** **Organizer:** Jong Chul Jeong (Wild Bugs Eco-Environment institute)

S4. Expanding Our Horizons with Ecological Entomology

4. 25. Fri | **SAPPHIER I (2F)** | **Organizer:** Doo-Hyung Lee (Gacton University)
Yun-sik Lee (Pusan National University)

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09:10~09:40
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S4-4
10:20~10:40
Understanding of adaptive traits of insect host with environmental acquisition mechanism of symbiotic bacteria ········ 15
Joo-Young Kim, Jung-Wook Kho and Doo-Hyung Lee

S4-5
10:40~11:00
Tiny hunters, big insights: Unveiling insect defences against jumping spiders ········ 16
Won Bin Lim and Chang Ku Kang

S4-6
11:00~11:20
Food switching and dietary preferences for soil cyanobacteria in *Allonychiurus kimi* (Collembola: Onychiuridae) after 30 years of continuous inbreeding on a yeast monodiet ········ 16
JeongWon Choi, Jimin Shin, Seonghyeok Kim, Nakyeong Lee, Hyeon-Gi Min and Yun-Sik Lee

11:20~11:30 Concluding Remarks

S5. Current Research Trends in Entomology

4. 25. Fri | **SAPPHIER II (2F)** | **Organizer:** Jin-Kyung Choi (Daegu National University of Education)

S5-1
09:00~09:30
Genome browser construction and bioinformatic analysis for the genome and transcriptome of the endangered Korean spurred beetle (*Damaster mirabilissimus mirabilissimus*) ········ 17
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S6. Bridging Disciplines and Borders in Insect Biodiversity Research

4. 25. Fri | **EMERALD (3F)** | **Organizer:** Seunghwan Lee (Seoul National University)
Seunghyun Lee (Seoul National University)

Oral Presentation - Non-Competition

1. General_All Subject I

4. 24. Thu **GRAND BALLROOM I (3F)** **Organizer:** Yonggyun Kim (Andong National University)

2. General - All Subject II

4. 24. Thu **GRAND BALLROOM II (3F)** **Organizer:** Myeoungcheol Kim (SOKN)

Oral Presentation - Competition

3. Taxonomy_Phylogeny

4. 24. Thu EMERALD (3F)
Organizer: Il-Kwon Kim (Korea National Arboretum)
Sunghoon Jung (Chungnam National University)

4. Taxonomy_Morphology

4. 24. Thu SAPPHIER I (2F) **Organizer:** Tak-gi Lee (Incheon National Universtiy)
Bayarsaikhan Ulziijargal (Incheon National Universtiy)

5. Ecology

4. 24. Thu **SAPPHIER II (2F)** **Organizer:** Moon Bo Choi (Kyungpook National University)

SAPPHIER II (2F) **Organizer:** Youngjin Park (Andong National University)
Doo-Hyung Lee (Gachon University)

6. Pest Control / Molecular Biology

4. 24. Thu **SAPPHIER Ⅲ (2F)** **Organizer:** Ji Hyoun Kang (Korea University)

SAPPHIER Ⅲ (2F) **Organizer:** Young Su Lee (Gyeonggi-do Agricultural Research and Extension Services)
Jong-Hoon Kim (Pukyong National University)

7. Physiology / Medical Entomology

4. 24. Thu RUBY I (2F)

Organizer: Kyungjae Andrew Yoon (Chungbuk National University)
Jinmo Koo (Kyungpook National University)

Poster Presentation

1. Taxonomy

2. Ecology

3. Morphology

4. Molecular Biology

5. Phylogeny

6. Pest Control

7. Medical Entomology

8. ETC

Poster Presentation - Competition

1. Undergraduate_All subjects

Organizer: Kwang-Ho Kim (National Institute of Agricultural Sciences)
Jong Ho Park (National Institute of Agricultural Sciences)

2. Graduate_Taxonomy

Organizer: Bo-Sun Park (National Institute of Agricultural, Science)
Minwoong Son (National Institute of Agricultural, Science)

3. Graduate_Taxonomy, Phylogeny

Organizer: Dong June Lee (Honam National Institute of Biological Resources)
Moo-Sung Kim (Korea National Arboretum)

4. Graduate_Physiology, Pest Control

Organizer: Seulki Kim (Jeonbuk National University)
Sumin Oh (Chungnam National University)

5. Graduate_Molecular Biology

Organizer: Kwang-Ho Kim (National Institute of Agricultural Sciences)
Jong Ho Park (National Institute of Agricultural Sciences)

6. Graduate_Ecology, Applied Entomology

Organizer: Sung-Wook Jeon (National Institute of Agricultural Science)
Jinsol Hong (Korea University)

7. General_Taxonomy, Morphology

Organizer: Jong-Seok Park (Chungbuk National University)
Hee-A Lee (EcoVision Inc.)

8. General_Pest Control, Ecology, Applied Entomology

Organizer: June Wee (Chungnam National University)
Jong-Kook Jung (Kangwon National University)

Poster Presentation - Non Competition

1. All members_Taxonomy

2. All members_Pest Control

3. All members_Molecular Biology

4. All members_Ecology

5. All members_Applied Entomology

Small Group Meeting

1. Issues on Forest Insect Pests and Future Research

4. 24. Thu	EMERALD (3F)	**Organizer:** Jong-Kook Jung (Kangwon National University)

2. Modeling Insect Ecology Using Machine Learning

4. 24. Thu	SAPPHIER I (2F)	**Organizer**: Dong Gun KIM (Sahmyook University)

3. Academic Committee Meeting

4. 24. Thu	RUBY I (2F)	**Organizer:** Dong Woon Lee (Kyungpook National University) Donghun Kim (Kyungpook National University)

4. Research on Pesticide Resistance Bioassays

4. 24. Thu RUBY Ⅱ (2F) **Organizer:** Dong Woon Lee (Kyungpook National University)

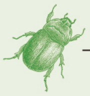
5. Sustainable Agriculture through dsRNA Technology: Reality and Future

4. 24. Thu SAPPHIER Ⅱ (2F) **Organizer:** June-Sun Yoon (Jeonbuk National University)

6. Research on Automatic trap and Digital Pest Control

4. 24. Thu SAPPHIER III (2F) **Organizer:** Kyungsan Choi (BySTo)

Keynote Address



Keynote Address I

Advancing from climate response strategies to innovation challenges: Envisioning the future of entomology through the ESG paradigm

Woo-Jin Lee
Science & Technology Policy Coordination Division Director, Ministry of Sciense and ICT

최근 과학기술 분야에서는 개별 연구자 중심의 접근을 넘어서, 국가 정책의 흐름과 연구현장의 실천을 연계하는 통합적 시각이 요구되고 있다. 이공계 연구자의 시각에서 지난 20년간 범부처 과학기술 정책의 수립과 조정 과정을 고찰하면, 과학기술혁신 거버넌스 체계의 정비, 기후변화 대응을 위한 녹색성장(Green Growth) 전략, 창조경제(Creative Economy) 기반 창의문화 조성, 소프트웨어 활용을 통한 서비스화, 지식재산(IP)을 통한 R&D 완결성 제고, 추격형에서 선도형으로의 전환을 도모한 혁신도전형 R&D(APRO), 사회문제 해결형 임무중심 혁신정책(Mission-Oriented Innovation Policy) 등 다수의 정책이 추진되어 왔다.

이러한 정책적 축적은 곤충학과 같이 기초연구와 산업화의 연계 가능성이 높은 분야에도 중요한 인사이트를 제공한다. 곤충을 기반으로 한 바이오소재 개발, 생물방제, 환경 감시 등의 응용 연구는 ESG (Environment, Social, Governance) 측면에서도 높은 잠재력을 지니며, 정부 정책과의 전략적 정합성을 모색할 수 있는 대표 사례로 주목된다.

이에 따라 과학기술정책의 ‘원거리적 관점(far-field focus)’과 연구자의 '현장 중심 시각(near-field focus)'을 접목함으로써, 특정 과학기술 분야 연구자들이 정책 방향성과 ESG 가치를 연구 설계에 통합할 수 있는 방법을 논의하고자 한다. 본 발표는 과학기술정책과 기초과학 현장의 연결을 통해 지속가능한 과학기술 생태계를 모색하는 출발점이 될 것이다.

Keynote Address II

The role of insect chemical ecology in ESG: Sustainable solutions for a better future

Il-Kwon Park[1,2]
[1]Department of Agriculture, Forest, and Bioresources, College of Agriculture and Life Sciences, Seoul National University;
[2]Research Institute of Agriculture and Life Science, College of Agriculture and Life Sciences, Seoul National University

곤충화학생태학은 곤충과 환경 간의 화학적 상호작용을 연구하는 학문으로, ESG 원칙을 준수하는 지속 가능한 미래를 구축하는 데 중요한 역할을 할 수 있다. 특히, 곤충 화학생태학 연구는 생물학적 방제, 공중보건 개선, 친환경 산업 육성 및 정책 개선과 같은 분야에서 혁신적인 솔루션을 제공할 수 있으며, 이는 기업, 정부, 학계가 지속 가능한 미래를 위한 전략을 수립하는 데 중요한 기반이 될 것이다. 산림 또한 ESG의 핵심 요소로서 지속 가능한 발전에 필수적인 역할을 한다. 이러한 산림을 보호하기 위해 화학생태학을 이용하여 산림해충의 피해를 예방하고 관리하는 것은 매우 중요하다. 이번 발표에서는 연구자가 그동안 수행해온 산림곤충 화학생태학 연구를 소개하고, 향후 발전 방향에 대해 논의하고자 한다. 먼저, 소나무재선충 매개충인 솔수염하늘소와 북방수염하늘소의 집합-성페로몬을 비롯하여, 솔껍질깍지벌레, 솔알락명나방, 회양목명나방, 복숭아명나방, 복숭아유리나방, 별박이자나방 등의 페로몬 성분을 규명하고, 야외 유인력 검정 연구를 수행하였다. 또한, 트랩별 색깔에 따른 유인력 검정, 트랩 형태별 및 페로몬 농도가 페로몬 트랩의 포획 효율에 미치는 영향을 분석하였다. 특히, 솔껍질깍지벌레 페로몬을 이용한 전국 단위 발생 분포 모니터링을 통해, 국내 전역에 솔껍질깍지벌레가 분포하고 있음을 최초로 확인하였다. 앞으로도 다양한 산림해충의 화학통신물질을 규명하고, 안테나 감각기의 전기생리 반응을 이용한 후보물질 선발, 후각 수용에 관여하는 유전자 탐색 등의 연구를 지속적으로 수행하여 산림해충 화학생태학 발전에 기여하고자 한다.

검색어: 곤충화학생태학, 정보화학통신물질, 페로몬, 카이로몬, 산림곤충

Keynote Address III

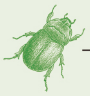
Beetle diversity: From the field to the lab

Seunghyun Lee[1,2]
[1]Insect Biosystematics Laboratory, Department of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea
[2]Research Institute for Agricultural and Life Sciences, Seoul National University, Seoul, Republic of Korea

발표자가 진행해온 곤충 분류학을 기반으로 한 딱정벌레목의 다양성 연구를 폭넓게 소개합니다. 먼저 발표자의 박사학위논문에 수록된 3개 파트: 하늘소아과의 분류, DNA 바코딩을 이용한 유충동정, 생태/형태/DNA를 이용한 계통학진화적 연구를 소개합니다. 이어서 학위논문의 각 파트를 작성하면서 얻었던 경험과 통찰이 다른 연구들로 어떻게 이어졌는지 설명합니다. 이 중에는 하늘소가 아닌 다른 분류군에 같은 접근방식을 적용한 연구들과 개체군유전학을 이용한 침입종 판별이나 생물학적 방제제 선별과 같은 기존의 접근법을 활용한 연구들이 있습니다. 더불어 시선추적기를 활용한 연구나 3D 프린터를 이용한 트랩 개발처럼 보다 실험적인 연구도 함께 소개합니다.

검색어: 딱정벌레, 하늘소과, 밑빠진벌레과, 풍뎅이과, 분류학, 분자계통학

Symposia





(사)한국곤충학회
The Entomological Society of Korea

(사)한국응용곤충학회
Korean Society of Applied Entomology

S1-1

A study on the current status and management of insect outbreaks

Sun-Jae Park, Seung-Gyu Lee, Min Jeong Baek and Taemin Kang
Climate change and environmental biology research division, National Institute of Biological Resources (NIBR)

최근(2011~2020년) 전 지구 연평균 기온은 산업화 이전(1850~1900년)보다 1.09℃ 상승하였고, 우리나라도 최근 30년(1911~2020년)간 과거(1912~1940년)보다 1.6℃ 상승하였다. 이런 기후변화는 곤충을 비롯한 생물의 대발생에도 영향을 준다. 최근 수도권 및 도심지역을 중심으로 대발생하고 있는 붉은등우단털파리(2022년~), 대벌레(2020년~), 동양하루살이(2006년~) 등의 대발생도 기후변화로 인한 현상으로 추정되고 있다. 생물이 대발생하는 데에는 기후변화 외에도 서식환경의 변화, 먹이자원의 변화, 천적의 변화 등 여러 가지 요소들이 복합적으로 작용해야 가능할 것이다. 이런 생물 대발생 현황을 파악하고 선제적으로 대응하기 위해 국립생물자원관은 1) 국내외 대발생 생물 및 근연종의 목록을 구축(140종)하고, 2) 이들의 분류·생태학적 자료를 확보(14종)하며, 3) 대발생 원인 파악 연구를 진행(5종) 중에 있다. 이를 통해 시민들에게 사전에 생물 대발생을 대비하고 대응할 수 있도록 카드뉴스(20종 제작) 등을 활용해 서울시 등 유관기관에 정보를 제공하였다. 아울러 대발생 빈번지역 모니터링, 신속 종판별, 친환경적 관리방법 제안 등 현장 지원을 강화하여, 국민의 불안함을 최소화할 수 있도록 대응 관리체계 마련에 노력하고 있다.

검색어: 곤충, 대발생, 기후변화, 환경변화, 발생원인, 관리방안

S1-2

Sustainable ecological intervention approaches for insect mass emergences: Integration with environmental, social, and governance frameworks

Dong Gun Kim
Smith College of Liberal Arts, Sahmyook University

Since the early 2000s, recurrent mass emergences of *Ephemera orientalis* have been observed along the Hangang River, causing significant inconvenience to the public. This phenomenon has been particularly pronounced in Namyangju-si, Gyeonggi-do, where annual mass emergences of adult mayflies have required substantial financial investment in management and control efforts by local authorities.

In recent years, the emergence zones have expanded to areas such as Seongsu-dong in Seoul, resulting in a noticeable increase in public complaints and discomfort, particularly during the spring season. These mass emergence events are not unique to Korea; similar occurrences have been documented in other countries, including China, where they have also led to notable environmental and social impacts.

This presentation aims to investigate the ecological and environmental drivers behind these mass emergences, and to evaluate their broader implications through the lens of ecosystem service valuation and ESG. Furthermore, it will explore how climate change and ongoing environmental transformations may contribute to ecosystem disturbances and influence the future dynamics and spatial distribution of *E. orientalis* and other aquatic insect populations.

Key words: Mass emergence, *Ephemera orientalis*, Ecosystem services, ESG, Climate change

S1-3

Environment friendly agriculture policy of Republic of Korea

Gyu Il Choi
Environment Friendly Agriculture Ddivision Deputy Director, MAFRA

농식품부는 생물의 다양성을 증진하고, 농업생태계를 건강하게 보전하며, 국민에게 건강한 먹거리를 제공하기 위하여 친환경농업 육성 정책을 추진하고 있으며, 이를 통해 생산자와 소비자를 함께 보호할 수 있도록 노력하고 있다 2001년부터는 친환경농업법에 따라 5년 단위로 친환경농업 육성계획을 수립하고 있으며, 현재는 제5차 계획('21~'25)을 수립하여 추진하고 있다. 제5차 기본계획은 「환경과 미래세대를 위한 지속 가능한 농업 확산」이라는 비전하에 ▲친환경농산물 판로 다변화 및 소비 활성화, 이에 대응한 ▲안정적인 생산기반 구축, ▲농업환경관리를 통한 친환경농업 전환 유도를 주요과제로 정해 추진하고 있다. 특히, 최근 들어 기후 위기의 심각성이 높아지는 상황에서는 농업분야의 탄소중립과 환경친화적 농업으로의 전환이 매우 중요하다 할 수 있다. 이에 맞게 농식품부는 환경과 미래세대를 위한 지속 가능한 농업 확산이 전개되도록 정책을 추진해 나아갈 계획이다.

검색어: 농식품부, 친환경농업, 육성계획, 탄소중립

S1-4

Current status and future plans of industrial insect R&D for the promotion of a sustainable green-bio industry

Young Woong Byeon, Hae-Yong Kweon, Seong Ryul Kim, Kwanho Park, Joon Ha Lee and Ji hae Lee
Department of Agricultural Biology, National Institute of Agricultural Sciences

유엔식량농업기구(FAO)에서 식용곤충을 미래식량으로 지목한 바 있다(2013). 곤충은 단백질 1kg을 생산하는 데 소보다 물이나 사료는 적게 들고 이산화탄소 배출량은 1/10~1/350밖에 되지 않는 효율적인 영양공급원이기 때문이다. 우리나라에서는 2010년 곤충산업법이 제정되고 식품원료로 10종의 식용곤충이 등록되었고, 2025년 1월에는 그린바이오산업법이 시행되어 산업 육성을 위한 법적, 제도적 기반을 갖추었다.

국립농업과학원 산업곤충과에서는 곤충산업 육성을 위해 사료곤충, 식용곤충의 산업적 활용을 위한 연구를 중점적으로 추진하고 있다. 생산성 향상을 위해서는 산업곤충 우수품종 육성, ICT 활용 스마트 대량생산체계 구축, 표준 먹이원 개발을 추진하고 아울러 농산 부산물을 활용한 먹이원 생산비 절감 연구와 산업곤충 수확 후 위생관리 및 일관처리 시스템(세척-데침-건조) 개발을 추진 중이다. 기능성 연구 분야에서는 홍잠(5령8일 누에, 익힌숙잠)의 비알코올성 간 건강 개선 효능, 기전 및 기능물질을 밝혔다. 또한 흰점박이꽃무지 유충 추출물의 면역 세포 활성화 등 효능을 세포시험, 동물시험을 통해 밝힌 바 있으며, 현재 홍잠과 꽃무지 유충 추출물은 건강기능식품 원료 등록을 위해 인체적용시험을 수행하고 있다. 향후에는 곤충 대체단백질의 중요성과 기능성이 구명되어 곤충의 새로운 가치를 발굴해야 할 것이다.

검색어: 그린바이오산업, 산업곤충 R&D

S2-1

Current distribution status of tomato leafminer in Korea

Kwang-Ho Kim, Jong Ho park, HyunOh Sun, Sung-Wook Jun and Boyoon Seo
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남미 페루가 원산지로 알려진 토마토뿔나방(*Phthorimaea absoluta*)은 현재 전세계적으로 원산으로 100여개 국가에 분포하는 해충으로 보고되고 있으며, 국내에는 ’23년 7월 확인된 이후 ’24년에는 전국적으로 발생이 보고되고 있으며, 2025년 3월 현재 81개 시군의 토마토재배농가에서 피해가 확인되었다. 토마토뿔나방은 2006년 스페인에서 처음 침입이 확인되었고 이후 지중해와 서유럽의 많은 국가로 빠르게 확산되었고, 이어 아시아의 터키에서 2009년, 인도와 파키스탄에서 2014년, 방글라데시와 네팔에서 2016년, 미얀마 2017년, 중국의 신장지역에서 2018년, 대만에서 2020년, 일본에서 2021년에 발생이 보고되었다. 전세계적으로 토마토뿔나방의 기주식물은 토마토를 비롯하여 감자, 까마중, 가시비름 등 28여종이 보고되고 있다. 국내에서도 토마토뿔나방의 기주식물은 토마토 등 16여종이 보고되고 있다. 따라서 토마토뿔나방의 효과적인 방제를 위해서는 주요기주식물인 토마토에서의 생태뿐만 아니라 야생잡초에서 월동하고 증식한 후 주기주인 토마토를 이동하는 시기 및 주요 이동시간대 등에 대한 연구가 많이 필요할 것으로 여겨진다.

검색어: 토마토, 토마토뿔나방, 분포, 확산, 기주식물

S2-2

Organic management field case of tomato leafminer in tomato greenhouses

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토마토뿔나방(*Phthorimaea absoluta*)은 남미가 원산으로 100여 개 국가에 분포하는 해충이다. 국내에는 ’23년에 발견된 이후 전국적으로 토마토농가에서 피해가 확대되었다. 특히 친환경 재배농가에서 큰 피해가 나타났으나 적절한 유기농 관리 기술은 부족한 상황이다. 이를 해결하기 위해 국내외 사례를 기반으로 개발한 친환경 매뉴얼을 현장에 적용하였다. 봄작기 해당 토마토뿔나방의 피해를 받은 토마토 유기재배농가에서 가을작기에 종합적 관리기술을 투입하여 효과를 확인하였다. 유묘장은 소형망실 설치, 피해잎 제거, 유기농업자재 살포를 실시하였다. 재배온실에서는 전작기 피해 토마토 기주제거, 측창 미세방충망 설치, 교미교란제·끈끈이롤트랩 활용, 유기농업자제 살포 등으로 관리하였다. 관리 후, 온실에 트랩에 초기 13마리(일)까지 발생했던 성충은 0마리로 감소하였고 피해엽은 초기 0.5%에서 후기 0%로 나타났다. 수확 시 피해과실은 보이지 않았다.

검색어: 토마토, 토마토뿔나방, 친환경

S2-3

Current status of mating disruption control for *Tuta absoluta* (Lepidoptera: Gelechiidae) in Korea

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토마토뿔나방(*Tuta absoluta*)은 유충이 잎에 터널을 만들고 줄기 및 과실 속을 가해하는 해충으로 가지과 작물 중 특히 토마토를 가장 선호하는 것으로 알려져 있다. 우리나라에는 2023년 제주에서 첫 발생 후 전국적으로 피해가 확산되고 있으며 잔류농약 문제로 인해 친환경 방제법 개발이 시급하다. 본 연구에서는 이러한 문제를 해결할 수 있는 대안으로 국내 교미교란제를 이용한 최적 활용 기준을 구명하고자 한다. 토마토뿔나방 방제를 위한 성페로몬 성분은 E3,Z8,Z11-tetradecatrienyl acetate과 E3,Z8-tetradecatrienyl acetate의 혼합물이며 방출기로는 페로몬 흡착실리콘과 폴리에틸렌 재질의 통기성 파우치를 이용하였다. 교미교란제는 10a당 100개를 과원내에 균일하게 배치하였으며 지면에서 약 50~70cm 높이에 설치하였다. 교미교란제 처리 효과는 페로몬트랩에 유인된 수컷 성충수를 무처리구와 비교하여 조사하였는데 처리 50일 후, 무처리구에서 총 40마리가 유인되었으나 처리구에는 유인되는 개체가 없었다. 토마토의 피해엽율을 조사한 결과 무처리구의 경우 7.5%의 피해율을 보였으나 처리구의 경우 1% 이하로 유충에 의한 피해도 경감되는 것을 확인하였다. 추후 토마토 재배작형별 교미교란제의 설치시기 및 설치 횟수를 구명하여 우리나라에 가장 효과적인 교미교란제 활용 기준을 마련할 계획이다.

검색어: 토마토, 토마토뿔나방, 교미교란제, 방제

S2-4

Research trends on biological control of tomato leafminer, *Phthorimaea absoluta* (Metrick) (Lepidoptera: Gelechiidae) using natural enemies and Methods for exploration of domestic natural enemy resources

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토마토뿔나방(*Phthorimaea absoluta*)은 현재 전 세계 토마토 재배에 심각한 문제를 초래하는 해충이며 국내에서는 2023년에 처음 발견된 이후. 전국적으로 퍼져 국내 토마토 재배 농가에 많은 경제적 손실을 입히고 있다. 특히 친환경 토마토 재배 농가에 대한 피해가 크게 발생하였지만 친환경 방제 방법이 부족한 상황이다. 북아프리카와 유럽에서는 토마토뿔나방의 포식성 천적인 담배장님노린재(*Nesidiocoris tenuis*)를 상업적으로 이용하고 있으며, 스페인에서 알벌류(*Tricogrammatidae*)를 토마토뿔나방 방제에 활용하는 등 친환경 방제수단으로써 천적을 활용하고 있다. 국외에서의 천적을 이용한 토마토뿔나방 방제 사례를 수집하여 기존 국내 천적의 활용성을 검증하고 이를 토대로 국내 토착 천적의 탐색 및 효과 검증을 통한 종합적인 천적 활용 친환경 방제 전략 수립에 이용하고자 한다.

검색어: 토마토, 토마토뿔나방, 생물적방제, 천적

S2-5

Research trends in chemical control strategies and insecticide resistance of *Tuta absoluta*

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토마토뿔나방(*Tuta absoluta*)은 토마토를 기주식물로 하며 전 세계적으로 심각한 피해를 주고 있는 해충으로, 국내에서는 23년 7월 제주에서 유입 사실을 확인하였고, 24년 3월 이후 예찰 및 분포조사 과정에서 전국적으로 분포하고 있는 것으로 확인되었으며, 특히 친환경재배농가에 심각한 피해를 끼치고 있다. 국외에서는 토마토뿔나방을 효과적으로 방제하기 위한 다양한 살충제에 대한 약효 평가 연구가 수행되고 있다. 국내에서는 토마토뿔나방 방제를 위해 등록된 주요 살충제는 메타플루미존, 사이안트라닐리프롤, 스피네토람, 에마멕틴벤조에이트, 플룩사메타마이드, 피리달릴 6종이 있다. 최근 몇 년간의 국외 연구결과에 따르면, 주요 나비목 해충 방제약제인 디아마이드 계열에 대한 저항성 돌연변이가 토마토뿔나방에서 보고되고 있으며 주요 살충제에 대해 교차저항성도 보고되고 있는 상황이다. 따라서 토마토뿔나방에 대한 화학적 방제 기술 및 저항성 연구 결과들을 종합하여 국내 토마토뿔나방 방제를 위한 효과적인 전략 제안 및 향후 지속 가능한 농업을 위한 방향성을 제시하고자 한다.

검색어: 토마토뿔나방, 살충제, 저항성, 외래해충

S2-6

Biological control strategies for *Tuta absoluta*: Eco-Friendly approaches and practical applications

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The devastating pest of tomato, *Tuta absoluta* (Merick, 1917) (Lepidoptera: Gelechiidae) poses a significant threat to tomato production globally. The tomato leafminer native to South America, was discovered in Spain in 2006 and widely spread to Africa and Asia, and has recently been reported in Korea and Japan. *T. absoluta* has high pesticide resistance, which necessitates biological control for sustainable and environmentally sound management strategies. Biological control has emerged as a key component of Integrated Pest Management (IPM) for mitigating the impact of this pest while minimizing environmental damage. Currently, *T. absoluta* management in South America and European countries is moving from chemical control using pesticides in the past to integrated pest management, and there is a need for an eco-friendly approach and practical application suitable for Korea based on relevant data. This presentation will examine *T. absoluta* management strategies in South America and Europe and discuss control strategies tailored to Korean conditions.

Key words: Integrated Pest Management, Biological control, tomato, *Tuta absoluta*

S2-7

Predicting the potential distribution of major pests, including *Tuta absoluta*, using species distribution modeling

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Species distribution modeling (SDM), a tool used to predict the potential distribution of species based on climate and environmental factors, has been widely applied to assess the occurrence probability and habitat changes of major agricultural pests. SDMs can be constructed based on various factors, including the biological and ecological characteristics of the target species, the availability of data and predictor variables, and the spatial extent of the prediction area. Recent advancements in SDM research have focused on enhancing model performance and reducing uncertainty in predicted regions through the implementation of multiple algorithms, the integration of complex factors, and the optimization of model structures. In Korea, the application of SDMs has been expanding in response to increasing threats posed by invasive species and pest habitat shifts driven by environmental changes, including climate change. This study evaluates the feasibility of using SDM to predict the spatial distribution of agricultural pests in Korea by introducing recent techniques. Additionally, we explore case studies where species distribution modeling has been applied to *Tuta absoluta*, a significant threat to domestic agriculture, to provide insights for future monitoring and control strategies.

Key words: Ecological niche modeling, habitat evaluation, spatial analysis, species distribution model, *Tuta absoluta*

S3-1

Improvement and optimization of molecular diagnostic methods for mosquito, tick, and chigger mite-borne infectious diseases

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As climate change alters the density patterns and northern limit lines of disease vectors such as mosquitoes, ticks, and chigger mites, the risk of various infectious diseases becoming endemic or newly introduced in Korea is increasing. Mosquitoes are known to transmit Dengue, Zika, Chikungunya, Japanese encephalitis, Yellow fever, and West Nile fever; ticks transmit Q-fever, bartonellosis, SFTSV, Lyme disease, among others; and mites transmit scrub typhus. These disease vectors are gaining prominence due to their significant public health impact. PCR-based molecular diagnostic methods have been employed in vector and pathogen research since before 2010; however, challenges including high costs, insufficient genetic information, and limited understanding of PCR inhibitors have created ongoing demands for diagnostic improvements. This research analyzes the technical advancements in both nucleic acid extraction phases and PCR diagnostic processes to effectively detect pathogens from disease-carrying insects. By presenting case studies of current molecular diagnostic technology applications and optimization strategies, we aim to contribute to the advancement of vector-borne disease surveillance and prevention systems in Korea. This presentation focuses on practical improvement measures that enhance both the sensitivity and specificity of molecular diagnostic methods while increasing cost-effectiveness.

Key words: Vector-borne diseases, Molecular diagnostics, PCR optimization, Nucleic acid extraction, Climate change, Disease vectors

S3-2

Capturing 3D models of arthropods including mosquitoes and ticks

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Morphology is fundamental to understanding biodiversity. Various imaging technology have been developed to obtain 2D and 3D morphological data of insects. 3D imaging techniques such an Confocal laser scanning microscopy (CLSM) and computed tomography (CT)-based techniques are useful for reconstructing internal structures. Although these techniques are very useful, they do not express colors well, which are important for identifying insects including arthropods. Color is very important feature along with morphological structure in the In the field of taxonomy and system biology. A structured illumination-based method was developed to provided natural color and 3D morphological information. In this study, a multi-view image fusion system was used to obtain high-resolution full-color 3D images and 3D morphological data of arthropods including mosquitoes and ticks. High-resolution images were obtained using an objective lens, and texture information was processed to make a color-mapped 3D model. Using this method, 3D images of arthropods including insects would be useful for taxonomy and functional morphology, and could also be used as an educational tool and 3D electronic library for arthropods.

Key words: 3D image, insect, taxonomy, 3D electric library

S3-3

The future of Malaria in the world

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Malaria is an infectious disease caused by *Plasmodium* protozoan parasites and transmitted by mosquitoes of the *Anopheles* genus. It remains the leading cause of death among single infectious diseases worldwide. In South Korea, over 700 cases of *Plasmodium vivax* malaria are reported annually. Despite long-standing global control efforts, including those led by the World Health Organization (WHO), new challenges continue to emerge. These include ecological shifts in mosquito vectors driven by climate change, reduced sensitivity in diagnostic and therapeutic measures, the emergence of novel *Plasmodium* species, and the increasing spread of asymptomatic infections. As definitive solutions remain elusive, it is imperative to reassess our strategies in addressing these persistent challenges.

Key words: Malaria, Vector, *Plasmodium*, *Anopheles,* Parasite

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S4-1

Ecological insights into *Vespa mandarinia*: Dietary habits, nesting sites, natural enemies, and inquilines

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Vespa mandarinia, the world's largest hornet, possesses potent venom and aggressive behavior, posing risks to humans and beekeeping. In Korea, autumn grass-cutting increases the likelihood of mass attack incidents, and the species threatens managed honeybee colonies. Its 2019 detection in North America raised ecological concerns, prompting eradication efforts in Washington State. This study examines *V. mandarinia*'s diet, nesting sites, natural enemies, and inquilines in Korea. DNA metabarcoding analysis revealed a broader diet than in North America, with social Hymenoptera as the primary prey. While most nests were found underground, some were located in tree cavities and rooftops. Additionally, six parasitoid and inquiline species were identified, providing insights into potential biological control strategies.

Key words: *Vespa mandarinia*, dietary, metabarcoding, parasitoid, inquiline

S4-2

Developing an integrated agricultural model for climate risk adaptation

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Successful climate risk management for agriculture requires comprehensive understanding of various components. However, most of the climate change research focuses on simulating the climate impacts on individual factors. In the previous 7-year project, MOTIVE (2014–2020), primarily aimed to develop intra- and inter-sectoral climate change impact assessment models. After 2020, the launch of the 3rd National Climate Change Adaptation Plan (2021–2025) marked a key transition, emphasizing ‘national climate risks’ and ‘adaptation’ as main themes. In response to this national agenda, a new 7-year project, DIRECTION (2022–2028), was initiated. DIRECTION focuses on developing comprehensive assessment tools capable of evaluating multiple sectors and supporting the effective implementation of the adaptation plan. For the agricultural sector, the new project aims to update and develop an integrated agriculture model using a meta-modeling approach to support local governments in formulating future climate change adaptation plans. First, key components of Korean agriculture were identified based on national climate risks in the agricultural sector, including crop production and suitability, soil erosion, pest impacts, and livestock. Second, an interlinked framework of these factors was established, with a particular focus on cultivation management. Finally, a meta-model was developed using machine learning techniques, leveraging this interlinked structure. This talk presents the ongoing project and explores future improvements for developing an integrated model to address climate risks from an ecological perspective.

Key words: Climate Change, Risk, Adaptation, Agriculture

S4-3

Bacterial symbionts of *Agapanthia amurensis*: Interactions with fungal pathogens and host integrity

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The stem-boring beetle *Agapanthia amurensis* inhabits senescing stalks of *Erigeron annuus*, where its sequential stalk-cutting behavior exposes larvae to airborne fungal pathogens, particularly *Beauveria bassiana*. Given that fungal infections were detected in only 4.35% of sampled larvae (11 out of 253 individuals), despite high exposure risk, we hypothesize that microbial associations play a role in mitigating fungal infection. To investigate this, we analyzed bacterial communities associated with larval surfaces and habitat structures and tested their potential role in fungal inhibition. Bacteria from larval surface exhibited strong antifungal properties, and experimental larval re-inoculation confirmed increased resistance to fungal infection. Further analyses suggest that fungal suppression may be mediated by microbial interactions involving resource competition and antagonistic secondary metabolites. These findings highlight the ecological significance of insect-associated microbiome and suggest that microbial symbioses may be an essential component of fungal resistance strategies in endophytic insect herbivores.

Key words: *Agapanthia amurensis,* symbiosis, fungal pathogen

S4-4

Understanding of adaptive traits of insect host with environmental acquisition mechanism of symbiotic bacteria

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Riptortus pedestris (Hemiptera: Alydidae) acquire their symbiotic bacteria from soil environments in every generation. Unlike the vertical transmission of the symbionts, the environmental acquisition mechanism entails a risk of variations in symbiotic associations. However, this strategy persists in insects belonging to Alydidae and Coreidae, suggesting its adaptive values in the evolution of insect-microbe interactions. Therefore, we attempt to characterize the flexibility of the environmental acquisition mechanism with *R. pedestris* to better understand its ecological and evolutionary implications. First, this study aims to investigate the flexibility of symbiont strains in *R. pedestris* and their symbiotic effects on the insect host. Second, we investigate the flexibility with regard to the timing of symbiont acquisition from the environments and its effects on the insect host. Finally, we aim to address how the flexibility would exert an effect on the host population growth. Taken together, these results would serve as baseline information to better understand evolutionary context in which the environmental acquisition is in favor of natural selection while shaping insect-microbe associations.

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

S4-5

Tiny hunters, big insights: Unveiling insect defences against jumping spiders

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Studies on visual anti-predator defences (such as camouflage, aposematism, and mimicry) have been a vibrant research focus in behavioural ecology. However, the defensive functions and mechanisms of traits in ‘tiny’ insects remain poorly understood. This knowledge gap likely arises from the predominant focus on avian predators as primary selective agents. Alternatively, jumping spiders (Araneae, Salticidae), invertebrate visual predators, may shape the evolution of defensive traits in ‘tiny’ insects. Here, we present ongoing behavioural and comparative studies on Lepidopteran adaptations to jumping spider predation. We propose novel phenomena and concepts that may be overlooked in avian-focused research, along with a more comprehensive understanding of defensive strategies in specific taxa.

Key words: Batesian mimicry, False head, Glyphipterigidae, Gracillariidae, Lycaenidae, Stathmopodidae

S4-6

Food switching and dietary preferences for soil cyanobacteria in *Allonychiurus kimi* (Collembola: Onychiuridae) after 30 years of continuous inbreeding on a yeast monodiet

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Food switching, the process by which predators transition to novel food sources, plays a crucial role in ecosystem function and is significantly influenced by predator food preferences. In this study, the dietary preferences and traits of *Allonychiurus kimi* during food switching to two species of soil cyanobacteria were investigated using a laboratory population that had been maintained on a monodiet of Saccharomyces cerevisiae with continuous inbreeding for 30 years. This study was conducted through two experiments: food preference experiments and food switching experiments. In the food preference experiment, *A. kimi* showed a strong preference for *S. cerevisiae* at the beginning of the feeding period during the first four days, but this preference gradually shifted toward Pseudoaliinostoc sp. over a span of two days. In contrast, *A. kimi* significantly avoided *N. neudorfense* throughout the entire experimental period. In the food switching experiment, the food transition time to both cyanobacteria was observed to be one week, during which the egg production and molting frequency were lower compared to the treatment group fed with S. cerevisiae. This study confirmed that despite 30 years of inbreeding on a single food source, preferences for new food sources could be reestablished after food switching, suggesting that food preferences are not solely determined by the current prey.

Key words: Collembola, *Allonychiurus kimi*, Cyanobacteria, Food switching, Inbreeding

S5-1

Genome browser construction and bioinformatic analysis for the genome and transcriptome of the endangered Korean spurred beetle (*Damaster mirabilissimus mirabilissimus*)

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This study was conducted with the goal of securing transcriptome and genome data for the endangered beetle *Damaster mirabilissimus mirabilissimus*, designated as a Class II endangered wild animal by the Ministry of Environment, and building a genome browser to effectively use this data in species restoration and conservation research. Since most wild invertebrates do not have reference genome data, de novo assembly is essential; however, traditional methods are often complicated and time-consuming. To overcome these challenges, we developed SCHDNA ver1.0, a program that supports researchers in efficiently generating and analyzing unigenes and scaffolds. Research on endangered species is crucial for formulating effective restoration and conservation strategies, but it is often restricted by the rarity of the species and a lack of genetic resources. Overcoming these limitations requires the secure and effective analysis and utilization of genomic and transcriptomic data for endangered species lacking reference genomes. This study focuses on improving the research environment, enabling researchers to directly utilize the data. We collected specimens of *D. m. mirabilissimus*, extracted DNA and RNA for library construction, and conducted sequencing. Using SCHDNA ver1.0, we performed *de novo* assembly to produce unigenes and scaffolds, which were then annotated. Furthermore, we employed AlphaFold2 to predict the 3D protein structures of mitochondrial tRNA, underscoring its importance to our research objectives. To provide a more intuitive display of the results, we developed a genome browser based on JBrowse2, creating an interactive web database for researchers. This study proposes a standard method for the bioinformatic analysis of genome and transcriptome data in endangered wild animals without reference genomes through the development of SCHDNA ver1.0. The analyzed results, visualized through the genome browser, offer valuable insights for researchers conducting similar studies. This initiative is expected to serve as a foundational resource for biodiversity conservation, ecosystem restoration strategies, and various biological studies.

Key words: *Damaster mirabilissimus mirabilissimus*, Redlist, Genome, Transcriptome, Database

S5-2

Documenting the research progress on Spilomelinae (Lepidoptera: Crambidae) in Korea

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한반도에서 기록된 Spilomelinae의 현황을 파악하기 위하여, 한국 기록 및 해당 종들의 분포 기록과 관련된 문헌을 조사한 결과 약 300여 편을 주요 문헌으로 판단하였다. 기록의 정리는 우선 시간 순서를 고려하여, Spilomelinae 종의 한국 기록을 최초로 남긴 Leech (1889)를 기준으로 삼아 그 전 · 후를 조사하였다. 광복 이후 한국인 연구자에 의한 연구를 추적한 결과, 1956년 조복성&김창환의 기록에서 2종이 기록된 것을 시점으로 추정하였다. 이후 다양한 연구자들의 기록에 의해 한국의 Spilomelinae 종다양성이 증가하고 정리되어 왔으나, 최근에 이르러서도 단순 종 목록만이 제시되는 경우가 많고, 각 종의 국내 초기록이나 동종이명관계, 분포 등의 기록을 명시하지 않거나 정보의 출처를 생략하는 경우가 많다. 이에 후대 연구자들이 이러한 내용을 확인하기 위해서는 일일이 개별 기록을 찾아 확인해야만 하는 상황으로, 이를 조금이나마 타개하기 위하여 Spilomelinae 연구를 진행하며 조사 · 분석한 문헌을 정리하여 제시하였다.

검색어: 나비목, 풀명나방과, 초기록, 동종이명관계, 분포

S5-3

Evaluation of adhesive traps for *Vespa mandarinia* control: Effects of presence, vital status, and colony specificity on attraction and non-target impact

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Vespa mandarinia, the world's largest hornet, poses significant threats to human safety and apiculture due to its aggressive behavior and potent venom. Its collective predation strategy allows for rapid decimation of honeybee colonies, causing severe economic losses. In Korea, adhesive traps are increasingly used in apiaries for control, though their effectiveness remains largely unverified. This study assessed trap efficiency based on hornet presence, vital status, colony origin, and trap location. Live hornets significantly increased capture rates, while dead hornets had minimal effect. Colony-specific attraction was observed, whereas intercolony attraction was negligible. No hornets were captured in forested areas, suggesting reliance on colony pheromones. However, only 9.79% of trapped insects were *V. mandarinia*, indicating high non-target capture. These findings highlight the benefits and limitations of adhesive traps, informing more effective control strategies for *V. mandarinia* management.

Key words: *Vespa mandarinia*, adhesive trap, control, pheromone, non-target

S6-1

International collaboration and citizen science in Korean Heteroptera research

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Taxonomy, stemming from an interest in nature, is the foundation of biological research, and its importance has not diminished despite the paradigm shifts accelerated by technological advancements. In particular, insect taxonomy remains a challenging field due to its high species diversity and complexity. The deletion or redesignation of existing taxa is as active as the discovery of new species. In the 21st century, increased accessibility of literature through the internet and the ease of information exchange among researchers have reduced the likelihood of such errors. However, a large number of taxa still suffer from unclear information and inconsistent standards, necessitating continuous attention and research. In this presentation, we will review cases that have occurred during the taxonomic study of Korean Heteroptera and adjacent countries, and discuss the positive aspects of collaboration between researchers in neighboring areas, and the importance of citizen science, where amateurs are central to discovery.

Key words: Heteroptera, taxonomy, international collaboration, citizen science

S6-2

Exploring the invasive potential of *Psacothea hilaris* (Coleoptera, Cerambycidae) through species distribution modeling and haplotype analysis

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Psacothea hilaris (Pascoe, 1858) (Coleoptera, Cerambycidae, Lamiinae) is a species native to Eastern Asia, currently invasive in Italy and Japan. *Psacothea hilaris* primarily develops on figs (especially *Ficus carica*, F. *erecta*, and *F. macrocarpa*), mulberries (notably *Morus alba* and *M. indica*) (Moraceae), and Japanese aralia (*Fatsia japonica*, Araliaceae). The larval feeding behavior, which involves tunneling through the wood, results in significant damage to the trunk and branches of the host plant, often causing dieback and eventual death. The species has recently been the subject of two studies aimed at exploring its potential distribution in China, in relation to the effects of climate change, and in the invasion area in Italy, considering both habitat and climate effects. Specifically, regarding the invaded area in Italy, although the species distribution model, based on the species' native occurrences, suggests generally low suitability for the region, the species continues to successfully expand its range. Given this fenomenon, questions have been raised about the origin of the Italian population and whether its origin, related to a specific ecotype, is what determines its higher invasiveness compared to what is observed for the species when considered as a whole.

Key words: *Psacothea hilaris*, Invasive species, Host plants, Climate suitability, Ecotype origin

S6-3

Evolutionary radiation in wings of lacewing: Mode, dynamics, and driving force

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Evolutionary radiations are considered key processes underlying the origin of biodiversity. Notably, the mechanisms driving these radiations can vary across organisms and often involve a complex interplay of abiotic and biotic factors. The superorder Neuropterida (lacewings and allies) is an archaic holometabolous insect group, which might have undergone a Mesozoic radiation and a Cenozoic decline through its macroevolution. Here I present two case studies tackling the questions on the evolutionary radiations in Neuroptera and Megaloptera. First, the role of the raptorial appendages, with evolutionary novelties for predation, in the Superfamily Mantispoidea (mantidflies, beaded lacewings, thorny lacewings, and dipteromantispids) was unraveled, based on a new dated phylogeny and quantitative evolutionary analyses on modern and fossil species. The raptorial foreleg and its associated novelties was found as key innovations triggering an early radiation of raptorial mantispoids from the Late Triassic to the Early Jurassic. Subsequently, the evolution of the raptorial foreleg influenced the diversification in different modes among lineages. At times, it might have limited the morphological diversity of other body parts and lead to lineage constraint by intensifying competition and lowering environmental resilience, e.g., in thorny lacewings, whose extant diversity is meagre. Conversely, in mantidflies, reduced emphasis on foreleg novelties and increased plasticity in other body parts may lead to better adaptation to predator-prey interactions and environmental shifts, thus maintaining a stable or accelerated level of diversification. Second, the spatiotemporal mode of diversification of the most species-rich megalopteran genus Protohermes was recovered using genome-scale data of ultraconserved elements (UCEs) and mitochondrial genes. The results suggest that vicariance events, likely attributed to the Cenozoic Himalayan orogeny as well as climate change in East Asia, triggered speciation that coincided with the accumulation of genital divergence. Further enhancement of genital and phenotypic diversification might have been promoted by secondary contacts of allopatric or parapatric lineages following the build-up of species richness, likely facilitating species coexistence and lineage accumulation. Thus, the current high species diversity of Protohermes is likely to be resulted from a non-adaptive radiation.

Key words: Neuropterida, phylogenetics, evolutionary radiation, diversification, adaptive trait

S6-4

Morphological basis and driving force of beetle flourishing

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Beetles are the largest group of organisms, accounting for one-fifth of all known species. Why there are so many beetles is a very important scientific question, but also has important practical implications. Most of the studies on this issue are based on samples obtained through active collection, and small-scale studies, including functional morphology and genome, are lacking of larger scale ecological quantified sample level studies. Firstly, this study developed a series of beetle specimen acquisition devices. On the one hand, a large number of rare beetle samples were obtained to fill the gaps such as lack of materials, and on the other hand, the ecological information of these beetle samples was also preserved. Secondly, we use a multidisciplinary approach to study the three-dimensional morphology of beetles, functional morphology of special behaviors, morphological big data, fossil morphology, etc., in an attempt to answer the morphological basis of beetle flourishing. Thirdly, under the framework of SITE-100 international Big Science Program, we established a standardized sample SITE for global beetle diversity monitoring, and analyzed the driving force of beetle flourishing in the three data dimensions of species diversity, ecosystem service function diversity and genetic diversity, combined with environmental factors and the prediction of suitable areas.

Key words: Coleoptera, Diversity, Functional morphology, Multidisciplinary approach

S6-5

How we ‘eye-dentify’ beetles: Eye-tracking reveals cognitive differences based on expertise

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Identification is crucial for understanding biodiversity but faces significant challenges due to declining expertise, especially within hyperdiverse groups like insects. Beetles (Coleoptera), accounting for nearly 40% of described animal species, present significantly diverse morphological characters and thus offer an ideal model for investigating how taxonomists visually perceive and distinguish species. Although extensive taxonomic literature exists, the cognitive processes underlying expert species identification, specifically the visual prioritization of morphological features, remain poorly understood.

This study employs eye-tracking technology to quantitatively examine the visual attention patterns of observers with varying expertise—expert taxonomists, entomology students, and laypersons—as they identify beetle species. Participants viewed standardized beetle images, some featuring distinctive morphological traits, for fixed intervals while their eye movements were recorded.

Our findings demonstrated clear differences in general eye-movement patterns based on expertise levels. Experts consistently focused on specific anatomical regions more frequently and systematically compared to non-experts, indicating that visual attention is strongly correlated with taxonomic expertise. Furthermore, expert gaze patterns closely corresponded with established phylogenetic and taxonomic relationships, suggesting a deliberate cognitive strategy in prioritizing diagnostically significant anatomical features. Visually unique or distinctive morphological traits captured attention across all expertise levels, indicating a universal human bias toward visually prominent characteristics regardless of taxonomic knowledge.

The insights from this research contribute to a deeper understanding of visual cognition in taxonomic expertise, emphasizing the role of eye-tracking as a powerful tool for capturing and preserving expert taxonomic skills. Ultimately, this approach provides valuable empirical evidence to support training programs and conservation efforts, underlining the essential role of human expertise in biodiversity research and species conservation.

Key words: Visual Cognition, Eye-tracking, Expertise, Coleoptera, Morphology

Oral Presentation

Non-Competition

(사)한국곤충학회
The Entomological Society of Korea

(사)한국응용곤충학회
Korean Society of Applied Entomology

01

Strong negative effects of recent wildfires on the Madeiran Green Bush-Cricket (*Psalmatophanes barretoi*)

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Madeira is a volcanic island located in the Atlantic Ocean. Due to arson, burning and artificial climate change, wildfires are one of the critical threats to biodiversity on the island.

The Madeiran Green-Bush Cricket (*Psalmatophanes barretoi*) is an endemic species to Madeira. It was assumed that the species is threatened by wildfires. Based on this assumption, the species is listed on the IUCN Red List as Vulnerable. Thus, we hypothesised that wildfires affect populations of *P. barretoi* negatively. As expected, the species disappeared in many recently burnt areas (2016-2019). However, the species occurred in several oldy burnt regions (2006-2015). The possibilities of recolonisation and the effects of the seasonality of wildfires on *P. barretoi* were discussed.

Key words: Madeira, Wildfires, Fire Ecology, Acoustic Monitoring, The Madeiran Green Bush-Cricket

02

The impact of temperatures on the overwintered honey bee

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The seasonal cycle plays a crucial role in honey bee survival. In this cycle, winter bees exhibit significantly greater longevity than summer bees, a pattern that is altered by climate change. To simulate global warming, we maintained hives at 25°C (Group 25) and 35°C (Group 35) from June to October, while the control group experienced natural conditions. Overwintered workers exhibited temperature-driven physiological and gene expression differences, including the upregulation of *HSP70, ilp2,* and *TOR1* in Group 35. These findings highlight the impact of summer warming on winter bees and may inform strategies to mitigate colony losses and enhance insect model studies.

Key words: honey bees, climate change, physiology, molecular markers, overwintering

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03

A Natural Language Processing (NLP) approach to understanding *Trogoderma granarium* in South Korea

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The khapra beetle, *Trogoderma granarium*, is a globally significant quarantine pest due to its destructive feeding on stored products. Its presence in Korea was first documented in 1928. This study addresses the persistent misinterpretation of *T.granarium*'*s* presence in Korea within global scientific literature. Despite its official exclusion from the Korean national insect species list since 1998, inaccurate records continue to circulate. Employing NLP, this study conducted a systematic literature analysis to identify patterns of information dissemination and citation practices that contribute to this discrepancy. This research aims to quantify the extent of historical misinterpretations, reveal the mechanisms of their perpetuation, and demonstrate the species' exclusion from the Korean fauna. By leveraging NLP, this study provides a data-driven approach to rectifying scientific records and emphasizing the importance of critical evaluation in invasion biology literature.

Key words: Qurantine record, data verification, stored product pest

04

Prediction of annual insect pest population dynamics using cumulative density model and evaluation of its usability

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해충 모니터링 자료를 이용한 개체군 동태 모형은 연간 해충 발생을 예측하는 데에 쓰인다. 이 개체군 동태 모형과 발육데이터에 의거한 복합 개체군모형을 비교하고 실용성을 확인하고자 하였다. 연중 다회 발생 나방해충 데이터를 이용하여, 누적온량(degree days)에 대해 표준화된 해충 누적발생밀도 수식을 얻었다 약제 살포, 장거리 이주, 천적과 같은 외부 압력이 없다고 가정하였을 때, 해충 발육에 영향을 미치는 주된 요인은 일평균온도로, 각 세대의 누적발생밀도는 복합 개체군 모형과 마찬가지로 동일하게 수렴하는 것으로 표현할 수 있다. 단, 계절초기 발생세대는 중간 발육단계부터 생육이 시작될 수 있는 점, 마지막세대의 경우는 개체군 증가 도중에 월동에 접어 우화개체가 더 이상 증가하지 않는 점으로 인하여 별도의 개체군 동태 모형이 필요하였다.

검색어: 복숭아순나방, 담배나방, 개체군동태, 예측모형, 페로몬트랩

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05

Bench-scale production of biodiesel from insect lipids

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최근 바이오연료 의무 혼합비율 증가로 인해 바이오디젤 수요가 급증하고 있다. 국내에서는 주로 폐식용유를 원료로 하여 바이오디젤을 생산하고 있으나, 원료 공급이 부족한 실정이다. 따라서, 새로운 원료의 확보가 시급하다. 본 연구에서는 곤충 지질을 활용한 바이오디젤 제조를 실험실 규모에서 벤치 규모로 확장하는 연구를 수행하였다. 곤충 지질 유래 바이오디젤 전환율은 지방산 메틸 에스테르 함량 분석 및 GC-FID 분석을 통해 확인되었다. 연구 결과, 곤충 지질은 실험실 및 벤치 규모에서 모두 효율적으로 바이오디젤로 전환되었으며, 이러한 결과는 향후 대규모 생산을 위한 기초 자료로 활용될 수 있을 것이다.

검색어: 곤충 지질, 바이오 디젤, 벤치 스케일

06

Evaluation of insect lipids for the development of eco-friendly bio-lubricants

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석유화학제품으로부터 제조되는 윤활기유는 윤활유의 원료물질로써 식물성 지질인 대두유와 같은 탄소중립 원료로의 전환연구가 진행되고 있지만 식용이 가능한 식물성 지질의 한계로 인한 지속가능성에 대한 우려가 있다. 동애등에와 같은 곤충은 높은 지질 함량과 짧은 생애주기를 가지며, 사육조건에 따라 지질의 함량과 조성을 조절할 수 있는 장점이 있다. 특히, 곤충은 음식물 쓰레기를 먹이로 활용할 수 있어 자원 활용 측면에서 효율적이다. 본 연구에서는 곤충지질을 원료로 하여 바이오윤활기유로의 전환을 실험실 규모에서 검증하였다. 이를 위하여 곤충지질의 Epoxidation 공정을 통하여 곤충지질에 포함된 불포화지방산에 산소관능기가 형성됨을 확인하였으며, 기초적인 윤활기유 물성을 비교 조사하였다. 본 연구를 통하여 곤충지질의 바이오윤활기유로써의 활용성을 검토하고, 국내 곤충자원의 활용 가능성을 제고하고자 한다.

검색어: 동애등에, 곤충지질, 탄소중립, 윤활기유, 윤활유

O7

Updated chromosome-level genome assembly of *Ctenoplusia agnata* and its potential application in Plusiinae pest management

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We sequenced the genome of a Korean *Ctenoplusia agnata* (Yanggu strain, looper_JK_23b) using PacBio Revio long-read (ca. 235×) sequencing combined with Pore-C scaffolding. The final assembly (ASM4114632v1, 406.7Mb) comprises 70 scaffolds, with the largest 31 scaffolds representing 95.1% of the assembly, corresponding to the expected 31 chromosomes (n = 31). BUSCO analysis confirmed high completeness with 98.8% gene coverage and 36% GC content. The assembly achieved a scaffold N50 of 13.2 Mb, scaffold L50 of 14, and 28.57% repeat sequence content. We annotated 12,726 protein-coding genes, with 12,635 functionally annotated. Comparative analysis with *Chrysodeixis includens* and *Trichoplusia ni* from the same Plusiinae subfamily revealed that *C. agnata* shares the chromosome number (31) with *C. includens* but shows closer genomic similarity to *T. ni*. Analysis of five major detoxification enzyme gene families (CYP, CCE, GST, UGT, and ABC) showed *C. agnata* has fewer detoxification genes than both *T. ni* and *Spodoptera frugiperda*, potentially influencing its host range and insecticide resistance development.

Key words: *Ctenoplusia agnata*, Genome assembly, Plusiinae, Noctuidae, Pest management

O8

A simultaneous control of two sucking insect pests, *Bemisia tabaci* and *Frankliniella occidentalis*, infesting hot peppers using spraying BioClay-formulated dsRNA specific to vATPase subunit B gene

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Whiteflies and thrips are serious insect pests by feeding plant tissues and transmitting plant viruses to crops. To avoid excessive uses of chemical insecticides, spraying double-stranded RNA (dsRNA) has been proposed alternative control measure against these sucking insect pests. A potent dsRNA was generated against a vacuolar type ATPase subunit B (*vATPase-B*) gene of the silverleaf whitefly, *Bemisia tabaci*, which shares a high sequence homology (85.7%) with that of the western flower thrips, *Frankliniella occidentalis*. The gene was well expressed in the intestine of the whitefly at nymph and adult stages, in which it was highly expressed at the filter chamber and midgut areas from FISH analysis. Due to its sucking mouth parts, it was considered impossible to deliver the sprayed dsRNA by feeding to the internal body of the whiteflies. This study showed the difference between the two insects, in which the thrips could uptake the sprayed dsRNA while the whiteflies could not. To prove the poor dsRNA delivery in *B. tabaci*, the dsRNA was expressed in the host plant by virus-induced gene silence (VIGS). As expected, dsRNA expressed in the VIGS-treated plant hosts was well delivered to the intestine of *B. tabaci* as well as to *F. occidentalis*. To facilitate the dsRNA delivery to the plant tissues, two dsRNA formulations were compared in the control efficacy of the insects. Chitosan- or layered double hydroxide (LDH)- formulation was effective to enhance the control efficacy against both sucking insects. Especially, LDH formulation was much effective to control *B. tabaci* as well as *F. occidentalis*. When LDH-formulated dsRNA was sprayed to hot peppers infested by thrips and whiteflies, it resulted in > 85% control efficacy against the whiteflies and the thrips. These control efficacies were similar those of a chemical insecticide, spinosad. Furthermore, the LDH-formulated dsRNA exhibited a relatively long residual control efficacy. These results suggest that LDH formulation is ideal for dsRNA delivery against sucking insects.

Key words: Whitefly, Thrips, dsRNA, SIGS, VIGS, layered double hydroxide, hot pepper

O9

Foraging benefits of age polyethism in termite tunneling behavior: A simulation study

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Our study examines how age polyethism influences foraging efficiency in termite colonies. Using an individual-based model, we simulated termite tunneling behavior, where older termites have higher energy reserves. Simulations show that younger termites boost efficiency in less mature colonies, while older termites play a key role in mature colonies. By comparing energy expenditures for searching and transporting food, we found that age polyethism significantly enhances efficiency when searching requires more energy than transporting. However, its impact is minimal when transport costs exceed search costs. These findings highlight the ecological benefits of age polyethism in termite foraging.

Key words: Age polyethism, termite, labor division, foraging efficiency

O10

Revision of the genus *Gastrobothrus* Broun (Pselaphinae: Brachyglutini) from New Zealand based on a molecular phylogeny

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Brachyglutini Raffray, the only tribe of the New Zealand Goniaceritae, comprises eight genera. Among them, the endemic genera *Eupinogitus* Broun, *Gastrobothrus* Broun, and *Physobryaxis* Hetschko were previously represented by one, four, and one species, respectively. A recent molecular phylogenetic study indicated that these three genera are paraphyletic, with moderately supported nodes, probably attributed to dataset being limited to only two genes (*COI* and *28S*). In this study, we describe ten new species, providing illustrations of their diagnostic characters. Additionally, we conducted a molecular phylogenetic analysis of New Zealand Brachyglutini, focusing specifically on the three genera, incorporating new species. The dataset included ree mitochondrial genes (*COI*, *COII* and *16S*) and three nuclear ribosomal genes (*18S*, *28S* and *wingless*). The resulting trees revealed that species of *Gastrobothrus* and *Physobryaxis* are scattered across the three genera, and that the clade encompassing all species from the three genera are clearly separated from the outgroup with strong support values.

Key words: phylogeny, ant-loving beetles, New Zealand, new species, evolution

O11

Commercial forests beetle community responses to thinning intensity in Ontario, Canada

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Thinning is a silvicultural practice designed to boost harvest productivity. Given the need for sustainable forest management, understanding how environmental changes induced by different thinning intensities affect biological communities is essential. Our study examined the impact of thinning on beetle biodiversity in both above-ground and ground habitats across five forest types in Nipigon, Ontario, Canada. Although overall beetle abundance remained similar, species diversity was highest in the natural forest, with biodiversity estimates varying among thinning intensities. The results of the community structure analysis showed that thinning intensity was an important variable, and the structural variation patterns were different between the flying beetle community and the ground beetle community. Based on our results, we propose that thinning practices be adjusted by using the beetle communities as indicators.

Key words: beetle, Canada, commercial forest, conservation, thinning

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O12

Comprehensive detection of rodent-borne pathogens in the Republic of Korea using a TaqMan array card

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Rodents are widely recognized as carriers, reservoirs, and hosts for various infectious diseases. Additionally, the impact of global climate change and shifts in human settlement patterns may contribute to a rise in issues associated with rodent-borne pathogens. Given these concerns, this study aims to develop a comprehensive screening approach using TaqMan array cards (TAC). In this study, 45-well microfluidic card designed to perform up to 45 simultaneous detection of various pathogens using real-time PCR (qPCR).

We selected 45 rodent-borne pathogens that are either currently prevalent in the Republic of Korea or pose a potential risk of introduction from external sources. The selected pathogens comprise 16 viruses, 13 bacteria, and 16 parasites, all of which have been customized for a TAC, which provides a distinct advantage for the simultaneous detection of multiple pathogens. The manufactured TAC was verified as suitable for pathogen screening through our own validation, and a method was employed to enhance sensitivity by performing preamplification during RT-PCR. The experimental subject specimens will be spleens from the internal organs of wild rodents sampled nationwide in 2022, and a total of 160 specimens will be screened for pathogens. Positive samples confirmed through these experiments will undergo conventional PCR individually to obtain target sequences, followed by phylogenetic analysis using the obtained sequences.

Key words: rodents-borne diseases, screening, TAC

O13

Evaluation of vector competence of *Culex tritaeniorhynchus* and *Culex pipiens pallens* for Japanese encephalitis virus genotypes GV

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Japanese encephalitis virus (JEV) is a significant mosquito-borne zoonotic pathogen with five genotypes (GI-V), primarily transmitted by *Culex* (*Cx.*) mosquitoes. Before the 1990s, genotype GIII was predominant, but infections with GI have notably increased since then. In the Republic of Korea (ROK), genotype GV has become the dominant strain since its first identification in 2010, suggesting its successful establishment in the region. This study evaluates the vector competence of two domestic mosquito species, *Cx. tritaeniorhynchus* and *Cx. pipiens pallens*, for JEV genotype GV under laboratory conditions.

At 14 days post-infection, *Cx. tritaeniorhynchus* exhibited an infection rate of 97.9% and a dissemination rate of 95.7%. Additionally, viral RNA was detected in saliva samples, with a transmission rate of 91.3%. This species demonstrated significantly higher vector competence for GV, with robust viral replication and efficient transmission to the salivary glands. In contrast, *Cx. pipiens pallens* showed a lower infection rate of 36.9% and a dissemination rate of 42.2%, with a transmission rate of 31.1%. Although *Cx. pipiens pallens* exhibited lower vector competence compared to *Cx. tritaeniorhynchus*, viral RNA was present in some saliva samples, indicating its potential role in JEV transmission.

These findings highlight the critical role of *Cx. tritaeniorhynchus* in JEV transmission in the ROK, while also suggesting that *Cx. pipiens pallens* could contribute to JEV spread, particularly in urban areas.

Key words: Japanese encephalitis virus; *Culex tritaeniorhynchu*; *Culex pipien pallens*; vectos competency; genotype V

014

Medico-legal entomology-based estimation of minimum postmortem interval (PMI-min) in Busan, South Korea: A case study using growth models and machine learning

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Accurately estimating the minimum post-mortem interval (PMI-min) is critical for determining the time and circumstances of death in forensic investigations. Traditional post-mortem indicators are reliable only within 48–72 hours, requiring alternative methods for extended PMI estimation. This study analyzed three forensic cases in Busan, South Korea, involving insect specimens collected from bodies discovered in 2023. Collected specimens were preserved and identified through morphological and DNA analyses. Corrected death scene temperatures were calculated using a thermo-hygrometer and meteorological data, analyzed using quadratic regression and a Support Vector Machine (SVM) model. PMI-min was estimated using growth models and developmental data. Various stages of *Lucilia sericata* (2nd, 3rd instar, and 3rd instar post-feeding), *Calliphora vicina* (3rd instar post-feeding), and *Sarcophaga crassipalpis* (3rd instar) were identified. Estimated PMI-min deviated from the deceased's last known activity by 5–16 days, likely due to pre-colonization interval (PCI) and factors such as weather, oviposition timing, mixed fly populations, and maggot-generated heat. Future research should integrate these variables and leverage machine learning to enhance accuracy.

Key words: Medico-legal entomology, Minimum postmortem interval (PMI-min), Necrophagous flies, Pre-colonization interval (PCI), Growth mdodels

O15

Effects of pig manure-sawdust mixture by black soldier fly (*Hermetia illucens* L.) larvae on biogradation and composting

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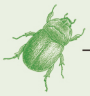
최근 축산분뇨를 처리하기 위한 환경적 문제를 최소화하는 방법은 곤충을 활용하는 것이다. 곤충들 중 동애등에(*Hermetia illucens* L.) 유충은 유기성 폐기물을 변형하는 데 가장 강력한 잠재력을 보여주고 있으며. 번식하고 자랄 수 환경에 최적화 되어 있는 곤충으로 알려져 있다. 본 연구에서는 동애등에 유충의 성장 단계 별로 돈분-톱밥 혼합물에 첨가하여 분해 능력과 그 특성에 초점을 맞추었다. 두 실험 그룹은 돈분 4kg을 톱밥 1kg과 섞은 다음 동애등에 유충 2령(그룹 1) 또는 3령(그룹 2) 0.5kg을 각각 처리했다. 실험 1에서는 동애등에 2령 유충이 3령 유충보다 분해 능력이 증가되었다. 실험 2의 경우 두 동애등에 유충 그룹은 돈분-톱밥 처리가 pH, 수분, ADF, NDF 및 헤미셀룰로스 함량에는 큰 영향을 주지 못했다. 이점은 추후의 연구를 통해 규명할 필요성을 가지고 있다.

검색어: 동애등에, 돈분, 톱밥, 분해능력, 돈분과 톱밥 혼합처리의 특성

Oral Presentation



Competition

(사)한국곤충학회
The Entomological Society of Korea

(사)한국응용곤충학회
Korean Society of Applied Entomology

O16

Molecular phylogenetic evidence for the revival of the subfamily Pterocommatinae (Hemiptera: Aphididae) and its systematic reestablishment

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The synonymized aphid group Pterocomatinae Wilson, 1910 (Hemiptera: Aphididae) was systematically reestablished. We analyzed nuclear gene (EF-1α) and four mitochondrial genes (COI, tRNA + COII, 16S) from 48 terminal taxa representing Aphididae, including recognized major genera and an outgroup. Our findings suggest the phylogenetic revival of the subfamily Pterocommatinae using maximum likelihood with strong support values. Furthermore, taxonomic classification, host-plant association, and ecological approaches were interpreted together.

Key words: aphids, phylogeny, Pterocommatinae, Aphididae

O17

Phylogenic study of the subfamily Aphidiinae (Hymenoptera: Braconidae)

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The subfamily Aphidiinae consists of 55 genera 700 species worldwide, with 15 genera 65 speceies recorded in South Korea. Aphidiinae parasitoids exhibit host specificity toward aphids, making them widely utilized as biological control agents. In this study, we conducted a genus-level phylogenetic analysis using mitochondrial and nuclear gene regions, comprising between four (1451 bp) and seven (3122 bp) genes, including all genera recorded from South Korea as well as several genera known from other regions but not yet reported in South Korea. Our findings indicate that the previously recognized subtribe Trioxina warrants elevation to tribe status as Trioxini. Within Trioxini, phylogenetic relationships were demonstrated to align more closely with aphid host associations rather than traditional morphological classifications. This research provides critical insights into the phylogenetic positioning of the Aphidiinae occurring in South Korea.

Key words: parasitoid wasp, Aphidius, Praon, Ephedrus, Pauesia

O18

Phylogeny and biogeography of the subfamily Alysiinae/Opiinae (Hymenoptera: Braconidae)

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Alysiinae and Opiinae are among the most diverse subfamilies within Braconidae, yet no comprehensive phylogenetic studies have been conducted despite their remarkable species richness and ongoing taxonomic controversies. Here, we present a molecular phylogenetic analysis of these subfamilies using a multilocus dataset comprising five genetic markers (1865 bp) from 175 taxa. Maximum likelihood (ML) and Bayesian inference (BI) methods were employed to infer phylogenetic relationships, while divergence time estimation and biogeographic reconstruction analyses were conducted to explore their evolutionary history. We find that Opiinae forms a clade within Alysiinae. Furthermore, the two previously recognized tribes of Alysiinae, Alysiini and Dacnusini, were not recovered as monophyletic. Based on these findings, we propose a revised classification with three tribes: the newly recorded Asobarini stat. n., alongside Alysiini and Dacnusini. Ancestral state reconstruction suggests that the common ancestor of Alysiinae and Opiinae originated in the Western Palearctic during the Late Cretaceous, followed by diversification primarily driven by geographic dispersal and host specialization. These findings provide new insights into the evolutionary history, classification, and historical biogeography of these ecologically significant parasitoid wasps.

Key words: Hymenoptera, new tribe, new to science, parasitoid wasp, taxonomy

O19

Phylogenomics of cavecrickets reveals the evolution of habitat preference

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Cave crickets (Rhaphidophoridae) prefer dark and moist environments and are often found in residential areas. However, they adapt to diverse habitats across different lineages. In a multilocus phylogenetic study, we discovered a close relationship between Anoplophilinae in Far East Asia and Gammarotettiginae in California, both of which prefer an arboreal habitat. While some cave crickets commonly inhabit human dwellings, others have adapted to a range of environments, such as arboreal habitats, caves, and even deserts. To investigate the evolution of habitat preference in the cave crickets, we performed a phylogenomic analysis using an Orthoptera-specific target enrichment (OR-TE) probe set. This study provides the first phylogenomic tree of cave crickets including all extant subfamilies. We reveal a correlation between their morphological traits and habitat adaptation.

Key words: Orthoptera, Phylogenomics, Anchored hybrid enrichment, Divergence time estimation, Ancestral state reconstruction

O20

Molecular phylogeny of the family Histeridae (Coleoptera: Histeridae)

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Histeridae, commonly known as clown beetles, consist of over 400 genera and 4,800 species belonging to nine subfamilies. Although they are predominantly generalist predators, histerid beetles adapt to various environments. Consequently, they exhibit morphological diversity according to their microhabitats. These morphologically and ecologically fascinating beetles have continuously attracted numerous taxonomists, resulting in several classifications based on morphology. Although multiple phylogenetic studies on Histeridae were performed, their results were inconsistent and limited by reliance on cladistic analyses of morphological characters or the use of only a few molecular markers. To revisit and investigate the internal relationships of Histeridae, we reconstructed a phylogenetic tree, using datasets of 16,175 bp from 15 mitochondrial genes and two nuclear ribosomal RNA (18S, 28S). In this study, we explored the validity of internal classification and relationships among the subfamilies of Histeridae. Also, we provide new suggestions for the positions of some histerid groups.

Key words: Histeridae, mitogenome, molecular, phylogeny, classification

O21

Investigation of the biodiversity of soil invertebrates from Dokdo, Korea

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독도는 한반도 최동단에 위치한 섬으로, 독특한 생태계를 지니고 있다. 독도의 식물, 조류, 곤충, 토양선충, 토양미생물, 해저생물 등 다양한 생물의 다양성이 보고되었으나, 토양 절지동물 연구는 2000년대 톡토기 7종(미동정 6종) 이외의 후속 연구는 보고되지 않았다. 본 연구에서는 2023년부터 2024년까지 3회에 걸쳐 독도의 토양 시료를 채취한 뒤, Berlese-Tullgren funnel trap을 사용하여 응애와 톡토기를 추출하였다. 형태 및 분자 진단을 통해서 종 동정을 수행한 결과, 토양 응애 14과 10속 18종, 톡토기 3과 6속 8종을 확인하였다. 종 수준으로 동정된 샘플은 응애 4종(*Gamasiphis pulchellus*, *Macrocheles penicilliger*, *Punctoribates punctum*, *Tectocepheus sarekensis*)과 톡토기 6종(*Ceratophysella denticulate*, *Desoria trispinata*, *Entomobrya monopunctata*, *Folsomina onychiurina*, *Homidia grisea*, *Hypogastrura garcilis*)이며, Mesostigmata에 속하는 *Macrocheles pencilliger* (Berlese, 1904)는 국내에 처음으로 보고된 종이다. 이 연구는 독도의 생물다양성 및 토양생태계 연구에 대한 중요한 자료를 제공한다.

검색어: 독도, 토양절지동물, 응애, 톡토기, 생물다양성

O22

Regional analysis of *COI* gene variations among *Spodoptera litura* populations across Korea in 2024

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국내에서 주요 농업해충인 담배거세미나방(*Spodoptera litura*)은 최근 기후변화의 영향으로 발생이 증가하고 있다. 이번 연구는 2024년에 경북, 경남, 경기, 강원, 충북, 제주지역(총 78개 시, 군)에서 담배거세미나방 성충을 채집하였으며, 지역별 담배거세미나방을 대상으로 *cytochrome C oxidase I* (*COI*) 유전자에 대한 염기서열의 차이를 비교하였다. 우선, 담배거세미나방의 지역별 발생에서 경남지역이 가장 높았으며, 충북지역이 가장 낮았다. *COI* 분석결과, 모든 지역에서 유사한 single nucleotide polymorphism (SNP) 패턴을 보여주었다. 대부분 406번째 위치의 C가 T로 나타나는 변이 패턴을 보였으나, 경북 울진, 경기 포천, 강원 태백에서는 407번째 위치의 C가 T로 변이가 있었다. 특히, 경북 울진과 경주에서는 이와는 다른 SNP 패턴이 관찰되었다. 이 연구를 통해 국내 분포 담배거세미나방의 지역별 유전적 다양성 정보를 확보하였으며, 이는 담배거세미나방의 집단유전학을 이해하는데 기여할 수 있을 것이다.

검색어: *Spodoptera litura, cytochrome C oxidase I,* single nucleotide polymorphism, climate change

O23

Systematic study on family Stathmopodidae from the Korean Peninsula

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The family Stathmopodidae was first described by Meyrick in 1913 and now comprises more than 40 genera and 400 species. Members of this family feed on crops, pines, mosses, and fern spores, and some are carnivorous, consuming aphids or spider eggs. Despite this ecological diversity, research on Stathmopodidae has been limited due to their small size and the morphological similarity among species. Furthermore, only around 20 species have been reported in the Korean Peninsula, compared to more than 50 in neighboring Japan, indicating a significant gap in domestic research. This study aims to identify and analyze the relationships of Stathmopodidae species collected from the Korean Peninsula by integrating traditional morphological methods, modern molecular techiniques, and the latest technology, machine learning approach.

Key words: Stathmopodidae, Korean Peninsula, Taxonomy, Phylogeny

O24

Biogeography of *Allochthonius* (Pseudoscorpiones: Pseudotyrannochthoniidae) demonstrated dynamic evolutionary history in East Asia

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East Asia is a geologically complex region with exterme levels of biodiversity but the origins and diversity of many invertebrate lineages remain poorly understood. Herein, we suggest two hypotheses about the diversification patterns of *Allochthonius*: i) the ‘isolation’ hypothesis, which explains the diversification of *Allochthonius* happened by several biogeographical barriers and got isolated; ii) the ‘overlapping’ hypothesis that repeated interconnection and separation between the mainland and islands have facilitated the overlapping distribution of *Allochthonius*. For investigating the biogeographical history of *Allochthonius*, we used a combination of phylogenetic analyses, divergence time analyses, and biogeographical methods for phylogenetic and biogeographical reconstructions. A total of 69 species including 61 *Allochthonius* samples were used for phylogenetic analyses, with four loci (18S, 28S, CO1, and H3), total 2550 bp, were sequenced. Our analyses suggest that the current distributions of *Allochthonius* can be explained by a several tectonic events and climate changes in East Asia.

Key words: Arachnida, dispersal, East Asia, historical biogeography, phylogeny, pseudoscorpions, vicariance

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O25

Larval feeding evolution of dung flies (Diptera: Calyptratae: Scathophagidae)

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Dung flies (Scathophagidae) are a small calyptrate family comprising approximately 380 described species worldwide. Their name originates from the type genus *Scathophaga*, which is commonly associated with herbivore feces, but larval feeding habits within the family are remarkably diverse, including phytophagy, saprophagy, and even predation. Despite this diversity, the evolutionary history of these feeding habits remains largely unexplored. In this study, we perform ancestral character state reconstruction to infer the evolutionary history of larval feeding habits and examine patterns of evolutionary transitions within the dung fly lineage.

Key words: Ancestral Character State Reconstruction, Larval Feeding Habits, Scathophagidae

O26

Cryptic species in genus *Maculolachnus* (Hemiptera: Aphididae: Lachninae): from South Korea

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Cryptic species complexes challenge taxonomy by obscuring genetically distinct taxa under a single species name. *Maculolachnus submacula* (Walker, 1848), widely distributed across Eurasia, including South Korea, has long been considered a homogeneous taxon. However, integrative analyses combining morphology and mitochondrial COI barcoding reveal significant genetic divergence and subtle morphological differences, indicating a cryptic species within the *M. submacula* complex. This study re-evaluates its taxonomic status in South Korea as a new species. These findings underscore the importance of modern taxonomic approaches in uncovering hidden biodiversity and refining aphid systematics.

Key words: aphids, new species, DNA barcoding, SEM

O27

Taxonomic review of the Korean Scarabaeinae, Aphodiinae, and Aegialiinae (Coleoptera: Scarabaeidae)

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The family Scarabaeidae Latreille comprises approximately 36,400 species and 460 genera worldwide, classified into 21 subfamilies. Among these, three subfamilies—Scarabaeinae Latreille, Aphodiinae Leach, and Aegialiinae Laporte—are generally recognized as exhibiting both coprophagous and saprophagous feeding behaviors. Prior to this study, a total of 96 species belonging to 19 genera from these three subfamilies had been reported from the Korean Peninsula. In this paper, we describe four new species and document 11 species newly recorded in Korea. Additionally, two synonymies are proposed, and four previous misidentifications are corrected. Consequently, the Korean fauna of these three subfamilies is now represented by 107 species in 53 genera. Here, we provide a comprehensive taxonomic review of the Scarabaeinae, Aphodiinae, and Aegialiinae from Korea, incorporating morphological diagnoses and recent taxonomic revisions, along with a general introduction to each subfamily.

Key words: Scarabaeinae, Aphodiinae, Aegialiinae, taxonomic review

O28

Taxonomic notes of tribe Rhynchitini Gistel (Coleoptera: Rhynchitidae) from Korea

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A total of 220 species belonging to 28 genera are included in the tribe Rhynchitini Gistel (Coleoptera: Rhynchitidae: Rhynchitinae) worldwide, with most species distributed in subtropical and tropical regions. Since Voss (1920) recorded *Cneminvolvulus* (*Cneminvolvulus*) *rugosicollis* Voss and *C.* (*Opacoinvolvulus*) *gensanensis* Voss, a total of 18 species from eight genera have been documented in Korea. However, the lack of detailed descriptions, illustrations, and ecological information makes species identification challenging and increases the risk of misidentification. In this study, we provide an updated taxonomic review of Korean Rhynchitini and discuss its taxonomic history.

Key words: Coleoptera, Korea, Rhynchitidae, Rhynchitini

O29

Taxonomic studies on the family Latridiidae (Coleoptera: Coccinelloidea) in Korea

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The family Latridiidae (Coleoptera: Coccinelloidea) consists of small species, typically measuring 0.5–3.3 mm, with colors ranging from yellow to black. Most species in this family are mycetophagous, feeding on fungi, mycelium, and spores, and some species are found in fungi or spores within ant nests. Latridiidae includes two subfamilies: Latridiinae Erichson and Corticariinae Curtis. Latridiinae comprises 289 species within 19 genera, while Corticariinae includes 550 species within 12 genera, with a total of over 840 species recorded worldwide. In Korea, four species within three genera of Latridiinae and six species within four genera of Corticariinae have been recorded. This study identifies two new species and two newly recorded species from each subfamily, adding eight species to Korea's fauna.

Key words: Lathridiidae, minute brown scavenger beetle, new record, taxonomy

O30

Taxonomy of the family Sarcophagidae (Diptera: Oestroidea) in Korea

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The family Sarcophagidae (Diptera: Oestroidea) is globally distributed comprising over 3,000 species. The larvae of sarcophagid flies exhibit necrophagous, sarcophagous, coprophagous, and parasitic habits, making them not only a taxonomic group of significant forensic relevance but also important ecological roles.

Total 57 species, including one new to science species and 13 newly recorded species were examined with genitalia illustrations. Additionally, cladistic analysis based on 61 selected morphological characters from male adults was conducted to investigate the phylogenetic relationships of Korean Sarcophagidae species. The results showed that the family Sarcophagidae was divided into two clades: Miltogramminae + Paramacronychiinae and Sarcophaginae. The three subfamilies—Miltogramminae, Paramacronychiinae, and Sarcophaginae were strongly supported as monophyletic, forming distinct clades. All genera within the subfamilies Miltogramminae and Paramacronychiinae were also recovered as monophyletic groups. However, within the subfamily Sarcophaginae, the genera and subgenera belonging to the genus *Sarcophaga* did not clearly form monophyletic lineages.

Key words: Sarcophagidae, morphological phylogeny, Korea

O31

A historical review of the classification of superfamily Alucitoidea (Lepidoptera: Apoditrysia) in East Asia

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Alucitoidea commonly known as many-plumed moths, comprises approximately 280 species in 21 genera worldwide, primarily inhabiting tropical and temperate regions. The Alucitoidea is distinguished by its unique plume-like wing structure, which has made it a continuous subject of interest in morphological studies. While traditionally regarded as the sister group to Pterophoroidea due to wing morphology, recent larval characteristics indicate a closer relationship to Copromorphoidea or Epermenioidea rather than to Pterophoroidea. This necessitates a re-evaluation of previous taxonomic data and the re-establishment of its phylogeny. In this study, we review the historical classification of Alucitoidea in East Asia and propose further research directions. By reviewing past taxonomic data, we aim to achieve a more nuanced understanding of the superfamily's systematic position.

Key words: Lepidoptera, Alucitoidea, taxonomy, many-plumed moths, history

O32

Morphological variation among *Pryeria sinica* Moore (Lepidoptera: Zygaenidae) populations across different geographic regions

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Pryeria sinica Moore is a significant pest of Celastraceae and Pentaphylacaceae plants, causing extensive defoliation in East Asia. While its morphology and biology have been studied in China and Japan, research on the Korean population remains limited. This study examined the morphological characteristics of *P. sinica* across all developmental stages in Korea and compared them with populations from Japan, China, and Taiwan. Quantitative and qualitative analyses revealed distinct differences in body size, setal density, spiracle distribution, wing venation, and genital structures among populations, suggesting potential intraspecific divergence. These findings highlight the need for further molecular studies to determine whether the observed variations are due to environmental adaptation or cryptic speciation.

Key words: *Pryeria sinica* Moore, morphological characteristics, regional variation, intraspecific variation

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O33

Photo capturing and 3D model reconstruction of insects

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The demand for 3D model development is increasing rapidly and is widely applied in various fields, especially for virtual reality (VR) and augmented reality (AR) technology to create more interactive and vivid environments. This work presents methodologies combining photography and computational techniques to capture and construct detailed 3D views of insects. High-resolution imaging is utilized to document morphological features, followed by advanced photogrammetry to generate three-dimensional reconstructions. These models provide a valuable tool for various fields, including entomology, education, art, entertainment, and conservation efforts. This approach bridges the gap between traditional observation and modern technology, offering new perspectives on these vital components of ecosystems.

Key words: 3D model, 360 view, insect, photogrammetry

O34

Potential habitat prediction of mosquito species in the Republic of Korea based on Maximum Entropy Modeling

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This study employed species distribution modeling to predict the geographical distribution of 18 mosquito species inhabiting the Republic of Korea. Occurrence data with precise geographic coordinates were compiled from authoritative sources including the Animal and Plant Quarantine Agency, Korea Disease Control and Prevention Agency, GBIF, and scientific publications. Environmental variables were selected through a two-step process: initial contribution assessment followed by correlation analysis (removing variables with lower contributions when $|r|>0.85$). This approach, combining WorldClim bioclimatic variables with land cover, TWI, and DEM data, yielded 8-11 species-specific variables. Model optimization was conducted through ENMeval, generating candidate models with various regularization multipliers and feature combinations, with optimal models determined through information-theoretic approach (delta.AICc=0). The analysis predicted potential habitats for all 18 mosquito species, reflecting species-specific ecological requirements across the Republic of Korea. These findings provide a scientific foundation for public health interventions and ecosystem management strategies, including prioritization of vector control areas and risk assessment for invasive species. The habitat suitability maps represent valuable baseline data for ecological research and vector-borne disease prevention efforts.

Key words: species distribution modeling, MaxEnt, mosquito vectors, habitat suitability, vector-borne disease

O35

Predation effects of two predators, *Toxorhynchites christophi* and *Lutzia vorax* (Diptera: Culicidae), on larval mosquito communities in Korean forest

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Two obligate predators of mosquito larvae, *Tx. christophi* (Portschinsky) and *Lt. vorax* Edwards, are widely distributed across forested areas in Korea, yet their general biology and ecological roles remain poorly understood. In this study, field monitoring was conducted in the Gwangneung Forest from 2023 to 2024. The two predators revealed distinct seasonal occurrence patterns, indicating mutually exclusive temporal niches. Notably, mosquito larval communities associated with *Tx. christophi* exhibited higher species richness and diversity but lower dominance and prey mosquito density. In contrast, communities with *Lt. vorax* showed higher dominance and lower species richness, diversity, and prey density. Our findings suggest that both predators could play a key natural enemies in controlling vector mosquitoes, but differ in their modes of predation, which are related to their adaptive feeding strategies.

Key words: larval mosquito community, natural enemy, predacious mosquito, top-down regulation

O36

Suggestion of optimal pesticide application timing for *Carposina sasakii* based on its AI model

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최근 기후변화의 영향으로 예측이 어려운 급격한 기상 변화로 인해 해충 발생 예측의 정확도가 낮아지고 있다. 이에, 급격한 기상 변화를 반영할 수 있는 해충 모형의 요구가 전 세계적으로 급증하고 있다. 본 연구에서는 농촌진흥청에서 제공받은 2011년부터 2022년 복숭아심식나방의 발생데이터를 활용하여 머신러닝 기법으로 복숭아심식나방 성충의 발생 예측 모델을 개발하였다. 개발된 모델은 통계적으로 검증하고, 2023년과 2024년 복숭아심식나방 발생데이터로 검증하였고, 2023년과 2024년 데이터를 추가하여 모델을 고도화하였다. 현재 복숭아심식나방의 최적 방제 적기는 1령으로 알려져 있기 때문에, 성충 발생 모델을 기반으로 성충으로부터 1령 발생까지 요구되는 온열량을 기존에 발표된 논문을 기반으로 추정하였다. 이렇게 생성된 성충 발생 예측 모델과 방제 적기는 매일 기상 예측 정보를 기상청으로부터 API로 수신하여 모델을 재학습시켜서 급격한 기상 변화를 반영할 수 있는 모델과 방제 적기 제시 기술을 개발하였다. 현재 본 기술은 16개 병해충에 적용되었으며, 보다 많은 병해충에 적용될 수 있을 것으로 기대된다.

검색어: AI 모델, 복숭아심식나방, 방제적기, 머신러닝, 사과

O37

Survival and reproduction of *Nesidiocoris tenuis* on alternative prey sources

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담배장님노린재 (*Nesidiocoris tenuis*)는 가루이를 포함한 다양한 해충을 포식하는 광포식성 천적으로, 생물학적 방제를 위한 대량 사육 기술이 요구된다. 본 연구에서는 세 가지 대체 먹이[줄알락명나방 알, 갈색거저리(밀웜) 유충, 새우(*Altemia* sp.) 알]에 따른 담배장님노린재의 생존 및 번식 특성을 비교하였다. 담배장님노린재의 약충 발육기간은 각각 14.03일, 14.76일, 17.82일로 나타났고, 생존율은 각각 87.5%, 85%, 42.5%이었다. 성충의 평균 수명은 각각 먹이의 경우에 수컷은 27.5일, 28.7일, 20.5일이었고 암컷은 17.3일, 17.5일, 13.7일이었다. 산란량은 115.8개, 88.4개, 72.6개이었다. 줄알락명나방의 알이 가장 적합한 대체먹이지만 이 나방이 해충으로 분류되며, 인편 발생 등으로 인해 작업자의 건강에 악영향을 줄 수 있다. 반면 밀웜은 담배장님노린재가 일정 수준 이상의 생존과 번식력을 보이면서 상업적 대량 공급이 가능해 대체 먹이로 활용 가치가 높다고 판단된다. 또한 밀웜은 천적곤충 생산업체의 새로운 수익원으로 활용될 수 있으며, 파라필름 등을 이용한 인공 먹이 캡슐 개발 등을 통해 담배장님노린재의 안정적인 대량사육 및 상업적 이용이 가능할 것으로 기대된다.

검색어: 천적, 대량생산, 담배장님노린재, 대체먹이, 생명표

O38

Disruptive camouflage and the funciton of stripes in hawkmoth caterpillars

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Camouflage is known of widespread defensive strategy. Disruptive coloration proposed by cott (1940), obscures body outlines to hinder predator detection. While artificial studies support is benefits, its role in wild animals remains uncertain. Poulton (1890) suggested hawkmoth caterpillar stripes break up body shape for concealment. According to Poulton (1890), the stripes on the caterpillar of Hawk moth play a crucial role in helping it blend into the background. This observation known as 'disruptive coloration', possible to stripes disrupt the predator's visual detection. This study evaluates whether hawkmoth caterpillar stripes have survival advantage by disrupting predator vision and highlight the evolutionary pathway of stripes trait in caterpillar of hawkmoth.

Key words: caterpillar, camouflage, hawkmoth, disruptive

O39

Nationwide monitoring of *Matsucoccus matsumurae* Kuwana (Hemiptera: Matsucoccidae) occurrence using pheromone traps

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Matsucoccus matsumurae (Kuwana, 1905) is a significant forest pest that attacks *Pinus* species in Korea. This study conducted the nationwide monitoring of *M. matsumurae* to provide accurate information on the occurrence of this pest. Three pheromone traps were installed in each 164 regions (2022) and 65 regions (2023). Captured males on the trap sheets were photographed with a smartphone camera and automatically counted using a deep-learning-based system. The total number of individuals, seasonal occurrence times, and reoccurrence characteristics were analyzed. We developed an XGBoost-based model to predict the spatial distribution of *M. matsumurae* abundance and phenology. Input features included satellite-derived land surface temperature and vegetation indices, bioclimatic variables, elevation, and the proportion of *Pinus thunbergii* in each grid cell. The monitoring results showed that *M. matsumurae* is distributed nationwide, with many individuals in southwestern coastal areas and Jeju Island. First and peak occurrences were observed earlier in low-latitude and southwestern coastal areas. Moreover, small reoccurrences were detected from late July to October, except in southwestern Jeonnam and Jeju Island. The model outperformed a spatial interpolation baseline in predicting both abundance and phenology, and effectively captured regional variation in outbreak dynamics, with temperature, temperature seasonality, and NDVI emerging as the most influential predictors.

Key words: *Matsucoccus matsumurae*, Japanese pine blast scale, nationwide monitoring, pheromone trap, forest pest prediction

040

Effect of host tree condition on occurrence patterns and diurnal activity of *Aromia bungii* (Coleoptera: Cerambycidae) in urban landscape

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벚나무사향하늘소는 도시 가로수와 과수에 심각한 피해를 주는 천공성 해충이다. 일반적으로 천공성 해충의 특성상 수세가 약해진 나무를 산란처로 선택할 가능성이 높다. 따라서 본 연구는 벚나무사향하늘소 성충의 출현 시기와 행동 패턴을 분석하고, 기주 수목의 생리적 상태와의 관계를 분석하고자 수행되었다. 이를 위해 2022년부터 2024년까지 왕벚나무(*Prunus* × *yedoensis*) 가로수를 대상으로 전기저항도를 측정하고, 성충의 활동이 관찰되는 낮 시간 동안 주요 행동을 기록하였다. 조사 결과, 성충이 발견되는 나무의 전기저항도가 낮은 경향을 보였다. 이는 기주 수목의 생리적 상태가 벚나무사향하늘소의 초기 정착에 영향을 미칠 가능성이 있음을 시사한다. 다만, 전기저항도는 시간대별로 변화하는 특성이 확인되어 보다 면밀한 추가 조사가 요구된다.

Key words: longhorn beetle, tree-boring insects, diurnal activity, urban tree, tree condition

041

Comparison in assemblage strucutre of weevils (Coleoptera: Curculionoidea) across post-forest fire management

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산불 후 곤충 군집 구조는 산불의 직접적인 영향보다는 서식지 구조 변화와 같은 간접적인 요인에 의해 결정된다. 따라서 본 연구는 생태학적 기능군이 다양한 바구미상과(Coleoptera: Curculionoidea)가 산불 후 생태계 복원을 평가하는데 유용한 분류군이 될 수 있을지 검증하는 것을 목적으로 수행되었다. 대형 산불이 빈번하게 발생하는 동해안 지역에서 2019년에 발생한 산불 피해지를 대상으로 2024년 4월부터 9월까지, 월 1회 2주 동안 조사하였다. 서로 다른 관리 방법으로 인해 각기 달라진 5유형의 서식지 패치(대조구, 자연 복원지, 소나무 조림지, 관목지, 초지를 조사하였다. 각 서식지 유형별로 세 개의 방형구를 설정하고, 각 방형구에서 함정트랩, 토양우화트랩, 다중깔대기트랩을 활용하여 바구미상과의 군집 구조를 비교하였다.

검색어: 바구미상과, 산불, 복원방법, 천공성 곤충, 식식성 곤충, 산림생태계, 군집 구조

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042

Comparison of wild bee pollinator assemblages between semi-natural grassland and clear-cut area in a temperate forest

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Pollinating insects, particularly wild bees, are declining globally due to habitat loss. In South Korea, where forests cover 63% of land but grasslands only 2%, this study examined clear-cut areas as potential alternative habitats for wild bees. A total of 57 bee species were identified across both habitat types. While semi-natural grasslands had more individuals (4,183 vs 1,477), clear-cut areas supported greater species richness (51 vs 40) and large-sized specimens. The distinct ecological characteristics of clear-cut areas, with unoccupied ecological niches near the ground, suggest they could serve as alternative habitats for wild bees in early vegetation succession progresses.

Key words: Wild bees, Habitat, Grassland, Clear-cut area, Pollinator

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043

Role of *Tm*Tube on AMPs production against microbial infection in *Tenebrio molitor*

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Tube, an intracellular protein of the Toll-pathway, is known to form a complex with Pelle and MyD88 to regulate antimicrobial peptide (AMP) production by activating NF-κB in *Drosophila*. However, the function of Tube has not yet been studied in *Tenebrio molitor*. To characterize the role of *Tm*Tube, we identified its sequence from the RNA-seq Database. To understand its function in AMP production, we investigated the effects of *TmTube* RNAi on larval mortality and tissue-specific AMP expression after microbial challenge. Our findings will provide insights into the immunological function of *Tm*Tube in response to microbial infections.

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

O44

Characterization of *Tm*TRAF on antimicrobial peptide production in *T. molitor*

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Tumor necrosis factor receptor-associated factor (TRAF) is an adaptor protein in the TLR/IL-1R pathway of mammals, playing an important role in innate immunity and inflammatory responses. In insects, TRAF has been suggested to be involved in antimicrobial peptides production through the Toll signaling pathway, but its function is not well studied. Here, to understand the function of TRAF in *Tenebrio molitor*, we investigated the temporal and spatial expression patterns of *TmTRAF* and its induction patterns against microbial infection. Also, we investigated the effects of *TmTRAF* RNAi on larval mortality and AMP expression patterns in response to microbial infection. This study provides insights into the function of *Tm*TRAF.

Key words: *TmTRAF*, *Tenebrio molitor*, Antimicrobial peptides, Toll pathway, RNAi

O45

Characterization of *TmPellino* on immune memory in *Tenebrio molitor*

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Recent studies have demonstrated that invertebrates possess immune memory, known as immune priming (IP). To investigate the mechanisms underlying IP, we focused on Pellino, a potential regulator of the Toll signaling pathway. First, we performed a mortality assay with sequential infection experiment. To elucidate the relationship between *Tenebrio molitor* Pellino (*Tm*Pellino) and immune priming, we investigate the larval mortality with *TmPellino* silenced *T. molitor* larvae by sequential infection experiment. This study aims to provide fundamental insights into the role of *Tm*Pellino in immune priming.

Key words: *Tenebrio molitor*, *TmPellino*, Toll pathway, RNAi, immune priming

046

Performance evaluation of SCHDNA (SoonChunHyang *De Novo* Assembly), an automated insect transcriptome *De novo* assembly pipeline

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차세대 염기서열 분석(Next-Generation Sequencing, NGS) 기술의 발달은 곤충 유전체 및 전사체 데이터의 폭발적인 증가를 가져왔으며, 이에 따라 방대한 데이터를 신속하고 효율적으로 처리할 수 있는 자동화된 분석 시스템 구축의 필요성이 대두되고 있다. 특히, 참조 유전체 없이 전사체를 분석하는 *De novo* assembly 방식은 mapped 방식에 비해 계산 자원 소모가 크고 과정이 복잡하여 자동화 파이프라인 구축의 요구가 더욱 절실하다. *De novo* assembly는 참조 유전체없이 분석을 수행하는 방식으로, 유전체 정보가 부족한 비모델 생물종 연구에 필수적일 뿐만 아니라, 유전체 변이가 심하거나 새로운 유전자 발견에 유용하다는 점에서 학술적 의의가 크다.

이 연구에서는 연구진들에 의해 기 확보된 곤충 전사체 데이터를 활용하여 기존의 수동 파이프라인 방식과 새롭게 개발된 자동화 프로그램인 SCHDNA(SoonChunHyang *De Novo* Assembly)의 성능을 비교 평가하였다. 두 방식의 분석 시간과 결과의 정확성을 비교 분석한 결과, 두 방식 모두 유사한 크기의 Unigene을 생성하였으며, 평균 분석 시간은 약 5시간으로 유의미한 차이를 보이지 않았다. 그러나 기존 분석 방식은 각 프로그램의 종료 시점을 연구자가 수동으로 확인해야 하는 반면, SCHDNA는 자동 분석을 수행하여 지속적인 모니터링이 불필요하였다. 이는 효율적이고 일관된 분석 결과를 위한 자동화 시스템 도입의 당위성을 시사한다. 이번 연구를 통해 개발된 전사체 *De novo* assembly 자동화 파이프라인인 SCHDNA는 향후 지속적인 개선과 최적화를 통해 다양한 곤충 전사체 및 생물다양성 연구에 효과적으로 활용될 수 있을 것으로 기대된다.

검색어: Insect, Transcriptome, NGS, SCHDNA, De novo assembly, Automatic

047

Analysis of the fumigation effect of methyl benzoate on *Sitophilus oryzae* and *Rhizopertha dominica*

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포스핀(phosphine)은 검역 및 저장곡물해충 방제를 위한 훈증제로 사용되고 있으나, 최근 농산물에서 포스핀 저항성 개체군이 증가함에 저장곡물해충 방제에 어려움이 발생하고 있다. 본 연구에서는 살충 활성을 가진 식물유래 천연 휘발성 유기화합물인 Methyl benzoate(MBe)를 활용하여 쌀바구미(Sitophilus oryzae)와 가루개나무좀(Rhyzopertha dominica)의 포스핀 감수성 및 저항성 개체들에 대한 훈증 효과를 분석하였다. 쌀바구미의 감수성 개체와 저항성 개체의 MBe의 LC_{90} 농도는 각 21.5 mg/L 및 13.8 mg/L이었으며, 가루개나무좀은 각 15.5 mg/L 및 17.6 mg/L로 나타났다. 쌀바구미에서는 포스핀 감수성 및 저항성 개체 간의 유의한 차이가 확인되었으나 가루개나무좀의 경우는 차이가 관찰되지 않았다. 본 연구 결과는 두 종의 저장곡물해충에서 포스핀 저항성 여부와 관계없이 MBe가 효과적으로 작용함을 시사하며, 포스핀 저항성 해충의 소독 및 방제에 유용한 대안이 될 것으로 기대된다.

검색어: 검역, 훈증, 저항성, 살충효과

048

Study on the characteristics of a novel *Bacillus thuringiensis* isolate from Korea

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곤충병원성 세균 *Bacillus thuringiensis* (Bt)는 곤충병원성 세균으로 생물농약으로 개발되어 사용되고 있다. 국내에 존재하는 다양한 Bt 자원을 확보하기 위해 강원도 평창의 천궁 재배지 토양에서 균주 분리를 시도하였다. 이를 위해 채집한 토양을 멸균증류수와 혼합하여 고온에서 1시간 동안 열처리한 후 TSA 배지에 도말하여 단일 균총을 분리하였다. 분리한 균주는 16S-rRNA 유전자 분석을 통해 분자동정과 배추좀나방 유충을 대상으로 병원성을 검증하였다. BLAST 결과 NCBI에 등록된 기존의 *B. thuringiensis* subsp. *kurstaki*와 100%의 유사도를 보여주었으며, 시험곤충에 대해서 96시간에 100% 살충효과를 나타내어 Bt 균주로 동정 및 Bt IPTL3로 명명하였다. 또한, Bt IPTL3 균주는 콩명나방, 파밤나방, 조명나방 및 열대거세미나방 2령 유충에 대한 살충효과와 식물병원성 곰팡이 1종에 대한 길항효과가 있었다. 따라서, 본 연구결과는 국내에서 분리한 신규 Bt 균주의 생물적 방제 인자로써 높은 활용 가능성을 제시한다.

검색어: *Bacillus thuringiensis*, biopesticide, *Spodoptera frugiperda*, entomopathogenic fungi

O49

Effects of temperature, relative humidity, and ultraviolet radiation on the germination of *Beauveria bassiana* AAD16

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The efficacy of entomopathogenic fungi is influenced by environmental factors. We examined the effects of temperature, relative humidity (RH), ultraviolet (UV) radiation, and oil concentration on *Beauveria bassiana* AAD16, a native pathogen of *Allomyrina dichotoma* beetle. Optimal germination was recorded at 24°C, while extreme temperatures 32°C, significantly reduced germination rate. Hyphal length was longest at 24°C but significantly decreased at both lower and higher temperatures, indicating that temperature stress negatively affects fungal growth. At 95% RH, germination remained high but significantly dropped at 35% RH, highlighting the fungus's dependence on high moisture conditions. UV exposure significantly reduced germination over time, confirming susceptibility to prolonged radiation ($R^2 = 0.89$). Higher oil concentrations negatively affected conidial viability while 0.1% oil was found to be most appropriate among the concentration tested. These findings emphasize the need for optimized environmental conditions and protective formulations, such as oil-based carriers and UV protectants, to enhance *B. bassiana*'s field efficacy in pest management.

Key words: entomopathogenic fungus, oil formulation, conidial germination, abiotic factors

O50

Comparative evaluation of different oil concentrations in *Beauveria bassiana* ARP14 for enhanced virulence

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Oil-based formulations of entomopathogenic fungi offer the added advantage of prolonged conidial survival and increased infection potential. In this study, we compared the virulence of *Beauveria bassiana* (Balsamo) Vuillemin ARP14 formulated with different oil concentrations (0.1%, 0.2%, and 0.4%) against *Plodia interpunctella* (Hübner) larvae. Laboratory bioassays were conducted using topical application and the filter paper pipetting method with a concentration of 1×10^8 conidia/ml. In both methods, ARP14+0.1% oil resulted in the fastest larval mortality compared to 0.2%, 0.4%, and ARP14 alone. In the topical application method, mycosis in larvae treated with ARP14+0.1% oil reached 96.7% at 25 days, whereas 0.2%, 0.4%, and ARP14 alone showed mycosis rates of 73.3, 43.3, and 90%, respectively. In the filter paper pipetting method, ARP14+0.1% oil achieved 100% mycosis at 7 days, while 0.2%, 0.4%, and ARP14 alone resulted in mycosis rates of 76.7, 66.7, and 100%, respectively. These findings suggest that a 0.1% oil concentration is the most effective in enhancing the virulence of *B. bassiana* ARP14.

Key words: entomopathogenic fungus, microbial control, stored-product pest, mortality, mycosis rate

O51

A study on insect pupae in forensic entomology: X-ray imaging method for enhanced precision in post-mortem interval (PMI) estimation

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Finding the exact time of occurrence of a dead body by estimating the post-mortem interval (PMI) is most important in the field of forensic entomology. The study focused on blow fly pupae, which are some of the earliest insects to colonize decomposing bodies. The pupae have the longest development period in the blow fly life history, but we have trouble viewing the inside of the pupae because of the puparium. Therefore, the division experiment that the developmental internal x-ray imaging stage carried out could reveal a difference in growth based on temperatures in two different environments. All experiments were recorded accurately with an indoor Wireless-Fidelity (Wi-Fi) camera. There is a significant difference in developmental time between the individuals sampled at 20℃ and 30℃. During the internal developmental stage at two different temperatures, it is distinctly divided by their morphological characteristics. The internal developmental stages, subdivided into four distinct phases, improve the precision of post-mortem interval estimation. The x-ray imaging method is more economical and easier to use than the current method, but it requires collecting more data through additional experiments in various environments to apply this method effectively.

Key words: developmental stage, forensic entomology, post-mortem interval estimation, x-ray analysis

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O52

Reproductive strategy and tick-borne pathogens prevalence in *Haemaphysalis longicornis* in the Republic of Korea

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The Asian longhorned tick, *Haemaphysalis longicornis*, is the predominant hard tick species and a major vector of Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV) in the Republic of Korea. In nature, *H. longicornis* is maintained through two reproductive strategies, bisexual and parthenogenesis. Parthenogenetic and bisexual individuals predominated from the northeastern and southwestern ROK, respectively. There is no study to screen other tick-borne pathogens, although SFTS virus is well-known as transmitted by *H. longicornis*. In this study, we identified the putative tick-borne pathogens, including *Rickettsia*, *Theileria*, *Babesia*, *Borrelia*, and *Anaplasma*, from both reproductive lineages. Two species of *Anaplasma* and a single species from each *Ehrlichia*, *Rickettsia*, and *Theileria* were further identified through conventional and nested PCR. This study provides new insight into the tick-borne pathogens associated with the two reproductive lineages of *H. longicornis*, which will contribute to expanding our understanding of vectorial capacity for *H. longicornis*.

Key words: *Haemaphysalis longicornis*, reproductive system, population genetics, tick-borne pathogen

053

Cross-species microRNA transfer between body lice and humans

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Host-parasite co-evolution has shaped cross-species physiological regulation through molecules like microRNAs (miRNAs). The body louse, an obligate blood-feeding ectoparasite, may ingest human-derived miRNAs and inject its own via saliva, enabling bidirectional molecular exchange. In this study, we identified miRNAs from saliva, salivary glands and alimentary tracts of adult lice, as well as from whole bodies of unfed nymph and mixed stage lice to investigate these cross-species interactions. Our analysis revealed 105 body louse miRNAs, 98 salivary gland miRNAs, 62 saliva miRNAs, and 155 human-origin miRNAs present in lice after blood feeding. Interestingly, louse-derived miRNAs that are transferred to humans are likely to be involved in gene expression regulation and immune responses. The potential roles of these miRNAs and their cross-species interaction will be discussed in this talk.

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

054

Inhibition of digestive α-amylase in *Helicoverpa armigera* by proteinaceous seed extracts: Biochemical and genetic insights

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Helicoverpa armigera is a major agricultural pest worldwide. Due to resistance, enzyme inhibitors are being explored as an alternative to chemical pesticides. This study evaluated the inhibition effects of seed protein extracts on α-amylase (Amy) acitivity in *H. armigera* larvae. The results showed concentration-dependent Amy inhibition and revealed three isozyme bands. A BLAST search identified three mRNA sequences for *H. armigera Amy* genes. Phylogenetic analysis showed these isoforms were closely related, though one had lower similarity to neighboring sequences. Candidate gene for *Amy* were analyzed and visualized. Our findings suggest that proteinaceous seed extracts and the *Amy* gene may serve as potential tools for pest control.

Key words: *Helicoverpa armigera*, proteinaceous extracts, inhibitors, α-amylase

O55

RNA-seq-based identification of imidacloprid resistance mechanisms in *Nilaparvata lugens* and development of diagnostic tools for the CYP6ER1 variant

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Neonicotinoid insecticides, such as imidacloprid, have been used for over three decades to control major agricultural pests, including brown planthopper. However, the extensive use of imidacloprid has led to widespread resistance across Asia in many pest populations. Bioassay results demonstrated significant resistance in *N. lugens*, with a resistance ratio 38. RNA-seq analysis revealed that the overexpression of detoxification enzyme genes plays a central role in resistance, with CYP6ER1 being the most significantly upregulated gene, showing a 28-fold increase in resistant strain compared to susceptible strain. To date, six main variants of CYP6ER1 have been reported. The current study, CYP6ER1vA has been identified as the predominant variant across all resistant strains, field populations collected in 2024, and museum samples from 1975. This suggests that the vA variant predated the widespread use of imidacloprid and that its expression level, rather than its mere presence, is the key factor driving resistance.

Key words: *Nilaparvata lugens*, Imidacloprid resistance, CYP6ER1, RNA-seq, Diagnostic tools

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O56

In silico functional analysis of the T115N mutation in the octopamine receptor associated with amitraz resistance in *Varroa destructor*

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The *Varroa destructor*, an ectoparasitic mite, poses a significant threat to global beekeeping by compromising the vitality and immunity of Western honey bees, *Apis mellifera,* and transmitting various honey bee viruses. Previous studies have identified a novel T115N mutation in the β2-adrenergic-like octopamine receptor gene (*Octβ*$_2$*R*) in Korean populations of *Varroa* mite, and confirmed its role in amitraz resistance. The mites homozygous for the T115 allele exhibited early intoxication responses, whereas those with the N115 allele had delayed responses and a 2.8-fold longer median lethal time, confirming the amitraz resistance conferred by the T115N mutation. *In silico* homology modeling and molecular docking simulations of *Octβ*$_2$*R* variants suggested that the T115N mutation reduced binding affinity specifically for amitraz, whereas other previously reported mutations (N87S, Y215H, F290L, and Y337F) exhibited reduced affinity for amitraz's primary metabolite, N-(2,4-dimethylphenyl)-N'-methylmethanimidamide (DPMF). The docking simulation data suggested the potential link between high-dose versus low-dose amitraz applications and the region-specific selection of *Octβ*$_2$*R* mutations.

Key words: *Varroa* mite, Amitraz resistance, Octopamine receptor, 3D modeling, Molecular docking

057

Neurotoxic pesticides impair homing ability in honey bee by disrupting energy metabolism and cognitive function

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Foraging is crucial for honey bees as it provides essential dietary resources for the entire colony. However, previous studies have reported that pesticide exposure can impair foraging ability. In this study, we investigated the effects of acetamiprid (ACE), imidacloprid (IMI), carbaryl (CAR), and fenitrothion (FEN) on the homing ability of honey bees. Furthermore, to elucidate the underlying mechanisms, we analyzed the expression of genes related to cognition and energy metabolism. Our results showed that all four pesticides generally reduced homing ability. In ACE-, IMI-, and CAR-treated foragers, cognitive function-related genes were upregulated, whereas genes involved in energy metabolism were downregulated, suggesting that reduced cellular energy availability may underlie the decline in homing ability. In contrast, FEN-exposed honey bees exhibited downregulation of insulin signaling-related genes but upregulation of cellular respiration-related genes. In addition, foraging-related gene expression was suppressed in FEN-treated bees, indicating that disruptions in both energy metabolism and cognitive function may contribute to the failure of homing in FEN-exposed bees. These findings provide insights into how neurotoxic pesticides differentially impact honey bee homing ability by disrupting energy metabolism and cognitive processes, highlighting potential risks to bee health.

Key words: Honey bee, Homing ability, Coginition-related genes, Energy metabolism-related genes

O58

Propolis-fed *Drosophila melanogaster* exhibits enhanced ethanol tolerance via antimicrobial peptides induction

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In our previous studies, we observed a significant induction of antimicrobial peptides (AMPs) expression in *Drosophila melanogaster* exposed to ethanol, and transgenic flies with reduced AMPs expression exhibited significantly lower ethanol tolerance. In this study, we found that expressions of AMPs were elevated in *D. melanogaster* reared on an artificial diet containing 1% propolis. Interestingly, flies fed with propolis exhibited a higher survival rate than those on a normal diet when exposed to ethanol, further confirming the physiological role of AMPs in ethanol tolerance. To investigate the potential involvement of oxidative stress in this process, we analyzed the expression levels of antioxidant enzymes (AOEs) in flies reared on propolis following ethanol exposure. Notably, AOEs were not induced by ethanol exposure, suggesting that AMPs, rather than AOEs, play a key role in mitigating ethanol-induced oxidative stress in flies with high AMP expression. Given that ethanol exposure generates oxidative stress and AOEs typically function to reduce its toxicity, our findings suggest that AMPs may contribute to ethanol tolerance by participating in oxidative stress metabolism. These results provide new insights into the physiological functions of AMPs beyond immunity, highlighting their potential role in stress resistance mechanisms.

Key words: *Drosophila melanogaster*, oxidative stress, propolis, antimicrobial peptides, antioxidant enzymes

O59

Activities of mitochondrial respiratory chain complexes in *Tribolium castaneum* under carbonyl sulfide exposure

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A new fumigant, carbonyl sulfide (COS), has potential as a replacement for methyl bromide, phosphine and ethyl formate, however its mechanism of toxicity to insects remains poorly understood. In this study, transmission electron microscopy (TEM) analysis, mitochondrial respiratory complexes activities (Complex I, II, III, IV) and ATP assay were performed on the *Tribolium castaneum* to investigate the effects of COS exposure. TEM analysis was conducted on the fat body tissues of *T. castaneum*, which play a key role in mitochondrial energy metabolism in insects. COS-treated *T. castaneum* adults exhibited distinct variations in mitochondrial morphology with rarefaction and vacuolation in their mitochondrial matrix, compared to the control group. Additionally, COS exposure significantly altered mitochondrial function, with the activities of Complex I and Complex IV increasing by 1.31-fold and 2.79-fold, respectively, while ATP content decreased by 0.89-fold. In contrast, COS-treated *T. castaneum* adults did not significantly increase mitochondrial Complex II and III activities compared to the control group. These mitochondrial alternations suggest that COS may exert its insecticidal effect by targeting the respiratory system. This study highlights the potential efficacy of the COS as a fumigant against major stored-product pest, *T. castaneum*.

Key words: red flour beetle, carbonyl sulfide, mode of action, TEM analysis, mitochondrial respiratory system complex activity

O60

Nanoparticle-based RNAi targeting vATPase B for effective management of three aphid species

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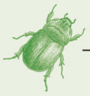
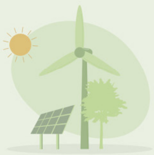
Aphids are major agricultural pests capable of transmitting plant viruses including cucumber mosaic virus (CMV), pepper veinal mottle virus (PVMV), and potyviruses, and causing significant crop damage through their piercing-sucking mouthparts, which allow them to efficiently extract phloem sap and uptake viral particles from infected plants. RNA interference (RNAi) has emerged as a promising strategy for aphid pest control by silencing essential genes through double-stranded RNA (dsRNA) delivery. However, aphid salivary and gut nucleases rapidly degrade unprotected dsRNA, reducing RNAi efficiency. A previous study showed an improved transdermal dsRNA delivery system using a cost-effective nanocarrier against soybean aphid *Aphis glycines*, demonstrating high gene silencing efficiency and potential for RNAi-based aphid management. In our study, we focus on the development of a common double-stranded RNA (dsRNA) targeting the vacuolar ATPase subunit B (vATPase B) gene to control three economically significant aphid species: *Myzus persicae*, *Aulacorthum solani*, and *Aphis gossypii*. To enhance the stability and efficacy of dsRNA delivery, we employ protective strategies using chitosan and layered double hydroxide (LDH) nanoparticles. The effectiveness of the dsRNA treatment is assessed through molecular analyses to determine its impact on gene silencing and aphid survival. Our findings demonstrate that nanoparticle-coated dsRNA significantly enhances gene silencing efficiency compared to unprotected dsRNA. This approach prolongs dsRNA stability in the aphid gut and improves systemic RNAi effects, leading to increased aphid mortality and reduced crop damage. Future studies will focus on optimizing nanoparticle formulations and evaluating field-level efficacy to advance the practical application of RNAi-based aphid control.

Key words: *Myzus persicae*, *Aulacorthum solani*, *Aphis gossypii*, dsRNA, vATPase B, Chitosan, LDH

Poster Presentation





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A1

Taxonomic study of the Oestridae (Diptera) reported in the Korean Peninsula

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The family Oestridae (Diptera) are obligatory parasitic flies that cause myiasis in mammals, with various species parasitizing the skin or tissues of livestock, wild mammals, and even humans. According to the 2024 National Species List of Korea (NIBR), two species from the genus *Hypoderma* and one species each from the genera *Gasterophilus* and *Rhinoestrus* were recorded in Korea. However, except for *H. bovis*, all these records are from North Korea. *H. bovis* is believed to have been introduced through the importation of dairy cattle and other livestock. In our surveys conducted in 2018, 2019, 2022 and 2023, we newly collected a species of *Hypoderma* in the Gapyeong and Hongcheon, and samples of *Cephenemyia* in Inje and Yanggu. In this study, we conducted a taxonomic review of the Oestridae in the Korean Peninsula using phylogenetic analysis based on the mtDNA barcode region and morphological analysis of the samples from South Korea.

A2

Review of the genus *Greensladella* Johnson (Coleoptera: Ptiliidae: Ptiliini): A new combination with first Korean record

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The genus *Greensladella* was first described as a monotypic genus from the Solomon Islands. With the addition of two species in 2021, a total of three species are currently known worldwide. That this genus is morphologically related to the genera *Ptilium*, *Micridium*, and *Ptiliolum*. However, the phylogenetic position of these genera remains unclear. We examined 16 specimens collected in South Korea and identified them as *Ptiliolum hiranoi*. However, based on the type species of *Greensladella* and three subgenera of *Ptiliolum*, we propose transferring of *Ptiliolum hiranoi* to the genus *Greensladella*, resulting in *Greensladella hiranoi* **comb. nov.** Updated illustrations of the diagnostic characters of *Greensladella* and a key to the worldwide *Greensladella* species are also provided.

Key words: new record; featherwing beetle; taxonomy

A3

Faunistic study of Coleoptera (Buprestidae, Carabidae, Cerambycidae, Lucanidae, and Melyridae) on Gageodo Island, including a newly recorded species from the Korean Peninsula

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The Korean archipelago comprises over 3,348 islands, many of which have well-preserved biodiversity. Although Gageodo Island, the southwesternmost island in the Korean Peninsula, has unique flora and fauna distinct from the mainland making it biogeographically significant, it was underexplored, especially in terms of its coleopteran fauna. In this study, we surveyed five beetle families: Buprestidae, Carabidae, Cerambycidae, Lucanidae, and Melyridae on Gageodo Island. To update the coleopteran list for the island, previous studies that examined specimens from Gageodo Island were also compiled and organized. As a result, 31 species and three families are recorded on the island for the first time, for a total of 93 species within 16 families. Of these, the melyrid species, *Intybia tsushimensis* (Satô & Ohbayashi, 1968) is reported for the first time in the Korean Peninsula. This study would serve as a foundational piece for understanding the fauna of Gageodo Island.

Key words: biodiversity, *Intybia*, island fauna, new record, Korean archipelago

A4

A new pselaphine genus from Eastern Australia (Coleoptera: Staphylinidae: Pselaphinae: Faronitae) with nine new species

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The family Staphylinidae is one of the most speciose groups in the world. Within this family, the subfamily Pselaphinae is among the largest groups. Pselaphinae comprises six supertribes: Batrisitae, Goniaceritae, Pselaphitae, Euplectitae, Clavigeritae, and Faronitae. The supertribe Faronitae consists of 30 genera worldwide, with 14 genera found in Australia and New Zealand. While examining faronite specimens, we identified 167 specimens that did not belong to any known faronite genera. Species of this genus can be distinguished from other Faronitae genera by their frontal sulcus, features of the aedeagus, and restricted collection localities, as they have only been found in the eastern part of Australia. In this study, we describe nine new species.

Key words: Pselaphinae; Faronitae; Australia; Taxonomy

A5

An integrative systematic study on the green bush-cricket genus *Tettigonia* (Orthoptera: Tettigoniidae) in South Korea

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The green bush-cricket genus *Tettigonia* comprises 26 species worldwide, including four species in Korea. Previous studies have reported taxonomic confusion, particularly focusing on morphological characteristics such as tegminal length and male genitalia. We conducted an integrative systematic study of three South Korean species—*T. ussuriana*, *T. dolichoptera* and *T. jungi*—including morphological, bioacoustic, and molecular characteristics. As a result, we identified incongruencies in *T. ussuriana* across these characteristics. Morphological and bioacoustic analyses revealed that *T. ussuriana* formed two distinct groups, while *COI* phylogenetic tree indicated polyphyly. These discrepancies strongly support the need for an integrative approach to resolving the taxonomic conflicts in *Tettigonia* species.

Key words: Orthoptera, Tettigoniidae, *COI*, *Tettigonia ussuriana*, phylogeny

A6

Taxonomic study of the genus *Amiota* Loew (Diptera: Drosophilidae) from South Korea based on morphology and DNA barcoding

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The genus *Amiota* Loew in Drosophilidae is distinguished by its lachryphagous behavior, and is typically characterized by a glossy black body with milky-white patches on the pleura and face. Up to date, 154 species of *Amiota* are recorded worldwide, including 78 species from China and 33 from Japan, whereas only seven species have been recognized from South Korea. In this study, we recognized ten species from the country, including seven additional species that represent new to the country or new to science. We provide detailed taxonomic information, including the images of the habitus and genital structures and a phylogenetic tree inferred from mitochondrial *COI* barcode sequences. Furthermore, we discuss the potential existence of a novel species group, as suggested by the analysis result based on genital morphology and molecular phylogenetic data.

Key words: Diptera, Drosophilidae, Amiota, DNA barcoding, new species group

A7

Molecular and morphological insights into the taxonomic classification and introduction pathways of *Vespa crabro* L. (Hymenoptera: Vespidae)

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[2]Korea Hemp Institute, Konkuk University, Seoul, Korea
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The traditional color pattern–based classification of *Vespa crabro* into six subspecies remains unreliable. This study integrated morphological and genetic analyses to reassess taxonomy and introduction pathways, focusing on two Korean subspecies, *V. c. crabroniformis* and *V. c. flavofasciata*. Analysis of 163 Korean specimens revealed 27 color pattern variants, with weak correlations between thoracic and abdominal patterns, challenging color-based classification. CO1 gene analysis identified nine haplogroups in Korea, inconsistent with subspecies classification. Unique Korean single nucleotide polymorphisms distinguished them from Japanese, European, and North American populations. Phylogenetic analysis showed significant genetic differences between Korean and Japanese populations, despite previous classification as the same subspecies. North American populations exhibited genetic links to both European and Korean populations, suggesting multiple introduction pathways. These findings support unifying *V. crabro* subspecies and emphasize the importance of molecular data in refining taxonomy and tracking introductions.

Key words: CO 1, color pattern variation, *Vespa crabro*, *V. crabro crabroniformis*, *V. crabro flavofasciata*

A8

Additional records of the family Corylophidae (Coleoptera: Coccinelloidea) from South Korea

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The family Corylophidae LeConte is a cosmopolitan family, comprising 28 genera and approximately 300 species worldwide. This family is known as minute hooded beetles due to their small body size and morphological character of head concealed by the pronotum. Both larvae and adults feed on fungi spores and thrive in a variety of habitats. In Korea, three genera and six species have been recorded. In this study, we reports three additional species: *Sericoderus brevicornis* Matthews, *Arthrolips* sp.1, and *Arthrolips* sp.2. Illustrations of habitus, genitalia, diagnostic characters, and a distribution map are also provided.

Key words: minute hooded beetles, new records, *Arthrolips*, *Sericoderus*, taxonomy

* This research was supported by the research program of RDA (RS-2021-RD009884).

A9

First report of the *Batrisodes abdominalis* (Coleoptera, Staphylinidae, Pselaphinae) from South Korea

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The genus *Batrisodes* Reitter is currently known to contain 150 species in the Holarctic region (Chandler, 1997; Schülke and Smetana, 2015; Jiang and Yin, 2017). Only one species, *B. baejeongdoki*, has been recorded in South Korea, which is significantly fewer compared to the 21 species in Japan and 12 species in China. The only species recorded in South Korea was collected from Mt. Jiri and described as a new species by Nomura in 1993. During specimen research at the Korea National Arboretum, we identified one species, *B. abdominalis*, collected by a window trap in Gwangneung forest. This species was described by Yin (2017) in China, including information on its habitus and male genitalia. Therefore, we are reporting this unrecorded species from South Korea for the first time. Information on the species, including diagnosis, habitus, and male genitalia, will be provided.

Key words: Batrisitae, *Batrisodes*, Myrmecophilous beetle, Taxonomy

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A10

New records and a new combination in the Korean *Borophaga* and *Peromitra* (Diptera: Phoridae)

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The South Korean species of the scuttle fly genus *Borophaga* are reviewed and three species are newly recognized. Among them, One species is described as new to science and *B. femorata*, is new to South Korea. The other newly recorded species *B. tibialis*, along with a Burmese species *B. thoracalis*, is transferred to the genus *Peromitra* based on morphological and molecular characteristics, and the two species are possibly conspecific. Brief diagnoses with photographs of the *Borophaga* and *Peromitra* species are provided.

Key words: *Borophaga*, Korea, new combination, *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).

A11

One more sand fly species (Diptera: Psychodidae) newly recorded from Korea

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Sergentomyia is a genus of hematophagous Phlebotomine sand flies, primarily herpetophilic and known to transmit reptile leishmaniasis. Recent studies suggest some species may also serve as potential vectors of *Leishmania* causing human infections. Previously, *Sergentomyia hivernus* was firstly recorded species of this genus in Korea (in prep.) In this study, sand flies collected using malaise traps from various regions in Korea were identified and newly recorded as *Sergentomyia squamirostris*. This species has been recorded in Japan and China and is known to transmit *Trypanosoma bocagei*, a hemoparasite of toads. Since sand flies are an important group in terms of public health and veterinary concerns, which is completely unknown in Korea before our studies, continuous monitoring is necessary to comprehend the distribution of this possible disease vector species within the subfamily Phlebotominae and the potential presence of unrecorded species in Korea.

Key words: blood-feeding, hematophagous insects, leishmaniasis, sand flies, *Sergentomyia*

A12

A subgroup-level classification and distribution of *Pholcus phungiformes*-group from Korea (Araneae: Pholcidae)

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[2]Department of Plant Medicine, Division of Bio-Resource Sciences, Kangwon National University

Pholcus phungiformes-group is a highly diverse species-group of the cellar spider genus *Pholcus* Walckenaer (Araneae: Pholcidae), containing more than a hundred species mostly endemic (> 99%) to their mountainous habitats from Far East Asia. Taxonomic studies have been frequently conducted in Korea, and currently 44 valid species have been recorded in the country. Although these species is now classified as belonging to a single species group, genital morphology of them is astonishingly diverse and these radiation is presumably correlated to their geographic distribution. In this study, we propose morphological species-subgroups for classifying Korean members of the species-group more effectively, and provide their diagnostic characteristics and specific distribution ranges.

Key words: cellar spiders, distribution, *Pholcus phungiformes*-group, species-subgroup, taxonomy

A13

Four new species of the genus *Pholcus* (Araneae: Pholcidae) from Korea

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[2]Department of Plant Medicine, Division of Bio-Resource Sciences, Kangwon National University

Currently 44 valid species of the *Pholcus phungiformes*-group (Araneae: Pholcidae) have been known from Korea, and undoubtedly many species still await discovery. In this study, four new species belonging to this species group were found in mountainous regions from Danyang and Yeongwol, Korea. These new species have common characteristics with *Pholcus gosuensis*, such as claw-like exaggerated sclerotized prolateral process of procursus and auriculate uncus with small blunt triangular distal projection in male palp and strongly extended epigynal knob area in female genitalia. Brief diagnoses, photographs and a distribution map for the new species and *P. gosuensis* are provided.

Key words: Araneae, cellar spider, new species, *Pholcus phungiformes*-group, taxonomy

A14

Three new records of *Neoplatyura* Malloch (Diptera: Keroplatidae) from South Korea

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The family Keroplatidae (Diptera), commonly known as predaceous fungus gnats, is one of the most diverse groups within the superfamily Sciaroidea. Globally, around 100 genera and 1,000 species of Keroplatidae have been documented, yet only five species has been recorded in South Korea. The genus *Neoplatyura* Malloch (Diptera: Keroplatidae: Keroplatinae) is known to include 51 species worldwide, among which only two species, *Neoplatyura cognata* Uesugi, 2002 and *Neoplatyura maruyamaensis* Uesugi, 2002, have been recorded in South Korea. In this study, three keroplatids species in the genus *Neoplatyura* Malloch, 1928, *Neoplatyura elongata* Uesugi, 2002, *Neoplatyura* sp.1 (new species), and *Neoplatyura* sp.2 (new species) are newly recorded from South Korea. Specimens were collected from Ulleng-gun in Gyeongsangbuk-do, Seoguipo-si in Jeju-do, and Namhae-gun in Gyeongsangnam-do using Malaise traps. The species are described and illustrated.

Key words: fungus gnats, Korea peninsula, Orfeliini, taxonomy

A15

Taxonomy of the genus *Condylostylus* Bigot (Diptera: Dolichopodidae) from Korea

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The genus *Condylostylus* Bigot, 1859, one of the most commonly found long-legged flies in Korea, is easily identified by other species by their black spot of wing. Up to now, only one species, *C. nebulosus* (Matsumura, 1916), was recorded in Korean fauna. In the course of taxonomic survey on the long-legged flies in Korean peninsula, the authors have found two firstly recorded species, *C. itoi* Kasagi, 2006 and *C. japonicus* Kasagi, 1984 and a new species, *Condylostylus* sp. nov. Some morphological characteristics of firstly recorded and new species are provided here.

Key words: Empidoidea, Sciapodinae, long-legged fly, new species

A16

Two new species of the genus *Meroplius* Rondani (Diptera: Sepsidae) with a key of Palaearctic species

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Two new species, *Meroplius* sp. nov. 1 and *Meroplius* sp. nov. 2, are described from Korea. The morphological characteristics of both species are provided in detail. Additionally, a key for the identification of Palaearctic species of *Meroplius* is presented.

Key words: Sciomyzoidea, black scavenger fly, Korea, taxonomy

A17

First report of the genus *Azelia* Robineau-Desvoidy (Diptera: Muscidae) from Korea

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The genus *Azelia* Robineau-Desvoidy, 1830, which is associated with the dung of herbivorous or omnivorous animals and flowers, comprises 15 species worldwide. However, this genus has not been recorded on the Korean Peninsula. In this study, we report this genus for the first time in Korea with the previously unrecorded species *Azelia cilipes* (Haliday, 1838). External photographs and taxonomic information are presented herein.

Key words: Muscoidea, Azeliinae, Azeliini, new record

A18

First record of the family Mythicomyiidae (Diptera: Asiloidea) from Korea, with description of a new species

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[4]Institute of Plant Medicine, Kyungpook National University

In this study, we report the first record of the family Mythicomyiidae on the Korean Peninsula, based on the discovery of a new species, *Glabellula* sp. nov. This finding also represents the first record of the genus *Glabellula* in the eastern Palearctic region. A detailed description of the new species is provided, along with photographs and detailed illustrations. Additionally, an updated checklist of the genus *Glabellula* in the Palearctic region is presented herein.

Keywords: micro bee fly, *Glabellula*, taxonomy

A19

First record of the genus *Compsoptesis* Villeneuve, 1915 (Diptera: Tachinidae) from South Korea

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The genus *Compsoptesis*, belonging to the subfamily Phasiinae, is a small group of tachinid flies with only three species known worldwide: *C. klossi* (Malloch, 1930), *C. rufula* Villeneuve, 1915, and *C. phoenix* Villeneuve, 1915 (the type species). All previously known species are distributed within the Indomalayan region. In this study, we recognized for the first time the presence of *Compsoptesis* sp. feeding on nectar from *Chrysanthemum indicum* in November in Busan, South Korea. This species is presumed to be new to science. The discovery expands the known geographic range of the genus *Compsoptesis* beyond the Indomalayan region to the Palearctic region, suggesting a broader distribution than previously recognized. We provide detailed photographs and diagnostic characters, contributing to the understanding of the diversity and ecology of this taxa.

Key words: Tachinidae, Phasiinae, *Compsoptesis*, New species, Korea

A20

A new species of genus S*ciaphyes* Jeannel, 1924 (Coleoptera: Leiodidae: Cholevinae) from South Korea

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The subfamily Cholevinae Kirby, 1837, commonly known as cave-dwelling beetles, includes approximately 2,200 species recorded worldwide. Cholevid beetles inhabit ground, subterranean habitats, and caves, and they are found in organic matter such as animal carcasses and excrement. To date, 17 species belonging to four tribes have been recorded in Korea. In the present study, we report the tribe Sciaphyini Perreau, 2000 from South Korea for the first time, along with a new species of the genus *Sciaphyes*. The previously unrecorded genus *Sciaphyes* is anophthalmic and apterous. This new species was collected on Geogeum Island (Goheung-gun) using a deep-soil trap. Illustrations of the adult, aedeagus, and diagnostic characters are also provided.

Key words: *Sciaphyes*, new species, Cholevinae, Taxonomy

A21

Cheklist of the subfamily Xoridinae (Hymenoptera: Ichneumonidae) from South Korea with descriptions of two unrecorded species

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The subfamily Xoridinae (Hymenoptera: Ichneumonidae) is a small group of parasitoid wasps which are known to parasitize ‘wood-boring’ coleopteran and woodwasps. This subfamily is comprised more than 220 species from worldwide (Yu et al., 2016). Xoridinae can be distinguished by some charaters: usually elongated body, fore wing vein 2*rs-m* very short and 3*rs-m* absent; lacking glymma; ovipositor longer than the metasoma, lower valve of ovipositor with teeth apically. In this study, checklist of the South Korean Xoridinae, redescriptions of two unrecorded species, and photographs are provided.

Key words: Ichneumonids, parasitoids, taxonomy, wasp, wood-boring

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B1

Species diversity of *Culicoides* in southern part of the Republic of Korea

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등에모기속(Genus *Culicoides*)은 1~3mm 크기의 흡혈곤충으로 세계적으로 여러 가지 축산질병을 매개한다. 국내에서는 4종의 Culicoides에 대해 Akabane, Chuzan, Ibaraki 등의 병원체가 검출되었으며 9종은 해외 매개체로써 질병 전파에 주의해야 할 대상이다. 본 연구는 2023년, 2024년 5월부터 10월까지 한국 남부 지방 및 제주도의 15개 축사에서 채집을 진행하여 이들의 발생 분포를 조사하였다. 그 결과 14종 220,757마리의 기록종이 채집되어 채집 지역에 대한 이들 종의 월별 분포 상황과 3종의 우점종(*Culicoides arakawae*, *Culicoides punctatus*, *Culicoides tainanus*)도 확인할 수 있었다. 또한 4종의 미기록종(*Culicoides asiana*, *Culicoides palawanensis*, *Culicoides verbosus*, *Culicoides thurmanae*)을 확인하여 보고하고자 한다. 본 연구 자료는 국내 축산질병 방제를 위한 자료로 유용하게 사용될 수 있을 것으로 기대된다.

검색어: *Culicoides,* Distribution, Unrecorded species, Species diversity

B2

Distribution of bisexual and parthenogenetic populations of *Haemaphysalis longicornis* in the Republic of Korea

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작은소피참진드기는 현재 대한민국에서 우점하는 참진드기 종으로, 법정감염병으로 지정되어 있는 중증열성혈소판감소증후군의 주요 매개체이며, 이배체 양성생식 개체와 삼배체 단위생식 개체로 구성되어 있다. 작은소피참진드기의 단위생식 개체는 양성생식 개체보다 자손을 약 2배 정도 많이 낳으며 분산률 역시 높아 질병 매개에 큰 영향을 미칠 수 있다. 그러나 현재까지 작은소피참진드기의 양성생식과 단위생식에 대한 대한민국의 전국 분포 조사가 자세하게 이루어지지 않고 있는 상황이다. 이에 본 연구에서는 작은소피참진드기의 양성생식 및 단위생식에 대한 전국 분포 현황 조사를 진행하였다. 채집은 18개 지역에서 수행되었으며, 미토콘드리아 12S rDNA 영역을 활용하여 양성 및 단위생식을 구분하였다. 서울과 철원의 경우, 모든 샘플이 단위생식 개체인 반면, 제주 지역의 경우 양성생식 개체가 73.4%의 큰 비율을 차지하였다. 본 연구 결과를 통해 작은소피참진드기 두 생식 개체에 대한 전국 분포 현황을 알아보았으며, 이 분야의 후속 연구를 위한 기초 자료로 활용이 가능할 것으로 기대한다.

검색어: *Haemaphysalis longicornis*, distribution, bisexual population, parthenogenetic population

B3

Mosquito (Diptera: Culicidae) surveillance in southern part of Gyeongsangbuk-do in the Republic of Korea, 2021-2023

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모기(Diptera: Culicidae)는 속마다 다양한 질병을 매개하는데, *Aedes*속이 매개하는 뎅기열, 황열, 지카바이러스감염증, *Anopheles*속이 매개하는 말라리아, *Culex*속이 매개하는 일본뇌염, 웨스트나일열이 있다. 이렇게 인간에게 치명적인 질병을 매개하는 모기의 종별 개체수 및 바이러스 보유 여부를 조사하기 위해 2021년부터 2023년까지 대구의 도심과 철새도래지 2가지 환경을 선정하여 3월부터 11월까지 채집을 실시하였다. 총 5속 10종 20,488마리의 모기가 채집되었으며 2021년에는 7,140마리, 2022년에는 2,481마리, 2023년에는 10,867마리가 채집되었다. 채집된 모기의 개체수는 2021년 대비 2022년에 약 65.3% 감소하였고 2022년 대비 2023년은 약 338% 증가하였다. 도심지역에서는 총 19,654마리의 모기가 채집되었으며, *Culex pipens* complex가 12,810마리(65.18%)로 가장 많이 채집되었다. 철새도래지에서는 총 834마리의 모기가 채집되었으며, *Armigeres subalbatus*가 253마리(30.34%)로 가장 많이 채집되었다. 채집된 모기의 Flavivirus 보유 여부를 확인하기 위하여 *Anopheles* spp.를 제외하고 최대 30마리씩 pooling하여 Real-time PCR을 이용해 조사한 결과 2023년 7월에 채집된 *Aedes vexans* 1개의 pool에서 차오양 바이러스가 검출되었다. 2021년 대비 2022년에 모기 개체수가 감소한 것은 대구를 포함한 한반도 남부지방의 극심한 가뭄 현상과 관련이 있는 것으로 여겨지고, 본 조사 결과는 대구 지역의 질병 매개체 관리를 위한 기초 자료로 활용될 수 있으리라 기대한다.

검색어: *Anopheles*, *Aedes*, *Armigeres*, *Culex*, Flavivirus

B4

The effect of climate change on indicator wetland insects: Predicting the current and future distribution of two giant water bugs (Hemiptera: Belostomatidae) in South Korea

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Giant water bugs (*Appasus japonicus* and *Diplonychus esakii*) are key wetland predators and biological indicators. This study predicts their distribution under three climate change scenarios using MaxEnt modeling with climatic and non-climatic variables. Results indicate that *A. japonicus* will face a northward range contraction, while *D. esakii* will expand northward without range loss, potentially altering aquatic communities. Elevation primarily influences *A. japonicus*, whereas annual mean temperature is crucial for *D. esakii*. These findings highlight their climate sensitivity and provide insights for wetland conservation in South Korea.

Key words: *Appasus japonicus*, aquatic insects, conservation, *Diplonychus esakii*, maximum entropy model, range shift

B5

Ecological characteristics of social wasps in Seoul: Distribution, abundance, and the spread of *Vespa velutina nigrithorax*

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The increasing occurrence of social wasps in urban areas and the rising number of sting incidents have led to heightened public concern. Additionally, the invasion of *V. velutina nigrithorax* has caused significant ecological damage, emphasizing the need for further research. This study aims to investigate the diversity and distribution of social wasps in Seoul, the capital of South Korea, and assess their ecological and urban impact. From 2023 to 2024, traps were set at 36 sites across the city, collected 1,628 individuals from 12 species. The most abundant species were *V. velutina nigrithorax* (34.4%) and *Vespa crabro* (31.4%). Regarding habitat preferences, *V. crabro* abundance was highest in areas with approximately 50% green space, while *V. velutina nigrithorax* was more frequently found in residential areas and along roads than other species. suggesting a strong adaptation to urban environments. These findings provide crucial data for understanding urban wasp distribution and guiding ecological management efforts.

Key words: Seoul, Urban, Social wasps, Green space ratio, Vaspinae, *Vespa velutina nigrithorax,*

B6

Comparison of terrestrial insects in the 3rd and 5th national ecosystem surveys

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본 연구는 전국자연환경조사(육상곤충 분야)에서 도엽 중심으로 수행된 제3차(2006–2012)와 제5차(2019–2023) 조사 결과를 비교·분석하여 곤충 종다양성의 변화를 파악하였다. 3차 조사에서는 총 21목 299과 4,728종이 확인된 반면, 5차 조사에서는 25목 410과 7,634종이 확인되어 종수가 약 61.5% 증가하였다. 두 조사에서 공통으로 확인된 종은 4,134종이었으며, 3차 조사에서만 확인된 종은 594종, 5차 조사에서만 확인된 종은 3,500종이었다. Shannon 다양성 지수(H′) 분석 결과, 3차 조사(2.89)에 비해 5차 조사(4.09)에서 유의미하게 증가하였으며(Wilcoxon rank-sum test, $p < 0.0001$), 이 결과는 5차에서 곤충 군집의 균등도와 종 다양성이 증가한 것으로 판단된다. Simpson 다양성 지수(1–D) 역시 3차 조사(0.91)보다 5차 조사(0.96)에서 증가하여, 특정 종의 우점도가 감소하고 균등하게 분포하고 있음을 의미한다($p < 0.0001$). 5차에서 균등도와 종다양성이 증가한 요인으로 “제5차 전국자연환경조사 지침” 개선으로 트랩조사법 도입과 분류·동정팀 운영 등 조사체계가 변화한 점이 영향을 미친 것으로 판단된다. 향후에는 환경 요인의 변화, 조사 방식의 차이, 분류군별 특성 등을 종합적으로 고려한 분석이 필요하며, 특히 종 증가율이 특정 지역이나 서식지 유형에 따라 차이를 나타내는지에 대한 검토가 필요할 것으로 판단된다.

검색어: 전국자연환경조사, 육상곤충, 종다양성, 균등도

B7

Parasitization rate and host specificity of *Xenos* spp. (Strepsiptera: Xenidae) in South Korea

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In South Korea, two species of the genus *Xenos* Rossi, 1793, *Xenos moutoni* du Buysson, 1903 and *Xenos oxyodontes* Nakase & Kato, 2013, have been reported. *X. oxyodontes* specifically prefers to stylopize *Vespa analis* Fabricius, 1775, whereas *X. moutoni* is known to stylopize other *Vespa* species. This study aims to expand knowledge on the parasitization rate and host preference of *Xenos* spp. in South Korea by examining *Vespa* specimens collected through trapping. As a result of the investigation, a total of 146 out of 21,866 hornets were confirmed to be stylopized by *Xenos.* the proportion of stylopized individuals was confirmed to be 0.46% in *Vespa ducalis* Smith, 1852, 1.41% in *Vespa mandarinia* Smith, 1852, 0.33% in *Vespa crabro* Linnaeus, 1758, and 1.99% in *V. analis*. The two species exhibit significant variation in stylopization rates across microregions, suggesting that *Xenos* spp. may inhabit certain areas densely. Notably, as in previous studies, the two *Xenos* species parasitized only their respective preferred hosts (100%). *X. moutoni* showed a significantly higher number of female individuals compared to males (90.82%), whereas *X. oxyodontes* had a nearly equal number of males and females. Our results show that the distinct ecological traits of *V. analis*, the preferred host of *X. oxyodontes*, or a unique parasitization strategy of *X. oxyodontes* may be contributing factors. Further studies are needed to investigate these aspects.

B8

Stylopization of *Vespula* spp. by *Nipponoxenos* (Strepsiptera: Xenidae) in South Korea: Host range and parasitization rates

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Nipponoxenos Kifune & Maeta, 1975 has been reported as a monotypic genus, with *Nipponoxenos vespularum* Kifune & Maeta as its only species. This species is known to stylopize *Vespula flaviceps* Smith, 1870, and *Vespula shidai* Ishikawa, Yamane & Wagner, 1980 and has been recorded in Japan and Russia. This study aimed to supplement knowledge on the stylopization rate and biological characteristics of *Nipponoxenos* sp., which parasitizes *Vl. flaviceps* and *Vespula koreensis* Radoszkowski, 1887, both of which are major yellowjacket species in South Korea. A total of 7,617 samples of *V. koreensis* and 9,758 individuals of *V. flaviceps* were examined, revealing stylopization rates of 1.27% and 0.31%, respectively. Stylopization was observed only in female hosts, with multiple stylopization found in three workers of *V. koreensis*. Female *Nipponoxenos* sp. were predominantly found on the fourth abdominal segment of the host (99.11%), while males were mainly observed on the fifth segment (92.31%). Since *Nipponoxenos* has not been previously recorded in South Korea, it is considered an unrecorded genus. Additionally, *Vl. koreensis* is an endemic species of Korea and has not been previously reported as a host of Xenidae. Therefore, further studies should consider the possibility of a new species parasitizing *Vl. koreensis*.

B9

Effects of temperature and female age on the hatching success and duration of *Callipogon relictus*

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장수하늘소(*Callipogon relictus*)는 우리나라의 천연기념물이자 멸종위기종으로, 효과적인 증식 및 보전 방안을 마련하기 위해 최적의 사육 환경을 규명하는 것이 중요하다. 본 연구에서는 장수하늘소의 부화 단계에 영향을 미치는 다양한 요인을 평가하여 최적의 사육 환경을 조성하고자 하였다. 실험은 장수하늘소의 서식지 환경을 고려하여 설정한 다양한 온도 조건(20°C, 23°C, 25°C, 27°C, 30°C)에서 수행되었으며, 암컷 성충의 나이에 따른 알의 부화율과 부화 기간을 측정하였다. 연구 결과, 알의 부화율은 암컷 성충의 나이와 밀접한 관련이 있으며, 부화 기간은 온도에 따라 유의한 차이를 보였다. 이러한 결과는 장수하늘소의 인공 대량증식 및 개체군 복원 시 최적의 온도 범위와 산란 시점을 설정하는 데 중요한 자료가 될 것으로 기대된다. 앞으로 성장 속도 및 산란에 미치는 영향 등을 평가하는 추가 연구의 필요성이 제기된다.

검색어: 장수하늘소, 최적 사육 온도, 부화율, 생존율, 보전

B10

MaxEnt를 활용한 시식성 파리, 큰검정파리(*Calliphora lata*)의 잠재 분포와 출현 패턴에 대한 연구

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파리 종은 인간의 시체에 가장 먼저 접근하는 시식성 곤충으로 이들에 대한 정보는 수사나 법의학적 사실규명에 중요하게 활용되고 있으며, 미국, 중국 등 다른나라의 자료에 의존하는 수준에서 최근들어 우리나라의 곤충에 대한 자료를 독자적으로 구축하는 움직임이 활발해지고 있다. 특히 큰검정파리는 시기나 장소에 큰 영향이 없이 유사한 출현 양상을 보이는 다른 검정파리과의 곤충들에 비해 사체에 출현하는 빈도가 높지만 계절적인 출현 시기 편중성향이 강해 기온이 상승하는 여름철에 높은 고도로 이동하는 것으로 알려져 있다. 따라서 본 연구에서는 저지대에서 연구되고 확인된 분포자료를 기반으로 기온과 강수량 등 기상요인에 의한 서식 예상공간을 추정하고, 다양한 요인에 의한 출현 패턴을 제시하고자 한다.

Key words: Calliphoridae, blow flies, GIS, Climate change, forensic science

B11

Population genomics of a spiny crawler mayfly, *Drunella ishiyamana* (Ephemeroptera: Ephemerellidae), in Mongolia

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Mayflies play a crucial role in freshwater ecosystems as bioindicators of water quality and ecosystem health. The spiny crawler mayflies (genus *Drunella*, family Ephemerellidae) are known for their altitudinal distribution and microhabitat specialization. This study examines the population genomics of *Drunella ishiyamana* from eight populations in Mongolia to assess altitudinal population structures and ecological adaptations. Genetic diversity analysis showed moderate variation, with heterozygosity ranging from 0.298 to 0.371 and inbreeding coefficients between -0.097 and 0.055. Pairwise F_{ST} values indicated moderate genetic differentiation, suggesting localized adaptation or restricted gene flow. Using Stacks, 17,592 SNP loci were identified, and STRUCTURE analysis determined K=4 as the optimal number of genetic clusters, indicating structured differentiation likely driven by altitude and local adaptation. This study provides valuable insights into gene flow, population structure, and local adaptation in *D. ishiyamana*, emphasizing its role as a key indicator species in freshwater ecosystems.

Key words: Altitudinal adaptation, freshwater ecosystem, mayfly, Mongolia, population genomics

* This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MIST) (2022R1A2C1009024, RS-2024-00350469).

B12

Population genetic structure and overwintering potential of *Pantala flavescens* in Korea

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Pantala flavescens, commonly known as the wandering glider, exhibits the widest geographic distribution among Odonata. This species migrate for several generations covering distances of over 10,000 km in search of suitable breeding habitats. Although it is known that they are unable to overwinter in temperate regions due to their sensitivity to temperature, it has not been confirmed whether they can overwinter in Korea. In this study, we analyzed mitochondrial *COI* gene sequences of *P. flavescens* collected in Korea to assess genetic diversity, population structure, and the possibility of overwintering in Korea. Understanding the genetic diversity and population structure of *P. flavescens* can provide insights into their migratory routes and emergence patterns, thereby contributing to assessments of global climate change impacts.

Keywords: *COI*, haplotype analysis, population genetics, wandering glider

* 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 (NIBR202505104).

B13

Infection-induced modifications of wing morphology and gut microbiota in *Monochamus saltuarius* by *Bursaphelenchus xylophilus*

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Finding The pine wood nematode *Bursaphelenchus xylophilus*, the causative agent of pine wilt disease, represents a serious ecological threat to pine forests across East Asia. Its primary vector, the pine sawyer beetle (*Monochamus saltuarius*), plays a pivotal role in disease dissemination. This study investigates the effects of *B. xylophilus* infection on the wing morphology and gut microbial community of *M. saltuarius*. A total of 160 beetle specimens were collected and screened for nematode infection. Wing shape variation was quantified using landmark-based geometric morphometrics, while gut microbiota composition was analyzed via 16S rRNA gene sequencing. Canonical variate analysis, along with Mahalanobis and Procrustes distance metrics, revealed significant differences in wing morphology and microbial community structure between infected and uninfected individuals. Notably, female beetles exhibited more pronounced morphological alterations. These infection-associated changes suggest a potential impairment in the dispersal ability of the vector, which may, in turn, influence its efficiency in transmitting the pathogen. The findings highlight the importance of understanding physiological changes induced by parasitic infection and their implications for vector competence. Future research should further explore how these alterations impact beetle behavior and transmission dynamics under varying ecological conditions to inform targeted strategies for managing pine wilt disease.

Key words: gut microbiota, pathogen, wing morphology

B14

Molecular Characterization and Immune-Inducible Expression of Dipterícin Paralogs in the Black Soldier Fly (*Hermetia illucens*)

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The black soldier fly (*Hermetia illucens*) is a promising agent for sustainable biowaste recycling, owing to its high bioconversion efficiency and innate resistance to pathogenic microbes. This study investigates the molecular characteristics and immune-responsive expression of diptericin, a glycine-rich antimicrobial peptide (AMP) primarily active against gram-negative bacteria, in H. illucens larvae (BSFL). We identified seven full-length cDNA sequences encoding diptericin paralogs, which are tandemly clustered on chromosome 2 over a 38.6 kb region, with an average intergenic spacing of 5.5 kb. Sequence analysis revealed that three genes (HipDptA/B/C) are pseudogenized due to premature stop codons, while the remaining four (HiDpt1/2/3/4) encode functional diptericins featuring conserved proline-rich N-terminal (P-domain) and glycine-rich C-terminal domains (G-domain), separated by one or two putative furin cleavage sites (R-X-R/K-R). These cleavage motifs likely generate glycine-rich AMPs and additional peptides of yet unknown function. Upon bacterial challenge, expression of HiDpt1/2/3/4 was markedly induced—by over 1,000-fold in response to gram-negative bacteria and significantly, though to a lesser extent, by gram-positive *Micrococcus luteus*. These results suggest that HiDpt genes encode key effectors in BSFL's innate immunity, functioning as a rapid and broad-spectrum first-line defense against microbial threats. This study provides the first comprehensive molecular insight into BSFL diptericins, highlighting their potential role in enhancing microbial resistance in industrial or ecological applications involving *H. illucens*.

Key words: biowaste recycling, black soldier fly, sustainable

B15

Probabilistic Reinforcement Learning Framework for Predicting River Habitat Degradation and Optimizing Adaptive Management Strategies

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This study proposes a probabilistic reinforcement learning (RL) framework for predicting river habitat degradation and optimizing adaptive ecosystem management strategies. Traditional assessment methods, which rely heavily on physicochemical indicators or static statistical models, often fall short in capturing ecological complexity and adapting to changing environmental conditions. To overcome these limitations, we integrate key water quality variables (dissolved oxygen, temperature, pH, conductivity, and flow velocity) with biological indicators (macroinvertebrate abundance and tolerance ratings) to quantify river degradation levels. We employ a deep ensemble modeling approach using Monte Carlo Dropout to account for predictive uncertainty, with additional performance improvements achieved through log transformation and outlier filtering. On this basis, an RL-based policy optimization framework is developed to dynamically explore and evaluate various river management interventions. Results demonstrate that multi-faceted strategies—particularly those combining biological restoration with pollution control—achieve more significant reductions in degradation than single-action approaches. This work underscores the value of integrating probabilistic modeling with reinforcement learning for data-driven, adaptive river ecosystem management. The proposed framework enables more resilient and flexible decision-making under uncertainty. Future research should focus on refining reward functions, incorporating multi-agent architectures, and validating the model using longitudinal real-world environmental datasets.

Key words: biological indicators, habitat degradation, water quality variables

C1

Revisiting the functional morphology of mandibular tusks in burrowing mayfly larvae (Insecta: Ephemeroptera) using micro-computed tomography and 3D morphometrics

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The superfamily Ephemeroidea is distinguished by mandibular tusks in the larval stage, resembling those of elephants and wild boars. To investigate the functional morphology of tusks across all six tusked families, we applied 3D morphometrics using micro-CT scanning with an artificial landmarking method. Our findings quantitatively support and refine Bae and McCafferty's (1995) hypothesis, revealing how tusk curvature and robustness are functionally linked to adaptation. Evolutionary trends based on the current Ephemeroidea phylogeny suggests that interstitial dwelling may have evolved in basal lineages of Potamanthidae and Euthyplociidae, while burrowing dwellers and substrate dwellers (e.g., *Povilla*) evolved in parallel, enhancing burrowing efficiency. These findings provide a more comprehensive insgiht into the functional and ecological adaptations of these unique structures among aquatic insects.

Key words: aquatic insects, artificial landmarks, Ephemeroidea, micro-CT, point cloud registration

D1

RNAi-mediated knockdown of *TmIAP1* in *Tenebrio molitor* induces apoptosis and external morphological defects

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Apoptosis is a tightly regulated process essential for maintaining viability of organism. Inhibitor of apoptosis proteins (IAPs) play a crucial role in preventing excessive cell death by regulating caspase activity. In this study, RNA interference (RNAi)-mediated knockdown of *TmIAP1* in *Tenebrio molitor* induced apoptosis and resulted in severe morphological defects. Notably, larvae exhibited prolapse at the terminal end and ceased movement from 6 day post-injection. Since *TmIAP1* is known to inhibit DRONC (Caspase-9), its suppression likely triggered caspase activation, leading to extensive cell death. These findings suggest that *TmIAP1* is essential for maintaining tissue integrity and survival in *T. molitor.*

Key words: *Tenebrio molitor,* Apoptosis, *TmIAP1,* RNA interference

D2

Investigation of *TmTab2* in immune defense and AMPs regulation in *Tenebrio molitor*

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The immune deficiency (Imd) pathway, a highly conserved immune signaling pathway in invertebrates, plays a crucial role in regulating the production of antimicrobial peptides (AMPs). One of its key components is TAK1-associated binding protein 2 (TAB2), an intracellular signaling molecule essential for Imd pathway regulation. To investigate the role of *TmTab2* in *T. molitor*, we performed RNA interference (RNAi)-mediated knockdown of *TmTab2*, followed by infection with *E. coli*, *S. aureus*, *C. albicans*, and *L. monocytogenes*. Survivability was monitored for 10 days post-infection, revealing a significant reduction in survival rates, particularly in response to *C. albicans* infection. Additionally, the expression levels of 15 different AMPs were assessed following *TmTab2* knockdown and pathogen injection, providing insights into the regulatory role of *TmTab2* in AMP expression.

Key words: *Tenebrio molitor*, *TmTab2*, Antimicrobial peptiedes

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D3

The immune role of *TmDorX1* in the regulation of antimicrobial peptides in *Tenebrio molitor*

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Antimicrobial peptides (AMPs) are key components of innate immunity, playing a crucial role in the immediate immune response against bacterial, fungal, and viral infections. *Tenebrio molitor* dorsal 1 (*TmDorX1*) is an NF-κB transcription factor involved in the Toll signaling pathway and regulates AMP gene expression. In this study, we investigated the immune function of *TmDorX1* using RNA interference (RNAi). Systemic infections were induced in *T. molitor* larvae with *E. coli*, *S. aureus*, *L. monocytogenes*, and *C. albicans* following *TmDorX1* knockdown, and AMP gene expression patterns were analyzed. Among the 14 AMP genes examined, the expression levels of *TmTenecin-1*, *-2*, *-4*, *TmColeoptericin-A*, *-B*, *-C*, *TmAttacin1b*, and *TmAttacin2* were significantly downregulated upon *TmDorX1* suppression. These findings suggest that *TmDorX1* acts as a key regulator of Toll pathway-mediated innate immunity in T. molitor and is essential for the expression of multiple AMP genes.

Key words: Toll pathway, DorX1, *Tenebrio molitor*, RNAi, Antimicrobial peptides

D4

Characterization and functional analysis of caspase-9 (*TmDRONC*) in *Tenebrio molitor*

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Apoptosis plays a crucial role in embryonic cell formation and organ differentiation through caspases. DRONC is an initiator caspase with a caspase recruitment domain (CARD) and undergoes auto-cleavage to activate DrICE, triggering apoptosis. qPCR analysis of *TmDRONC* gene expression in different developmental stages and tissues of *Tenebrio molitor* revealed a significant increase in expression during the larval, early pupal, and late pupal stages. High expression of *TmDRONC* was observed in the gut of larvae and the ovary of female adults. Following microbial challenge with *S. aureus*, *TmDRONC* expression was significantly higher in the gut, compared to other tissues. During *C. albicans* infection, *TmDRONC* expression was initially high in the integuments and Malpighian tubules. These findings suggest that *TmDRONC* plays a key role in development and immune responses.

Key words: Apoptosis, DRONC, *Tenebrio molitor*

D5

The role of caspase-1 in apoptosis of *Tenebrio molitor*

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Caspase-1 is a well-known mediator of inflammatory cell death in mammals, but its role in insect apoptosis remains unclear. This study aims to investigate whether Caspase-1 is involved in apoptosis in *Tenebrio molitor.* The *TmCaspase-1* gene was cloned and its characteristics were analyzed. Gene expression patterns were examined using qPCR, revealing that *TmCaspase-1* expression increased during the larval and adult stages of development. At the tissue level, its expression was notably elevated in the gut. Furthermore, when *E. coli, S. aureus, C. albicans and L.monocytogenes* were injected into larvae, significant results were observed in each tissues, particularly upon injection of *E. coli, C. albicans*.

Key words: *Tenebrio molitor,* caspase-1, Apoptosis, microbial injection

D6

Population genetic analysis of South Korean *Anopheles sinensis* based on ITS2 sequencing

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Anopheles sinensis is a key malaria vector in East Asia, yet its population structure and genetic diversity in South Korea remain underexplored. This study utilizes the Internal Transcribed Spacer 2 (ITS2) region to investigate genetic variation among *A. sinensis* populations across 5 different locations in the country. DNA was extracted from field-collected specimens, and ITS2 sequences were analyzed to assess polymorphisms, haplotype diversity, and phylogenetic relationships. Preliminary findings suggest genetic differentiation among populations, which may be influenced by environmental and geographic factors. Ongoing analyses aim to clarify gene flow patterns and potential lineage divergence. These findings could contribute to a better understanding of *A. sinensis* population dynamics and provide a molecular bases for improved vector surveillance and malaria control strategies in South Korea.

Key words: *Anopheles sinensis*, ITS2, population genetics, gene flow, phylogenetics, malaria vector, South Korea

* This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (RS-2024-00461502).

D7

Inflammatory induction of *TmEgr*, *Tmpvf-1*, and *Tmpvf-3* in *Tenebrio molitor*

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The cytokines are generated in response to an immune stimulus and play a crucial role in regulating the immune response. In this study, we identified the ORF sequences of potential cytokines such as Eiger, pvf-1, and –3 from *Tenebrio molitor* (*Tm*Egr, *Tm*pvf-1, and –3). The temporal expression patterns of the these genes were investigated, resulting that *TmEgr* was highly induced at 12 h after *E. coli* injection in gut. The highest expression of *Tmpvf-1* was detected at 3 h after *E. coli* injection in whole body. While *Tmpvf-3* was highly expressed at 9 h after *E. coli* injection in hemocytes. We will investigate the effects of these genes on hemocytes differentiation and apoptosis. This study will provide information to understand inflammation in *T. molitor*.

D8

Identification and expression analyses of iNOS in *Tenebrio molitor*

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Nitric oxide synthase (NOS) plays an important role in immune responses through production of nitric oxide (NO). It is well known that the inducible NOS (iNOS) is specifically induced during inflammatory responses. In this study, we identified and investigated the developmental and tissue specific expression patterns of *iNOS* in *T. molitor* using qRT-PCR. Additionally, *TmiNOS* expression patterns were analyzed following pathogenic infection. Our results may help to understand the immunological function of *Tm*iNOS.

Key words: *Tenebrio molitor*, iNOS, inflammation, pathogenic infection

D9

Predicting protein-protein interactions between *H. longicornis* salivary proteins and SFTS virus using AlphaFold3

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The Asian longhorned tick, *Haemaphysalis longicornis*, can serve as a vector for pathogens such as the Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV). To identify key molecules involved in SFTSV transmission, differentially expressed proteins in the salivary glands of *H. longicornis* across blood-feeding stages were analyzed. The potential interactions between these salivary proteins and SFTSV surface glycoprotein were screened using an *in silico* approach based on AlphaFold3. Complex structures were modeled using AlphaFold3 for 41 *H. longicornis* salivary proteins and SFTSV glycoprotein. Residues involved in potential interactions such as hydrogen bonds and salt bridges at the protein-protein interface were identified. In addition to interaction residues, confidence scores of structural predictions and interface area measurements were evaluated to rank the interaction potential of these proteins. Limitations of *in silico* predictions were discussed, and the methodological efficiency and applicability of AlphaFold3, which has demonstrated significant advancements in accuracy and speed for complex structure prediction, were highlighted.

Key words: *Haemaphysalis longicornis,* Severe Fever with Thrombocytopenia Syndrome Virus, AlphaFold3, protein-protein interaction

E1

Molecular reclassification of Tenebrionidae and novel evidence from mitochondrial genome diversity

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Taxonomic discrepancy in the family Tenebrionidae, based on molecular and morphological characteristics remains unsolved. Mitochondrial genome is well-documented as a genetic marker that provides improved phylogenetic resolution and evolutionary plasticity in previous studies. This study characterizes the complete mitochondrial genome of *Pedinus strigosus*, and performs a comparative analysis including 48 tenebrionid species, focusing on gene order, codon usage, and intergenic composition. As a result, rearrangements in two cassettes of 2 to 3 tRNA genes and inversions within eight tRNA genes and control region were observed in several species. The usage frequency of amino acids reveals distinct biases in three tRNAs. A conserved intergenic region of 16-17 bp in length is identified between *trnS2* and *ND1* across all species in this study. This study highlights potential applicability of gene order and amino acid frequencies as apomorphy within the family as well as sequence-based phylogenetic resolution in mitochondrial genome.

Key words: Tenebrionidae, *Pedinus strigosus*, mitochondrial genome, gene order, intergenic region

E2

Taxonomic history and evolutionary phylogenomics of gall mites (Acari: Prostigmata: Eriophyoidea)

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Eriophyoidea, a superfamily within the order Trombidiformes, comprises three families and over 4000 species. These mites, approximately 200 μm in size, possess a vermiform body, 4 legs, stylet-like chelicerae, and radiated claws. They are phytophagous, highly host-specific, and often induce gall formation in plant tissues. The taxonomic and phylogenetic study of this group spans nearly 300 years, from morphological characteristics in the 18th century to molecular phylogenomics in the present. However, their classification and phylogenetic placement remain unresolved. In this study, we reconstruct the maximum likelihood (ML) phylogeny of Eriophyoidea using *18S rRNA*, *28S rRNA*, *COI*, and concatenated sequences of mitochondrial 13 protein coding genes (PCG), respectively. Our analysis clarifies the phylogenetic relationships among subgroups within the superfamily.

Key words: Eriophyoidea, maximum likelihood (ML), nuclear and mitochondrial gene, PCG, molecular phylogeny

E3

Comparative mitogenomic analysis of Korean and Chinese *Onthophagus fodiens* (Coleoptera: Scarabaeidae: Scarabaeinae: Onthophagini)

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The dung beetle *Onthophagus fodiens* (Coleoptera: Scarabaeidae) is a coprophagous species. In this study, we first characterized the mitochondrial genome (mitogenome) of Korean *O. fodiens* and compared it with that of Chinese *O. fodiens*. The nearly complete mitogenome of Korean *O. fodiens* is 14,315 bp in length, excluding the control region and three tRNA genes (*trnI*, *trnQ*, and *trnM*), which were not recovered in this study. It contains 13 protein-coding genes (PCGs), 19 tRNA genes, and two rRNA genes, with the same gene order those of Chinese *O. fodiens*. Furthermore, we perform phylogentic analysis based on 13 mitochondrial PCGs and examined tRNA secondary structure and codon usage pattern. Phylogenetic analysis supports the polyphyly of the genus *Onthophagus,* consistent with previous stuides. This study suggests necessity of re-examination of the genus *Onthophagus* with integrated approaches including morphological and molecular characteristics.

Key words: *Onthophagus fodiens*, dung beetle, Scarabaeinae, mitochondrial genome, phylogeny

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E4

Inferring for the inanimate pathway of Lumpy Skin Disease (LSD) vector, *Stomoxys calcitrans* (Diptera, Muscidae) in South Korea

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Stomoxys flies (Muscidae) are hematophagous ectoparasites of medical and veterinary importance. In this study, *Stomoxys calcitrans,* were collected 464 individuals from 38 sites in South Korea for a genetic diversity study based on the cytochrome *c* oxidase subunit I (COI). As a result of the Pairwise comparison of the COI gene base sequence, it was largely divided into two groups, showing a sequence difference of 1.4% to 3.3%. A total of 53 haplotypes were identified, of which H1 (34 indiv.) and H2 (309 indiv.) were found to dominate. In the median-joining network analysis, a network was largely formed around the two major Haplotypes (H1, H2), and the mutation point between these two haplotypes was found to be at least 11 times. Genetic diversity in the COI gene were found to be large, so it is inferred that there may have been an influx of individuals from abroad.

Key words: Lumpy Skin Disease (LSD), *Stomoxys calcitrans*, Genetic diversity, COI, inanimate pathway

E5

The first mitochondrial genome for Sterictiphorinae (Hymenoptera: Argidae) and insights into argid phylogeny

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The mitochondrial genome (mitogenome) of *Sterictiphora koreana*, a Korean endemic species of Sterictiphorinae, has been fully sequenced and analyzed for the first time. The nucleotide base composition reveals a relatively high AT bias, with *S. koreana* exhibiting slightly lower AT content than Arginae species. The gene order is largely conserved among Argidae, but *S. koreana* exhibits rearrangements in the *trnK*-*trnD* and *trnI*-*trnM* gene clusters. Ka/Ks ratios of all PCGs are less than 1, meaning there is little change in the amino acid. Phylogenetic based on nucleotide and amino acid sequences of the 13 PCGs strongly support the monophyly of Argidae with a well-defined subfamily structure and its close relationship with Pergidae. Divergence time estimation suggests that Argidae originated around 153.47 Ma in the Late Jurassic, with subsequent diversification occurring from the Early Eocene to the Late Oligocene. These findings not only illuminate mitogenome evolution within Argidae but also provide a foundation for broader investigations into symphytan phylogenetics and taxonomy.

Key words: AT content, divergence time, phylogeny, Symphyta, Tenthredinoidea

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F1

Investigation of the infection patterns of *Orientia tsutsugamushi* in Chigger mites (Acari: Trombiculidae) parasitizing wild rodents in Asan, Chungcheongnam-do

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쯔쯔가무시증은 *Orientia tsutsugamushi* 감염에 의한 급성 발열성 질환으로, 털진드기 유충이 주요 매개체인 것으로 알려져있다. 충청남도는 전국적으로 쯔쯔가무시증 발생률이 높은 지역 중 하나이며, 특히 아산시는 인구 10만 명당 발생률이 충남 및 전국 평균을 상회하는 것으로 보고되어, 지속적인 매개체 및 병원체 관련 연구가 필요하다. 이번 연구는 충남 아산시 소재의 순천향대학교 캠퍼스 내 서식하는 설치류와 털진드기의 현황을 조사하고, 털진드기의 *O. tsutsugamushi* 감염 실태를 조사하여 지역 내 쯔쯔가무시증 유행 가능성을 확인하고, 효과적인 예방 및 관리 대책 수립의 기초 자료를 제공하고자 수행되었다.

연구 대상 지역인 순천향대학교 캠퍼스는 주거 지역 및 경작지와 인접하고, 교내에 넓은 야산과 산책로가 조성되어 있어 설치류 및 털진드기 서식에 적합한 환경을 갖추고 있다. 조사 수행 지역의 환경적 특성을 고려하여 채집 수행 장소를 세 구역 (학성산 인근, 학교 인근, 교내) 으로 구분하였으며, 2024년 5월부터 10월까지 월 1회 Sherman live trap을 20개씩(총 60개) 약 5m 간격으로 설치하여 설치류 채집을 진행하였다. 채집된 설치류에서 털진드기를 분리하였으며, 분리된 털진드기를 대상으로 Nested PCR를 수행하여 *O. tsutsugamushi* 감염 여부를 확인하였다.

조사 결과 총 14마리의 설치류와 288마리의 털진드기가 채집되었으며, 교내에서 채집된 생쥐(*Mus musculus*)에서 분리된 털진드기에서 *O. tsutsugamushi* 양성이 검출되어 혈청형을 분석한 결과, 해당 균주는 Boryong 혈청형으로 확인되었다.

이번 연구를 통해 순천향대학교 내 서식하는 털진드기의 *O. tsutsugamushi* (Boryong type) 감염을 확인하였으며, 이는 캠퍼스 내 쯔쯔가무시증 발생 가능성을 시사한다. 이러한 연구 결과는 향후 순천향대학교 인근의 쯔쯔가무시증 예방 및 관리를 위한 기초자료로 사용될 수 있으며, 관련하여 지속적인 역학 조사와 방역 대책 마련이 필요한 것으로 사료된다.

검색어: 쯔쯔가무시증, *Orientia tsutsugamushi*, 털진드기, Boryong 혈청형, 설치류, 아산시

G1

Complete mitochondrial genomes of two types of the Japanese encephalitis virus vector *Culex tritaeniorhynchus*

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*Culex tritaeniorhynchus*는 일본뇌염 (Japanese encephalitis)의 주요 매개체이며, 전 세계적으로 매년 약 2만여 명이 일본뇌염으로 인해 사망하는 것으로 알려져 있다. 최근 대한민국, 일본, 중국에서 수행된 연구 결과에 따르면 mtDNA인 cytochrome oxidase subunit 1 (*COI*) 영역에 기반해 *Culex tritaeniorhynchus*에는 2개의 타입 (Continental type: Ct-C, Japaneses type: Ct-J)이 존재하고 있는 것이 밝혀졌다. 그러나 현재까지 *COI* 영역 외에 추가적인 유전적 차이에 대해서는 알려진 바 없다. 이에 본 연구에서는 2개의 타입에 대한 mtDNA 전체 서열을 확보하여, 이를 토대로 *Culex* 속 모기류 내 이들의 계통학적 위치를 추론하였다. 분석 결과 Ct-C와 Ct-J 개체들은 기존의 *COI* 영역뿐만 아니라 mtDNA 전 영역에서 두 타입 간 변이가 존재함을 추가로 확인하여 유전적으로 명확히 구분되는 분류군임을 알 수 있었다. 본 연구 결과는 이들의 진화적 관계를 파악하기 위한 기초 자료로 유용하게 활용될 수 있을 것이다.

검색어: Japanese encephalitis, *Culex tritaeniorhynchus*, Mitochondrial genome, Vector mosquito

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G2

Surveillance of chigger mites as a scrub typhus vector during the epidemic season in Honam region, 2024

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A surveillance of chigger mites was conducted to monitor for occurrence to scrub typhus vectors from each four environmental collection points in three locations (Sunchang and Goheung) in the Honam region of Korea from August to December 2024. During the surveillance period, 1,957 chigger mites were collected and the predominant species were *Leptotrombidium scutellare* (84.4%). The number of patients had the peaked at 44 week (10.24~10.30), while the density of chigger mites peaked at 48 week (11.21~11.28) respectively. This result suggests that higher temperature (2.7℃) and precipitation (149.6mm) was limited scrub typhus vectors activity in Autumn than the average year. However, long-term periodic surveillance is needed to investigate the relationship between chigger mites density and the number of patients with tsutsugamushi disease.

Key words: scrub typhus, chigger mites, *Leptotrombidium scutellare*, vectors activity

G3

Application of photo-catalyzed TiO_2 for inactivation of inhalant allergens

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Capturing and eliminating allergens in the air could be an effective strategy against respiratory allergic diseases. In this study, we tested the capability of TiO_2 to degrade allergens upon activation by a photocatalyst. House dust mite (HDM), cat, and oak pollen extracts were incubated with TiO_2 powder for 24 h in either dark or light exposure. Regarding protein concentrations, 69.9% of HDM, 27.1% of cat, and 21.5% of oak pollen were degraded by TiO_2 compared to the extracts incubated in the dark without TiO_2. More specifically, 96.6% of Der f 1 and 81.2% of Fel d 1 were degraded by investigatory rutile TiO_2. However, no significant degradation of Que ac 1 was observed. Immunoblot analyses using monoclonal antibodies and IgE antibodies from patients' sera showed diminished allergen bands. In the inhibition ELISA of HDM extract, 87.1% and 96.5% of IgE reactivity was reduced by TiO_2, whereas 47.0% of self-degradation was observed. In conclusion, TiO_2 eliminated each allergen at a different degradation rate. TiO_2 may be useful in reducing indoor allergenic molecules. However, more detailed studies are needed to optimize its efficacy.

Key words: allergen, cat, house dust mite, oak, TiO_2, photocatalyst

G4

Myiasis by *Musca domestica* in a patient with sinonasal carcinoma: A case report (Diptera: Muscidae)

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An 83-year-old woman with sinonasal carcinoma was found dead in her residence and was reported to the police by her family on June 11, 2024. According to the family's statement, her death was first noticed on June 10, one day prior to the report. During the postmortem examination, empty puparia, pupae, and larvae of flies were discovered, raising suspicion of myiasis, a condition in which fly larvae invade living tissues. Morphological observations and DNA barcoding confirmed that all collected specimens belonged to *Musca domestica* (housefly). This finding indicated that at least one life cycle of the housefly had passed since the initial infestation. Since the ambient temperature at the scene was not recorded, the most conservative estimate of the oviposition (egg-laying) time was determined to be June 5, 2024, at 00:24 or earlier. This estimation suggests that the infestation occurred at least five days before the death was noticed on June 10. Identifying myiasis is crucial in forensic investigations, particularly in cases involving potential neglect or abuse. While myiasis can be caused by various fly species, this report appears to be the first documented case of housefly-induced myiasis in South Korea.

Key words: house fly, forensic entomology, myiasis

G5

Simultaneous detection of *Bandavirus dabieense* and multiple tick-borne pathogens in *Haemaphysalis longicornis* ticks using droplet digital PCR

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Haemaphysalis longicornis, a tick species prevalent in South Korea, is a major vector of *Bandavirus dabieense*, which causes Severe Fever with Thrombocytopenia Syndrome (SFTS). However, these ticks may also harbor other tick-borne bacteria and protozoa, which suggests frequent co-infection in wild populations. Identifying this co-infection is crucial for understanding the prevalence and co-transmission potential of multiple pathogens.

Here, we aimed to confirm *B. dabieense* infection and co-infection with other pathogens in field-collected *H. longicornis* ticks using droplet digital PCR (ddPCR). We detected *B. dabieense* in nucleic acids extracted from *H. longicornis* ticks. We then screened for co-infection with other tick-borne pathogens commonly found in South Korea, including *Orientia tsutsugamushi*, *Anaplasma phagocytophilum*, *Coxiella burnetii*, *Borrelia* spp. and *Babesia* spp. After confirming co-infection by ddPCR, we analyzed gene expression patterns related to immune response and pathogen transmission in *B. dabieense*-only ticks and co-infected ticks to assess biological impacts.

We accurately identified *H. longicornis* ticks co-infected with *B. dabieense* and other pathogens using ddPCR-based molecular diagnostics. These findings show the precision of ddPCR in detecting multiple pathogens and suggest a potential for simultaneous pathogen transmission to humans. In addition, gene expression analysis of co-infected *H. longicornis* ticks can improve our understanding of tick physiology and *B. dabieense* transmission, which possibly reduces the risk of co-transmission to humans.

Key words: SFTSV, Tick-borne pathogen, Co-infection, *Haemaphysalis longicornis*, Droplet digital PCR

H1

Digitization and utilization of biological collections at Nakdonggang National Institute of Biological Resources

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The Nakdonggang National Institute of Biological Resources (NNIBR), a freshwater biological research institution, manages seven biological specimen repositories with approximately 550,000 specimens. Since 2021, NNIBR has established a photography studio to support comprehensive specimen digitization. Using specialized equipment, including microscopes, DSLR cameras, and X-ray microscopy, NNIBR has successfully produced and archived high-resolution multifocal 2D images as well as detailed 3D rendered images of biological specimens. To date, over 1,300 species of freshwater organisms have been successfully digitized. Digital images are made publicly available via the institute's official website. Furthermore, NNIBR has utilized these images to create diverse digital content supporting researches, exhibitions, and educational programs. Ultimately, these digitization initiatives play a crucial role in biodiversity conservation efforts by raising awareness and ensuring sustainable utilization and long-term preservation of biological resources.

Key words: digital imaging technology, X-ray microscopy, 2D image, 3D video

H2

Alien hitchhiker insect detected on empty containers entering South Korea in 2024

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The increasing globalization of trade and transportation has intensified the risk of unintentional introductions of non-native organisms. Among them, hitchhiker insects pose significant ecological risks. This study investigates the presence of alien hitchhiker insect species detected in international empty containers entering South Korea in 2024. Total 12 species were found, among them six species are not distributed in South Korea. Among them, *E. fullo* and *T. desjardinsi* were identified as stored-product pests, if established in Korea, they could lead to both agricultural and ecological disruptions, emphasizing the importance of rigorous inspections. These findings emphasize the necessity of rigorous inspections and continuous monitoring of various entry pathways to mitigate the risks associated with hitchhiker insects.

H3

Seasonal and regional variations in blowfly (Diptera: Calliphoridae) assemblages in urban and forest habitats of Jeollanam-do, South Korea

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Understanding the biodiversity and distribution of blowflies (Diptera: Calliphoridae) is crucial for improving the accuracy of Post-Mortem Interval (PMI) estimation in forensic entomology. This study aims to investigate the seasonal and regional variation of blowfly assemblages across five sites in Jeollanam-do, South Korea, focusing on differences between urban and forest habitats. Rat-baited fly traps were deployed bi-monthly for 48 hours from January to December 2023. A total of 9,276 adult flies, representing 13 species from 5 genera, were collected. The overall dominant species were *Chrysomya megacephala* (27.88%) and *Chrysomya pinguis* (27.59%), which were rarely observed in spring and autumn, regardless of habitat type. However, species dominance varied by habitat type: while *Chrysomya megacephala* was the most frequently collected species overall, *Lucilia sericata* was the most dominant species in urban habitats, whereas *Chrysomya pinguis* was the most dominant species in forest habitats. These findings underscore the importance of understanding the ecological and seasonal dynamics of Calliphoridae assemblages to improve the accuracy of PMI estimation in forensic investigations. The observed regional variations suggest that habitat and climate factors should be incorporated into forensic entomological models. Future studies should involve long-term monitoring across diverse environmental settings to establish more comprehensive forensic entomological baselines and improve species-level resolution through molecular analysis.

Key words: Calliphoridae, Season, Habitat, Fly Trap, Legal Investigation

H4

Influence of concealment on decomposition and insect succession patterns in pig carcasses: Implications for PMI-min estimation

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Estimating the minimum post-mortem interval (PMI-min) using insect succession patterns has shown increasing potential in forensic investigations. However, body concealment can delay insect colonization and alter the rate of decomposition, complicating PMI-min estimation. This study investigated the effects of concealment on decomposition and insect succession using pig carcasses as human analogs in forested areas of Uiseong and Iksan, South Korea. One pig carcass at each site was concealed in a suitcase, while the other was fully exposed as a control. Insect colonization occurred earlier in exposed carcasses, beginning during the fresh stage, whereas colonization in concealed carcasses was delayed until the bloated stage. *Lucilia caesar* (Linnaeus, 1758) and *Chrysomya pinguis* (Walker, 1858) were observed on the first day in exposed carcasses, with oviposition occurring on the second day. In contrast, these species were first detected on the second day in Uiseong and the fourth day in Iksan in concealed carcasses, with oviposition occurring the following day. Exposed carcasses reached the dry stage at approximately 160 accumulated degree days (ADD), whereas concealed carcasses entered the decay stage at around 160 ADD and remained in that stage until approximately 500 ADD. These findings enhance the understanding of decomposition dynamics and insect succession patterns in concealed environments, contributing to more accurate PMI-min estimation in forensic cases involving concealed bodies.

Key words: Medico-legal entomology, Insect succession, Concealed carcass, suitcase, Decomposition

H5

Using micro-computed tomography to reveal the morphological structure of *Scambocarabus kruberi hallasanensis* (Carabidae, Carabinae)

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Scambocarabus kruberi hallasanensis (Carabidae, Carabinae), living only in Hallasan mountain, Jeju island. This subspecies has been known to entomologist for 30 years. However, details of its morphology and anatomy remain poorly understood. A relatively recent technique, known as micro-computed tomography (micro-CT), which is based on X-ray, allows visualization of the internal structure without the need to dissect the insect. Therefore, we tried to identify morphological structures using the dried specimen of *S. kruberi hallasanensis* (male, NNIBRIN213223), in order to describe the internal and external structure of *S. kruberi hallasanensis* with use of micro-CT. This technique enables us to perform a detailed morpological study, without damaging specimens.

Key words: Hallasan mountain, micro-CT, Nakdonggang National Institute of Biological Resources (NNIBR), specimen

H6

Microbiome composition of *Haemaphysalis flava* in Korea and diversity analysis based on region, developmental stage, and sex

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Ticks are well-known vectors of various diseases and are widely distributed globally. In this study, we investigated the microbial community of *Haemaphysalis flava*, a common tick species in Korea, using 16S rRNA gene analysis. Alpha diversity analysis revealed that adult ticks had higher microbial richness and complexity than nymphs, and the highest diversity was observed in adult females. Significant regional differences were also found, with samples from Jinju and Boseong showing higher richness and samples from Jeju showing lower richness. Beta diversity analysis showed that microbial communities were clustered according to region and developmental stage, with unique clusters observed in Samcheok and Gokseong, which may be due to regional environmental factors. Proteobacteria dominated the microbial community in most samples, followed by Actinobacteriota and Firmicutes. At the genus level, *Coxiella* and *Pseudomonas* were dominant, and *Coxiella* may be associated with pathogen transmission. The abundance of other genera varied by region and developmental stage, reflecting complex host-microbe interactions. These findings highlight the influence of environmental, developmental, and biological factors on the *H. flava* microbiota, emphasizing the need for further research to understand the ecological role of the microbiota in pathogen transmission and to develop effective strategies for preventing tick-borne diseases.

H7

Mitochondrial genome assembly and annotation of *Laccotrephes japonensis*

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장구애비(*Laccotrephes japonensis*)는 Hemiptera 목 Nepidae 과에 속하며, 한반도 전역에 분포하는 종으로 알려져 있다. 이 종은 물속에서 서식하며 물고기, 올챙이, 모기 유충 등의 체액을 섭취하는 포식자로, 해충 방제 및 생태계 유지에 중요한 역할을 수행한다고 알려져 있다. 그러나 현재까지 *L. japonensis*의 유전체 정보는 NCBI에 등록된 Nucleotide 30건, Protein 10건, SRA 1건에 불과할 정도로 부족한 실정이다. 나고야 의정서(ABS, Access and Benefit-Sharing) 체결 이후, 각국은 자국의 생물 유전자원을 체계적으로 연구하고 관리하는 방향으로 나아가고 있으며, 한국 또한 국내 생물자원의 확보와 연구 활성화를 중요한 과제로 삼고 있다. 이에 따라 본 연구에서는 *L. japonensis*의 미토콘드리아 유전체를 분석하여 국내 생물 유전자원의 확보 및 보존을 위한 기초 데이터를 제공하는 것을 목표로 하였다. 단일 개체에서 Whole Genomic DNA를 추출한 후, Illumina HiSeq 2500 플랫폼을 이용하여 raw data를 확보하였다. 이후 MitoZ 파이프라인을 활용하여 assembly 및 annotation을 진행하였으며, 미토콘드리아 유전체 내 tRNA 유전자의 위치와 구조를 분석하기 위해 tRNAscan-SE v.2.0을 사용하였다. 분석 결과, *L. japonensis*의 미토콘드리아 유전체 길이는 15,591 bp로 확인되었으며, 13개의 단백질 코딩 유전자, 22개의 tRNA 유전자, 그리고 12S 및 16S rRNA 유전자를 포함하는 것으로 확인되었다. 또한, tRNAscan-SE v.2.0 분석을 통해 총 16개의 tRNA 유전자가 예측되었다. 본 연구를 통해 *L. japonensis*의 미토콘드리아 유전체 구조 및 유전자 구성을 확인하였으며, 이는 향후 분자계통학 및 생물다양성 연구에 활용될 수 있을 것으로 사료된다. 또한, 나고야 의정서의 취지에 따라 국내 생물 유전자원의 확보를 위한 기초 데이터를 제공하며, 확보된 유전체 정보는 생태계 보존 연구에 기초 자료 활용될 수 있을 것으로 사료된다.

검색어: Mitochondrial Genome, *Laccotrephes japonensis*

H8

Transcriptome sequencing analysis and SSR markers of the critically endangered *Cicindela* (*Abroscelis*) *anchoralis* (Athropoda: Carabidae)

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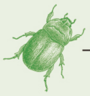
Carabidae과에 속하는 *Cicindela* (*Abroscelis*) *anchoralis*는 한국 고유종으로 충남 태안과 전남 신안에 분포하는 것으로 알려져 있으며, 주요 서식 환경인 해안사구의 훼손 및 지속적인 개체수 감소로 인해 2006년 멸종위기 야생생물 II급으로 지정되었다. 종 보존과 관련된 지속적인 노력인 필요함에도 확보된 *Cicindela* (*Abroscelis*) *anchoralis*의 유전정보는 Nucleotide 29건, Protein 43건, SRA Experiments 1건으로 확인되어, 적극적인 기초자료 확보가 필요할 것으로 사료된다.

이번 연구에서는 *Cicindela* (*Abroscelis*) *anchoralis* 1개체를 사용하여 Illumina HiSeq 4000으로 시퀀싱을 진행하였다. 그 결과 7,615,641,533개의 raw data를 확보하였으며, Trinity program을 이용하여 *de novo* assembly를 수행한 결과, 평균 길이 2,352bp인 24,048개의 unigene을 확보하였다. KOG, GO, KEGG 및 InterProScan 데이터베이스를 활용하여 분석을 진행한 결과, 각각의 데이터베이스에 annotation된 20,265개, 14,308개, 423개 및 25,526개의 unigene을 확인하였다. 그 결과 Collagen alpha-1(I) chain, Solute carrier family 및 Adenylate cyclase와 같은 적응에 관여하는 유전자들이 확인되었다. 또한 3,983개 dinucleotide repeats (AT/AT 및 AC/GT)로부터 3,388개의 SSR marker를 확인하였다. 이러한 연구 결과들은 멸종 위기종의 환경 적응과 관련된 생리 기작을 파악하기 위한 기초 자료로서 활용될 수 있으며, 나아가 유전정보를 기반으로 한 멸종위기종의 계통 유연관계 분석 및 집단유전학 등의 연구 수행에 활용될 수 있을 것으로 기대된다.

검색어: Transcriptome, *Cicindela* (*Abroscelis*) *anchoralis*, Endangered species, Adaptation genes, SSR markers

Poster Presentation



Competition

P1

Comparative study of semi-synthetic artificial diets on *Spodoptera frugiperda* larvae for mass rearing

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열대거세미나방(*Spodoptera frudiperda*)은 나비목 밤나방과의 해충으로 연구목적의 대량사육을 위해 미국산 인공사료를 사용하였다. 본 연구에서는 국산 인공사료를 대체하기 위해 국내에서 사용중인 나비목 곤충의 인공사료를 일부 개량한 인공사료(IPTL-J1과 IPTL-J2)를 만들어 사육 적합도를 조사하였다. 본 연구에서 사육 적합도 실험은 열대거세미나방 1세대를 기준으로 유충에게 인공사료를 제공한 후 용화율, 우화율, 산란율을 대상으로 비교하였다. 그 결과, 용화률은 미국산 인공사료보다 IPTL-J1에서 80%, 우화률은 미국산 인공사료에서 90.5%로 가장 높았다. 산란율은 30개 이상으로 산란한 난괴를 대상으로 측정하였으며, 미국산 인공사료와 IPTL-J2에서 가장 높았다. 우화 후 산란까지의 기간은 IPTL-J2은 3일로 미국산 인공사료보다 1일 정도 더 빨랐으며, 부화한 유충 수는 IPTL-J2에서 415마리로 다른 사료와 비교하여 통계적으로 유의미하게 높았다. 따라서, 실험에 사용한 IPTL-J2 사료는 기존의 인공사료를 대체할 수 있을 것으로 기대된다.

검색어: *Spodoptera frugiperda*, artificial diet, eclosion rate, oviposition rate, mass rearing

P2

Surveillance of insect pests on tree fruits in Gyeonggi and Gangwon provinces

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Pest monitoring provides fundamental information for developing management programs. In this study, we surveyed seasonal occurrence of three agricultural pests from four orchards in Gyeonggi and Gangwon provinces twice a month from April to November in 2024. First, two fruit moths, *Carposina sasakii* (Lepidoptera: Carposinidae) in two apple and one peach orchards, and *Grapholita molesta* (Lepidoptera: Tortricidae) in one pear orchard, were monitored using conventional sticky traps (Delta trap) and remotely operated sticky traps (Autoroll trap) with pheromone lures. From the four orchards, Autoroll traps collected up to 12.7-fold greater numbers of moths while detecting adult emergence 15 days earlier than the Delta traps. Second, brown marmorated stink bug, *Halyomorpha halys* (Hemiptera: Pentatomidae), was monitored using clear sticky traps with pheromone lures in the four orchards. The total number of *H. halys* collected significantly differed across the orchards, with a maximum of 5.1-fold difference observed. These results can serve as a baseline information for predicting occurrence of the pests and making decision for insecticide application in fruit orchards.

Keywords: peach fruit moth, oriental fruit moth, brown marmorated stink bug, seasonal abundance

P3

Spatial repellent effects of natural products against *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae): Electrophysiological responses and field tests

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The brown marmorated stink bug (BMSB), *Halyomorpha halys*, is an invasive pest that damages over 170 plant species, causing significant agricultural losses. This pest pressure has led farmers to heavily rely on insecticides, increasing the risk of pesticide resistance and environmental contamination. Therefore, we conducted experiments to evaluate the spatial repellent effects of natural products as an eco-friendly pest management strategy through electroantennogram (EAG) and field tests. In EAG screening with fifteen natural compounds, four compounds (*A*, *B*, *K*, and *M*) exhibited significant EAG responses at a 1mg dose in both sexes. In subsequent field tests, we evaluated the spatial repellent effects of the EAG-active compounds on male and female attraction to the aggregation pheromone, methyl (2*E*,4*E*,6*Z*)-decatrienoate (MDT), compared with MDT alone (positive control) and a blank control (negative control). Compounds *A* significantly decreased female trap catches by 35.4% compared to the positive control, but there was no effect on male trap catches. In addition, compound *B* significantly reduced male and female trap catches by 54.3% and 41.1%, respectively, compared to the positive control. Our findings provide useful information for future control development via a push–pull strategy in integrated BMSB management. These approaches would help conserve the environment by reducing pesticide use and slowing the development of pesticide resistance.

Key words: pesticide resistance, methyl (2*E*,4*E*,6*Z*)-decatrienoate, push-pull, eco-friendly

P4

A comparative analysis of life tables between parthenogenetic and bisexual *Haemaphysalis longicornis*

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The Asian longhorned tick, *Haemaphysalis longicornis*, is the most abundant hard tick species in the Republic of Korea and is also known as a vector of various pathogens including severe fever with thrombocytopenia syndrome virus (SFTSV). Their populations are maintained by two reproductive strategies: parthenogenesis and bisexual. The analysis of 16S rRNA sequence is an easy and precise way to distinguish their reproductive lineage. However, their fundamental biology, such as the life table, is still unclear. In this study, we examined various biological parameters, including blood-feeding duration, pre-molting and oviposition periods, and body weight across different developmental stages, to identify key physiological distinctions between the two reproductive types. The period of time for blood feeding, pre-molting, oviposition and body weight were significantly different at each stage between the two reproductive types. Parthenogenetic individuals were significantly heavier than bisexual individuals and exhibited shorter period for blood feeding and pre-oviposition, except the larvae stage. In contrast, the pre-molting period was shorter for bisexual individuals. The comparison of biological characteristics between two reproductive lineages is crucial for assessing their ecological adaptability and vectorial capacity, particularly in regions where both populations coexist.

Key words: *Haemaphysalis longicornis*, parthenogenetic, bisexual, blood feeding, pre-molting, pre-oviposition

P5

Evaluation of volatile chemicals as a UV-A mosquito trap enhancement

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Mosquitoes are one of the most annoying insect pests for both indoor and outdoor activities. Insect repellents such as DEET and IR3535 are recommended to prevent mosquito bites during outdoor activities, although they need to be applied every few hours. Indoor mosquito traps utilizing UV-A have been widely used in various places such as restaurants, to collect endophagic and endophilic mosquitoes, such as *Aedes albopictus*. To improve the rate of mosquito trapping, it is suggested to apply volatile chemicals that mosquitoes utilize as host location cues. There are several proposed mosquito attractants such as sulcation, ethyl butylate, and 2-methyl-3-pentanol. In this study, we tested our hypothesis that mosquito attractants help the UV-A mosquito trap increase the efficiency of mosquito trapping. The volatile chemicals were prepared with the solvent hexane and placed at different concentrations on beaker traps placed in mosquito cages. The number of mosquitoes caught in the beaker traps was monitored at 8-hour intervals for 72 hours. The attraction rates varied depending on the chemicals and concentrations. These findings suggest that incorporating volatile attractants into UV-A mosquito traps can substantially enhance their effectiveness, suggesting a more effective mosquito control strategy for indoor environments.

Keywords: *Aedes albopictus,* attractant, sulcatone, ethyl butyrate, 2-methyl-3-pentanol

P6

First record of genus *Cremastobaeus* Ashmead, 1893 (Hymenoptera: Scelionidae) from Korea

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The genus *Cremastobaeus* Ashmead belongs to the subfamily Scelioninae, with 44 valid species distributed worldwide. In the Palearctic region, two species are known to be distributed, *C. artus* Kozlov et Kononova, reported from Honshu, Japan, and *C. siculus* Mineo, reported from Sicily, Italy. This genus is clearly differentiated from other genera by antennomeres A2–A4 with dorsal serrations and the fusion of A3 and A4.

In this study, the genus *Cremastobaeus* is recorded first time from Korea, with one new record, *C. artus*. Diagnosis and photographs of *C. artus*, and the geographical distribution of Palearctic *Cremastobaeus* species are provided.

Key words: parasitoid, Scelioninae, new record, Korea

P7

Review of the bat ectoparasite mites, *Spinturnix* (Acari: Spinturnicidae) in the Korean peninsula

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The entire members of family Spinturnicidae (approx. 110 species) are highly adapted ectoparasitic groups of bats. Especially, the genus *Spinturnix* is comprised of 50 species worldwide, inhabit the patagium and skins, and feeding on the host's blood. Despite the genus *Spinturnix* is one of the diverse groups within the family Spinturnicidae, research remains limited due to their unique habitat and ecology. According to the National Species List of Korea, six species from four genera of Spinturnicid mites have been recorded, three of which belong to the genus *Spinturnix* (*S. aviaton*, *S. plecotinus*, and *S. vespertilionis*). However, except for the *S. plecotinus*, the other two species were listed based on records from North Korea, which raises issues about their validity. In this study, we provide a revised list of the Korean *Spinturnix* and discuss the validity of the North Korean records.

Key words: Acari, distributional record, ectoparasite, Mesostigmata, Spinturnicidae

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P8

Four new species of *Spelaeochthonius* Morikawa, 1954 (Pseudoscorpiones: Pseudotyrannochthoniidae) in South Korea revealed by integrative taxonomy

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Karst research in Korea is still in its infancies and the invertebrate fauna of subterranean systems across the country is poorly known. One of the very diverse lineages in caves across Korea, the pseudoscorpions, are almost undocumented although they represent stunning examples of cave adaptations and troglomorphism. In this study, we provide a phylogenetic analyes for the pseudoscorpion *Spelaeochthonius* Morikawa, 1954 (Pseudoscorpiones: Pseudotyrannochthoniidae) using four loci (18S, 28S, CO1, and H3). Also, we report four new species based on molecular, distributional, and morphological data. All speices are strongly cave-adapted and known from a single cave or karst system only, emphasizing the need to implement conservation strategies for Korean karst systems and their fauna.

Key words: caves, false scorpions, Korean, Peninsula, phylogeny, species delimitation, taxonomy

P9

First records of two species within the subfamily Erebinae (Lepidoptera, Erebidae) from the Korean Peninsula

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The taxonomic status of two genera—*Chrysopera* and *Entomogramma*—within the subfamily Erebinae is still up for debate. This is because there are not many thorough phylogenetic studies based on large sampling and the Erebinae is one of the most speciose subfamilies of Lepidoptera with a high degree of diversity. They also lack in-depth comparative studies with morphologically related species. In this study, we report new records of two erebine genera, *Chrysopera* and *Entomogramma*, based on *C. combinans* and *E. fautrix* from Korea. We also provide taxonomic diagnoses for all species and distribution data, as well as illustrations of adults and genitalia. Furthermore, we present detailed descriptions of both species for the first time.

Key words: erebine moths, Korean peninsula, new record, owlet moths

P10

Taxonomic notes of the genera *Daphnis* and *Hippotion* (Lepidoptera: Sphingidae: Macroglossinae) in Korea

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Subfamily Macroglossinae (Lepidoptera: Bombycoidea: Sphingidae) is presented, recording 27 species in 12 genera in Korea. In Korea, the genus *Daphnis* Hübner, 1819 has not been recorded, and the genus *Hippotion* Hübner, 1816 is recorded only one species from North Korea. These two species are distributed in the Palaeotropical region. In this study, we present *Daphnis nerii* Linnaeus, 1758 and *Hippotion celerio* Linnaeus, 1758 as newly recorded species in Korea. Herein, the morphological key to the genera, diagnosis, photographs of adults and genitalia, and ecological information on *Daphnis nerii* Linnaeus, 1758 are presented.

Key words: *Daphnis*, *Hippotion*, newly record, Korea

P11

A new species of the ectoparasitic genus *Bethylus* Latreille (Hymenoptera, Bethylidae) in South Korea, with the description and barcode analysis

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A new species of *Bethylus* Latreille, the type genus of Bethylidae (Hymenoptera, Chrysidoidea, Bethylinae), is reported from the Korean Peninsula based on materials collected from Gangwon Province. The new species is described and illustrated with detailed diagnostic features and a phylogenetic analysis was conducted using mitochondrial cytochrome oxidase subunit I sequences from common *Bethylus* species to better understand the evolutionary relationships within the genus. The resulting phylogeny supports the distinction between *Bethylus* sp. nov. and the other species. Additionally, a key to the species of *Bethylus* in East Asia is provided.

Key words: DNA barcodes, *Bethylus*, ectoparasitoid, Korean Peninsula, new species, taxonomy

P12

Taxonomic review of the genus *Stilbus* Seiditz (Coleoptera: Phalacridae) in Korea with descriptions of two new species

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The family Phalacridae Leach (Coleoptera: Cucujoidea) includes 52 genera and 635 species within two subfamilies distributed worldwide. Most phalacrids are fungivores, but some feed on the flower heads. Phalacridae exhibits the highest species diversity in tropical regions. Although species diversity is lower in temperate regions, a significant population is still present. The genus *Stilbus* Seidlitz includes 74 species worldwide. However, it has not been recorded in Korea. In this study, the genus *Stilbus* is recorded for the first time with four species new to Korea: *Stilbus longurius*, **new species**, *Stilbus petiolus*, **new species**, *Stilbus coxalis* Švec and *Stilbus merkli* Švec. Illustrations of their habitus, diagnostic characters and male genitalia, a distribution map, and an identification key to the Korean *Stilbus* species are provided.

Key words: new records, Palearctic, Phalacridae, shining flower beetles, *Stilbus*

P13

A checklist of Korean *Curculio* Species (Coleoptera: Curculionidae), their host plants and distribution

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Insects of the genus *Curculio* (Coleoptera: Curculionidae) primarily use host plants from the family Fagaceae, and some species are known as economically significant pests that damage nut production. To date, a total of 25 *Curculio* species have been recorded in Korea. In this study, we reviewed existing literature and specimen data to compile a list of *Curculio* species inhabiting Korea and systematically organized information on their host plants. Through this approach, we aimed to understand the ecological characteristics and host selection tendencies of *Curculio* species in Korea and provide fundamental data for future taxonomic and genetic research.

Key words: *Curculio*, Coleoptera, distribution, Korea, host plants

P14

New marker, same task: Stathmopodidae species delimitation

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Insects exhibit a high degree of morphological similarity between species, making species identification based solely on morphology challenging. To address this issue, molecular identification using DNA markers with low intraspecific variation has become widely adopted. In the species delimitation of insects, the *COI* gene is commonly used, whereas different markers are employed for other taxa, such as *rbcL* for plants and *ITS* for fungi. A previous study on the genus *Stathmopoda* Herrich-Schäffer, 1853, which represents the largest proportion of the family Stathmopodidae, revealed that the *EF1α* gene, specifically amplified by the Starsky-Luke primers, is more effective for species differentiation than the commonly used *COI* gene. Based on these findings, this study aims to compare and evaluate the species delimitation performance of the mitochondria, nuclear, and ribosomal RNA genes.

Key words: Stathmopodidae, *Stathmopoda*, Delimitation, *EF1α*

P15

From microdiversity to megadiversity: Focusing on *Atkinsonia* Stainton, 1859

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Species of the genus *Atkinsonia* Stainton, 1859 (Stathmopodidae) exhibit diverse traits and broad host associations from aphids to oaks yet have received limited study. To investigate the diversity of this genus with its varied characteristics, we selected two morphologically similar species with opposite feeding habits and compared their traits. We examined *Atkinsonia ignipicta* (Korea, aphid feeder) and *A. beijingana* (Japan, oak feeder), focusing on unstudied aspects. Using SEM (Scanning Electron Microscopy), we identified scale microstructural differences, then applied 3D (three dimensions) modeling and fluid simulations. *A. ignipicta*, lacking specialized structures, showed rapid vortex formation, whereas *A. beijingana* displayed slower but intensifying vortices. We propose that *A. ignipicta*, facing heavy predation, evolved faster flight scales to evade threats. These findings may inform biomimetic designs, improving aerodynamic efficiency in drones and vehicles.

Key words: Stathmopodidae, *Atkinsonia*, SEM, 3D modeling, Simulation

P16

Report on two new species of *Casmara* from Oriental Realm based on Micro-CT

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The genus *Casmara* Walker, 1863 was long classified within Oecophoridae, but a 2016 molecular phylogenetic study reclassified it under Stathmopodidae. Since then, no follow-up research has been conducted, and no new species have been reported for over a decade, leaving critical gaps in understanding of this genus. Moreover, species of *Casmara* are pests that bore into plant stems, highlighting the importance of clarifying their diversity and distribution. In this study, we describe two new *Casmara* species collected from the Oriental Realm, thereby expanding the known diversity and distribution of the genus. These species were identified without dissection using Micro-CT (Computed Tomography), and by comparing the results with dissected genitalia, we assess the significance of Micro-CT in species diagnosis.

Key words: Stathmopodidae, *Casmara*, New species, Micro-CT

P17

Automated identification and classification of the genus *Stathmopoda* using YOLO

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Among the more than 40 genera and 400 species reported worldwide in the family Stathmopodidae, and the genus *Stathmopoda* with over 200 described species comprises the largest proportion. Although members of this genus display diverse ecological traits, ranging from feeding on agricultural crops to preying on aphids, their high degree of morphological similarity has made species identification difficult and hindered extensive research. In this study, we employ the latest version of the YOLO object detection algorithm, YOLOv11 widely used across various fields for its speed and accuracy to identify and classify *Stathmopoda* species collected from the Korean Peninsula. Forewings, which most clearly reflect species-specific characteristics, were used as training data. The entire process, from data preprocessing to result visualization, was conducted on the Roboflow platform without coding, making it accessible to non-experts as well.

Key words: Stathmopodidae, *Stathmopoda*, Artificial Intellgence, Identification, Classification

P18

First discovery of *Homodecatoma mallotae* (Hymenoptera: Eurytomidae) in Korea, with its complete mitochondrial genome

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The monotypic genus *Homodecatoma* Liao, 1979 is recorded in Korea for the first time, following its initial discovery in China. Specimens of *H. mallotae* emerged from the seeds of *Mallotus japonicus* (Euphorbiaceae) collected from Jeju Island. The complete mitochondrial genome of *H. mallotae* was sequenced and analyzed, revealing a circular genome of 16,405 bp in length, comprising the typical set of 37 genes: 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), and 2 ribosomal RNAs (rRNAs). The nucleotide composition exhibits a high A+T content, consistent with other Eurytomidae species. A graphical representation of the mitochondrial genome of *H. mallotae* is provided, along with a phylogenetic analysis comparing it to closely related species, offering insights into its evolutionary relationships within Eurytomidae.

Key words: Mitochondrial genome, Monotypic genus, Phylogeny, Phytophagous, Jeju Island

P19

Taxonomic clarification of *Argyresthia brevalbella* Lee, Lee & Liu, 2023 as a synonym of *Argyresthia festiva* Moriuti, 1969 (Lepidoptera: Argyresthiidae)

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In this study, the taxonomic status of *Argyresthia brevalbella* Lee, Lee & Liu, 2023 was clarified. *A. brevalbella* was reported as a new species by Lee et al. (2023). However, it shows strong morphological similarity to the Japanese species, *A. festiva* Moriuti, 1969, and the original description dose not include a comparison with this species. To compare these two species, adult morphology, genital examination, and DNA analysis were conducted. Through this study, the two species were confirmed to be conspecific, and we proposed that *A. brevalbella* should be treated as a synonym of *A. festiva*.

Key words: Lepidoptera, Yponomeutoidea, Argyresthiidae, Synonym

P20

A new species of *Opostegoides* Kozlov, 1985 (Lepidoptera: Opostegidae) from the Korean Peninsula with a checklist of the genus in Korea

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Opostegidae is a microlepidopteran family (Lepidoptera: Nepticuloidea) that includes almost 200 species belonging to seven genera worldwide. Among them, the genus *Opostegoides* Kozlov, 1985 has been recorded in Korea with three species and *O. minodensis* is known to infest *Betula*. Herein, we report the discovery of a new species of the genus *Opostegoides*. Adult and male genitalia are provided based on illustrations. Additionally, a checklist of Korean *Opostegoides* is provided.

Key words: Opostegidae, *Opostegoides*, Korea, Taxonomy

P21

Checklist of Lepidoptera in Yeoseo Island with one newly recorded species

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Despite covering only a small fraction of the Earth's land area, islands play a vital role in biodiversity by hosting numerous endemic species. This study reports on the biological and conservation value of Yeoseo Island, where limited research has been conducted. Collections of the Order Lepidoptera (butterflies and moths) were conducted over two periods in August, 2023 in Yeoseo Island. Lepidoptera is recognized as ecological indicators due to their diverse ecologies and habitats. Specimen are collected by sweeping, light trap, and bucket trap. A checklist of Lepidoptera identifying a total of 154 species belonging to 27 families is provided. The checklist includes four species currently under management and one newly recorded species. Additionally, this study presents information on the adult morphology, genitalia structures, and ecology of the unrecorded species.

Key words: Checklist, Lepidoptera, New record, Yeoseo Island

P22

Study on morphology, biology of *Cinara shinjii* (Hemiptera: Aphididae: Lachninae) in South Korea

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The genus *Cinara* Curtis, 1835 (Hemiptera: Aphididae: Lachninae) is a large aphid genus comprising 256 known species worldwide, associated with coniferous trees (Cupressaceae and Pinaceae families) as host plants.

Cinara (*Cinara*) *shinjii* Inouye, 1938 has been recorded in Japan and South Korea, with additional reports from Europe (Germany). In this study, we reassessed the host range of this species in South Korea, confirming its association with *Pinus parviflora*, *P.koraiensis*, and *P.pentaphylla*. Additionally, we provide detailed morphological descriptions of all developmental stages and investigate its life-cycle.

Key words: Aphids, *Pinus*, morph, life-cycle

P23

First record of *Dysaphis foeniculus* (Hemiptera: Aphididae: Aphidinae) from South Korea

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The genus *Dysaphis* Börner, 1931 (Hemiptera: Aphididae: Aphidinae: Macrosiphini) is a Palaearctic taxon comprising approximately 110 species, many of which exhibit a heteroecious life cycle. In spring, colonies establish on primary hosts within the Pyroideae (*Amelanchier*, *Cotoneaster*, *Crataegus*, *Malus*, *Pyrus*, *Sorbus*), where they induce leaf distortion and discoloration. Subsequently, they migrate to secondary hosts, predominantly within Umbelliferae/Apiaceae, but also across several other plant families, including Campanulaceae, Compositae, Valerianaceae, Plantaginaceae, and Polygonaceae.

Dysaphis (*Dysaphis*) *foeniculus* (Theobald, 1923) predominantly forms dense colonies on the basal parts of various host plants within the Apiaceae(*Anethum*, *Apium*, *Daucus*, *Foeniculum*, and *Ferula*), with occasional records from *Rumex* (Polygonaceae). Native to Egypt, this species has rapidly expanded populations reported in Africa, Australia, Central Asia, India, Japan, Mediterranean area, Middle East, New Zealand, North and South America, Pakistan, southern Europe.

In this study, we report the first occurrence of *Dysaphis foeniculus*on *Heracleum moellendorffii*in South Korea. We provide: (1) redescriptions of the apterous and alate viviparous females and (2) DNA barcoding analysis.

Key words: Aphids, *Heracleum moellendorffii*, exotic species, COI

P24

First record of *Lachnus sorini* (Hemiptera: Aphididae: Lachninae) from Jeju, South Korea

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The Holarctic genus *Lachnus* Burmeister, 1835 comprises approximately 23 valid species and is mostly associated with *Quercus* spp. (Fagaceae). This genus is morphologically distinguished from other Lachnid genera by the presence of darkly pigmented wings in alatae. To date, three species of *Lachnus* have been documented in Korea: *Lachnus chosoni* Szelegiewicz, 1975; *L. quercihabitans* (Takahashi, 1924); *L. tropicalis* (van der Goot, 1916).

Lachnus sorini Binazzi & Remaudière, 2006 was first described from *Quercus* spp. in Japan. In this study, we report its first occurrence on *Quercus glauca* and *Q. phillyraeoides* in Jeju, South Korea. We provide redescriptions of the apterous, alate, and oviparous viviparous females.

Key words: Aphids, *Quercus,* diversity, morph

P25

New report of Lachninae tribe from South Korea: Miyalachnini (Hemiptera: Aphididae: Lachninae)

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This study reports the first occurrence of *Miyalachnus sorini* (Aphididae: Lachninae) in South Korea, expanding its known distribution beyond Japan and identifying *Prunus sargentii* as a new host. Key morphological traits across life stages are described, and comparative analyses with Japanese populations reveal morphological variations. Mitochondrial COI barcoding shows low intraspecific divergence (0.2%) but high interspecific divergence (10.5%) between *Miyalachnus* sp. and *M. sorini*. TCS network analysis was conducted to examine haplotype relationships and cryptic genetic diversity. The observed morphological and genetic differences suggest potential ecological adaptations, contributing to a better understanding of *M. sorini*'s diversity and distribution.

Key words: Aphids, *Prunus*, COI, haplotype

P26

A newly recorded *Microcolona* (Lepidoptera: Elachistidae) species from South Korea with DNA barcoding analysis

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This study presents the first record of a *Microcolona* Meyrick, 1897 species from South Korea. The genus *Microcolona* is distributed across Asia, Oceania, and Africa, and is known for leaf-mining biology in its larval stages. Here, we provide faunistic data for this species and descriptions of adult morphology including detailed illustrations. Additionally, we perform DNA barcoding analysis to compare the obtained sequences with global barcode reference at the species level.

Key words: Taxonomy, Gelechioidea, leaf-mining moth, description, distribution, CO1

P27

First report of genus *Xenocorixa* Hungerford (Hemiptera: Corixidae) in Korea

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Corixidae is one of the largest families of aquatic bugs (Hemiptera: Nepomorpha) and includes more than 400 valid species. In Korea, 13 species in four genera of Corixidae have been reported. In this study, we report a genus *Xenocorixa* Hungerford, 1947 for the first time from the Korean Peninsula. *Xenocorixa* is the monotypic genus that have known to be distributed in Japan and China. We provide taxonomic accounts and ecological information of the species with photographs and also provide a key to genus of Korean Corixidae to facilitate identification.

Key words: Aquatic bugs, Corixidae, taxonomy, water boatman, *Xenocorixa*

P28

Redescription of *Cylindralcides takahashii* (Kôno) (Coleoptera, Curculionidae, Molytinae, Mecysolobini) damaged on the Thunberg's bay-tree

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Several specimens of *Cylindralcides* (*s. str.*) *takahashii* (Kôno, 1930), belonging to the tribe Mecysolobini (Curculionidae: Molytinae), were collected on new shoots of Thunberg's bay-tree, *Machilus thunbergii* Siebold & Zucc. from Is. Jeju of Korea. This represents the first record of the genus *Cylindralcides* Heller, 1918 in Korea and the first documented record of *M. thunbergii* as the host plant for this species. The original description of *C. takahashii* was brief and lacked detailed diagnostic features leading to misidentification. This study provides a redescription with accurate diagnosis information including detailed illustrations adult and larva and and ecological information, aiming to clarify the taxonomic status of the species. Additionally, the 682 bp of COI DNA barcode data support to assess molecular relationships within the tribe Mecysolobini.

Keywords: Curculionidae, Redescription, *Cylindralcides takahashii*, *Machilus thunbergii*, Korea

P29

First record of the genus *Plococerus* (Curculionidae: Molytinae: Cryptorhynchini) from Sri Lanka

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The genus *Plococerus* Marshall, 1923, belonging to the tribe Cryptorhynchini of the subfamily Molytinae, is discovered for the first time from Sri Lanka. Several specimens of the nominotypical species, *Plococerus denticollis* Marshall, 1923, were collected from the damaged stems of a *Euphorbia* species in the North Central Province. This species is readily recognized by its distinctive dentate prothorax. Males are distinguishable by plumose antennae inserted at one-third from the apex of the rostrum. A comprehensive redescription of both the adult and larval stages is provided, supported by detailed morphological illustrations and ecological information.

Keywords: Curculionidae, Cryptorhynchini, *Plococerus denticollis*, First record, Sri Lanka

P30

Unraveling the evolution of basal Ensifera through phylogenomics with Orthoptera-specific target enrichment

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Basal Ensifera includes groups such as cave crickets (Rhaphidophoridae), raspy crickets (Gryllacrididae), Jerusalem crickets (Stenopelmatidae), wētā and king crickets (Anostostomatidae), along with other related groups. These lineages exhibit diverse evolutionary adaptations, including wing reduction and complex biogeographical histories. Despite their evolutionary and ecological significance, phylogenomic research has been slow to progress due to challenges posed by their large genome sizes, extensive global distribution, and limited prior studies. In this study, we employed the Orthoptera-specific target enrichment (OR-TE) probe set to perform a phylogenomic analysis of basal Ensifera. Our results provided clarity on key taxonomic issues that had remained unresolved in previous studies. This research represents a critical advancement in Ensifera systematics and underscores the importance of incorporating newly established phylogenetic frameworks in future evolutionary studies.

Key words: Orthoptera, Phylogenomics, Anchored hybrid enrichment, Rhaphidophoridae, Gryllacrididae

P31

Systematic revision and larval feeding evolution of dung flies (Diptera: Calyptratae: Scathophagidae)

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Dung flies (Scathophagidae) are commonly associated with herbivore feces, yet their larval biology spans a remarkable diversity of feeding strategies, including phytophagy, saprophagy, and even predation. However, the evolutionary history of these diverse feeding habits remains poorly underexplored, largely due to the absence of a well-resolved phylogeny and the limited biological data available for many species. This study integrates systematic revision and evolutionary analysis to reconstruct the phylogenetic framework of Scathophagidae and infer the evolutionary transitions in larval feeding habits.

Using a multigene dataset including both subfamilies of Scathophagidae and a broad Calyptratae outgroup, this study reconstructs a robust phylogeny and evolutionary timescale to reassess the systematics of dung flies and trace the evolution of their life histories. The results challenge previous hypotheses on scathophagid phylogeny, revealing novel relationships within the family and clarifying the placement of Delininae. Ancestral character state reconstruction indicates that stem-boring was the ancestral larval feeding habits in Scathophagidae, from which multiple independent transitions to other feeding habits, such as leaf-mining, seed-feeding, coprophagy, and predation, have occurred.

This study establishes a robust phylogenetic framework for Scathophagidae and provides the first insights into the evolutionary transitions of larval feeding habits within the family. While these findings clarify long-standing taxonomic uncertainties and reveal novel evolutionary patterns, challenges remain due to low support values in some clades and limited taxon coverage. Future research incorporating genome-scale datasets and broader taxonomic sampling will be crucial to further refine these results. Despite these limitations, this study serves as an essential groundwork for understanding feeding evolution in dung flies and provides a comparative framework for investigating the diversification of ecological histories across Diptera.

Key words: Ancestral Character State Reconstruction, Divergence Time Estimation, Larval Feeding Habits, Multigene phylogeny, Scathophagidae

P32

Ultrastructural characterization of antennal sensilla in *Bradysia procera* (Diptera: Sciaridae), the ginseng stem fungus gnat, using scanning and transmission electron microscopy

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The ginseng stem fungus gnat, *Bradysia procera*, is a major insect pest of Korean ginseng (*Panax ginseng*), significantly impacting plant growth. Moreover, as a boring pest that burrows into the ginseng stem, early detection and control are challenging. In this study, the classification, distribution, and functional inference of antennal sensilla in male and female *B. procera* were examined using scanning electron microscopy (SEM) and transmission electron microscopy (TEM). The antennae consist of a scape, pedicel, and flagellum, with a total of 16 antennomeres. Four types of sensilla, including six subtypes, were identified: chaetica, trichodea, basiconica, and coeloconica. There was no difference in the types of sensilla between males and females, but males had a significantly higher number of sensilla than females. This study provides a foundational reference for future Single Sensillum Recording (SSR) experiments and research on chemical communication behavior in *B. procera*.

Key words: *Bradysia procera*, antennal sensilla, ultrastructure, SEM, TEM

P33

A conceptual model for the diapause intensity curve in overwintering Japanese pine sawyer larvae, *Monochamus alternatus* (Coleoptera: Cerambycidae)

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The Japanese pine sawyer (*Monochamus alternatus* Hope; Coleoptera: Cerambycidae) is a primary vector of the pine wood nematode, *Bursaphelenchus xylophilus* (Steiner and Buhrer), which causes pine wilt disease (PWD). This study aimed to elucidate the diapause development process of *M. alternatus*, with a particular focus on changes in diapause intensity in response to chilling periods at 9°C. We conceptualized the diapause process of *M. alternatus* based on the established framework of insect diapause ecology, which includes pre-diapause, diapause, post-diapause, and non-diapause phases. Larvae collected on October 24, representing the initial diapause state, did not pupate after chilling for 0 or 10 days. However, during chilling periods ranging from 30 to 130 days, the time required for pupation decreased significantly, indicating a progressive decline in diapause intensity. The depth of diapause was inferred to peak between 10 and 30 days of chilling, suggesting an initial refractory phase, followed by a gradual decrease in diapause intensity, forming a peak-shaped curve indicative of the maintenance and termination phases. The completion of diapause termination was observed at 110 days, at which point diapause intensity reached zero, possibly coinciding with the loss of diapause symptoms and transition to a quiescent developmental state. This study successfully delineates the entire diapause intensity curve of *M. alternatus* using experimental data, contributing to a better understanding of its life cycle in the context of climate change and facilitating predictions of adult emergence in spring

Key words: Pine trees, overwintering biology, diapause development, chilling period, pupal chamber

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P34

Preference for pesticide-contaminated food sources in honey bee with pesticide exposure history and olfactory/gustatory electrophysiological responses to pesticides

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The honey bee, *Apis mellifera*, is a vital agricultural and ecological pollinator that is frequently exposed to pesticides, raising concerns about the impact of agrochemicals on its foraging behavior. The present study demonstrates that honey bee previously exposed to pesticides exhibit a preference for food sources contaminated with the same pesticide. To elucidate the underlying mechanisms, we quantified the natural volatilization of pesticide active ingredients and assessed the olfactory and gustatory responses of honey bee to these compounds. Our results indicated that although pesticides volatilize in trace amounts, they are not detected by olfactory receptors and may instead be perceived through gustatory pathways. These findings suggest a potential mechanism underlying pesticide-dependent foraging behavior in honey bee, providing insights into how agrochemical exposure may alter pollinator foraging preferences.

Key words: honey bee, pesticide, behavior, electrophysiology

P35

Development of a LAMP-based molecular species diagnostic tool for the invasive pest, tomato leaf miner, *Tuta absoluta* (Lepidoptera, Gelechiidae)

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The tomato leaf miner (*Tuta absoluta*, TLM) is a voracious predator that mainly attacks Solanaceae crops and is a significant pest of tomatoes grown in fields and greenhouses. It belongs to the Gelechiidae family. This species is native to the Andes region of South America. However, it is now well known as a serious invasive pest of tomato crops in Europe, Africa, and Asia. It was officially confirmed in Korea in 2024, and damage was reported in many Gangwon Province farms. However, it has a high degree of morphological similarity, and it sometimes occurs together with a closely related species that attacks the same Solanaceae crop, the potato tuber moth (*Phthorimaea operculella*, PTM), so it was necessary to develop a diagnostic method for it. Here, we developed a loop-mediated isothermal amplification (LAMP) assay for rapid and effective species diagnosis and PCR to identify Korean field-collected or overseas samples. Species-specific primers were designed by aligning and comparing the mitochondrial genomes of related species, including two main species. TLM sensitivity is good enough to allow visual discrimination when reacted at 61°C for 20 minutes. This simple and accurate LAMP assay can be used for intensive field monitoring and integrated management of these species.

Key words: *Tuta absoluta*, *Phthorimaea operculella*, LAMP, invasive pest, Diagnostic tool

P36

Evaluation of different concentrations of ARP14 against whitefly and mite using the leaf-dipping method

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This study evaluates the efficacy of different concentrations of the entomopathogenic fungus ARP14 against *Tetranychus kanzawai* and *Bemisia tabaci* using the leaf-dipping method under controlled conditions. Mortality and mycosis rates were recorded over 15 days. Results showed a concentration-dependent reduction in survival, with *B. tabaci* being more susceptible than *T. kanzawai*. At 1×10^9 conidia/mL, mortality reached 99% in *B. tabaci* adults and 42% in nymphs, while *T. kanzawai* mortality was 85% in adults and 93% in nymphs after six days. By day 15, both mite and whitefly populations exhibited 100% mortality across all fungal concentrations. Mycosis rates exceeded 90% at 1×10^9 conidia/mL. The LC_{50} values were 1.2×10^6 conidia/mL for *B. tabaci* and 2.8×10^7 conidia/mL for *T. kanzawai*, with statistical significance. These findings suggest that 1×10^9 conidia/mL is the most effective concentration against *T. kanzawai* and *B. tabaci*.

Key words: entomopathogenic fungi, mortality rate, mycosis, LC_{50}, probit analysis

P37

Comparison of different treatment methods of the neem oil for the control of *Tuta absoluta* (Lepidoptera: Gelechiidae)

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Tomato (*Solanum lycopersicum* L.) is a globally significant vegetable crop that suffers substantial economic losses due to insect pests, notably the tomato leafminer *Tuta absoluta* (Lepidoptera: Gelechiidae). It has become a significant pest worldwide. Due to the resistance development of synthetic pesticides, neem oil, a plant-derived natural pesticide, has been widely used for sustainable pest management. This study evaluated the efficacy of neem oil at three different application methods against the mortality of larval instars of *T. absoluta* under lab conditions. Neem oil solutions were prepared at azadirachtin concentrations of 0 to 15 ppm. The mortality was assessed using the direct spray, leaf dip, and soil-drenched methods. Results indicated that the effects of the soil-drenching was comparable with direct spray and leaf-dipping assay. The results of this study may lead to an easier and more effective neem oil treatment method to maximize the control of *T. absoluta*.

Key words: azadirachtin, neem, tomato leaf miner, invasive species, tomato, biopesticides

P38

Identification of a novel amitraz resistance mutation in the β₂-octopamine receptor of Korean *Varroa destructor* populations

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The *Varroa* mite (*Varroa destructor*) is an ectoparasitic mite of the honey bee (*Apis mellifera*) and a major threat to beekeeping. In Korea, amitraz has been extensively used for *Varroa* mite control. Despite concerns over potential resistance development, previously identified octopamine receptor mutations (N87S, Y215H, and F290L), associated with amitraz resistance, have not been detected in Korea. However, a novel mutation (T115N) was identified recently. In this study, we investigated the impact of the T115N mutation on amitraz susceptibility by comparing time-dependent intoxication response and median lethal time between mites carrying the T115 and N115 genotypes. Compared to mites with the T115 genotype, N115 genotype mites exhibited a delayed intoxication response and a median lethal time approximately 2.8-fold longer, suggesting increased resistance to amitraz. Over five years (2020–2024), the T115N mutation has spread within *Varroa* mite populations in Korea. Further research is needed to understand the underlying factors driving this region-specific T115N mutation in Korea.

Key words: *Varroa destructor*, amitraz resistance, octopamine receptor, T115N mutation

P39

Construction of recombinant *Bacillus thuringiensis* expressing nematicidal crystal proteins

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Plant-pathogenic nematodes are significant agricultural pests that cause substantial yield losses and economic damage globally. However, traditional chemical control methods for nematodes are environmentally harmful. To address this challenge, *Bacillus thuringiensis* (Bt), a widely used microbial pesticides, offers promising biocontrol potential due to its insecticidal proteins which are safe for humans and environment. Among these proteins, Cry5Ba and App6Aa have been reported to have nematicidal activities. In this study, recombinant nematicidal Bt strains were constructed by introducing plasmid carring the *cry5Ba* and *app6Aa* genes. These Bt strains exhibited stable expression of the Cry5Ba and App6Aa proteins. This study provides a novel strategy for improving Bt-based biocontrol by expressing multiple nematicidal proteins, contributing to sustainable pest management in agriculture.

Key words: nematode control, *Bacillus thuringiensis*, Cry5Ba, App6Aa

P40

Improved insecticidal activity against *Spodoptera exigua* through co-infection of AcMNPV and LdMNPV

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Autographa californica multiple nucleopolyhedrovirus (AcMNPV) has been considered as an effective agent to control *Spodoptera exigua* which is a globally distributed agricultural pest insects. It has been reported that the insecticidal activity of co-infection of two different baculoviruses was higher than that of individual viruses. In this study, *Lymantria dispar* multiple nucleopolyhedrovirus (LdMNPV) was used as a synergist to improve AcMNPV performance. The polyhedra of AcMNPV and LdMNPV were co-applied to *S. exigua* larvae in lab experiments. Although the synergistic effect did not show at the AcMNPV concentration of 5×10^2 PIBs/larva, the insecticidal activity of AcMNPV against *S. exigua* was significantly enhanced by 2.4-fold when LdMNPV (1×10^6 PIBs/larva) was added to the AcMNPV concentration of 2.5×10^2 PIBs/larva. Additionally, even when the concentration of LdMNPV was reduced to 1×10^4 PIBs/larva, the synergistic effect continued to markedly improve AcMNPV lethality against *S. exigua*. These results suggests that LdMNPV markedly augments the insecticidal activity of AcMNPV against *S. exigua,* likely due to synergistic interactions during co-infection.

Key words: AcMNPV, LdMNPV, *Spodoptera exigua,* synergistic effect, insecticidal activity

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P41

Insecticidal effect of a novel entomopathogenic fungus, *Beauveria bassiana*, isolated from the invasive hornet, *Vespa velutina nigrithorax*, in Korea

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등검은말벌(*Vespa velutina nigrithorax* du Buysson)은 꿀벌의 중요한 포식성 해충으로 2003년 이후 국내에 침입한 후 양봉산업에 경제적 피해를 주고 있다. 본 연구에서는 곰팡이에 감염된 등검은말벌 사체에서 병원균을 분리하여 ITS 영역의 염기 서열을 분석하였다. 그 결과 NCBI에 등록된 곤충병원성 곰팡이인 *Beauveria bassiana*와 99.8%의 유사도로 확인되어 동일 종으로 동정하였다. 또한, 분리한 병원성 곰팡이의 병원성을 벌목(Hymenopter)과 나비목(Lepidoptera)을 대상으로 평가하였다. 살충효과는 벌목의 등검은말벌 1종과 나비목의 뿔나방과 2종, 밤나방과 2종의 유충을 대상으로 검증하였다. 본 연구는 국내에서 최초로 등검은말벌에서 분리한 *B. bassiana*를 보고하는 사례이다.

검색어: *Beauveria bassiana*, *Vespa velutina*, *Tuta absoluta*, entomopathogenic fungi, honey bee

P42

Mortality effects of three chitin synthesis inhibitors on subterranean termite *Reticulitermes speratus*

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The subterranean termite, *Reticulitermes speratus* (Isoptera: Rhinotermitidae), is one of the most frequently encountered termite species in South Korea. The *R. speratus* causes irreversible damage to wooden structures, Hanok, and cultural heritage sites. To mitigate both economic and structural damage, eliminating the colony by targeting and removing the reproductive caste is essential. One of the most effective methods for collapsing *R. speratus* colonies is implementing a baiting system that utilizes chitin synthesis inhibitors (CSIs). The CSIs, as active ingredients in baits, should not induce feeding deterrence in *R. speratus* at lethal concentrations. In this study, we investigated the feeding deterrence and lethal effects of three CSIs on *R. speratus*. We conducted behavioral and electrophysiological tests on *R. speratus* with three CSIs (*A*, *B*, and *C*) at 1500 ppm, 2500 ppm, and 5000 ppm. The tests included a two-choice test, a no-choice test, and electroantennography (EAG). In the two-choice test, only CSI *A* at 5000 ppm exhibited feeding deterrence in *R. speratus*, while no deterrence was observed at any concentration of CSIs. In the no-choice test, 100% mortality was observed at 12 weeks for CSI *A* at 1500 ppm and 2500 ppm. For CSI *B*, 100% mortality was recorded at 8 weeks for 1500 ppm, 10 weeks for 2500 ppm, and 12 weeks for 5000 ppm. In the electrophysiological tests, only CSI *A* at 5000 ppm elicited a significant response in *R. speratus*, while no significant electrophysiological response was observed at any concentration of CSIs. In this research, We propose that our findings may contribute to the development of baits for the effective control of subterranean termites in South Korea.

Key words: subterranean termite, chitin synthesis inhibitors, behavioral tests, electroantennography

P43

One-year tracking of *Gryllus bimaculatus* densovirus infection status in South Korea and the potential for virus control using RNAi

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2023년 쌍별귀뚜라미 덴소바이러스(*Gryllus bimaculatus* Denso virus, GbDV)의 발생으로 국내 쌍별귀뚜라미 사육 농가는 심각한 피해를 입었으며, 일부 농가는 바이러스를 극복하지 못하고 폐업에 이르렀다. 이에 따라, GbDV의 전국적인 재확산을 방지하기 위해 감염양상을 지속적으로 모니터링하고, 효과적인 대응 방안을 마련해야 할 필요가 있다. 본 연구에서는 2023년부터 2024년까지 전국 쌍별귀뚜라미 사육 농가의 존폐와 바이러스 감염양상을 조사하였으며, 감염 정도에 따라 감염 수준을 분류하였다. 또한, Sanger sequencing을 통해 바이러스의 유전적 변이를 분석한 결과, 동일한 Structure protein내 동일한 부위에서만 발생한 5가지 유형의 Non-synonymous SNP를 확인했다. 끝으로, 본 연구에서는 이러한 돌연변이를 포함한 GbDV를 효과적으로 저감하기 위해 RNA interference를 활용한 바이러스 저감제를 개발하기 위해 시도함으로써, GbDV를 극복하는 데 기여하고자 한다.

검색어: 쌍별귀뚜라미, *Gryllus bimaculatus* denso virus, Non-synonymous SNP, RNA interference

P44

Production of recombinant factor C in insect virus expression system

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Recombinant factor C (rFC)는 의약품의 세균 감염 여부 판별에 이용되는 투구게(Japanese horseshoe crab) 유래 재조합 단백질이다. rFc는 분비 당단백질(secreted glycoprotein)로서 기능적 특성을 유지하기 위해서는 재조합 단백질의 생산 중 올바른 단백질 접힘과 분비 과정이 필수적으로 요구된다. 현재 rFC는 주로 대장균(*Escherichia coli*) 및 효모(yeast)에서 생산되고 있지만, 당쇄화와 분비 효율에서 명확한 한계점을 보인다. 곤충 바이러스인 baculovirus를 이용한 baculovirus expression system (BES)은 진핵생물인 곤충 세포를 이용해 재조합 단백질을 생산하기 때문에 포유동물 발현계 수준의 번역 후 수정 과정을 제공하여, 재조합 단백질의 올바른 구조와 높은 활성 수준을 유도할 수 있다. 따라서, 본 연구에서는 BES를 활용하여 그 활성이 더욱 증대된 rFC를 생산하고자 하였다. 이를 위해 투구게(*Tachypleus tridentatus*) 유전체 정보로부터 획득한 Fc 유전자 서열을 BES에 코돈 최적화 후 *polyhedrin* 프로모터 하에 발현시켰다. 재조합 바이러스들은 분비 과정의 최적화를 위해 다양한 분비 신호를 가지도록 제작하여 그 발현 효율을 비교 평가하였다. 또한 재조합 단백질의 안정성에 영향을 주는 바이러스 분해효소에 의한 rFc의 안정성에 대해 비교 평가하였다.

검색어: 곤충 바이러스, baculovirus expression system, recombinant factor C, 분비 신호

P45

DNA barcoding of two hard tick species transmitting SFTSV and haplotype network analysis to investigate regional genetic variations

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The hard tick is a three-host tick, meaning it selects a different host for each developmental stage. During the feeding process, ticks can transmit diseases to animals. In particular, Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV), which is transmitted by hard ticks, is a zoonotic disease characterized by high fever, gastrointestinal symptoms, thrombocytopenia, and leukopenia. The case fatality rate due to SFTSV in domestic infections has been reported to be 15.7%. In this study, DNA barcoding was performed on two tick species that transmit SFTSV. Samples of *Haemaphysalis flava* were collected from nine locations (Inje-gun, Gwangju-si, Ulju-gun, Andong-si, Ganghwa-gun, Boseong-gun, Jeju-si, Seongbuk-ri, and Gunsan-si). Samples of *Ixodes nipponensis* were collected from nine locations (Yeoju-si, Hwaseong-si, Goseong-gun, Pyeongchang-gun, Jeongeup-si, Uiseong-gun, Cheongsong-gun, Cheongdo-gun, and Gunsan-si). Four sets of DNA markers (COI, 16S rDNA, 12S rDNA, and ITS2) were used for barcoding. Genomic DNA (gDNA) was obtained from 97 samples of *Haemaphysalis flava* and 135 samples of *Ixodes nipponensis*. The barcode data were then subjected to haplotype network analysis to examine the genetic variations due to regional isolation. This study will provide fundamental data for future investigations of SFTSV vector-borne pests.

Key words: hard tick, vector, tick born disease, South Korea

P46

Microbiome diversity and site-specific variation of *Culex pipiens molestus* and *Culex pipiens pallens* in Korea

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Mosquitoes harbor diverse microbiota that influence reproduction, digestion, and pathogen transmission. Understanding the composition and structure of mosquito microbiomes can provide valuable insights into vector control strategies. In this study, we analyzed the gut microbiomes of adult female *Culex pipiens* subspecies (*Culex pipiens molestus* and *Culex pipiens pallens*) collected from seven locations in Korea. Using 16S rRNA sequencing, we observed significant site-specific variations in microbiome composition, particularly in *Wolbachia* abundance. While *Wolbachia* was dominant in most locations, its proportion varied significantly between sites, suggesting potential environmental influences. Additionally, microbial communities associated with *Culex pipiens* exhibited distinct patterns based on geographical location, with two taxa identified as site-specific. Our findings highlight the role of environmental factors in shaping mosquito-associated microbiomes and suggest that microbiome-based vector control strategies should consider site-specific microbial dynamics.

Keywords: *Culex pipiens*, microbiome, *Wolbachia*, mosquito-borne disease, vector control

P47

Population structure of *Psychoda alternata* (Diptera: Psychodidae): high-rise buildings—genetic islands in the city for moth flies?

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The trickling filter fly, *Psychoda alternata* Say, 1824 (Diptera: Psychodidae), is one of the moth fly species commonly found in urban areas across the world. Despite the pervasiveness of this species, its population structure and dispersal routes remain largely unexplored. To address this gap, we sequenced 82 individual genomes of *P. alternata* collected from nine localities in South Korea and one locality in Taiwan. We also performed *de novo* genome assembly of *P. alternata* using Illumina sequencing to construct the first reference genome of the genus *Psychoda*. Population analyses were conducted based on single nucleotide polymorphism (SNP) markers. Unexpectedly, most samples from Gwangju formed a separate cluster distinct from the rest of South Korea. Furthermore, high levels of inbreeding were detected in individuals collected from hotels, apartment complexes, and mixed-use buildings (“officetels” in South Korea), including samples from Taiwan and Gwangju. These results suggest that high-rise buildings may act as islands isolating moth fly populations in urban areas.

Key words: drain fly, genetic structure, inbreeding, population genomics, SNP, urban pest

P48

Frankliniella occidentalis monitoring using Random forest algorithm

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Insect pests cause damage to crops, resulting in economic losses. Insect pest management is necessary to reduce such damage. Generally, insect pest management is carried out in three stages: occurrence, monitoring, and control. Among these, monitoring is crucial for determining insect pest density. However, monitoring has limitations as it requires significant time and labor, necessitating methods to overcome these challenges. Monitoring can be conducted in this context by utilizing the relationships between insect pests, crops, and the environment. In this study, we used the machine learning algorithm Random Forest, which learns patterns based on input data, to predict the patterns of *F. occidentalis* density in a greenhouse using crop health, and the environmental factors in the greenhouse

Key words: *Frankliniella occidentalis*, monitoring, Random forest

P49

Development of system dynamics model for exploring relationships between *Bursaphelenchus xylophilus* and various factors using stock and flow diagram

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Pine wilt disease, caused by *Bursaphelenchus xylophilus*, poses a significant threat to pine forests in the Korean Peninsula, affecting forestry, local economies, and biodiversity. The spread of this disease depends on its insect vector, *Monochamus alternatus*, and is influenced by various biological, environmental, and economic factors. To better understand the complex relationship governing the occurrence and impact of pine wilt disease, this study explores a system dynamics approach. Stock and flow diagram (SFD) is developed to represent key relationships among *B. xylophilus*, *M. alternatus*, and factors such as climate conditions, forest structure, and human activities. This modeling framework aims to provide insights into insect pest and plant disease dynamics and potential management strategies.

Key words: system dynamics model, stock and flow diagram, pine tree, *Monochamus alternatus*, *Bursaphelenchus xylophilus*

P50

A tentative method optimizing the model parameters using a machine learnig algorithm, L-BFGS-B: A case study for diapause termination rate curve in black pine bast scale

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The approach to developing a prediction model of insect pests can be largely divided into a mechanical model and a statistical model. Unlike a mechanical model that parameterizes the innate characteristics of organisms, such as a temperature-dependent growth rate model, the latter develops a model based on observation data such as presence or absence. In this study, we propose a method to optimize and estimate the parameters of a mechanical model using empirical data. The black pine bast scale was selected as a model pest, and the parameters of the summer diapause termination rate model were estimated using field observation data. The parameters were optimized using the Python scipy.optimize.minimize function using L-BFGS (or Limited-memory BFGS, LM-BFGS), which belongs to the optimization algorithm of quasi-Newton methods. The parameters of the objective function were changed so that the deviation between the predicted and the observed date of summer diapause completion was minimized. As a result, the optimal parameter approximation was obtained, and when the summer diapause completion date was predicted by applying these parameters, the deviation from the actual value was 2.0 days on average, showing excellent performance. This parameter estimation method appears to be useful for developing mechanistic models of biological properties using only fragmentary empirical observation data.

Key words: Empirical data, Parameter estimation, Forecasting models, Temperature, Objective function

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P51

Antennal olfactory receptor neurons for the host plant volatiles and sex pheromone in *Dioryctria abietella* (Denis & Schiffermüller, 1775) (Lepidoptera: Pyralidae)

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Dioryctria abietella (Denis & Schiffermüller, 1775) (Lepidoptera: Pyralidae) is considered a major pest affecting seed production of various *Pinus* species in the Republic of Korea. In this study, we investigated the response profiles of antennal olfactory receptor neurons (ORNs) in adult *D. abietella* to 15 host plant volatiles and two sex pheromone compounds using the single sensillum recording (SSR) technique. We identified seven types of olfactory sensilla along with various types of ORNs in the antennae of *D. abietella*. Of these seven olfactory sensilla types, two were present in both sexes, whereas five were sex-specific. The most abundant type contained one or two ORNs, which exhibited high specificity for *α*-pinene enantiomers and *β*-pinene, with minor responsiveness to geranyl acetate and (−)-bornyl acetate. Another common sensilla type contained one specialized ORN responsive to *β*-caryophyllene and *α*-humulene. In females, a pheromone-sensitive sensilla type contained two highly specialized ORNs, one responsive to (*Z*,*Z*,*Z*,*Z*,*Z*)-3,6,9,12,15-pentacosapentaene and the other to (*Z*,*E*)-9,11-tetradecadienyl acetate. Another female-specific sensilla type responded to *α*-phellandrene, *α*-terpinolene, and (±)-limonene. In males, a pheromone-sensitive sensilla type contained two ORNs, of which only one responded to (*Z*,*E*)-9,11-tetradecadienyl acetate. Similarly, a male-specific sensilla type also contained two ORNs, but only one responded exclusively to geranyl acetate. Another male-specific sensilla type contained two ORNs, with one responsive to *α*-pinene enantiomers and *β*-pinene, while the other was responsive to (*E*)-2-hexenal. These findings suggest that *D. abietella* possesses a set of specialized ORNs for the host plant volatiles and sex pheromone compounds, providing initial understanding into its olfactory communication system. However, further experiments are needed for more precise characterization of ORNs in this species.

Key words: *Dioryctria abietella*, host plant volatiles, sex pheromone, olfactory receptor neurons (ORNs), single sensillum recording (SSR)

P52

RNA-based analyses of feeding response in *Allonychiurus kimi*: Relationship between peptide expression and food consumption

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Organisms that function as consumers in ecosystems acquire most of their energy through food consumption for growth, survival, and reproduction. To achieve this successfully, organisms tend to store energy advantageously for survival or reproduction after sufficient food consumption. In this regard, determining whether individuals have consumed sufficient food can be essential for understanding the relationship between specific behaviors and energy intake in certain species. This study aimed to establish a method to assess the response of *Allonychiurus kimi* to food from an RNA perspective. Laboratory-reared *A. kimi* were subjected to food restriction for 1 week before being allowed to feed for 24 hours, with RNA extracted at various intervals (30 minutes, 2, 6, 12, and 24 hours). RNA was also collected after food removal (24 hours, 48 hours, and 1 week later). Results showed that CCHamide-2 expression gradually decreased after feeding. Conversely, ILPs-7 expression increased after feeding and showed an inverse relationship with CCHamide-2. These findings demonstrate that food consumption of *A. kimi* is regulated by peptide expression and that this method can determine the intensity of food consumption.

Key words: Collembola, food consumption, CCHamide, ILPs, appetite regulation, mRNA, RT-qPCR

P53

Production of foot-and-mouth disease virus-like particles using baculovirus expression system

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구제역(foot-and-mouth disease, FMD)은 소, 돼지 등 우제류에서 발생하는 높은 전염성을 지닌 질병으로, 가축 산업에 있어 심각한 경제적 손실을 초래한다. 바이러스 유사입자(virus-like particle, VLP)는 유전물질이 결여된 형태의 바이러스 구조 단백질만을 포함하며 감염 위험 없이 강력한 면역 반응을 유도할 수 있는 차세대 백신으로 주목받고 있다. 본 연구에서는 높은 수준의 번역 후 수정능력을 나타내 VLP 생산에 탁월한 것으로 알려진 배큘로바이러스 발현계(baculovirus expression system, BES)를 활용하여 구제역 바이러스 유사입자(FMD-VLP)를 효과적으로 생산하고자 하였다. 효율적인 구제역 바이러스 유사입자의 생산을 위하여 P1 구조 단백질의 발현량을 증대시키고, 구조 단백질을 절단하여 VLP 조립에 기여하는 3C protease의 발현량을 조절할 수 있는 최적의 프로모터 조합을 선정했다. 본 연구를 통해 최적화된 발현 전략은 FMD-VLP의 생산성을 향상시키는 효과적인 접근법을 제시하며, 향후 구제역 백신 개발 및 바이러스 유사입자 기반 백신 플랫폼 개선에 기여할 것으로 기대된다.

검색어: 구제역, 바이러스 유사입자, 배큘로바이러스 발현계

P54

Secretion efficiency of recombinant target proteins according to signal peptide in baculovirus expression system

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배큘로바이러스 발현계(baculovirus expression system, BES)는 높은 수준의 번역 후 수정 과정을 제공하여 다양한 유용 목적 단백질 생산에 활용된다. 신호 펩타이드를 목적 단백질에 적용하면 분비 경로를 통해 단백질의 올바른 접힘 및 당쇄화가 촉진되어 단백질 품질이 향상된다. 더불어, 배양액으로의 분비를 유도하여 단백질 수거 및 정제를 용이하게 할 수 있다. 그러나 BES에서 목적 단백질에 따른 신호 펩타이드의 최적화에 대한 연구는 아직 미흡한 실정이다. 이에 본 연구에서는 다양한 신호 펩타이드를 가진 다양한 종류의 목적 단백질을 발현할 수 있는 재조합 바이러스들을 제작하고 목적 단백질들의 발현 및 분비 효율을 평가하였다. 세포 추출물과 배양액에서 목적 단백질의 발현을 비교 분석하여 신호 펩타이드에 따른 분비 효율을 확인하고 BES에서 목적 단백질에 따른 최적 신호 펩타이드를 결정하였다. 본 연구 결과는 다양한 재조합 목적 단백질의 생산에 있어서 최적의 신호 펩타이드 선택을 위한 기초 자료로 활용될 수 있을 것이다.

검색어: 배큘로바이러스, 신호 펩타이드, 재조합 단백질, 세포 외 분비

P55

Evaluation of increased recombinant virus stability by novel bacmid in baculovirus expression system

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배큘로바이러스 발현계(baculovirus expression system, BES)는 높은 수준의 번역 후 변형과정을 제공하기 때문에, 외래 단백질 생산에 널리 이용되는 유용한 발현계이다. BES는 목적 유전자를 가진 재조합 바이러스를 제작하여 재조합 단백질을 생산한다. 이러한 재조합 바이러스 제작에 널리 이용되는 방법 중 하나인, 대장균에서 bacmid를 이용한 유전자의 전위(transposition)에 의한 재조합 바이러스 제작 방법은 매우 편리하다는 장점을 가진 반면, 목적 유전자의 낮은 안정성이 가장 큰 문제점으로 지적되고 있다. 본 연구에서는 bacmid에서 목적 유전자의 전위 위치를 변화시켜 그 안정성을 높인 새로운 재조합 bacmid를 제작하고 그 유용성을 평가하였다. 새로운 bacmid를 이용하여 다양한 종류의 목적 단백질을 발현하는 재조합 바이러스들을 제작하고 바이러스의 연속 계대 증식을 통해 목적 단백질의 생산 안정성 및 유전자의 안정성을 평가하였다. 본 연구 결과는 BES를 이용한 목적 단백질의 생산성 향상에 유용하게 활용될 수 있을 것이다.

검색어: 배큘로바이러스 발현계, bacmid, 재조합 단백질, 생산 안정성, 유전자 안정성

P56

Development of *in silico*-based diagnostic antibodies for Korean rhinoceros beetle nudivirus

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Nudiviruses have significantly impacted the entomological industry by causing substantial damage to *Trypoxylus dichotomus* populations over the past decade. This study aimed to develop antibodies for fundamental research in viral diagnostics. The ODV-E66 gene, encoding a viral envelope protein, was selected as the target for antibody production. Epitope prediction was performed using *in silico* analysis, considering conserved motif regions and peptide secondary structure. Physicochemical properties of the selected peptide were analyzed to validate its suitability as an immunogen. The study demonstrated that antibody production was achievable using nudivirus mimotopes. These findings provide novel insights into insect virus diagnostics and contribute to the broader understanding of peptide immunogens.

Key words: mimotope, nudivirus, ODV-E66, diagnosis, *Trypoxylus dichotomus*

P57

Development of an AI-based automated counting method with *Allonychiurus kimi* (Collembola)

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This study developed an AI-based method to automatically count adults and juveniles of *Allonychiurus kimi.* Using YOLOv8, a highly accurate model was developed to detect and count adults and juveniles (Precision=1.0, Recall=0.95 for adults; Precision=0.95, Recall=0.83 for juveniles). Statistical analysis showed no significant difference between manual and automated counts. Additionally, the system can automatically measure the body area of each individual, allowing for more detailed evaluations of growth and development. This method significantly improves the efficiency of large-scale toxicity evaluations while reducing researcher workload.

Key words: Soil invertebrate, Artificial intelligence,. Automatic counting, Collembola

P58

Development of assessment techniques to determine the level of *Nosema ceranae* infection in honeybees

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농작물의 수분 매개자이며 생태계 유지에 필수적인 역할을 하는 꿀벌의 노제마병(nosemosis)은 꿀벌 집단 붕괴현상(colony collapse disorder: CCD)의 원인 중 하나로 알려져 있다. 또한, 노제마병은 봉군 약화를 초래할 뿐 아니라 여러 가지 양봉 산물의 생산성을 낮추는 원인이기도 하다. 국내에서는 *Nosema ceranae*가 노제마병의 주요 병원체로 알려져 있다. 노제마 감염을 확인하기 위해서는 꿀벌의 중장을 적출한 후 노제마 포자의 확인 및 계수를 통해 감염 수준을 평가할 수 있다. 본 연구에서는 더욱 빠르고 정확하게 노제마 감염 수준을 평가할 수 있는 새로운 방법으로 포자 염색법과 qPCR 방법을 개발하였다. 노제마 포자에 대해 특이적인 염색이 가능한 Fluorescent Brightener를 이용하여 노제마 감염 꿀벌 중장을 염색한 결과, 형광 발현으로 노제마의 감염 여부를 확인할 수 있었다. 또한, 중장내 포자량에 비례한 형광 발현도 확인할 수 있었다. 그러나, 노제마 감염에 대한 특이도 및 포자량에 비례한 형광 발현 민감도는 신뢰하기 어려웠다. 그에 비해, 노제마 특이 유전자를 이용한 qPCR 방법은 노제마의 감염 여부 뿐만 아니라 포자량에 비례한 감염 수준 결정이 가능함을 확인하였다. 특히, 많은 시료들에서 노제마 감염 수준의 신속하고 정확한 평가에 qPCR 방법은 유용하게 활용될 수 있을 것으로 기대되었다.

검색어: 꿀벌, 노제마병, *Nosema ceranae*, 형광염색, quantitative PCR

P59

Analysis of genetic characteristics of the oriental fruit fly, *Bactrocera dorsalis*, in Southeastern Asia

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The oriental fruit fly, *Bactrocera dorsalis*, is a major agricultural pest that damages over 400 plant species, including crops and fruits. *B. dorsalis* is native to Southeast Asia, Taiwan, and has recently expanded its distribution to Japan and China. To investigate the origin and epidemiological route of *B. dorsalis*, mitochondrial cytochrome c oxidase subunit I (COI) sequences were employed in this study. The genetic characteristics of *B. dorsalis* were compared by assessing haplotypes and genetic variation among populations from Southeast Asia, including Thailand, Taiwan, Vietnam, and Cambodia. Additionally, mitochondrial COI sequences from surrounding countries of the Republic of Korea were obtained from previous studies and/or Genbank to further investigate genetic diversity. Based on the result of the study, *B. dorsalis* had considerable haplotype diversity among individuals and populations. The present study might enhance our understanding of the genetic diversity of *B. dorsalis* in neighboring countries and expand our knowledge about predicting the origin and invasive pathway for *B. dorsalis.*

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

P60

A report of Lepidopteran pest in plant quarantine inspect from Taiwanese pineapple

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Pineapple is one of the most valuable fruit crops produced in Taiwan. In the last few years, 420,000 tons of pineapples were produced annually. Of them, over 90% of crops exported to mainland China.

During the previous two decades, a total of 152 cases and 1,039 tons of fresh pineapples were imported into Korea. However, the import volume of fresh pineapples rapidly increased in 2024 with 43 cases and 435 tons. Meanwhile, APQA inspectors detected lepidopteran larvae from Taiwanese pineapple from June to July and identified them using morphological characters and mitochondrian genomic sequence analysis.

In the present study, we report the results of pineapple pest discovery, and their morphological and genomic data were provided.

Key words: COI, pineapple, lepidoptera, plant quarantine

P61

New *Dudusa* in the Oriental region with an annotated checklist (Lepidoptera, Notodontidae)

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The present paper describes a new *Dudusa* Walker, 1865 species, *Dudusa* **sp. nov.** with an annotated checklist and type localities of the genus. Also we discuss about true *D. nobilis* Walker and its distribution. Figures of adults and genitalia of the examined species are provided.

Key words: Noctuoidea, Dudusinae, *Dudusa* species-group, taxonomy, Oriental Region

P62

A new *Toerpenola* László, Ronkay & Witt, 2010 (Lepidoptera, Nolidae) from Laos with a checklist of known species

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A new *Toerpenola* László, Ronkay & Witt, 2010 species, *Toerpenola* **sp. nov.** is described with illustrations of both sexes. A checklist of them and some discussions are also presented.

Key words: Noctuoidea, Nolinae, Oriental regions, Indochina, misidentification

P63

New record of genus *Heterotoma* (Hemiptera: Miridae) from Korea, with discussion on its distribution and biology

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Orthotylinae is one of the mirid subfamilies, comprising approximately six tribes, 260 genera, and 2,100 species. Diverse orthotyline species display predatory feeding habits, with some acting as natural enemies of significant plant pests. Heterotoma species are zoophytophagous and recognized as natural enemies of various arthropod pests. For example, H. planicornis prey on various pests including mites, aphids, psyllids, gall midges, eggs and larvae of Chrysomelidae, and eggs of heteropteran and lepidopteran insects. Currently, four Heterotoma species are known, all originating from the Western Palearctic. In this paper, we present a new distribution record and observed biological data of Heterotoma from the Korean Peninsula with one species, H. planicornis. A morphological diagnosis accompanied by figures of dorsal habitus, male, and female genital structures is provided.

Key words: Orthotylinae, Heterotoma, New record, Invasive population, Biology

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P64

Two new records of Haltichellinae (Hymenoptera: Chalcididae) from Korea

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The subfamily Haltichellinae Ashmead, 1904 is the most diverse subfamily in Chalcididae (Hymenoptera: Chalcidoidea) with over 500 described species. Despite the diversity of this taxon, only three species in two genera have been recorded in Korea: *Antrocephalus sepyra* (Walker, 1846), *A. japonicus* (Masi, 1936) and *Uga menoni* Kerrich, 1960. In this study, specimens were collected sweeping various flowering plants and using Malaise traps and Lindgren funnel traps. We report new records of *Antrocephalus ishii* Habu, 1960 and *Haltichella nipponensis* Habu, 1960 from Korea. Among these species, genus *Haltichella* Spinola, 1811 reported in Korea for the first time. We provide photographs and detailed descriptions of both species, with additional morphological characters of both sexes of *Haltichella nipponensis*.

Key words: *Antrocephalus*, *Haltichella*, new record, South Korea, taxonomy

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P65

Taxonomic insights of *Schoutedenia ralumensis* (Hemiptera: Aphididae) from Cambodia: Redescription of poorly known morphology and DNA barcoding

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Schoutedenia ralumensis Rübsaamen, 1905, an aphid species within the subfamily Greenideinae (Hemiptera: Aphididae), is newly recorded from Cambodia on *Phyllanthus* sp. (Phyllanthaceae). The poorly known morphology of oviparous females is redescribed with live photographs, biometric measurements, and photomicrographic illustrations. Additionally, DNA barcoding based on mitochondrial cytochrome c oxidase (COI) sequences is conducted within the genus *Schoutedenia*, updating the Cambodian specimen in global datasets. These findings expand the known distribution of *Schoutedenia ralumensis* and contribute to a better understanding of Cambodian aphid diversity.

Key words: aphid, COI, Cambodia, *Phyllanthus*, *Schoutedenia ralumensis*.

P66

Species delimitation analysis of the genus *Grapholita* (Lepidoptera: Olethreutinae) from Korea, based on DNA barcoding analysis

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The genus *Grapholita* (Lepidoptera: Olethreutinae) has been known as a difficult group to distinguish due to their similar characteristics among the species. In this study, we conducted species delimitation analysis within Korean *Grapholita* using DNA barcoding. We analyzed 43 specimens of 8 species, with four species delimitation methods (ABGD, ASAP, GMYC, and bPTP) showing 87.5% agreement with morphological identification. During the present study, cryptic diversity was detected among the *G. dimorpha* species group, and described as new to science. All available information, including the images of adults and genitalia structures is provided.

Key words: Lepidoptera, *Grapholita*, species delimitation, new species, DNA barcode, Korea.

P67

A new species of *Nipponogarypus* (Pseudoscorpiones: Olpiidae) from South Korea

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In this study, we reported new species, *Nipponogarypus seosanensis* sp. nov., which are positioned in newly recorded family Olpiidae from South Korea. Detailed descriptions, habitus pictures, and illustrations of new species are provided. Also, type localities of all Nipponogarypus are mapped.

Key words: Olpiidae, East Asia, false scorpions, new species

P68

Unveiling hidden diversity: New records of *Chaitophorus* aphids in Korea from historical specimens

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The aphid genus *Chaitophorus* Koch, 1854 (Hemiptera: Aphididae: Chaitophorinae) has been reviewed in South Korea from historical specimens. A total of fourteen species of Korean *Chaitophorus* have been confirmed, including four new records: *C. horii* Takahashi, 1939; *C. leucomelas* Koch, 1854; *C. salijaponicus* Essig and Kuwana, 1918; and *C. tremulae* Koch, 1854. These four newly recorded species are described with biometric measurements and illustrations. Modified taxonomic key for Korean *Chaitophorus* spp. and remarks are presented.

Key words: aphids, Salicaceae, East Asia

P69

A morphological study on the larva of *Chrysochroa coreana* (Coleoptera: Buprestidae)

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전남 해남군 대흥사에서 비단벌레 유충을 채집하여 광학현미경(Zeiss Stemi2000-c)으로 관찰한 결과를 이미지와 함께 기재하였다. 유충은 종령의 경우 몸길이가 54.0~64.7mm, 가장 넓은 폭인 앞가슴에서 9.6~12.7mm로 나타났다. 몸은 얇고 길며 앞가슴이 가로로 둥글게 부풀어 있는 형태다. 몸은 전체적으로 유백색을 띠며, 경화되지 않은 부분은 백색, 경화된 부분은 적갈색에서 진한 적갈색, 가장 경화된 큰턱은 검정색을 띤다. 외피에는 산발적으로 긴 금색털들과 촘촘하게 짧고 뾰족한 털들이 나 있다. 머리는 작고, 대부분 경화되었으며, 앞가슴 안쪽으로 함입될 수 있다. 앞가슴등판과 배판에는 각각 뒤집어진 V자 모양과 세로선모양의 홈(groove)이 있고, 양쪽 판 모두 치모양의 경화된 돌기(sclerotized microteeth)들로 뒤덮여 있다. 두 번째부터 아홉 번째 배마디의 옆면마다 주름이 발달하였다. 기문은 가운데가슴 옆면과 첫 번째에서 여덟 번째 배마디 옆면에 각각 있고, 콩팥 모양이며, 약하게 경화되어 있고, 가슴기문이 배기문 보다 크고 길다. 본 연구를 통해 관찰된 형태학적 형질들 중 가슴등판과 배판, 배마디 옆면의 주름들은 뱀처럼 좌우로 텐션을 주어 이동하는 특성이 있는 비단벌레 유충의 보행에 쓰이는 것으로 보인다. 이러한 결과는 천연기념물이자 멸종위기 야생생물 I급인 비단벌레의 연구에 기초자료가 되며 향후 국내 자생하는 비단벌레와 근연종 유충의 형태학적 차이 규명에도 활용될 수 있을 것이다.

검색어: 비단벌레, 유충, 천연기념물, larval morphology, *Chrysochroa coreana*, jewel beetle

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P70

Nematicidal activity of entomopathogenic fungi extracts against *Bursaphelenchus xylophilus*

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Pine wilt disease (PWD), caused by the infection of the pinewood nematode (PWN), *Bursaphelenchus xylophilus*, results in significant environmental damage to pine forest ecosystems. This study evaluated the nematicidal activity of seven entomopathogenic fungi extracts to develop nematicide against PWN. Fungi were cultured and extracted, and their nematicidal activity was assessed in a 96-well plate at various concentrations. *Cordyceps pruinosa* extract showed the highest mortality rate of 84.7% at 5 mg/mL, with an LC_{50} value of 0.130 mg/mL. *Ophiocordyceps nutans* extract exhibited the mortality rate of 76.2% at the same concentration. The mortality by other five fungi extract was 42.8% – 62.0%. The high nematicidal activity of *Cordyceps* extracts suggests potential for developing biological nematicides, pending further identification of active compounds.

Key words: *Cordyceps*, *Bursaphelenchus xylophilus*, Pine Wood Disease, Fungal Extractsl

P71

Toxicity evaluation of two diamide insecticides on *Monochamus saltuarius* adults (Coleoptera: Cerambycidae)

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북방수염하늘소는 주로 잣나무에 소나무재선충을 매개하는 해충으로 중부지방의 잣나무림에서 큰 문제가 되고 있다. 그러나 북방수염하늘소 방제를 위해 기존에 등록된 약제는 꿀벌 독성문제로 인하여 사용이 중지되어 기존 약제를 대체할 약제가 필요한 실정이다. 그 중 디아마이드계 살충제는 나비목 곤충의 근육세포에 존재하는 라이아노딘 수용체를 표적으로 작용하여 근육세포 내 Ca^{2+}의 지속적인 방출을 통해 Ca^{2+}을 고갈되게 만들어 근육의 마비와 섭식 억제를 일으켜 치사시키는 작용기작을 가진 약제로 비교적 인축독성이 낮고 안전하다고 알려져 있다. 이번 연구는 2종의 디아마이드계 살충제를 이용하여 각 약제의 농도에 따른 북방수염하늘소 성충의 약제 감수성을 조사하였다. 2종의 디아마이드계 약제 모두 농도에 따른 살충효과의 차이는 크지 않았으며, 분무법을 이용한 충체분무 결과 2가지 약제 모두 모든 농도에서 7일차에 약 90%의 방제가를 보였고, 약제 간 살충효과는 비슷한 것으로 나타났다. ULV(초미립자살포기)를 이용하여 약제처리를 한 결과 2가지 약제 중 cyclaniliprole이 5일차에 100% 살충률을 보여 cyantraniiliprole에 비해 더 높은 살충효과를 보였다.

검색어: 북방수염하늘소, *Monochamus saltuarius*, diamide insecticides, cyclaniliprole, cyantraniiliprole, ULV

P72

Construction of mosquitocidal recombinant *Bacillus thuringiensis* strains

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Mosquitoes are major vectors of infectious diseases such as malaria, dengue fever, and Zika virus. However, excessive use of chemical insecticides has raised concerns about resistance development and environmental toxicity. As an environmentally friendly alternative, *Bacillus thuringiensis* (*Bt*) has been recognized as an effective biopesticide due to its highly specific insecticidal toxins. Several Bt toxins have been identified as highly effective against mosquitoes.

In this study, recombinant *Bt* strains were developed to express the binary toxins (BinA and BinB) from *B. sphaericu*s and the Cry11B toxin from *Bt jegathesan*, all of which are known for their mosquitocidal activity. The recombinant *Bt* strains exhibited strong insecticidal activity against mosquitoes, suggesting their potential for the development of more effective mosquito larvicides.

Key words: mosquito control, *Bacillus thuringiensis*, recombinant, insecticidal protein

P73

Nondetrimental impact of *Beauveria bassiana* ARP14 on *Aphidius colemani*

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Assessing the effect of *Beauveria bassiana* ARP14 on non-target beneficial species is essential for ensuring its compatibility with integrated pest management (IPM). In this study, we compared the virulence of a native entomopathogenic fungus *B. bassiana* ARP14 with a commercial strain (GHA) of the same species against *Aphidius colemani* adults. The leaf dipping method was used in the laboratory, with a concentration of 1×10^8 conidia/ml. The ST_{50} value of the ARP14 strain was not statistically different from that of the GHA strain or the control. Similarly, survival analysis showed that the mortality of fungal treatments was not different from that of control. However, mycosis rates reached 96% in *A. colemani* treated with the ARP14 strain and 100% with the GHA strain at 6 days after treatment. The reason for the high mycosis rates observed in *A. colemani* remains unknown. We conclude that *Beauveria bassiana* ARP14 is compatible with *A. colemani,* as it did not affect the mortality. However further investigation is needed to clarify the high mycosis rates observed.

Key words: entomopathogenic fungus, natural enemy, microbial control, mortality, mycosis rate.

P74

Virome analysis of *Varroa destructor* in South Korea

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꿀벌응애(*Varroa destructor)*는 꿀벌에 기생하는 외부 기생성 해충으로, 다양한 바이러스를 꿀벌에 매개하는 것으로 알려져 있다. 이러한 질병 매개체(Vector)를 통해 전파되는 바이러스 종류를 확인하는 것이 중요한 일임에도 불구하고, 국내 꿀벌응애에 대한 바이러스체(Virome) 조사가 부족한 실정이다. 본 연구는 차세대 염기서열 분석(High-throughput sequencing, HTS)을 이용하여 꿀벌응애 체내에 존재하는 바이러스의 군집(Viral community)을 분석하였다. 꿀벌응애는 국내 5개 지역의 양봉농가에서 채집되었으며, 채집된 개체마다 바이러스의 감염 여부와 바이러스의 구성에 차이가 있음을 확인하였다. 채집된 모든 개체에서 Deformed wing virus (DWV) 바이러스의 전사체가 확인되었으며, 이 밖에도 꿀벌에서 발견되는 Black queen cell virus (BQCV), Israeli acute paralysis virus (IAPV), Sacbrood virus (SBV), Chronic bee paralysis virus (CBPV) 등의 전사체는 개체별로 다른 감염 분포(Distribution)와 풍부도(Abundance)를 보였다. 본 연구는 꿀벌응애에서 발견되는 다양한 바이러스의 구성을 보여주며, 응애 매개 바이러스에 대한 기초 자료를 제공할 것으로 기대된다.

검색어: 꿀벌응애, 바이러스, 메타게놈 분석, 차세대염기서열 분석

P75

Assessment of ecological and environmental changes following the transition to eco-friendly apple and grape orchards

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This indicates that the transition to eco-friendly apple and grape farming is extremely challenging. This study aimed to provide necessary technologies to farmers seeking to transition to eco-friendly farming and objectively assess the resulting ecological and environmental changes from 2024 to 2026. The research was conducted to enhance the public benefits of eco-friendly and organic agriculture, such as environmental conservation effects and biodiversity. Following the “Agricultural Ecological Environment Survey and Evaluation Standards and Manual (Draft)” by the Ministry of Agriculture, Food, and Rural Affairs (2020), a second survey was conducted in 2024 on six taxonomic groups at one open-field apple farm and three grape farms (open-field and greenhouse). The survey results were quantified and analyzed. The comprehensive ecological and environmental assessment (graded A–E) indicated that all farms received a rating of C or higher. Additionally, the ecological environment was found to be superior in open-field cultivation compared to greenhouse cultivation.

Key words: Ecological environment, Eco-friendly transition, Apple, Grape

P76

Recent wild records of endangered bumblebee, *Bombus koreanus*

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참호박뒤영벌은 과거에는 전국적으로 널리 분포했으나 최근 발견 지역이 줄어들면서 멸종위기 야생생물 2급으로 지정된 종이다. 기존에 보고된 지점에서는 더 이상 확인되지 않고 있어 개체수 감소에 대한 우려가 커지고 있다. 우리는 2018년부터 2024년까지 다양한 충매현화식물에서 참호박뒤영벌을 발견했고, 이를 다음과 같이 보고하고자 한다.

경북 김천 수도산(2018), 경기 남한산성(2019), 강원 홍천 북방면(2021), 경기 포천 국립수목원(2022), 경기 군포 초막골생태공원(2024)에서 참호박뒤영벌을 확인할 수 있었다. 기존 문헌에서 참호박뒤영벌이 주로 방문한 충매현화식물은 참깨, 호박, 무궁화, 진달래, 철쭉, 황기였다. 우리는 현장 조사를 통해 한련화, 큰제비고깔, 황금, 털부처꽃, 개박하류, 참조팝나무, 프렌치라벤더, 배초향, 모라르다 등 참호박뒤영벌의 방화식물을 추가로 확인할 수 있었다. 이를 통해 참호박뒤영벌이 자생식물뿐만 아니라 정원용으로 식재한 외래종에도 방문함을 알 수 있었다. 시민과학을 통해 새롭게 알게 된 참호박뒤영벌의 방화식물 목록은 이 종의 보전에 중요한 기초자료가 될 것이다.

검색어: Citizen science, Endangered species, Foraging plants, Insect-pollinated plants, Long-tongued bumblebee, Pollinator

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P77

Sub-lethal effects of 2,4-Dichlorophenoxyacetic acid on nursing and foraging behaviors in honey bees

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2,4-D, a common herbicide, disrupts honey bee behavior. This study found LD50 values of 104.1, 456.6, and 221.6μg/bee for different bee stages. Sub-lethal exposure impaired nursing by reducing gland size and AmGr10 expression. Foragers showed decreased responsiveness, learning, and memory due to lowered AmGr1 and AmOA1 expression, threatening colony health.

Key words: 2,4-D, honey bee, nursing behavior, foraging behavior, hypopharyngeal gland, learning and memory

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Insect fauna of Jeoji Gotjawal in Jeju, Korea

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본 연구는 제주도 저지곶자왈 일대의 곤충 종 조성 현황을 파악하고, 제주 곶자왈 지역의 곤충상 기초데이터 수집을 위해 수행되었다. 4개 조사지(보전지, 복원지, 폐목장, 훼손지)에서 2024년 4월, 6월 및 8월에 각 1회씩, 총 3회에 걸쳐 조사하였다. 조사 방법으로는 솔껍질깍지벌레 페로몬 트랩을 설치하고 2주 간격으로 수거하였으며, 각 조사지에 2개의 버킷식 유아등 트랩을 설치하고, 다음 날에 수거하였다. 또한, 6월과 8월에는 털어잡기를 수행하였다. 채집된 곤충은 연구실에서 표본으로 제작한 후, 종 수준까지 분류 및 동정을 수행하였다. 조사결과, 솔껍질깍지벌레는 총 27마리가 채집되어 낮은 밀도를 보였으나, 훼손지에서 가장 높은 밀도를 나타냈다. 버킷식 유아등 트랩에서는 총 2목 43과 536종의 곤충류가 조사되었으며, 훼손지에서 8월에 다른 지역에 비해 종 풍부도가 가장 낮았고, 모든 조사시점에서 특정 종이 우점하는 경향이 확인되었다. 털어잡기에서는 6월에 16종, 8월에 9종의 식식성 곤충이 확인되었으며 훼손지에서 솔나방 유충의 밀도가 상대적으로 높게 확인되었다. 본 연구에서는 수종 다양성이 낮고, 소나무가 밀식된 훼손지에서 특정 곤충 종의 개체수가 높았으며, 이들이 해당 지역에서 잠재적으로 해충화될 가능성이 있는 것으로 확인되었다.

검색어: 제주도, 저지곶자왈, 곤충상, 훼손지, 생물다양성

P79

Analysis of arthropod diversity and ecological functions in organic floury rice fields

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The conservation of biodiversity in agricultural ecosystems is essential not only for crop productivity but also for enhancing ecosystem services. This study aims to evaluate the diversity of arthropods in organic floury rice fields under different cultivation environments and assess their impact on improving ecological functions. Arthropods were collected and species diversity was analyzed. Additionally, the effects of installing straw bundles and managing levee vegetation on enhancing ecological functions were examined. A total of 72 species were identified in the floury rice fields. The highest species richness was observed in paddies where both levee vegetation and straw bundles were present. The spider population was 3.3 times higher in vegetated levees than in mowed ones, and their abundance inside straw bundles was significantly higher in the paddy than on the levees. These results confirm that the cultivation environment of floury rice influences arthropod diversity. Furthermore, levee vegetation and straw bundles can serve as habitats for natural enemies, contributing to the enhancement of ecological functions.

Key words: arthropod diversity, ecological function, floury rice, organic farming, rice field

P80

Attractiveness of sex pheromones and analogues to tobacco cutworm (*Spodoptera litura*) moths in the field

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The tobacco cutworm moth (*Spodoptera litura*) is a globally distributed polyphagous pest, attacking a wide range of crops. Although it is polyphagous, it exhibits species-specific range of host preferences, and some components of the female sex pheromone are similar across different species within the same genus. In this study, we conducted field trapping tests to evaluate the behavioral responses of *S. litura* to a total of 17 compounds, including four female sex pheromone components and 13 structurally related analogues. Our results showed that some of the compounds either enhanced or inhibited the attractiveness of its female sex pheromone to conspecific males. These findings provide new insights into the chemical communication system of *S. litura* and may contribute to the development of eco-friendly behavioral control strategies using semiochemicals.

Key words: analogue, antagonist, attractant, field trapping, sex pheromone

P81

Characterization of selectively bred strains of *Protaetia brevitarsis seulensis*

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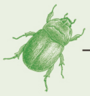
Protaetia brevitarsis seulensis, which is one of a mass-produced insect for industry, has been widely utilized as a functional insect due to its benefits in blood circulation improvement and inflammation reduction. To enhance the functional component of industrial insect and optimize the mass production, selective breeding is necessary. This study aims to analyze the morphology, growth characteristics, and nutritional composition of these selectively bred strains of *P. brevitarsis seulensis.* The morphological analysis reveals that the dorsal, ventral, and tarsus regions are consistently purple (J301) or green (J302) in the bred strains, whereas the wild-type has a mixture of purple and green with diverse coloration. The pupation period of J301 is the shortest one as 14.3 days, while J301 larvae contain the highest level of tyrosine. Based on these findings, a gene expression study will be conducted to investigate the mechanisms of the strains' color variations. Furthermore, color traits will be integrated with growth traits through selective breeding to establish that color is a phenotypic indicator for strain differentiation.

Key words: *Protaetia brevitarsis seulensis*, selective breeding, strain, color variation, nutritional composition

Poster Presentation



Non-Competition

P82

A newly recorded species of the genus *Taleporia* (Lepidoptera, Psychidae) from Korea

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Taleporia tubulosa Retzius, 1783 is reported for the first time from Jeju island, Korea. The genus *Taleporia* comprised 24 species in the world, and two species (*T. nigropterella, T. trichopterella*) have been reported in Korea. The morphology of adult males, including genitalia of *T. tubulosa* are presented. Additonally, DNA barcode for the species are provided.

Key words: Lepidoptera, Psychidae, *Taleporia*, newly record, DNA barcode

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P83

New records of three species of the family Coleophoridae Hübner (Lepidoptera: Gelechioidea) in Korea

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We report three coleophorids in Korea for the first time: *Coleophora helgada* (Anikin, 2005); *C. milvipennis* Zeller, 1839; and *C. obscuripalpella* Kanerva, 1941. As a result, these new records increase the total number of known coleophorid species in Korea from 43 to 46. The diagnostic characteristics of each species, along with photographs of the adults and genitalia, are provided.

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

P84

Genetic analysis of red imported fire ants (*Solenopsis invicta* Buren) collected in Vietnam and study of colony social structure

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2024년 베트남 북부지역에서 채집한 개미(300마리)의 DNA를 추출하여 *COI* 염기서열로 종 동정한 결과 *Solenopsis invicta*로 확인되었다. *COI* 바코드 서열뿐만 아니라 *COI* 후반부와 *COII* 전반부(tRNA Leu 포함)를 포함한 미토콘드리아 DNA (Mt DNA) 서열을 증폭하여 하플로타입을 분석한 결과, 확보한 붉은불개미 집단 내에서 H5 및 H22 하플로타입이 혼재되어 있었다. 추가적으로 군체 사회 구조 분석을 위해 *Gp-9* 유전자형을 분석하여 해당 집단이 다수여왕(polygyne) 형태의 군체 구조를 가지는 것을 확인하였다. 이는 붉은불개미의 확산 및 정착 전략과 관련하여 중요한 생태학적 정보를 제공한다. 현재, 개체군 유전자 구조를 보다 정밀하게 분석하기 위해 Microsatellite 마커를 활용한 연구를 진행 중이며, 보다 신뢰성 있는 데이터를 확보하기 위한 재실험을 수행하고 있다. 특히, 본 연구에서 확보한 베트남 붉은불개미 샘플은 기존에 유전적 분석이 진행된 한국, 중국, 대만, 미국 개체군 외 국가에서 최초로 확보된 샘플이라는 점에서 중요한 의의를 가진다. 이를 통해 향후 붉은불개미의 침입 경로 추적과 확산 양상 연구를 위한 유전적 레퍼런스를 확장하는 데 기여할 것으로 기대된다.

검색어: *Solenopsis invicta*, red imported fire ant, *COI* 염기서열, 하플로타입 분석, *Gp-9*, 다수여왕 군체, 베트남, 분자역학 조사

P85

Genetic analysis and distribution study of hunting billbug (*Sphenophorus venatus vestitus* Chittendon) in South Korea, *COI* sequencing and phylogeny

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잔디왕바구미(*Sphenophorus venatus* vestitus)는 북미 원산으로 멕시코, 중동, 일본, 중국 등에 분포하며, 국내·외 골프장에서 발견되는 등 골프장, 공원 등의 잔디류에 피해를 주는 심각한 해충이다. 2024년 12월 제주지역 골프장에서 발견된 유충의 종 동정 및 유전적 특성을 분석하고, 기존 보고된 개체들과의 유전적 유사성을 비교하여 침입 경로를 추정하기 위해 본 연구를 수행하였다. 발견 지역에서 채집된 5개체의 DNA를 추출하여 *COI* 유전자 영역을 증폭(LCO1490/HCO2198 프라이머)하였으며, NCBI BLAST 분석을 통해 *S. venatus*와 100%, *S. v. vestitus*와 99.09% 일치함을 확인하였다. 국내에서는 그동안 골프장에서만 발견되는 것으로 보아 골프 여행객의 소지품을 통한 편승 유입 가능성도 추정할 수 있다. 본 연구는 잔디왕바구미의 유전적 특성을 이용하여 침입 경로 추적 및 향후 방제전략 수립을 위한 분자 연구적 근거를 제공한다. 이를 바탕으로 지속적인 예찰과 효과적인 관리 전략 마련이 필요하며, 추가적인 유전자 마커 분석 및 샘플 확장을 통해 보다 정밀한 침입 경로 연구가 수행될 필요가 있다.

검색어: *Sphenophorus venatus vestitus*, Hunting Bilbug, *COI* 염기서열 분석, 계통 분석, 침입 해충, 잔디 해충, 한국

P86

A new record of the genus *Aleiodes* (Hymenoptera: Braconidae: Rogadinae) from South Korea

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The genus *Aleiodes* Wesmael is the most diverse genus within the subfamily Rogadinae (Hymenoptera: Braconidae), with a global distribution and 632 known species. All *Aleiodes* species are koinobiont endoparasitoids of various Lepidoptera and mummify their hosts. *Aleiodes euproctis* was first recorded in China in 1990, parasitizing *Euproctis bipunctapex*. In this study, *Aleiodes euproctis* is reported for the first time in Korea. We provide diagnosis, description, distribution, and illustrations.

Key words: Natural enemy, Rogadinae, Taxonomy, Unrecorded species

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P87

Two newly reported species of *Dasyhelea* (Diptera: Ceratopogonidae) from *Aristolochia contorta* Bunge in Korea

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A new record, *Dasyhelea bilineata* Goetghebuer, 1920 and a new species, *Dasyhelea aristolochiae* Bang **sp**. **nov**., were collected and firstly described from Korea, based on female adult specimens. Both species were collected from the glabrous, tube-shaped flowers of *Aristolochia contorta* Bunge during the summer season. DNA barcodes for two species have been added, and morphological-molecular identification confirmed that the collected samples showed a new record and new species. Further research is needed to examine the male adults, immature specimens, and life cycles to better understand the interaction between the specimens and host plants.

Key words: Biting-mdiges, Birthwort, Dasyhelea, DNA barcodes

P88

A new record of the genus *Mollitrichosiphum* Suenaga (Hemiptera: Aphididae: Greenideinae) from South Korea

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The genus *Mollitrichosiphum* Suenaga belongs to the subfamily Greenideinae, with 19 species have been recorded worldwide. Three genera have been recorded in the Greenideinae of South Korea: *Cervaphis*, *Eutrichosiphum*, *Greenidea*. We collected *Mollitrichosiphum* (*Metatrichosiphon*) *luchuanum* (Takahashi, 1930) on *Meliosma myriantha* in Jeju-do. This species has been recorded in Japan and China. In this study, we report this species for the first time in South Korea, and describe morphological features of apterous viviparous females.

Key words: Greenideini, *Mollitrichosiphum*, New record, *Meliosma myriantha*, South Korea

P89

Lepidoptera survey and collection in Cleopatra's needle critical habitat, Palawan, Philippines

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The Philippines, one of the world's 18 megadiverse countries, ranks fifth in floral diversity and harbors 5% of the world's plant species. It is also recognized as a biodiversity hotspot, with over 700 threatened species, making it a priority for global conservation efforts (CI, 2013; DENR, 2015). Despite its rich biodiversity, numerous species remain undescribed, and the extent of endemism is still insufficiently understood. Palawan, the focal area of this survey, is often referred to as the Philippines "last ecological frontier" due to its abundant natural resources and exceptional biodiversity.

This study presents a review of insect fauna documented during expeditions in the Philippines conducted from 2022 to 2024, with an emphasis on Lepidoptera. 200 species from 82 genera in 24 families were identified as Lepidoptera. However, additional taxonomic examination is necessary to confirm species identities.

Key words: Oriental region, tropical ecosystem, Lepidoptera, species diversity

P90

Taxonomic study of subfamilies Epipaschiinae and Pyralinae (Lepidoptera, Pyraloidea, Pyralidae) from Korea

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The subfamily Epipaschiinae is belonging to the family Pyralidae in the superfamily Pyraloidea. Moths of the epipaschiine are mostly medium-sized, and around 737 described species have been described in the worldwide, mostly distributed in the Tropical and Temperate Regions. Moths of the pyraline are also mostly medium-sized, more than 1,300 species have been recorded worldwide, especially common in Africa and Asia (Nuss *et al*., 2024).

In this study, a total of 24 species of 10 genera of the subfamily Epipaschiinae, and 34 species of 13 genera of the subfamily Pyralinae are reviewed from Korea. We reexamined checklist of Korea, based on external characters of the subfamilies Epipaschiinae and Pyralinae.

Key words: Lepidoptera, Pyralidae, new record, taxonomy, Palaearctic, Korea

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P91

Genus *Sacculocornutia* Roesler, 1971 (Lepidoptera: Pyralidae: Phycitinae) newly recorded from Korea, with descriptions of two species

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Sacculocornutia Roesler, 1971 is a genus in the subfamily Phycitinae, established by Roesler based on *Nephopteryx monotonella* Caradja, 1927. Four species belong to this genus and have been reported only in China. Here we report the genus *Sacculocornutia* Roesler, 1971 from Korea for the first time with two species: *Sacculocornutia sinicolella* (Caradja, 1926) and *Sacculocornutia zhengi* Du, Li & Wang, 2002. Diagnoses and photographs of adults and their genitalia are provided.

Key words: East Asia, Korea peninsula, snout moth, *Juglans mandshurica* Maxim.

P92

Taxonomy of the genus *Thrinax* (Hymenoptera: Tenthredinidae, Selandriinae) from South Korea

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Thrinax is a moderately medium-sized genus of Selandriinae, 27 described species worldwide and three species occur in South Korea (Taeger et al. 2010). *Thrinax* is similar to genus *Strongylogaster* but, it can be distinguished by the anal crossvein, occipital ridge, and the length of the antennal pedicel. This genus can be recognized as such by the occipital ridge present, antennal pedicel as long as wide, epicnemial furrow straight, mesoscutum lateral lobe without pits, and fore wing anal cell with almost perpendicular crossvein (Smith, 1969). In this study, we provide a diagnosis of four South Korean *Thrinax* included one newly recorded species and photographs.

Key words: *Thrinax angustatus, athyrii,, flexa, paucipunctatus*

P93

A new species of the genus *Deladenus* isolated from a dead red pine tree in the Republic of Korea

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The new species is characterized by its lateral fields with six to seven lines, pharyngeal corpus without a distinct median bulb and lacking a chamber, oesophageal-intestinal junction located immediately behind the nerve ring, hemizonid located posterior to nerve ring, excretory pore opening within the contour of hemizonid or just at the base of hemizonid, vulva with no lateral vulval flaps, post-uterine sac rudimentary or absent, vulva-anus distance ca equal to tail length, tail conoid, gradually tapering to a broadly rounded terminus, and slender spicules, 18.5-21.5μm long.

Key words: Molecular characterization, morphology, morphometrics, phylogeny, taxonomy

P94

The first report of *Greenidea* (*Trichosiphum*) *prunicola* Ghosh, Banerjee & Raychaudhuri, 1971 (Hemiptera: Aphididae: Greenideinae) in South Korea

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The Genus *Greenidea* Schouteden, 1905 consists of three subgenera worldwide: *Greenidea*, *Paragreenidea*, *Trichosiphum*. Only *Greenidea* (*Trichosiphum*) have been recorded in South Korea. We collected *Greenidea* (*Trichosiphum*) *prunicola* Ghosh, Banerjee & Raychaudhuri, 1971 on *Castanopsis sieboldii* in Tongyeong. In this study, we report this species for the first time in South Korea, and illustrations, description of apterous viviparous females, host plants and distributions are provided.

Key words: Greenideinae, *Greenidea*, New record, *Castanopsis sieboldii*, South Korea

P95

Investigation of the growth characteristics of *Metcalfa pruinosa* and *Neodryinus typhlocybae* in wild-simulated ginseng cultivation area

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산양삼 재배포지 주변과 기존에 발표된 문헌 등에서 보고된 기주에서 미국선녀벌레 발생 밀도를 조사하여 미국선녀벌레 기주식물 298종을 선발하였고, 피해지수를 선정하여 3점(심) 이상의 수종 중 재배포지에 인위적으로 식재가 가능한 초목과 관목 3종을 유인식물로 선발하였다. 선발한 유인식물에서 미국선녀벌레의 생육적합도와 천적인 선녀벌레집게벌의 생태 특성을 조사하였다. 선녀벌레집게벌과 미국선녀벌레 계절발생 동시성 평가를 통해 선녀벌레집게벌의 우리나라 기후조건에서의 적합성을 평가하고, 선녀벌레집게벌의 산양삼재배지에서의 정착율을 조사하였다. 산얌삼 재배포지 내에 분포하는 각 수종별 선녀벌레집게벌의 기생성공률과 잎면적당 기생 효율에 관하여 분석한 결과 잎 면적과 선녀벌레집게벌의 기생 효율과 상관관계를 확인하였다.

검색어: 산양삼, 미국선녀벌레, 선녀벌레집게벌, 기후적합도, 천적

P96

Spatiotemporal dynamics of trunk-injected pesticide residue and efficacy in *Pinus koraiensis*

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This study focused on the persistence, distribution, and efficacy of trunk-injected pesticides in *Pinus koraiensis* (Korean pine) to control pinewood nematodes (PWNs, *Bursaphelenchus xylophilus*), the causative agent of pine wilt disease (PWD). In this study, we compared pesticide residues in the needles and branches of Korean pine, revealing significant declines in pesticide residues over time in treatments. Notably, abamectin residues decreased from 0.2325 mg/kg to 0.0901 mg/kg in branches over 18 months. In contrast, emamectin benzoate showed a variation in residue decline depending on the formulation, with the residue level in branches decreasing from 0.1220 mg/kg to 0.0328 mg/kg over the same period. From the spatial perspective, the results revealed minimal differences in pesticide residue along the height of trees, although a decrease in upper canopy residue was observed in some cases. The nematicidal efficacy test demonstrated that none of the treated trees developed PWN symptoms. Overall, the findings suggest that the trunk-injected pesticides abamectin and emamectin benzoate can persist for two years, with the residue levels being sufficient to prevent PWN propagation, even when the levels are below critical inhibition concentrations.

Key words: Korean pine, Abamectin, emamectin benzoate, pine wood nematode, pine wilt disease, *Bursaphelenchus xylophilus*

P97

Occurrence patterns of major plant pests in the Korea National Arboretum - *Ligustrum obtusifolium* and *Hemerocallis* spp.

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국립수목원 내 해충 피해 정도가 큰 주요 식물 중 쥐똥나무와 원추리류의 문제 해충 파악을 위해 2024년 5월부터 10월까지 24회에 걸쳐 해충 발생 시기와 밀도를 조사하였다. 그 결과 쥐똥나무에서는 3목 8과 8종의 해충이 조사되었고, 별박이자나방에 의한 피해가 가장 심각한 것으로 확인되었다. 별박이자나방은 부화 직후인 8월 초에 밀도가 높았으며, 잎을 완전 섭식하여 수목의 가지만 잔존하게 하였다. 원추리 품종(아이스 카니발, 애기원추리, 젠틀 사라, 어섬 블로섬)에서는 6목 8과 8종의 해충 분류군이 확인되었고, 모든 집단에서 인도볼록진딧물과 잎응애류가 발견되었다. 관찰 결과 인도볼록진딧물은 토착 천적인 진디벌류와 혹파리류에 의해 밀도가 안정적으로 조절되었으나, 잎응애는 6월 중순 이후 밀도가 증가하여 일부 개체의 식물개화에 장애를 일으켰다. 전시원 내 해충 발생에 대한 선제적이고 효율적인 방제전략 수립을 위해 지속적인 해충 발생 양상 조사가 필요할 것으로 판단된다.

검색어: 국립수목원, 원추리류, 쥐똥나무, 해충, 별박이자나방, 잎응애류

P98

Effect of insecticides on lepidopteran larval parasitoids, *Exorista japonica* and *Meteorus pulchricornis*

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밤나방과 유충의 기생성 토착천적인 긴등기생파리와 예쁜가는배고치벌에 대한 살충제의 독성정도를 확인하였다. 콩에 등록된 작물보호제 16종을 작물체에 처리한 후 경과일에 따른 두 종 천적의 성충을 노출시키는 잔류독성 실내검정을 수행하였다. 긴등기생파리의 경우 acrinathrin 5.7% 액상수화제 처리 후 1일, 3일 경과한 작물체에 노출 시 40.0%의 사충율을 보였다. 하지만 살포 후 7일이 경과한 작물체에 노출시 사충율은 23.3%로 떨어졌다. Acrinathrin을 제외한 15종의 살충제의 경우, 처리 후 1일차 작물체에 긴등기생파리 성충을 노출시켰음에도 사충율은 25% 미만으로 확인되었다. 따라서 콩에 등록된 대부분의 살충제는 긴등기생파리에 부정적인 영향을 주지 않을 것으로 판단된다. 긴등기생파리에 독성을 보인 acrinathrin 5.7% 액상수화제는 예쁜가는배고치벌에 대해서도 처리 후 1일 경과된 작물체에 노출시 96.7%의 사충율을 보였다. flubendiamide 20% 액상수화제를 포함한 5종 살충제가 예쁜가는배고치벌에 대해 사충율 25~50% 미만의 보통독성을 나타냈다. Pyrifluquinazone 6.5% 액상수화제를 포함한 8종 살충제들은 예쁜가는배고치벌에 대해 모두 사충율 25% 미만의 저독성 약제로 확인되었다. 2022년부터 2024년까지 전남북 4개 시군의 콩 재배지에서 파밤나방과 담배거세미나방 유충을 채집하여 긴등기생파리와 예쁜가는배고치벌에 의한 자연기생율을 조사한 결과, 약 8.1~35.0%까지 확인되었다. 두 종 나방류 유충 토착천적의 국내 노지에서의 분포상황을 고려할 때 추후 방제를 위한 천적 현장 가능성은 충분하다고 판단되며, 농가에서의 살충제 사용시 이러한 천적을 보호·유지할 수 있도록 저독성 약제를 선택적으로 사용해야 할 것으로 판단된다.

검색어: 담배거세미나방, 기생성 천적, 저독성작물보호제

P99

HIPVs enhanced biological control potential of an aphid parasitoid, *Binodoxys communis* (Hymenoptera: Braconidae) in cucumber greenhouses

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고치벌과 곤충에 유인효과가 확인된 식물휘발성물질 9종을 대상으로 진딧물 기생성 토착천적인 쌍꼬리진디벌에 대한 유인효과를 조사했다. Dual choice cage test 및 비커트랩 실내검정을 통해, (z)-3-hexenyl acetate 처리구와 무처리구의 쌍꼬리진디벌 유인에 의한 오이 목화진딧물 기생율(머미 형성율) 및 쌍꼬리진디벌 성충 포획율 차이를 확인하였다. (z)-3-hexenyl acetate를 오이 비닐하우스 2개 동 각각 4개 지점에 처리 후(무처리 하우스는 용매만 처리) 하우스 중앙에 쌍꼬리진디벌 성충을 1쌍/3.3㎡ 방사하였다. 진디벌 방사 후 4주 동안 주 1회 오이 엽당 진딧물 및 머미수를 조사한 결과, 유인물질이 처리된 곳과 처리 인접지점에서의 쌍꼬리진디벌 유인에 의한 엽당 머미수가 상대적으로 높게 나타났다. 진딧물 방제효과는 천적 방사 후 21일차에 42.3%, 28일차에는 98.5%로 나타나며 유인물질 처리에 따른 쌍꼬리진디벌의 진딧물 방제 증대효과를 확인할 수 있었다.

검색어: 진딧물 기생성 천적, 목화진딧물, 천적유인물질

P100

Environmentally friendly control effect of thrips on the facility lettuce

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전북 익산시 시설상추 재배지에서 발생하는 총채벌레의 환경친화적 종합 방제기술을 개발하기 위해 검정방충망을 창가 출입구에 설치해 유입을 차단하고, 총채벌레 번데기는 백강균으로 방제 처리한 후 밀도가 높을 경우 마늘오일을 살포하여 방제하였으며, 청색끈끈이 트랩을 설치하여 유인 포획함과 동시에 포획밀도를 조사하였다. 방제효과는 관행(화학적방제구)와 무처리구를 대조구로 하여 포획밀도를 비교하였다. 상추 재배시기별 총채벌레 발생상황 조사결과, 봄재배(4.20.~6.20.) 무처리구에서는 5월 중순 발생을 시작하여 수확기인 6월 중순까지 5,820마리까지 포획밀도가 급증하였으나, 종합방제 처리구에서는 3,000마리 이하로 낮았다. 여름재배(7.10.~8.20.) 무처리구에서는 7월 하순부터 발생하여 수확기까지 밀도가 증가하였으나, 포획밀도는 500마리 이하였고, 종합방제 처리구에서는 200마리 이하였다. 가을재배(9.10.~11.10.)에서는 정식 직후 가장 높은 밀도를 보였고, 이후 감소하는 경향으로 수확기(10월 하순) 포획밀도는 10마리 이하로 큰 피해는 없었지만, 무처리구에 비해 정식 직후부터 포획밀도가 현저하게 낮은 것을 확인하였다. 이러한 환경친화적 총채벌레 방제체계는 총채벌레뿐만 아니라 토마토반점위조바이러스(TSWV) 피해도 크게 줄여준다는 것을 확인하였고, 화학적방제와 유사한 방제효과를 얻을 수 있었다.

검색어: 총채벌레, 시설상추, 발생밀도, 방제효과

P101

Exploration of insect pests and natural enemies resources on *Eleutherococcus senticosus* and *Eleutherococcus sessiliflorus* (Araliaceae)

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Medicinal herbs are valuable crops widely used in herbal medicine for disease treatment. While extensive research has been conducted in pharmacology, toxicology, and pharmaceutical sciences, studies on pests affecting medicinal plants remain limited compared to those on cultivated crops. This study examines insect pests and natural enemy resources associated with *Eleutherococcus senticosus* (Rupr. & Maxim.) Maxim. in Taean and *E. sessiliflorus* (Rupr. & Maxim.) S.Y.Hu (Araliaceae) in Asan. Our findings identified 39 insect pest species and 15 natural enemy species from *E. senticosus*, and 32 insect pest species and 14 natural enemy species from *E. sessiliflorus*. These results contribute to the development of effective pest management strategies, supporting the stable production and supply of medicinal herbs.

Key words: medicinal herb, insect pest, natural enemy, *Eleutherococcus senticosus*, *Eleutherococcus sessiliflorus*, Korea

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P102

The developmental processes of *Dolycoris baccarum* L. (Heteroptera: Pentatomidae) on sesame (*Sesamum indicum*) under different temperature regimes

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The *Dolycoris baccarum* L. (Heteroptera: Pentatomidae) is a highly destructive insect pest, damaging a wide range of field crops in Korea, particularly sesame (*Sesamum indicum*). To better understand its population dynamics and support pest management strategies, we developed a predictive model based on its developmental characteristics. Temperatures (15.3, 20.8, 25.0, 27.0, 30.1, 35.0, and 40.0°C) induced developmental parameters, mortality, and longevity of *D. baccarum* examined on the sesame seed pod in this study. The total duration for egg development varied from 30.56 days at 15.3°C to 2.07 days at 40°C, whereas the nymphs' developmental period ranged from 64.75 days at 20.8°C to 21.17 days at 35.0°C. The LDT and K for the overall development completion were 14.22°C and 492.22-day (DD), respectively, on the sesame seed pods. The data generated from this study can help forecast spring emergence, number of generations, and population trends of *D. baccarum*, which further facilitates the development of IPM measures against pentatomid bugs.

Key words: Sloe bug, models, spring emergence, forecasting, generations, management

P103

Electrophysiological responses of antennal sensilla in *Monochamus saltuarius* Gebler to pheromone, bark beetle pheromone, and host volatiles

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Electroantennogram (EAG) and single sensillum recordings (SSR) were conducted on *Monochamus saltuarius* Gebler (Coleoptera: Cerambycidae) using 22 semiochemicals, including aggregation-sex pheromones, bark beetle pheromones, and host volatiles. The majority of host volatiles such as α-pinene, 3-carene, and camphor, elicited stronger EAG responses than monochamol, their aggregation-sex pheromone. Within the two types of olfactory sensilla - thin (SBaA) and thick (SBaB) sensilla basiconica - 10 subtypes of olfactory sensory neurons were identified and clustered based on their functional responses to specific volatiles. These findings contribute to deeper understanding of the chemical ecology of *M. saltuarius* and provide insights for suggesting potential attractant candidates.

Key words: *Monochamus saltuarius*, electroantennogram, single sensillum recording, antennae, sensilla, olfactory sensory neuron

P104

Occurrence and susceptibility to insecticides of *Spodoptera frugiperda* on corn in Chungbuk Province

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충북지역 내 열대거세미나방의 발생생태를 비교하기 위하여 충청북도 북부, 중부, 남부 지역인 단양, 괴산, 영동에 페로몬트랩을 설치하여 발생밀도를 조사하였다. 페로몬 트랩은 옥수수가 재배중인 5월 상순부터 10월 중순까지 설치되었다. 3개 지역 모두 열대거세미나방은 9월상순부터 발생하기 시작하였으며, 괴산과 영동은 10월 중순까지 밀도가 증가하는 추세를 보였다. 하지만 단양은 10월 상순에 가장 많은 개체가 유인되었으며, 10월 중순에는 유인된 개체가 감소한 경향을 보였다. 또한 비래해충인 열대거세미나방을 효율적으로 방제하기 위하여 화학약제에 대한 살충률을 비교하였다. 살충효과는 추천농도 및 접촉법으로 검정되었으며, 화학약제 중 사이안트라닐리프롤, 인독사카브, 스피네토람, 플루벤디아마이드 등 4종 약제에서 처리 후 24시간에 100%의 살충률을 보였다.

검색어: 열대거세미나방, 발생밀도, 약제선발

P105

Accessing the efficacy of alternative insecticides against pyrethroid-resistant mosquitoes in South Korea

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Anopheles sinensis and *Culex pipiens* complex have developed resistance to pyrethroids due to their continuous use in Korea. We evaluated alternative insecticides with different modes of action, including acetamiprid, chlorfenapyr, and spinosad, against field-collected *An. sinensis* (44.5-fold resistant to λ-cyhalothrin) and *Cx. pipiens* complex (14.6-fold resistant to permethrin). Spinosad exhibited greater larvicidal efficacy against both λ-cyhalothrin-resistant *An. sinensis* and permethrin-resistant *Cx. pipiens* complex. In addition, adult mosquitoes showed >90% mortality when exposed to 20 μg per bottle of chlorfenapyr, regardless of their pyrethroid resistance level. These results suggest that spinosad is an effective larvicide, while chlorfenapyr is a promising adulticide for managing pyrethroid-resistant mosquito populations.

Key words: *Anopheles sinensis*, *Culex pipiens* complex, insecticide resistance, pyrethroid

P106

Evaluation of feeding deterrence and electrophysiological response induced by three chitin synthesis inhibitors on western drywood termite *Incisitermes minor*

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The western drywood termite, *Incisitermes minor* (Isoptera: Kalotermitidae), is a native pest in southwestern USA and northwestern Mexico. The *I. minor* is one of the most destructive termites, causing serious structural damage and an estimated economic impact of 250 million USD. The *I. minor* has spread across the USA, Canada, Australia, China, and Japan as an invasive pest, and its invasion was first detected in South Korea in 2023. The *I. minor* is primarily controlled through fumigation or removal of infected wood, but the baiting system has also been investigated as an alternative approach. In this study, we evaluated the feeding deterrence and electrophysiological response of three chitin synthesis inhibitors (CSIs) on *I. minor*. We conducted two-choice tests and electroantennography (EAG) on *I. minor* with three CSIs (*A*, *B*, and *C*) at 1500 ppm, 2500 ppm, and 5000 ppm. In the two-choice test, no deterrence was observed at any CSI concentration. Similarly, in the electrophysiological tests, no significant response was detected at any CSI concentration. The results of this study may contribute to improving baiting systems for the management of *I. minor*.

Key words: western drywood termite, chitin synthesis inhibitors, behavioral tests, electroantennography

P107

Managing soil dwelling pupae and overwintering stages of *Frankliniella occidentalis* using soil fumigants and soil granular insecticides

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고추에 발생하는 총채벌레는 섭식 또는 산란에 의해 고추에 직접적인 피해를 주며, TSWV(칼라병)을 매개하여 2차 피해를 준다. 비가림하우스의 경우 꽃노랑총채벌레가 우점하여 발생하며, 겨울철 내부에서 월동을 하며 이듬해 3월부터 발생 증가하는 것으로 조사되었다. 비가림하우스 내부에서 월동하는 꽃노랑총채벌레의 방제가능성을 검토하기 위하여 고추에 등록된 토양소독제 3종(Dimethyl disulfide, Metam sodium, Dazomet)을 훈증소독한 결과, 3약제 모두 자연발생개체, 접종한 사육개체에 대하여 100%의 치사율을 나타내었다. 고추에 등록된 토양살충제 4종(Bifenthrin GR, Cadusafos GR, Diazinon GR, Terbufos GR)의 총채벌레 번데기 적용가능성 검토 결과, 실내 접종 5일 후 각각 21.7%, 99.3%, 95.8%, 100%의 사충률을 나타으며, 포장 검토에어는 정식 21일 후 23.9%, 36.4%, 63.1%, 53.0%, 정식 35일 후 15.3%, 14.3%, 63.1%, 60.0%의 방제효과를 나타내었다.

검색어: 고추, 총채벌레, 방제, 토양소독제, 토양살충제

P108

Study of developing markers for tracing the origin of vector mosquito of foreign infection disease

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To facilitate the early detection and effective prevention of foreign infectious disease vector mosquitoes, this study analyzed the genetic characteristics of *Aedes albopictus* populations in South Korea and developed genetic markers for origin tracing. 459 mosquito specimens were collected from 16 regions in South Korea and three regions in Vietnam. Population genetic analyses were conducted using COI gene and microsatellite (MS) markers. COI haplotype analysis identified 30 haplotypes, with minimal genetic differentiation (2.66%) between the South Korean and Vietnamese populations. MS marker-based analysis revealed extensive gene flow among domestic populations, although some regions exhibited relatively isolated genetic structures. Bayesian analysis indicated a high genetic similarity between the Vietnamese population and the capital region 1 population, suggesting a potential foreign introduction. Comparisons with previous international studies suggest that the *Aedes albopictus* populations in South Korea were not the result of a single introduction but rather multiple independent introductions, followed by widespread dissemination within the country.

Key words: Infectious disease, origin tracing, introduction pathway, population genetics

P109

Host-dependent emergence and morphological variations in *Zeugodacus tau* Walker (Diptera: Tephritidae)

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The pumpkin fruit fly, *Zeugodacus tau*, is a polyphagous pest infesting diverse fruits and vegetables. This study evaluated the adult emergence patterns and morphological varations of *Z. tau* across 12 fruits and 9 vegetables. Adult emergence periods varied significantly among hosts, with morphological measurements indicating host-specific variations in body size and proportions. The findings highlight the host-dependent adaptability of *Z. tau*, offering insights for developing targeted pest management strategies.

Key words: *Zeugodacus tau,* emergence patterns, host crops, morphology

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P110

Phenology of three important rice field spiders in Korea

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Spiders play an important role as a predator group in regulating insect pests in the agricultural ecosystem. From 2021 to 2023, the phenology of three important sice gield spiders, *Ummeliata insecticeps* (Linyphiidae), *Pachygnatha clercki* (Tetragnathidae), and *Pirata subpiraticus* (Lycosidae), which are known as important natural enemies of major rice pests such as planthoppers and leafhoppers, was intensively monitored. The study was conducted in five regions of Korea with different average temperatures, where rice was cultivated conventionally in collective farming systems: Anseong-si (Gyeonggi-do), Nonsan-si (Chungchenongnam-do), Imsil-gun and Namwon-si (Jeonbuk State), and Gurye-gun (Jeollanam-do). Monitoring was conducted at 10-day intervals from the early transplanting stage to just before harvest to analyze abundance, age structure, activity range, occurrence date, and occurrence duration.

Key words: natural enemy, phenology, rice field, spiders, Korea

P111

Comparison of insect community characteristics in organic and conventional paddy fields in Gangwon Province

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Understanding differences in insect communities according to agricultural practices is crucial for evaluating their ecological impact. This study compares insect communities in organic and conventional paddy fields by analyzing species diversity, abundance, and community composition. The results showed that organic fields support a higher species diversity than conventional fields, but there was no significant difference in abundance between the two systems. These findings suggest that organic farming may contribute to biodiversity conservation in rice agroecosystems.

Key words: diversity, abundance, Shannon, benthic, flooding period

P112

Assessment of suitable host plants for mass rearing *Phanuromyia ricaniae* (Hymenoptera: Scelionidae), an parasitoid of *Ricania* spp.

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Phanuromyia ricaniae, an egg parasitoid of *Ricania* spp., is a native natural enemy discovered in Gurye, South Korea, in 2015. To support its mass rearing, we investigated the oviposition host plants of *Ricania* spp. in various orchards and collected egg masses to evaluate the parasitism rate of *P. ricaniae* among different plant species. A survey of 27 host plants showed that cherry, Asian hazel, plum, kousa dogwood, and peach had the highest densities of *Ricania* spp. egg masses. The parasitism and emergence rates of *P. ricaniae* were highest on royal azalea, hydrangea, blueberry, and Asian hazel, with parasitism rates exceeding 10% and emergence rates over 80%. These results suggest that royal azalea, hydrangea, and blueberry are suitable for mass-rearing *P. ricaniae* for field releases. Future studies will verify its parasitism rate on these plants under controlled conditions.

Key words: *Ricania* spp., *Phanuromyia ricaniae*, Egg mass, Parasitism

P113

Seasonal occurrence of oriental tobacco budworm (Lepidoptera: Noctuidae) at red pepper field in Jeonbuk state

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고추의 주요 해충인 담배나방의 방제를 위하여 연중 발생 세대수 변화와 피해정도를 조사하였다. 전북 익산지역의 고추포장에서 페로몬트랩을 이용하여 성충의 발생소장을 조사한 결과 전체 발생기간은 5월 상순부터 11월 중순까지였으며, 8월부터 발생량이 증가하여 9월 중 채집량이 가장 많았다. 발생최성기는 6월 하순, 7월 하순, 8월 중순, 9월 중순이었다. 발생소장 자료와 유효적산온도를 토대로 연중 발생세대수를 추정한 결과 월동세대는 5월 하순~7월 상순, 1세대는 7월 중순~8월 상순, 2세대는 8월 중순~9월 상순이었으며, 9월 중순이후에 유인되는 것은 3세대로 판단되었다. 최근 여름철 온도가 높아짐에 따라 과거에 비해 한 세대가 더 경과할 수 있는 것으로 분석되었다. 담배나방 피해는 8월 중순부터 많아져 2세대 유충에 의해 발생한 것으로 생각된다.

검색어: 담배나방, 고추, 페로몬트랩, 발생소장

P114

Occurrence and distribution of plant-parasitic nematodes in Jeonbuk state

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전북 지역에서 재배하는 작물에 발생하는 식물기생선충의 감염현황을 조사하기 위해 고추, 국화, 무, 생강 재배지에서 토양과 뿌리 등의 시료를 채취하여 선충을 분리하고 동정하였다. 전체 86점의 시료 중 27점(31.3%)에서 식물기생선충이 발견되었는데 확인된 선충은 궁침선충(*Trichodorus*) 등 9종이었으며 이 중 궁침선충과 뿌리혹선충(*Meloidogyne*)이 많이 검출되었다. 고추에서는 궁침선충, 국화에서는 침선충(*Paratylenchus*), 무에서는 곤봉선충(*Psilenchus*), 생강에서는 뿌리혹선충이 많이 검출되었으나 일부 포장을 제외하고 발생밀도는 높지않았다. 식물기생선충이 가장 많이 검출된 작물은 생강으로 뿌리혹선충 등 7종을 확인하였으며 총 34점의 시료 중 13점(38.2%)에서 발견되었다. 그 이유로는 생강의 재배기간이 길고 연작함에 따라 선충의 검출률과 밀도가 증가한 것으로 생각된다.

검색어: 식물기생선충, 감염현황, 검출률

P115

Field empirical study of the effects of alternative feed on mealworms, *Tenebrio molitor* (Coleoptera: Tenebrionidae)

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갈색거저리 유충의 먹이원인 밀기울 가격 상승으로 생산비 증가와 식용곤충 판매가격 하락에 따라 사료비 절감과 유충 품질 향상을 위하여 대체 먹이원 개발이 요구되고 있다. 다양한 농업부산물을 이용한 대체 먹이원 실험 결과를 토대로, 2 종류의 대체사료를 선발하였고 밀기울과 대체사료의 배합비율을 70:30으로 설정하였다. 본 연구는 갈색거저리 사육농가를 대상으로 선발된 대체사료의 급이 효과를 검증하였다. 밀기울만 급이한 대조구와 밀기울+유채유박(70:30) 처리구에서 유충무게는 차이가 없음을 확인하였다. 급이 처리 10주 후 유충을 수확하여 건조 전과 후의 무게를 비교해보니 밀기울+유채유박(70:30) 처리에서 건조수율이 약 11% 높게 나타났다. 갈색거저리 유충의 조단백질과 조지방 함량은 밀기울+유채유박(70:30) 급이처리에서 대조구보다 약 8.8%, 4.6% 증가하였다. 이를 통해 유채유박이 사육 원가를 절감하여 유충을 생산할 수 있는 대체사료 소재로 활용할 수 있을 것으로 판단된다.

검색어: 갈색거저리, 대체사료, 생육특성, 현장실증

P116

Production and immunogenicity of human papillomavirus virus like particles by baculovirus hyper expression system

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The baculovirus insect cell expression vector system has been effective and widely used method for the recombinant protein expression. Human papillomavirus (HPV) is a significant causative agent of cervical cancer, necessitating effective vaccine antigens. In this study analysis the production and characterization of HPV virus-like particles (VLPs) as vaccine antigens. using baculovirus hyper expression system. Furthermore, we applied baculovirus hyper expression system to produce HPV L1 protein and assessed its actual yield and immunogenicity. This research conducted an evaluation of the expression levels, purification efficiency and VLPs formation capability of the produced L1 protein. Additionally, the study aimed to demonstrate the potential industrial applicability of baculovirus hyper expression system. These assessments were conducted to provide comprehensive data supporting the potential of baculovirus hyper expression system for large scale production of biopharmaceuticals, particularly in the context of vaccine manufacturing.

Key words: Baculovirus, Human papillomavirus, Cervical cancer, VLPs, immunogenicity, vaccine

P117

Artificial diets for *Locusta migratoria* as a sustainable alternative to host plants

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This study examined the growth and developmental responses of *Locusta migratoria* nymphs to different artificial diet formulations and explored efficient feeding strategies to optimize their performance. The diet formulated with wheat bran and fish meal (WF) was more suitable for *L. migratoria* than the other diets, supporting improved growth and survival. Contrastingly, casein- and sucrose-containing diets (WCS) demonstrated higher cannibalism rates and lower survival. Further fish meal ratio optimization in WF diets demonstrated that wheat bran + fish meal 8% (WF8) provided the most suitable growth and survival balance. WF8 exhibited slightly lower feed efficiency and weight gain than the natural host plants, wheat and corn; however, the developmental period was comparable. This indicated WF8's potential as a promising alternative diet. Particularly, transitioning to artificial diets from the fourth instar after feeding natural host plants until the third instar led to substantially higher survival rates and adult body weight than continuous feeding on a single diet. These results establish WF8 as a promising artificial diet for *L. migratoria* and provide valuable insights into sustainable and efficient feeding strategies for large-scale insect farming. This study supports the development of sustainable insect production systems and promotes the advancement of the edible insect industry as an alternative protein source.

Key words: Artificial diet, Development characteristics, Food efficiency, *Locusta migratoria*

P118

Evaluation of insect lipid-based renewable diesel production via hydroprocessing

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앞선 연구에서 곤충지질을 활용한 탄소중립형 물질로 전환하기 위한 연구를 진행하였으며, 그 결과로 FAME계 바이오디젤의 전환 및 스케일-업에 대한 가능성을 평가하였다. FAME계 바이오디젤은 연료분자에 포함된 산소와 같은 화학물질로 인하여 기존연료대비 낮은 적용성을 보이며, 대량 혼합에 한계를 가지고 있다. 이를 극복하기 위한 수첨촉매공정 기반 지속가능 바이오디젤(Renewable Diesel, RD)에 대한 연구가 진행되고 있다. 본 연구에서는 동애등에 지질을 기반으로 RD 전환가능성을 평가하고자 한다. 이를 위하여 수첨촉매공정을 통하여 RD성분이 포함된 탄화수소 화합물을 제조하고, EN15940에서 제시하는 인화점 세탄가 70 이상, 밀도 765 ~ 800kg/L등의 규격에 적합여부를 조사하였으며, 만족함을 확인하였다.

검색어: 동애등에, 곤충지질, 탄소중립, RD, 디젤

P119

Developmental and genetic diversity of *Trypoxylus dichotomus* (Linnaeus, 1771) populations in South Korea (Coleoptera: Scarabaeidae)

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In this study, we collected eight *Trypoxylus dichotomus* (Linnaeus) populations from commercial insect farms in different regions of South Korea and investigated their developmental characteristics and genetic diversity. Significant differences in larval weight were observed among the populations at all measured time points, but these differences decreased after 11 weeks post-hatching. In adults, all measured developmental traits showed statistically significant differences between populations. Although fecundity varied greatly among populations, no statistically significant differences were detected between them. Mitochondrial COI barcode analysis, including publicly available data from other countries, identified a total of eleven haplotypes. Among these, eight haplotypes were present in South Korean populations, showing no clear regional structuring. The average genetic diversity in South Korean *T. dichotomus* was estimated at 0.19±0.16%, indicating relatively low intraspecific genetic diversity. However, the presence of multiple haplotypes and the lack of population structure suggest gene flow among populations, likely facilitated by human-mediated breeding and trade.

Key words: COI haplotype, developmental characteristics, genetic diversity, *Trypoxylus dichotomus*

P120

Investigation of symptoms of Deformed Wing Virus (DWV) in domestic *Bombus terrestris*

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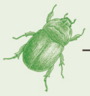
Between 2023 and 2024, an investigation was conducted in domestic bumblebee rearing facilities to examine the clinical symptoms associated with DWV infection. DWV was detected across all castes—including workers, drones, and queens. In colonies where fewer than 50 workers were present, the detection of DWV-infected individuals was typically associated with the failure to develop a colony with 50 or more workers. Similarly, in reproductive colonies, the presence of DWV-positive individuals corresponded with inadequate colony formation. The characteristic symptoms observed were as follows: **Wing Deformities:** Infected bees exhibited complete wing loss, unilateral wing presence with the opposite wing nearly absent, and various degrees of wing deformation. **Leg Abnormalities and Dorsal Indentations:** Some individuals showed shortened legs, resembling either metathoracic legs or mesothoracic legs, accompanied by indentations on the dorsal side. **Flight Impairment:** All DWV-affected individuals were unable to fly. **Queen-Specific Symptoms:** A subset of queens demonstrated a lack of oviposition, and dissections revealed the presence of abnormal tissue or parasitic signs around the ovaries. These findings suggest that DWV infection can significantly impair colony formation and reproductive functions in bumblebees. Further research into the infection routes, inter-individual transmission, rearing environments, and nutritional sources is essential. In addition, breeding programs aimed at developing DWV-resistant bumblebee strains should be prioritized to support sustainable bumblebee management and production.

Key words: *Bombus terrestris*, deformed wing virus, Symptoms

Small Group Meeting



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Korean Society of Applied Entomology

SG1-1

Population dynamics of *Ramulus mikado* caught between winter temperature and entomopathogenic fungi

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Since 2020, *Ramulus mikado* has been occurred in some hillocks in central Korea. Although most population of the insect are showed rapidly decline in their abundance, while some of them are still maintained high population density resulting in seriously defoliation. In recent, stick insect-specific entomopathogenic fungi, *Metharizium phasmatodeae* was newly reported in Korea, which fungi was considered as one of major control agents to *R. mikado*. However, temperature is the other important agent because every insect species are ectotherms. This study was conducted to examine which biotic and abiotic factors are influence on the population dynamics of *R. mikado* from 2020 to 2024.

Key words: stick insect, forest insect pest, outbreak, pest management

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SG1-2

Distributional changes of *Matsucoccus masumurae* (Hemiptera: Matsucoccidae) and population occurrence patterns in Gangwon-do, Republic of Korea

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솔껍질깍지벌레(*Matsucoccus masumurae*)는 국내에서 1963년에 최초 발생한 것으로 추정되며, 소나무와 곰솔을 가해하는 대표적인 흡즙성 산림 해충이다. 처음 피해가 발생한 지역은 전라남도 고흥, 목포, 무안 등으로 주로 해안 지역에만 분포하는 것으로 보고되었으나, 현재는 제주도를 포함하여 전국적인 분포가 확인되었다. 본 연구에서는 강원 지역에서 솔껍질깍지벌레의 발생 밀도 및 발생 패턴을 규명하기 위해 2022년부터 2024년까지 수행되었으며, 2022년에는 18개, 2023년에는 8개, 2024년에는 4개의 시·군에서 수행되었다. 각 조사 지역에 황색 점착 트랩 3개를 설치하고 성페로몬을 이용하여 1-2주 간격으로 포획되는 수컷 성충 개체수를 확인하였다. 조사 결과, 수컷 성충의 우화는 3월 하순~5월 초순에 시작되었으며, 우화 최성기는 5월 하순~6월 초순으로 나타났다. 조사 기간 중 가장 많은 개체가 포획된 지역은 2023년 양 구(9,695개체)였으며, 가장 적은 개체가 포획된 지역은 2022년 양양(502개체)이었다. 또한 2023년 수컷 성충 밀도 자료를 이용하여 발생 시기 예측 모형을 개발하고 2024년 자료로 검증한 결과, 예측 오차는 ±7일로 나타났다. 한편 솔껍질깍지벌레가 1년 1세대로 알려진 것과 달리, 조사 결과 봄 개체군의 활동 종료 이후 8월부터 11월까지 활동하는 수컷 성충 개체군이 확인되었다.

검색어: 솔껍질깍지벌레, 강원지역, 분포, 발생시기예측, 발생패턴

SG1-3

Development of a deep learning model for measuring the damage of Pine Needle Gall Midge (*Thecodiplosis japonensis*) using smartphone and drone images

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Pine Needle Gall Midge (PNGM, *Thecodiplosis japonensis*), a major pest damaging pine trees, has spread across Korea since its initial detection in 1929. Current assessment method for damage of PNGM rely on manual inspection, which is labor-intensive and inefficient for large areas. This study developed a deep learning model using smartphone and drone images to measure damage more efficiently. As a result, the feasibility of measuring the damage was confirmed using deep learning-based image analysis techniques with smartphone and drone images. The proposed method provides a standardized and efficient approach to managing forest health.

Key words: deep learning model, drone, pine needle gall midge, *Thecodiplosis japonensis*, smartphone

SG1-4

Current status of the occurrence of Korean pine pests in the Gyeonggi region

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경기도 지역의 잣나무림 면적은 40,406ha로 경기도 전체 산림의 7.9%를 차지하고 있다. 경기도 북부 지역에서는 산림의 대표적인 임산물인 잣을 생산하고 있어 산림에서 매우 중요한 수종이다. 최근 경기도 지역의 잣 생산량은 2016년 4,268ton 290억 원을 기점으로 2023년에는 99.4% 수준으로 떨어져 큰 위기를 맞고 있다. 이는 기후변화, 잣나무림의 노령화, 병해충 피해 등 다양한 원인이 문제가 되고 있지만, 병해충에 의한 피해도 큰 문제로 자리잡고 있다. 경기도 지역의 잣나무림의 병해충 문제는 소나무재선충병의 확산, 대표적인 잣 생산지인 가평군 지역에 2018~2020년경에 침입한 것으로 추정되는 외래해충인 소나무허리노린재에 의한 잣나무 구과 피해 문제, 과거부터 지속적으로 문제가 되어 항공방제를 실시되었으나 최근에도 22.5% 내외의 잣나무 구과 피해를 일으키는 대표적인 구과해충인 솔알락명나방 피해, 1990년 초반까지 피해가 심하였으나 최근에는 피해가 발견되지 않았던 잣나무넓적잎벌 피해가 2023년 포천시 지역에 돌발적으로 11.4ha가 발생하기 시작하여 지속적인 피해로 인하여 잣나무 생육이 문제가 되고 있다. 이와 같이 경기도 지역의 잣나무에 발생하는 해충 문제로 인하여 경기도 잣나무 생육과 잣 구과 생산에 큰 문제를 일으키고 있다.

검색어: 잣나무, 소나무재선충병, 소나무허리노린재, 솔알락명나방, 잣나무넓적잎벌

SG1-5

Monitoring of new and exotic insect pests with analyzing domestic spread and risk

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In recent years, the number of exotic and emergent insect pests has increased dramatically, requiring proactive outbreak surveys to develop control plans. This study selected vulnerable areas for insect pest outbreaks in Korea in 2024 and investigated new and exotic pests occurring in these areas. As a result, four lepidopteran pest species were investigated as potential new emerging pests. In addition, the spread path of a certain clearwing moths, which has already occurred throughout Korea, was traced to select risk areas for large outbreaks.

Key words: exotic and emergent insect pest, monitoring, outbreak, risk areas

SG4-1

Bioassay for the detection of insecticide resistance in the western flower thrips

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In peppers, western flower thrips (*Frankliniella occidentalis,* WFT) are collected by shaking off the flowers that are their habitat or by picking the flowers. To test for insecticide resistance against the WTFs, immerse pepper leaves in a diluted insecticide solution for 30 seconds and then dry in the shade for 30 minutes. Place five pieces of filter paper soaked in distilled water on the bottom of the insect breeding container, then place a 5 × 5 cm piece of Parafilm in the center of the filter paper. Place the pepper leaves soaked in the insecticide on top and dry them, then carefully inoculate them with 20 adult WFTs using a brush. In the case of long-acting insecticides, experiments are conducted using first-instar larvae, and 7 sheets of filter paper are laid out to maintain moisture. The efficacy of the insecticide is tested after 3 days for adults and after 7 days for nymphs.

Key words: efficacy, *Frankliniella occidentalis,* hot pepper, insecticide, resistance

SG4-2

An improved mass rearing method for western flower thrips, *Frankliniella occidentalis*

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Western flower thrips (*Frankliniella occidentalis*) is widely reared for studies on insecticide resistance and other experimental purposes. In this study, we developed an improved rearing method that saves both time and space. The notable improvements include using harvested cotyledons without washing, maintaining proper moisture levels in the rearing containers to prevent drying of the cotyledons during oviposition, reducing moisture from the egg stage to the late nymphal stage to avoid excessive humidity, and slightly increasing moisture levels from the late nymphal stage to pupation. The number of adults produced per container ranged from 50 to 100, with some containers yielding as many as 150 to 200 adults.

Key words: bioassay, cotyledon, kidney bean, rearing efficacy, test insect

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SG4-3

Mornitoring of farmhouse insecticides use practice in Korea

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약제저항성의 모니터링을 통해 지역별 농가 포장의 약제저항성 정도를 조사하고 농가 포장별 약제저항성의 발달을 분석하는 기초 자료로 농가에서 사용된 농약의 이력이 매우 중요하다. 또한 이러한 기초 정보는 데이터베이스 자료로 축적 함으로서 약제저항성의 관리를 위한 중요한 자료로 활용 가치가 높다. 이러한 목적을 위해 농가 농약 사용 현황의 조사 항목을 약제저항성 관리 시 기초 자료로 필요한 항목을 표준화하여 작물, 재배형태, 농약(살충제), 시기, 횟수 등을 고려하여 분석할 수 있는 농가 농약 사용 실태조사 표준안을 작물별로 순차적으로 제시코 져 한다. 이 제시된 표준안은 데이터베이스로 변환되어 농가별 포장의 약제저항성 관리와 방제력 조정에 활용할 수 있게 만드는 것이 목표이며 또한 농가 농약사용 실태 자료를 편리하고 체계적인 방법으로 데이터가 수집, 분석. 활용되게 시스템을 순차적으로 개발하는 것이 최종 목표이다. 이번에 제시된 농가 농약사용 실태조사 표준안은 시설 고추의 총채벌레에 대한 조사 표준안으로서 지역별 시설고추의 작형별 살충제의 사용 실태를 농가의 구매 이력 정보와 사용 경험을 취합하여 조사항목을 선정하여 만든 표준안이며 실제 이 표준안으로 농가와 함께하는 모니터링 조사방법의 유형을 개발 발전시켜 실용화를 하고 져 한다.

검색어: 농가농약사용 실태, 약제저항성 모니터링, 시설고추, 총채벌레, 방제력

SG4-4

Standardized method for evaluating insecticide resistance of *Aphis gossypii* (Hemiptera: Aphididae) collected in the field

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Aphis gossypii (Hemiptera: Aphididae) is a polyphagous agricultural pest that damages host plants by direct feeding and transmitting plant viruses. Synthetic chemical insecticides are the primary tools for the management of *A. gossypii.* However, the pest has repeatedly developed resistance against a wide range of insecticides. As the level of resistance varies with the insecticide and local pest population, consistent monitoring is crucial for effective management. In our study, we present a standardized method for monitoring insecticide resistance of *A. gossypii* from pepper fields in South Korea. Based on the method proposed by Insecticide Resistance Action Committee, we established a thorough protocol for leaf-dip bioassay ranging from collecting the sample population to testing dose-dependent response. Our standardized method provides prospective researchers with guideline for the leaf-dipping method, allowing them to conduct insecticide resistance monitoring efficiently.

Keywords: pest management, aphid, probit assay, lethal concentration

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SG4-5

Acaricide bioassay with two-spotted spider mite (*Tetranychus urticae*): Evaluation of method for resistance monitoring

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점박이응애는 250과 1400여 종의 식물에 피해를 주고 있는 해충으로 높은 번식력, 근친 교배, 무성생식, 짧은 수명주기로 년간 발생 횟수가 많아 약제에 대한 저항성이 빠르게 발달하는 종이다. 약제저항성 발달을 평가하는 독성시험방법으로 slide dip, leaf dip, leaf disc, topical application, pray potter tower, glass vial, vial leaf dipping 등이 있으며 최근에는 분자학적 진단법 등도 개발되어 있으나 이들 방법은 해충 종이나 발육단계, 약제에 따라 정확도가 달라지므로 현장에 가장 맞는 방법을 찾아야 할 것이다. 최근 확립된 생물검정법은 페트리디쉬에 2% agar 용액을 5ml 붓고 agar 표면만 굳을 때(상온 2시간) 강낭콩잎을 붙인다. 충체는 성충을 대상으로 한 반복당 20마리 이상을 접종한 후 30cm 거리에서 1~2ml의 약액을 분무한다. 항온기(25℃; 광주기 14L:10D)기에 보관하여 72시간 후 사충수를 조사한다. 조사는 붓으로 충체를 건드렸을 때 움직이지 않은 개체를 죽은 것으로 간주한다.

검색어: 점박이응애, 약제저항성, 생물검정

SG4-6

Monitoring insecticide resistance of *Bemisia tabaci* in the Republic of Korea

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담배가루이(*Bemisia tabaci*)는 주요 시설 작물을 직접 가해 또는 식물 바이러스를 매개하여 심각한 경제적 피해를 유발하는 주요 해충이다. 시설재배지에서 담배가루이는 연간 10세대 이상 발생하며 화학적 방제법으로 관리되고 있다. 지속적인 살충제 살포는 담배가루이의 약제 저항성 발달로 이어져 효율적인 방제를 방해하는 주요 요인이 된다. 따라서 시설재배지에서 발생하는 담배가루이의 약제저항성 평가를 통해 약제 선정 및 대체 약제 제시 등 지속가능한 해충관리법을 제시하고자 한다. 본 연구에서는 작용기작별 사용량이 많은 살충제를 선발하여 전국 5개 권역에서 채집된 담배가루이의 약제저항성을 평가하였다. 담배가루이 3령 약충을 대상으로 엽침지법을 통해 살충률을 조사하였다. 살충제 저항성 조사를 위해 필요한 담배가루이 사육법과 생물검정법을 공유하여, 전국 시설재배지에서 발생하는 담배가루이의 저항성 수준을 조사하는데 활용하고자 한다.

검색어: 담배가루이, 저항성, 생물검정, 엽침지법

SG5-1

Current trends in RNAi research in USA

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Since its first discovery in 1998, RNA interference (RNAi) has been extensively studied in insects as a pest control tool. Our knowledge in the mechanism of RNAi in different insects accumulated significantly over the last two decades. Currently, RNAi research in agriculture is undergoing major shifts towards commercialization. Here, we show major accomplishments in RNAi research that led to commercialized products, such as double-stranded RNA-based biopesticides. In addition, some of the ongoing research that will lead to more commercialized products in the future will be highlighted. Lastly, limitations for the current RNAi technology and ongoing research that could potentially make breakthroughs will be discussed.

Key words: RNAi, biopesticide, commercialization, USA

SG5-2

Application of dsRNA in plant-protection: Current status of research at the Fraunhofer IME-BR, Germany

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RNA interference (RNAi) technology, utilizing double-stranded RNA (dsRNA), offers a promising eco-friendly approach to pest control in agriculture. This mechanism disrupts the expression of essential genes in target pests through sequence-specific silencing. The Fraunhofer Institute for Molecular Biology and Applied Ecology, branch of Bioresources (IME-BR) is developing innovative applications of RNAi for plant protection, focusing on optimal chemical formulations to enhance dsRNA stability and efficacy. Current approaches involve micro- and nanoparticle colloidal dispersions that protect dsRNA on plant surfaces and in insect digestive tracts while facilitating cellular uptake. This technology aims to provide a sustainable alternative to conventional pesticides, addressing the challenges of insect resistance and regulatory restrictions while minimizing environmental impact.

Key words: double-strandes RNA (dsRNA), RNA interference (RNAi), pest insects, nanoformulation, sustainable agriculture

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SG5-3

Sustainable agriculture through dsRNA technology: Reality and future

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dsRNA (이중가닥 RNA)를 이용한 해충방제 연구 및 상용화는 가속도가 붙고 있으며, 식물 바이러스와 진균 방제에 dsRNA가 활용되면서 식물보호제로써의 가능성도 상당한 단계에 올라와 있다. 또한, 해충방제제로서의 dsRNA는 IRAC의 Group 35로 분류될 만큼 하나의 농약으로 자리 잡았다. 최근 스프레이 형식의 dsRNA생물농약(Spray induced gene silencing, SIGS)의 개발로 GMO (Genetically modified) 작물이 가지고 있던 규제적 한계를 넘어서서, 완화된 규제를 통해 더욱 더 다양한 해충 종을 방제하려는 움직임이 미국을 비롯해 유럽 및 호주에서도 이루어지고 있다. 우리는 지속 가능한 농업을 위해 dsRNA의 연구와 활용의 현재를 되짚어보며, 한국에서 dsRNA를 이용한 해충방제제 개발의 미래를 논의해 보고자 한다.

검색어: RNAi, dsRNA, 생물농약, 해충방제

SG6-1

Introduction to researches on automatic trap and digital pest control

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현재 우리나라 농업은 기후변화로 인한 농작물 피해 증가와 농촌 고령화와 인구감소로 인한 농촌 소멸 위기를 직면하고 있다. 스마트농업 활성화와 디지털전환 정책은 인력의존형 농업을 디지털기반의 무인자동화로 전환하여 기후변화로 인한 농업생산성 감소 문제와 농촌문제를 해결할 수 있는 좋은 대안이 될 수 있다.

해충 예찰과 방제를 무인자동화하기 위해서는 주요 농업 해충들을 예찰할 수 있는 무인트랩 개발과 예찰체제 구축이 선행되어야 하고, 예찰정보를 활용한 방제시기 예측, 예측정보를 활용하여 농업인에게 서비스할 수 있는 방제 지원 정보 생산이 필요하다.

본 소모임에서는 무인예찰 개발과 관련 예찰기술 개발 및 방제지원을 위한 디지털방제력 등 예측 기술에 대하여 현황정보를 공유하고 해충 예찰방제 무인자동화 개발에 나아갈 방향을 논의하고자 한다.

검색어: 무인트랩, 디지털방제, 예찰, 예측, 병해충

SG6-2

Development of an auto trap system for rapid pest identification

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본 연구는 예찰의 신속한 동정을 위해 오토트랩을 활용한 예찰방법 개선 결과이다. 기존의 예찰시 동정 방식은 전문가의 현장 방문이나 장거리 출장이 필요하여, 현장 대응이 늦어지고 인력 자원의 효율적 활용에 어려움이 존재하였다. 이에 따라, 해충이 트랩에 들어오면 360도 카메라를 통해 촬영된 사진을 자동으로 서버로 전송하는 오토트랩 시스템을 도입하고 있다. 서버에서는 전송된 이미지를 실시간으로 분석하여 해충을 동정하는 과정을 거친다. 이 시스템은 장거리 출장이나 현장 방문 없이도 빠르게 동정을 할 수 있어, 발생 초기 단계에서의 신속한 대응이 가능하다. 또한, 루시드키, 인공지능(AI) 및 머신러닝 알고리즘을 활용하여 비전문가도 더욱 정확한 동정이 가능하며, 전문가의 실시간 검토를 통해 동정의 정확도를 높일 수 있다. 이 연구 결과는 해충 방제의 효율성을 높이고, 인력 자원의 활용도를 극대화 할 수 있는 중요한 기술적 진전을 나타낸다. 향후 추가적인 테스트 및 개선을 통해 상용화가 이루어질 것으로 기대한다.

검색어: 오토트랩, 예찰, 동정, 인공지능, 실시간

SG6-3

Development of the unmanned surveillance AI trap developed by NICS

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작물에서 발생하는 해충을 예찰하기 위해서는 관행적으로 인력이 트랩을 조사하는 방식이 사용된다. 하지만 이러한 방식은 많은 시간과 인력이 소요되며, 표준화된 데이터를 주기적으로 수집하는 데 어려움이 있다. 이를 대체하기 위해서 무인예찰 시스템이 필요하며 본 연구에서 노지 밭작물의 나방류와 노린재류에 적합한 무인예찰 AI 트랩을 개발하였다. 이 트랩은 고화질 이미지를 획득한 후 해충을 분쇄·배출하여 자가청소가 가능하며, 파밤나방, 담배거세미나방, 톱다리개미허리노린재 등의 딥러닝 모델이 탑재되어 있어 이미지 기반 마릿수 분석이 가능하다. 또한, 설치 지점의 온도, 습도, 풍향 등 환경 데이터를 동시에 취득하여 해충 발생 분석에 활용할 수 있다. 이 개발 기술은 KC, CE, ISO 등의 공인인증을 취득하였으며, 현재 시범사업에 활용되고 있다. 트랩의 무인예찰이 원활하게 이루어지기 위해서는 자가관리, 무선 송수신 등의 기능이 필요하며, 자동 분석을 위해서는 AI가 구동 가능한 서버 운영과 데이터 관리도 지속적으로 고려해야 한다. 앞으로 무인예찰 기술의 현장 활용을 확대하기 위해 현재의 개발 현황을 점검하고, 발전 방향에 대해 논의하고자 한다.

검색어: 트랩, 무인예찰, 모니터링, AI트랩, 자동인식

SG6-4

Field test of automated insect monitoring trap (Auto-Rolltrap)

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Monitoring is the most important method for an efficient and effective pest control. However, more labor and higher expenses are required. For monitoring pests, colored sticky traps have been used for those small insects like thrips, aphids, whiteflies, etc and also such sex pheromone traps as delta trap, wing trap, and so on have been used sticky plate for capturing lepidopteran pests. Auto-Rolltrap was developed to monitor insect pests having been conduced with those traps. One of the signature of Auto-Rolltrap is a self refreshing function. A part of a roll-typed sticky trap in the trap is unwrapped and exposed to the outside for capture. Captured pests on the exposed are taken by dual cameras inside while wrapping. All images taken are sent to the server for user. This make it possible the unmanned monitoring for a long time until a roll-type sticky trap are consumed.

Key words: Auto-Rolltrap, Insect, Monitoring

SG6-5

Monitoring the occurrence of moth pests and developing the phenology model using 'TrapCam' trap

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최근 기후변화에 따라 해충의 발생 시기가 변화하고 있으며, 따라서 특정 해충의 정확한 발생시기를 보다 더 정밀하게 예측하기 위해서는 예측모형 개발과 더불어 이를 필드에서 검정할 수 있는 시스템이나 새로운 모니터링 기술 개발이 매우 중요하다. 현재 농촌진흥청의 국가농작물병해충관리시스템(NCPMS)서는 6개 작물, 17종 해충에 대한 발생 예측정보가 서비스되고 있다. 이 시스템에서는 개별 해충의 발육영점온도를 기준으로 한 유효적산온도(Degree-Day) 모형을 기반으로 실제 야외에서의 발생시기를 예측하고 있다. 하지만 대부분의 해충에 대하여 모델이 예측하는 시기와 실제 포장에서 발생하는 시기에 대한 검정이 이루어지지 않아 필드에서의 실제 발생시기 자료와 모델이 예측하는 날짜를 서로 일치시키기 위한 조정과정이 매우 필요한 시점이다. 따라서 본연구에서는 가루깍지벌레와 감자뿔나방에 대하여 필드에서의 정확한 발생자료를 얻기 위하여 예찰 트랩에 소형카메라를 설치하여 이들 해충의 일별 시간별 트랩에 유인된 개체수를 촬영하여 초발생일과 발생최성기를 확보하였고, 조사 지역별 트랩설치 지점에서의 일별 기상자료에 기반한 예측모형의 발생예측 시기와 비교분석하였다.

검색어: 기후변화, 가루깍지벌레, 감자뿔나방, 온도발육모형, 예측방법


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적용대상

가지, 감(단감 포함), 감귤, 감자, 고추(단고추류 포함), 국화, 꽃양배추(브로콜리, 콜리플라워 포함), 무, 배, 배추, 복숭아, 사과, 상추(양상추 포함), 수박(복수박 포함), 오이, 자두, 참외, 토마토(방울토마토 포함), 호박(단호박 포함)

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