

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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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

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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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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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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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

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

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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

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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 Diptericin 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

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

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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

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

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