台灣昆蟲學會一〇四年（第三十六屆）年會
論文宣讀摘要

How land use change influences human health: insights into vector-borne diseases

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Vector-borne diseases, including such as plague, malaria, and dengue fever, have long been a great threat to human society. Because disease vectors are typically arthropods, which are themselves regulated by the environment, a change in land use could have profound influence on the number of the vectors, thus the risks to human health. In this talk, the significance of land use change to human health will be exemplified by two vector-borne diseases, tick-borne Lyme disease and mite-borne scrub typhus (恙蟲病). Lyme disease is prevalent primarily in temperate regions and recent studies have revealed that a reduction in forest areas could increase human risks to Lyme disease. This is mediated mainly by an increase in reservoir hosts, which happen to be habitat generalists that prosper following habitat fragmentation. Scrub typhus is endemic to the West Pacific, including Taiwan. Taiwan's acceding to World Trade Organization has left many rice fields fallowed, with the consequence of elevated number of mites that could transmit scrub typhus because these mites can't survive in flooded rice paddies. Both studies demonstrate that land use change could have unexpected ramifications for public health, and underscore the necessity of research on vector-borne diseases and their control from broader perspectives.

Key words: arthropod vector, disease control and prevention, ecological study, environmental change, infectious disease

Termites and fire: A trans-boundary research in exploring termite biodiversity in Southeast Asian tropical degraded peatland

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Tropical peat swamp forests in Southeast Asia occupy approximately 72% of the global peatland. Peat swamp forests are thought to support lower species diversity than tropical rainforests. Countries with extensive peat swamp forests, such as Malaysia and Indonesia, have always regarded them as unproductive wastelands, except for the presence of valuable logs, and governments have tended to convert natural peatlands to more productive land use. Thus, the present stage of tropical swamp forest is a mosaic of different land uses, including agroindustrial planted forests and silvicultural plantations (e.g., rubber and oil palm). However, extensive forest exploitation following peat drainage for agricultural expansion leads to catastrophic peat fires. In general, cultivated peats experience fire once every four to five years. The high level of repeated fires may explain why the area covered by abandoned secondary peatland has increased two-fold from 1.2 to 3.5 Mha since 1990. Given that the absence of earthworms in acidic soil conditions in which is well known of their ecosystem service, termites are viewed as a potentially major player in a variety of ecosystem functions, as has been shown in other landscapes. Trans-boundary research effort is underway to assess the sustainability of land use in degraded peatland. The presentation will address on the impact of fire on the termite assemblage in fire-impacted peat and their possible ecosystem function at post fire. In addition, it is necessary to understand the strategies that termites adaptively employ to survive in the harsh environment. Understanding species vulnerability is fundamental for developing conservation strategies that harness ecosystem services provided by certain groups, such as restoring the fertility of increasingly degraded fire-impacted peatlands for agricultural purposes.

Key words: deforestation, degraded peatland, landscape disturbance, insect biodiversity, peat fire

BD01

台江濕地不同棲地昆蟲之組成
The composition of insect assemblage in different habitats in Taijiang wetland

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台江地區包含「台江國家公園」及其鄰近地區，陸域環境以濕地為主，鹽生草澤為主要的生態樣貌，林澤代表為沿感潮溝生長的紅樹林，故其昆蟲相具有相當大的獨特性。本研究選定紅樹林、防風林（木麻黃林）、濕草地優勢植物、乾草地優勢植物，以及陸地水域環境作為研究樣區，並依據昆蟲葉棲、地棲、水棲與飛行等的活動特性，以相對應的採集方法進行採集，自 2015 年 1 月起為期一年每月以定量方法調查，並比較各種棲地昆蟲組成與季節性變化。本研究採用 Wainstein 相似性指標（Wainstein's Similarity Index, K_w）來分析不同方法或不同棲地所採集昆蟲組成結構的相似性。不同採集方法所捕獲昆蟲的組成結構相似性均不足 5%，相似性最高的採集方法為馬式網與窗式陷阱（K_w= 4.62），而飛行昆蟲與地棲昆蟲組成相似性則低於 0.1%，由此可見使用多種不同的採集方法較能反映出該地的昆蟲組成情形。1 月份不同棲地間（防風林、紅樹林與乾草地）的昆蟲組成相似性指標皆不足 5%。防風林與紅樹林以馬氏網與窗式陷阱所採集的飛行昆蟲組成結構相似性約 4~5%，而以掉落式陷阱採於防風林與乾草地所採集的地棲昆蟲組成結構相似性為 0.68%，此顯示各類型濕地棲地的昆蟲組成有其獨特性。

關鍵詞（Key words）: 台江國家公園（Taijiang National Park）、濕地（wetland）、棲地（habitats）、昆蟲組成（insect assemblages composition）、Wainstein 相似性指標（Wainstein's Similarity Index）

BD02

臺灣恙蟎分類研究與分子鑑定
Taxonomic study and molecular identification of chigger mites in Taiwan

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本研究主要針對臺灣各地低海拔鼠類及鼩鼱類進行恙蟎採集，同時蒐集高海拔鼠類、鼩鼱類及其他野生動物如蝙蝠、鳥類、蜥蜴及食肉目動物等身上所發現之恙蟎，進行外部形態觀察和鑑定，同時測量、拍照及繪圖，共彙整了 2 科 2 亞科 12 屬 38 種的恙蟎種類，包括 3 個新種：連氏背展恙蟎 (*Gahrliepia* (*Gateria*) *lieni*)、微小背展恙蟎 (*Gahrliepia* (*Gateria*) *minuta*)、宜蘭背展恙蟎 (*Gahrliepia* (*Gateria*) *yilanensis*)，23 個新紀錄種及 12 個已知種；其中在宜蘭縣大同鄉思源埡口所調查之 21 隻鼠類當中，就發現 2 種恙蟎新種以及 9 種新紀錄種，顯示臺灣的恙蟎種類，尤其是高海拔山區，仍有很大的調查空間。連同文獻記載但此次未採獲的 9 個已知種，臺灣恙蟎目前有 2 科 2 亞科 13 屬 47 種。恙蟎分子鑑定部分，則針對核糖體 DNA 中 ITS1-5.8S-ITS2 片段，以及專為纖恙蟎屬 (*Leptotrombidium*) 物種設計之粒線體 DNA 細胞色素氧化酶 I (cytochrome oxidase I, COI) 片段進行巢式聚合酶連鎖反應 (nested PCR)。前者已成功定出 20 種恙蟎物種之序列，其中纖恙蟎屬部分物種無法藉由此片段有效區分，故近一步進行 COI 基因 nested PCR，目前已定出 7 種纖恙蟎屬物種之序列。本研究結果希冀可充實臺灣生物多樣性資料庫，並做為相關後繼研究之基礎。

關鍵詞 (Key words): 恙蟎 (chigger mite)、分類 (taxonomy)、核醣體 DNA (ribosomal DNA)、細胞色素氧化酶 I (cytochrome oxidase I)

BD03

增温激發胡麻斑星天牛的棲群分化

On population stratification of *Anoplophora macularia* (Thomson) escalated by climate warming

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本文以三個層面來探討胡麻斑星天牛棲群分化和附呈現的翅鞘斑型（elytra pattern）變異的可能理由。三個面相是：1. 年度間成蟲羽化峯的時間距離；2. 年度間成蟲羽化峯的數目和年積溫；3. 成蟲其白斑在翅鞘上的四列斑（SS1, SS2, SS3, SS4）分佈的變異及消融。依據本研究歷年來檢視所採集樣本得知，星天牛翅鞘白斑變異：以 SS1 逐年消減的最多；SS2 消減的最少。而所有 SS 斑皆消失者，在 2012 年前，不曾檢視過。但是，自 2013 年以來，部分或全部 SS 白斑消失者，却發生在當年成蟲羽化期的末期。2014 年之年均温屬異常昇高。隨之而來，2015 年 1 月至 6 月均温異常昇高而導致胡麻斑星天牛翅鞘背脊縱軸上的所有 SS 白斑消失。而同年七月的月均温更進一步的異常昇高，導致七月羽化者，背脊縱軸上的所有白斑，全部消失；竟而呈現翅鞘全黑的天牛。本文試就他人所悉：室內全年在常温下飼育星天牛一世代蟲所得觀察記錄；及本研究：2013、2014 及 2015 全年所得室外觀察記錄，作彼此比對，試着探討，氣候異常導致白斑消融及翅鞘全黑的形態，生態或生理現象的影響。

關鍵詞（Key words）: 胡麻斑星天牛（*Anoplohora macularia* (Thomson)）、棲群分化（population stratification）、翅鞘斑型（pattern of elytra maculation）、增温（climatic warming）

BD04

聖嬰年增温導致胡麻斑星天牛翅鞘斑型的消融

On diminution of elytra maculae of *Anoplohora macularia* (Thomson) on account of climate warming due to El Niño

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繼 2013、2014 年在臺北市北投關渡紅樹林保護區的樣本點及參考點，所採集的胡麻斑星天牛 *Anoplophora macularia* (Thomson) (Cerambycidae: Coleoptera) 及 2015 年新北市淡水竹圍的星天牛，三個族群成蟲的翅鞘斑型 (pattern of elytra maculation) 的記錄，並行統計及分析。以該蟲左右翅鞘背 HH 斑下方；中尾端的四對 SS 斑 (Lingafelter and Hoebeke, 2002) 皆具足者，為第壹組參數；以第一對斑消融或變異者為次組參數；以第二對斑消融或變異者為第三組參數；第三或第四對斑，有任何變異者為第四組參數；以四對斑中有兩對以上斑呈消融者為第五組參數；所有背斑消失者為末組參數共得到 17 項參數。參數的記錄資料以 Excel 檔下載，以多態生物統計軟體程式 (PRIMER 5) 進行統計分析。結果顯示：1. 四對斑具足者，逐年遞減；2. 第一對斑消融率則逐年增加；3. 2013 及 2014 年天牛，兩對以上斑的消融率劇增；4. 2015 天牛，有翅鞘背脊斑型全部消失者。

關鍵詞 (Key words): 竹圍紅樹林 (Chuwei mangrove forest)、胡麻斑星天牛(*Anoplohora macularia* (Thomson))、翅鞘斑 (elytra maculation)、消融變異 (diminution)、聖嬰年 (El Niño year)

BD05

兩種扁葉蟬其塗抹與梳刷行為之分析（半翅目：葉蟬科：扁葉蟬亞科）

Analysis of the anointing and grooming behavior of two *Penthimia* species (Hemiptera: Cicadellidae: Penthiminae)

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Brochosomes are currently considered a unique characteristic for the family Cicadellidae. The brochosomes coatings of leafhoppers result from the anointing and grooming behavior. About fifteen leafhopper species in 8 subfamilies of Cicadellidae have been studied on the anointing and grooming behavior and brochosomes in the past two decades. It shows that the anointing and grooming behavior and brochosomes with potential as taxonomic characteristics in Cicadellidae. We are reporting the anointing and grooming behavior and morphology of brochosomes of Penthiminae for the first time. Two penthiminine species, *Penthimia formosana* and *Penthimia guttula*, were examined and analysed in this study. The results show both the anointing and grooming behavior and brochosomes have potential as taxonomic characteristics in different taxonomic category.

關鍵詞 (Key words): 葉蟬 (leafhopper)、扁葉蟬屬 (*Penthimia*)、塗抹與梳刷行為 (anointing and grooming behavior)、微小體 (brochosome)

BD06

臺灣產兩種造癭沫蟬初步研究（半翅目: 沫蟬總科）
The preliminary study of two galling froghoppers from Taiwan (Hemiptera: Cercopoidea)

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全世界已記錄之造癭沫蟬計有兩種，其分類地位均為尖胸沫蟬科 (Aphrophoridae)，分別為 *Philaenus spumarius* (Linnaeus, 1758) 與 *Aphilaenus nigripectus* (Matsumura, 1903)。此兩種沫蟬若蟲所造成的蟲癭，係使寄主葉緣以不規則的捲曲程度朝向葉脈中肋，屬於開放式蟲癭，若蟲則藏匿其中取食中肋或葉脈的木質部導管汁液。本文作者於臺灣發現兩種造癭沫蟬，屬於全世界第三及第四例，分類地位分別為尖胸沫蟬科的 *Philaenus* 屬及沫蟬科 (Cercopidae) 的 *Cosmoscarta* 屬，後者則為全球首例沫蟬科昆蟲的造癭紀錄。本文將擇要報告此兩種沫蟬之分類修訂、寄主範圍及蟲癭形態，詳細研究結果將另文發表。

關鍵詞 (Key words): 造癭沫蟬 (galling froghopper)、沫蟬科 (Cercopidae)、尖胸沫蟬科 (Aphrophoridae)、台灣 (Taiwan)

BD07

螞蟻中跳躍基因多重水平轉移之可能性探討

Multiple putative recent horizontal transfers of a transposon in ants

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Transposable elements (TEs) occupy significant fractions of the genomes of metazoans, including 44.8% in human and about 1.4~8.8% in ants. They are selfish elements that can increase their copy number via inserting into new locations in the host genome. TEs can cross species boundary through horizontal transposon transfer (HTT). HTT is well documented in prokaryotes and is increasingly recognized among eukaryotes. In ants, however, there have been only a few studies examining TEs. The mechanisms or vectors mediating HTT are also unknown in social insects. To identify putative HTT events, we investigated TEs in the red imported fire ant (*Solenopsis invicta*). Analysis of RNA-seq data from male and female germlines revealed a highly expressed TE, *mariner-2DF,* with 97% identity to the consensus orthologous sequence in two *Drosophila* species. The number of synonymous substitutions for the *mariner-2DF* transposase was less than that for three nuclear genes consistent with the possibility that the fire ant gained *mariner-2DF* through a relatively recent HTT. To test if other ants also have *mariner-2DF*, we used a PCR assay to surveyed 20 ant species, which represented five major ant subfamilies from Taiwan. Nine species, which had a patchy phylogenetic distribution, were positive for *mariner-2DF*, suggesting that multiple independent HTT events of this TE into ants. We further tried to determine if a mite commonly associated with the fire ant could be a potential vector for the HTT of *mariner-2DF*. We found support for this possibility as a similar sequence in this mite was detected. We plan to test if this mite might be a potential vector for HTT among ants. Our results suggest the HTT of *mariner-2DF* is a common feature that has not been carefully examined before.

關鍵詞 (Key words): 跳躍基因 (transposable element)、水平轉移 (horizontal transfer)、入侵紅火蟻 (*Solenopsis invicta*)

BD08

台灣各地蜂蟎的遺傳組成與種系發生
Genetic composition and phylogenetic analysis of varroa mite (Acari: Varroidae) in Taiwan

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Among the serious threats to the bee industry, varroa mite feeding on haemolymph of its host evolved highly specialization in honey bee parasitism and drived factors that have led to an upsurge in viral titres such as Acute-Kashmir-Israeli complex and Deformed Wing Virus. Until a past decade and a half, a misleading systematic statement in *Varroa* taxonomy, i.e. *V. destructor* identified within *V. jacobsoni,* was always done. According to a combined mitochondrial COI and morphological evidences, *V. destructor* was nominated as a distinct species from *V. jacobsoni*. In fact, no single morphological character could be applied to distinguish *V. destructor* from *V. jacobsoni*. In this study, molecular evidences of the mitochondrial COI and the nuclear intertranscribed spacer (ITS) are employed to elucidate varroa mites distributing in Taiwan. Genotype composition and phylogenetic analysis show that all varroa mites in Taiwan are *V. destructor*. Moreover, only two genotypes, i.e. Korea genotype and Japan-Thailand genotype, among more than 10 genotypes in the world could be found in Taiwan. Moreover, evidences from ITS, a new data never being exposure in varroa systematics, show a putative hybridization events in varroa evolutionary history.

關鍵詞 (Key words): 狄斯瓦蟎 (*Varroa destructor*)、細胞色素 C 氧化酶 I 基因 (COI)、內轉錄區間 (ITS)

BD09

應用 ITS1 專一性引子探討石蒜科上常見根蟎的組成與分佈

Specific primers based on the nuclear inter transcribed spacer 1 to identify commonly bulb mites (Acari: Acaridae: *Rhizoglyphus*) in the cultured Amaryllidaceae plants in Taiwan

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Rhizoglyphus belonging to the family Acaridae (Acari: Acariformes) would damage host plants by biting their bulb, corm, tuber, tuberous root and/or rhizome. The damaged root would be rotten and then affect the leaf becoming yellow and the branch being distortion and even made host plant death causing a great economic loss. Traditionally, *Rhizoglyphus* was identified based on the adult features, however, the tiny bulb mites with insufficient characteristics makes it difficult to identify the closely related *Rhizoglyphus* and their populations. The study herein, the specific primers from the nuclear inter transcribed spacer 1 (ITS1) are applied to provide a rapid method in bulb mites identification. The specific primers were applied in multiplex PCR to identified *R. echinopus*, *R. robini* and *R. setosus* which were commonly found in the cultured Amaryllidaceae plants. Results show that both mites of *R. robini* and *R. setosus* have a cross infection in scallion in Taichung county, while only bulb mite of *R. robini* was examined in Pingtung county except the *R. echinopus* which infected onion in District Checheng, Pingtung. However, that primers producing unclear specific band in *R. echinopus* indicates its current specific primers should be refined. Moreover, more bulb mite specimens across Taiwan should be acquired to elucidate the distribution and the cross infection possibility in these three bulb mites.

關鍵詞 (Key words): 根蟎屬 (*Rhizoglyphus*)、內轉錄區間 1 (inter transcribed spacer 1)、專一性引子 (specific primer)、多重聚合酶鏈鎖反應 (multiplex PCR)

BD10

台灣的喜蟻性與喜白蟻性昆蟲之生物多樣性初探
The preliminary biodiversity survey of myrmecophilous and termitophilous insects in Taiwan

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喜蟻（白蟻）性生物泛指對螞蟻或白蟻有依賴關係的生物，根據其與寄主之間的互動關係分為蟻盜（synechthrans）、客蟲（synoeketes）、真蟻客（symphiles）、寄生者（ecto- and endoparasites）與取食共生者（trophobionts）。喜蟻（白蟻）性生物的多樣性高，絕大部分為昆蟲，但在台灣的相關研究不多。根據前人研究的結果，喜蟻（白蟻）性昆蟲在台灣共紀錄 5 目 12 科，分別為鞘翅目（Coleoptera）之隱翅蟲科（Staphylinidae）、步行蟲科（Carabidae）與擬步行蟲科（Tenebrionidae）；雙翅目（Diptera）之蚤蠅科（Phoridae）與食蚜蠅科（Syrphidae）；半翅目（Hemiptera）之介殼蟲科（Coccidae）、粉介殼蟲科（Pseudococcidae）與角蟬科（Membracidae）；膜翅目（Hymenoptera）之蟻科（Formidae）與蟻小蜂科（Eucharitidae）；鱗翅目之灰蝶科（Lycaenidae）；直翅目（Orthoptera）之蟻蟋科（Myrmecophilidae）；其中以灰蝶科與粉介殼蟲科之喜蟻性生物學研究較多，其他類群之研究則匱乏。本研究藉由檢視國內標本館館藏、野外觀察及室內飼養的行為觀察，共記錄台灣喜蟻（白蟻）性昆蟲 7 目 21 科，新紀錄有 2 目與 9 科之喜蟻（白蟻）性昆蟲，分別為鞘翅目之牙蟲科（Hydrophilidae）、纓毛蕈蟲科（Ptiliidae）、金龜子科（Scarabaeidae）、僞瓢蟲科（Endomychidae）與朽葉蟲科（Cerylonidae）；雙翅目之麗蠅科（Calliphoridae）與角菌蚊科（Keroplatidae）；蜚蠊目（Blattodea）之穴蠊科（Nocticolidae）；纓尾目（Thysanura）之土衣魚科（Nicoletiidae）。本研究提供各類群於台灣之研究現況、部分類群之採集方式以及初步生態與行為觀察結果。

關鍵詞（Key words）: 喜蟻性生物（myrmecophile）、喜白蟻性生物（termitophile）、寄居動物（inquilines）、共生生物（symbionts）、社會性昆蟲（social insects）

BD11

臺灣產捕植蟎標本困境之解決對策–以天祥亦盲走蟎為例

A clue in puzzle of phytoseiid specimens (Acari: Mesostigmata: Phytoseiidae) from Taiwan - with a practical example, *Scapulaseius tienhsainensis* (Tseng, 1983)

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Acarological studies on phytoseiid mites were discovered for 53 species of Taiwan. The framework on phytoseiid fauna was provided and 48 species including 20 species that named by Mr. Yi-Hsiung Tseng. However, his collections, including type specimens, were no longer available after he retired. We started to collect Taiwanese phytoseiid mites since 1985 and faced a challenge in describing our specimens – we could not compare the type specimens with those new species described by Tseng. Take *Scapulaseius tienhsainensis* as an example, we solved this problem by applying Principle Component Analysis (PCA) to analyze the setal length variation between specimens we collected and the original descriptions. Eight female and two male specimens collected from Mei-Feng, Dongpu, and Anma Mountain were identified as *S. tienhsainensis.* It shows no distinct group in the two axes of the PCA analysis. Morphometrical analysis supports those specimens and holotype description belonging to the same species. The neotype of *S. tienhsainensis* is designated, described and provided with habitus photos and illustrations. It also reveals the importance of setal length variation on phytoseiids identification, and PCA can be used to solve the problems in the alpha-taxonomy of the family Phytoseiidae. For now, we have found half of the species described by Tseng during our survey. We are surveying persistently and trying to collect all phytoseiids' "new species" described by Y. H. Tseng in the coming future.

關鍵詞 (Key words): 捕植蟎 (phytoseiids)、新模標本 (neotype)、主成分分析 (principal components analysis, PCA)

EC01

原生與入侵種白蟻在森林中的資源競爭
Resource competition between endemic and invasive termites in forest

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外來入侵種格斯特家白蟻 (*Coptotermes gestroi* (*Wasmann*)) 是都市地區重要的害蟲，而台灣土白蟻 (*Odontotermes formosanus* (Shiraki)) 是都市及郊區常見的本土原生種白蟻，兩種白蟻共同被發現於國立臺灣大學實驗林管理處所轄之下坪熱帶植物園中。根據該地自 2013 年二月至 2014 年十月間在 595 根木樁上的每月白蟻發生資料，台灣土白蟻的活動範圍是格斯特家白蟻的 23.3 倍 (396:17 根木樁)，遠大於格斯特家白蟻，且格斯特家白蟻有 70.6% (12/17 根木樁) 的活動範圍與台灣土白蟻重疊，在重疊的區域內，兩種白蟻雖然會取食相同位置的木樁，但鮮少共同出現 (3.6%)，主要是以輪替的方式占據木樁，且兩者輪替的機率相近，因此，雖然台灣土白蟻在森林中較格斯特家白蟻優勢，但格斯特家白蟻能在其領地內與台灣土白蟻維持均勢。另外，室內實驗發現兩種白蟻相遇時會打鬥，可解釋兩種白蟻具有明顯的領域行為。自 2014 年十月至 2015 年的八月，我們以 Recruit HD 白蟻餌劑防治該地的格斯特家白蟻族群，這段時間內木樁上共發生 6 次白蟻物種取代，皆是由台灣土白蟻取代格斯特家白蟻，且兩種白蟻活動範圍的重疊率升高為 82.4%，顯示在格斯特家白蟻衰弱後，台灣土白蟻將入侵並佔據格斯特家白蟻的領地。

關鍵詞 (Key words): 外來入侵種 (invasive species)、本土物種 (endemic species)、種間競爭 (interspecific competition)、多屬白蟻群落 (multi-genera termite fauna)

EC02

節角捲葉蛾 (*Strepsicrates rhothia* (Meyrick)) 於番石榴上之生活史
A preliminary study on the life history of *Strepsicrates rhothia* ((Meyrick) on guava

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節角捲葉蛾 (*Strepsicrates rhothia* (Meyrick)) 分類地位為鱗翅目(Lepidoptera)、捲葉蛾科(Tortricidae)，多分布於熱帶及亞熱帶地區，主要寄主作物為桃金孃科之番石榴及蒲桃等，雌成蟲產卵於番石榴之嫩葉或新芽處，孵化後幼蟲取食嫩葉，並吐絲將嫩葉綴合，嚴重為害葉片，密度高時亦會為害花苞及幼果，對番石榴品質與產量造成影響。本研究於 20、25℃二種定溫，相對溼度為 70±10% 及光週期 12D：12L 下，以番石榴葉飼養觀察其生長發育，卵孵化率分別為 99% 及 96%，卵期分別為 5.5 日及 4 日，幼蟲期共五齡，幼蟲期發育所需時間分別為 41.2 日及 30 日；而成蟲壽命分別可存活 13.6 日及 6.7 日；雌蟲每日平均產卵量分別為 2.02 及 2.6 粒，一生平均總產卵量為 36.3 及 38.97 粒卵。於 20 及 25℃下之族群介量，內在增值率 (γ) 為 0.05、0.08，淨增值率 (Ro) 為 12.58、15.73，平均完成一世代所需時間 (T) 為 48.68、34.55 日，終極增殖率 (λ) 為 1.05、1.08。

關鍵詞 (Key words): 節角捲葉蛾 (*Strepsicrates rhothia*)、生活史 (life history)、族群介量 (population parameter)

EC03

熱帶火蟻工蟻體型與種子選擇

Seed selection and worker size in the tropical fire ant *Solenopsis geminata*

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熱帶火蟻（*Solenopsis geminata*）會收集植物種子並儲存於蟻巢內，工蟻收集該棲地內多種植物種子並作為食物來源之一。本研究採集臺灣中南部八個縣市的熱帶火蟻蟻巢內種子，經鑑定後共 15 科 49 種，多以草本植物為主，其中禾本科植物佔 21 種。本研究選取八個縣市中熱帶火蟻收集最多的 10 種植物種子，分別於臺中與嘉義火蟻發生地進行野外種子偏好試驗，結果顯示熱帶火蟻優先選擇搬運芒稷，其次為木麻黃，最後選擇的種子為飛揚草。此外，本研究另以飼養於實驗室的熱帶火蟻為對象，選取 11 種野外熱帶火蟻收集之種子，觀察工蟻優先選取的種子種類，結果顯示熱帶火蟻優先選擇搬運木麻黃，芒稷次之，最後選擇的種子為龍爪茅。試驗中進一步測量搬運種子的工蟻頭寬，以及該工蟻搬運的種子重量，試驗過程中多為中小型工蟻搬運種子，但結果仍顯示工蟻體型與其搬運的種子重量呈正相關。透過本研究的結果，希冀瞭解熱帶火蟻偏好取食的種子種類，及其行為對臺灣禾草植物豐度與組成的影響。

關鍵詞 (Key words): 熱帶火蟻 (*Solenopsis geminata*)、禾本科 (Poaceae)、種子選擇 (seed selection)、種子重量 (seed weight)、工蟻體型 (worker size)

EC04

熱帶火蟻與多樣擬大頭家蟻之種間競爭試驗
Interspecific competition between the tropical fire ant (*Solenopsis geminata*) and Asian marauder ant (*Pheidologeton diversus*)

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熱帶火蟻（*Solenopsis geminata*）為臺灣中南部常見的入侵種螞蟻，不僅攻擊土棲無脊椎動物，亦會對人類健康造成危害，其族群入侵臺灣三十餘年，對於臺灣農業生態系統造成不小衝擊。多樣擬大頭家蟻（*Pheidologeton diversus*）被稱為亞洲掠食蟻，多蟻后型，族群數量龐大，藉由群體獵食（group hunting）迅速獲得食物。在靜宜大學校園發現，熱帶火蟻與多樣擬大頭家蟻為常見之優勢螞蟻，為瞭解兩物種之互動情形，本研究透過實驗室內個體與群體競爭試驗，評估兩物種之競爭能力與侵略性行為。個體試驗部分，顯示熱帶火蟻多採取主動攻擊。試驗 24 小時後，多樣擬大頭家蟻的死亡率顯著高於熱帶火蟻。群體競爭試驗部分，熱帶火蟻會直接侵入對方區域並主動攻擊。試驗後 2 小時與 24 小時兩物種死亡率，多樣擬大頭家蟻死亡率亦顯著高於熱帶火蟻。熱帶火蟻行動速度較多樣擬大頭家蟻快，且攻擊性強，並分泌毒液做為攻擊武器。當兩物種相遇時，多樣擬大頭家蟻會選擇迴避。面對資源時，多樣擬大頭家蟻個體數量多，經常能以量取勝獲取資源，推測多樣擬大頭家蟻在野外獲取資源的效率應較熱帶火蟻高。實驗室內試驗雖無法直接反應野外族群之互動情形，初步仍可瞭解熱帶火蟻的競爭能力以及在臺灣生態環境中與其他螞蟻物種之互動情形。

關鍵詞（Key words）: 熱帶火蟻（*Solenopsis geminata*）、多樣擬大頭家蟻（*Pheidologeton diversus*）、種間競爭試驗（interspecific competition）、死亡率（mortality）

EC05

非洲真葉蟎 *Eutetranychus africanus* (Tucker) (Acari: Tetrnychidae) 於台灣之發生及其生活史初探

A preliminary study of occurrence and life history of *Eutetranychus africanus* (Tucker) (Acari: Tetrnychidae)

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非洲真葉蟎 (*Eutetranychus africanus* (Tucker)) 分類地位為蟎蜱亞綱 (Acari)、葉蟎科 (Tetranychidae)，於台灣之分布為台中、雲林、高雄、屏東等地，其寄主植物達 12 科 19 種植物之多，非洲真葉蟎主要為害植物葉面，造成葉面密布白色小斑點，降低植株行光合作用效率及提早落葉，而影響作物之產量及品質。本研究於 25、28℃二種定溫，相對溼度為 70±10% 及光週期 12D：12L 下，以豔紅西番蓮 (*Passiflora vitifolis*) 葉飼養觀察其生長發育，卵孵化率分別為 76% 及 73%，卵期分別為 4.8 日及 4.5 日，雌雄蟎由卵至成蟎發育所需時間分別為 10.2、9.9 日及 8.6、8.9 日；而有交尾及未交委雌成蟎壽命分別為 10.7、11.1 日及 9.7、9.8 日；雌蟲每日平均產卵量分別為 3.2、2.1 及 4.4、3.0 粒，一生平均總產卵量為 19.5、13.1 及 28.9、18.4 粒卵；後代性比分別為 0.87 及 0.76。於 25 及 28℃下之族群介量，內在增值率 (γ) 為 0.1168、0.1718，淨增值率 (Ro) 為 6.31、9.72，平均完成一世代所需時間 (T) 為 15.83、13.27 日，終極增殖率 (λ) 為 1.123、1.187。未交尾雌蟎產生之後代全為雄性，顯示非洲真葉蟎為孤雌產雄生殖。

關鍵詞 (Key words): 非洲真葉蟎 (*Eutetranychus africanus*)、生活史 (life history)、族群介量 (population parameter)

EC06

早期腐敗對麗蠅產卵之影響

Effects of early decomposition on blow fly (Diptera: Calliphoridae) oviposition

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從屍體死亡發生到麗蠅完成其生命史的過程可以分為五個階段，暴露期 (exposure phase)、偵測期 (detection phase)、接受期 (acceptance phase)、消耗期 (consumption phase) 以及散佈期 (dispersal phase)。先前大部分的研究主要都致力於後拓殖期 (post-colonization stage; 消耗期與散佈期) 中，不同環境因子對幼蟲和成蟲生長發育的影響。然而從暴露期到接受期的前拓殖期 (pre-colonization stage) 的研究也是很重要，卻十分的缺乏。此研究針對大頭金蠅 (*Chrysomya megacephala*) 的接受期進行研究。接受期的定義為從麗蠅抵達屍體到產卵的這段時期，產卵的延遲會導致死後間隔時間 (post-mortem interval; PMI) 估計的偏差。在此研究中，我們假設不同腐敗程度的豬肝可能會影響大頭金蠅產卵的決定。在野外試驗中，我們使用不同腐敗程度的豬肝做為產卵基質，結果顯示在不同處理間 (新鮮~腐敗 8 天) 的卵數具有顯著差異，在後測中，結果顯示腐敗 2 天的處理與新鮮及腐敗 8 天的處理組間具有顯著差異。而在偏好實驗中，不同的產卵處理間的卵數也具有顯著差異。我們的結果指出不同腐敗程度確實會影響麗蠅產卵行為，大頭金蠅偏好腐敗 2 天與 4 天的產卵基質，且幾乎不產卵在腐敗 8 天以上的產卵基質。而產卵在新鮮處理組的產卵基質上的卵量也低於預期。應用這樣產卵偏好的結果可以在未來幫助我們調校 PMI 的估算。

關鍵詞 (Key words): 產卵 (oviposition)、腐敗程度 (decomposition level)、接受期 (acceptance phase)、法醫昆蟲學 (forensic entomology)、大頭金蠅 (*Chrysomya megacephala*)

EC07

如何吸引螞蟻？談雀榕、授粉蜂與螞蟻的三重共生關係

Tripartite mutualism between ants, *Ficus subpisocarpa* and its pollinating fig wasp: How to attract ants?

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Mutualistic interactions are open to exploitation by one or other of the partners and a diversity of other organisms, and hence are best understood as being embedded in a network of biotic interactions. Figs participate in an obligate mutualism in that figs are dependent on agaonid fig wasps for pollination and the wasps are dependent on fig ovules for brood sites. Ants have been recorded on approximately 11% of fig species, including all six subgenera, and often affect the fig-fig pollinator interaction through their predation. *Ficus subpisocarpa* and their associated ant species have been studied in Taiwan since 2009. The colonization by ants on this fig species displayed a great variability of settlements and activities on these trees with no apparent domination of ant species over others. But their presence is a strong repellent for the nonpollinating fig wasps which are parasitizing the obligate mutualism between the *Ficus* trees and their pollinating wasps. We present here data showing that the simple presence of ants over a fig crop can protect very efficiently from the parasites of the mutualism. *Ficus subpisocarpa* is one of the two *Ficus* species that can shelter ant nests within its branches leading to speculate about the coevolution between the ant species dwelling on *F. subpisocarpa* and the fig species itself. We will also discuss about the prerequisite factors that can lead to a tripartite mutualism.

關鍵詞 (Key words): 螞蟻 (ant)、共演化 (coevolution)、榕屬植物 (*Ficus*)、榕小蜂 (fig wasp)、三重互利共生 (tripartite mutualism)

EC08

合歡山地區不同海拔梯度之蝴蝶組成及多樣性

Butterfly composition and diversity along the elevation gradient in Hehuan Mountain area

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Butterfly is one amongst the vulnerable organisms affected by climate factor and vegetation structure in its immediate surroundings. Alpine area in mountainous Taiwan is always facing the habitat destruction for culture activity and the development for recreation. Therefore, we would like to employ butterfly to address how the butterfly composition and distribution along the elevation gradient in Hehuan mountain area. Eight transects each in a 200 m division from Cingjing farm (1800 m) to Wuling (3200 m) were set for butterfly sampling early in the month monthly in 2005, 2006, 2012, and 2013. Totally, 2572 individuals within 130 species of five butterfly families were recorded. Analysis of similarity (ANOSIM) in species abundance and composition shown insignificant differences among the survey years (Global R = 0.028, P = 0.267). Butterflies abundance and richness were mostly found during May to November, and have a particular maximum in September. ANOSIM shown a significantly different composition between the separation transects (Global R = 0.64, P = 0.001). While the highest richness and abundance located in 2,000 m (588 individuals in 99 species) as well as diversity (Shannon-Wiener index, 3.92) that multidimensional scaling analysis (MDS) and cluster analysis shown butterfly composition changeable gradually along the elevation gradient. Butterflies distribute in elevation 1800-2000 m forming distinctly from 2600-3200 m with that of the 2200-2400 m as an intermediate. The vegetation community in the surrounding transect as well as the temperature should be included in upon the elucidation of butterfly composition and dynamics along the elevated gradient alpine area.

關鍵詞 (Key words): 蝶類群聚 (butterfly community)、海拔梯度 (elevation gradient)、合歡山 (Hehuan Mountain)、多樣性 (diversity)

EC09

競爭密度對尼泊爾埋葬蟲雌蟲繁殖策略的影響

The effect of competition density on female reproductive strategy of *Nicrophorus nepalensis* Hope (Coleoptera: Silphidae)

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在族群密度升高的情況下，埋葬蟲有呈現少子化，以增加後代競爭力的現象，本研究即探討尼泊爾埋葬蟲 (*Nicrophorus nepalensis* Hope) 在不同競爭密度下，雌蟲對幼蟲數量的調控，以及對於子代形態的影響。在先前的研究裡，尼泊爾埋葬蟲親代雌蟲在幼蟲時期的「成長密度」，或雌蟲成蟲時期的「遭遇密度」，皆顯示對其子代的數量與形態並無顯著的影響，本研究則進一步檢測雌蟲在資源存在下，「競爭密度」對其繁殖策略的影響。將交配過的雌蟲置於鼠屍與競爭者數量分別為 0 隻、7 隻、15 隻的環境中，檢視「競爭密度」對雌蟲繁殖策略的影響；初步實驗結果顯示，無競爭者的雌蟲產下幼蟲平均數量為 21.5 隻、標準差 9.42 (n = 13)，而面對 15 隻競爭者的雌蟲，其幼蟲數量為 14 (n = 1)，目前數據呈現競爭密度對尼泊爾埋葬蟲雌蟲的繁殖策略可能產生影響。

關鍵詞 (Key words): 埋葬蟲 (burying beetles)、尼泊爾埋葬蟲 (*Nicrophorus nepalensis*)、競爭密度 (competition density)、幼蟲調控 (brood regulation)、育雛數 (brood size)、繁殖策略 (reproductive strategy)

MB01

探索螞蟻的新穎性別決定基因
Mapping a novel sex determination gene in ants

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Sex determination is a fundamental biological process that is regulated by a bewildering large number of molecular mechanisms. In about 20% of animals, including all ants and bees, sex is determined by the ploidy of the individual. Males are haploid and develop from unfertilized eggs with one set of chromosomes. Females are diploid and obtain two sets of chromosomes from fertilization. In these species, the mechanism to ascertain ploidy has been proposed to be complementary sex determination (csd): individuals heterozygous at the sex locus develop into females, whereas hemizygous haploid or homozygous diploid individuals develop into males. Studies in the honeybees, *Apis mellifera,* have identified a single locus, *csd*, as the master sex determination gene. Although ants and honeybees share many putative homologs in the sex determination pathway, evidence for their functional conservation is still lacking in ants. We are using the fire ant *Solenopsis invicta* as a model organism to study sex determination. Our genetic analyses have revealed that the fire ants have evolved a novel master sex determination gene. We have mapped the sex locus to a 131 Kb region, which contains ten predicted genes, none with homology to any known sex genes. An analysis of low coverage genome sequence data of multiple individuals revealed a hypervariable region (HVR) among the sex alleles. Thus far, we have identified 10 sex alleles from individuals sampled from Taiwan and USA in the invasive range. These data are consistent with balancing selection acting on the sex determination locus. Finally, we have detected a ~400bp putatively non-coding RNA transcribed from the HVR locus during embryogenesis, coincident with the timing of sex determination. We are currently conducting functional tests to characterize this novel sex determination gene in ants.

關鍵詞 (Key words): 紅火蟻 (fire ants)、單雙套系統 (haplodiploidy)、補償性性別決定 (complementary sex determination)、高度變異區 (hypervariable region)

MB02

cncC 及 *keap1* 在東方果實蠅 (*Bactrocera dorsalis* Hendel) 不同生長期與青春機素類似物後處理下之反應

Expression of *cncC* and *keap1* in the oriental fruit fly at different developmental stages and treatments of juvenile hormone analogues

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cap'n'collar isoform C (cncC) 是解毒相關基因的上游調節因子，而 Kelch-like ECH-associating protein 1 (keap1) 是他的抑制因子。平時透過兩者的結合，而使 cncC 被降解，影響下游基因的表現。當細胞遭受逆境時，如氧化物或外來毒物刺激，會使得 keap1 與 cncC 的結合能力下降，使 cncC 得以進入核中刺激轉錄下游基因，以抵抗逆境。近期的研究中發現，cncC 及 keap1 可能也與昆蟲的生長發育有關，且會影響到蛻皮激素的合成基因 (如 disembodied (dib) 及 shadow (sad) 等) 及受蛻皮激素調控的下游基因 (如 E75 及 Sgs-3 等) 之表現。為確認其是否參與昆蟲激素調控生長發育，本研究以即時定量聚合酶連鎖反應 (real-time PCR) 探討 cncC 及 keap1 於東方果實蠅 (*Bactrocera dorsalis* Hendel) 不同生長期，如老熟幼蟲、1 及 5 日齡的蛹及初羽化的雌雄成蟲之結果顯示，蛹期的 keap1 表現量較老熟幼蟲高，而 5 日齡蛹的 keap1 表現量比 1 日蛹高接近一倍。以青春機素類似物－百利普芬 (pyriproxyfen) 處理 5 日齡幼蟲後發現，百利普芬雖不影響幼蟲化蛹率，但會對其羽化造成影響。以百利普芬處理後，幼蟲雖然仍會化蛹，但羽化率會受到劑量的影響，且發現 cncC 及 keap1 兩基因的表現量均會受到抑制；再者，蛻皮激素合成基因及蛻皮激素調控的下游基因表現量亦會受到抑制，顯示 cncC 及 keap1 可能參與昆蟲蛻皮激素相關的生理反應，且青春激素可能透過 cncC 及 keap1 調節蛻皮激素。

關鍵詞 (Key words): cap'n'collar isoform C (cncC)、百利普芬 (pyriproxyfen)、東方果實蠅 (*Bactrocera dorsalis* Hendel)、蛻皮激素 (ecdysteroids)

MB03

柑橘鳳蝶視覺系統內組織胺調控型氯離子通道的鑑定與定位

Identification and localization of histamine-gated chloride channels in the visual system of the Japanese yellow swallowtail butterfly, *Papilio Xuthus*

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Spectral opponency is one of the most important mechanisms for processing chromatic information, which has been observed even at the level of photoreceptors in some butterflies. The origin of the photoreceptor spectral opponency is controversial. Since synapse-like structures have been found between photoreceptors in *Papilio xuthus*, and histamine is the only neurotransmitter so far identified in insect photoreceptors, we tried to identify histaminergic channels in their visual system. Two specific antisera against peptides specific to the *Papilio xuthus*-homologs of (*Drosophila*) histamine-gated chloride channels, PxHClA and PxHClB, have been raised. The possible localization of histaminergic synapses has been visualized via fluorescence immunohistochemical staining of anti-PxHClA and -PxHClB. The distinct labeling patterns indicate that PxHClA exists in the second-order neurons postsynaptic to photoreceptors as found in the *Drosophila* lamina monopolar cells (LMCs). On the other hand, the anti-PxHClB labeling is detected in the retina where photoreceptor cell bodies are located: if the PxHClB exist exclusively in photoreceptors around the interphotoreceptor synapses, this channel may be involved in the spectral opponency of photoreceptors.

關鍵詞 (Key words): 光感受器光譜拮抗 (photoreceptor spectral opponency)、組織胺性通道 (histaminergic channel)、免疫組織化學 (immunohistochemistry)、視覺 (vision)、蝴蝶 (butterfly)

MB04

Consumption of dietary sugar by gut bacteria protects *Drosophila* against hyperlipidemia

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Gut microorganisms are essential for the nutritional health of many animals, but the underlying mechanisms are poorly understood. This study investigated how lipid accumulation by adult *Drosophila melanogaster* is reduced in flies associated with the bacterium *Acetobacter tropicalis* which displays oral-fecal cycling between the gut and food. We demonstrate that the lower lipid content of *A. tropicalis*-colonized flies relative to bacteria-free flies is linked with a parallel bacterial-mediated reduction in food glucose content; and can be accounted for quantitatively by the amount of glucose acquired by the flies, as determined from the feeding rate and assimilation efficiency of bacteria-free and *A. tropicalis*-colonized flies. We recommend that nutritional studies on *Drosophila* include empirical quantification of food nutrient content, to account for likely microbial-mediated effects on diet composition. More broadly, gut microorganisms are known to enhance animal nutrition by providing nutrients or degrading foods intractable to animal digestion. This study demonstrates that the microorganisms can additionally contribute to host nutrition by selective consumption of dietary constituents in excess, to improve the nutritional balance of the animal diet.

Key words: *Acetobacter*, *Drosophila*, gut microbiota, sugar utilization, symbiosis

MB05

東方果實蠅對乃力松抗藥性相關之羧酸酯酶身分鑑定
Identification of a carboxylesterase associated with resistance to naled in *Bactrocera dorsalis* (Hendel)

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我國以含乃力松之甲基丁香油作為東方果實蠅 (*Bactrocera dorsalis*) 共同防治及田間族群密度監測之主要藥劑，然現今台灣地區田間東方果實蠅對乃力松已普遍產生抗藥性。本研究針對東方果實蠅乃力松抗性品系中，一種在蛋白質表現量上有明顯提升的羧酸酯酶 *Bd*E5，探討其在乃力松抗藥性中扮演的角色。原態膠體電泳 (native-PAGE) 之酯酶活性染色的結果指出，在抗性品系中帶有高強度 *Bd*E5 條帶之個體出現頻度顯著高於感性品系，顯示 *Bd*E5 條帶的存在與否與果實蠅對乃力松的感受性有關。在抑制試驗中，抗、感性品系之 *BdE5* 在體內 (*in vivo*) 與體外 (*in vitro*) 皆可被乃力松抑制。然而，酯酶總體被抑制的程度則是在抗性品系高於感性品系。以奈米級流速高效能液相層析串聯質譜儀 (NanoLC-nanoESi-MS/MS) 分析進行 *Bd*E5 身分鑑定，經比對 NCBI 蛋白質資料庫而將其註解為東方果實蠅 esterase FE4-like (XP_011200445.1)。進一步以 cDNA 末端快速擴增法 (rapid amplification of cDNA) 取得 2012 鹼基對之 *BdE5* cDNA 全長，包含 1770 鹼基對之開放閱讀框架 (open reading frame)，其可轉譯為 590 個胺基酸長度的假定蛋白。親緣分析則揭露 *Bd*E5 屬於分泌性 β-esterases (E clade)，且與黑腹果蠅 (*Drosophila melanogaster*) 羧酸酯酶 CG6414 (NP_570089) 的親緣關係最接近。此研究確認了 *Bd*E5 與乃力松抗藥性的相關性，並對 *Bd*E5 之身分鑑定與分子特徵提供進一步的了解。

關鍵詞 (Key words): 乃力松 (naled)、羧酸酯酶 (carboxylesterase)、隔離 (sequestration)、東方果實蠅 (*Bactrocera dorsalis*)

MB06

開發益達胺的免疫分析殘留檢測方法
Development of immunoassay in imidacloprid residue detection method

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農藥在農業上具不可取代的地位，適當的使用農藥有助於作物免於病蟲草害的侵擾，減少經濟損失。其中，益達胺 (imidacloprid) 因具系統性及速效性等優點，在田間被廣泛使用於刺吸式口器害蟲的防治。因此，這些農藥在蔬果間的殘留是非常重要的議題。目前常見的農藥殘留檢測方法為儀器分析，如氣相層析串聯質譜儀 (GC-MS/MS) 與液相層析串聯質譜儀 (LC-MS/MS)，但儀器分析耗時、昂貴且需要專業的操作人員。若能開發出一個快速、簡單、低成本的檢測方法，將可提供民眾一個更好的管道進行農藥檢測。因此我們嘗試開發一個利用益達胺單株抗體的免疫分析技術做為新的農藥殘留檢測元件，首先，將益達胺抗原注射進小鼠腹腔內促成免疫反應。免疫數次後，免疫反應最佳的老鼠會被犧牲以製備得以產生單株抗體的融合瘤細胞。生產出的單株抗體經測試效價高達 64,000 倍，對六種新尼古丁類藥劑進行交互反應測試，抗體對高濃度的亞滅培、可尼丁、賽果培有交互反應，對其他新尼古丁類藥劑則無。利用生產的益達胺單株抗體進行酵素鍵結免疫分析 (ELISA) 免疫分析，結果顯示對益達胺的最小偵測極限為 12.5 ppb，變異係數為 3.46%，線性範圍介於 10~1000 ppb 之間。以單株抗體檢測農藥極具發展潛力，未來更能進一步開發出適合大眾使用的農藥殘留檢測工具。

關鍵詞 (Key words): 益達胺 (imidacloprid)、農藥殘留 (pesticide residue)、單株抗體 (monoclonal antibody)

MB07

間隙基因 *hunchback* 於豌豆蚜之非典型表現與發育角色之探討

Non-canonical expression and developmental roles of *hunchback* in the pea aphid *Acyrthosiphon pisum*

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Orthologs of *hunchback* (*hb*) genes play conserved roles in anteroposterior (A-P) patterning, segmentation, and neurogenesis during insect development. These developmental features of *hb* have been identified in both holometabolous and hemimetabolous insects – *Drosophila melanogaster* (fly) and *Acyrthosiphon pisum* (pea aphid) are the examples, respectively. Apart from the conserved patterns, we identified non-canonical expressions of pea aphid *hb* (*Aphb*): (1) localization of *Aphb* mRNA to the anterior pole in the oocytes and early embryos prior to blastulation suggests that *Aphb*, like *Drosophila bcd*, is involved in the specification of the anterior axis; and (2) *Aphb* mRNA and protein are colocalized with gene products of *Apvas1* (a germline marker in the pea aphid), suggesting that *Aphb* may be involved in germline development. The germline expression of *hb* was also identified in the green peach aphid *Myzus persicae*, implying that this is a norm among aphids. We further examined expressions of other gap genes in the pea aphid but did not find similar patterns. Accordingly, we infer that *hb* is a versatile gene for both somatic and germline development in the parthenogenetic and viviparous aphids.

關鍵詞 (Key words): 豌豆蚜 (*Acyrthosiphon pisum*)、體軸 (body axis)、生殖細胞 (germ cells)

ME01

Systemic responses to tissue damage through S-adenosyl-methionine metabolism in *Drosophila*

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Tissue damage triggers an inflammatory response that is required for tissue repair. Organisms may have various systemic responses including an adaptive mechanism for the protection against tissue damage. Metabolism is tightly regulated by organisms under normal physiological states but exhibits flexibility in response to pathologic conditions. We found that glycine N-methyltransferase (Gnmt) that catabolites S-adenosyl-methionine (SAM) is regulated by transcription factor FOXO under necrotic tissue damage, starvation and aging. Our genetic study suggested that Gnmt-mediated SAM buffering is a protective mechanism against energy loss under necrotic inflammation and starvation conditions. Furthermore, we found genetic enhancement of the activity of Gnmt suppressed age-dependent SAM increase, and extended longevity. Deficiency in *gnmt* abrogated the lifespan-extending effect of dietary restriction (DR), the most successful regimen to delay aging and extend longevity. Thus SAM metabolism is a key mediator for DR-dependent benefit.

ME02

The role of gut in pathogen-transmitting mosquito: barrier or gate?

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Vector-borne diseases rely upon organisms, named vectors, such as mosquitoes, ticks or sandflies that have an active role in the transmission of a pathogen from one host to the other. A critical stage in pathogen transmission occurs in the vector midgut, when the pathogens ingested with blood, first makes contact with the gut epithelial surface. To understand the response mechanisms within the midgut environment, including those influenced by resident microbiota against pathogens, we focus on both midgut bacteria specie and vector-pathogen interaction that confers diversity to the vector's competency for pathogen transmission. *Serratia marcescens* isolated from either laboratory-reared mosquitoes or wild populations in Burkina Faso shows great phenotypic variation in its cellular and structural features. Importantly, this variation is directly correlated with its ability to inhibit *Plasmodium* development within the mosquito midgut. Furthermore, this anti-*Plasmodium* function conferred by *Serratia marcescens* requires increased expression of the flagellum biosynthetic pathway that is modulated by the motility master regulatory operon, flhDC. These findings point to new strategies for controlling malaria through genetic manipulation of midgut bacteria within the mosquito.

ME03

台灣地區蜱與小獸類無形體及艾利希氏體監測
Surveillance of *Anaplasma* spp. and *Ehrlichia* spp. in ticks and small mammals in Taiwan

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Anaplasmosis and Ehrlichiosis are tick-borne diseases. To understand the potential risk of *Anaplasma* and *Ehrlichia* infections in Taiwan, tick and small mammal samples were surveyed by SYBR Green real-time polymerase chain reaction (PCR) using *Anaplasma* and *Ehrlichia*-specific primers, in addition, samples from the human highly risk group were also selected for screening. A total of 648 parasitzing ticks of small mammals collected from 2006 to 2010 in ten Counties in Taiwan were tested. The infection rate of *Anaplasma* or *Ehrlichia* in all ticks was 19.9% (129/648). Three species of ticks were found to be positive by PCR, *Ixodes granulatus* tick has the highest infection rate (33.2%; 77/232), followed by *Haemaphysalis bandicota* (17.0%; 40/236), and *Rhipicephalus haemaphysaloides* (6.67%; 12/180). Seven species of *Anaplasma* and *Ehrlichia* were identified in this study. Among them, three species are zoonotic agents, including *Anaplasma phagocytophilum*, *Ehrlichia chaffeensis*, *Candidatus Neoehrlichia mikurensis*, in addition, we also found a pathogen of bovines (*Anaplasma bovis*). To detect the *Anaplasma* and *Ehrlichia* infections in small mammal hosts for ticks, spleen and blood specimens from small mammal hosts were collected and tested by real-time PCR. The infection rates of *Anaplasma* and *Ehrlichia* were 64.1% (59/92) and 48.4% (44/91), respectively. Pairwise nucleotide sequence analysis of 16S rRNA genes showed that *A. phagocytophilum* and *A. bovis* discovered in Taiwan were new variants, whereas *Candidatus Neoehrlichia mikurensis* was identical with strains from other areas of the world. Due to the high infection rates of *A. phagocytophilum* in ticks and small mammals, and the same habitats for ticks and chiggers (vectors of scrub typhus) in Kinmen County, we tested *A. phagocytophilum* infections in patients with suspected scrub typhus in Kinmen County in 2011-2012. The seropositive rate of *A. phagocytophilum* of suspected scrub typhus patients was 19.7% (57/289), and 6.38% (3/47) for healthy control group volunteers. The results showed significant difference ($X^2 = 4.9$, $p = 0.0268$) between these two groups and suggested the occurrence of Anaplasmosis in Kinmen County.

Key words: *Anaplasma* spp., *Ehrlichia* spp., ticks, small mammals, polymerase chain reaction

ME04

麗蠅（雙翅目：麗蠅科）產卵研究及其法醫昆蟲學重要性
Blow fly (Diptera: Calliphoridae) oviposition and its significances in forensic entomology

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Undoubtedly, necrophagous blow fly species in family Calliphoridae is one of the most important groups which has been intensively studied and applied in the field of forensic entomology. Developmental profiles of blow fly larvae are essential in estimating the minimum postmortem interval of victims in forensic investigation; thus, the blow fly oviposition, the beginning of a fly life's, is a crucial factor. Unfortunately, we don't know too much about its biological attributes so far. This study is trying to review our recent discoveries about blow fly oviposition with special focus on ecological and behavioral aspects from the application viewpoints of forensic entomology; and concluding the following: 1) significant oviposition preference was confirmed in blow flies; 2) visual cue should be crucial for blow flies during oviposition; 3) blow flies could recognize their environments, conspecific and xenospecific companions or competitors before laying eggs; 4) gregarious oviposition was proved as a special behavior in blow flies under controlled experiments; 5) nocturnal oviposition of blow flies is still controversial, whereas gravid female flies did show this behavior under laboratory condition. 6) both decomposition level and egg load affect the laying time and the selection of laying sites.

關鍵詞 (Key words): 產卵偏好 (oviposition preference)、聚集產卵 (gregarious ovipositon)、夜間產卵 (nocturnal oviposition)、視覺因子 (visual cues)、金蠅屬 (Chrysomya)

ME05

Pathobiology of vector tick-host interactions and anti-inflammatory molecules in tick-saliva

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Ticks are obligatory blood-sucking ectoparasites and while feeding for a single blood-meal, ticks remain attached to hosts by firmly embedding their barbed mouthparts for several days. Like mosquitoes, they cannot canulate an individual blood vessel; rather, they cause extensive damage in vascular beds and underlying tissues leading to the development of a blood pool, a feeding lesion of ticks. In the blood pool, blood and tissue fluid accumulate from where ticks gradually become engorged after several consecutive days of feeding. Extensive tissue damage and development of a blood pool are common features of tick feeding. In fact, a blood pool is a battlefield where a highly organized submicroscopic molecular war takes place among host, vector and invading pathogen, and each axis wants to win to survive. However, ticks can cleverly manage the host responses developed against the biting insult to ensure an adequate blood meal. Tick salivary gland molecules are thought to have pivotal roles in successful feeding on blood meals from hosts. We discovered that tick-saliva contained haemagin, an anti-angiogenic agent and longistatin, a plasminogen activator efficiently inhibited wound healing and hemostasis, respectively, during acquisition of blood meals from hosts. Moreover, longistatin bound with the receptor for advanced glycation end products (RAGE), the central player in inflammation; thus, down-regulated production of vital inflammatory effectors including adhesion molecules and cytokines, and eventually counteracted amplification of inflammatory signal transduction elicited during tick bites. Our works shed light deeply into the tri-angular interaction among hosts, vectors, and pathogens which may play critical roles to control disease vectors and/or vector-borne diseases.

ME06

Horizontal gene transfer of a vertebrate vasodilatory hormone into ticks

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The horizontal gene transfer (HGT) of functional molecules is found in higher eukaryotes, but its influence on their evolution has not been fully evaluated. Here we describe the HGT of a vertebrate vasodilator, adrenomedullin (ADM), into ticks of the genus *Ornithodoros* and hypothesize its involvement in tick evolution[1)]. The salivary glands of *Ornithodoros* ticks contain ADM-like vasodilators, tick-adrenomedullin (TAM). ADM-like molecules, including TAM, are conserved in all vertebrates and *Ornithodoros* ticks but not in any other invertebrates, including *Argas* ticks, which share a common ancestor with *Ornithodoros* ticks. In addition, the close evolutionarily relationship between TAM and ADM is supported through genomic sequence and phylogenetic relatedness analyses. *Ornithodoros* ticks horizontally acquired vertebrate ADM and currently employ it to facilitate blood feeding. The acquisition of TAM might result in a beneficial change in feeding behavior and influence the divergence of *Ornithodoros* ticks.

ME07

蟲媒立克次體之分離培養與血清學檢驗

Isolation of vector-borne rickettsiae and their serological diagnostics

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Among vector-borne rickettsial diseases, scrub typhus and murine typhus are the two known zoonotic diseases in Taiwan. Scrub typhus caused by *Orientia tsutsugamushi* is the most important acute febrile illness associated with the major rickettsioses. Murine typhus caused by *Rickettsia typhi* which is transmitted by rat flea. Flea-borne rickettsioses caused by *Rickettsia felis* were recently designated as a transitional group and have been identified in cat fleas in Taiwan. Development of the shell vial cell culture isolation technique and the extensive use of bacterial identification based on molecular techniques have greatly improved the detection of novel rickettsial species and the understanding of newly described rickettsioses in recent decades. For example, many novel species of spotted group rickettsiae (SFG) have been isolated from ticks in Taiwan. Because of the lack of a specific reference bacterial antigen, the diagnosis for SFG often relied on a commercial immunofluorescence assay (IFA), which offered only *R. rickettsii* and *R. conorii* antigens, and positive cases were identified though serologic cross-reaction. In this study, we describe the shell-vial isolation technique for establishment of local rickettsiae. Using these rickettsial antigens, we develop the micro-IFA as the reference standard for serodiagnosis of vector-borne rickettsioses.

關鍵詞 (Key words): 立克次體 (rickettsia)、恙蟲病立克次體 (*Orientia tsutsugamushi*)、斑點熱立克次體 (spotted fever group rickettsiae)、地方性斑疹傷寒立克次體 (*Rickettsia typhi*)、免疫螢光抗體分析 (immunofluorescence assay)

MK01

Biology and ecology of an endoparasitoid fly *Misotermes mindeni* (Diptera: Phoridae) of subterranean termite *Macrotermes gilvus* (Blattodea: Termitidae)

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Macrotermes gilvus (Hagen) is an important mound building termite species in Southeast Asia. It is an agricultural pest of sugarcane plantation, and also secondary pest of buildings and structures. In 2008, we discovered a new species of scuttle fly (*Misotermes mindeni* Disney & Neoh) parasitizing on the major soldier of *M. gilvus*. The behavioral, physiological and morphological changes in the parasitized termite host were evaluated. An abnormally rounded head capsule and remarkably short mandibles are characteristics of a parasitized soldier. The older larval fly stages were found only in major soldiers. We found that parasitism mainly occurred in termite mounds overgrown with grass and mounds that had been broken up previously for other experiments. The parasitized soldiers showed a significantly lower level of interspecific aggressiveness compared with healthy soldiers ($P < 0.05$). Parasitized soldiers also changed in habitat preference to one isolated chamber of the nest. This might be an adaptive strategy that facilitates parasitoid dispersal, provides protection to parasitoids, and reduces the risk of parasitism to host colony. The metabolic rate of parasitized hosts was significantly higher than that of unparasitized termites. Mean total body water content of parasitized major soldiers was significantly lower than that of unparasitized termites. Parasitized hosts also had significantly lower total body water loss rates and higher cuticular permeability than unparasitized major soldiers. Parasitized major soldiers survived almost twice as long as unparasitized termites and they had significantly higher tolerance to water loss compared to unparasitized termites. Body lipid content in parasitized hosts was significantly higher than that of unparasitized termites. Finally, parasitized hosts had a significantly lower percentage of cuticular water content than unparasitized major soldiers.

關鍵詞 (Key words): endoparasitoid, Macrotermes, termites

MK02

檢測間斷式呼吸之水分節約假說及發展機制性模式
A test of hygric hypothesis for discontinuous gas exchanges and development of mechanistic models

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本演講將包含昆蟲呼吸演化及機制性模式發展兩個主題。第一主題是檢驗昆蟲間斷式呼吸 (discontinuous gas exchange, DGC) 之演化假說。許多昆蟲在休息時，其呼吸 (spiracle) 呈現關閉、快速開合及打開三階段重複動作。水分節約假說 (hygric hypothesis) 解釋 DGC 是昆蟲因應乾旱環境下的演化產物，因為關閉呼吸孔能阻止呼吸水分蒸散 (respiratory evaporative water loss, REWL)。為了檢測此假說，我們測量在以色列不同氣候區的近緣種蝗蟲於 DGC 及連續呼吸期間之 REWL 及氣囊體積。結果顯示：在控制代謝量的影響後，來自潮濕棲地的物種 (*Ocneropsis bethlemita*, *O. lividipes*) 之 REWL 在兩種呼吸形式之間並無顯著差異。沙漠物種 *Tmethis pulchripennis* 之 DGC 有水分節約效果，這可能與其氣囊較大有關。因此，我們認為 DGC 並非是為了節約水分而產生，但氣囊大小會影響氧氣儲存量、呼吸孔關閉程度及時間長短，進而影響 REWL 的量。第二主題是發展機制性模式預測沙漠蝗蟲 (*Schistocerca gregaria*) 之生態表現。機制性模式可整合地貌、氣候、動物生理及行為特徵，模擬動物在地景尺度下的生存指標，目前已被用於入侵種及氣候變遷相關的生態議題上。本研究目標為預測此害蟲入侵以色列後之適育地、孵化時間及發育速度。目前正在蒐集生物參數，包括幼體在不同體溫時之發育及生長速度、偏好溫度等，預計將於明年夏季進行野外工作驗證模式之預測能力。

關鍵詞 (Key words): 蝗蟲 (grasshopper)、氣囊體積 (tracheal volume)、水分散失 (water loss)

MK03

微核醣核酸在果蠅化蛹前後的表現及演化

Evolutionary dynamics of microRNA expression at the onset of *Drosophila* metamorphosis

葉淑丹

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MicroRNAs (miRNAs) are ~22 nucleotide non-coding RNA molecules that regulate gene expression post-transcriptionally. Changes in miRNA abundance may result in different pathologies or morphological variation. However, the extent to which miRNA expression levels have evolved overtime, the role of different evolutionary forces play in shaping these changes, and whether this variation in miRNA expression can reveal the interplay between miRNAs and mRNAs remains poorly understood. Using deep-sequencing and multi-species microarrays, we assayed miRNA expression levels immediately before (≥18BPF) and after (PF) the increase of ecdysone titer responsible for triggering metamorphosis in four strains of *D. melanogaster* and two closely-related species. In contrast to their sequence conservation, approximately 25% of miRNAs showed significant within-specie variation in male expression levels at ≥18BPF and/or PF. Modifications in expression bias between two developmental stages appeared in approximately 33% of miRNAs. Further analysis in interspecific comparison revealed that changes in miRNA abundance accumulate linearly over evolutionary time at PF but not at ≥18BPF. Importantly, ≥18BPF-enriched miRNAs showed the greatest variation in expression levels both within and between species, so they are less likely to evolve under stabilizing selection. Functional attributes, such as expression ubiquity, appeared more tightly associated with lower levels of miRNA expression polymorphism at PF than at ≥18BPF. Furthermore, ≥18BPF- and PF-enriched miRNAs showed opposite patterns of covariation in expression with mRNAs, which denoted the type of regulatory relationship between miRNAs and mRNAs. Collectively, our results show contrasting patterns of functional divergence associated with miRNA expression levels during *Drosophila* ontogeny.

關鍵詞 (Key words): 果蠅 (*Drosophila*)、基因表現變化量之演化 (evolution of expression profiles)、微核醣核酸 (miRNAs)、昆蟲變態(metamorphosis)、微核醣核酸與信息核醣核酸的關聯性 (miRNA-mRNA associations)

PC01_BD

分子糞便學：褐河烏只獵取水面下的食餌？
Molecular scatology: Have drown dippers only hunt for food underwater?

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河烏雖然身為燕雀目的一員，但卻是擁有潛入水中覓食本領的溪流鳥類。根據以往研究顯示，河烏以水棲昆蟲為主食，偶爾取食魚、蝦、蟹等生物。而瞭解生物食性有三種方法：直接觀察、侵入性調查，以及分子定序技術。直接觀察較難準確鑑定且耗時，侵入性調查會傷害研究目標，本研究利用分子定序技術鑑定糞便中獵物碎片。於河烏非繁殖季（2014 年 10 月）進行涵蓋七家灣溪流域之五個地點糞便採樣，再以次世代定序（next generation sequencing，NGS）來鑑定褐河烏（*Cinclus pallasii*）之獵物身分。已定序出 382 萬多條序列(可區分出 16 萬多種序列)，再與 NCBI (national center for biotechnology information) 比對序列(取序列重複數大於 1000 次的 87 種，佔所有序列量的 75%)，可鑑定出 6 目 8 科 10 屬，解析度達屬階級。前兩名的序列量已佔 86%，分別是家蠅科黑蠅屬（*Ophyra*）為最多（58%序列量），且同一性（identities）最高可達 95%；其次為扁蜉蝣科 *Rhithrogena* 屬（28%序列量），同一性最高可達 90%。此外，在此地的水棲昆蟲調查中發現，目前並無家蠅科黑蠅屬採集紀錄，且解剖顯微鏡下觀察河烏糞便也沒有發現相似的陸生昆蟲碎片，因此推測原因可能河烏有取食到陸生昆蟲，或排泄後之糞便受到黑蠅屬昆蟲產卵汙染，尚須進一步調查釐清。

關鍵詞 (Key words): 河烏（*Cinclus pallasii*）、食性（diet）、次世代定序（next generation sequencing）

PC02_MB

孤雌胎生豌豆蚜胚胎發育:體軸決定與形式生成

Embryonic development of the parthenogenetic and viviparous pea aphid: axis determination and pattern formation

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The pea aphid *Acyrthosiphon pisum*, a rising model for genomics and developmental studies, propagate offspring parthenogenetically and viviparously. Hence oogenesis is followed by embryogenesis within the same ovariole. Previously, we identified anterior localization of *hunchback* (*Aphb*) mRNA in oocytes and early embryos of the asexual pea aphid, suggesting that the symmetry breaking in the anterior pole specifies the anterior axis. Expression of *caudal* (*Apcad*) mRNA, however, was first identified in the egg posterior until blastoderm formation, implicating that determination of the anteroposterior (AP) axis is not synchronous in the asexual pea aphid. For studying the formation of the dorsoventral (DV) axis, we detected expressions of *decapentaplegic* (*Apdpp*) and *short gastrulation* (*Apsog*), both of which are toolkit genes for DV axis formation in insects. Asymmetric distribution of mRNAs transcribed by the four *Apdpp* genes (*Apdpp1-4*) was not observed whilst *Apsog* could be identified in the ventral region of the cellularized embryos. Before blastoderm formation, mRNAs of both genes were randomly distributed. We thus argue whether DV axis is determined after the embryo becomes cellularized. Interestingly, we identified colocalization of mRNA transcribed by *Aphb* and the germline gene *Apvas1* in the germ cells throughout development. Whether *Aphb* is involved in the germline development requires further investigation using functional tools, such as RNA interference. Besides, we also examined the patterning of *Hox* genes. All of the efforts described above, we expect, can enable us to understand how a parthenogenetic and viviparous aphid constructs its body plan at the molecular basis.

關鍵詞 (Key words): 豌豆蚜 (pea aphid)、體軸 (body axis)、發育基因 (developmental genes)、不對稱分佈 (asymmetric distribution)

PC03_BD

探討入侵紅火蟻蟻后氣味分子之來源

Identification of the origin of the olfactory cue(s) in the fire ant queens *Solenopsis invicta*

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The two types of social organization, monogyny and polygyny, in the fire ant (*Solenopsis invicta*) are known to be perfectly associated with a single gene *Gp-9*. In monogyne colonies, all individuals have the *Gp-9BB* genotype, and workers show strong aggression toward any additional queens. Polygyne workers (have either the *Gp9-BB* or *Gp-9Bb* genotype) can accept additional *Gp-9Bb* queens but reject all *Gp-9BB* queens. Polygyne workers rubbed against introduced *Gp-9BB* queens get attacked by their nestmates, showed that there is (are) a unique odor cue(s) differentiating *Gp-9BB* and *Gp-9Bb* queens causing distinct behavior in polygyne workers. To localize the olfactory cue(s) on *Gp-9BB* queens, we conducted rubbing experiments on 30 mature monogyne virgin queens (VQs) from three different colonies (using polygyne VQs as control). We found rubbing monogyne VQs elicited significantly stronger aggression compared to the controls. Rubbing against the abdomen showed the closest behavior to rubbing against the full body. However, our results suggested that rubbing order may also affect the aggression instances and the odor cue(s) may be spread throughout the whole body of the VQ.

關鍵詞 (Key words): 入侵紅火蟻 (*Solenopsis invicta*)、社會型態 (social organization)、Gp-9、社會行為 (social behavior)、氣味分子 (olfactory cue)

PC04_MB

鑑定先天性免疫反應和多去氧核糖核酸病毒之小分子

Identification of innate immune response and microRNA function from *Spodoptera litura* (Fabricius) and *Snellenius manilae* (Ashmead) infected by polydnavirus

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Innate immune responses are the most significant defense against micro-organisms infections. Antimicrobial responses, Toll, Imd, Jak-STAT, and RNAi pathways, produce different kinds of antimicrobial peptides (AMPs) to protect insects when triggered, but Polydnaviruses (PDVs) can suppress these kinds of immune reactions. PDVs are symbiotic viruses used by parasitoid wasps to manipulate the physiology of lepidopteran hosts and induce parasitism. Virus particles are only produced by calyx cells in female wasp ovaries and enter lepidopteran hosts alongside wasp eggs. Viral products are essential for wasp development and ensure wasp survival in lepidopteran larvae by interfering with the immune responses and development of lepidopteran hosts. The proviral genome is comprised of two components, the core gene and the encapsidated genome, which produce gene products essential for replication and virulence. Encapsidated genomes are the main weapons used to suppress immune responses as they not only decrease gene expression, but also reduce amounts of AMPs from the lepidopteran host. The genome is made up of 15 segments (lettered A to O), which are individually packaged into virions. The noncoding regions of the encapsidated genome are responsible for immunosuppression. MicroRNAs (miRNAs) are small noncoding RNAs that play a key role in regulating gene expression in eukaryotes. The encapsidated genome segments J, B, and C have been found to persist in host genomes through integration and can potentially express several miRNAs through structural prediction. It is theorized that these predicted miRNAs are able to suppress the immune responses of *Spodoptera litura*. This study seeks to explore the novel roles of miRNAs in the immunosuppression of PDV hosts and the mechanisms underlying this phenomenon. Combined with other microbiological control agents, this unique feature may hold potential for pest management control in the future.

關鍵詞 (Key words): Polydnaviruses (PDV), miRNA, *Spodoptera litura*, *Snellenius manilae*, immunosurppression

PC05_EC

人為噪音對黃斑黑蟋蟀鳴叫行為之影響初報
Preliminary report on the impacts of anthropogenic noise on calling behavior of *Gryllus bimaculatus*

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許多種環境污染會對生物造成傷害，其中人為噪音更被認為是全球性汙染，並會影響使用聲訊溝通的生物。根據 Yager1999 年的報告，昆蟲在偵測聲音上已獨立演化至少 19 次，可用多元方式及身體各段感受 10Hz 至 100kHz 的聲音，期中，蟋蟀及蟬最低能感受 2Hz 至 6kHz 的聲音。而大多數昆蟲使用低於 10kHz 聲音傳訊，又能接收極大部分的人為噪音，因此，昆蟲在傳訊時受噪音干擾可能比想象中嚴重。本研究使用低海拔常見的黃斑黑蟋蟀 (*Gryllus bimaculatus* De Geer，1773) 作為研究物種，比較道路旁不同環境噪音分貝下的蟋蟀鳴叫聲學特徵變化，包含頻率、唧聲率及脈衝比等，觀察面對人為噪音環境時，黃斑黑蟋蟀的適應方式。以往相關實驗多針對脊椎動物進行研究，鮮少以昆蟲作為研究物種。隸屬食物網底層的昆蟲是許多生物的食物來源，自環境中消失的話，將會嚴重影響生態系平衡。因此，若能更深入的了解人為噪音對昆蟲的影響，未來在人為開發或環境保育等相關議題上，可提供不同層面的資訊。

關鍵詞 (Key words): 黃斑黑蟋蟀 (*Gryllus bimaculatus*)、人為噪音 (anthropogenic noise)

PC06_BD

熱帶火蟻的性別決定系統
What type of sex determination does *Solenopsis geminata* use?

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For most insect species, the downstream components of the sex determination pathway are conserved, but the upstream genes and mechanisms are very diverse. The honey bee (*Apis mellifera*) and the red imported fire ant (*Solenopsis invicta*) are both eusocial Hymenoptera and use the single-locus complementary sex determination (sl-CSD) mechanism whereby heterozygosity at a single sex locus results in females and hemizygosity (or homozygosity) at this locus yields males. Although both species use sl-CSD our results have shown that *S invicta* use a novel sex locus, which we call the *sex determination locus* (*SDL*). I would like to determine the sex determination gene in the related tropical fire ant (*Solenopsis geminata*). It is likely that *S. geminata* also uses *SDL*, but since the upstream sex determination genes appear to evolve very quickly it may be that *S. geminata* uses another gene. Female heterozygosity at orthologous microsatellite markers tightly linked to *SDL* on many independent samples would support orthology of the *SDL* gene. In contrast, observing any homozygosity at these loci would exclude *SDL*. Thus far, genotyping of female samples has revealed heterozygosity at many, but not all, loci near *SDL*. The homozygous loci have low allele numbers and thus probably have low information content. I plan to identify additional loci with greater allele number and test them for heterozygosity. Genotyping of males has revealed at least 12 sex haplotypes in the Taiwan population. While my data are compatible with *SDL* being the sex locus, stronger evidence would be the observation that all diploid males are homozygous at *SDL*. No diploid males have been reported in *S. geminata*, so I am also trying to create “match matings” artificially.

Key words: sex determination, haplodiploidy, single-locus complementary sex determination, *Solenopsis geminata*, microsatellite

PC07_MB

以昆蟲桿狀病毒轉導 shRNA 的表現來抑制前列腺癌細胞之 IL-8 基因的表現

Expression of shRNA to inhibit IL-8 gene expression in prostate cancer cells transduced with recombinant baculovirus

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前列腺癌是目前發生率以及死亡率皆很高的癌症，研究發現雄激素非依賴型癌細胞中 IL-8 的表現量會顯著上升，而且 IL-8 已被證實與前列腺癌的惡化有關。本研究首先比較四種前列腺細胞之 IL-8 的表現，結果顯示雄激素非依賴型 (Androgen independent prostate cancer, AIPC) 前列腺癌細胞 DU145 及 PC-3 之 IL-8 的表現明顯比偏正常之前列腺細胞 RWPE1 及雄激素依賴型 (Androgen dependent prostate cancer, ADPC) 前列腺癌細胞 LNCaP 之表現量多，尤其是 PC-3 之 IL-8 的表現量比 RWPE1 高約 6 倍。接著以 Oligoengine 軟體針對人類 IL-8 之 cDNA 序列找出受 shRNA 抑制性較高的五個位置來設計基因片段，並利用重組昆蟲桿狀病毒作為哺乳動物細胞基因轉殖載體的技術平台，以 Bac-to-Bac 表現載體系統套組構築建構可表現 IL-8 之 shRNA 的重組加州苜蓿夜蛾核多角體病毒 (*Autographa californica* nucleopolyhedrovirus, AcMNPV) 命名為 vAcMNPV-shRNA。轉導試驗顯示 PC-3 接受重組感狀病毒轉導之效率最高，因此後續實驗即進一步探討 PC-3 受 vAcMNPV-shRNA 轉導之影響。以 M.O.I = 750 之病毒液轉導 PC-3 細胞，於 48 小時觀察結果顯示 118 與 338 位置之 vAcMNPV-shRNA，抑制癌細胞生長的效果最明顯達到 40%以上。以西方墨點法來檢測 PC-3 細胞之 IL-8 基因之表現，證實明顯受 vAcMNPV-shRNA 的轉導而被抑制。本研究結論顯示昆蟲桿狀病毒可轉導前列腺癌細胞，藉由 IL-8 基因之 shRNA 的表現來抑制前列腺癌細胞之 IL-8 基因的表現，以達到抑制癌細胞生長之效果，未來可望成為基因療法的途徑之一。

關鍵詞 (Key words): 昆蟲桿狀病毒 (baculovirus)、shRNA (short hairpin Ribonucleic acid)、白血球介素-8 (interleukin-8, IL-8)、基因療法 (gene therapy)

PC08_MB

*Hz*NV-1 病毒的微小核醣核酸藉由表觀遺傳調控於宿主體內建立潛伏性感染

Heliothis zea Nudivirus-1 miRNA establishes latent infection in host via epigenetic regulation

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Heliothis zea nudivirus-1 (*Hz*NV-1) is an insect virus that can induce both lytic and latent infections in many insect cell lines. During latent infection, the persistency-associated gene 1 (*pag*1) expresses several microRNAs (miRNAs) and is the only detectable *Hz*NV-1 gene. Two of the miRNAs derived from pag1 have been found to suppress and silence an early gene, *Hz*NV-1 HindIII-I 1 (*hhi*1), and furthermore can promote the establishment of latent infections. Previous reports have shown that persistent infection of Herpes simplex virus (HSV) is highly associated with epigenetic regulation of chromatin structure and is regulated by latent-specific miRNAs. Since *pag*1 is a non-coding transcript, it could regulate host chromatin structures through miRNAs to further establish latent infections. Nevertheless, the exact *pag*1 mechanism that alters viral infections is still unknown. In this study, CHIP (Chromatin Immunoprecipitation) experiments were performed to examine whether miRNAs encoded by pag1 target histone-modification related enzymes. This study not only provides a better understanding of the *Hz*NV-1 infection mechanism but also the relationship between viral miRNAs and their hosts.

關鍵詞 (Key words): *Heliothis zea* nudivirus (*Hz*NV-1)、微小核醣核酸 (miRNA)、持續性感染 (persistent infection)、表觀遺傳調控 (epigenetic regulation)

PC09_EC

臺灣臺北的雀榕上榕果小蜂種間關係

Species interactions between chalcid wasps (Hymenoptera: Chalcidoidea) on *Ficus subpisocarpa* in Taipei, Taiwan

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Ficus species have the species-specific mutualistic relationship with Agaonidae pollinating wasps. Meanwhile the non-pollinating fig wasps, including gall-maker, parasitoid and inquilines, are important in the study of the community structuration: species with diverse trophic levels are gathered around one fig opening great opportunities for the understanding of community ecology. *Ficus subpisocarpa* had highly diverse wasp fauna with most of the wasp species still undescribed and little is known about interspecific interactions. Thus, trees in NTU Campus and Daan Park, in Taipei city, were surveyed for studying the wasp fauna of *F. subpisocarpa*, and investigate the wasp interactions by describing the oviposition sequence. Moreover, wasp exclusion experiments were also done on the same trees. In this study, 19 chalcid wasp species were observed and identified. Through oviposition sequence, *Camarothorax* sp1 and *Acophila mikii*, which laid eggs in A phase figs, were considered to be gall-makers. The wasps that oviposited in B or C phase figs, such as *Arachonia* sp., *Sycoryctes* sp., and most of *Sycophila* spp., should be parasitoids or inquilines. While the species *Philotrypesis* sp1 was considered as parasitoid due to the late egg-laying period. Neverthless most of the non-pollinating fig wasps, which could affect the population of pollinators, laid eggs in C phase figs. Thus, when the figs were protected from the non-pollinating wasps inside fabric bags, the abundance of pollinators increased by almost 50%. The results of A-bagged and control figs also showed that, the population of pollinators remain one-third of the wasp community. Therefore, even there were high diversity and density in non-pollinators, the affection on pollinator abundance was small. The synchronous fig production of *F. subpisocarpa*, and the dispersive egg-laying strategy of non-pollinators could also lower the threats on flower overused.

關鍵詞 (Key words): 雀榕 (*Ficus subpisocarpa*)、榕果小蜂 (fig wasp)、小蜂相 (wasp fauna)、產卵時序 (oviposition sequence)、種間關係 (species interaction)

PC10_PM

水稻瘤野螟抗性之篩選

Screen for rice leaffolder *Cnaphalocrocis medinalis* (Guenée) resistant rice genotype in Taiwan (Lepidoptera: Pyralidae)

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Rice is the major cereal crop in Taiwan and has the most cultivated area and crop production in Taiwan. Recently, brown planthopper, white backed planthopper, and rice leaffolder (*Cnaphalocrocis medinalis* Guenée) are three major rice pests in Taiwan. Planthopper-resistant rice varieties have been widely used. However, we have no rice leaffolder rice variety in Taiwan. Thus, we are trying to do large screening of all Taiwan rice genotypes and expect to have rice leaffolder resistant rice genotypes. Furthermore, we have been tested several successful artificial insect diets (fall armyworm corn strain, fall armyworm rice strain, and even the suggestion recipe of rice leaffolder artificial diets in several publications.) However, all tested artificial diet failed to rear rice leaffolder. Thus, we suggested that the previous corn seedling rearing technique is still the best rearing method for rice leaffolder. In addition, rice leaffolder in Taiwan is a migratory insect which immigrate from Mainland China every year. The maximum population of rice leaffolder in Taiwan is usually observed at rice tillering and panicle initiation stages on second crop season. However, rice leaffolder seems not over-winter in Taiwan. It may lack optimal host plants or cannot survive under lower temperature during winter season. Thus, we collected rice leaffolder throughout Taiwan to gain the information of the genetic variation of rice leaffolder in Taiwan and will use this information for further rice laeffolder screening process.

關鍵詞 (Key words): 瘤野螟 (*Cnaphalocrocis medinalis* Guenée)、抗性 (resistance)、水稻基因型 (rice genotype)

PC11_BD

台灣的象白蟻屬(蜚蠊目: 白蟻科)之分類、物種分布模擬與生物學
Taxonomy, species distribution modeling and biology of *Nasutitermes* (Blattodea: Termitidae) from Taiwan

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Nasutitermes Dudley is the most speciose genus of Termitidae and its taxonomy was mainly based on the morphology of the soldier caste. Lately, application of cuticle hydrocarbons analysis and gene sequencing had revealed several cryptic species and synonyms. In Taiwan, taxonomy of *Nasutitermes* remains some long-existed problems. In addition to basic science, *Nasutitermes* had been recorded as an agricultural pest and emerged urban pest, but no study focus on its potential threat to Taiwan. In this study, *Nasutitermes* from Taiwan is revised. According to DNA sequence and morphometric analysis, monophyly of the three Taiwanese species, *Nasutitermes kinoshitai* (Hozawa, 1915), *Nasutitermes parvonasutus* (Nawa, 1911) and *Nasutitermes takasagoensis* (Nawa, 1911) are confirmed. The identification keys of the three species are provided based on alate, soldier and worker castes. Species distribution modeling of the tree species were used to quantify their ecological niche and to define major factors may result in niche segregation. Based on 438 colony samples, the polymorphism of soldier and worker, dispersal flight season of alate, and their termitophiles of the three species were discussed.

關鍵詞 (Key words): 象白蟻亞科 (Nasutitermitinae)、生態棲位模擬 (Niche modeling)、物種界定 (Species delimitation)、隱翅蟲科 (Staphylinidae)、牙蟲科 (Hydrophilidae)

PC12_MB

雙翅目昆蟲的「奧斯卡」：探究 *oskar* 基因對調控蠅類生殖漿組裝的角色演化

"Oskar" in the Diptera: investigating the evolutionary roles of *oskar* genes in the assembly of germ plasm in flies

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生殖細胞為專司遺傳訊息傳遞之細胞，其特化 (specification) 通常發生於動物發育的早期。已知黃果蠅 (*Drosophila melanogaster*) 的初始生殖細胞 (primordial germ cells, PGCs) 為最早特化的胚胎細胞，其形成須倚賴聚集在蚤腔後端的生殖漿 (germ plasm)。*oskar* (*osk*) 基因產物預先集中表現於生殖漿已被證實為驅動整個特化過程的關鍵。相較於黃果蠅，黃斑黑蟋蟀 (*Gryllus bimaculatus*) 雖亦擁有 *osk* 同源基因，但卻不涉入生殖細胞之特化，僅影響神經的發育。由此推測，*osk* 為一快速演化 (fast-evolving) 基因，甚或可能在親緣關係相近的雙翅目昆蟲當中有歧異之發育角色。為驗證此一假設，我們選殖和黃果蠅同屬家蠅總科之東方果實蠅 (*Bactrocera dorsalis*) 之 *osk* 同源基因 (*Bdosk*)，檢視 *Bdosk* 之發育表現，並同時和果蠅 *osk* 的分佈做一比較，藉此得知表現之差異性。我們成功選殖 *Dmosk* 與 *Bdosk* 片段製作核醣核酸探針標定卵的發育過程。透過整體原位雜合法我們發現東方果實蠅之卵發育與被廣泛研究之黃果蠅相似。於卵的發育早期，*Bdosk* 均勻表現於卵之細胞質中。直至卵發育中期以後，*Bdosk* 始表現於卵之後端。為探討 DmOsk 與 BdOsk 於卵發育過程中的表現與功能，我們將合成抗體以利後續研究。並希冀透過轉基因黃果蠅，進一步探討 *Bdosk* mRNA 在 *Dmosk* 基因剔除之黃果蠅的表現是否聚集於卵後端與是否成功恢復驅動生殖細胞的特化過程。

關鍵詞 (Key words): 東方果實蠅 (*Bactrocera dorsalis*)、*oskar*、生殖漿 (germ plasm)、生殖細胞 (germ cells)

PC13_EC

天蠶蛾的警戒性眼紋具有高度的演化可塑性

The warning eye spots on Saturniidae wings are highly plastic in evolution

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鱗翅目昆蟲翅面中央位置的眼紋通常被認為具有威嚇天敵的功能，雖然其威嚇的機制仍存在數個互斥假說，然而根據日行性蝶類的研究顯示相對醒目的眼紋通常被認為具有嚇阻天敵的作用，而相對隱匿的眼紋則有助於降低被天敵偵測到的風險。眼紋在蛺蝶科被認為是一個經歷過多次退化的祖徵，而眼紋在同一種蛺蝶上的變化則與季節有關。然而不具備季節多態性的天蠶蛾的眼紋功能與演化趨勢卻很少被檢驗。大多數天蠶蛾的中室（discoidal cell）斑紋在發育上是同源的，這個斑紋在部分物種小且不醒目，但在另一些物種則是大而顯眼並形眼紋與月眉紋。此外眼紋的發達程度在前後翅也可能所不同。為了探索天蠶蛾眼紋的演化趨勢以及可能涉及的防禦型態之間的關聯，我們在此採用 Baber *et al*. (2015) 所重建的天蠶蛾科親緣關係架構，並試圖將眼紋的尺寸、形狀、眼紋複雜性、醒目程度與展示方式等特徵最適化之後映像（mapping）到親緣關係術上，並偵測這個特徵之間在演化上的關聯性。根據我們得到的結果，具有高度警戒性的眼紋與展示方式獨立出現在美洲、亞洲與非洲的物種，然而相對於展示方式來說，眼紋的複雜度與尺寸卻與警戒性沒有演化上的相關性。我們也懷疑夜行性視覺掠食者的多樣性越高，越有可能在演化塑造出眼紋龐大、醒目且複雜的眼紋。

關鍵詞（Key words）：眼紋（eyespot）、翅盤斑（discoidal pattern）、天蠶蛾（Saturniidae）、環境背景（environmental background）、警戒性（aposematism）

PC14_BD

以 DNA 生命條碼探討台灣入侵種板栗癭蜂之寄生蜂來源
The origin of parasitoids associate with the invasive species *Dryocosmus kuriphilus* in Taiwan through DNA barcodes

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橡樹癭蜂蟲癭為封閉的生態體系，支持著多樣且食性專化於癭蜂的寄生蜂，這使得橡樹蟲癭成為研究生物群聚形成的演化及生態機制之重要模式，然而，寄生蜂分類的建立是研究此生物群聚的重要前提。台灣近來遭受多種造癭昆蟲的入侵，並有未知的寄生蜂物種取食外來種的紀錄，但這些寄生蜂的來源尚待釐清，也顯示台灣原生蟲癭寄生蜂的分類亟待建立。板栗癭蜂 (*Dryocosmus kuriphilus* Yasumatsu)(膜翅目：癭蜂科) 為原產於中國的殼斗科栗屬 (*Castanea*) 果樹之重要害蟲，於近年入侵台灣並在嘉義縣中埔鄉的板栗主要產區造成危害，栽培於南投縣北東眼山的日本栗亦有板栗癭蜂的發生，同時，板栗癭蜂與台灣原生癭蜂之蟲癭皆記錄到依形態鑑定為 *Torymus beneficus* Yasumatsu & Kamijo 與 *Megastigmus nipponicus* Yasumatsu & Kamijo 之膜翅目長尾小蜂科寄生蜂形態種，為釐清這兩種寄生蜂是否由原生癭蜂寄主徵集 (recruit) 至板栗癭蜂，本研究以 DNA 生命條碼 (DNA barcode) 驗證不同癭蜂寄主來源的寄生蜂形態鑑定結果。DNA barcode 序列取自 COI 及 ITS2 基因片段，並與 GenBank 相同物種或近似物種之序列比較種間關係。兩段基因的分析結果皆支持板栗癭蜂與原生癭蜂之寄生蜂為不同的單系群，寄生原生癭蜂的 *T. beneficus* 形態種與日本的 *T. beneficus* 個體及另一形態近似種 *T. sinensis* 另成一個單系群，而寄生板栗癭蜂的 *M. nipponicus* 與日本同物種個體形成一單系群。這些結果不支持寄生蜂由原生癭蜂被徵集至外來癭蜂的假設，不同的單系群也可能代表未知的隱蔽種，而形態鑑定與序列比對結果的不一致性，也暗示 *T. beneficus*、*T. sinensis* 與 *M. nipponicus* 的分類有待重新檢討。

關鍵詞 (Key words): 蟲癭 (gall)、寄生蜂 (parasitoids)、板栗癭蜂 (*Dryocosmus kuriphilus*)、長尾小蜂科 (Torymidae)、DNA 生命條碼 (DNA barcode)

PD01_EC

光週期對玉帶鳳蝶 (*Papilio polytes polytes* L.) 發育之影響
Effect of photoperiod on the development of the *Papilio polytes polytes* L.

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本研究探討光週期對玉帶鳳蝶 (*Papilio polytes polytes* L.) (鱗翅目：鳳蝶科)育之影響。在網室中採集玉帶鳳蝶當日產下的卵，置於 25 ± 1℃，80 ± 5% RH，五種光週期 (8L:16D、10L:14D、12L:12D、14L:10D、16L:8D) 之生長箱內，玉帶鳳蝶幼蟲以檸檬 (*Citrus limon*)，單隻飼育至羽化成蝶，每日調查五種光週期對其各蟲期生長發育之情形。結果顯示，玉帶鳳蝶在日長 14 hr 組卵孵化率只有 56%，而日長 10 hr 組和日長 8 hr 組高達 98 和 92%。第一齡幼蟲發育至羽化成蟲的存活率，在五種光週期處理下為 47.6~57.1%，皆無差異。卵發育至羽化成蟲的平均發育日數，以日長 14 hr 組最短為 34.87 日，而日長 8 hr 組最長為 43.04 日，相差約 8 日。在五種光週期處理下，玉帶鳳蝶第五齡幼蟲頭殼寬需超過 4.53 mm 的閥值方可化蛹。幼蟲頭殼寬度的常用對數與齡期間呈迴歸直線關係，符合戴爾法則。玉帶鳳蝶雌、雄蝶性比為 1:1，可知此蝶性比不受五種光週期影響。由結果可知，在 25 ± 1℃條件下飼育玉帶鳳蝶，以日長 10 和 14 hr 組飼養較佳。

關鍵詞 (Key words): 玉帶鳳蝶、光週期、發育

PD02_EC

光週期對淡紋青斑蝶 (*Tirumala limniace limniace* (Cramer)) 發育之影響

Effect of photoperiod on the development of the *Tirumala limniace limniace* (Cramer)

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本研究探討光週期對淡紋青斑蝶 (*Tirumala limniace limniace* (Cramer)) (鱗翅目：蛺蝶科) 發育之影響。在網室中採集淡紋青斑蝶當日產的卵，置於 25 ± 1℃, 80 ± 5% RH，五種光週期 (8L:16D、10L:14D、12L:12D、14L:10D、16L:8D) 之生長箱內，淡紋青斑蝶幼蟲以華他卡藤 (*Dregea volubilis*)葉片，單隻飼育至羽化成蝶,每日調查各蟲期發育情形。結果顯示，淡紋青斑蝶於日長 14 hr 組時孵化率為 76% 較低，以日長 12 hr 組達 90%。第一齡幼蟲發育至羽化成蟲的存活率，以日長 8 hr 組最高為 92.5%。卵發育至羽化為成蟲的平均發育日數，以日長 10 hr 組最短為 25.05 日，而日長 16 hr 組最長為 33.91 日，相差約 9 日。在五種光週期處理下，淡紋青斑蝶第五齡幼蟲頭殼寬必需超過 3.39 mm 的閥值方可化蛹。頭殼寬度的常用對數與幼蟲齡期間呈正相關，符合戴爾法則。雌、雄蝶性比為 1:1,可知此蝶性比不受五種光週期影響，且成蟲翅長翅寬皆無差異。本結果得知，淡紋青斑蝶以 25 ± 1℃及日長 8、14 hr 組飼育下之存活率最好，而發育日數則以日長 10 hr 組 25.05 日最短。

關鍵詞 (Key words): 淡紋青斑蝶、光週期、發育

PD03_EC

上升二氧化碳對於植物品質及植食性昆蟲斜紋夜蛾生長表現之影響

Influence of elevated CO_2 condition on leaf's quality and consequently affect the performance of herbivorous insect of *Spodoptera litura*

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The increasing of carbon dioxide (CO_2) in atmosphere accompany with temperature are raising concern on environmental issue of global warming. CO_2 as the primary raw material utilized by plants to produce the organic matter as well as construct their tissues, consequently, the more CO_2 in the air, the better plants can grow. Insect as herbivores rely on host plant for necessary nutrition to develop. But plants, in the defense strategy to attackers, have produced allele-chemicals that cause negative effect on insect performance. In this study, we address the question of whether leaf's quality will be change under elevated CO_2 of 900 ppm and consequently affect to the performance of herbivorous insect (*Spodoptera litura*). Result of this can be highlighting the insect-plant interaction in the context of global warming condition.

關鍵詞 (Key words): 斜紋夜蛾 (*Spodoptera litura*)、二氧化碳 (Carbon dioxide)、昆蟲與植物交互作用 (Insect-plant interaction)

PD04_EC

菜心螟 (*Hellulla undalis*) 生活史概述
Life cycle of *Hellulla undalis* fed on Chinese cabbage crop

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本研究探討菜心螟 (*Hellulla undalis*) 之生活史，以供未來室內飼養之選擇。菜心螟屬於鱗翅目 (Lepidoptera) 螟蛾科 (Pyralidae)，為寡食性 (oligophagous) 的植食性昆蟲，十字花科作物 (Brassicaceae) 為其主要之寄主植物，本蟲會造成苗期之死亡。本實驗自小白菜田採回 45 個蛹，待羽化後交配產卵，所孵化之幼蟲仍以小白菜葉片飼養，作為蟲源，飼養一代後進行以下之實驗，以小白菜葉片為食料，選用的溫度為 25℃。小白菜飼養之平均發育時間，在卵期為 3.33 ± 0.06 天；幼蟲期為 24.64 ± 0.32 天；蛹期為 7.62 ± 0.13 天；成蟲期為 10.33 ± 0.65 天；產卵狀況為少數雌成蟲未產卵，產卵之母成蟲產卵數量由 1~167 粒不等，平均產卵量為 67.18 粒/隻。若就生活史參數而言，小白菜飼養之 r_m 值為 0.074365；Ro 為 12.32；λ 為 1.0772；T 為 33.77。未來仍會繼續探討餵飼不同十字花科作物之生活史以資比較。

關鍵詞 (Key words): 菜心螟 (*Hellulla undalis*)、生活史 (life cycle)、小白菜 (Chinese cabbage)

PD05_PM

蓮霧新興造癭害蟲–米爾頓釉小蜂之生物學
Biology of a new galling pest – *Anselmella miltoni* on wax apple

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米爾頓釉小蜂 (*Anselmella miltoni* Girault) 為釉小蜂科 (Eulophidae) 的造癭昆蟲，寄主為蓮霧 (*Syzygium samarangense*) 等赤楠屬植物，引起種子部位膨大變形。近年來台灣出口的蓮霧於輸入國屢遭發現此小蜂感染，影響蓮霧果實的外銷。由於米爾頓釉小蜂生物學資訊極為缺乏，加上造癭昆蟲難以飼養之特性，造成防治策略擬定的障礙，因此本研究於蓮霧果園進行監測與觀察，以建立米爾頓釉小蜂基礎資訊，提供防治參考。米爾頓釉小蜂產卵時機為蓮霧開花後，產卵時雌蟲停棲在蓮霧雌蕊基部，將卵產在胚珠表面，自卵發育至成蟲都在果實內的癭室發生，歷時約 35 天。成蟲羽化時鑽出果實，留下隧道，但並不同時羽化，迴歸分析顯示癭室數量與持續羽化天數呈正相關 ($y = 0.0973x + 3.8651$, $R^2 = 0.3997$, $p < 0.05$)，每個蟲癭包含約 20.8 ± 11.5 個癭室 (N = 57)，一個感染種子持續有小蜂羽化的天數最久約 9~10 天。以不同食物於室內飼養成蟲，結果顯示不同處理間的成蟲壽命並無顯著差異，約為 2~3 天。除蓮霧外，也於蒲桃 (*S. jambos*) 記錄到米爾頓釉小蜂。防治此新興害蟲應把握正確時機，本研究根據目前生物學資料，提供田間耕作防治建議，若配合其他蓮霧害蟲的化學防治，則務必掌握盛花期到套袋前。造癭昆蟲發生需配合植物生長，米爾頓釉小蜂分批羽化及成蟲壽命不長，推論台灣可能還存有已記錄之外的可利用寄主。

關鍵詞 (Key words): 米爾頓釉小蜂 (*Anselmella miltoni* Girault)、造癭昆蟲 (galling insect)、蓮霧 (*Syzygium samarangense*)、生物學資訊 (information of biology)

PD06_MB

組蛋白去乙醯化酶對西方蜜蜂免疫與抗病機制之研究

A study of the immune and resistance mechanism of the histone deacetylase inhibitor in western honeybees (*Apis mllifera*)

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Western honeybees (*Apis mellifera*) are important economic insects and also play an essential role in nature. Western honeybees impact greatly on the ecosystem as they are pollinators of flowers. Recently, the colony collapse disease (CCD) has been reported in many regions, the main causes of which still remain unknown, but it is theorized that several factors may be involved, such as bee viruses and stress from the environment. This study examines the relationship between hostone deacetylase inhibitor (HDACi) and honeybee resistance through bioassays and gene expression analysis. HDACi mainly inhibits histone deacetylase in cells and induces gene expression due to loose chromatin structure. In our bioassays, honeybees that were treated with several concentrations of HDACi for a week showed lower mortality rates compared to non-treated groups when exposed to pressures of imidacloprid. The results of our gene analysis showed elevations of cytochrome P450, which play a role in the detoxification mechanism, and Dorsal-2, which is part of the immune pathway. HDACi may potentially protect honeybees against pesticides or microorganisms. Our results indicated that HDACi displays specificity; although HDACi modifies chromatin structure and gene expression, not all gene expressions were raised, and GST and Relish showed no significant differences when treated with HDACi

關鍵詞 (Key words): 西方蜜蜂 (*Apis mellifera*)、組蛋白去乙醯化酵素抑制劑 (HDAC inhibitor)、免疫機制 (immune mechanism)、解毒機制 (detoxification mechanism)、殺蟲劑 (desticides)

PD07_PM

蓮霧之造癭昆蟲--米爾頓釉小蜂的非破壞性檢疫
Nondestructive quarantine for galling insect -- *Anselmella miltoni* Girault on wax apple

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蓮霧 (*Syzygium samarangense*) 為台灣重要農產及外銷農產水果之一。近年來自台灣出口的蓮霧，多次被輸入國攔截受到米爾頓釉小蜂 (*Anselmella miltoni* Girault) 感染，嚴重影響蓮霧產品輸出。米爾頓釉小蜂主要於蓮霧種子部位造癭，造成感染部位變形。由於受感染蓮霧果實外表完全沒有徵狀，因此果實包裝時無法由外表進行篩檢，目前出口檢驗僅能靠傳統剖檢。X 光非破壞性檢測系統以 X 光進行果實透視，藉由果實內部受害後造成緻密度差異的情形，達到檢疫效果，此系統研發時以果實蠅類受害情形為出發點，但目前測試結果顯示配合適當的電壓電流值，亦可觀察到受感染蓮霧果實內部的變化。迄今利用此項技術檢視會受到米爾頓釉小蜂感染的 3 個蓮霧品種，皆可明顯觀察到果實內部的蟲癭，顯示此項技術對於受到米爾頓釉小蜂感染之蓮霧果實檢測是可行的有效方法。建立可作為檢疫人員 X 光影像判讀訓練參考的影像資料庫，進一步開發自動影像判讀系統，顯示效果顯著，未來期望可利用 X 光檢測系統，並配合傳統剖檢，加強米爾頓釉小蜂檢出效率，減少出口蓮霧被攔截銷毀機會，穩固台灣蓮霧出口之市場，甚至將此檢驗技術擴展至其他不同類水果之檢驗。

關鍵詞 (key words): 蓮霧 (*Syzygium samarangense*)、米爾頓釉小蜂 (*Anselmella miltoni* Girault)、X 光非破壞性檢測系統 (X-ray nondestructive quarantine system)、檢疫 (quarantine)

PD08_PM

瓜實蠅寄生蜂 (*Psyttalia fletcheri* (Silvestri)) 形態描述及生活史研究 (膜翅目：小繭蜂科)

Morphology and life cycle of larval parasitoid wasps, *Psyttalia fletcheri* (Silvestri) (Hymenoptera: Braconidae), of melon flies, *Bactrocera cucurbitae* (Coquillett)

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瓜實蠅為臺灣重要的經濟害蟲，對瓜類生產的影響甚大，化學防治之方法已經行之有年，因此另闢新的防治道路是目前的一個方向。在對於瓜實蠅的寄生蜂、生物防治上，一直以來研究不多，而目前最常被研究及利用在瓜實蠅防治上之寄生蜂為一種幼蟲寄生性小繭蜂 *Psyttalia fletcheri* (Silvestri)，此種幼蟲寄生蜂會於瓜實蠅的末齡幼蟲離開瓜果跳入土壤化蛹前的階段寄生，並於瓜實蠅化蛹後取用其內部組織，造成瓜實蠅無法羽化並死亡。對於該寄生蜂之大量飼養及採集在臺灣都還在嘗試階段，對於該種類之形態分類亦少有描述，另外對於該種寄生蜂之生活習性也需更多的資料。本次研究首先著重於該種寄生蜂之形態描述及種類再確認，利用比對國外文獻及高倍率電子顯微鏡下的觀察拍照，給予該種寄生蜂之重新描述。討論該種寄生蜂常用之分類特徵，例如頭部後方的後頭脊 (occipital carina)、大顎及頭楯片的形狀、胸背板及腹板上之花紋、胸背板上的盾側溝 (notaulus) 等。另外也進行寄生蜂之生活史及生態觀察。綜合以上的研究結果，以期建立在利用該種寄生蜂生物防治時之基礎參考資料。

關鍵詞 (Key words): 形態 (morphology)、分類 (taxonomy)、生活史 (life cycle)、瓜實蠅幼蟲寄生蜂 (*Psyttalia fletcheri*)、瓜實蠅 (*Bactrocera cucurbitae*)

PD09_PM

米爾頓釉小蜂有效產卵管長度與不同品種蓮霧感染率之關係初探

Preliminary study on the effective ovipositor length of *Anselmella miltoni* (Hymenoptera: Chalcidoidae: Eulophidae) and its relationship to different infected rate of wax apple varieties

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米爾頓釉小蜂 (*Anselmella miltoni* Girault) 具造癭習性，引起種子部位變形，為台灣蓮霧新興害蟲，影響蓮霧出口市場。目前出口檢疫資料顯示，感染情形於品種有別，驗出感染者為南洋種和印尼種，泰國種則未有感染紀錄。由於小蜂雌蟲產卵時會停棲在蓮霧雌蕊基部，插入產卵管後將卵產在胚珠表面，推測不同品種的感染可能跟蓮霧與小蜂結構的配合有關。測量 3 種蓮霧品系各 60 個樣本，其雌蕊基部至胚珠之距離三者均有顯著差異。本實驗進一步測量米爾頓釉小蜂的有效產卵管長度，及其上述 3 種蓮霧品系之上述測量值，以測試此假說。目前以 (1) 從產卵管鞘末端拉出產卵管，(2) 量測完整產卵管長度再扣除留在體內長度，分別估算釉小蜂有效產卵管長度。並以核密度函數 (Kernel densitiy estimation) 將有效產卵管長度與 3 種蓮霧雌蕊基部至胚珠距離之資料轉換為機率密度分佈，計算兩兩間機率密度分佈之重疊率，兩種測量法結果皆顯示，有效產卵管長度與印尼及南洋種重疊率高，與泰國種重疊率低，推測釉小蜂較容易感染印尼及南洋種，較難感染泰國種，而雌蕊基部至胚珠距離可能為不同品種蓮霧感染率差異因素之一。由於目前無法透過實驗直接取得有效產卵管長度，日後將持續確認釉小蜂產卵行為，加強結果可信度。

關鍵詞 (Key words): 米爾頓釉小蜂 (*Anselmella miltoni* Girault)、蓮霧 (*Syzygium samarangenes*)、產卵管長度 (length of ovipositor)、感染 (infect)

PD10_BD

墾丁國家公園象鼻總科概述
Outline of the weevil fauna (Coleoptera: Curculionoidea) in Kenting National Park

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Weevils or the superfamily Curculionoidea are one of the largest groups in Coleoptera. According to the Catalogue of Life in Taiwan (TaiBNET), at present (2015), there are 697 species of Curculionoidea in Taiwan, including Anthribidae (114), Attelabidae (35), Rhinchitidae (29), Apionidae (10), Nanophyidae (6), Brenchidae (49), Dryophthoridae (24), Erirhinidae (1), Brachyceridae (1), Curculionidae (251), Scolytidae (140) and Platypodidae (24). Taiwanese weevil fauna are characterized by mixing oriental and palearctic biogeographical elements, so they are different depending on the location's altitude or climate. In this study, 855 dry specimens of Curculionoidea from the survey of insect fauna in Kenting National Park from 2010 to 2015 were examined. The specimens were collected by hand searching, beating, sweeping and light trap. Since that Kenting National Park is located southernmost point of Taiwan, so the tropical environment shapes the weevil fauna as it was strongly affected by oriental element. The results showed that 155 species of Curculionoidea were found, which comprised 8 families, 22 subfamilies, 56 Tribes and 119 Genus except species of Scolytidae and Platypodidae. This implied that approximately 22% of Curculionoidea species in Taiwan reside in Kenting National Park. In this poster, some identified noteworthy species in the collection will be discussed.

關鍵詞 (Key words): 象鼻總科 (Curculionoidea)、象鼻蟲 (weevil)、昆蟲相 (insect fauna)

PD11_EC

探討昆蟲與植物的交互關係：揮發性有機化合物在三層營養階層交互作用中所扮演的角色

Assessing insect-plant interactions: the roles of volatile organic compounds in tritrophic interactions

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One of the most challenging approaches for current ecologists is to integrate new concepts and tools toward comprehending the structural and functional complexity of ecological relationships between plants and animals. The breadth of the ecological scope, from molecular mediation to the structuration of ecological food webs, and its bottom-up and top-down effects along its range render even more complex the studies of animal-plant interactions. We used chemical ecology tools to assess tritrophic plant-insect interactions with or without obligate partnership. Two systems involving ants as third partner were chosen: the obligate mutualism between *Ficus* (Moraceae) and their pollinating fig wasps and insect carnivory by *Nepenthes* pitcher plants (Nepenthaceae). In both systems, the plants produce and emit a large variety of volatile organic compounds (VOCs) that play critical roles in attracting potential pollinators that act as vectors of pollen to ensure reproduction (*Ficus*) or as prey to ensure growth in nutrient-limited habitat (*Nepenthes*). We highlight three key roles of ants on tritrophic interactions: (1) Ants use the olfactory signals emitted by the plants for their own benefit, (2) ants affect the stability of the plant-pollinator interactions in both positive and negative ways, (3) the likely mutualistic role of the ant-plant relationship in both systems. Finally, we recommend a set of questions to be investigated in such chemically-mediated communities.

關鍵詞 (Key words): chemical ecology, plant-insect relationships, tritrophic interactions

PD12_EC

台灣直翅目昆蟲的海拔分布初報
The preliminary study of altitude distribution on Orthoptera insect in Taiwan

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台灣地形特色造成昆蟲海拔分布由陳德浩 (2008) 黑蝗亞科種間分布及 Chalida (2009) 直翅目科間分布初步發現特性，需要再深入探討。本研究沿中部橫貫公路系統化掃網採集，共有 16 個樣區，選定 13 種植群類型作為樣區，探討台灣直翅目昆蟲的海拔分布特性，2015 年 1 月起已進行採集較完整的資料 (1 月份及 2 月份)，共採集 54 隻，且加入 Chalida (2009) 的初探 92 隻標本做討論，將海拔以 1000 公尺為級距分成低海拔、中海拔、高海拔，低、中海拔為蝗科 (Acrididae) 數量最多，分別佔整體的 38.6% 和 73.7%；而高海拔則是以螽斯科 (Tettigoniidae) 佔整體 83.3% 最多而蟋蟀的數量少，除了採集方法之限制外，也與地棲型蟋蟀海拔分布較低有關。未來我們將鑑定型態種，作為直翅目海拔分布的資料庫。

關鍵詞 (Key words): 直翅目 (Orthoptera)、海拔分布 (altitude distribution)、掃網採集 (SWP)

PD13_BD

來自昆蟲生命週期的選擇壓力如何影響榕樹的物候

The selective pressure from an insect lifespan on the fig tree phenology

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The prevalence of dioecy in *Ficus* is atypical in Taiwan: out of 26 species, 22 are dioecious. Pollinators of these species, the fig wasps, must then travel from one individual to another to insure pollination. Whatever the habitat of the fig trees, dioecy imposes a high selective pressure on the fig trees to insure that figs are always available for the fig wasps. Because fig trees in Taiwan occupy very different habitats, they constitute a suitable model to identify specific adaptations related to dioecy and environmental constraints. We investigated the reproductive phenology of three dioecious *Ficus* species with distinct ecologies in northern and southern Taiwan. *Ficus erecta* is a common fig tree all over Taiwan with a preference for higher elevation habitats. In contrast, *Ficus pedunculosa* var. *mearnsii* and *Ficus tinctoria* subsp. *swinhoei* are shrubs growing on exposed locations such as coral reef remnants of seashores. All species showed a common trait: the continuous presence of figs on male trees. However, their reproductive phenology was quite different among sites, even within a single species. At an individual level, each *Ficus pedunculosa* shrub produced figs continuously, so that fresh receptive figs were always available for the pollinating wasps. *Ficus tinctoria* extended the period of receptivity of its figs, so that receptive figs waiting for pollinating wasps were almost always available. These two last adaptations to the survival of pollinating wasp populations may have been selected by the harsh environment and the extremely short lifespan of the pollinators (few hours to one day). Although further observations are needed, it appears that dioecious figs in Taiwan remarkably vary in their phenology, both within species among locations and within location among species. Cost-benefit analyses of such strategies could provide further insights on the maintenance and evolution of dioecy in fig trees.

關鍵詞 (Key words): 共演化 (coevolution)、榕屬植物 (*Ficus*)、榕小蜂 (fig wasp)、互利共生 (mutualism)、物候 (phenology)

PD14_PM

金門地區小黃腹鼠恙蟲病病媒調查

Vector surveillance for scrub typhus on *Rattus losea* in Kinmen area

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自 1998-2014 年全國各縣市共 6,342 名本土性恙蟲病 (scrub typhus) 個案，其中以金門縣 999 例占全國第一位，由此可見金門地區恙蟲病發生率之嚴重性。此疾病藉由恙蟲叮咬傳播，病原體為恙蟲病立克次體 (*Orientia tsutsugamushi*)。恙蟲生活史共分卵、次卵、幼蟎、若蟎及成蟎，病原體由親代獲得，即卵已帶有立克次體；恙蟲僅於幼蟎期叮咬寄主一次，當人被帶有病原體的恙蟲叮咬，可能會得到恙蟲病。恙蟎屬蛛形綱 (Arachnida)、真蟎目 (Acariformes)、恙蟎科 (Trombiculidae)。本研究於 2010 年 1-12 月在金門選取 6 個採樣點進行小黃腹鼠 (*Rattus losea*) 恙蟲採集及鑑定。小黃腹鼠體外寄生蟲除了恙蟎之外，同時也發現厲蟎、蜱類、蝨類及蚤類等 5 類體外寄生蟲，總侵染率為 100% (127/127)。恙蟎之侵染率為 74.0% (94/127)，共採集到 3 種恙蟎，分別為地里恙蟎 (*Leptotrombidium deliense*) 為 6,894 隻、小板恙蟎 (*Leptotrombidium scutellare*) 458 隻及中華無前恙蟎 (*Walchia chinensis*) 171 隻。地里恙蟎於 4-11 月出現，為金門的夏季優勢種，小板恙蟎僅出現於 11 月至隔年 3 月，是冬季優勢種。6 個採集點中，以陽翟所採集恙蟲之帶蟎率 (12.9%) 及恙蟎指數 (11.93) 最低，料羅及新湖所採集之帶蟎率 (100%) 最高，嚨口所採集之恙蟎指數 (182.78) 為最高。

關鍵詞 (Key words): 恙蟲病 (scrub typhus)、恙蟎 (chiggers)、小黃腹鼠 (*Rattus losea*)、金門 (Kinmen)

PD15_BD

台灣螳螂 (Mantodea) 近十年研究概況
The research status on Taiwan praying mantis (Mantodea) over the past decade

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台灣螳螂目分類尚待修訂，未來將進行形態特徵的重新描述及分類修訂，近十年來台灣螳螂相關研究以文獻回顧與分析結果，2004 年周倖瑜對分類資料初步整理出台灣螳螂目 2 科 14 屬 23 種，包含未檢視到標本的 6 種；本研究以該資料為基礎名錄，以種名為關鍵詞在 Google Scholar 搜尋得到 75 份自 2004 年至 2015 年的台灣螳螂相關研究，將內容依行為學 (Behavior)、生態學 (Ecology)、形態學 (Morphology)、系統發生學 (Phylogeny)、生理學 (Physiology)、分類學 (Taxonomy)、動物相研究 (Fauna)、蟲害防治管理 (Pest control)、生物資訊 (Bioinformatics)、應用科學 (Applied science) 10 個主題分類；文獻中被分類到 3 個主題的研究篇數佔 5.3%，2 主題的佔 12%，而主題分類結果有 98 項，行為學研究佔 30%，數量最多，生態學、形態學研究各佔 13.2%，生理學 12.2%，動物相研究 11.2%，分類學 6.1%，系統發生學 5.1%，蟲害防治管理、生物資訊研究各 3%，應用科學 2%，研究對象種類集中於 *Hierodula (Hierodula) patellifera*、*Mantis religiosa*、*Tenodera aridifolia*、*Tenodera sinensis*，而在回顧的文獻中分類研究比例確實較少，由此分析可見台灣螳螂目的分類研究刻不容緩。

關鍵詞 (Key words): 台灣 (Taiwan)、螳螂 (praying mantis)、螳螂目 (Mantodea)、文獻回顧 (review)

PD16_MB

黑腹果蠅之脂肪酸去飽和酶對乾燥逆境所扮演的角色
The desiccation tolerance roles of fatty acid *desaturases* in *Drosophila melanogaster*

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昆蟲能夠成功的在陸地環境生存，主要歸功於牠們能夠有效的容忍乾燥，昆蟲失水方式主要是因為水分穿過角質層所造成的表皮失水。前人研究發現失水率的轉變與脂質層屬性的改變有關，當表面脂質在臨界溫度熔化時，表皮脂質會由固態轉變為液態，表皮則會從水分不可滲透的狀態轉變成水分輕易流失的狀態，因此可以推測出熔點與失水率有關。前人的體外試驗指出，碳氫化合物的鏈越長，熔點越高；碳氫化合物的雙鍵越多，熔點越低；本研究以黑腹果蠅 (*D. melanogaster*) 為材料，利用 *UAS-GAL4* 系統分別將果蠅的 *desaturase 1.2.F* 基因分別在全身、絳細胞、脂肪體過表現之後，再將果蠅放置在乾燥環境觀察其生存率變化。本研究發現將 *desaturase* 基因過表現的雄蟲及雌蟲，其在乾燥環境下的生存時間皆比控制組還要少，*desaturase* 基因的過表現會使表皮脂質的不飽和脂肪酸的增加，導致果蠅耐旱性降低。

關鍵詞 (Key words): 黑腹果蠅 (*Drosophila melanogaster*)、去飽和酶 (desaturase)、乾燥

PD17_MB

台灣銳蠓卵巢結構與生殖決定基因之分析

Characterization of ovarian structure and germ line determination genes in *Forcipomyia taiwana* (Diptera: Ceratopogonadiae)

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The biting midge, *Forcipomyia taiwana* (Diptera: Ceratopogonadiae) is a tiny, blood feeding insect prevalently found in Taiwan. The female midge is feeding on human blood for egg formation. Bites of *F. taiwana* cause intense pruritic and allergic response in sensitive individuals and thus is disrupting the development of tourism. While the ecological study of *Forcipomyia taiwana* has been performed, little is known about its ovarian structure and oogeneisis. Here, we investigated the ultrastructure of *F. taiwana* ovary which is composed of ovarioles of the meroistic polytrophic type. In particular, the follicle of *F. taiwana* ovarioles possesses a single nurse cell which is distinct in dipteran. By using Vasa as a marker, we further identified the existence of nuage in the nurse cell. Through transcriptome analysis, we further identified germ plasm components such as oskar, vasa, and nanos. Particularly, two out of three oskar homologues presented specific localization of their transcripts in the oocyte posterior which might involve in the formation of germ plasm and the determination of germ cell. Taken together, our work represents a fundamental step in understanding the ovarian structure of *F. taiwana* together with identifying critical genes involved in germ plasm assembly. We believe the understanding of oogenesis could provide an insight in finding a strategy to control the population of *F. taiwana* in the future.

關鍵詞 (Key words): 台灣銳蠓 (*Forcipomyia taiwana*)、卵母細胞發育 (oogenesis)、生殖漿 (germ plasm)

PD18_PM

寄主轉換會影響小菜蛾 (*Plutella xylostella*) 在兩種十字花科上之生活史嗎?
The host plant change will affect life table of *Plutella xylostella* fed on two cruciferous crop

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本研究探討寄主轉換對小菜蛾 (*Plutella xylostella*) 生活史之影響，以供未來室內飼養之選擇。小菜蛾屬鱗翅目 (Lepidoptera) 菜蛾科 (Plutellidae)，為寡食性 (oligophagous) 的植食性昆蟲，十字花科作物 (Brassicaceae) 為其主要之寄主植物，會造成重大產量損失，全球每年用在防治的費用可達 10 億美金 (Talekar, 1992)。本實驗自甘藍菜田採回約 1000 個蛹待羽化後產卵孵化之幼蟲仍以甘藍菜葉片飼養，作為蟲源，飼養一代後進行以下之實驗，一組以幼蟲以油菜餵飼，另一組以小白菜餵飼，選用的溫度為 15、20、25、30℃。油菜飼養之平均發育時間，在卵期為依續為 7 ± 0、7 ± 0、3.99 ± 0.01、2 ± 0 天；幼蟲期為 27.54 ± 0.58、25.5 ± 0.5、16.5 ± 0.43、11.38 ± 0.32 天；蛹期為 7.82 ± 0.19、6.5 ± 0.29、3.67 ± 0.21、3 ± 0.27 天；成蟲期為 13.91 ± 1.07、11.5 ± 1.56、16.5 ± 0.43、10 ± 2.75 天。小白菜飼養之平均發育時間，在卵期為依續為 4.93 ± 0.05、5 ± 0、3 ± 0、2 ± 0 天；幼蟲期為 25.36 ± 0.45、20.89 ± 0.14、14.04 ± 0.08、10.42 ± 0.15 天；蛹期為 7.31 ± 0.21、5.39 ± 0.08、4.23 ± 0.05、3.42 ± 0.15 天；成蟲期為 11.38 ± 1.23、9.09 ± 0.33、11.15 ± 0.63、7 ± 1.1 天。若就生活史參數而言，以油菜飼養之 rm 值依溫度低至高序為 0.053985、0.016203、0.042088 、0.054278；Ro 為 5.39、1.69、2.34、2.26；λ為 1.0555、1.0163、1.043、1.0558；T 為 31.2、32.38、20.2、15.04。以小白菜飼養之 r_m 值依溫度低至高序為 0.044061、0.190574、0.245、0.137512；Ro 為 3.79、81.51、75.36、6.75；λ為 1.045、1.2099、1.2776、1.1474；T 為 30.24、23.09、17.64、13.89。由上述結果顯示子代取食不同寄主確有齡期縮短及子代數減少之情形。

關鍵詞 (Key words): 小菜蛾 (*Plutella xylostella*)、生活史 (life cycle)、白菜 (Chinese cabbage)、油菜 (kale)

PD19_BD

天蠶蛾科無法以口器形態作為功能性判斷依據

Proboscis morphology is not a good predictor of the functionality in Saturniidae (Lepidoptera)

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The proboscis, formed by the coupled specialized maxillae is one of the most remarkable evolutionary innovations in the evolution of the glossatan Lepidoptera This organ has enabled the majority of moths and butterflies to absorb and uptake water, chemicals and nutrients from environment in an efficient way, reduction of proboscis, therefore, is considered an evolutionary trade-off in the taxa of which the adult life span is short and the energy investment during courtship is limited. Among the behaviors that require functionality of proboscis, puddling is usually associated with the males that need accumulating sodium or regulating body temperature. Discovery of this behavior in Saturniidae, that is well-known for the absence of coiled and long proboscis in both sexes, is therefore intriguing. In the present study, we summarize the observation records of puddling behavior of the saturniids from Taiwan, India, Nepal and Africa, and examined the morphology of reduced proboscis to investigate the phylogenetic correlations between geographical source, morphology, habitat and evolutionary history. We used 29 saturniid species, including those with records of puddling and representing the major lineages of the entire family, and then assessed the phylogenetic correlations between these features. The results show that the longer proboscis is plesiomorphic in Saturniidae but the derived groups in Asia and Africa also possess this character state. However, no phylogenetic correlation between functionality and proboscis morphology is detected because it seems that the puddling behavior cannot be predicted by using the type of proboscis. The fact that the galeae of the species having puddling behavior are not fused suggests that the fluid uptake is possibly accomplished by capillarity, but not the action of the cranial sucking pump.

關鍵詞 (Key words): 天蠶蛾科 (Saturniidae)、退化口器 (reduced probosci) 、吸水行為 (puddling behavior)

PM01

溫度對青翅蟻形隱翅蟲 (*Paederus fuscipes* Curtis) 發育與繁殖之影響
Effects of temperature on development and reproduction of *Paederus fuscipes* Curtis feeding on *Nilaparvata lugens* (Stål)

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青翅蟻形隱翅蟲 (*Paederus fuscipes* Curtis) 為台灣水稻田常見重要捕食性天敵之一，可捕食水稻飛蝨、葉蟬及多種鱗翅目害蟲的卵與幼蟲。本研究在 15, 20, 25 及 30℃下進行，初步結果顯示在 20-30℃間，卵之孵化率為 85-95%。卵期、幼蟲期及蛹期在 30℃下之發育時間最短，分別為 3.6, 11.6 及 3.0 天；發育臨界溫度分別為 9.18, 9.57 及 12.65℃；有效積溫分別為 70.73, 231.61 及 51.66 日度。合併計算未成熟期之發育臨界溫度為 10.14℃，有效積溫為 354.28 日度。雌成蟲壽命在 30℃下最短 (平均 58.3 天)，產卵量於 25℃下最多 (平均 190.8 粒)。以供應褐飛蝨 1-3 齡若蟲為食餌，若蟲期之取食量以 25 及 20℃之 37.6 及 29.1 隻最多，以不同溫度下若蟲取食量及壽命之比值計算，則以 25℃之每日平均取食 2.6 隻最高，其次為 30℃之 1.7 隻。雌成蟲於 25℃之取食量最高 (平均 279.8)；雌蟲取食量及壽命之比值，則以 25℃之每日平均取食 3.5 隻最高，其次為 30℃之 2.9 隻；以雌蟲產卵量及壽命之比值計算，於 25℃之每日平均產卵 2.4 粒最高，其次為 30℃之 2.2 粒。雄成蟲在 25℃下之取食量最高 (202.2 隻)，其取食量及壽命之比值，以 30℃之每日平均取食 3.1 隻最高，25℃僅為 2.5 隻左右。比較雌、雄成蟲在 25℃下之取食量及壽命比值，雌成蟲平均每日 (3.5 隻) 比雄成蟲多取食 0.95 隻食餌；在 30℃下，雌、雄成蟲每日取食量在 2.9-3.1 隻之間。

關鍵詞 (Key words): 青翅蟻形隱翅蟲 (*Paederus fuscipes* Curtis)、發育 (development)、繁殖 (reproduction)

PM02

評估套袋保護時間點對於台農 1 號荔枝果實品質影響及荔枝細蛾防治效果

Effect of fruit bagging at different times to fruit quality and litchi fruit borer (*Conopomorpha sinensis* Bradley) infestation on 'Taiung No. 1' litchi (*Litchi chinensis* Sonn.)

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荔枝細蛾 (*Conopomorpha sinensis* Bradley) 為荔枝果實生育期最重要的害蟲。一般除了使用化學藥劑防治外，亦可利用套袋保護以隔絕荔枝細蛾入侵危害。由於荔枝果實發育過程歷經生理落果及荔枝細蛾入侵危害，何時套袋保護將是關鍵性的問題。本研究以'台農 1 號'荔枝作為試驗品種，以偏雌花盛開當作描述果實生育期起始，以綠色網袋於偏雌花盛開後第 3 週、第 5 週與第 7 週進行套袋保護，並以不套袋及偏雌花盛開後第 3 週破壞網袋當作對照組，每週調查穗上果實數並計算週間相對落果率，於偏雌花盛開後 76 天採收，計算果實受害率及評估果實品質分析。試驗結果顯示不同週數套袋的相對落果率並無差異，而未套袋對照組於第 11 週出現落果率較高的形況。果實品質分析顯示各種處理之果重、果肉重與糖度皆優於未套袋對照組；惟果皮重、種子重、酸度與糖酸比並無顯著差異。荔枝細蛾的受害率在第 3 週與第 5 週套袋處理並無遭受危害，但是第 7 週套袋與破壞網袋處理的受害率為 10.6-17.1%，未套袋對照組的受害率更高達 97.5%。雖然第 3 週與第 5 週套袋處理皆無遭受荔枝細蛾的危害，但第 3 週之每穗平均結果率為 3.4 個，較第 5 週的 1.8 個佳。本研究結果顯示欲利用套袋進行荔枝果實的保護，如能於偏雌花盛開後第 3 週開始進行套袋為最佳的時機。

關鍵詞 (Key words): 荔枝細蛾 (*Conopomorpha sinensis*)、套袋保護 (bagging protection)、台農 1 號荔枝 ('Taiung No. 1' litchi)

PM03

螞蟻對甲基丁香油誘蟲器內果實蠅樣本影響之初探
Effect of ants on tephritid fly samples in methyl eugenol-baited traps

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甲基丁香油誘蟲器常用來監測果實蠅族群密度，為詳實反應田間果實蠅密度，許多研究致力探討誘引效力的相關物化因子，但影響密度估算之外在生物因子似乎較少受到重視。故本研究以此議題為主軸，探討螞蟻存在是否影響果實蠅誘蟲器中之蟲數，與影響螞蟻進入陷阱之因素。本研究於苗栗縣及新北市共 17 處樣點，懸掛黏蟲膠處理誘蟲器（懸掛鐵絲以黏蟲膠包覆）與慣行誘蟲器各一，每兩周收集誘蟲器內果實蠅及螞蟻數量並鑑定種類。結果發現，多種螞蟻可於慣行誘蟲器中發現，以舉尾家蟻屬（Crematogaster）及管琉璃蟻屬（Ochetellus）為大宗，且螞蟻數量與果實蠅破損比例皆高於黏蟲膠處理組，顯示黏蟲膠能防止螞蟻進入誘蟲器以及樣本破損的發生。本研究進一步以舉尾家蟻為例，探討螞蟻是否受甲基丁香油誘引而進入誘蟲器，結果指出，相較於甲基丁香油處理組別，舉尾家蟻優先取食冷凍處理之果實蠅，顯示螞蟻對甲基丁香油無偏好。若餵食含農藥甲基丁香油處理過之果實蠅，則可在試驗裝置中發現死亡之舉尾家蟻。上述結果證實螞蟻受果實蠅誘引而進入誘蟲器中取食，因此，未來將深入解析其取食行為與含農藥甲基丁香油間之交互關係，盼此研究能首次揭開螞蟻對誘蟲器樣本之影響，並於慣行操作之框架下提供實用的防範建議。

關鍵詞 (Key words): 螞蟻 (ant)、東方果實蠅誘蟲器 (oriental fruit fly trap)、黏蟲膠 (sticky glue)

PM04

4 種蟲害誘導之植物揮發性成分對天敵之誘效評估
Evaluation of the effectiveness of four herbivore induced plant volatiles on attracting natural enemies

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本研究使用 4 種經昆蟲取食傷害誘導後會產生之植物揮發性成分水楊酸甲酯、順式 3-己烯-1-醇、2-苯乙醇及沉香醇，搭配黃色黏板於農業試驗所調查所捕獲之天敵種類及數量。4 種成分中，僅水楊酸甲酯對小黑花蝽象具顯著誘引效果，而所有成分對其它天敵皆無明顯誘引效果。經過進一步調查發現，水楊酸甲酯對於小黑花蝽象之誘引效果會因濃度不同而有所差異，以 99.0% 水楊酸甲酯效果最好 (5.2 隻/黏板)，顯著高於最差的 10.0% (2.1 隻/黏板)。將水楊酸甲酯與其他成分混合後，與順式 3-己烯-1-醇混合可捕獲最多小黑花蝽象 (3.3 隻/黏板)，顯著高於對照組 (0.6 隻/黏板)。在 2014 及 2015 年 1-2 月間於梅園連續進行 4 週調查後，水楊酸甲酯處理組於各時間點捕獲小黑花蝽象之數量均顯著高於對照組。而除了梅園外，水楊酸甲酯於枇杷、玉米及萬苣田 3 種不同作物之環境中，亦可有效誘引小黑花蝽象。綜合上述之結果，水楊酸甲酯具有作為小黑花蝽象田間誘引劑之開發潛力，但必須考慮到不同濃度以及與不同化學成分混合後對於誘引效果之影響。

關鍵詞 (Key words): 蟲害誘導之植物揮發性成分 (herbivore induced plant volatiles)、水楊酸甲酯 (methyl salicylate)、小黑花蝽象 (*Orius*)、誘引劑 (attractant)

PM05

水楊酸甲酯吸引天敵並降低小黃瓜上蚜蟲族群數量

Methyl salicylate attracts natural enemies and reduces cucumber aphids population

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本研究使用水楊酸甲酯於農業試驗所以小黃瓜盆栽試驗，評估對棉蚜族群影響及所吸引之天敵種類及數量。小黃瓜盆栽（含有 20 隻棉蚜）懸掛不同濃度水楊酸甲酯經 1 日後，以 0.1% 處理組小黃瓜盆栽上棉蚜數量最少（5.0 隻/株），其次為 10.0%（13.7 隻/株）、99.0%（14.4 隻/株）及 1.0%（15.3 隻/株），4 處理組均顯著低於對照組的 18.7 隻/株。比較距水楊酸甲酯不同距離對小黃瓜盆栽（含有 20 隻棉蚜）上原接棉蚜數量影響，結果經 3 日後，以懸掛水楊酸甲酯中心處小黃瓜上棉蚜數量最少（3.5 隻/株），其次為距懸掛處 1.25 m 的 4.2 隻/株及 2.5 m 的 5.9 隻/株，3 處理組棉蚜數量均顯著低於 5.0 m 的 10.0 隻/株及 10.0 m 的 9.0 隻/株，上述 5 處理組棉蚜數量亦均顯著低於對照組的 13.2 隻/株。比較懸掛水楊酸甲酯後對小黃瓜上害蟲族群及吸引天敵之影響，水楊酸甲酯處理組小黃瓜植株上棉蚜及薊馬的數量於 9 週的試驗中均顯著低於對照組，粉蝨及潛葉蠅的數量則與對照組無顯著差異；於天敵誘引方面，水楊酸甲酯處理組較對照組顯著誘引更多的東小瓢蟲、小黑花蝽象及中華斑腿盲蝽象，小黃瓜懸掛水楊酸甲酯與對照組相較對食蚜虻、東方蚜小蜂、蚜繭蜂、綠草蛉、褐草蛉、六條瓢蟲及蜘蛛等天敵無顯著誘引效果。

關鍵詞 (Key words): 水楊酸甲酯（methyl salicylate）、棉蚜（*Aphis gossypii*）、小黑花蝽象（*Orius*）、中華斑腿盲蝽象（*Campylomma chinensis*）、東小瓢蟲（*Scymnus sodalis*）

PM06

以行為學與解剖學角度探討益達胺對黑棘蟻之亞致死效應
Ethological and anatomical approaches unravel sublethal effects of imidacloprid on the gray black spiny ant, *Polyrhachis dives*

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使用殺蟲劑的主要目的為消滅害蟲，但往往可能會造成其他非標的生物的影響，如授粉者（蜜蜂）。益達胺為目前廣泛使用之系統性殺蟲劑，作用於昆蟲尼古丁型之乙醯膽鹼受器（nicotinic acetylcholine receptor, nAChR），導致神經興奮過度（hyperpolarization）而麻痺死亡。研究顯示亞致死劑量之益達胺將對昆蟲行為造成顯著之影響，其中以造成外勤蜂不正常的覓食行為最為顯著。但同為社會性昆蟲之螞蟻卻幾乎無此類研究。螞蟻於覓食過程中，可能會直接接觸環境中殘留之藥劑或取食遭受藥劑殺死之昆蟲，使毒性累積於螞蟻體內；並可能經由交哺作用（trophallaxis）傳遞給幼蟲，進而導致蟻巢衰弱。益達胺作用之 nAChR 多分布於昆蟲腦部和學習與記憶有關的區域，因此，本研究推測接觸低濃度藥劑之螞蟻，其學習能力可能也會受到影響，進而導致覓食行為不正常。本研究選用黑棘蟻（*Polyrhachis dives*）作為研究材料，首先以不同濃度的益達胺建立口服毒性資料，試驗結果 LC50 為 2.625 mg/L，再以不同濃度之益達胺（LC1、LC15 及 LC50）處理黑棘蟻，觀察該藥劑對其覓食行為及食物搜尋能力之影響。未來將對黑棘蟻進行解剖，探討益達胺造成之行為改變是否與腦中突觸數量與密度的改變具相關性。

關鍵詞（Key words）：覓食行為（forage activity）、益達胺（imidacloprid）、黑棘蟻（*Polyrhachis dives*）、亞致死效應（sublethal effect）

PM07

螞蟻液體餌劑對疣胸琉璃蟻群落的防治效果評估

Evaluation of ant liquid baits on colony control of *Dolichoderus thoracicus* (Hymenoptera: Formicidae)

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疣胸琉璃蟻 (*Dolichoderus thoracicus*) 最早由 Mayr (1862) 於菲律賓所發現以雙疣琉璃蟻 (*D*. bituberculatus) 發表命名，Shattuck (1994) 認為雙疣琉璃蟻是同物異名的分類報告；中國將此屬命名為臭蟻屬。疣胸琉璃蟻主要分布於東南亞地區，目前發現地區包括：菲律賓、印尼、新加坡、馬來西亞、印度、緬甸、越南、寮國、中國華南及台灣等地均有疣胸琉璃蟻的分布紀錄。A. Forel 於 1912 年發表台灣蟻類名錄中首次記錄此種類於台灣之分佈，所發表之標本採集地點為 Pilam (台東縣卑南)。疣胸琉璃蟻分布於台灣棲地環境，主要是海拔 500~600 公尺以下的山麓環境，以竹林、次生林、雜木林、果園、檳榔園等環境，但因這些地區鄰近村落、農舍、社區、學校、廟宇等人為環境，常造成社區居民生活、環境與農作上的困擾。疣胸琉璃蟻近年來入侵人類的生活環境中而造成各式危害，影響生活品質。然而因為不同螞蟻的食性與取食偏好不逕相同，因此若要有效防治特定害蟲螞蟻，是須對不同螞蟻設計不同餌劑，包括：劑型、誘引配方、藥劑種類、施放方式與時期等。本研究於實驗室內進行探討疣胸琉璃蟻的食性偏好及不同濃度、成份的餌劑的效力評估，進而設計出更具吸引力的餌劑，並提供防治田間疣胸琉璃蟻族群的參考策略。以不同濃度的硼酸和硼砂搭配不同比例的誘引配方製成餌劑，評估餌劑對疣胸琉璃蟻工蟻、蟻后及子代的防治效果。結果顯示所有處理在第 11 天，對疣胸琉璃蟻工蟻、蟻后及子代均達 100%的防治效果。

關鍵詞 (Key words): 螞蟻餌劑 (ant baits)、液體 (liquid)、食餌偏好 (bait preference)、硼酸 (broic acid) 、有害螞蟻 (pest ant)

PM08

小紅鰹節蟲於台灣之發生調查

Investigation of the occurrence status of *Trogoderma granarium* in Taiwan

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小紅鰹節蟲 (*Trogoderma granarium* (Everts)) 是屬於檢疫類積穀害蟲，曾在於 1970 至 1984 年間隨國外穀物進口而入侵本土稻穀倉，為此現象曾有報告說明其在台灣之危害狀況，導致台灣被各國視為此蟲之疫區。為了解此蟲是否有持續發生或立足，自 2012 年起利用此蟲性費洛蒙在台灣穀倉進行害蟲誘引監測，以確認此蟲在台灣是否存在。針對進口穀物部分，包含台中及高雄港兩處進口穀倉、農糧署從澳洲及東南亞輸入之進口米倉約 30 處、2 處民營進口雜糧倉。而針對本土穀倉部分，包含稻穀倉 48 處及碾米廠區 58 處，調查範圍均勻分布於全台灣各處。監測點每 6 週更換一次性費洛蒙餌劑，並將監測後黏板寄回農業試驗所進行檢驗，持續 3 年以上。調查結果顯示，不論進口穀物倉、本土稻穀倉及碾米廠區之監測樣品，均未發現此檢疫害蟲，由此結果推測可能因倉庫害蟲防治推薦藥劑之更替或環境因子之變遷等，導致此蟲並未在台灣穀倉立足。

關鍵詞 (Key words): 小紅鰹節蟲 (*Trogoderma granarium* (Everts))、性費洛蒙 (sex pheromone)、監測 (monitoring)

PM09

稻穀倉應用防蟲網對害蟲隔絕之效果評估

Evaluation of insect-proof screens applied to prevent of stored-product insects in rough rice storehouses

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政府為保護農民及穩定糧價等，每年會定期收購稻穀貯藏，但常因倉容不足或力霸式開放穀倉，導致不同期別稻穀或穀種之混倉貯藏狀況。此種貯藏模式常引起新穀進倉後，受倉內原有蟲源快速侵入，使稻穀內害蟲密度快速增加。針對此類穀倉，為避免新穀受舊蟲源入侵，分別在彰化伸港農會混倉貯藏倉及霧峰源福順碾米廠之力霸倉，進行 32 目防蟲網覆蓋新穀試驗，以了解防蟲網對阻隔舊蟲源之效果。在伸港分別調查 8 號倉 101-2 期粳稻及 5 號倉 102-2 期粳稻之害蟲密度變化，進倉日期為當年 11 月底，結果顯示 8 號倉之害蟲密度，以防蟲網阻隔在貯藏 6、9、12、18 個月後，分別為開放對照組之 13.3、16.9、26、66.2%。5 號倉之害蟲密度，以防蟲網阻隔在貯藏 6、9、12、18 個月後，分別為開放對照組之 41.4、25.4、27.7、51.6%。對主要害蟲穀蠹 (*Rhyzopertha dominica*) 及麥蛾 (*Sitotroga cerealella*) 均有阻隔效果，其中對麥蛾阻隔最為明顯。在源福順之力霸倉，調查 1 號倉 103-1 期粳稻，進倉日期為當年 7 月底，結果顯示 1 號倉之害蟲密度，以防蟲網阻隔在貯藏 3、6、9、12 個月後，分別為開放對照組之 393、557、266、125%，防蟲網處理反而高於對照組之害蟲密度。其原因可能為力霸倉新穀堆疊時，正是害蟲最嚴重發生時期，其覆蓋防蟲網在堆疊 2 個月後才處理，可能導致蟲源已先入侵，覆蓋後防蟲效果反無法彰顯。由兩處之試驗結果，為提升防蟲網阻隔效果，建議稻穀堆疊後能立即覆蓋防蟲網，方能達到阻隔新穀被舊蟲源之入侵，否則可能導致反效果。

關鍵詞 (Key words): 積穀害蟲 (stored-product insects)、防蟲網 (insect-proof screens)、穀蠹 (*Rhyzopertha dominica*)、麥蛾 (*Sitotroga cerealella*)

PM10

無毒甲基丁香油誘殺器在田間之誘捕效果
The efficiency of different traps attracted with *Bactrocera dorsalis* by nontoxic methyl eugenol in fields

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東方果實蠅為熱帶及亞熱帶地區重要的果樹害蟲，每年造成大量農損，現有防治手段多以含毒甲基丁香油誘殺雄蟲降低田間族群密度。含毒甲基丁香油常因藥劑失效造成誘殺效率降低。基於此點，本實驗設計測試兩種新型誘殺器以無毒甲基丁香油進行誘捕。新型誘殺器利用 2000 ml 透明寶特瓶 (NCHU-T15) 及底半徑 5.5 cm 高 15 cm 之塑膠罐 (NCHU-T14)，以內陷管作為入口，具易進難出的效果。NCHU-T15 設置不同數量開口進行測試，結果開口以八及十二孔時具較佳的誘殺效果，四孔則顯著較差。NCHU-T15、T14、市售渦漩式誘集器（安啦）及長效型誘集器以不含毒甲基丁香油，於田間進行試驗，結果 T15 較佳與渦漩式無顯著差異，T14 次之，長效型誘捕數為 0。再將 NCHU-T15、T14 及渦漩式誘集器以不含毒甲基丁香油，及長效型誘集器以含毒甲基丁香油，進行試驗，結果長效型誘集器效果最佳，與無毒組具顯著差異，T15 與渦漩式無顯著差異，T14 最差。另外，以 NCHU-T15 及 T14 誘殺器以含毒及不含毒的甲基丁香油進行誘殺比較，發現這兩種誘集器在不含毒的情況下，T15 比 T14 顯著較高，在含毒時 T15 和 T14 則無顯著差異。

關鍵詞 (Key words): 東方果實蠅 (*Bactrocera dorsalis*)、甲基丁香油 (methyl eugenol)、物理陷阱 (physical trap)

PM11

瓜螟 (*Diaphania indica*) 性費洛蒙誘餌配方之探討

Study on the attractiveness of the cucumber moth, *Diaphania indica,* sex pheromone with different formulations

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於彰化縣田尾鄉網室苦瓜園，分別以瓜螟 (*Diaphania indica*) 雌、雄成蟲當誘引源，結果顯示僅雌蟲顯示誘引性，顯示瓜螟的性費洛蒙由雌蟲分泌。依文獻瓜螟性費洛蒙組成分 I: E11-16: Ald、II: E,E-10,12-16: Ald 配製瓜螟性費洛蒙誘餌，結果顯示瓜螟性費洛蒙誘餌在田間約可持效 3-5 周，其誘蟲數隨誘餌劑量增加而增多。因此，探討 I/II 不同比例、加入不同抗氧化劑、蠟油等對瓜螟誘引性之影響。配製 I/II = 1/0、0/1、1/1、2/1、3/1、4/1、5/1 等不同比例性費洛蒙配方對其雄蟲的誘引性，經六角型木質轉盤、飛行轉盤生物檢定及田間試驗，分別以 I/II = 3/1、5/1、2/1 配方較具誘引效果。誘餌中加入 BHT、Vit-A、Vit-E、小麥胚芽油、荷荷葩油等不同抗氧化劑，以加入 Vit-E 者無誘蟲效果，其餘對誘餌的誘蟲效果與持效期沒有增加。配方中加入蠟油，以 1 mg 者在田間可持效 5 周，其至第 7 周對瓜螟仍具誘引效果。

關鍵詞 (Key words): 瓜螟 (*Diaphania indica*)、昆蟲性費洛蒙 (insect sex pheromone)

PM12

利用昆蟲性費洛蒙偵/監測春、秋作胡麻害蟲發生情形之初報

Preliminary study on detection and monitoring insect's pests of spring and fall sesame with insect sex pheromone

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2014 年於嘉義、台中大肚秋作胡麻，發現危害胡麻新梢花及果莢之芝麻莢野螟 (*Antigastra catalaunalis*)。以花姬捲葉蛾、粗腳姬捲葉蛾、甜菜夜蛾、斜紋夜蛾、番茄夜蛾、豆莢斑螟、白緣螟蛾 (Ez-A, Ez-E, Ez-st)、亞洲玉米螟、粉斑螟蛾、印度穀蛾等 12 種害蟲性費洛蒙誘餌，偵測朴子、東石鄉胡麻害蟲發生情形。於朴子分場內偵測到斜紋夜蛾 (*Spodoptera litura*)、甜菜夜蛾 (*Spodoptera exigua*)、番茄夜蛾 (*Helicoverpa armigera*)、豆莢斑螟 (*Etiella behrii*)、及亞洲玉米螟 (*Ostrinia furnacalis*) 等。於東石鄉除偵測到上述害蟲種類，亦誘得粗腳姬捲葉蛾 (*Cryptophlebia ombrodelta*)。於 2015 年春作胡麻於朴子分場、東石鄉繼續以斜紋夜蛾、甜菜夜蛾、番茄夜蛾、豆莢斑螟、白緣螟蛾、粗腳姬捲葉蛾、亞洲玉米螟等害蟲性費洛蒙監測，又增加偵測擬尺蠖、小白紋毒蛾等，結果顯示以斜紋夜蛾族群密度較高，其次依序為甜菜夜蛾、亞洲玉米螟、小白紋毒蛾等，擬尺蠖於 5 月底至 6 月初族群密度升高。實際於田間調查不同地區蟲相有差異，春作胡麻銀葉粉蝨、甜菜夜蛾、蚜蟲、煙盲椿 (*Nesidiocoris* sp.)、粉介殼蟲、蟎等害蟲普遍發生。以胡麻葉及碩果餵食斜紋夜蛾、甜菜夜蛾、番茄夜蛾、擬尺蠖，顯示其取食良好，證實其能危害胡麻作物。

關鍵詞 (Key words): 胡麻 (sesame)、昆蟲性費洛蒙 (insect sex pheromone)、偵測 (detection)、監測 (monitoring)、害蟲 (insect's pests)

PM13

薊馬警戒費洛蒙生物檢定條件與其對小黃薊馬 (*Scirtothrips dorsalis*) 的警戒效果

Conditions of thrip Alarm pheromone bioassay and the alarm effect on the chilli thrips, *Scirtothrips dorsalis*

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本研究探討薊馬警戒費洛蒙製劑生物檢定條件，包括薊馬成蟲不同週齡、光度、警戒有效距離等，進而測試其對小黃薊馬的警戒效果。比較台灣花薊馬成蟲 1 週、2 週、3 週等不同週齡成蟲對警戒費洛蒙的生物活性，隨其成蟲週齡的增加對警戒費洛蒙的反應率下降，以 1 週齡成蟲對警戒費洛蒙的反應率較佳，兩次試驗反應率分別為 50.2、49.0%。試驗時的光度影響薊馬對警戒費洛蒙的反應率，以光度 525 lux 至 580 lux 較佳。將台灣花薊馬若蟲分別置放於距離薊馬警戒費洛蒙製劑 0、50、100、150、200、250、300 cm 處，經 1 hr 檢視其外出率，結果顯示薊馬警戒費洛蒙塑膠微管及橡皮帽製劑之有效距離分別約為 50 及 100 cm。將含有小黃薊馬的花豆子葉、薊馬警戒費洛蒙製劑、及新鮮的花豆子葉，同時置放於玻璃培養皿中，分別經 1、2、6、12 及 24 hr 取出新鮮花豆子葉，再置放約 21 日等小黃薊馬發育為成蟲，記錄蟲數。與對照組比較，再換算為因警戒費洛蒙處理花豆子葉受薊馬為害產卵數下降的比率。結果顯示經警戒費洛蒙處理可降低小黃薊馬的產卵數，經 1、2、6、12 及 24 hr 花豆子葉受薊馬為害產卵數下降的比率，於第一次試驗分別為 73.6、31.7、40.1、69.9 及 41.4%。於第二次試驗分別為 100、100、72、85.5 及 87.8%。

關鍵詞 (Key words): 台灣花薊馬 (*Frankliniella intonsa*)、小黃薊馬 (*Scirtothrips dorsalis*)、警戒費洛蒙 (alarm pheromone)

PM14

薊馬警戒費洛蒙及殺蟲劑綜合應用之室內防治效果評估與田間持續應用之防治效果

Evaluation of integrated control effect with thrip alarm pheromone and insecticides in the laboratory and the control effect on thrips with continuous applications in the field

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本研究於 2009 年選用防治薊馬常用藥劑，如亞滅培、益達胺、賜諾殺、芬殺松、納乃得、馬拉松、畢芬寧、第滅寧、丁基加保扶等 9 種殺蟲劑對台灣花薊馬的防治效果。測試於室內以表層附藥的花豆子葉靠接含有薊馬的花豆子葉，經 24 hr 薊馬的死亡率，以處理賜諾殺、芬殺松藥劑者較高，分別為 72.2、48.7%；其餘藥劑處理之死亡率為 1.3~6.7%。2013 年增加克凡派、賽洛寧，共測試 11 種殺蟲劑，僅賜諾殺、芬殺松顯示對台灣花薊馬具防治效果。對小黃薊馬之燻殺效果以賜諾殺、丁基加保扶、克凡派較佳，而亞滅培、納乃得沒有防治效果。薊馬警戒費洛蒙與殺蟲劑綜合應用之效果探討，台灣花薊馬選用芬殺松 10,000x，小黃薊馬選用賽洛寧進行試驗。比較藥劑、藥劑及薊馬警戒費洛蒙分別處理台灣花薊馬與小黃薊馬之死亡率，結果顯示兩種處理對兩種薊馬之死亡率均無差異；經探討處理薊馬警戒費洛蒙主要在降低薊馬產卵數。於 2012 年 8 月至 2014 年 10 月，連續利用薊馬警戒費洛蒙在彰化縣社頭鄉番石榴果園綜合防治薊馬，共進行 3 次試驗。結果顯示警戒費洛蒙處理區其果實危害率逐年下降，由 2012、2013、2014 年分別 69.3、36.4、26.9%；對照區果實危害率由 2012 年 92.8%，陸續降為 2013 年 71%，2014 年 46.7%，顯示持續使用薊馬警戒費洛蒙，使薊馬在果園內的族群密度逐漸下降，果實危害率因而逐年下降。

關鍵詞 (Key words): 台灣花薊馬 (*Frankliniella intonsa*)、小黃薊馬 (*Scirtothrips dorsalis*)、警戒費洛蒙 (alarm pheromone)、番石榴 (guava)、綜合防治 (integrated control)

PM15

四種稻穀品種之穎殼完整性對穀蠹及麥蛾繁殖影響

Effects of husk integrity of four rice varieties on the reproduction of *Rhyzopertha dominica* and *Sitotroga cerealella*

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台灣稻穀收割已全然邁入機械化時代，在田間以濕穀形式收割，進倉前先經稻穀烘乾機乾燥後才進倉貯藏。在濕穀收割過程或進倉前之烘乾過程，常因稻穀本身生理特性或處理機械之傷害，導致稻穀破損率增加，影響後續之害蟲發生。為了解不同稻穀品種收穫後其破損多寡對害蟲繁殖之影響，本研究將比較四種重要稻穀品種（台南 11 號、台粳 9 號、台農 71 號、台中秈 10 號）在完整粒及 2、4、8、12% 破損率下，對穀蠹及麥蛾之繁殖影響。結果顯示穀蠹及麥蛾均能侵入四種稻穀品種之完整粒，繁殖數則隨稻穀破損率增加而增加，兩者成正相關，在各處理中 4 種稻穀品種之完整粒與 12% 破損率均呈現顯著差異。兩種害蟲之繁殖數均以台中秈 10 號最高，其中穀蠹在 12% 破損率的台中秈 10 號處理組是完整粒之 4.5 倍，而麥蛾僅達 2.16 倍。而穀蠹及麥蛾對稻穀損失量亦與稻穀破損率成正相關，其損失量以台中秈 10 號最高。顯示完整穎殼無法阻止穀蠹、麥蛾之侵入，但破損率多寡對兩種害蟲繁殖成正相關，其中對穀蠹之影響高於麥蛾。

關鍵詞 (Key words): 積穀害蟲 (stored-product insects)、稻穀品種 (rice varieties)、穀蠹 (*Rhyzopertha dominica*)、麥蛾 (*Sitotroga cerealella*)

PM16

傳播玉米褪綠斑駁病毒之玉米薊馬鑑定與防治
Identification and control of maize thrips (*Frankliniella williamsi*) transmitted *Maize chlorotic mottle virus*

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玉米薊馬 (*Frankliniella williamsi* Hood) 為傳播玉米褪綠斑駁病毒 (*Maize chlorotic mottle virus*, MCMV) 之媒介昆蟲之一，2014 年台灣玉米大面積感染 MCMV 而產量大減，罹病植株矮化，葉片明顯點狀白化斑駁、黃化或兩側壞疽，幼苗感染時，植株明顯矮化、生長不良甚至乾枯壞死，成株則結實不捻。於田間罹患病毒玉米上收集 3 種薊馬，經鑑定分別為玉米薊馬、台灣花薊馬 (*F. intonsa* Trybom) 及稻薊馬 (*Stenchaetothrips biformis* (Bagnall))，其中以玉米薊馬族群數量最多，經 PCR 檢測體內帶有玉米褪綠斑駁病毒。以室內育出不帶毒的玉米薊馬成蟲經飢餓處理後，接種至罹病植株進行獲毒及傳毒試驗，結果顯示可將褪綠斑駁病毒傳至健康植株上，確認玉米薊馬為該病毒之媒介昆蟲。為利未來田間玉米薊馬發生密度之監測及防治之參考，分別以黃色、藍色黏板連續 8 周進行監測調查。結果顯示以黃色黏板誘集效果較藍色黏板佳，且與實際檢視植株調查薊馬發生密度相符。以登記防治玉米害蟲之 7 種藥劑，在室內測試對玉米薊馬殺蟲效果，其中以 5.87% 賜諾特 (Spinetoram) 水懸劑 1600 倍及 50% 撲滅松 (Fenitrothion) 乳劑 1500 倍稀釋液處理，經處理 24 hr 後的成蟲與幼蟲死亡率均達 90% 以上，後經防檢局公告為防治玉米薊馬傳播病毒之緊急用藥。

關鍵詞 (Key words): 玉米薊馬 (*Frankliniella williamsi*)、玉米褪綠斑駁病毒 (*Maize chlorotic mottle virus*, MCMV)、媒介昆蟲 (insect vector)、防治 (control)

PM17

台灣都市地區白蟻危害問卷調查及鑑定網站

Accessing termite problem in Taiwan through questionnaire survey and termite identification website

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台灣都市地區長久以來受到白蟻危害的困擾，全面量化分析台灣白蟻危害與防治現況是發展防治策略與技術最重要的一步。本研究分別以台灣住宅白蟻危害現況調查問卷及白蟻鑑定服務網站兩種方式進行研究。問卷調查以街頭訪問路人的方式，收集受訪人觀察到房屋現況、住家白蟻受害情形、採取防治策略以及受訪人背景資料進行分析，我們關心的問題是台灣住宅白蟻的危害率、危害建築物類型、民眾過去採取的防治措施以及白蟻的防治費用與其造成的經濟損失。問卷內容包括民眾對防蟲公司在白蟻防治工作上的重視條件與合理收費範圍作調查；白蟻鑑定服務網的設立主要是提供民眾一個諮詢白蟻問題的管道，透過民眾登錄的採集資訊以及寄送來的白蟻標本，我們可以分析各縣市白蟻危害的物種，進而建議各地防蟲公司與民眾適當的防治策略，此外取得大量台灣各地白蟻標本，對相關白蟻基礎研究之重要性也不言可喻。目前設定各縣市至少有 100 份有效問卷，白蟻樣本採集也以各縣市至少有 100 份樣本為目標。

關鍵詞 (Key words): 白蟻防治 (termite control)、電腦輔助人員訪問 (computer assisted personal interviewing，CAPI)、公民科學 (citizen science)

PM18

亞洲柑橘木蝨的行為在柑橘黃龍病媒介傳播之研究

Studies of the behavior of asian citrus psyllid (*Diaphorina citri* Kuwayama) (Hemiptera: psyllidae) on the vectorship of citrus Huanglongbing pathogen (*Candidatus* Liberibacter asiaticus)

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柑橘黃龍病為近年危害柑橘產業最嚴重病害之一，缺乏有效治療藥劑，且可由媒介昆蟲傳播，增加病害防堵上困難性，如何預測並避免媒介昆蟲亞州柑橘木蝨（*Diaphorina citri*）向外傳播黃龍病成為防治的重要手段。本研究藉人為釋放健康柑橘木蝨成蟲進入原始不具柑橘木蝨族群之柑橘園內（30.8 × 28 m^2），以估計新入侵柑橘木蝨在田區內擴散的特性。兩次釋放結果顯示，擴散範圍在首週後不再擴大，擴散平均距離約 7-9 m，皆與首週的風向一致。由田區迎風面及逆風面同時釋放約 400 隻木蝨，分析擴散距離分別為 46 cm 及 7 cm，迎風面釋放呈現較廣擴散面積及距離，結果支持風向對柑橘木蝨擴散方向性之影響。前人研究提出柑橘木蝨在病株間具選擇偏好性，然本次試驗結果顯示偏好性無統計上之顯著差異。鑒於風向為目前探討因子中與柑橘木蝨田間擴散方向最為相關，而黃色黏板為目前推薦用於柑橘木蝨族群監測，懸掛黃色黏板於田間逆風及順風面，但均未誘集到柑橘木蝨，顯示黃色黏板在田間柑橘木蝨處於低密度時誘集效果不佳。藉由試驗所得之柑橘木蝨田間生態及行為資訊，探討黃色黏板監測柑橘木蝨族群動態之有效性，期作為未來柑橘黃龍病防治策略擬定之參考依據。

關鍵詞 (Key words): 媒介特性（vectorship）、擴散（dispersal）、寄主偏好（host preference）、亞洲柑橘木蝨（*Diaphorina citri*）

SC01

昆蟲免疫系統決定桿狀病毒寄主專一性
Insect immune system to determine baculoviruses host specificity

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Baculoviruses are insect-specific DNA viruses with restricted host range, and serve as viral vectors for bioindustry applications such as foreign gene expression, vaccine production, and pest control. *Autographa californica* nucleopolyhedrovirus (AcMNPV), a prototype of a commercially available and widely used baculovirus, can infect 39 species in 13 families. *Bombyx mori* nucleopolyhedrovirus (BmNPV) is a major pathogen of silkworms and has developed high host specificity to *Bombyx mori*. Interestingly, on a genomic level, the AcMNPV and BmNPV are highly homologous, but they share no overlapping host range. These two quite similar viruses have extremely different infection outcomes in *Bombyx mori*. We theorize that the determination of host specificity may depend on virus-host interactions, and that several genes may be involved in determining host specificity. Therefore, we used next-generation sequencing (NGS) to analyze the transcriptome response of the hosts to these viruses. The transcriptome library was constructed, annotated, and grouped after sequence assembly. A comparison of gene expressions shows several significant differences in the gene expression profiles of BmNPV and AcMNPV, especially in cases where genes involved in immune responses are verified by RNA interference. The manipulation of virus-host specificity could provide a breakthrough for the application of baculovirus in protein expression systems and in the development of bio-control agents.

關鍵詞 (Key words): 桿狀病毒 (Baculovirus)、次世代定序 (Next-generation sequencing)、寄主專一性 (Host specificity)

SC02

木蝨近緣種之聲學分化及物種辨識（半翅目：木蝨總科）
Acoustic divergence and specific recognition of allied psylloid species (Hemiptera: Psylloidea)

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Acoustic signals often play an essential role in mating behavior among species of Hemiptera. These signals usually covey specific information and may contribute to reproductive isolation between different species. In Psylloidea, the acoustic signals are highly specific and usually used in mating behavior. However, reports of acoustic comparison and mate recognition of psylloids were scarce. The role of acoustics in species divergence of psylloids remains unexplored. Therefore, the purposes of this study were 1) to examine the acoustic divergence of allied psylloid species; 2) to understand the role of acoustic recognition in pre-reproductive isolation of psylloids. Different groups of closely related psylloids, including three *Cacopsylla* species (Psyllidae), two *Trioza* species (Triozidae) and two *Macrohomotoma* species (Homotomidae), were studied for acoustic divergence. Among these, two *Cacopsylla* species and two *Trioza* species were used in acoustic recognition via cross experiments. Three *Cacopsylla* species revealed multiple distinct acoustic characteristics, including chirp duration, chirp number, chirp interval, trill duration and dominant frequency. Two *Trioza* and two *Macrohomotoma* species were clearly distinguishable by chirp duration. As these three groups each belong to different families, the results of acoustic comparison provided consistent evidences of acoustic divergence in psylloids. It indicates that acoustic characteristics are invaluable to distinguish closely related species of psylloids and provides supplementary characters in classification. The results of cross experiments presented that psylloids recognize conspecific signals to facilitate mating and prevent unnecessary hybridization via refusing of heterospecific signals. It suggests that acoustic signals reveal strong correlation with the mechanism of psylloid speciation.

關鍵詞（Key words）：木蝨總科（Psylloidea）、聲學（acoustics）、生殖隔離(reproductive isolation)、物種辨識（specific recognition）

SC03

白蟻與螞蟻在樹木腐朽過程中的物種演替
Termites and ants succession along tree decay process

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本研究砍伐不同腐朽程度的柳杉 81 棵，調查白蟻與螞蟻多樣性及空間分布，以瞭解兩者在樹木腐朽過程中的物種演替。結果顯示活立木、枯死立木與倒木等三種木材腐朽狀態皆棲息著散白蟻 (*Reticulitermes* sp.) 與樹白蟻 (*Glyptotermes* sp.)，但在活立木上，樹白蟻出現的頻率較散白蟻高，而在枯死立木及倒木上，則是散白蟻出現的頻率較高，顯示兩種白蟻對樹木的腐朽程度有不同的偏好。分析柳杉腐朽程度與白蟻出現率的關係，發現枯死立木上的白蟻出現率顯著高於活立木與倒木，顯示白蟻偏好取食死亡但未倒伏的樹木。本研究共採集到 16 種螞蟻，活樹上發現 3 種，枯死立木與倒木皆發現 13 種，而且螞蟻的出現率在枯死立木及倒木上顯著高於活立木，顯示大部分的螞蟻都是在樹木死亡後入侵，另外，廣義線性模型分析顯示部分螞蟻種類的出現與白蟻有正相關，包含散白蟻對日本皺家蟻 (*Tetramorium nipponense*)以及樹白蟻對台灣隱針蟻 (*Cryptopone taivanae*)，這兩種螞蟻可能是白蟻的捕食者、或偏好相同的築巢環境，但其餘的螞蟻與白蟻的出現無關。分析白蟻與螞蟻在樹木上的空間分布，發現不論是活立木、枯死立木或是倒木上，基部的白蟻與螞蟻出現頻率都較高，推測大部分的白蟻與螞蟻自基部入侵樹木。根據以上結果推測，在木材自然腐朽的過程中，樹白蟻最先入侵活樹，而在樹木死亡後，散白蟻與多種螞蟻開始入侵，但在枯立木倒下後，部分的白蟻會離開，而螞蟻則會繼續利用倒木。

關鍵詞 (Key words): 柳杉 (Japanese cedar)、社會性昆蟲 (social insects)、空間分布 (space distribution)、森林昆蟲學 (forest entomology)

SC04

Brain gene expression profiling in the fire ant *Solenopsis invicta*: division of labor

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Differential gene expression in the brain may underlie some behavioral differences among individuals. In eusocial insects, the behavior is different amongst castes: queens reproduce and workers work. To this end we have dissected brains from virgin queens and workers at two stages: pupae and adults. Four biological replicates of each sample were obtained (16 in total). These samples are subjected to RNA-sequencing (RNA-seq). A preliminary analysis comparing the two castes (queens vs. workers) revealed 205 (1% of total) and 293 (1.5% of total) genes differentially expressed in the pupal and adult stages, respectively. We will present the results of our ongoing analysis.

關鍵詞 (Key words): *Solenopsis invicta*, brain, division of labor

SC05

高溫對豌豆蚜（*Acyrthosiphon pisum*）生殖和發育的影響
Effects of high temperature on the reproduction and development of the pea aphid, *Acyrthosiphon pisum*

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昆蟲的生長發育受環境因素影響，溫度為其中一個重要因子。研究顯示溫度變化對於孤雌生殖胎生豌豆蚜的生存率、生長速率、壽命和子代數目皆有所影響。當環境溫度高於最適溫度 (20-25°C)，豌豆蚜存活率、壽命和子代數下降。溫度超過 30°C 時，存活率約為 70%，但已無子代產生。然而，高溫環境下造成豌豆蚜存活率下降與子代數減少的機制目前仍未明。我們以孤雌生殖胎生豌豆蚜為實驗物種，透過顯微解剖技術分析微卵管與卵室數目變化，並觀察胚胎形態發育。透過原位雜合法標定生殖發育基因 *Apvasa1* mRNA 的表現位置以探討高溫是否會影響生殖基因的表現。實驗結果發現卵室數目在不同飼養溫度的豌豆蚜中無顯著差異。然而 30°C 飼養之豌豆蚜晚期胚胎的長度顯著小於 20°C 飼養之豌豆蚜。已選殖成功 *Apvasa1* 片段製作核醣核酸探針標定生殖細胞，比較飼養於 20°C、25°C 與 30°C 之豌豆蚜 *Apvasa1* mRNA 表現位置，發現並無差異。但飼養於 30°C 之豌豆蚜其 *Apvasa1* mRNA 表現量較飼養於 20°C 之豌豆蚜弱。因此推論高溫飼養並不會影響 *Apvasa1* mRNA 在生殖細胞中的表現位置，但是否會抑制生殖細胞相關基因的表現，仍需以即時聚合酶鏈鎖反應確認。透過將高溫飼養豌豆蚜於不同時間移至最適溫度飼養，觀察是否能恢復正常的卵室數與基因表現量，從而分析高溫飼養時間對生殖發育之影響。

關鍵詞 (Key words): 豌豆蚜（*Acyrthosiphon pisum*）、溫度（temperature）、*Apvasa1*、生殖細胞（germ cells）

SC06

利用昆蟲桿狀病毒作為仿流感病毒以建構抗血球凝集素之單源抗體庫

Baculovirus as pseudotyped influenza viruses for the construction of monoclonal antibody library against hemagglutinin

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流感病毒為重要人畜病原，其中血球凝集素 (Hemagglutinin, HA) 在病毒感染的過程中極重要，為此病毒表面上的主要抗原，同時也是宿主產生免疫抗體的主要標的。本研究以我們實驗室發展成功的昆蟲桿狀病毒表面抗原呈現技術，成功的將 HA 表現在桿狀病毒的包膜 (envelope) 上，以之改善流感病毒血球凝集素之單株抗體生產流程，並比較小鼠施打不同抗原所引起之免疫反應。由於 HA 展示於桿狀病毒包膜上具天然三結合體構型，進一步我們又將桿狀病毒做特殊設計，使其同時具有在昆蟲細胞與哺乳類細胞中表現 HA 的能力，有助於增強 B 細胞對 HA 之免疫性。在融合瘤細胞篩選過程，亦能利用昆蟲桿狀病毒可於哺乳類細胞表面僅展示 HA 抗原的原理，安全且專一地以免疫螢光法篩選正確的融合瘤細胞。本實驗發現，桿狀病毒在展示 HA 後可造成凝血反應，因此可取代真正的流感病毒作血清反應試驗。在施打 1×10^9 pfu 之 HA-Bac 於小鼠後，以第二次免疫後第六週血清進行血球凝集抑制試驗之結果，顯示出能夠產生抑制 HA-Bac 上 HA 蛋白功能的抗體。本實驗所建立之 HA-Bac 抗原系統能以超越傳統方法，安全而有效率地製備出各種單株抗體。其可作為獨特工具篩選不同型病毒的特異性、小範圍及通用性 (universal antibody)、以及具病毒中和效力的單源抗體等全面性之應用。

關鍵詞 (Key words): 桿狀病毒表面展示系統 (baculovirus-display system)、A 型流感病毒 (influenza virus A)、血球凝集素 (hemagglutinin, HA)、單源抗體 (monoclonal antibody)