구두발표
세미나실 1

○ **Oral presentation**
육종 및 생리생태

O-21　　　　Oral presentation - 육종 및 생리생태

Exploring Genetic Variation and Phylogenetic Patterns of *Tropilaelaps mercedesae* (Mesostigmata: Laelapidae) Populations in Asia

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The mites belonging to the genus *Tropilaelaps* are ectoparasites of honeybees, primarily infesting the larval and pupal stages. Originating from subtropical regions, these mites can cause brood malformation, bee mortality, and subsequent decline or absconding of colonies. During field surveys conducted in Nepal, South Korea, and Uzbekistan to investigate honeybee pests, several populations of *T. mercedesae* were collected. The intraspecific genetic divergence of the populations of *T. mercedesae* were analyzed based on the sequences obtained from forty-eight samples from South Korea, Nepal and Uzbekistan and previously deposited sequences from different Asian countries, available in GenBank. The molecular analysis of cytochrome oxidase I gene revealed high similarity between Uzbekistan and Pakistan populations alarming the potential invasion of subtropical honey bee parasites into the Central Asian beekeeping sectors. Phylogenetic analysis indicated the presence of four distinct lineages within the Mainland-Indonesian populations of *T. mercedesae*. Notably, an evolutionary divergence was observed between the haplotypes from Sri Lanka and the Philippines compared to the remaining mainland Asian and Indonesian haplotypes, suggesting the possible existence of subspecies or separate species in these isolated locations. To gain a deeper understanding of this phenomenon, it is essential to continue monitoring the spread of this significant honeybee pest and conduct comprehensive morphological and molecular analyses of samples collected from these specific localities.

Key words: mtDNA, South Korea, Nepal, Uzbekistan, genetic variation, climate change, invasive species.

O-22   Oral presentation - 육종 및 생리생태

Amino Acid Dynamics in Bee Feed: Implications for Honey Bee Foraging Behavior and Nutrition

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The foraging behavior of honey bees can be attributed to the nutritional rewards they gain from their activities. In a previous experiment, we established that foragers' pollen selection is influenced by its protein content. However, a longstanding question remained regarding how the nutritional composition, especially in terms of protein, changes during the process of converting pollen into bee bread. To address this question, we pursued two approaches. Initially, we provided honey bees with *ad libitum* pollen patty and observed them as they transformed it into bee bread. We quantified the amino acid content of the resulting bee bread and compared it with that of the pollen patty. In a parallel approach, we estimated the amino acid content of the original pollen, the bee pollen collected by the honey bees, and the bee bread produced after collecting the same pollen. In all the cases the pollen was rapeseed pollen. The results of our research revealed that pollen exhibited markedly higher levels of individual amino acids, leading to a substantially greater overall amino acid content compared to bee pollen. During the initial 3 to 7 days, no significant difference in the total amino acid content was observed between bee bread, and bee pollen or the pollen patty, although there were notable changes in individual amino acid levels. However, interestingly, in contrast to the majority of amino acids, we observed a distinct pattern of proline content in the bee bread, which was higher than that in bee pollen or the pollen patty. This change in amino acid content is likely a result of the addition of nectar and other secretions during the bee bread processing. Moreover, over a period of about 14 days in hive conditions, the amino acid content of the bee bread increased. This could possibly be attributed to the nutritional contributions by microbiome in the hive environment. In conclusion, the nutritional reward, especially in terms of amino acids, plays a significant role in honey bees' physiology. The transformation of pollen into bee bread involves dynamic changes in the amino acid content, influenced by both intrinsic bee-related factors and external hive environment factors.

O-23 **Oral presentation -** 육종 및 생리생태

Vitellogenin and Overwintering Success in Honey Bee Workers: Unraveling the Connection Between Protein Levels and Body Weight

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Vitellogenin (*Vg*) is a protein precursor of egg yolk commonly found in oviparous animals, and it is abundantly present in honey bee workers, a caste of helpers that typically do not lay eggs. However, honey bee *Vg* serves various roles beyond reproduction, playing critical parts in hormone signaling, food-related behavior, immunity, stress resistance, and longevity. To investigate the potential relationship between *Vg* and the survival of overwintering honeybees, we conducted an analysis of *Vg* levels during the overwintering period, along with its correlation with the weight of overwintering workers. From October to December, we performed weekly weight measurements of a mixed-aged nurse bee population. The expression level of *Vg* was assessed through RNA extraction from the nurse bee abdomen, utilizing Real-Time PCR. Additionally, we quantified the amount of *Vg* protein using SDS-PAGE methods. Our study unveiled a decrease in the weight of honey bee workers during the overwintering period. Interestingly, while the level of *Vg* expression dropped rapidly during the investigation period, the amount of body Vg protein reduced gradually throughout the study, suggesting that a high amount of *Vg* is produced and stored inside the body during autumn and gradually consumed during the overwintering period. These observations indicate a potential link between the weight changes and the decline in *Vg* protein levels. These findings shed light on the dynamic physiological changes that occur in honey bee workers during overwintering and highlight the importance of *Vg* in their overall health and survival. Further research into the specific mechanisms underlying *Vg* regulation and its impact on honey bee longevity could contribute to a better understanding of bee health and the factors affecting their population dynamics. Such insights are crucial for addressing the challenges faced by honey bee colonies and their conservation in the face of environmental pressures and other stressors.

Key words: Honey bee, Vitellogenin, overwintering, body weight changes, gene expression

O-24　Oral presentation - 육종 및 생리생태

Rapid Acquisition of the odor by Honey Bee Queens at an Early Age

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Virgin queens leave the nest and successfully navigate during nuptial flights, demonstrating the crucial role of learning and memorization for colony success. This study aimed to investigates olfactory learning and memory in queens at different ages (5 days, 1 month, 3 months, and 2 years) and foraging workers using the proboscis extension reflex (PER). 1-nonanol served as the conditioned stimulus (CS), and 50% sugar as the unconditioned stimulus (US). Our findings reveal that queens of all ages possess the ability to learn and memorize odors. However, 5-day-old queens exhibit significantly higher learning performance than queens at every other age tested. Additionally, the memory retention percentage of 5-day-old queens is significantly higher than that of 3-month and 2-year-old queens and insignificant with foraging workers. The peak learning and memory ability of queens may occur during their mating flight days. Nevertheless, throughout the rest of their lives, hormonal guidance likely accounts for the reduction in learning and memory abilities.

Key words: Learning, Memory, Queen, Proboscis Extension Reflex, Mating flight

O-25　Oral presentation - 육종 및 생리생태

솔라비하이브를 이용한 양봉꿀벌 봉군 특성과 내외부 환경 측정 기술의 적용과 응용(활용)

정원기[1]

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최근 꿀벌의 실종과 원인을 특정할 수 없는 폐사가 잇따르면서 봉군의 활동을 수시 관찰하고 영향 요인을 식별해 대응책을 마련하기 위한 연구가 이어지고 있다. 스마트 양봉 시스템은 벌통의 무게, 온도, 습도 및 CO_2와 같은 봉군 상태와 관련된 매개변수의 실시간 및 장기 측정을 위해 사용될 수 있도록 개발되고 있다. 본 연구는 한국농수산대학교 양봉장에 설치된 탄소중립형 스마트 양봉 시스템인 솔라비하이브를 통해 수행하였다. 나무로 제작된 8매상 벌통에 4G LTE망을 통해 원격 서버로 전송이 가능한 MCU(비온팜)를 설치하여 온도, 습도, CO_2, 벌통 무게, 꿀벌 이동량을 측정해 30분마다 기록된다. 또한 외부 환경에 따른 이동량 변화를 비교 분석할 수 있도록 별도 MCU를 설치해 양봉장의 외기 온도, 습도, CO_2를 측정했다. 이번 연구를 통해 꿀벌의 활동량과 벌통 내부 및 외부 환경 요인의 상관관계를 살펴볼 수 있었으며, 향후 꿀벌 활동량 인식의 정확도를 높일 수 있는 개선 연구와 함께 봉군 내부 및 외부의 소리 데이터를 통해 꿀벌의 행동 특성을 추가로 분석하는데 유용한 도구로 사용될 수 있을 것이다.

검색어: 스마트 양봉, 꿀벌 활동량, 벌통

O-26   Oral presentation - 육종 및 생리생태

A Study on Enhancements for Honeybee Mining Environment Analysis and Activity index

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Increased frequency of extreme weather events due to climate change is causing regional shifts in flowering times and constraining beekeeping activities, which has impacted bee populations and productivity. To minimize this damage, we have developed a system that allows beekeepers to manage their apiary environment and support efficient activities during swarming season. In this study, we created a productivity class map using high-resolution grid data from the Korea Meteorological Administration and forest environment data. Through this, the productivity of the target area was identified and indicators for services were derived. The decision-making service for beekeeping activities that considers local weather information can be used as a basis for stable beehive operation and bee population management.

Key words: Migratory beekeeping, Extreme weather, High-resolution grid data, Activity index

O-27   Oral presentation - 육종 및 생리생태

A comparison of basal expression level of the detoxification enzyme cytochrome P450 between *Apis cerana* and *Apis mellifera* (Hymenoptera: Apidae)

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The Asian honey bee (*Apis cerana*) and the European honey bee (*Apis mellifera*) (Hymenoptera: Apidae) are two major honey bee species in Korea. These two closely related species show different responses to various pests and diseases, leading to different exposure pathways to different pesticides. It is known that *A. cerana* is more sensitive to various miticides for the varroa mite than *A. melllifera*, including amitraz, fenitrothion, and fipronil. The main object of this study is to find the reasons for the different toxicological responses of two closely related species, with a particular emphasis on metabolic processes in honey bees. Since P450s in the CYP3 and CYP4 clans, especially the CYP9Q family, are known to be major enzymes for detoxification of xenobiotics, including various pesticides, this study focuses on the spatial differences in the basal expression level of P450s belonging to the CYP3 and CYP4 clans in *A. cerana* and *A. mellifera*. Furthermore, the CYPomes of two closely related honey bee species were compared for the first time, shedding light on the molecular causes of the toxicological variations.

Key words: *Apis mellifera*, *Apis cerana*, bioactivation, detoxification, cytochrome P450

심포지엄
세미나실 2

○ **Symposium**

농업생태계 기후변화로 인한 먹이사슬 변화

S-03   Symposium - 농업생태계 기후변화로 인한 먹이사슬 변화

Climate change effects of Vespa phenology and distribution and its possible impact on food web in agroecosystem

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Temperature change and climatic variability impact phenology and distribution of organisms threatening the ecosystem stability. We had monitored Vespa hornets in the family of Vespidae in Hymenoptera, Insecta over the country where existing Vespid hornets are interacting with the newly invaded species of Vespa velutina. With the monitoring data we had constructed phenology model of spring emergence of overwintered queen adopting degree day accumulation with the empirical fitting of the developmental threshold. Developmental threshold and thermal constant was estimated given the biofix as January 1 which indicate the hornet began to have the physiological changes even before March when the ambient temperature reach 8. Further using the bioclimatic variables and landscape factors, we also have developed the Vespa velutina distribution model. Both model will serve as the platform for future interaction prediction based on the climate and landscape changes. Here we provide one example of honey bee and pollinator community changes after the hornet invasion. In our case, we still have to look at the food web structural changes as well as the food web cascade partly because of extreme bee hive density and superabundance of vespa hornets in Korea.

S-04   Symposium - 농업생태계 기후변화로 인한 먹이사슬 변화

Improvement of Detection Accuracy for Hornet using an Advanced YOLOX Structure

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말벌 모니터링을 위해서는 작은 객체에 대한 검출 성능이 중요하다. 본 연구에서는 작은 객체 검출 성능이 가장 우수한 YOLOX-X의 구조를 개선하는 방법을 제안한다. 이를 위해 특징추출부(Backbone)에 존재하는 4개의 CSPLayer를 ShuffleLayer로 변경하여 모델의 깊이가 깊어질수록 발생하는 공간 정보의 손실을 방지하면서 출력 채널의 크기를 유지하였다. IoU 50%에서 테스트 데이터에 대한 mAP정확도는 제안한 YOLOX가 93.8%로 기존 모델 대비 4.2% 높게 나타났다. 실제 봉군 환경을 고려하여, 테스트 말벌 영상을 각 입력영상 크기 대비 객체의 비율이 0.3%가 되도록 만든 후 정확도를 평가하는 실험에서는 제안한 모델이 mAP 87.35%로 기존 YOLOX 대비 1.14% 높은 결과를 보였다. 백본에서 모델의 총 파라미터 수는 19,720으로 기존 모델에 비해 91.82%감소하였으며 따라서 전체 실행 속도에서 1.35배 더 빨랐다. 따라서 제안한 모델을 말벌 모니터링 시스템에 적용할 경우 기존 모델에 비해 정확도 및 속도에서 우수한 검출 성능을 기대할 수 있다.

S-05   Symposium - 농업생태계 기후변화로 인한 먹이사슬 변화

A Preliminary Result on UAV-based Rotational Antenna System for Localization and Tracking of *Vespa velutina*

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In this study, we propose an approach for localizing and autonomously tracking radio-tagged flying insects using an unmanned aerial vehicle (UAV)-based rotational antenna system. In the proposed system, a motor-driven rotational antenna with 360-degree coverage is attached to an unmanned aerial vehicle, the signal strength for a given angle is measured in real time, and the UAV's position is controlled by considering the direction of the strongest signal. Moreover, we designed a system architecture that comprised a tracking sensor system and a UAV system for radio-tagged flying insects. The effectiveness of the proposed system for estimating and autonomously tracking the target's position was evaluated by performing a numerical dynamics simulation.

S-06   Symposium - 농업생태계 기후변화로 인한 먹이사슬 변화

Early foraging activity possibility in winter bees exposed to abnormally high temperatures

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월동기는 낮은 외기온도에 대해 벌들이 에너지를 축적하며 버티는 시기이다. 월동기의 영양상태는 차세대 봉군 양성 전까지 세력 유지를 위해 중요하며, 해당 시기의 벌은 내역봉 상태에 머무르다 이른 봄철 외역 행위를 개시하기 위해 외역봉로 전환하는 특징을 보인다. 본 연구는 발달단계의 외기온도 스트레스가 월동벌의 영양상태 및 계급 전환에 미치는 영향을 확인하기 위해 진행되었으며, 전년도 7월 ~10월간 세 가지 외기온도(wildtype, 25℃, 35℃)에 지속적으로 노출된 월동군을 대상으로 3가지 실험을 수행하였다. 그 결과, 35℃에서 발육한 벌에서 상대적으로 저조한 fat boy 축적량 및 작은 크기의 하인두 샘(Hypopharyngeal glands)이 확인되었으며, 생리적 상태 또한 외역봉에 가까운 것으로 확인되었다. 따라서, 고온에서 발육한 벌은 이른 봄철 상대적으로 빠른 외역 활동을 개시할 것으로 추정된다.

Key words: *Apis mellifera*, Thermal stress, Winter bee, Nutrition, Caste transition

S-07   Symposium - 농업생태계 기후변화로 인한 먹이사슬 변화

Population changes of climatic change indicator butterflies in agroecosytem across Korea

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나비는 화려한 날개와 주간 활동성으로 서식지 변화와 기후변화를 나타내는 지표종으로 많이 이용되고 있다. 우리나라에서도 농업생태계에 서식하는 나비 중 배추흰나비, 노랑나비, 남방노랑나비, 호랑나비 4종을 기후변화 지표종으로 선정하여 농업생태계에서 기후변화에 따른 개체군 변동을 파악하고 있다. 우리는 2020년 이후 2022년까지 전국 6개 지점에서 매주 선조사법을 이용한 나비모니터링을 4월부터 10월까지 실시하여 이들 기후변화 지표종 변화를 전국적인 양상에서 살펴보았다. 그 결과 기후변화 지표종의 출현은 남부지방에서 1주일 먼저 관찰되는 양상을 나타내었고 이후 변동 양상은 다른 지역과 유사하였다. 이들 개체군 출현 양상을 통하여 기온변화에 따른 개체군 증감 여부를 누적분포함수와 확률밀도함수를 추정하였다. 이러한 연구결과를 통하여 농업생태계에서 주요한 역할을 하는 화분매개곤충이자 초식곤충인 나비 개체군 변동이 기후변화에 어떻게 영향을 받는가를 추적하여 먹이사슬 내 변동을 관찰할 필요가 있다.

검색어: 나비, 기후변화지표종, 농업생태계, 화분매개

Climate Change based Distribution of Honey Plants in Korea

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전 세계의 작물의 3/4은 화분매개곤충에 의해 수분을 하고 있다고 FAO에 의해 보고되었습니다. 이는 꿀벌과 나비와 같은 화분매개곤충이 작물 수확량에 미치는 영향이 큰 것을 알 수 있습니다. 기후변화는 화분매개곤충의 개체수를 빠르게 감소시키고 있는데 나비는 1991년이후에 거의 절반으로 줄었고, 특히 꿀벌은 최근에 개체수가 급격하게 감소하고 있습니다. 국내에는 화분매개군충의 먹이원이 되는 밀원식물은 약 600종류의 식물이 분포하고 있는 것으로 알려져 있고 이중 초본류는 337종류, 목본류는 237종류로 보고되어 있다. 이들 밀원식물은 농경지 및 가장자리 서식지, 산지, 계곡 등 다양한 환경에서 분포하고 있고 전국적으로 분포하는 종은 약 478종류이고 중부지방에 56종류, 남부지방에 66종류 등이 분포하고 있다. 주요 밀원식물의 적산온도를 예측한 미래의 잠재서식지를 통해 미래의 밀원식물의 분포범위를 확인하였다. 밀원식물의 분포범위의 이동은 화분매개곤충의 이동을 동반할 수 있고 이는 수분이 필요한 많은 작물의 영향을 미쳐 향후 작물의 생산량에도 영향을 미칠 것으로 판단이 가능하였다. 따라서 지속적인 밀원식물의 이동, 개화기 등의 모니터링이 필요하다.

Potential Changes in the Distribution of Four Indicator Plant Species in Response to Climate Change at Agroecosystem

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지구 온난화는 식물의 출현시기뿐만 아니라 개화나 개엽시기 그리고 휴면타파에 상당한 영향을 줄 수 있으며 기후변화로 인한 강수량 변화는 식물 군집과 종 풍부도에 영향을 미친다. 미래 기후변화는 많은 종의 서식지와 분포 변화를 초래하여 생물다양성 감소와 생태계 교란이 예상된다. 따라서 본 연구는 농업생태계 기후변화 지표식물 4종(서양금혼초, 큰망초, 큰개불알풀, 광대나물)의 현재와 미래의 분포 특성을 예측하고자 수행하였다. 전국을 대상으로 200여 지점의 실제 분포 유무 자료를 수집하고 Maxent모형을 적용하여 현재와 기후변화 시나리오에 따른 미래의 잠재적 분포를 예측하였다. 기후변화에 따른 미래 분포예측에서 광대나물, 큰개불알풀, 큰망초는 분포면적이 확대되는 것으로 예측되었다. 서양금혼초는 미래에는 소폭 축소되는 것으로 나타났다. 이와 같은 기후변화 지표식물의 모니터링 자료는 장기간에 걸쳐 일어나는 기후변화에 따른 생태계의 반응을 파악하고 농업생태계 관리 계획 설정에 활용될 것으로 기대된다.