台灣昆蟲學會

Taiwan Entomological Society 37th Annual Meeting

第37屆年會

國立臺灣大學應用力學館
2016年10月14、15號

National Taiwan University
October 14th & 15th, 2016

第三十七屆台灣昆蟲學會年會

The 37th Annual Meeting of Taiwan Entomological Society

2016 年 10 月 14-15 日
台灣，台北，國立臺灣大學
October 14-15, 2016
National Taiwan University
Taipei, Taiwan

內容 Contents

大會資訊 Meeting Information

大會地點 Meeting Venue

本年度之年會於國立臺灣大學應用力學館舉行。所有的演講及活動分別於一樓視聽教室、一樓教室及大廳舉行。報到處與服務台位於近前門處。

The 37th annual meeting of Taiwan Entomological Society is to be held in the Institute of Applied Mechanics Building of National Taiwan University. All the talks and activities take place in the hall/classrooms of the first floor. Registration and information desks are near the front door of the building.

論文宣讀者注意事項 Guidelines for Oral Presenters

每一間教室皆備有筆記型電腦及投影機，所有講者請於每一場次開始前將檔案上傳至會場電腦，上傳檔案請使用 Office 2003 以下之格式。每位講者演講時間為 10-12 分鐘，討論時間 2-3 分鐘，共計 15 分鐘。

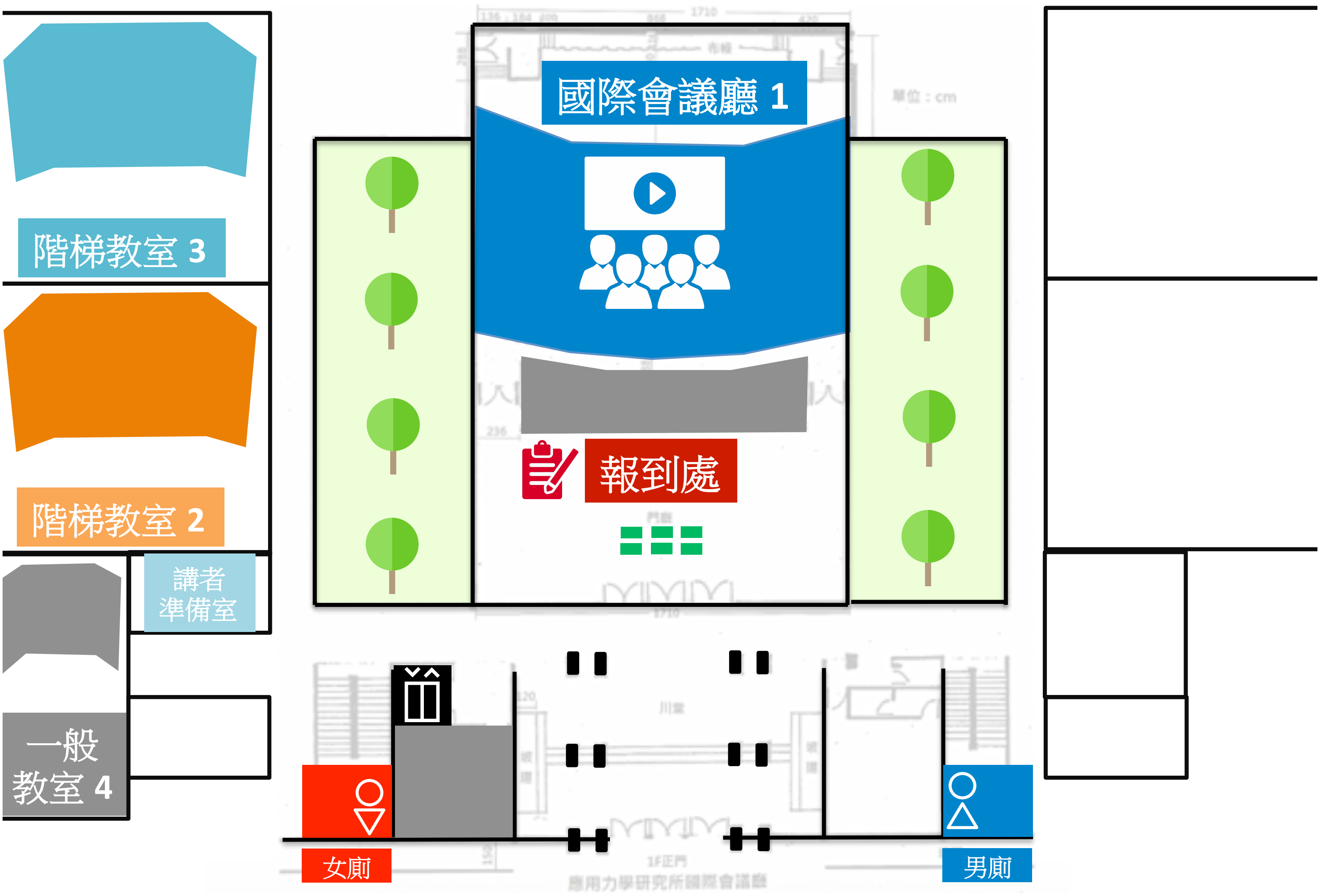
Laptops and projectors are provided for all classrooms. All presentation files should be uploaded to the laptops before the beginning of the sessions. The presentation medium for the Meeting is limited to Office 2003. There are 15 minutes for each speaker; 10-12 minutes for oral presentation and 2-3 minutes for discussion.

海報宣讀者注意事項 Guidelines for Poster Presenters

海報宣讀者請分別於第一天 (10 月 14 日) 之上午 09:00-09:50 以及第二天 (10 月 15 日) 之上午 08:30-09:00 依所指定之編號張貼，海報編號請見大會手冊，會場備有圖釘、膠帶和剪刀。海報展示地點為一樓大廳，請海報宣讀者於議程上指定之場次向參觀會友介紹展示內容並回答問題。海報下架時為第二天 (10 月 15 日) 下午 3:00。

The posters can be mounted respectively according to the assigned poster number on the first day of the Meeting at 09:00A.M.-09:50A.M. and the second day at 08:30A.M.-09:00A.M. The assigned poster numbers are listed in the programme. Tape, thumbtack and scissors are provided from the information desk. The poster exhibit is located in the hall on the first floor. Poster presenters have to be in attendance besides their posters to introduce the contents and answer questions. Posters must be removed during the ten-minute break (at 3:00P.M.) of the second day of the Meeting.

會場平面圖 Floor Plan



議程大綱 Programme at a Glance

105 年 10 月 14 日 (星期五) / Friday 14th October, 2016

時間 / Time	主題 / Activity	地點 / Place
09:30-10:10	報到 / 壁報張貼	大廳
10:20-11:10	大會專題演講 01	國際會議廳
11:10-11:20	休息	大廳
11:20-12:10	大會專題演講 02	國際會議廳
12:10-13:30	午餐 / 休息 / 壁報賞析	大廳
13:30-15:30	研究生演講比賽	國際會議廳
15:30-16:00	茶敘	大廳
16:00-17:00	會員大會	國際會議廳
17:00-17:30	壁報賞析	大廳
17:30-18:30	晚餐 / 壁報賞析	大廳
18:30-20:00	瘋狂昆蟲大賓果	大廳

議程大綱 Programme at a Glance

105 年 10 月 15 日 (星期六) / Saturday 15st October, 2016

時間 / Time	主題 / Activity	地點 / Place
08:30-09:00	報到 / 壁報張貼	大廳
09:00-10:30	壁報宣讀 01	大廳
	醫用昆蟲及病媒生態討論會 01	國際會議廳
	蟲害管理討論會 01	階梯教室 02
	昆蟲分子生物學討論會	階梯教室 03
	昆蟲多樣性調查討論會 01	一般教室
10:30-11:00	茶敘	大廳
11:00-12:30	醫用昆蟲及病媒生態討論會 02	國際會議廳
	蟲害管理討論會 02	階梯教室 02
	生物防治討論會 01	階梯教室 03
	昆蟲多樣性調查討論會 02	一般教室
12:30-13:30	午餐時間	大廳
13:30-15:00	壁報宣讀 02	大廳
	樹藝/都市生態論壇	國際會議廳
	昆蟲分類學討論會	階梯教室 02
	生物防治討論會 02	階梯教室 03
	昆蟲生活史及人工飼料討論會	一般教室
15:00-15:10	休息 / 壁報下架	大廳
15:10-17:10	生物物理及科技應用討論會	國際會議廳
	全球變遷對昆蟲影響討論會	階梯教室 02
	昆蟲行為生態討論會	階梯教室 03
	昆蟲抗藥性討論會	一般教室
17:10-17:30	閉幕頒獎 (優良論文、研究生比賽頒獎)	國際會議廳
17:30-18:00	第十九屆理監事改選開票	國際會議廳

第 37 屆台灣昆蟲學會年會議程大綱

Program

105 年 10 月 14 日 (星期五) / Friday 14th October, 2016

	大廳	國際會議廳 01	階梯教室 02	階梯教室 03	一般教室 04
09:30-10:10	報到/壁報張貼				
10:20-11:10		大會專題演講 01			
11:10-11:20		休息			
11:20-12:10		大會專題演講 02			
12:10-13:30	午餐/休息/壁報賞析				
13:30-15:30		研究生演講比賽			
15:30-16:00	茶敘				
16:00-17:00		會員大會			
17:00-17:30	壁報賞析				
17:30-18:30	晚餐/壁報賞析				
18:30-20:00		瘋狂昆蟲大賓果			

第 37 屆台灣昆蟲學會年會議程大綱

Program

105 年 10 月 15 日 (星期六) / Saturday 15th October, 2016

	大廳	國際會議廳 01	階梯教室 02	階梯教室 03	一般教室 04
08:30-09:00	報到/壁報張貼				
09:00-10:30	壁報宣讀 01	醫用昆蟲及病媒生態討論會 01（陳錦生）	蟲害管理討論會 01（段淑人）	昆蟲分子生物學討論會（路光暉）	昆蟲多樣性調查討論會 01（李後鋒）
10:30-11:00	茶敘				
11:00-12:30		醫用昆蟲及病媒生態討論會 02（蔡坤憲）	蟲害管理討論會 02（吳文哲）	生物防治討論會 01（賴麗娟）	昆蟲多樣性查討論會 02（楊曼妙）
12:30-13:30	午餐時間				
13:30-15:00	壁報宣讀 02	樹藝/都市生態論壇（楊平世）	昆蟲分類學討論會（蔡經甫）	生物防治討論會 02（謝佳宏）	昆蟲生活史及人工飼料討論會（陳文華）
15:00-15:10	茶敘/壁報下架				
15:10-17:10		生物物理及科技應用討論會（紀凱容）	全球變遷對昆蟲影響討論會（何傳愷）	昆蟲行為生態討論會（林宗岐）	昆蟲抗藥性討論會（戴淑美）
17:10-18:00		閉幕頒獎(優良論文、研究生比賽)與第十九屆理監事選舉投票			

The 37th Annual Meeting of Taiwan Entomological Society

Program

Friday 14th October, 2016

	HALL	Conference room 01	Classroom 2	Classroom 3	Classroom 4
09:30-10:10	Registration/ Poster Mounting				
10:20-11:10		Keynote Speech 01			
11:10-11:20		Break			
11:20-12:10		Keynote Speech 02			
12:10-13:30	Lunch/ Poster Session				
13:30-15:30		Student Oral Presentation Competition			
15:30-16:00	Tea break				
16:00-17:00		TES General Assembly			
17:00-17:30	Poster session				
17:30-18:30	Dinner/ Poster session				
18:30-20:00		Slingo Challenge			

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Program

Saturday 15th October, 2016

	HALL	Conference room 01	Classroom 2	Classroom 3	Classroom 4
08:30-09:00	Registration/ Poster Mounting				
09:00-10:30	Poster Competition Session 01	Medical Entomology & Vector Ecology 1 (Chin-Seng Chen)	Pest Management 01 (Shu-Jen Tuan)	Insect Molecular Biology (Kuang-Hui Lu)	Insect Diversity Survey 01 (Hou-Feng Li)
10:30-11:00	Tea Break				
11:00-12:30		Medical Entomology & Vector Ecology 2 (Kun-Hsien Tsai)	Pest Management 02 (Wen-Jer Wu)	Biological Control 01 (Li-Chuan Lai)	Insect Diversity Survey 02 (Man-Miao Yang)
12:30-13:30	Lunch				
13:30-15:00	Poster Competition Session 02	Arboriculture & Urban Ecology Forum (Ping-Shih Yang)	Insect Taxonomy (Jing-Fu Tsai)	Biological Control 02 (Chia-Hung Hsieh)	Life History & Artificial Diet (Wen-Hua Chen)
15:00-15:10	Break/ Poster Unmounting				
15:10-17:10		Biophysics & Scientific Application (Kai-Jung Chi)	Impacts of Global Change on Insects (Chuan-Kai Ho)	Behavioral Ecology (Chung-Chi Lin)	Insect Resistance (Shu-Mei Dai)
17:10-17:30		Award ceremony & Closing Remarks			

大會專題演講 Keynote Speech

第一天：105 年 10 月 14 日（星期五）10：20-11：10

地點：國立臺灣大學應用力學館 國際會議廳

講者：Dr. Serguei V. Triapitsyn, Department of Entomology, University of California at Riverside, USA

第一天：105 年 10 月 14 日（星期五）11：20-12：10

地點：國立臺灣大學應用力學館 國際會議廳

講者：Prof. Tsuyoshi Yoshimura, Research Institute for Sustainable Humanosphere, Kyoto University, Japan

大會專題演講 **Keynote Speech**

Taxonomy and biology of egg parasitoids of Auchenorrhyncha of economic importance in the world, and what we know about them in Taiwan

Serguei V. Triapitsyn
Department of Entomology, University of California at Riverside, USA

Most common and speciose egg parasitoids of members of the suborder Auchenorrhyncha (Hemiptera) belong to two families of Hymenoptera, Mymaridae and Trichogrammatidae in the superfamily Chalcidoidea. Worldwide, along with some nymphal and adult parasitoids such as Dryinidae (Hymenoptera) and Pipunculidae (Diptera), they are largely responsible for the natural control of leafhopper (Cicadellidae), planthopper (Delphacidae), and treehopper (Membracidae) species, including the economically important pests. Therefore, knowledge of their taxonomy (for identification) and biology is very important for biological control, ecological, and biodiversity studies. An overview of the history and current status of the taxonomy and biology of these two groups of egg parasitoids in the world, with special focus on Taiwan and the adjacent countries, is provided. While generic identifications of most Mymaridae and Trichogrammatidae in the region are generally relatively easily available, species identifications are still a major problem. Biogeographically, the fauna of Taiwan is primarily Oriental, although at high altitudes it arguably fits more in the Palaearctic ecozone, possibly with some Himalayan elements. The faunas of the adjacent countries are either within the Oriental or Palaearctic ecozones, or both. The entire region also has a number of cosmopolitan or Old World taxa, some transpacific elements (genera and species) that occur from Australasia to the eastern Palaearctic, endemic, relict, and possibly a few unintentionally introduced species. Historically, dealing with such diversity has been challenging for taxonomists of parasitic Hymenoptera (now being very few everywhere including Taiwan), particularly due to the fact that many species of egg parasitoids of Auchenorrhyncha, including economically important ones, are often widespread in distribution. A “single country” focal approach (rather than regional or hemisphere, or global) to parasitoid taxonomy thus has been particularly problematic and detrimental for these groups of insects: to be able to correctly identify a parasitoid from one country in east and southeast Asia, a taxonomist needs to have knowledge (combined with quality preparation of the voucher specimens and access to the type specimens), at a minimum, of the congeneric taxa from the northern Australasian,

Oriental, and Palaearctic regions. Also presented is vision of the future research on the egg parasitoids, such as promoting tri-trophic studies (i.e., collecting data on the host plant, the herbivore, and its parasitoids and hyperparasitoids, if any). Examples of some recent such studies are given, and the role of Auchenorrhyncha taxonomists and ecologists is discussed.

關鍵詞 (Key words)：Auchenorrhyncha, biological control, egg parasitoid, Taiwan

大會專題演講 Keynote Speech

Termite researches in Japan: from biodiversity to control

Tsuyoshi Yoshimura
Research Institute for Sustainable Humanosphere, Kyoto University, Japan

Japan is one of the leading countries on termite researches these days due to fruitful experience with serious termite problems in historical wooden buildings and products from the ancient days. The first description on termite infestation in the history can be dated back to the book “Nihon Ryoi-ki” published on 810-824. At present, we have four economically important termites out of 22 species in Japan, and the termite controlling market is estimated around 500 - 700 million USD per year. The modern termite research in Japan was initiated from Taiwan. The most important works were a series of termite survey by Mr. Masamitsu Oshima, whose name can be seen in three termite species including *Glyptotermes fuscus* Oshima, *Reticulitermes flaviceps* (Oshima), and *Sinocapritermes mushae* (Oshima et Maki). A total of six amazingly excellent research reports based on Mr. Oshima’s work, ranging from termite taxonomy to control strategies, were submitted to the government during 1909-1917. At the same period, Mr. Tokuichi Shiraki, who established the Entomology Laboratory in the Taihoku Imperial University (presently National Taiwan University) in 1928, made a comprehensive survey on pest insects in Taiwan in which he described 5 termite species: *Neotermes koshunensis* (Shiraki), *Coptotermes formosanus* Shiraki, *Odontotermes formosanus* (Shiraki), *Nasutitermes takasagoensis* (Shiraki), and *Pericapritermes nitobei* (Shiraki). Recently, we have published a book entitled “Termite Researches in Japan: from biodiversity to control” with 37 termite researchers in Japan as coauthors. In this talk, the contents of the book plus up-to-dated information will be addressed with special references to future possibility of collaboration between Japanese and Taiwanese termite researchers. For example, I have established a solid collaboration with Dr. Hou-Feng Li and Dr. Kok-Boon Neoh in National Chung Hsing University on termite infestation and diversity in Asia. More collaboration is expected in near future.

關鍵詞 (Key words)：Japan, research collaboration, Taiwan, termite research

論文宣讀議程 Program for Oral Presentation

研究生演講比賽

第一天：105年10月14日（星期五）13：30-15：30

Abstract QR code

地點：國立臺灣大學應用力學館 國際會議廳
主持人：楊景程博士
主題：研究生演講比賽

13：30-13：43	SC01_未折疊蛋白質反應參與病媒蚊生殖調控之研究–翁仕哲、蕭信宏
13：43-13：56	SC02_玉米穗蟲病毒的小分子 RNA 藉由後基因調控影響宿主並建立潛伏性感染–吳珮綺、吳岳隆
13：56-14：09	SC03_寬腹斧螳性食行為的可能肇因：飢餓與時機–林偉爵、蕭旭峰
14：09-14：22	SC04_利用單株抗體開發新尼古丁類藥劑免疫分析殘留檢測方法–蔡佳馨、何明勳、林韶凱、許如君
14：22-14：35	SC05_昆蟲桿狀病毒立即早期蛋白 IE2 形成新型聚合型結構體以增強基因表現–魏頌讚、董嬛、趙裕展
14：35-14：48	SC06_無取食行為的幼蟲與專食白蟻的成蟲：一新種喜白蟻性隱翅蟲之生活史與捕食行為–梁維仁、丸山宗利、李後鋒
14：48-15：01	SC07_溫度與二氧化碳濃度增加對於植食者表現的直接與間接影響：以綠點白粉蝶與葶藶為例–顏韶寬、劉騏銘、何傳愷
15：01-15：14	SC08_聖多美普林西比斑點熱立克次體之分子及血清流行病學研究–蕭穗文、曾蓮芬、吳文哲、王錫杰、蔡坤憲
15：14-15：27	SC09_多去氧核糖核酸病毒之小分子 RNA 於感病之斜紋夜蛾與馬尼拉小繭蜂的病理及免疫調控功能–唐政綱、吳岳隆

論文宣讀議程 Program for Oral Presentation

第二天：105 年 10 月 15 日（星期六）09：00-10：30

地點：國立臺灣大學應用力學館 國際會議廳
主持人：陳錦生教授
主題：醫用昆蟲及病媒生態討論會 01

Abstract QR code

09：00-09：20	MEVE01_Who is the better dengue vector?–陳維鈞
09：20-09：35	MEVE02_Genetic dissection of interaction between intermediate host and human tapeworm in red flour beetle, *Tribolium castaneum*–Hirotaka Kanuka
09：35-09：50	MEVE03_Dissecting molecular mechanism of taste sensation of ATP in fly and mosquito–Chisako Sakuma, Hirotaka Kanuka
09：50-10：50	MEVE04_埃及斑蚊唾腺蛋白對登革病毒複製能力之影響–查莉達、蕭信宏、杜武俊
10：05-10：20	MEVE05_以蚊蟲唾液蛋白抗體鑑別登革熱病媒蚊之叮咬–顏采瑩、蘇千玲、舒佩芸、蔡坤憲
10：20-10：35	MEVE06_臺灣地區小哺乳動物及外寄生蜱蟬媒病毒調查–廖顥竣、施函君、鍾珞璿、舒佩芸、王錫杰

地點：國立臺灣大學應用力學館 階梯教室 02
主持人：段淑人教授
主題：蟲害管理討論會 01

Abstract QR code

09：00-09：15	PM01_以直接噴灑藥劑及果實浸藥方式評估 9 種藥劑對於咖啡果小蠹防治效果–王泰權、朱宜芬、楊滿霞、張淑芬、陳柏宏
09：15-09：30	PM02_可濕性硫黃對葉蟎的致死影響–李啟陽、姚美吉
09：30-09：45	PM03_現行甘藷蟻象防治藥劑之室內藥效評估–陳柏宏、黃守宏、王泰權、黃瓊慧、朱宜芬

09：45-10：00	PM04_粗糙甘藷象鼻蟲 (*Blosyrus herthus* Herbst) (鞘翅目：象鼻蟲科) 不同定溫飼育發育日數調查及藥劑防治篩選–莊國鴻、陳巧燕、施錫彬
10：00-10：15	PM05_評估 6 種不同作用機制農藥於「沙坑」荔枝上對於荔枝細蛾防治效果–王泰權、陳柏宏、黃守宏、蔡志偉
10：15-10：30	PM06_農藥商品整合資訊查詢簡介–楊滿霞、呂椿棠

地點：國立臺灣大學應用力學館 階梯教室 03
主持人：路光暉教授
主題：昆蟲分子生物學討論會

Abstract QR code

09：00-09：15	MB01_Oral delivery of dsRNA encapsulated within liposomes induces RNAi effects in the German cockroach, *Blattella germanica*–黃佳欣、林育賢、劉耘、Xavier Belles、李後晶
09：15-09：30	MB02_東方果實蠅之膜蛋白型鳥苷酸環化酶 BdmGC2 可能參與馬氏管滲透壓之調節–李雅倩、劉振鐸、路光暉
09：30-09：45	MB03_重複胺基酸轉運蛋白基因之發育表現: 解析蚜蟲與其專一性胞內共生菌整合發育的作用–呂曉鈴、張俊哲、Alex C. C. Wilson
09：45-10：00	MB04_家蠶多角體病毒檢測抗體之開發與應用–林孟均、盧美君
10：00-10：15	MB05_無後蛋白：從果蠅上發現的基因體守護者–陳易呈、謝道時
10：15-10：30	MB06_台灣鋏蠓 巢結構與生殖漿成員之分析–Preethi Krishnaraj、王思捷、林明德

地點：國立臺灣大學應用力學館 一般教室
主持人：李後鋒助理教授
主題：昆蟲多樣性調查討論會 01

Abstract QR code

09：00-09：15	IDS01_北部地區小果油茶病蟲害種類及發生調查–陳巧燕、莊國鴻、吳信郁

09：15-09：30	IDS02_台灣春、秋作胡麻害蟲發生之初步調查–洪巧珍、吳昭儀、王文龍、張志弘、張慕瑋、李慧玉
09：30-09：45	IDS03_台灣都市地區白蟻危害問卷調查–蔡易穎、楊上禾、李後鋒
09：45-10：00	IDS04_珍貴老樹之白蟻危害現況調查–賴佑宜、李後鋒
10：00-10：15	IDS05_高屏地區植物上粉介殼蟲（半翅目）種類調查–蘇建中、陳文華
10：15-10：30	IDS06_黑茶蛀蟲與環境黴菌關係之探討–詹美鈴、王也珍、曾皓佑、李婉萱、張瑜庭

第二天：105 年 10 月 15 日（星期六）11：00-12：30

地點：國立臺灣大學應用力學館 國際會議廳
主持人：蔡坤憲副教授
主題：醫用昆蟲及病媒生態討論會 02

Abstract QR code

11：00-11：15	MEVE07_自生型地下家蚊於台北市和高雄市之族群分布–游凱迪、顏采瑩、陳錦生、蔡坤憲
11：15-11：30	MEVE08_以新型餵血器提升蚊蟲飼養效率–許北辰、戴淑美
11：30-11：45	MEVE09_台北市關鍵人物登革熱防治之知識態度與行為研究–張惠雯、胡晉福、黃基森
11：45-12：00	MEVE10_2015 年台南市登革熱流行特性與防治成效分析–黃基森、胡晉福
12：00-12：15	MEVE11_煙霧機空間噴灑對埃及斑蚊的防治效果–侯佳慧、羅怡珮
12：15-12：30	MEVE12_埃及斑蚊人工餵血系統–羅怡珮

地點：國立臺灣大學應用力學館 階梯教室 02
主持人：吳文哲教授
主題：蟲害管理討論會 02

Abstract QR code

11：00-11：15	PM07_未施肥之茄子作物對二點葉蟎族群的影響–賴韋翰、段

	淑人
11：15-11：30	PM08_四種小黃瓜品種對棉蚜 (*Aphis gossypii* (Glover)) 之防禦效果–董耀仁、黃紹毅
11：30-11：45	PM09_防蟲網對積穀害蟲之隔絕效果評估–姚美吉、李啟陽、蘇永倫
11：45-12：00	PM10_亞洲柑橘木蝨寄主偏好及以月橘作為陷阱作物之防治應用–陳建良、洪挺軒、蕭旭峰
12：00-12：15	PM11_設施花胡瓜南黃薊馬與甜瓜黃斑病毒病害之發生–陳怡如、林鳳琪、鄭櫻慧
12：15-12：30	PM12_番茄黃化捲葉泰國病毒於菸草粉蝨體內之感染、移行與經卵傳播–牟德芬、謝芊桂、蔡志偉

地點：國立臺灣大學應用力學館　階梯教室 03
主持人：賴麗娟副教授
主題：生物防治討論會 01

Abstract QR code

11：00-11：15	BC01_不同濃度水楊酸甲酯對天敵之誘引效果–董耀仁、黃紹毅
11：15-11：30	BC02_以蓖麻蠶卵飼育平腹小蜂後對荔枝椿象之寄生表現–吳怡慧、吳登楨、盧美君、莊益源
11：30-11：45	BC03_瓜實蠅幼蟲寄生蜂 (*Psyttalia fletcheri*) 之生物學及與格氏突闊小蜂之交互寄生習性探討–黃琬庭、吳怡慧、莊益源
11：45-12：00	BC04_利用平腹小蜂防治荔枝椿象之效果評估–張萃媖、陳文華、陳俊吉

地點：國立臺灣大學應用力學館　一般教室
主持人：楊曼妙教授
主題：昆蟲多樣性查討論會 02

Abstract QR code

11：00-11：15	IDS07_台江國家公園黃斑海黽分布調查–廖近妙、黃文伯
11：15-11：30	IDS08_台灣橡樹癭蜂多樣性及其在全球多樣性之意義–唐昌廸、楊曼妙

11：30-11：45	IDS09_武陵地區溪流扁蜉蝣 *Afronurus floreus* 與 *Rhithrogena ampla* 之族群變動–呂家榮、丘明智、郭美華
11：45-12：00	IDS10_穿山甲糞便中的白蟻物種組成–梁竣傑、孫敬閔、裴家騏、李後鋒
12：00-12：15	IDS11_海岸山脈南段台灣穿山甲排遺內螞蟻種類組成之分析–孫敬閔、梁竣傑、裴家騏、林宗岐、李後鋒
12：15-12：30	IDS12_臺南四草、七股地區防風林與草地地棲性昆蟲群聚之比較–蔡婷維、黃文伯

第二天：105 年 10 月 15 日（星期六）13：30-15：00

地點：國立臺灣大學應用力學館 階梯教室 02
主持人：蔡經甫博士
主題：昆蟲分類學討論會

Abstract QR code

13：30-13：45	IT01_The preliminary taxonomic study of the Tachinidae (Diptera) in Taiwan: tribe Blondeliini–Yu-Zen Huang, Takuji Tachi
13：45-14：00	IT02_中國中生代大花蚤科化石之首度發現與記述–蕭昀、俞雅麗、鄧從雙、龐虹
14：00-14：15	IT03_木鼻白蟻科 (等翅下目) 於台灣的發現紀錄與新種確立–吳佳倩、梁維仁、李後鋒
14：15-14：30	IT04_臺灣隱生性針蟻屬之分類回顧–梁志文、林宗岐、蕭旭峰
14：30-14：45	IT05_台灣直翅目昆蟲的海拔分布–詹明澍、楊正澤
14：45-15：00	IT06_台灣球蠼螋科之分類研究–劉人豪、張萃媖

地點：國立臺灣大學應用力學館 階梯教室 03
主持人：謝佳宏助理教授
主題：生物防治討論會 02

Abstract QR code

13：30-13：45	BC05_南方小黑花椿象捕食二點葉蟎後若蟎之族群特性及捕

	食率分析–鍾伊庭、段淑人
13：45-14：00	BC06_南方小黑花椿象捕食台灣花薊馬之族群特性與捕食潛能評估–丁漢彥、段淑人
14：00-14：15	BC07_基徵草蛉對銀葉粉蝨的防治效果探討–許北辰、余志儒
14：15-14：30	BC08_蓮霧新興害蟲米爾頓釉小蜂 (*Anselmella miltoni*) 在非經濟作物上的蟲癭發育及其寄生蜂相–鍾權承、楊曼妙

地點：國立臺灣大學應用力學館 一般教室
主持人：陳文華助理教授
主題：昆蟲生活史及人工飼料討論會

Abstract QR code

13：30-13：45	LHAD01_不同食草對茶角盲椿象生活史之影響–林敬桓、陳威嘉、莊益源
13：45-14：00	LHAD02_板栗癭蜂 (膜翅目：癭蜂科) 在台灣獨特生活史週期與其化學防治–林振睿、楊曼妙
14：00-14：15	LHAD03_家蠶人工飼料適性品種之選育–林孟均、詹雲貞、盧美君
14：15-14：30	LHAD04_溫度對瓜食酪蟎 (*Tyrophagus neiswanderi*) 生活史特性之影響–王家于、陳文華

第二天：105 年 10 月 15 日（星期六）15：10-17：10

地點：國立臺灣大學應用力學館 國際會議廳
主持人：紀凱容副教授
主題：生物物理及科技應用討論會

Abstract QR code

15：10-15：25	BPSA01_美國農業部國家農業圖書館 i5k Workspace 專案-節肢動物基因體之基因註解品質控制–陳玟如、Christopher Childers、Monica Poelchau
15：25-15：40	BPSA02_以微量元素分析建立台灣產龍眼蜜之鑑定技術–鄞智鈞、丁婕、張又文、盧美君、楊恩誠

15：40-15：55	BPSA03_雄性大龍蝨附著毛的可調式吸附機制–岳威廷、施明智、紀凱容
15：55-16：10	BPSA04_微電腦斷層掃描技術重構蜜蜂腦部構造–王庭碩、蔡逸峰、張涵涵、鄭穹祥、楊恩誠
16：10-16：25	BPSA05_運用能量守恆原理分析新渡戶歪白蟻兵蟻之高速大顎彈動–關貫之、紀凱容、李後鋒
16：25-16：40	BPSA06_「榕果與榕小蜂的共生關係」行動展示盒開發與教學成效之研究–林玳戎、蔡志偉
16：40-16：55	BPSA07_應用 WSN 技術對積穀害蟲之監測及回報機制–姚美吉、李啟陽、邱相文、張又文
16：55-17：10	BPSA08_應用蜂巢內影像監測系統於蜜蜂運動行為分析–蔡靜偉、吳詩雅、吳匡晉、楊恩誠、林達德

地點：國立臺灣大學應用力學館 階梯教室 02
主持人：何傳愷助理教授
主題：全球變遷對昆蟲影響討論會

Abstract QR code

15：10-15：25	IGC01_年積溫差與胡麻斑星天牛的表現型相關的探討–馬堪津、何鎧光、徐爾烈、吳文哲
15：25-15：40	IGC02_胡麻斑星天牛棲群因應日高溫的衝擊所呈現外在行為和內在適應的反應機制–馬堪津、彭武康、葉雲吟、趙榮台
15：40-15：55	IGC03_人工光害對黃緣螢幼蟲基因表現之影響–陳韻如、姜安容、楊恩誠
15：55-16：10	IGC04_初羽化蜜蜂頭部基因差異表現繼幼蟲時期接觸低致死劑量益達胺–吳明城、張又文、路光暉、楊恩誠
16：10-16：25	IGC05_氣候變遷如何影響北加州溪流大型無脊椎動物對農藥汙染之反應–丘明智、Lisa Hunt、Vincent Resh
16：25-16：40	IGC06_暖化對台灣不同地區小菜蛾之影響–吳冠毅、丘明智、郭美華
16：40-16：55	IGC07_暖化對台灣不同地區桃蚜之影響–張園、丘明智、郭美華
16：55-17：10	IGC08_暖化對基因轉殖東方果實蠅之影響–倪郁涵、丘明智、路光暉、郭美華

地點：國立臺灣大學應用力學館 階梯教室 03
主持人：林宗岐副教授
主題：昆蟲行為生態討論會

Abstract QR code

15：10-15：25	BE01_Worker reproduction in the invasive yellow crazy ant *Anoplolepis gracilipes* (Hymenoptera: Formicidae)–Ching-Chen Lee, Shu-Ping Tseng, Chung-Chi Lin, Chin-Cheng Yang
15：25-15：40	BE02_台灣土白蟻的多王多后初始族群在適存度及族群成長上的優勢–邱俊禕、李後鋒
15：40-15：55	BE03_台灣實例證明榕屬植物可成爲螞蟻共生–邊安台、周蓮香
15：55-16：10	BE04_尼泊爾埋葬蟲第二性徵對種內競爭之影響–林柏安、黃文伯
16：10-16：25	BE05_直角漢蜣築巢模式對子代發育之影響–吳秉錞、黃文伯
16：25-16：40	BE06_載卵壓力和聚集效應對於大頭金蠅產卵行為的影響–郭允、蕭旭峰
16：40-16：55	BE07_臺灣索鐵線蟲寄主專一性–邱名鍾、黃旌集、吳文哲、蕭旭峰

地點：國立臺灣大學應用力學館 一般教室
主持人：戴淑美副教授
主題：昆蟲抗藥性討論會

Abstract QR code

15：10-15：25	IR01_二化螟乙醯膽鹼酯酶的大量表現與純化–孟子翔、戴淑美
15：25-15：40	IR02_小菜蛾代謝相關抗藥性基因之功能性分析–王誌偉、葉庭維、張嘉哲、葉信宏、許如君
15：40-15：55	IR03_以轉錄基因體探討細胞色素 P450 與東方果實蠅有機磷抗性之關聯–余俊瑩、陳倩瑜、許如君
15：55-16：10	IR04_利用 RNA 干擾探討東方果實蠅 (*Bactrocera dorsalis*)

	穀胱甘肽硫轉移酶對有機磷類藥劑抗性相關性–吳昌昱、陳倩瑜、許如君
16：10-16：25	IR05_台灣地區小菜蛾的抗藥性調查及對因滅汀之抗藥性遺傳研究–方政威、戴淑美
16：25-16：40	IR06_小菜蛾對美文松抗藥性機制研究–許瑋真、戴淑美
16：40-16：55	IR07_聖多美普林西比民主共和國岡比亞瘧蚊種群之抗藥性分析–陳瀅安、曾蓮芬、鄭見福、連日清、蔡坤憲
16：55-17：10	IR08_褐飛蝨及白背飛蝨族群對不同抗性基因水稻之致害性表現–黃守宏、鄭清煥、王泰權、陳柏宏

壁報題目暨發表人 Poster Title & Presenter

壁報展覽

Abstract QR code

PD01_二點葉蟎 (*Tetranychus urticae*) 於台灣夏季自然變溫下之族群特性–陳沛享、林雍翔、段淑人

PD02_入侵紅火蟻成功入侵臺灣之基因體學探討–李志琦、丘祐坤、王忠信

PD03_不同溫度對黑豆蚜 (*Aphis craccivora* Koch) 生活史之影響–陳柏凱、陳奕均、黃郁涵、蕭文鳳

PD04_昆蟲免疫系統決定桿狀病毒寄主專一性–陳昱瑋、吳岳隆

PD05_開發防蚊液的檢測方法–吳詠群、黃子恆、羅怡珮

PD06_應用生化分析及分子檢測技術探討埃及斑蚊對除蟲菊劑的抗藥性–彭俊銘、吳彥霖、曾偉倫、羅怡珮

PD07_利用基因體增幅次世代定序技術完成火蟻共棲蟎類粒線基因體–李志琦、王忠信

PD08_How to revise the taxonomy of an insect genus with polymorphism, sexual dimorphism and conservative genitalia? A case study of *Elymnias* Hübner, 1818 (Nymphalidae, Satyrinae)–Chia-Hsuan Wei, David J. Lohman, Djunijanti Peggie, Shen-Horn Yen

PD09_浸水營地區(屏東縣轄)特有森林植物之伴生植食性昆蟲調查–顏聖紘、廖士睿、陳怡潔、杜士豪、蘇昱任、李書豪

PD10_楠梓仙溪野生動物保護區及其周邊濕地重要資源昆蟲普查及其棲地保育規畫–顏聖紘、廖士睿、陳怡潔、杜士豪、蘇昱任、李書豪

PD11_ *Philotrypesis* 屬榕小蜂雄蟲的非典型形態與行為-王達勉、邊安台、蕭旭峰、周蓮香

研究生壁報比賽

第二天：105 年 10 月 15 日（星期六）

第一場 09：00-10：30

第二場 13：30-15：00

Abstract QR code

PC01_日本與臺灣產白粉蝶 (*Pieris rapae*) 於相同溫度梯度下之生長表現–劉騏銘、顏韶寬、何傳愷

PC02_mir-100 表現量過低的原因及其對果蠅發育所造成的影響–林伯駿、葉淑丹

PC03_Walk with butterflies? Evaluating city sidewalks as habitat for *Pieris* butterflies–溫彝禎、何傳愷

PC04_入侵植物 (大花咸豐草) 如何在不同海拔影響本土植物 (葶藶) 和相關蝴蝶？–江怡安、歐家昂、何傳愷

PC05_台灣菌蠹蟲與線蟲族群關係之研究–張祁舜、余冠毅、施欣慧、林清山、陸聲山、楊爵因

PC06_光敏試劑對多種昆蟲細胞的胞殺影響與其對蚜蟲成蟲的效果之研究–王漢雍、吳岳隆

PC07_如何展示後翅眼紋才能獲得最佳的禦敵效果？–蘇昱任、顏聖紘

PC08_較低的蝶翅摩擦力是否有利逃離掠食者的攻擊？–杜士豪、顏聖紘

PC09_組織胺感受性氯離子通道於柑橘鳳蝶視覺系統中的免疫電顯定位–陳姵如、松下敦子、蟻川謙太郎

PC10_物聯網技術應用於蟲害管理之研究: 以東方果實蠅為例–廖敏勝、江昭皚、林明瑩、黃昱斌、楊恩誠、莊益源

PC11_時間稽延神經網路應用於蜂群預測之研究–陳韋勝、王健豪、邱奐絜、黃建朋、林弘人、楊恩誠、江昭皚

SC01_未折疊蛋白質反應參與病媒蚊生殖調控之研究

Essential role of unfolded protein response in the regulation of mosquito reproduction

翁仕哲、蕭信宏
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Autophagy is a process for degradation of proteins and organelles to maintain the homeostasis of macromolecules in eukaryotic cells. Previous studies have demonstrated that programmed autophagy in the mosquito fat body plays a pivotal role in maintaining of developmental switches required for normal progression of gonadotrophic cycles in the mosquitoes *Aedes aegypti*. Mosquitoes must feed on vertebrate blood for egg development. As a consequence, some mosquito species are vectors of pathogens that cause devastating diseases in humans, most importantly malaria, zika and dengue fever. Hence, dissecting mechanisms to control egg developmental cycles is of importance for developing novel approaches for mosquito control. During each egg developmental cycle, the fat body undergoes a developmental program that includes previtellogenic build-up of biosynthetic machinery, intense production of yolk protein precursors, and termination of vitellogenesis. However, the mechanisms of autophagy induction remain unclear. To investigate the autophagy in the fat body of female mosquitoes, we perform the qRT-PCR and Western blot analysis to examine the expression of autophagy-specific markers. Our data revealed that autophagy was activated during the synthesis phase of vitellogenesis, and the activation of autophagy was correlated to the unfolded protein response (UPR). To further examine the effects of the UPR and autophagy on vitellogenesis, we used the *in vitro* fat body culture system to assay the expression of the UPR and, autophagy specific markers. Our data show that UPR and autophagy was activated upon amino acids treatment. Interestingly, silencing of UPR related genes significantly reduced the expression of autophagy-specific markers and inhibited the fecundity of the female mosquitoes. Taken together, our results suggested that autophagy is induced during the synthesis phase of vitellogenesis in the fat body of *A. aegypti* and this induction is regulated via UPR.

關鍵詞 (Key words)：埃及斑蚊 (*Aedes aegypti*)、卵黃生成作用 (vitellogenesis)、未折疊蛋白質反應 (unfolded protein response, UPR)、細胞自噬 (autophagy)

SC02_玉米穗蟲病毒的小分子 RNA 藉由後基因調控影響宿主並建立潛伏性感染

Heliothis zea Nudivirus-1 miRNAs promote latent infection 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 (miRNA) and is the only detectable *Hz*NV-1 gene. Two of the miRNAs derived from *pag1* have been found to suppress and silence *Hind*III-I 1 (*hhi*1), an early gene of *Hz*NV-1. *Hhi1* induces strong apoptosis and increases the lytic to latent ratio. *Pag1* reduces the apoptosis caused by *hhi1* and further promotes the establishment of latent infections. Previous reports have shown that persistent infection of herpes simplex virus (HSV) is highly associated with epigenetic regulation of the chromatin structure and is regulated by latent-specific miRNAs. As *pag1* is a non-coding transcript, it could further establish latent infections through regulation of host chromatin structures via miRNAs. Our study discovered that histone modification associated enzymes changed upon *pag1* transfection. Furthermore, several miRNAs encoded from *pag1* have been found to target the message RNA of these transferases. We also performed CHIP (chromatin immunoprecipitation) assay to check histone acetylation/ methylation levels. These results suggest that HzNV-1 might directly influence epigenetic regulation of hosts through interaction with *pag1* miRNAs and promotion of latent infections.

關鍵詞 (Key words)：玉米穗蟲病毒 (*Heliothis zea* nudivirus, *Hz*NV-1)、小分子 RNA (miRNA)、潛伏性感染 (persistent infection)、後基因調控 (epigenetic regulation)

SC03_寬腹斧螳性食行為的可能肇因：飢餓與時機

Hunger or timing? The possible causation of sexual cannibalistic behavior in *Hierodula patellifera* (Mantodea: Mantidae)

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性食現象主要發生於無脊椎動物，以蜘蛛和螳螂的例子最廣為人知，嘗試解釋性食演化的假說多以這些生物為研究材料所建立。我們參考前人假說後提出三個修正假說：（一）若性食乃因雌性無法辨識同種雄性並將之視為食物，則預期雌性之攻擊行為可能近似於獵物選擇 (prey selection)；（二）若性食乃雌性辨識同種雄性失敗而將之視為食物，則預期雌性之攻擊行為將因雄性的求偶或接近行為而異，且較不受雌性飽食程度之影響；（三）若性食乃雌性可辨識同種雄性並將其視為食物，則預期雌性之攻擊行為將受雌性飽食程度與交配過與否影響。本研究以寬腹斧螳為材料，控制三假說中皆提及的因子──飽食程度以及雄性被雌性發現的時間點 (改良自舊因子)，觀察此兩因子對於交配成功與否及雄性存亡的影響。結果發現在本種中，雄性被發現的時間差異顯著影響性食的發生與否，雌性的飽食程反而對於性食發生與否的影響不大，且易遭性食之雄性體型較小，其結果支持我們所提出的假說二，較不支持假說一和三，並與過去大部分文獻之結果有出入。

關鍵詞 (Key words)：性食 (sexual cannibalism)、性食行為 (sexual cannibalistic behavior)、寬腹斧螳 (*Hierodula patellifera*)、兩性衝突 (sexual conflict)

SC04_利用單株抗體開發新尼古丁類藥劑免疫分析殘留檢測方法

Development of immunoassay in neonicotinoid pesticide residue detection method through monoclonal antibody

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隨著食安問題越趨嚴重，蔬果中的農藥殘留檢測逐漸成為一項重要的議題。目前常見的農藥殘留檢測方法為儀器分析，但其耗時、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。我們以新尼古丁類農藥為檢測目標，嘗試開發一個利用單株抗體的免疫分析技術做為新的農藥殘留檢測元件。將農藥半抗原與載體蛋白結合製備農藥抗原，注射進小鼠腹腔內促成免疫反應，免疫數次後，採血測試血清中抗體的效價，免疫反應最佳的小鼠會被犧牲，取小鼠脾臟細胞與癌細胞融合以製備得以產生抗體的融合瘤細胞。經過逐代篩選後，已挑選出得以辨識農藥益達胺 (imidacloprid)、可尼丁 (clothianidin)、亞滅培 (acetamiprid)、賽速安 (thiamethoxam) 等四株抗體細胞株。抗體細胞株放大培養後得以生產大量的單株抗體，利用競爭型酵素免疫分析方法 (enzyme-linked immunosorbent assay, ELISA) 評估抗體對農藥的靈敏度與交互反應性，四株單株抗體偵測極限皆低於 100 ng/mL，且皆具有高專一性。純化後的單株抗體可作為農藥檢測重要的元件，用於開發酵素免疫檢測套組及免疫快篩試紙 (immunochromotographic assay, ICA)，為農藥殘留的檢驗提供更多選擇。

關鍵詞 (Key words)：農藥殘留 (pesticide residue)、單株抗體 (monoclonal antibody)、新尼古丁類藥劑 (neonicotinoid pesticide)。

SC05_昆蟲桿狀病毒立即早期蛋白IE2形成新型聚合型結構體以增強基因表現

Baculovirus immediate early protein IE2 forms a novel clathrate cage-like structure to manipulate gene activation

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Baculovirus *Autographa californica* multiple nucleopolyhedrovirus (*Ac*MNPV) is an important insect pathogen and has been developed as a useful tool for foreign gene expression in both insect and mammalian cells. Previous studies showed that immediate early protein IE2 of baculovirus has important roles in viral gene expression and DNA replication. However, the mechanism for IE2 functioning remains unclear. Here, we found that IE2 could form a novel clathrate cage-like (CCL) structure, which co-localize with small ubiquitin like modifier (SUMO) proteins and viral DNA under confocal microscopy for strong transcriptional activation of target genes. We have also identified that during the expression of IE2, irregular nuclear domain 10 (ND10) nuclear bodies were found in the nuclei, suggesting IE2 might have the ability to disrupt ND10 nuclear body and related intrinsic antiviral responses. To further investigate protein disruption and binding activity of IE2, we have discovered two putative SUMO interacting motifs (SIMs) on the N-terminal region, which are crucial for functioning of this protein. Mutations of the SIMs of IE2 were not only affects its ability for CCL structure formation, but also eliminate its trans-activation function. By immunofluorescence staining, we also found a uniquely that class I Histone deacetylase (HDAC) could be specific expelled from IE2 CCL structure. By adding the HDAC inhibitor, trichostatin A and sodium butyrate, we observed a significant increasing trans-activation level of IE2 SIM double mutants. To further analyze the role of IE2 and HDAC interaction in viral replication, we produced numerous *ie2* mutated and knockout (KO) viruses. In Sf21 insect cell line, we have observed that *ie2* KO virus replicate ca. 100 times slower compare to normal virus. Based on these results, it is conceivable that IE2 activates viral promoters by affecting HDAC localization and in turn affects virus replication.

關鍵詞 (Key words)：Baculovirus、immediate-early protein IE2、RING domain E3 ligase、Small Ubiquitin like Modifier (SUMO)、Histone deacetylase (HDAC)

SC06_無取食行為的幼蟲與專食白蟻的成蟲：
一新種喜白蟻性隱翅蟲之生活史與捕食行為

Non-feeding larva and termitophagous adult: life cycle and predatory behavior of a new termitophilous rove beetle (Staphylinidae: Aleocharinae: Lomechusini)

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本研究始於野外觀察，由第一作者發現一種棲息於台灣土白蟻 (*Odontotermes formosanus* (Shiraki)) 覓食區域旁的隱翅蟲，且周圍伴隨有白蟻屍體殘骸。經由檢視外部形態及生殖器結構，該隱翅蟲屬於前角隱翅蟲亞科中的 *Zyras* 屬，且為一新物種。由於 *Zyras* 屬成員曾被記錄為喜蟻性或喜白蟻性，故本研究首先於實驗室中觀察其與土白蟻之間的互動，發現該隱翅蟲對土白蟻展現特殊的捕食行為，依序包含：觸角偵測、防禦行為、攻擊行為與取食行為；觸角偵測為對白蟻的位置、狀態或碰觸部位的感測，而進一步展現防禦或攻擊行為；防禦行為包含針對白蟻的頭部而展現的轉身行為或擺尾行為；攻擊行為則包含追趕白蟻以及破壞白蟻前胸之癱瘓行為；取食行為中首先進行斷頭行為，而後展現先食白蟻頭部的食腦行為。為瞭解其宿主專一性程度，以同棲地中之三科共六種白蟻進行取食偏好測試，結果顯示其僅取食台灣土白蟻單一物種，確認其為白蟻之專性捕食者。本研究於室內飼養中完整記錄其生活史，雌蟲每次只產下一顆卵，其發育階段（天數）為：卵 (3-4)、一齡幼蟲 (0.5-1)、二齡幼蟲 (1-2)、前蛹 (1-3)、蛹 (8-10)，本研究確認其幼蟲階段不取食之現象，為隱翅蟲科中之第一筆紀錄。本研究並以理論生態學原理探討此成蟲之捕食行為及其特殊生活史之可能成因。

關鍵詞 (Key words)：台灣土白蟻 (*Odontotermes formosanus*)、喜白蟻性生物 (termitophile)、專性捕食者 (obligatory predator)、最佳化覓食理論 (optimal foraging theory)、生活史策略 (life history strategy)

SC07_溫度與二氧化碳濃度增加對於植食者表現的直接與間接影響:以緣點白粉蝶與葶藶為例

Direct and indirect effects of elevated temperature and CO_2 on herbivore performance: a study of *Pieris canidia* and *Rorippa indica*

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Climate change (e.g., elevated temperature and CO_2) can affect species growth and development, subsequently shaping trophic interactions and community structure. However, less is known about how elevated temperature and CO_2 individually and collectively, as well as directly and indirectly, influence species performance. To help fill the knowledge gap, we studied the performance of *Pieris canidia* (herbivore) on *Rorippa indica* (host plant) by conducting three 3x2 factorial experiments. The 3x2 factorial design included temperature (ambient, +3°C, +6°C) and CO_2 (500, 1000 ppm) treatments, allowing us to examine the individual and collective effects of temperature and CO_2. The three experiments enabled us to compare the direct and indirect effects aforementioned: 1) Direct effect experiment – *P. canidia* under 6 temperature-CO_2 treatments fed on *R. indica* from common garden; 2) Indirect effect experiment – *P. canidia* in common garden fed on *R. indica* from 6 temperature-CO_2 treatments; 3) Combined effect experiment – *P. canidia* and *R. indica* were raised together in 6 temperature-CO_2 treatments. The results showed that temperature alone, but not CO_2, strongly affected *P. canidia* performance (e.g., reduced larval weight, larval and pupal period, and adult weight under warming). However, the collective effect (interaction) of temperature and CO_2 influenced forewing length and adult weight. Furthermore, elevated temperature, but not CO_2, affected *P. canidia* performance directly (reduced larval weight, larval period) and indirectly (increased larval period on +3°C host plants). Our study highlights the strong impact of elevated temperature on herbivore performance, which, however, is also mediated by a temperature-CO_2 interaction. Our attempt to untangle the complexity of individual, collective, direct, and indirect effects of climate change components should facilitate new models that will better predict community response to climate change.

關鍵詞 (Key words)：氣候變遷 (climate change)、植食者 (herbivore) 、寄主植物 (host-plant)、緣點白粉蝶 (*Pieris canidia*)、葶藶 (*Rorippa indica*)

SC08_聖多美普林西比斑點熱立克次體之分子及血清流行病學研究

Molecular and epidemiological study of spotted fever group rickettsiae in the Democratic Republic of Sao Tome and Principe

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Spotted fever group (SFG) rickettsioses are vector-borne diseases regarded as an emerging and reemerging disease around the world. Rickettsioses are caused by bacteria belonging to the genus *Rickettsia*, and are transmitted by ticks, fleas, lice and mites. In sub-Sahara Africa, the sero-prevalence of SFG was reported about 1.63% to 52%. However, there is no reports of tick species, SFG rickettsiae exposure or infection in the mid-African country, Democratic Republic of Sao Tome and Principe (DRSTP). In this study, dried blood spots (DBS) were collected from January 2016 to March 2016. The immunofluorescence assay (IFA) was used to detect IgG/A/M against SFG rickettsiae in 80 DBS samples randomly selected by age groups. The sero-positive rates to *R. africae*, *R. conorii*, and *R. felis* were 1.25% (1/80), 11.25% (9/80), and 1.25% (1/80), respectively. In addition, the sero-positive rate increases with age. No positive reaction was detected in age group of 0 to 15 years. Ectoparasites were collected from dogs, cattles and goats from August 2011 to August 2016. A total number of 1,187 cat fleas and 72 ixodid ticks were identified based on morphological characteristics and molecular methods. Rickettsiae DNA was detected by using polymerase chain reaction targeting the *gltA* and *ompA* genes as well as the pRF plasmid, and sequencing. The infection rate of fleas by *R. felis* was 21.01% (146/695). Partial *gltA*, *ompA* and pRF sequences from all *Ct. felis* fleas were 100% identical to those of *R. felis* strain URRWXCal2. Ticks were morphologically identified as *Amblyomma astrion* and *Amblyomma variegatum*. The SFG rickettsiae exposure was approved in DRSTP, public health department should informed the local residents and clinics for the risk of SFG exposure and the treatment.

關鍵詞 (Key words)：斑點熱立克次體 (spotted fever group rickettsiae)、seroepidemiology (血清流行病學)、貓蚤 (*Ctenocephalides felis*)、花蜱屬 (*Amblyomma* spp.)

SC09_多去氧核糖核酸病毒之小分子RNA於感病之斜紋夜蛾與馬尼拉小繭蜂的病理及免疫調控功能

Polydnavirus-encoded microRNA exerts different effects on the immune responses in *Spodoptera litura* and *Snellenius manilae*

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Insect immune systems are responsible for defending individuals against invasive organisms, meaning that parasitoid wasp larvae are liable to attack from the immune systems of their parasitized hosts. For this reason, parasitoid wasps have multiple mechanisms to inhibit the immune and physiological responses of their hosts. These mechanisms include the use of symbiotic viruses such as polydnaviruses (PDVs). PDVs differs from other viruses in that they are symbiotic with parasitoid wasps, and can help parasitoid wasp larvae infect lepidopteran larvae through the inhibition of host growth and immune reactions. PDVs display different infective symptoms in different hosts, and we believe that miRNAs are responsible for these differences. Rapid development of miRNA research has confirmed the involvement of miRNA in host-pathogen interactions. However, the role of miRNA has yet to be fully understood. This study aims to examine the role of miRNA in insect immune mechanisms through the differing immune responses that PDVs invoke in insects. PDV genomes contain many non-coding miRNAs, and these play a key role in regulating host gene expression. In this study, we focus on the novel role of miRNAs in the immunosuppression of PDV hosts and the mechanisms underlying this phenomenon. The Toll-7 expression levels of PDV-infected hosts are extremely down-regulated compared with wild-type and NPV-infected larvae. We performed next generation sequencing (NGS) to analyze RNA expression levels displayed upon PDV infection. These miRNAs account for 49.4% of the miRNAs species in our results and 45.0% of total reads compared with non-parasitized data. We hope to utilize RNAi technics, miRNA mimics and sponges in future experiments to manipulate miRNAs values in parasitized *Spodoptera litura* larvae and thus further examine the role of miRNAs. Finding the specific miRNAs responsible for immunosuppression and regulation of the immune system can not only improve our knowledge of insect pathology and provide potential methods for pest management control, but may also translate into better techniques for human medical sciences.

關鍵詞 (Key words)：多去氧核糖核酸病毒 (Polydnaviruses)、微小核醣核酸 (miRNA)、斜紋夜蛾 (*Spodoptera litura*)、馬尼拉小繭蜂 (*Snellenius manila*)、免疫抑制 (immunosurppression)

MEVE01_誰是比較重要的登革熱病媒蚊?

Who is the better dengue vector?

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Dengue fever has been one of important mosquito-borne viral diseases in most tropical and subtropical countries including Taiwan. Experimental evidence revealed that dengue virus causes minor damage in mosquito cells while it generally induces apoptosis in human (mammal) cells. This feature reflects an idea that partly elucidates how specific mosquitoes can be vectors of dengue fever. Currently, *Aedes aegypti* and *Aedes albopictus* are two species of mosquitoes considered to be significant vectors of dengue fever in nature because both of them are susceptible to dengue viruses and extensively distribute in dengue endemic areas. In Taiwan, most indigenous dengue cases have been recorded in regions down below the Tropic of Cancer (23.5°N), where *Ae*. *aegypti* and *Ae*. *albopictus* are sympatric. On the other hand, dengue outbreaks were scarcely reported from where only *Ae*. *albopictus* breeds according to surveillance in past decades. Similar phenomenon can also be seen in other countries located in Asia, America, and Africa. It raises an urgent question to be answered: Do these two mosquitoes play same roles in the transmission cycle of dengue virus in nature? In fact, differential susceptibility to dengue viruses has been demonstrated in the two mosquitoes; which is believed to be a major factor of determining vector competence. Generally, *Ae*. *aegypti* is more susceptible to dengue virus infection than *Ae*. *albopictus*. In addition, distinct mosquito behaviors including host preference, biting frequency, and larval breeding habitat are also assumed to be critical during establishment of dengue outbreaks. A hypothesis is thus inspired that a dengue outbreak, usually starting from a focal dengue virus transmission, is initiated more efficiently by *Ae*. *aegypti*. Subsequent participation of *Ae*. *albopictus* acts to expand or maintain the outbreak until the de novo herd immunity reaches high level.

關鍵詞 (Key words)：*Aedes*, dengue outbreaks, mosquito vectors, Taiwan

MEVE02_Genetic dissection of interaction between intermediate host and human tapeworm in red flour beetle, *Tribolium castaneum*

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Dwarf tapeworm, *Hymenolepis nana*, which belongs to phylum *Cyclophyllidea*, is the most common cestode of human. Its intermediate host is arthropods, in particular, beetles. Once the intermediate host ingests tapeworm eggs, oncospheres immediately hatch and pass through insect gut wall. Cysticercoids develop within the hemocoel where they survive without loss of infectivity until the intermediate host is ingested by a definitive host. To dissect the interaction between tapeworm and intermediate host, we employed a reverse genetic approach with red flour beetle, *Tribolium castaneum*, in which a robust systemic RNA interference (RNAi) response is observed, as a model system to explore host responses to tapeworm infection. Adult knock-down phenotypes in *T. castaneum* were induced by injection of double-stranded RNA (dsRNA) into late instar larvae. We performed RNAi screening targeting several gene transcripts of Toll and immune deficiency (IMD) pathways, which are two major signaling pathways of humoral immune response in insects. Reduction of Toll pathway function, which was induced by RNAi-mediated silencing of *MyD88, Dif1,* and *Dif2*, in addition to JAK/STAT and JNK components, caused increase of burden of cysticercoids. On the other hand, RNAi-mediated knockdown of IMD pathway components, *dredd* and *imd*, had no significant difference on cysticercoid load. Our findings suggest a pivotal role of specific pathway such as Toll signaling in regulating resistance to tapeworm infection.

關鍵詞 (Key words)：intermediate host, tapeworm, beetle, RNAi

MEVE03_Dissecting molecular mechanism of taste sensation of ATP in fly and mosquito

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Exploring the molecular mechanism of blood sucking behavior of female mosquitoes is one of the critical steps to fight against vector-borne disease such as dengue and malaria, since pathogens are transmitted when mosquitoes are gorging on blood. It has been known that adenine nucleotides in blood serve as a phagostimulant. Besides, the presence of chemoreceptive cells is suggested in labral apical sensilla and sensilla in cibarium (pre-oral mouth cavity). However, the molecular nature of chemoreceptors, corresponding primary sensory neurons, and processing of information in higher order centers remains to be examined. To identify the candidate chemoreceptor that perceives ATP in mosquitoes, we employed two approaches. First, we focused on gustatory receptors (Grs) of fruit fly *Drosophila melanogaster* from following two reasons: 1) sequence of P2X receptor that perceives ATP in broad animals is missing in mosquitoes and *Drosophila*, and 2) tasting food is generally facilitated by Grs in *Drosophila*. Two-choice behavior assay showed *Drosophila* with feeding preference to ATP. All Gr genes (60 genes) were examined using targeted expression of each dsRNA in ELAV-positive neurons and several Gr genes were identified as molecules modulating ATP preference. Second, expression pattern of genes in dengue virus-vector mosquito (*Aedes aegypti*) brains was compared between pre and post ATP suction using RNAseq analysis. In addition to Grs, mRNA expression levels of odorant receptors (Ors), innate immunity-related signaling molecules, chaperons, and microRNAs are increased in mosquito brain at 5-40 min after ATP-sucking. These results suggest that mosquitoes may adopt ATP-dependent signaling cue to control their blood-sucking behavior, in particular arresting feeding and leaving from host.

關鍵詞 (Key words)：mosquito, fruit fly, ATP, gustatory receptor (Gr)

MEVE04_埃及斑蚊唾腺蛋白對登革病毒複製能力之影響

Effects of salivary gland proteins in dengue virus replication in the mosquito *Aedes aegypti*

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Dengue fever is the most prevalent arthropod-borne viral disease in humans with no effective vaccine and medication. Previous studies have indicated that proteins from mosquito salivary gland may influence the infections of dengue virus (DENV) on human. However, the effects of salivary gland proteins on DENV infection in the mosquito *Aedes aegypti* remain largely unknown. Therefore, we hypothesize that some salivary gland proteins of *Ae. aegypti* may enhance or suppress the replication and transmission of dengue virus. The objective of this study is to determine the effect of salivary gland protein in the regulation of dengue virus replication and transmission. First of all, we identify several salivary gland proteins in the mosquito *Ae.aegypti*, namely D7, 34kDa and Apyrase. Our preliminary results showed that the transcripts of D7, 34kDa and Apyrase were up-regulated in the mosquito salivary gland post dengue virus infection. The replication of dengue virus was significantly inhibited with the absence of D7, 34kDa and Apyrase, by introduction of reverse genetic approach. Interestingly, we showed that the expression of E protein of dengue virus was inhibited when absence of 34kDa. Our findings indicated that salivary gland proteins are important for dengue virus replication and transmission in the mosquito *Ae. aegypti*.

關鍵詞 (Key words)：埃及斑蚊 (*Aedes aegypti*)、登革病毒 (dengue virus) 、唾腺蛋白 (salivary gland proteins) 、E 蛋白 (E protein)、基因默化 (gene silencing)

MEVE05_以蚊蟲唾液蛋白抗體鑑別登革熱病媒蚊之叮咬

Distinguish dengue vector exposure by antibodies against mosquito salivary protein

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Feeding of haematophagous arthropods involve not only taking blood but also injection of their saliva into the hosts. The saliva consists of many pharmacologically active, yet poorly understood molecules which function to break down haemostasis and modulate host immune responses and, in consequence, affect the progression of vector-borne diseases. The host antibodies elicited by mosquito salivary proteins (MSP) were proposed being used as indicators for vector exposure. Dengue fever is the most prominent arboviral infection in Taiwan. Although the two vector mosquitoes, *Aedes aegypti* and *Ae. albopictus*, distribute distinctly, frequent traffic and climate change could result in vector dispersal. In 2013, an indigenous dengue outbreak involving a total of 8 cases occurred in Taipei, where only *Ae. albopictus* thrives. Higher titer of antibody against *Ae. albopictus* salivary gland was found in 5 patients by immunofluorescence assay while the first patient exhibited stronger response against *Ae. aegypti*. Pre-adsorption was therefore carried out to reduce cross-reactions. The results showed that pre-absorption removed homologous antibodies. The experiments prove that the epidemic in Taipei in 2013 was indeed transmitted by *Ae. albopictus*. To further identify antigenic proteins in mosquito saliva, Western blot was applied. The blotting revealed the mosquito salivary proteins with molecular weight of 290-, 69- or 68-, 37-, and 30- kDa (representing SGS, apyrase, and D7-protein family, respectively) were highly immunogenic and prone to cross-reactions. The study employed human antibody responses against MSP to distinguish mosquito bites. The information about human exposure to dengue vectors should offer constructive suggestions to the scales of the coming epidemics and control strategies.

關鍵詞 (Key words)：登革熱 (dengue fever)、白線斑蚊 (*Aedes albopictus*)、蚊蟲唾液蛋白 (mosquito salivary protein)

MEVE06_臺灣地區小哺乳動物及外寄生蜱蜱媒病毒調查

Surveillance for tick-borne viruses in small mammals and their attached ticks in Taiwan

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蜱的生活史在幼蜱、若蜱、成蜱皆需更換寄主吸血，加上某些病原體可透過經發育期傳播 (transstadial transmission) 及經卵傳播 (transovarial transmission) 在蜱的體內代代相傳，使其成為傳播疾病的病媒中，重要性僅次於蚊子的病媒。蜱可傳播許多種類病原體，其中蜱媒病毒性疾病往往也是新興及人畜共通傳染病，例如最近發生於中國大陸、日本及南韓的發熱伴血小板減少綜合症 (severe fever with thrombocytopenia syndrome, SFTS)；此外蜱媒腦炎 (tick-borne encephalitis, TBE) 在歐洲、中國大陸及日本也有病例發生。本研究藉由建立蜱媒病毒的分子檢測法，先檢測黃病毒科 (Flaviviridae) 及布尼亞病毒科 (Bunyaviridae) SFTSV，再經由定序確認。同時調查採集臺灣西部、東部及離島小哺乳動物及外寄生蜱並檢測分離蜱媒病毒，藉以評估臺灣地區蜱種傳播 SFTS 及 TBE 等蜱媒病毒性疾病的潛在風險。自 103 年 1 月至 105 年 5 月完成臺灣本島 8 個縣市及離島 3 個縣市捕鼠採集，及小哺乳動物內臟檢體與外寄生蜱蜱媒病毒檢測。台灣西部、東部及離島三區小哺乳動物捕捉隻數分別為 196 隻、338隻及 290 隻，平均蜱侵染率 (蜱寄生動物數/全部動物數) 分別是 19.9%、4.44% 及 12.07%，所有動物內臟及蜱檢體 Flaviviruses 及 SFTSV 分子檢測結果皆為陰性。本研究目前並未發現小哺乳動物及外寄生蜱蜱媒病毒感染，顯示臺灣地區民眾感染蜱媒病毒的可能性較低。

關鍵詞 (Key words)：蜱 (tick)、蜱媒病毒 (tick-borne virus)、發熱伴血小板減少綜合症 (severe fever with thrombocytopenia syndrome)、蜱媒腦炎 (tick-borne encephalitis)、台灣 (Taiwan)

PM01_以直接噴灑藥劑及果實浸藥方式評估 9 種藥劑對於咖啡果小蠹防治效果

The control efficacy of nine insecticides for the coffee berry borer (Scolytidae: *Hypothemeus hampei*) by direct spraying and fruit dipping methods

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咖啡果小蠹為近年入侵台灣的咖啡重要害蟲，造成台灣咖啡產地的經濟嚴重損失。目前於植物保護手冊上尚無推薦藥劑可用於防治本害蟲，因此本研究以藥劑直接噴灑法與果實浸藥法於實驗室內進行藥劑篩選試驗，供試藥劑選擇 9 種市售成品農藥，分別為 85% 加保利可濕性粉劑 (850倍)、40.8% 陶斯松乳劑 (1,000倍)、2.4% 第滅寧水懸劑 (1,000 倍)、18.2% 益達胺水懸劑 (2,000倍)、2% 阿巴汀乳劑 (2,000倍)、11.6% 賜諾殺水懸劑 (3,000倍)、50% 培丹可溶性粉劑 (1,000倍)、18.4% 剋安勃水懸劑 (2,500倍)、11.7% 賜諾特水懸劑 (2,000倍)。藥劑直接噴灑試驗以噴藥塔直接對蟲體進行藥劑噴灑，每日觀察咖啡果小蠹的死亡率，試驗結果顯示藥劑處理 10 天後，以陶斯松及賜諾特處理最具毒殺效果，累積死亡率分別為 75.0% 及 69.5%，但是該 2 種藥劑卻未能有效於果實浸藥試驗造成咖啡果小蠹死亡。果實浸藥試驗於咖啡果小蠹接觸經藥劑處理的果實 24 小時後，以培丹及第滅寧的毒殺效果最好，死亡率分別為 97.5% 及 27.5%，但比較這 2 個藥劑的果實入侵率與平均入侵孔數，則以培丹 (16.7% 與 0.5 個) 優於第滅寧 (75.0% 與 4 個)，顯示培丹為最具防治效果的藥劑。因此根據本研究之 2 種室內藥劑篩選的結果，未來可於田間實際探討培丹用於防治咖啡果小蠹的效果。

關鍵詞 (Key words)：咖啡果小蠹 (*Hypothemeus hampei*)、防治效果 (control efficacy)、殺蟲劑 (insecticides)

PM02_可濕性硫黃對葉蟎的致死影響

Effect of wettable sulfur on the mortality of spider mites

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本次報告試驗資材為可濕性硫黃，其具殺菌、殺蟲、殺蟎作用，有登記使用在茶樹上防治葉蟎。衛福部雖將硫黃列為免殘留檢驗及世界各國有機農業也准許為有機農業資材，然我國農糧署並未將其列為有機栽培之病蟲害防治資材。硫黃在夏威夷為木瓜葉蟎的防治資材，然我國也尚未有合法登記於木瓜上使用，是以本試驗將予以驗證，並提出試驗資材的防蟲 (蟎) 對象與推薦用量，以提供農政單位參考。2014 年在網室木瓜上進行可濕性硫黃對神澤氏葉蟎 (*Tetranychus kanzawai* Kishida) 之 2 次田間防治試驗，試驗設計是依據我國農藥委託試驗設計採逢機完全區集設計。第 1 次試驗 4 種處理分別為 (1) 80% 硫黃WP 200 倍+sodasan (洗碗精) 1000倍、(2) 80% 硫黃 WP 400 倍+sodasan 1,000 倍、(3) 1% 密滅汀乳劑 1,500 倍、(4) CK組 sodasan 1,000 倍。施藥方法為硫黃組及CK組隔 5 天連續噴藥 2 次，密滅汀組僅噴藥 1 次，結果顯示在 2 種硫黃組在第 1 次施藥後第 7 天及第 12 天木瓜葉蟎防治率皆達 98.4% 以上並具有與 1% 密滅汀乳劑 1,500 倍相似防治葉蟎效果。第 2 次試驗 4 種處理分別為 (1) 80% 硫黃WP 400 倍、(2) 80% 硫黃WP 400 倍+一滴淨 (洗碗精) 1,000倍、(3) 1% 密滅汀乳劑 1500倍、(4) CK組 一滴淨 1,000 倍，施藥方法為硫黃組及CK組隔 4 天連續噴藥 2 次，密滅汀組僅噴藥 1 次，結果顯示在 2 種硫黃組在第 1 次施藥後第 7、14、21 天木瓜葉蟎防治率皆達 99.2% 以上並具有與 1% 密滅汀乳劑 1,500 倍相似防治葉蟎效果。2 次試驗期間木瓜葉片無明顯藥害。

關鍵詞 (Key words)：神澤氏葉蟎 (*Tetranychus kanzawai* Kishida)、可濕性硫黃 (wettable sulfur)、木瓜 (papaya)、防治 (control)

PM03_現行甘藷蟻象防治藥劑之室內藥效評估

Evaluation of insecticides recommended for controlling the adult of sweetpotato weevil, *Cylas formicarius* (Fabricius), in Taiwan

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甘藷蟻象 (*Cylas formicarius*) 為甘藷生產上之關鍵害蟲，防治上多以藥劑施用為主。本研究目的為檢測 5 種甘藷蟻象防治藥劑的殺蟲效果，比較藥劑噴佈法、藷塊浸藥法及藷葉浸藥法處理方式下，藥劑對甘藷蟻象成蟲之致死效果及其殘效性。試驗結果顯示，以 25% 陶斯松 (chlorpyrifos) 可濕性粉劑、43% 佈飛松 (profenofos) 乳劑及 50% 培丹 (cartap hydrochloride) 水溶性粉劑對成蟲的致死效果較佳。三種施藥方式處理下，以藷葉浸藥法處理所造成之殺蟲效果最高，藷塊浸藥法次之。此外，除 20% 亞滅培 (acetamiprid) 水溶性粉劑與 20% 達特南 (dinotefuran) 水溶性粒劑以外，殺蟲效果一般隨施用濃度提高而提升。藥劑殘效試驗結果顯示，25% 陶斯松可濕性粉劑以葉片浸藥處理，於處理後第 3 日與第 7 日仍分別保有 100% 與 46% 的殺蟲效果，其餘藥劑於處理後第 3 日的毒殺效果則顯著下降。

關鍵詞 (Key words)：蟲害防治 (pest control)、殺蟲劑 (pesticide)、甘藷蟻象 (sweetpotato weevil)

PM04_粗糙甘藷象鼻蟲 (*Blosyrus herthus* Herbst) (鞘翅目：象鼻蟲科) 不同定溫飼育發育日數調查及藥劑防治篩選

Developmental durations of Rough Sweet potato Weevil (*Blosyrus herthus* Herbst) (Coleoptera: Curculionidae) feeding on *Ipomoea batatas* at various temperatures and the selection of insecticide

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粗糙甘藷象鼻蟲 (*Blosyrus herthus* Herbst) 於2010年於新北市三芝區北新莊山區甘藷田發生，為該害蟲發生於台灣之新紀錄。其幼蟲嚙食甘藷塊根形成隧道狀溝槽食痕，致使甘藷失去商品價值。以新鮮藷塊於不同定溫飼育各蟲期發育日數，結果顯示20℃ 飼育卵期平均13.0 ± 0.5日、幼蟲期平均64.5 ± 6.2日、蛹期19.8 ± 2.6日，卵發育至成蟲總日數97.3 ± 7.3日，25℃飼育卵期8-9日，平均8.8 ± 0.4日，幼蟲7-8齡，幼蟲期平均46.5 ± 5.3日，蛹期9-17日，平均11.5 ± 1.7日，卵發育至成蟲總日數55-82日，平均66.9 ± 6.1日，30℃飼育卵期平均6.1 ± 0.3日、幼蟲期平均34.5 ± 3.5日、蛹期6.9 ± 1.6日，卵發育至成蟲總日數47.5 ± 3.5日，15℃飼育幼蟲1-2齡期即死亡，35℃卵無法孵化。隨飼育溫度上升，完成發育所需日數越短。推估20℃、25℃及30℃ 發育所需日數分別約為3個月、2個月及1.5個月。田間藥劑防治效果顯示以0.5%可尼丁粒劑每公頃每次施藥量60公斤，於定植初期、定植後30、55及75日各施藥一次，共計施藥4次，於甘藷收穫期藷塊遭幼蟲危害食痕指數1.3%為最低。

關鍵詞 (Key words)：粗糙甘藷象鼻蟲 (*Blosyrus herthus*)、生活史 (life history)

PM05_評估 6 種不同作用機制農藥於「沙坑」荔枝上對於荔枝細蛾防治效果

The control efficacy of six insecticides with different modes of action to the litchi fruit borer (*Conopomorpha sinensis* Bradley) on 'Sah Keng' litchi (*Litchi chinensis* Sonn.)

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荔枝細蛾 (*Conopomorpha sinensis* Bradley) 為荔枝果實生長期最重要的蛀果害蟲，生產者常以化學藥劑防治本害蟲。目前臺灣登記用於防治荔枝細蛾的農藥，根據作用機制分類分別為有機磷劑、胺基甲酸鹽及合成除蟲菊類。由於農民長期使用相同種類的藥劑防治害蟲，常造成田間荔枝細蛾的防治效果不佳。本研究測試 6 種作用機制不同的藥劑於「沙坑」荔枝 (*Litchi chinensis* Sonn.) 生產時防治荔枝細蛾效果，選用藥劑分別為 2% 阿巴汀 EC (稀釋 1,000 倍)、4.4% 祿芬隆 EC (稀釋 1,500 倍)、11.7% 賜諾特 (稀釋 2,000 倍)、18.4% 剋安勃 SC (稀釋 2,500 倍) 及 22.6% 滅芬諾 SC (稀釋 2,000 倍)，並以國內推薦藥劑 2.4% 第滅寧 SC (稀釋 1,500 倍) 及水作正負對照組。於荔枝花落後 10–20 天開始施藥，每隔 7–10 天施藥 1 次，於首次施藥起每週調查樹上果實害蟲產卵率，並於採收後調查果實危害率。結果顯示荔枝細蛾產卵率隨荔枝果實發育逐漸上升，於施藥後第 4 週即達77.5–97.5%，顯示施用藥劑無法減少荔枝細蛾於果實上產卵。收穫果實荔枝細蛾危害率以不施藥對照組最高為 95.6%；其次為第滅寧、祿芬隆及滅芬諾，危害率分別為 37.3%、35.3% 及31.3%；施用阿巴汀、賜諾特、剋安勃的危害率最低，分別為 12.5%、7.5% 及3.1%。根據收穫果實荔枝細蛾危害率顯示阿巴汀、剋安勃、賜諾特為較具有防治荔枝細蛾潛力的藥劑。

關鍵詞 (Key words)：荔枝細蛾 (*Conopomorpha sinensis*)、防治效果 (control efficacy)、「沙坑」荔枝 ('Sah Keng' litchi)、殺蟲劑 (insecticides)

PM06_農藥商品整合資訊查詢簡介

The Introduction to the search engine for integrated information of pesticides productions

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農作物生長期間普遍會受到病蟲的危害，以農藥進行預防與防治是目前最主要的策略之一，為提供農民購買農藥前，對於農藥之使用方法與殘留等訊息有更清楚的認識，農業試驗所在原開發的作物優質生產整合資訊平台下，新增加防檢局農藥商品查詢 (桌機版) 與行動版之作物病蟲害與農藥資訊查詢。本農藥商品整合資訊查詢系統自動介接植物防疫檢疫局之農藥資訊服網的農藥商品資訊，並結合農業藥物毒物試驗所之農藥作用機制及衛生福利部農藥殘留容許量標準資訊，以簡單易操作的條件式導引查詢畫面，提供農藥商品查詢服務與結果表單 EXCEL 下載功能及多筆農藥基本資料比較表格功能。本查詢系統期能使農藥商品資訊透明化，透過友善操作介面規劃，讓農民運用本系統之農藥商品比較表格了解各農藥商品之農藥基本資訊，依據實際需求挑選適宜之農藥商品並採取正確用藥方法，以免造成不必要的損失或農藥殘留情形。本查詢系統無需申請帳號或加入會員之程序，完全對外公開免費使用以服務更多農民。

關鍵詞 (Key words)：農藥商品 (pesticides productions)、農藥作用機制 (pesticides-mode of action)、農藥殘留容許量 (pesticide residue tolerance)、資通訊技術 (information and communication technology)

MB01_Oral delivery of dsRNA encapsulated within liposomes induces RNAi effects in the German cockroach, *Blattella germanica*

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The concept of RNA interference (RNAi) for the control of insect pests has been proposed and made significant progresses in the recent years. Many studies have examined this possibility by different approaches of double-stranded RNA (dsRNA) administration. However, oral delivery of dsRNAs, which is likely a practical application, has not worked in many insect species, in particular those with robust ribonuclease activity in the intestinal system. In the present study, we report the use of liposomes to encapsulate the dsRNA and examine the RNAi response after oral administration. In contrast to the dramatic depletion of essential *α-tubulin* gene and mortality by injecting dsRNA into the abdomen of the German cockroach, oral delivery of the naked dsRNA resulted in lower RNAi efficiency due to the action of RNA nuclease enzymes in the midgut juice, which rapidly degraded the dsRNA. Notably, we have further demonstrated that continuous ingestion of dsRNA lipoplexes, which dsRNA was encapsulated with a cationic liposome carrier, was sufficient to slow down the degradation of dsRNA in the midgut and to increase the mortality of the German cockroach accounted for significantly inhibiting *α-tubulin* expression in the midgut, but not apparently in other tissues. In conclusion, this study provides the empirical evidence that the formulation of dsRNA lipoplexes could be a plausible approach for insect pest control based on RNAi.

關鍵詞 (Key words)：*Blattella germanica*, liposome, pest control, RNAi

MB02_東方果實蠅之膜蛋白型鳥苷酸環化酶 *BdmGC2* 可能參與馬氏管滲透壓之調節

A membrane form guanylyl cyclase, *BdmGC2*, expressed in *Bactrocera dorsalis* might be involved in the osmotic regulation of Malpighian tubules

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A membrane form of guanylyl cyclase (mGC), namely *BdmGC-2* (accession number JN225448), was isolated in the oriental fruit fly, *Bactrocera dorsalis* (Hendel). *BdmGC-2* cDNA contains a 4524-bp open reading frame coding for a protein of 1508 amino acids; and the deduced protein possesses a characteristic domain organization similar to all known mGCs. RT-PCR analysis revealed that *BdmGC-2* were expressed in all developmental stages of *B. dorsalis*. In adults, *BdmGC-2* expression were detected in head, thorax and abdomen and in both males and females as well. Real-time PCR analysis further showed that *BdmGC-2* were expressed in *B. dorsalis* brain, testis and with the greatest expression in the Malpighian tubules. Further, whole-mount in situ hybridization assay confirmed that *BdmGC-2* was indeed expressed in the Malpighian tubules. Moreover, the upstream regulatory region of *BdmGC-2* was characterized by chromosome walking, and the putative transcription factor-binding sites prediction showed that there are two putative HOG-responsible elements located at upstream of the core promoter, suggesting that the expression of *BdmGC-2* may be involved in the osmotic regulation.

關鍵詞 (Key words)：鳥苷酸環化酶 (guanylyl cyclase)、馬氏管 (Malpighian tubules)、滲透壓調節 (osmotic regulation)、東方果實蠅 (*Bactrocera dorsalis*)

MB03_重複胺基酸轉運蛋白基因之發育表現:解析蚜蟲與其專一性胞內共生菌整合發育的作用

Developmental expression of duplicated amino acid transporter genes: insights into their roles in the developmental integration of the aphid and its obligate intracellular symbiont

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The best-studied model of insect symbiosis is that of the pea aphid, *Acyrthosiphon pisum* and its intracellular bacterial symbiont, *Buchnera aphidicola*. *Buchnera* are metabolically and developmentally integrated with their host. *Buchnera* live in large specialized aphid cells called bacteriocytes that assemble into an organ-like structure called the bacteriome. The amino acid biosynthesis occurs in the bacteriocytes to compensate for the low availability of some nutrients in the aphid's plant phloem sap diet. *Buchnera* are maternally inherited via transovarial transfer. Reproductive failure is observed when *Buchnera* are eliminated by antibiotic treatment. While the metabolic importance of the symbiosis is clear, the molecular mechanisms underlying *Buchnera* transmission and integration during aphid development are largely unknown. Extensive amino acid transporter (*AAT*) gene duplication has been identified in aphid genome; duplications which are important for sustaining the nutritional interactions of the host with its endosymbionts. Among the duplicated *AAT* genes, we first selected to study *ApGLNT1* for it was the only functionally characterized *AAT* gene. We tracked the expression and localization of *ApGLNT1* gene products and found that they localize to the embryonic follicular epithelium and sheath cells, but do not localize to the bacteriocyte membrane during embryogenesis. In contrast in the maternal bacteriome ApGLNT1 localizes to the bacteriocyte cell membrane. These ontogenetic shifts in localization of ApGLNT1 protein in the host bacteriome demonstrate that maternal and embryonic bacteriomes are not equivalent. In addition to *ApGLNT1*, we also studied the developmental expression of *ACYPI000536* and *ACYPI008904*, another two *AAT* genes whose transcripts are enriched in bacteriocytes. Unexpectedly we found that both genes were expressed in the posterior region of the blastula embryos where the embryos uptake the maternal endosymbionts. Our results suggest that expression of *ACYPI000536* and *ACYPI008904* genes may play novel developmental roles in symbiont recruitment and bacteriome development.

關鍵詞 (Key words)：胺基酸轉運蛋白 (amino acid transporter)、豌豆蚜麩醯胺酸轉運蛋白 (ApGLNT1)、蚜蟲 (aphid)、內共生菌 (endosymbiont)

MB04_家蠶多角體病毒檢測抗體之開發與應用

Development and Application of Polyhedrosis Virus Antibody in Silkworm (*Bombyx mori* L)

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病原監測系統的建立是家蠶種原庫維運及新用途開發之關鍵技術，臺灣家蠶常見的傳染性病毒包含核多角體病毒 (nuclear polyhedrosis virus , NPV) 及質多角體病毒 (cytoplasmic polyhedrosis virus, CPV)。本研究以建立多角體病毒偵測抗體為目標，利用大腸桿菌大量表現多角體病毒鞘蛋白，小鼠免疫後產生多株抗體。經抗原-抗體力價檢測顯示，多株抗體稀釋 625,000 倍後，仍可偵測到 0.1 μg 的抗原。以酵素連結免疫吸附分析法 (Enzyme-linked immunosorbent assay, ELISA)，監測本場家蠶種原庫 10 種品系潛伏病原，顯示 1~5 齡期 NPV 及 CPV 含量均低於發病門檻，且有隨齡期遞減之趨勢。配合家蠶人工飼料品種選育試驗，以病毒抗體建立之 ELISA 檢測系統，逐代淘汰帶原病卵，可有效降低蠶卵帶原率，降幅達 98.2%。已將家蠶多角體病毒檢測流程建立 SOP，可用來作為家蠶種原管理及清淨蠶生產之應用。

關鍵詞 (Key words)：家蠶 (*Bombyx mori* L.)、核多角體病毒 (nuclear polyhedrosis virus, NPV)、質多角體病毒 (cytoplasmic polyhedrosis virus, CPV)

MB05_無後蛋白：從果蠅上發現的基因體守護者

Wuho: a novel genome guardian isolated from Drosophila

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Accurate genome replication is essential for the transmission of genetic information, and this process is vulnerable to factors that can induce DNA damage or block replication. To avoid this and achieve genome stability, many enzymes need to coordinate their activities at the replication forks. We previously isolated a *Drosophila* mutation, *wuho* (meaning no progeny in Chinese), characterized by a severe fertility defect. Knockdown of Wuho by siRNA in insect and mammalian cells results in DNA damage of strand breaks. We identified that the flap endonuclease 1 (FEN1) is one of the interacting proteins with Wuho. FEN1 is required to remove RNA primer (also known as flap) on lagging strand during DNA replication. The nuclease activity of FEN1 while necessary for removing RNA primer and DNA damage, also presents a possible threat to genome integrity especially near replication fork. We showed that Wuho is able to modulate FEN1's endonucleolytic activities depending on the substrate DNA structure. The stimulatory or inhibitory effects of Wuho on FEN1's flap versus gap endonuclease activities are consistent with the proposed Wuho's functions in protecting the integrity of replication fork. These results suggest that Wuho is a new member of the guardians of genome stability.

關鍵詞 (Key words)：無後蛋白 (Wuho)、基因體穩定性 (genome stability)、flap endonuclease 1 (FEN1)、果蠅 (*Drosophila melanogaster*)

MB06_台灣鋏蠓卵巢結構與生殖漿成員之分析

Characterization of ovarian structure and germplasm components in *Forcipomyia taiwana* (Diptera: Ceratopogonadiae)

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Forcipomyia taiwana (Diptera: Ceratopogonadiae), is a tiny (1.4mm) hematophagic midge found predominantly in Taiwan. The female midge specifically requires the human blood for its oogenesis. The bites of these midges are often reported to cause intense pruritic and allergic response in sensitive individuals. *Therefore, th*e prevalence of *F. taiwana* curtails outdoor activities and causes a significant impact on tourism. Although the life cycle of *F. taiwana* had been extensively studied, their oogenesis is poorly understood. Here, we examined the ovarian structure of *F. taiwana.* Its ovary consists of meroistic polytrophic-type ovarioles, each of which having a developing follicle with a single oocyte connected to a single nurse cell. In dipteran, the formation of germ cells during early embryonic development relies on the deposition of germplasm components in specific regions of the oocyte. Through transcriptome analysis of female *F. taiwana*, we identified the presence of mRNAs encoding critical components of germplasm such as *vasa*, *nanos* and *oskar*. Through *in situ* hybridization and immunostaining, we found that *vasa* indeed expressed in germline cells. Especially, we identified punctate localization of Vasa proteins surrounding the nurse cell nucleus which resembles the nuage structure in *Drosophila*. While nuage shares common components with germplasm, we further present evidence to show that midge Vasa can be localized to the nuage in the nurse cells of *Drosophila* egg chamber, suggesting that Vasa could be a bona fide germplasm component. Taken together, our work represents a fundamental step in understanding both the ovarian structure and the genes involved in germplasm assembly which later could open the gateway in finding a strategy to control the population of *F. taiwana*.

關鍵詞 (Key words)：台灣鋏蠓 (*Forcipomyia taiwana*)、卵母細胞發育 (oogenesis)、生殖漿 (germplasm)

IDS01_北部地區小果油茶病蟲害種類及發生調查

Surveys on the diseases and pests and their occurrence on *Camellia brevistyla* in northern Taiwan

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本研究於北部小果油茶栽培地區調查病蟲種類及發生週期。調查結果顯示，小果油茶害蟲種類有 5 目 11 科 15 種，害蟎種類有 1 目 3 科 3 種，病害種類有7種。比對《臺灣油茶病蟲害圖鑑》及台灣農作物有害生物資料庫，油茶作物增加鞘線蟲、中華褐金龜、台灣青銅金龜、台灣花薊馬、茶黃薊馬、棉蚜、大灰枯葉蛾、懸巢舉尾蟻、二點葉蟎、杜克孔雀葉蟎及桔黃銹蜱等 11 種有害生物。利用黃色黏紙及花部採樣捕獲薊馬類害蟲數量調查結果，薊馬族群密度於開花期開始攀升，至落花後開始下降，10 月至 12 月每黏板平均為 58、641 及 331 隻薊馬，11 及 12 月花部採樣，每朵花平均有 8.7 及 12.8 隻薊馬。油茶鞘線蟲全年族群密度調查結果，族群密度最高可達每 100 公克根圈土壤 280 隻。油茶炭疽病周年發病調查，可發現 5 月及 8 月為罹病高峰，罹病高峰與月累積雨量具相關性。中華褐金龜危害調查結果，其食害程度為 36%。油茶彫木蛾危害調查結果，其發生率為 44%。

關鍵詞 (Key words)：小果油茶 (*Camellia brevistyla* (Hayata) Coh.-Stuart)、鞘線蟲 (*Hemicriconemoides kanayaensis* Nakasono & Ichinone)、炭疽病 (*Colletotrichum camelliae* (Cook) Battler)、中華褐金龜 (*Adoretus sinicus*)、彫木蛾 (*Casmara patrona*)

IDS02_台灣春、秋作胡麻害蟲發生之初步調查

Preliminary survey on pests of spring and fall sesame in Taiwan

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本研究為了解害蟲在胡麻作物的發生情形，春作胡麻分別於 2015 年 5 月 19、20 日在台南縣安定鄉、將軍鄉及 6 月 10 日台中市大肚區調查；秋作胡麻分別於 2015 年 11 月 16 日在台南縣安定鄉、11 月 20 日在嘉義縣東石鄉與朴子鄉進行調查。每區田依田區大小，分成 2–5 區，每區調查 35 棵，分別紀錄花苞碩果、植株葉片上病蟲害發生與被危害情形。危害病徵如蟲糞、蟲孔、捲葉、煤煙等；於植株上的害物發現有蚜蟲、粉蝨、粉介殼蟲、葉蟎、薊馬、擬尺蠖、胡麻莢野螟、斜紋夜蛾、白粉病等，另春作胡麻田發現捕食性煙盲椿象 (*Nesidiocoris* sp.) 普遍發生。調查結果顯示春、秋作胡麻害蟲種類有差異，不同地區病蟲害發生也有差異。春作胡麻安定三區胡麻田捕食性煙盲椿象發生率 10 – 48.6%，將軍兩區 29.5 – 49%，大肚四區 0 – 14.3%。害蟲為害情形安定以捲葉 (57.1 – 94.8%)、蟲孔 (44.3 – 78.6%)；將軍以捲葉 (37.1 – 47.1%)、蟲孔 (51 – 86.7%)；大肚以捲葉 (10 – 100%)、蟲孔 (15.7 – 100%) 較為嚴重。秋作胡麻安定以白粉病 (56.6 – 98.9%)、捲葉 (24.6 – 64%)、蟲孔 (24 – 44%)；東石、朴子以薊馬 (49.1 – 62.3%)、白粉病 (89.1 – 89.7%)、蟲孔 (58.3 – 99.4%) 較為嚴重。

關鍵詞 (Key words)：胡麻 (sesame)、調查 (survey)、害蟲 (pests)

IDS03_台灣都市地區白蟻危害問卷調查

Accessing termite problem in Taiwan through questionnaire survey

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本研究量化分析台灣白蟻危害與防治現況以協助發展防治策略與技術。以台灣住宅白蟻危害現況調查的電子問卷隨機訪問各縣市民眾，收集受訪者住宅近況、住家受害情形、防治策略以及個人資料進行分析。全台共收集 1733 份有效問卷，約 10% 住宅曾受到危害，南投縣的受害率顯著低於縣市平均。最多人在 6 月注意到白蟻有翅型的活動，但最多人注意到工、兵蟻活動則在 7 月。165 m^2 以上住宅受害率顯著高於 165 m^2 以下住宅，屋齡 41 年以上住宅受害率顯著高於屋齡 40 年以下住宅，屋況中牆面裂縫、漏水及壁癌與白蟻危害顯著相關，三種屋況在住宅中的比例隨著屋齡增加有上升的趨勢；同時具有三種屋況問題的住宅受害率顯著高於具有一或二種的住宅，沒有這三種屋況問題的住宅受害率顯著低於有屋況問題者。受害家具以木窗、木門、隔板及地板顯著高於平均受害率，但由防治公司處理的案件則是書櫃、天花板、木門及隔板顯著較平均受害率高。民眾自行防治白蟻顯著高於由防治公司處理，自行防治的民眾其住宅所有權在祖父母名下居多，但由防治公司處理的民眾住宅所有權則沒有顯著差異。民眾最重視的防治公司要素為防治成效、防治費用及使用政府核可用藥，但經過防治公司處理的民眾則較重視保固期長短而非防治費用。

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)

IDS04_珍貴老樹之白蟻危害現況調查

Termite infestation survey of protected old trees

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本研究調查珍貴老樹的白蟻發生率與危害物種，期望未來進行珍貴老樹白蟻發生特性分析、防治工法施作與防治方法開發時能有所依據。根據第一作者於105 年 11、12 月以台中市中區、南區與大里區三處行政區之台中市政府公告列管老樹進行調查後發現，共計 100 棵老樹的白蟻發生率為 23%，有一棵樹同時遭受兩種白蟻危害。其中以鼻白蟻科 (Rhinotermitidae) 物種占 12%最高，包含台灣家白蟻 (*Coptotermes formosanus* (Shiraki)) 與格斯特家白蟻 (*Coptotermes gestroi* (Wasmann))；木白蟻科 (Kalotermitidae) 物種的發生率為 7%，包含截頭堆砂白蟻 (*Cryptotermes domesticus* (Haviland)) 與恆春新白蟻 (*Neotermes koshunensis* (Shiraki))；白蟻科 (Termitidae) 物種的發生率則為 5%，目前僅發現台灣土白蟻 (*Odontotermes formosanus* (Shiraki))。台灣家白蟻、格斯特家白蟻與台灣土白蟻均會在取食部位的表面構築泥道，但台灣土白蟻僅取食樹皮，台灣家白蟻與格斯特家白蟻則會進一步取食樹木的木質部。截頭堆砂白蟻雖然也會取食木質部，但取食部位的表面較上述三種白蟻光滑，而且通常能在危害部位周圍發現六角柱狀的顆粒排遺。為使珍貴老樹的調查數據具有分析價值，後續調查樹種選擇栽種數量最多的榕樹 (*Ficus microcarpa* L. f.)、樟樹 (*Cinnamomum camphora* (L.) Presl.)、芒果 (*Mangifera indica* L.) 與茄苳 (*Bischofia javanica* Bl.) 進行大量調查，截至 105 年 9 月，各樹種調查數量分別為榕樹 66 棵、樟樹 14 棵、芒果 24 棵與茄苳 13 棵，共計 117 棵老樹之白蟻發生率為 24.8%。

關鍵詞 (Key words)：家白蟻屬 (*Coptotermes*)、木白蟻科 (Kalotermitidae)、白蟻危害方式 (termite damage patterns)、白蟻防治 (termite control)、樹木保護 (tree protection)

IDS05_高屏地區植物上粉介殼蟲（半翅目）種類調查

Survey of mealybug (Hemiptera: Pseudococcidae) in south Taiwan.

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本研究自 2015–2016 年採集台灣高屏地區之經濟作物、觀賞植物及雜草等 86 個樣品，所採寄主種類包括錦葵科(Malvaceae)、茄科 (Solanaceae)、菊科 (Asteraceae)、桑科 (Moraceae)、芭蕉科 (Musaceae)、番木瓜科 (Caricaceae)、禾本科 (Gramineae)、豆科 (Fabaceae)、大戟科 (Euphorbiaceae) 等，共計 24 科 47 種；並針對以上作物以圓餅圖分別呈現不同粉介殼蟲種類在不同作物科別所占之百分比，將所採得之粉介殼蟲製成玻片標本，採用雌蟲外部形態特徵進行鑑定，結果包含鳳梨嫡粉介殼蟲 (*Dysmicoccus brevipes*)、擬鳳梨嫡粉介殼蟲 (*D. neobrevipes*)、絲粉介殼蟲 (*Ferrisia virgata*)、桑粉介殼蟲 (*Maconellicoccus hirsutus*)、橘球粉介殼蟲 (*Nipaecoccus viridis*)、木瓜秀粉介殼蟲 (*Paracoccus marginatus*)、美地綿粉介殼蟲 (*Phenacoccus madeirensis*)、櫻丹綿粉介殼蟲 (*Ph. parvus*)、石蒜綿粉介殼蟲 (*Ph. solani*)、扶桑綿粉介殼蟲 (*Ph. solenopsis*)、橘臀紋粉介殼蟲 (*Planococcus citri*)、咖啡臀紋粉介殼蟲 (*Pl. lilacinus*)、太平洋臀紋粉介殼蟲 (*Pl. minor*)、茄疣粉介殼蟲 (*Coccidohystrix isolita*)、傑克貝爾長尾粉介殼蟲 (*Pseudococcus jackbeardsleyi*)、長尾粉介殼蟲 (*Ps. longispinus*)、刺平粉介殼蟲 (*Rastrococcus spinosus*)、糖梳粉介殼蟲 (*Saccharicoccs sacchari*)、多變根粉介殼蟲 (*Rhizoecus variavilis*) 等共計 11 屬 19 種粉介殼蟲，其中茄疣粉介殼蟲 (*Coccidohytrix insolita*) 為 2014 年新入侵台灣之害蟲 (已於 2016 年完成撲滅工作)。

關鍵詞 (Key words)：粉介殼蟲科 (Pseudococcidae)、特徵 (character)、新記錄 (new record)

IDS06_黑茶蛀蟲與環境黴菌關係之探討

A study on the relationship between mycophagous bird nest barklice and environmental fungi

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嚙蝨目 (Psocodea) 黑茶蛀蟲 (*Psoquilla marginepunctata*) 為菌食性昆蟲，近來大量出現在博物館浸液標本蒐藏庫中，雖不會對標本造成直接為害，但其屍體常成為其他博物館害蟲之食物，不利於標本蒐藏管理工作。為了解黑茶蛀蟲大發生原因，以做為未來防治之參考，本研究透過落菌試驗、無菌棉花棒塗抹環境表面、解剖蟲體腸道與收集蟲體糞便試驗，收集空氣與環境中的真菌，並將所收集之培養基置於 25℃ 生長箱培養，再進行純化與鑑定，了解黑茶蛀蟲與環境中黴菌的相關性及其食性。結果顯示空氣中黴菌主要為 *Penicillium*、*Fusarium*、*Aspergillus* 和 *Cladosporium* 等菌，其中以 *Penicillium* 最具優勢，*Fusarium* 次之，但當空調停止時，則多數培養基未收集到任何落菌 (73%)，或採集到未產孢真菌種類 (non sporulating fungi) (23%)，僅採到 3% 的 *Penicillium* 及 *Aspergillus* 種類，顯示空調開啓後，因氣流擾動而大大提高了落菌率。在塗抹試驗中，則以 *Penicillium* 和 *Aspergillus* 出現率最高，分別為 79% 及 36%，在空調口、儲存架、紙箱和標本瓶均能採到 *Penicillium* 及 *Aspergillus* 種類。黑茶蛀蟲腸道與糞便試驗中，則培養出未產孢真菌、*Penicillium* 及 *Aspergillus* 種類。初步測試，確認黑茶蛀蟲成蟲會取食 *Penicillium* 和 *Aspergillus*，並已存活超過一個月時間。我們在此認為黑茶蛀蟲可做為環境中存在 *Penicillium* 和 *Aspergillus* 黴菌之生物指標。

關鍵詞 (Key words)：黑茶蛀蟲 (*Psoquilla marginepunctata*)、青黴菌 (*Penicillium*)、麴菌 (*Aspergillus*)、落菌試驗 (settle plate)、棉花棒塗抹試驗 (cotton swab)

MEVE07_自生型地下家蚊於台北市和高雄市之族群分布

The population distribution of autogenous Culex pipiens molestus in metropolitan city of Taipei and Kaohsiung

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Culex pipiens molestus and *Cx. quinquefasciatus* are species of *Cx. pipiens* complex and live sympatrically in Taiwan. Both mosquitoes are stenogamous, but the *molestus* form is autogenous and hypogenous (develops in underground sites). *Culex p. molestus* was first documented in Taiwan in 1996. This follow-up study investigated its current distribution in metropolitan cities of Taipei and Kaohsiung two decades later. In the study, the larvae or adult of *Culex* mosquitoes were collected in underground facilities in 12 and 13 administrative districts in Taipei and Kaohsiung city, respectively during October 2012 to September 2016. The samples were identified by the morphological features including male genitalia, wing venation and abdominal patches of adult females. For those undistinguishable samples due to their non-intactness, molecular identification was utilized alternatively. Polymerase chain reactions (PCR) were performed with specific primers based on the polymorphisms of a nuclear intron of the *Drosophila Ace*-orthologous acetylcholinesterase (*Ace*) gene. Sequence variation of a putative bacteriophage locus (*orf7*) of *Wolbachia* was also used for evaluation. The testing revealed that *Cx. p. molestus* was dominant in the underground parking lots of public buildings in all administrative districts in Taipei, indicating a takeover (12/12; 100%) by the invasive species. *Culex p. molestus* was found in 53.8% (7/13) administrative districts in Kaohsiung. The biological characteristics and unique habitats of *Cx. p. molestus* should make it more challenging for control strategies. Laboratory experiments showed boric acid was an effective larvicide. The boric acid-based ovitrap can be applied as an inexpensive, accessible, and ecofriendly measure for mosquito control.

關鍵詞 (Key words)：自生型 (autogenous)、窄空間交配的 (stenogamous)、地面下生長的（hypogenous)、地下家蚊 (*Culex pipiens molestus*)

MEVE08_以新型餵血器提升蚊蟲飼養效率

Enhancement of rearing mosquito using a novel feeding device

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飼養昆蟲會面臨試驗空間、人力運用，及經費開銷問題，若能妥善利用空間，提升飼養密度，或是提升單位面積、體積內的能源密度，便能夠在有限的資源中，飼養出更大量且更經濟的試驗昆蟲。本研究開發一小型蚊蟲餵血器原型，期望以輕便、經濟，且易操作之人工餵血器取代活體生物做為病媒蚊繁殖所需的血源。以自由選擇法於相同空間中以累計飽血率評估餵血器與小鼠對埃及斑蚊雌蚊的誘引力，結果顯示在 5、10、15、20 分鐘四個時間點，餵血器組的累計飽血率分別為 30%、58.9%、64.4% 與 64.4%，而小鼠組則分別為 6.7%、17.8%、20% 與 21.7%，顯示餵血器對埃及斑蚊的誘引力遠高於小鼠，且累計飽血率於第 3 分鐘起便有顯著差異 ($P< 0.05$)。其次，以無選擇法比較吸食餵血器與小鼠對埃及斑蚊的飽血率與單次產卵量，結果顯示兩者於統計上皆無顯著差異 ($P < 0.05$)。本研究結果指出：在自由選擇條件下，餵血器對埃及斑蚊雌蚊有較強的誘引力，而在無選擇條件下，兩種供血方式對埃及斑蚊雌蚊具有相似的誘引力及繁殖潛能。因此新型餵血器有潛力取代活體動物血源以大量飼養埃及斑蚊。

關鍵詞 (Key words)：埃及斑蚊 (*Aedes aegypti*)、餵血器 (feeding device)、大量飼養技術 (mass rearing)、飽血率 (engorged rate)

MEVE09_台北市關鍵人物登革熱防治之知識態度與行為研究

Study on knowledge, attitudes and practices of key persons in Taipei city

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本研究旨在瞭解台北市主管機關人員、里鄰長與志工等關鍵人物對登革熱之知識、態度及行為的現況。採量化研究方法及運用自編問卷為研究工具，根據主管機關、里鄰長與志工等不同社群母體群進行問卷施放，同時以統計套裝軟體 (SPSS Statistics 20) 進行描述性統計與推論性分析，計回收有效樣本數為 208 份。研究結果顯示，台北市關鍵人物對登革熱相關知識與資訊來源主要為電視、政府機關與報紙、雜誌。有參加過相關訓練或研習達4小時以上者在知識得分高於其他，二者達顯著差異 ($p<0.05$)。整體而言，台北市關鍵人物在登革熱知識部分答對平均百分率為 61.33 %，其中答錯率最高為登革熱媒介傳播方式和成蟲防治方法。目前台北市關鍵人物對於登革熱防治態度尚未具有正向積極的防治態度，顯示政府機關仍應加強教育宣導民眾關切登革熱防治工作。由行為施測結果發現，目前台北市關鍵人物對於登革熱防治行為等相關議題缺少主動，不積極參與登革熱防治相關的環境活動。鄰里長與志工是影響社區登革熱病媒蚊防治的關鍵人物，可以幫助大家預防蟲媒傳染病。建議針對里鄰長與志工等經常舉辦登革熱相關議題的研習活動，才可有效提升大眾對登革熱知識的了解，同時提高民眾參與於登革熱防治的環境態度與活動的積極性，以因應登革熱與茲卡熱等蟲媒傳染病的危害風險。

關鍵詞 (Key words)：登革熱 (dengue)、蟲媒傳染病 (insect borne infectious disease)

MEVE10_2015 年台南市登革熱流行特性與防治成效分析

The analysis of control effectiveness and epidemiological features of dengue fever in Tainan, 2015

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本研究旨在分析臺南市 2015 年登革熱的流行特性、影響因素和防治成效評估，做為今後防治登革熱提供科學依據。研究使用描述性流行病學方法並以地理資訊系統與 SPSS 22.0 軟體進行統計分析。研究結果顯示，登革熱病例、重症與死亡病例、境外移入病例均日趨嚴重。2015 年臺南市通報確定病例占人口數的 1.21%，女性略高於男性和感染地點以市場為主有關；70 歲以上感染登革熱死亡病例多患有基礎疾病外，也因曾遭不同型別交叉感染有關。登革熱流行有明顯的季節性，好發於氣溫高和雨量豐沛的夏秋二季，且與病媒蚊密度消長一致。病例數主要分布於都會區，其擴散分布和人口密度與流動、病媒密度、氣候因子與環境特性顯著相關 (p<0.05)。地方政府在進行孳生清清除、告發取締與化學防治後，病媒幼蟲與病例數相繼大幅下降，有效減少登革熱擴散。臺南市登革熱流行具有反復性，境外與本土病例傳播並存、散發與多點同時爆發及季節性流行等特性，規劃採取都會區病媒蚊防治為重點的預防措施、中央與地方各部門動員聯防聯控與社區參與機制的執行力是控制登革熱流行的有效手段。

關鍵詞 (Key words)：登革熱 (dengue fever)、病媒蚊 (vector mosquitoes)、化學防治 (chemical control)、蟲媒傳染病 (vector-borne diseases)

MEVE11_煙霧機空間噴灑對埃及斑蚊的防治效果

Thermal fogging applications for managing dengue vector, *Aedes aegypti*

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為評估化學藥劑對埃及斑蚊的防治成效，以煙霧機進行不同化學藥劑對台南市東區 104 年品系、高雄市三民區 (敏感品系) 及高雄市苓雅區抗百滅寧品系 (LYPR) 埃及斑蚊的藥效測試。共測試 16 種市售防治藥劑，選擇含亞滅寧、賽滅寧、賽飛寧、第滅寧、賜百寧、賽酚寧、賽洛寧、依芬寧、芬化利、異治滅寧、治滅寧、普亞列寧及百滅寧等有效成分，含單一有效成分、複方及添加協力劑，試驗的劑型有乳劑、液劑、水基乳劑及微乳劑。將 20 隻供試埃及斑蚊置入紙杯製作的盛蟲容器，逢機分別懸掛於試驗空間的 3 個角落。將供試藥劑以水稀釋系列稀釋倍數，再以乙二醇等比例混合 (1：1) 進行藥效檢定。按每立方公尺施用 1 毫升稀釋藥液的用量，以德國 puls FOG 廠牌的熱煙霧機 (K-10 SP) 將藥液均勻噴灑於試驗空間。噴灑藥液後緊閉門窗30 分鐘，打開門窗及通風孔使空氣流通，取出供試昆蟲並記錄 30 分鐘的擊昏率 24 小時的死亡率。本藥劑試驗結果可作為選擇防治登革熱病媒蚊環境用藥的參考依據，也提供適當的稀釋倍數，得進行最有效的病媒蚊防治工作。

關鍵詞 (Key words)：埃及斑蚊 (*Aedes aegypti*)、煙霧機 (thermal fog)、殺蟲劑 (insecticide)

MEVE12_埃及斑蚊人工餵血系統

A multiple membrane blood-feeding system for *Aedes aegypti*

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開發新穎的多孔膜餵血系統提供埃及斑蚊血源，取代傳統志願者或脊椎動物的供血，可在實驗室內繼代繁殖埃及斑蚊。這個餵血系統使用的人工腸衣適合供試雌蚊取食，與使用石蠟膜的取食率差異不顯著性。取食效率與活老鼠供應的血源不具差異性，比較存活率、生殖力、化蛹率及羽化率皆不具顯著差異。豬血中加入 ATP 可明顯提升斑蚊的取食率。本人工餵血系統可以取代動物血源，提供斑蚊繁殖所需的血液，是一個簡單、便宜、方便且有效率的設備，可以在實驗室成功飼養斑蚊並進行相關研究。

關鍵詞 (Key words)：埃及斑蚊 (*Aedes aegypti*)、人工餵血系統 (artificial blood-feeding system)、人工腸衣 (sausage-casing membrane)、石臘膜 (Parafilm-M®)

PM07_未施肥之茄子作物對二點葉蟎族群的影響

Effect of non-fertilized eggplant on population increasing of *Tetranychus urticae* Koch (Acari: Tetranychus)

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二點葉蟎（*Tetranychus urticae* Koch）是全球性的重要害蟲之一，寄主植物種類高達 1200 種以上，主要危害植物葉面，降低光合作用效率而影響作物產量及品質。其發育速率快、世代短、繁殖力強，通常農民施用過多的肥料則可能加速該害蟎族群的猖獗。本實驗室擬探討氮肥施用量對其族群增長率之影響，現階段先以未施用氮肥之茄子植株進行研究。於 25 ± 1°C，相對溼度 60 ± 10%及 12D : 12L 光週期生長箱內，以麻芝茄 (*Solanum melongena* L.) 葉子飼養二點葉蟎，觀察該葉蟎之生長表現，並利用兩性生命表分析其族群介量。由初步結果顯示二點葉蟎在未施肥茄株葉子上的內在增殖率 (intrinsic rate of increase, r) 為 0.2778 d^{-1}、終極增殖率 (finite rate of increase, λ) 為 1.3022 d^{-1} 以及淨繁殖率 (net reproductive rate, R_0) 為 68.7，各齡期的發育時間則為卵期 4.5 天、成蟲前期 10.0 天以及成蟲 14.5 天，平均壽命 23.4 天。雌、雄蟲在各齡期發育時間並無顯著性差異，雌成蟲平均每日產卵量為 10.8 粒，一生平均總產卵量為 88.9 粒。日後將進行不同氮肥施用量對茄株及二點葉蟎族群成長之影響，以作為農民掌握正確肥培管理的參考。

關鍵詞 (Key words)：二點葉蟎 (*Tetranychus urticae* Koch)、麻芝茄 (*Solanum melongena* L.)、兩性生命表 (age-stage, two-sex life table)、族群介量 (population parameter)

PM08_四種小黃瓜品種對棉蚜 (*Aphis gossypii* (Glover)) 之防禦效果

Defenses of four cucumber cultivars to cotton aphid (*Aphis gossypii* (Glover)])

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本研究分別於室內及田間以盆栽測試自市售小黃瓜品種中選用之「秀燕」、「新蜜」、「阿秀」及「夏之輝」等4品種小黃瓜對棉蚜之防禦能力。試驗結果顯示，有翅型棉蚜於選擇性、非選擇性及田間試驗中，於「夏之輝」小黃瓜植株上停留之數量顯著少於其他3品種。在室內試驗中，「新蜜」小黃瓜延緩棉蚜族群發展效果最好，供試植株上平均棉蚜數量為399.7隻/株，顯著低於「夏之輝」(573.5隻/株)、「秀燕」(587.2隻/株) 及「阿秀」(875.0隻/株)，但4品種間產生有翅型棉蚜之機率並無差異。4品種小黃瓜植株遭受棉蚜危害於田間第3天，「新蜜」小黃瓜植株上天敵數量顯著高於其他3品種，原接棉蚜數量以「新蜜」及「秀燕」小黃瓜處理組最少，顯著低於「夏之輝」及「阿秀」處理組。供試4品種小黃瓜植株於田間經3 wk後，以「新蜜」小黃瓜植株上棉蚜數量最少 (40.0隻/株)，顯著低於「秀燕」(180.9隻/株)、「夏之輝」(248.6隻/株) 及「阿秀」(364.0隻/株)。天敵的數量則以「新蜜」(6.9隻/株) 及「秀燕」(5.2隻/株) 處理組最多，顯著高於「夏之輝」(2.5隻/株) 及「阿秀」(2.5隻/株) 處理組。綜合本試驗之結果，「新蜜」小黃瓜於4品種中，對棉蚜同時具有直接與間接防禦能力，「新蜜」小黃瓜在未來可納入棉蚜綜合防治體系中，並作為育種時，選育對棉蚜具良好防禦能力小黃瓜品種之參考。

關鍵詞 (Key words)：棉蚜 (cotton aphid)、品種 (cultivar)、防禦 (defense)、綜合防治 (integrated control)

PM09_防蟲網對積穀害蟲之隔絕效果評估

Evaluation of insect-proof screens applied to prevent of stored-product insects

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由於積穀害蟲抗藥性的產生與稻穀農藥殘留的疑慮，開發新型態的防治方法已成為研究人員主要目標。防蟲網本身具有物理阻隔，若蟲網含藥劑又能達到化學防治效果。為了瞭解不同網目對主要積穀害蟲穀蠹、米象與麥蛾的阻隔效果，並比較含有第滅寧藥劑之防蟲網與無藥防蟲網對害蟲死亡率之差別，選用16、24和32目防蟲網所製成的網袋，觀察害蟲24小時後穿出率與侵入率。結果顯示，穿出率方面，不管是在無藥或有藥防蟲網上，三種害蟲成蟲穿出16目和24目網袋均高達80%以上，32目無藥網袋穿出率則低於12%，32目有藥網袋穿出率依序穀蠹、米象和麥蛾為0、0和1.4%。侵入率方面，穀蠹和米象選用成蟲為材料，麥蛾則選用初齡幼蟲為材料，依照16目、24目和32目，穀蠹無藥網袋分別為83.5、90.6和7.8%，有藥網袋為46.7、34.8和0%；米象無藥網袋為55.6、34.1和0%，有藥網袋為6.5、3.5和0%；麥蛾無藥網袋為44.6、39.4和28%，有藥網袋為27.5、26.5和23.7%。此外，三種積穀害蟲成蟲接觸含藥防蟲網24小時後的死亡率與接觸無藥防蟲網死亡率有顯著差異。綜合本試驗結果可知，32目有藥防蟲網的阻隔及殺蟲效果均最好，適合推廣於穀倉防治積穀害蟲。

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

PM10_亞洲柑橘木蝨寄主偏好及以月橘作為陷阱作物之防治應用

Host preference and the application of using Jasmine orange as a trap crop for *Diaphorina citri* (Hemiptera: Liviidae)

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本研究主要探討柑橘黃龍病傳播媒介－亞洲柑橘木蝨 (*Diaphorina citri* Kuwayama) 對於不同芸香科寄主偏好性，並且實際應用常見寄主－月橘 (*Murraya paniculata* (L.) Jack.) 作為陷阱作物測試其阻擋木蝨侵入柑橘園之成效。以四種柑橘常見寄主植物分別與月橘進行選擇實驗結果顯示，木蝨在椪柑及柳丁這兩種品種上有較明顯的偏好，皆偏好取食月橘，表示月橘有作為陷阱作物之潛力。故選用椪柑和月橘進行陷阱植物應用試驗，結果也顯示月橘對於柑橘木蝨具有一定阻擋效果，使用與椪柑相同數量的月橘放置外圍可阻擋約 8 成在植株上被記錄到侵入的木蝨，而使用比椪柑多一倍數量之月橘則可阻擋約 9 成的木蝨侵入。兩次田間偏好性實驗結果顯示，將柑橘與月橘擺放於距木蝨釋放點等距離情況下，第一次釋放的木蝨較偏好於田區的柑橘上，但經過數週觀察發現，其產卵偏好受到新芽的影響，所以偏好在終年可抽芽的月橘上產卵，整體觀察結果，成蟲多半偏好棲息於田區的柑橘上；第二次釋放結果，木蝨初步有較多個體選擇取食田區的柑橘，而同樣偏好產卵在月橘上，整體分布在月橘的成蟲數量到後期有大幅提升，顯示月橘對木蝨具有一定程度之誘卵效果。

關鍵詞 (Key words)：柑橘木蝨 (Asian citrus psyllid)、黃龍病 (Huanglongbing)、月橘 (jasmine orange)、寄主偏好 (host preference)、陷阱作物 (trap crop)

PM11_設施花胡瓜南黃薊馬與甜瓜黃斑病毒病害之發生

Occurrence of *Thrips palmi* and melon yellow spot virus on cucumber in greenhouses

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南黃薊馬 (*Thrips palmi* Karny) 為甜瓜黃斑病 (Melon yellow spot virus, MYSV) 傳毒媒介昆蟲，造成病株葉片嵌紋黃化、產生黃斑或壞疽斑點、節間縮短，影響植株生長及產量。本研究調查中部設施花胡瓜南黃薊馬及其傳播 MYSV 病毒病害發生情形，每週每區懸掛黃色及藍色黏板監測薊馬發生密度，逢機檢視嫩心、幼葉及老葉等部位蟲數，並隨機取樣葉片 30 枚及蒐集病葉進行酵素結合免疫吸附分析 (Enzyme-linked immunosorbent assay, ELISA) 檢測 MYSV 病毒。薊馬發生初期黏板誘集成蟲以雄蟲居多，目視成蟲多發生於未展開嫩心處。因藍色黏板誘得南黃薊馬較多，以其監測數量與 ELISA 檢測所得罹病率進行相關性分析。莿桐地區資料顯示，瓜園第一期罹病率低於 10%，南黃薊馬密度低於3.5隻，第二期罹病率達 60%，薊馬密度達 37.5 隻，甜瓜黃斑病發生率與南黃薊馬密度呈正相關 ($R^2=0.66$，$P<0.05$)。第二期作南黃薊馬及其傳播之 MYSV 發生明顯受到花胡瓜連續栽培影響，建議連作務必確實清園以減少栽培初期之蟲源，有助於病蟲管理。

關鍵詞 (Key words)：南黃薊馬 (*Thrips palmi* Karny)、甜瓜黃斑病毒 (Melon yellow spot virus, MYSV)、蟲媒病害 (insect-borne disease)、媒介昆蟲 (insect vector)

PM12_番茄黃化捲葉泰國病毒於菸草粉蝨體內之感染、移行與經卵傳播

Infection, dissemination, and transovarial transmission of *Tomato yellow leaf curl Thailand virus* in *Bemisia tabaci*

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Tomato yellow leaf curl Thailand virus (TYLCTHV) is the major virus causing the tomato yellow leaf curl disease in Taiwan. Studies of the transmission biology of this virus and the relation with its insect vector, *Bemisia tabaci*, are critical to the disease control. We conducted an indirect immunofluorescence assay to detect the virus-infected organs of *B. tabaci* after 5-day acquisition of the virus. The results showed that TYLCTHV infected the midgut, gastric caecum, filter chamber, salivary gland, and ovariole of *B. tabaci*. Moreover, we conducted a time course PCR assay to investigate the dissemination of the virus in *B. tabaci*. The results illustrated that the hemolymph and the salivary glands were infected with the virus following the infection of the midgut. To sum up, the ovary of *B. tabaci* was infected with TYLCTHV, and it raised an intriguing question about the transovarial transmission of TYLCTHV by *B. tabaci*. We further investigated whether TYLCTHV can be inherited from the mother to the first generation progeny of *B. tabaci* and can be transmitted to healthy plants by them. The progeny of viruliferous females were analyzed by PCR and transmission assays. The results showed that TYLCTHV DNA was only detected in small portion (10%) of the first generation progeny, but no virus was detected in the test plants inoculated with them. We will further examine whether TYLCTHV replicates in *B. tabaci* to acquire the comprehensive knowledge of transmission biology of TYLCTHV by *B. tabaci*.

關鍵詞 (Key words)：豆類金黃嵌紋病毒 (*Begomovirus*)、間接免疫螢光檢測 (indirect immunofluorescence)、病媒昆蟲 (insect vector)、番茄 (tomato)

BC01_不同濃度水楊酸甲酯對天敵之誘引效果

Effectiveness of different concentration methyl salicylate on attracting natural enemies

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本研究使用不同濃度水楊酸甲酯 (99%、10%、1%、0.1%、0.01%) 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。於6個月調查期間水楊酸甲酯處理組黃色黏板累計所捕獲小黑花蝽象之數量均顯著高於對照組 (21.4隻/黏板)，其中 0.1% 處理組所捕獲之小黑花蝽象數量 (44.6隻/黏板) 顯著高於其 99% (31.8隻/黏板)、10% (32.4隻/黏板)、1% (28.0隻/黏板) 及0.01% (32.0隻/黏板) 處理組。水楊酸甲酯之各濃度處理組黃色黏板累計所捕獲之中華斑腿盲蝽象數量除1%處理組外 (7.2 隻/黏板) 均顯著高於對照組 (5.6隻/黏板)，其中0.1%處理組所捕獲之小黑花蝽象數量 (18.2隻/黏板) 顯著高於10% (10.2隻/黏板) 及0.01% (9.8隻/黏板) 處理組但與其 99% (11.6隻/黏板) 處理組無差異。0.1% 水楊酸甲酯搭配黃色黏板除顯著誘引小黑花蝽象及中華斑腿盲蝽象外，於6個月調查期間較對照組黃色黏板累計捕獲更多的六條瓢蟲、赤星瓢蟲、六星瓢蟲、小瓢蟲及褐草蛉等捕食性天敵，但二者間無顯著差異。

關鍵詞 (Key words)：水楊酸甲酯 (Methyl salicylate)、小黑花蝽象 (*Orius*)、中華斑腿盲蝽象 (*Campylomma chinensis*)

BC02_以蓖麻蠶卵飼育平腹小蜂後對荔枝椿象之寄生表現

Using *Samia cynthia* as mass production host for *Anastatus japonicas* for *Tessaratoma papillosa* suppression

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荔枝椿象 (*Tessaratoma papillosa*) 為近年來嚴重危害無患子科 (Sapindaceae) 果樹及行道樹的重要入侵害蟲，而平腹小蜂 (*Anastatus japonicus*) 則為目前田間發現可有效寄生此害蟲卵期的本土性寄生性天敵。蓖麻蠶屬鱗翅目 (Lepidoptera) 天蠶蛾科(Saturniidae)，在 25~27 ℃，70~80 % RH 的環境下，卵、幼蟲及蛹期分別約為 10、20-25 及 15-20 日，平均每一雌蛾約可產 300 多粒卵，此蟲可終年於實驗室內飼育繁殖，且其卵及蛹期具可延緩發育等特性。因此，本研究以蓖麻蠶 (*Samia cynthia*) 卵作為替代寄主，經過持續 12 個月繼代飼育，建立平腹小蜂室內飼育族群，平均 5-10 日齡雌寄生蜂每日可以成功寄生 4.2 ± 0.7 個蓖麻蠶卵，約經 20 日後可完成生活史羽化為子代寄生蜂。另以田間採集寄生於荔枝椿象卵的自然族群作為對照組，比較二者對荔枝椿象卵的寄生表現，結果顯示繼代飼育與自然族群平均每一雌蜂分別可成功產下 3.6 ± 0.7 及 4.8 ±0.7 隻子代寄生蜂，二者間無顯著差異；而二者子代的雌蟲與雄蟲比率分別為 3.0 : 0.6 及 4.4 : 0.5，彼此間亦無顯著差異。此初步結果顯示以蓖麻蠶卵作為替代寄主，室內飼育的平腹小蜂子代可發揮相當於自然寄生蜂族群之寄生效能，目前已建立相關大量飼育技術，有助於未來應用於果園區或行道樹上荔枝椿象的生物防治。

關鍵詞 (Key words)：荔枝椿象 (*Tessaratoma papillosa*)、平腹小蜂 (*Anastatus japonicus*)、蓖麻蠶 (*Samia cynthia*)、繼代飼育 (successive rearing)

BC03_瓜實蠅幼蟲寄生蜂 (*Psyttalia fletcheri*) 之生物學及與格氏突闊小蜂之交互寄生習性探討

Biology of a specialist larval parasitoid *Psyttalia fletcheri* and the parasitic interaction with a generalist pupal parasitoid *Dirhinus giffardii* in melon fly

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瓜實蠅 (*Bactrocera cucurbitae* (Coquillett)) 在台灣為葫蘆科 (Cucurbitaceae) 作物栽培期間的關鍵害蟲，本研究測試此害蟲幼蟲期寄生蜂 *Psyttalia fletcheri* Silvestri 在13、18、23、28、33℃ 等 5 種不同定溫環境下的生物表現，結果顯示 *P. fletcheri* 的雌、雄成蟲平均壽命在 18℃ 時最長，分別為 20.3 ± 8.9 及 18.7 ± 9.5 日；但只在 18、23、28℃ 等 3 種溫度環境下，具備成功寄生產出子代寄生蜂之能力，而以 23℃ 環境下具有最高的繁殖潛能，每一雌寄生蜂一生平均可產 116.6 ± 16.5 隻後代，與其他二種溫度處理者呈顯著差異。其次，觀察 *P. fletcheri* 的寄生行為，發現其寄生產卵位置大多在瓜實蠅幼蟲腹部中段背方或側方，被寄生的幼蟲呈現短暫麻痺情形。逐日解剖被寄生瓜實蠅個體，觀察此寄生蜂各蟲期發育情形，換算此寄生蜂在 23℃ 時從卵發育至蛹期約需 8.0 日，蛹體約經過 8.0 日後羽化為成蟲。此外，探討 *P. fletcheri* 與格氏突闊小蜂 (*Dirhinus giffardii* Silvestri) 對瓜實蠅的寄生交互作用，結果顯示瓜實蠅的幼蟲或蛹體分別單獨被 *P. fletcheri* 或格氏突闊小蜂寄生 24 h 後的處理組，瓜實蠅羽化率分別為 81.2 ± 2.6% 及 68.5 ± 7.4%，而瓜實蠅幼蟲先被 *P. fletcheri* 寄生，化蛹後再經格氏突闊小蜂寄生的處理組，瓜實蠅羽化率為 49.8 ± 8.8%，與前二種處理者呈顯著差異，此初步結果顯示當二種寄生蜂共同應用時，有助於提高瓜實蠅被寄生的比率。

關鍵詞 (Key words)：瓜實蠅 (*Bactrocera cucurbitae* (Coquillett))、幼蟲寄生蜂小繭蜂 (*Psyttalia fletcheri* Silvestri)、格氏突闊小蜂 (*Dirhinus giffardii* Silvestri)、寄生交互作用 (parasitic interaction)

BC04_利用平腹小蜂防治荔枝椿象之效果評估

Effect of releasing *Anastatus japonicus* (Hymenoptera: Eupelmidae) on controlling *Tessaratoma papillosa* (Hemiptera: Tessaratomidae) in Taiwan

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平腹小蜂 (*Anastatus japonicus*) 屬於膜翅目、旋小蜂科 (Hymenoptera: Eupelmidae) 之單元寄生性卵寄生蜂，104-105 年於田間釋放平腹小蜂防治荔枝椿象，其中 104 年釋放前調查高雄市橋頭區與田寮區之荔枝椿象卵被平腹小蜂寄生率分別僅有 3.8 及 2.1%，釋放後再調查橋頭區與田寮區卵被寄生率提升至 71.9% 及 63.2%，相較對照組 (未釋放區) 其荔枝椿象卵被寄生率僅有7.5%，隔年再次調查橋頭與田寮二區的釋放前自然寄生率，得知橋頭區荔枝椿象卵被平腹小蜂寄生率已達 20.7%，而田寮區雖受藥劑防治影響但仍有 11.8% 寄生率。105 年在橋頭與田寮二區釋放平腹小蜂，經調查得知：荔枝椿象卵的被寄生率隨著釋放次數持續提高，橋頭區從 56.8% 被寄生率、58.5%、61.9%、63.1%及78.6%，呈逐漸增加趨勢；而田寮區則從 30.4% 被寄生率、39.3%、44.8%、48.4% 及 68.7%；相較非釋放區的阿蓮區，其田間野外族群自整個荔枝椿象產卵結束時僅有 8.8% 寄生率，且針對荔枝椿象一齡若蟲族群調查，得知荔枝椿象因其卵被平腹小蜂寄生，導致族群量明顯下降外並縮短整個族群一齡若蟲的發生週期。研究結果得知，在實驗室內大量繁殖平腹小蜂再釋放至田間，不僅能完成階段性壓制野外荔枝椿象族群增長，且平腹小蜂於田間立足後，能有效且持續抑制荔枝椿象族群發生，可降低農民損失並同時兼顧環境生態的永續性。

關鍵詞 (Key words)：平腹小蜂 (*Anastatus japonicus*)、荔枝椿象 (*Tessaratoma papillosa*)、寄生蜂 (parasitoid)、生物防治 (biological control)

IDS07_台江國家公園黃斑海黽分布調查

The distribution research of the sea skater *Aslepios apicalis* Esaki (Hemiptera: Gerridae) in Taijiang National Park

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台江國家公園境內有多處主要由欖李及海茄冬所組成的紅樹林，大多紅樹林地與海洋相通形成感潮溝帶，於 2015 年在台江國家公園感潮溝帶發現自 1924 年以來未被再記錄的物種黃斑海黽 *Aslepios apicalis* (Esaki, 1924)，在先前的研究中僅描述該物種的特徵與分類，並沒有更進一步的物種研究及記錄。本研究以重新發現此物種的城西紅樹林及七股紅樹林作為研究樣區，分別於 2015 年以 D 型網捕撈及 2016 年樣框計數記錄黃斑海黽各月份成蟲與若蟲的分布數量，並測量兩年度所採集個體的體長及前胸背板寬，更進一步描述雌雄蟲及各齡期若蟲特徵。初步結果顯示黃斑海黽於 2015 年用 D 型網捕撈於 4 月及 10 月數量最多，2016 年目視計數以 5 月最多，並在 4～5 月時觀察記錄到成蟲配對，於 6 ~ 7 月則記錄到較多的低齡期若蟲；型態測量初步結果中雌蟲的體長平均值為 2.95 ± 0.32 mm，前胸背板寬平均值為 0.94 ± 0.08 mm，雄蟲體長平均值為 2.48 ± 0.16 mm，前胸背板寬平均值為 0.82 ± 0.04 mm，雌雄蟲的體長及前胸背板寬使用 t 檢定: p 值< 0.001, 雄蟲 n = 18, 雌蟲 n = 20。

關鍵字 (Key words)：黃斑海黽 (*Aslepios apicalis*)、分布 (distribution)、紅樹林 (mangrove forest)、台江國家公園 (Taijiang National Park)

IDS08_台灣橡樹癭蜂多樣性及其在全球多樣性之意義

The diversity of oak gallwasps in Taiwan and its significance to the global diversity

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全球約有 1,000 種橡樹癭蜂已知種，絕大多數的物種以殼斗科 (Fagaceae) 麻櫟屬麻櫟亞屬 (*Quercus* subgenus *Quercus*) 為造癭寄主，往昔研究多集中於歐洲 (西舊北區) 與北美 (新北區)，東亞 (東舊北區與東方區) 過去僅記錄 34 種以麻櫟亞屬為寄主的癭蜂有效種。然而，東亞為殼斗科苦櫧屬 (*Castanopsis*)、石櫟屬 (*Lithocarpus*) 與麻櫟屬青剛櫟亞屬 (*Quercus* subgenus *Cyclobalanopsis*) 的多樣性中心，這些植物曾有疑似橡樹癭蜂蟲癭之紀錄，近期的親緣關係研究指出東亞可能是橡樹癭蜂的起源中心，更顯出建立東亞橡樹癭蜂及其寄主多樣性資訊的重要性。台灣擁有的殼斗科物種涵蓋東亞的主要類群，這些潛在寄主曾有疑似癭蜂蟲癭的紀錄，為檢驗橡樹癭蜂與殼斗科之間的關係，提供絕佳的材料。本研究調查台灣全島殼斗科植物之癭蜂蟲癭多樣性，目前已記錄 115 種蟲癭形態種，確認 4 屬 28 種殼斗科為橡樹癭蜂之寄主，並採得 44 種橡樹癭蜂成蟲形態種。由於橡樹癭蜂為循環性孤雌生殖，有性世代與無性世代的蟲癭與成蟲形態皆不相同，進一步以粒線體 DNA 之 cytochrome b (cyt b) 基因檢測橡樹癭蜂形態種間之基因差異，確認其中兩形態種為 *Cerroneuroterus vonkuenburgi* 之不同世代，其餘形態種依形態檢查與基因差異比較之結果，另描述 7 屬 25 個新物種，其中 2 屬為新屬。本研究結果確認東亞殼斗科數個主要類群為橡樹癭蜂之寄主，提供探討橡樹癭蜂地理起源及與寄主之間演化關係的進一步關鍵訊息。

關鍵詞 (Key words)：橡樹癭蜂 (oak gallwasp)、殼斗科 (Fagaceae)、蟲癭 (gall)、形態種 (morphospecies)、循環性孤雌生殖 (cyclical parthenogenesis)

IDS09_武陵地區溪流扁蜉蝣 *Afronurus floreus* 與 *Rhithrogena ampla* 之族群變動

Population fluctuations of *Afronurus floreus* and *Rhithrogena ampla* between streams in Wuling

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本研究目的在研究大甲溪流域上游扁蜉蝣科 (Heptageniidae) *Afronurus floreus* 與 *Rhithrogena ampla* 兩物種的族群變動。自 2003 年 2 月至 2016 年 4 月，每年四次於桃山西溪、七家灣溪、高山溪及有勝溪設五個採樣站，每個樣站以舒伯氏水網 (Surber sampler) 採集 6 樣本，共計 14 年，攜回實驗室記錄個體數及測量體長，在各個樣站並同時測量水溫、pH、溶氧量、濁度及導電度等水質因子。研究結果顯示，扁蜉蝣稚蟲體長大小為 1.5 cm 以下，53 次採集到 45,410 隻扁蜉蝣 *R. ampla*，明顯較 *A. floreus* 僅 815 隻為多。由上游至下游，各樣站 *R. ampla* 族群平均數量顯著下降，*A. floreus* 則以有勝溪較多。扁蜉蝣密度在夏、秋雨季和颱風季時下降，冬、春乾季時密度較高，且流量過低過高的年份則無法採得 *A. floreus*。各水質因子的影響力大小不一，由上游至下游，濁度及導電度對 *R. ampla* 族群影響為負、水溫則對下游測站具負影響、溶氧量在上游為正影響，但在下游為負影響；七家灣溪下游 *A. floreus* 族群受濁度、導電度及水溫負影響、高山溪 *A. floreus* 族群受導電度負影響。由體長大小組成資料顯示不具明顯的世代間隔，且一年中有多個月持續具有大、小混合之稚蟲，推測應為一年多世代之生活史型態。

關鍵詞 (Key words)：水棲昆蟲 (aquatic insects)、扁蜉蝣科 (Heptageniidae)、溪流生態系 (stream ecosystem)

IDS10_穿山甲糞便中的白蟻物種組成

Termite species composition in the feces of Formosan pangolin (*Manis pentadactyla pentadactyla*)

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白蟻為社會性昆蟲，主要取食死亡的植物組織維生，在生態系中扮演清除者的角色。許多白蟻種類會在土壤中築巢與活動，是穿山甲重要的蛋白質來源。前人針對穿山甲取食白蟻之研究，多以侵入性的方法，如胃內含物，及野外行為觀察為之，所獲得的資料較為有限且缺少季節性的比較；非侵入性取樣 (non-invasive sampling) 對野生動物的傷害性小且樣本較容易收集，如排遺、毛髮等，在野生動物研究方面已廣為使用。本研究以台東鸞山地區穿山甲的排遺為樣本，分析民國 102 及 103 年不同季節的白蟻組成。比較排遺中未消化的白蟻頭部、大顎、小顎及翅後，除了未發現翅膀，大顎數量較小顎多且在數量上兩者呈相關性 (r = 0.7799)，故以白蟻大顎作為觀察標的，計算各類白蟻的出現頻度及季節性的生物量變化。目前於排遺分析中共發現四種白蟻，分別為台灣土白蟻 (*Odontotermes formosanus*)、小象白蟻 (*Nasutitermes parvonasutus*)、新渡戶歪白蟻 (*Pericapritermes nitobei*) 及黃胸散白蟻 (*Reticulitermes flaviceps*)。各物種出現頻度在乾季分別為 100%、75%、25% 及 0%；濕季則為 100%、80%、80% 及 20%。另外相對頻度在乾季為 50%、37.5%、12.5% 及 0%；濕季則為 35.7%、28.6%、28.6% 及 7.1%。台灣土白蟻的大顎總數量在乾季占 92.6%，濕季 78.5%。顯示出台灣土白蟻為穿山甲主要的食物來源，且以乾季更為重要。

關鍵字 (Key words)：穿山甲 (pangolin)、白蟻 (termite)、排遺分析 (fecal analysis)、食性 (food habit)

IDS11_海岸山脈南段台灣穿山甲排遺內螞蟻種類組成之分析

Analysis of ant species in the feces contents of Formosan pangolin (*Manis pentadactyla pentadactyla*) from the southern part of coastal mountain range, Taiwan

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為深入了解食蟻性 (myrmecophagous) 台灣穿山甲 (*Manis pentadactyla pentadactyla*) 的食物來源當中，螞蟻物種組成和季節變動，本研究於 2013 年至 2014 年，採集台東海岸山脈南段的穿山甲排遺，分析排遺中的螞蟻物種組成及季節變化 (濕季 4 月至 11 月；乾季 12 月至 3 月)。本研究由每份排遺中取 10 克 (乾重)，發展樣本處理及分析流程，以排遺殘留的螞蟻頭部作為鑑定物種及數量的依據；分析流程包含排遺篩洗、影像數化螞蟻殘骸、物種數和生物量計算等。結果顯示穿山甲排遺樣本中 (n = 36)，共分類出 5 個亞科 (家蟻亞科、山蟻亞科、針蟻亞科、琉璃蟻亞科以及軍蟻亞科) 之 40 種螞蟻 (32 種已知種及 8 種待鑑定種類)；比較所有排遺樣本的螞蟻物種出現頻率，8 種常見物種佔總覓食物種的 20%，依序為寬節大頭家蟻為 (*Pheidole nodus*) (100%)、厚毛巨山蟻 (*Camponotus monju*) (88%)、熱烈大頭家蟻 (*Pheidole fervens*) (69.4%)、席氏舉尾家蟻 (*Crematogaster schimmeri*) (66.6%)、吉悌細顎針蟻 (*Leptogenys kitteli*) (63.9%)、台灣偽毛山蟻 (*Pseudolasius binghami*) (63.9%)、麥氏棘山蟻 (*Polyrhachis illaudata*) (63.9%) 及矢野氏擬大頭家蟻 (*Pheidologeton yanoi*) (58.3%)。進一步分析，濕季的排遺中 (n = 20) 共發現 33 種螞蟻，每份排遺的平均螞蟻物種數為 9.6 種 (± 2.9)；與乾季排遺中 (n = 16) 發現 34 種螞蟻，每份排遺的平均螞蟻物種數為 10.3 種 (± 3.1) 相較，差異不大。此外，平均排遺內的無機質 (砂土等) 重量達 8.5 克 (每 10 克) 以上，顯示在穿山甲的排遺中，無機質含量偏高。

關鍵詞 (Key words)：台灣穿山甲 (*Manis pentadactyla pentadactyla*)、蟻科 (Formicidae)、食性 (food habit)、排遺 (feces)、海岸山脈 (coastal mountain range)

IDS12_臺南四草、七股地區防風林與草地地棲性昆蟲群聚之比較

The Comparison of epigeous insect communities in windbreak forest and grassland in Sicao and Qigu in Tainan

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本研究於 2015 年使用掉落式陷阱及誘餌掉落式陷阱比較臺南四草及七股地區防風林與草地的地棲性昆蟲多樣性及群聚相似性，實驗為期一年。每月調查的資料採用 Shannon-Wiener Index 分析物種多樣性及均勻度，並以 Wainstein'Index (K_w) 進行棲地間昆蟲組成的相似性比較。初步分析 1 至 10 月的調查資料，共鑑定出 13 目 43 科 239 種 7730 隻標本，豐度最高者為鞘翅目 97 種，相對豐量最高者為膜翅目，佔總捕獲數 50.05%；草地捕到的物種及個體數均比防風林多，分別為 198 種 5439 隻與 125 種 2301 隻。在不同棲地類型的多樣性及相似性比較中，誘餌式掉落陷阱調查到的防風林物種多樣性指數高於草地 (3.22, 2.47)，但掉落式陷阱的物種多樣性指數則較接近 (2.74, 2.76)。兩棲地在掉落式陷阱的相似性指數為 4.12，而誘餌式掉落陷阱的相似性指數為 2.65，顯示兩棲地間昆蟲組成差異大。探討同一棲地中兩方法間的差異，防風林的誘餌式掉落陷阱多樣性較掉落式陷阱高，而草地則相反，掉落式陷阱的多樣性比誘餌掉落式陷阱高；同一棲地方法間的相似性指數，分別為防風林 9.81 與草地 15.40。

關鍵詞 (Key words)：地棲性昆蟲 (epigeous insect)、防風林 (windbreak forest)、草地 (grassland)、掉落式陷阱 (pitfall trap)、誘餌式掉落陷阱 (baited pitfall trap)

IT01_The preliminary taxonomic study of the Tachinidae (Diptera) in Taiwan: tribe Blondeliini

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All Tachinidae are parasitoids of other insect or arthropods. This taxa have potential ability to be the biological agent because of their hosts are mainly herbivorous insects, such as larvae of Lepidoptera. However, there are two reasons that make the ecology and ethology of tachinid flies difficult to study: 1) because that tachinid is the second most speciose family of Diptera (8000 described species and more undescribed) and the most of the characters are homoplastic, the classification and identification of tachinids are difficult. 2) In contrast to the Palearctic and Nearctic regions, taxonomy of Tachinidae in the Oriental region has not been comprehensively studied. Therefore, this study began with the taxonomic research of tribe Blondeliini in Taiwan. The Blondeliini belong to the subfamily Exoristinae, which is the most well studied subfamily of Tachinidae, and highly diversity on the morphology and oviposition strategy. The identification of the study is mainly based on the keys of Crosskey (1976) and Shima (1979) at the level of tribe and genus. The materials are from Biosystematics Laboratory, Kyushu University, Kyushu University Museum, National Museum of Natural Science, National Taiwan University, Taiwan Agricultural Research Institute, and University of Kang Ning. In the previous record, there are 17 species belonging to 11 genera in Taiwan. Our results demonstrate 11 species of five genera newly recorded from Taiwan: *Admontia* Brauer & Bergenstamm, *Compsiluroides* Mesnil, *Lixophaga* Townsend, *Medina* Robineau-Desvoidy, and *Medinodexia* Townsend. The taxonomically important features such as male postabdomens are presented in this study.

關鍵詞 (Key words)：Blondeliini, Tachinidae, taxonomy

IT02_中國中生代大花蚤科化石之首度發現與記述

The first fossil wedge-shaped beetle (Coleoptera, Ripiphoridae) from the Mesozoic of China

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大花蚤科 (Ripiphoridae) 是一群具楔形身軀的陸生甲蟲，有著寄生性的幼期生活史，對象包括蜚蠊目、膜翅目和鞘翅目，已命名記述超過 400 個現生物種，已知的中生代大花蚤化石物種相當稀少，僅四例分別產於緬甸琥珀 (晚白堊紀) 和法國琥珀 (中白堊紀)。中國的鞘翅目化石研究始於 1923 年，並在過去三十年內迅速發展，透過對滅絕類群的研究，除了能追溯其起源外，尚可探討形態上的演化，並提供解析親緣關係的形態學證據。本研究檢查出土於內蒙古道虎溝的中生代鞘翅目化石，首度發現大花蚤科的物種，經由形態特徵上的比對，判定為新屬種，地質年代和層位為中侏儸紀九龍山組 (約 1.65 億年前)。本種的翅鞘修長並可完整覆蓋腹部，外形上相似於 Pelecotominae 和 Ptilophorinae 兩個亞科的成員，然而其頭部外形、觸角形式、前足脛節長度、脛節端部形態及脛距式等特徵別於這兩個亞科而無法進行歸類，故暫時置於亞科分類地位未確定 (*incertae sedis*)，本種為大花蚤科目前已知年代最早的化石紀錄，整體外形相似幼期寄生蛀木性甲蟲幼蟲的現生屬別 *Pelecotoma* (Pelecotominae)，加之相同地層亦出土蛀木性甲蟲化石物種，推測本種可能已建立與蛀木性甲蟲幼蟲間的寄生關係。未來以期能發現更多證據以探討大花蚤科的古生物學並結合現生物種進行本科的系統分類與演化學研究。

關鍵詞 (Key words)：鞘翅目 (Coleoptera)、大花蚤科 (Ripiphoridae)、基礎分類學 (alpha-taxonomy)、古生物學 (paleontology)、中侏儸紀 (Middle Jurassic)

IT03_木鼻白蟻科 (等翅下目) 於台灣的發現紀錄與新種確立

Discovery of Stylotermitidae (Isoptera) in Taiwan, with delimitation of a new species

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台灣百年來的白蟻紀錄穩定維持為4科，分別為原白蟻 (Archotermopsidae)、木白蟻科 (Kalotermitidae)、鼻白蟻科 (Rhinotermitidae)以及白蟻科 (Termitidae)，我們近年於台東鸞山地區之穿山甲棲地進行白蟻物種多樣性調查中發現一種尚未紀錄的木鼻白蟻科 (Stylotermitidae) 物種，此一發現不僅為台灣物種名錄新增一個科級分類群，更讓我們有機會釐清木鼻白蟻科在整個白蟻演化樹中的親緣關係。木鼻白蟻科僅存一現生屬木鼻白蟻屬 *Stylotermes*，已有44種被描述，分布侷限於中國、印度、孟加拉以及馬來西亞，由於其生態習性隱蔽與群體個體數少，木鼻白蟻科是現今等翅下目 9 個科中唯一沒有基因序列可供分析的類群，過去研究僅以形態特徵作為分類地位之判別依據。本研究首先整理木鼻白蟻屬中所有已描述物種之形質測量資訊，分別與台灣產木鼻白蟻的兵蟻、工蟻及有翅生殖型階級進行比較，經過形質與特徵比較後，判斷台灣產木鼻白蟻為一新種。本研究亦提供木鼻白蟻科首筆分子序列 (16S rRNA 與 COII)，後續將取得台灣產木鼻白蟻的粒線體全基因組，用以釐清木鼻白蟻科在白蟻演化樹上的位置。

關鍵詞 (Key words)：木鼻白蟻科 (Stylotermitidae)、食木白蟻 (wood-feeding termite)、新紀錄科 (new family record)、基因條碼 (DNA barcode)、物種界定 (species delimitation)

IT04_臺灣隱生性針蟻屬之分類回顧

Revision of the Taiwanese cryptobiosis ant species of genus *Ponera* (Hymenoptera: Formicidae)

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The ant genus *Ponera* Latreille, belonging to *Ponera* genus group of the subfamily Ponerinae, is represented by 57 extant and 5 fossil species in the world. They mainly distribute in the tropical and temperate areas, and nest in rotting logs or soil under stone. Particularly, genus *Ponera* has the highest biodiversity in Taiwanese ant fauna, and ten species have been recorded. *Ponera* species are cryptobiotic, mostly forage in leaf litter or soil; so they could only be collected using Berlese funnels or Winkler's extractor. However, only limited ecological information about *Ponera* ants have been published so far, except that Taylor has observed *Ponera* of New Guinea accepting diplurans, collembolans, and spiders as preys under laboratory condition in 1967. In 1986, Terayama described *Ponera alisana* from Fenchihu and *P. chiponensis* from Chihpen. He also reviewed Japanese *Ponera* species in 1996, and some paratypes of *P. tamon* were collected from Chihpen, Fenchihu and Jiuyuehtan of Taiwan. Then in 2009, Terayama described four new species from Taiwan: *P. rishen* from Riyuntan (Sun Moon Lake), *P. shennong* from Kenting, *P. taiyangshen* from Nanshan-Anleng, and *P. yuhnang* from Taipingshan. In 2014, Terayama reviewed myrmecofauna of Japan and found *P. bishamon* also presented in Taiwan. After that, additional two species of *P. takameni* and *P. japonica* were also recorded by Lin and Wu in 2003, and Wang in 1992 from Taiwan. In this study, we briefly review the Taiwanese *Ponera* species. And we report the first case of *Ponera* species hunting a young earthworm (Haplotaxida) in Laboratory as well as using an artificial trap to collect these cryptobiosis ants. On-going studies include the continuous basic taxonomic works; and hopefully, knowing more about the relationships between the *Ponera* species and their symphiles.

關鍵詞 (Key words)：分類學 (taxonomy)、隱生性 (cryptobiosis)、針蟻屬 (*Ponera*)、蟻科 (Formicidae)、膜翅目 (Hymenoptera)

IT05_台灣直翅目昆蟲的海拔分布

The altitude distribution of Orthopteran insects in Taiwan

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台灣的海拔高度差異是地形特色之一，地處熱帶卻有熱帶至亞寒帶不同類型的氣候區，海拔變化對生物分佈的影響，應該是台灣有趣的研究議題。本研究沿中部橫貫公路系統化掃網採集直翅目昆蟲，共有 18 個樣區，選定 13種植群類型作為樣區探討海拔分布特性，2015 年 2 月起每兩個月採集一次；已鑑定三個月的標本供分析，總計 705 個標本，鑑定後為 5 科 117 個形態種，佔已知直翅目 64 科的 12.8%。各科百分比分別為蝗科 (Acrididae) 454隻 (64.4%)、蟋蟀科 (Gryllidae) 92隻 (13.0%)、螽蟖科 (Tettigoniidae) 88隻 (12.5%)、菱蝗科 (Tetrigidae) 68隻 (9.6%)、蟋螽科 (Gryllacrididae) 2隻 (0.3%)。總計累積了 117 個型態種，各科百分比分別為蝗科 28.2%、螽蟖科 26.5%、蟋蟀科 22.2%、菱蝗科21.4%、蟋螽科 1.7%，型態種數目還在增加中，因此本結果數據僅供參考。海拔之間各科比例，以 1,000 公尺為級距分成低、中、高海拔，高海拔採集到的個體數最多為蝗科佔 74.5%，而中海拔則為佔 51.7% 的螽蟖科為最多，低海拔也是蝗科佔 64.6% 最多，用直翅目分類群的組成看不出海拔之間的分佈差異。以形態種個體數計算種豐富度指數 (species richness index)；結果顯示中海拔具有較高的種豐富度指數為 0.17，高海拔為 0.08 居中，而低海拔則數值最低為 0.03，此結果可能與昆蟲相物起源有關，可能是因為中海拔是物種分布的過渡區之緣故。

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

BC05_南方小黑花椿象捕食二點葉蟎後若蟎之族群特性及捕食率分析

The population property and predation rate of *Orius strigicollis* (Hemiptera: Anthocoridae) fed on protonymph of *Tetranychus urticae* (Acari: Tetranychidae)

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南方小黑花椿象 (*Orius strigicollis* (Poppius)) 為台灣田間與溫室中常見之本土捕食性天敵，其可捕食多種小型害蟲，如：葉蟎、薊馬、粉蝨等。此研究於 25±1℃ 定溫環境，相對溼度為 70±10% 及光週期 12:12 (L:D) h 下，以花豆 (*Phaseolus coccineus*) 葉飼養二點葉蟎 (*Tetranychus urticae* Koch)，再將後若蟎供給南方小黑花椿象捕食，進而記錄其生活史與捕食率。生活史中，小黑花椿象卵期平均為 3.8 日、若蟲期平均為 8.5 日、雌、雄成蟲期壽命平均分別為 18.2 及 17.6 日。雌成蟲的平均成蟲產卵前期 (adult pre-oviposition period, APOP)與總產卵前期 (total pre-oviposition period, TPOP) 為 3.7 與 16.2 日，一生平均總產卵量為 79.2 粒卵，淨增殖率 (net reproductive rate, R_0) 為 31.9 ，內在增殖率 (intrinsic rate of increase, r) 為 0.1571 ，平均完成一世代所需時間 (mean generation time, T) 為 22.04 日，終極增殖率 (finite rate of increase, λ) 為 1.1702。小黑花椿象若蟲期及成蟲期平均捕食率分別為 317.1 及 1205.4 隻二點葉蟎後若蟎，一生平均淨捕食率 (net predation rate, C_0) 為 1347.5。其中雌、雄蟲一生平均淨捕食率分別為 1565.2 及 1560.2 隻後若蟎，而小黑花椿象平均產生一有效卵之捕食率 (transformation rate, Q_p) 則為 42.2。上述資料提供南方小黑花椿象在 25℃環境下的族群特性與捕食量，可為將來溫室或田間試驗時提供生物防治之基礎資料。

關鍵詞 (Key words)：南花小黑花椿象 (*Orius strigicollis*)、二點葉蟎 (*Tetranychus urticae*)、兩性生命表 (two-sex life table)、捕食率 (predation rate)

BC06_南方小黑花椿象捕食台灣花薊馬之族群特性與捕食潛能評估

Demographic and predation potential of *Orius strigicollis* fed on *Frankliniella intonsa*

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南方小黑花椿象 (*Orius strigicollis* Poppius) 是田間常見的捕食性天敵，可捕食薊馬、葉蟎、蚜蟲等小型害蟲。在國外已有將小黑花蝽屬昆蟲商品化用於防治薊馬為害，是具有潛能的防治資材。台灣花薊馬 (*Frankliniella intonsa* Trybom) 則為台灣重要經濟害蟲之一，可危害花卉、豆科等經濟作物，造成植株乾枯萎凋。現今雖然主要以化學防治為主，但是薊馬生活習性隱蔽、繁殖能力強及抗藥性的潛在問題，開發替代防治策略實屬必要。本研究以二齡台灣花薊馬若蟲為南方小黑花椿象之食餌，以進行該族群增長率及捕食量之分析。每日觀察記錄此捕食性天敵之齡期變化、存活率及捕食量，並利用 TWOSEX-MSChart 結合 CONSUME-MSChart 來評估族群增長特性及捕食潛能。更進一步藉由 TIMING-MSChart 來評估南方小黑花椿象的族群變動來擬定防治的時機。在定溫25℃、相對溼度60 ± 10%、光週期12D：12L下，南方小黑花椿象若蟲所需的發育時間為13.8 ± 0.1日，雄蟲及雌蟲壽命分別為16.8 ± 2.8日及11.8 ± 1.6日。在族群介量部分，淨繁殖率 (net reproductive rate, R_0)、內在增殖率 (intrinsic rate of increase, r)及終極增殖率 (finite rate of increase, λ)，依序分別為18.2、0.1383d^{-1}及1.1483d^{-1}。捕食能力方面，淨捕食率 (net consumption rate, C_0) 為54.8，終極捕食率 (finite predation rate, ω) 為1.7611。結果顯示南方小黑花椿象除了卵期外各個齡期皆可捕食台灣花薊馬二齡若蟲並以其當作獵物完成其生活史，使族群能夠持續成長，此等基礎資料可應用於田間生物防治實務工作上。

關鍵詞 (Key words)：南方小黑花椿象 (*Orius strigicollis*)、台灣花薊馬 （*Frankliniella intonsa*）、生物防治 (biological control)、兩性生命表 (two sex life table)、族群介量 (population parameter)

BC07_基徵草蛉對銀葉粉蝨的防治效果探討

Efficiency of prey consumption of *Mallada basalis* larvae to nymphs of *Bemisia argentifolii*

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基徵草蛉 (*Mallada basalis* (Walker)) 已具有量產技術，可應用於大面積栽種之作物，能捕食蚜蟲、粉蝨，蟎類等多種小體形昆蟲，為農作害蟲防治上極具應用潛力之生物天敵。本研究探討不同溫度下基徵草蛉幼蟲對銀葉粉蝨 (*Bemisia argentifolii* (Bellows & Perring)) 的防治效果，結果顯示，在15ºC、20ºC、25ºC、30ºC環境下，基徵草蛉幼蟲一生可捕食 2295 ± 386.32、3806.4 ± 113.5、3449.8 ± 194.51、4800.8 ± 261.8隻銀葉粉蝨三齡幼蟲，且以三齡之基徵草蛉幼蟲捕食能力最強。進一步試驗銀葉粉蝨在不同溫度下的生活史，結合基徵草蛉對銀葉粉蝨之捕食量試驗結果，可做為未來草蛉應用技術的參考。

關鍵詞 (Key words)：基徵草蛉 (*Mallada basalis* (Walker))、銀葉粉蝨 (*Bemisia argentifolii* (Bellows & Perring))、捕食量 (prey consumption)

BC08_蓮霧新興害蟲米爾頓釉小蜂 (*Anselmella miltoni*) 在非經濟作物上的蟲癭發育及其寄生蜂相

Gall development and parasitic wasps of new invasive wax apple pest, *Anselmella miltoni* on non-economic crop

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米爾頓釉小蜂 (*Anselmella miltoni*) 在台灣以桃金孃科 (Myrtaceae) 赤楠屬的蓮霧 (*Syzygium samarangense*) 和蒲桃 (*S. jambos*) 為寄主，雌成蟲於寄主盛花期停棲於雌蕊基部將多個卵產於胚珠，受感染胚珠會發育成多癭室的蟲癭，對近幾年的台灣蓮霧產業造成負面影響，目前此害蟲在蓮霧上的感染情形及防治方式已有相當的研究成果，為了更充分瞭解米爾頓釉小蜂在不同寄主上的發生情形，本研究探討米爾頓釉小蜂在非經濟作物—蒲桃上的蟲癭發育及寄生蜂相，以作為防治參考。以嘉義縣觸口自然教育中心的蒲桃作為研究材料，解剖並觀察在不同的果實物候期蟲癭的發育狀況，可得知卵產下後，癭組織在胚仔期開始發育，並將蟲卵包覆，在種子膨大期形成癭室，幼蟲成長的過程中癭逐漸成熟定形，進入未熟果期後大部分的幼蟲會開始化蛹，果實成熟掉落以前成蟲幾乎都已咬出孔道離癭。此外，在蒲桃果實中觀察到另外三種小蜂自米爾頓釉小蜂的癭中羽化，分別是 *Aprostocetus* sp. (釉小蜂科)、*Megastigmus* sp. (長尾小蜂科)、*Eupelmus* sp. (旋小蜂科)，藉由解剖觀察，目前已確認 *Aprostocetus* sp.是米爾頓釉小蜂幼蟲的外寄生者，*Megastigmus* sp.是米爾頓釉小蜂和 *Aprostocetus* sp.幼蟲和蛹的外寄生者，而 *Eupelmus* sp.因數量稀少，難以確認其生態地位。

關鍵詞 (Key words)：米爾頓釉小蜂 (*Anselmella miltoni*)、蟲癭發育 (gall development)、寄生蜂 (parasitic wasp)

LHAD01_不同食草對茶角盲椿象生活史之影響

Life cycle of *Helopeltis fasciaticollis* (Hemiptera: Miridae) on different host plants

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茶角盲椿象 (*Helopeltis fasciaticollis* Poppius) 屬半翅目 (Hemiptera)、盲椿科 (Miridae)，近年來成為台灣中部埔里、魚池等地區茶樹 (*Camellia sinensis* (L.) O. Kuntze) 的主要害蟲，其成、若蟲均以刺吸式口器危害茶樹一心二葉部位，導致受害部位產生黑褐色斑痕，不僅造成植株芽體生長受阻，對茶葉的產量及品質影響甚鉅。目前針對埔里及魚池等地區茶園的初步調查，結果顯示此區域以台茶18 號及青心烏龍等品種受害較為嚴重；同時，亦發現此蟲會在大花咸豐草 (*Bidens pilosa* L. var. *radiata*) 及蔓澤蘭 (*Mikania cordata* (Burm. f.) B. L. Rob.) 等茶園常見雜草上棲息並取食新梢部位。本試驗於室內以大花咸豐草及台茶 18號飼育茶角盲椿象，比較其成、若蟲在二種不同食草上的發育情形。結果顯示在28.0 ± 2.0℃、75.0 ± 15.0% RH 及自然光照環境下，茶角盲椿象 1–5 齡若蟲取食大花咸豐草的發育時間分別為 1.9 ± 0.5、2.0 ± 0.6、1.4 ± 0.6、2.4 ± 0.5、3.3 ± 0.5天，取食台茶 18 號者分別為 2.2 ± 0.4、1.3 ± 0.5、2.4 ± 0.5、2.5 ± 0.7、3.6 ± 0.7天，餵食二種食草後茶角盲椿象均可完成生活史發育至成蟲，而二者完成若蟲期的發育時間分別為 10.8 ± 0.4 及 11.8 ± 1.3 天，彼此間並無顯著差異。雖然在茶園區茶角盲椿象偏好於茶樹上取食危害，但從飼育結果顯示大花咸豐草可做為代用寄主供其繼續存活，此初步結果可供茶園區雜草管理之參考。

關鍵詞 (Key words)：茶角盲椿象 (*Helopeltis fasciaticollis* Poppius)、茶樹 (*Camellia sinensis* (L.) O. Kuntze)、大花咸豐草 (*Bidens pilosa* L. var. *radiata*)、生活史 (life cycle)

LHAD02_板栗癭蜂 (膜翅目︰癭蜂科) 在台灣獨特生活史週期與其化學防治

The unique life cycle and chemical control of *Dryocosmus kuriphilus* (Hymenoptera: Cynipidae) in Taiwan

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板栗癭蜂 (*Dryocosmus kuriphilus* Yasumatsu) 為台灣新興的入侵造癭害蟲，在過去數十年間入侵北溫帶國家 (如日本、韓國、美國與義大利等)，造成栗屬 (*Castanea*) 果樹嚴重的經濟危害。其成蟲於 6–9 月離開蟲癭後，產卵於栗樹新生芽內，而後孵化為一齡幼蟲開始取食並刺激芽產生內部變異，至 10 月進入休眠期，翌年 4 月繼續生長發育，於 5 月下旬羽化為成蟲，蟄伏 10–15 天再行離癭。由於台灣氣候與溫帶國家大相逕庭，必須考量板栗癭蜂對亞熱帶氣候的適應性，先瞭解板栗癭蜂在台灣的生活史，再進一步測試化學防治的有效性。在田間調查後發現，台灣的板栗癭蜂幼蟲於 3 月中旬開始活動，至 7 月上旬成蟲完全離癭，較溫帶國家短且提前。此外，台灣有部分蟲癭在當年 10 月提早發育為早熟癭，並於隔年 4 月中記錄到離癭成蟲。這些生活史的差異意味著國外的防治時機在台灣需重新調整。因此，選擇不同時期以益達胺及第滅寧分別稀釋為 1000×、2000× 進行田間藥劑試驗。結果顯示，於成蟲離癭高峰期進行防治可將感染率降至 15% 以下；針對幼蟲防治時，如施藥於正要發育為蟲癭的芽，幼蟲致死率可達 60–80%，明顯優於施藥於蟲癭時 (2%)。由這些結果可得知，即便板栗癭蜂在台灣的生活史有其特殊性，如能準確地掌握成蟲離癭高峰與蟲癭即將發育時進行防治，仍可有效控制蟲害，降低損失。

關鍵詞 (Key words)︰入侵種、板栗癭蜂 (*Dryocosmus kuriphilus*)、物候、防治

LHAD03_家蠶人工飼料適性品種之選育

Breeding of silkworm (*Bombyx mori* L.) race adaptable to artificial diet

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家蠶人工飼料飼育系統之建立為高清淨度家蠶穩定生產的必要條件，也是家蠶生物反應器之重要關鍵技術。為提高家蠶之多元利用性，本研究針對家蠶種原庫之 136 個品系進行篩選，配合人工飼料配方之調整，蠶卵去病毒處理及飼育期病毒監測，以選育高清淨度之人工飼料之適性品種。試驗結果顯示，將 33 種強健之家蠶原原種品系，分別餵飼葉桑及修正後之日本 NOSAN 人工飼料，選出對人工飼料具較高適應性之品系共 7 種，再雜交組合成 43 種品種，經 3 代篩選並逐代淘汰帶病毒族群，於清淨環境下飼育，調查各齡期病毒帶原率、起蠶率、體重、上簇率及健蛹率等。經多代評估，選育出高人工飼料適性雜交品種 Bm-J10，五齡起蠶平均蠶重達 1.38 公克、五齡起蠶率為 95.0%、上簇率 96.4%，健蛹率 87.9%。

關鍵詞 (Key words)：家蠶 (*Bombyx mori* L.)、人工飼料 (artificial diet)、選育 (breeding)

LHAD04_溫度對瓜食酪蟎 (*Tyrophagus neiswanderi*) 生活史特性之影響

Temperature effect on the life history traits of *Tyrophagus neiswanderi*

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瓜食酪蟎 (*Tyrophagus neiswanderi*) 屬無氣門亞目 (Astigmata)、粉蟎科 (Acaridae)、食酪蟎屬 (*Tyrophagus*)，過去常紀錄為儲藏性食物害蟎。蝴蝶蘭 (*Phalaenopsis* spp.) 為我國農業旗艦農產品，在外銷上具有重要的地位，近年來在溫室栽培過程中常發生消苞落蕾之現象，影響其產量與品質，而該花卉受瓜食酪蟎為害之花苞外側表皮呈現皺縮現象，對於蘭業之切花、盆花造成重大損失，目前已知蝴蝶蘭之消苞落蕾可能與瓜食酪蟎相關。本試驗之研究於 20、25 及 30℃ 三種不同定溫下進行單隻飼育，於全黑無光照及相對濕度 70% ± 10% 之植物生長箱中進行，以人工飼料飼育瓜食酪蟎，探討不同溫度對其生活史特性之影響。結果顯示，於三種定溫下卵孵化率分別為 88.5、90 以及 88%。量測其體長及體寬均隨發育齡期之增加而增長。平均總發育日數分別為 17.4、10.4 及 9.9 日。於 25℃ 定溫下雌、雄成蟎之平均壽命分別為 24.9 及 40.2 日，雌成蟎之產卵期在交尾後第 11 日達高峰，平均每隻雌成蟎一生產 243.32 粒卵，平均每日產 3.92 粒卵。生長發育資料經兩性生命表分析，由齡別存活曲線可知其存活率自第 6 日即開始逐漸下降；而齡別繁殖曲線可知於 10.46 天達繁殖高峰，推估其族群介量分別為內在增殖率 (r) 0.28，淨增殖率 (R_o) 109.9，終極增殖率 (λ) 1.32，平均世代所需時間 (T) 16.9 日。

關鍵詞 (Key words)：瓜食酪蟎 (*Tyrophagus neiswanderi*)、生活史 (life history)、族群介量 (population parameter)

BPSA01_美國農業部國家農業圖書館 i5k Workspace 專案–節肢動物基因體之基因註解品質控制

The i5k Workspace@NAL – quality control of gene annotation for arthropod genomes

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The advances in sequencing technology have opened a new era in genome study. One of the essential challenges in current genome study is to annotate as many sequences as possible with biological information (such as protein/gene function). Some studies have revealed that community annotation, engaging biologists of the scientific community to annotate genes, distills invaluable knowledge for genome projects. However, such a data intensive approach demands a comprehensive bioinformatics infrastructure to support large-scale collaboration and requires gatekeepers to enforce rules of gene annotation. The i5k Workspace@NAL, a genome portal, is thus designed to meet the genome curation, visualization, and dissemination needs of the arthropod genomics community. Through hosting more than fifty arthropod genome projects, the i5k Workspace@NAL team observed various types of formatting errors that arose from community annotation. In this study, a quality control (QC) procedure is proposed to automatically detect and fix formatting errors in GFF3 (General Feature Format), the format for describing genomic features. The proposed procedure can detect 53 types of formatting errors, covering (a) intra-model, (b) inter-model and (c) single feature errors. The procedure has been applied to gene curations in eight insect genome projects. Overall, 15% to 30% of the manually curated models in these projects were found to be problematic after being screened with this procedure. The proposed procedure is shown to identify more existing errors than two other GFF3 validators, highlighting the need for this QC procedure. In conclusion, the automated QC procedure helps to ensure the quality of a gene set produced from community annotation and facilitates the genome annotation process of arthropod genomes.

關鍵詞 (Key words)：節肢動物 (arthropod)、基因體研究 (genome study)、基因註解 (gene annotation)

BPSA02_以微量元素分析建立台灣產龍眼蜜之鑑定技術

Identification of Taiwanese longan honey with microelement database

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蜂蜜具有豐富的營養價值與醫療成分，為國人於飲食文化中不可或缺的食物之一。然而由於臺灣龍眼蜜的經濟價值不斐，不肖業者往往為了降低成本、提高經濟利潤，混合國外龍眼蜜或添加高果糖漿、人工色素以及香料來合成假蜜進行販售。為確保蜂蜜品質和來源，我們檢測蜂蜜裡 14 種微量元素：鈉、鎂、鉀、鈣、鋁、鐵、銅、鋅等，並比較台灣與泰國兩地產龍眼蜜之間的差異。此外，將所有樣品連同已知混合比例 (果糖佔 30%、60%、90%) 的人工調和蜂蜜 (果糖與蜂蜜混合物) 和作為控制組的果糖進行相同的前處理後，一併使用感應耦合電漿質譜儀 (Inductively coupled plasma mass spectrometer, ICP-MS) 和感應耦合電漿原子發射光譜儀 (Inductively coupled plasma optical emission spectroscopy, ICP-OES) 進行微量元素測定，最後再利用主成份分析 (Principle component analysis, PCA) 法進行數據分析。結果顯示，此技術能有效利用常見微量元素之含量對於國內外蜂蜜、以及市面上的純蜂蜜及調和蜜進行區分。

關鍵詞 (Key words)：食品安全 (food safety)、蜂蜜 (honey)、微量元素 (microelements)、主成份分析 (principle component analysis)

BPSA03_雄性大龍蝨附著毛的可調式吸附機制

Tunable adhesion for life and sex: functioning mechanisms of adhesive hairs in male *Cybister* diving beetles

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Male diving beetles use specialized adhesive setae, in spatula or circular form, to mount on female elytra during underwater courtship; co-evolution of the contact surfaces has attracted much attention since Darwin. We for the first time directly measured and compared the performance of a single seta of each form. While the circular setae behave like typical suckers, the spatula ones with a modified shallow sucker and channels, found only in male *Cybister* beetles, use the combined mechanisms of suction and viscous resistance for adhesion. To decipher the physical mechanisms of the unusual velocity-dependent adhesion, we construct a conceptual "water-leaking model" combining spatula seta's surface geometry and properties, as well as its force and deformation throughout adhesion. Comparison between simulation and empirical results in *Cybister rugosus* reveals three functioning mechanisms: (i) water flowing through imperfectly sealed microfluidic channels leads to velocity-dependent adhesion; (ii) stalk-pulling action increases pressure difference to compress the channel wall, triggering seal-off of the micro-channels; (iii) stalk elasticity provides buffer for energy storage, further increasing the adhesion capacity. Such tunable adhesion mechanisms found in spatula setae not only allow the male *Cybister* beetles to succeed the premating courtship mount and easy release for respiration, but also provide us insights for future design of bio-inspired underwater adhesion devices.

關鍵詞 (Key words)：生物力學 (biomechanics)、橙斑大龍蝨 (*Cybister rugosus*)、模型模擬 (model simulation)、水下附著 (underwater attachment)、黏性吸附 (viscous adhesion)

BPSA04_微電腦斷層掃描技術重構蜜蜂腦部構造

Reconstruction of honey bee brain by using micro-CT technology

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The morphology of internal structures is difficult to observe without damaging the specimens. Even though a good quality result is available after a tedious and long-time dissecting or histological serial sectioning, soft tissues are easily distorted during the sample preparation, especially when studying the nervous system of insect. Furthermore, the infrastructure and position *in situ* are unavoidably sacrificed and accurate measurement is almost impossible. Micro-computed tomography (micro-CT) is very helpful to solve the problem mentioned above. To reveal the nervous system of an insect brain (a honey bee brain, in this case) for micro-CT scanning, a new perfusion staining method with microinjection of osmium tetroxide into the internal cavity of bee head has been developed. In the previous studies, open the head case to expose the brain for staining and removing the mouth parts, the hypopharyngeal and the head salivary glands were needed. The processes might have some negative impacts on the internal morphology. However, the perfusion staining method with microinjection minimized the damages caused by the processes. Three-dimensional image of honey bee brain was reconstructed digitally after a serial CT scan, and the morphological dimensions of the tissue can be measured with the help of software. In this study, the 3D visualization of honey bee brains by micro-CT was demonstrated, and our perfusion staining method can be easily employed for staining the soft tissues in the invertebrates.

關鍵詞 (Keywords)：蜜蜂 (honeybee)、微電腦斷層掃描 (micro-CT)、灌流 (perfusion)

BPSA05_運用能量守恆原理分析新渡戶歪白蟻兵蟻之高速大顎彈動

Analysis of mandible striking mechanics in soldiers of *Pericapritermes nitobei* using principle of energy conservation

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有些生物能透過彈性位能的儲存與釋放，產生超越肌肉收縮所致的極速運動，來提高避敵、捕食、防禦的優勢。具對稱型大顎的歪白蟻，會相互擠壓結構類似的兩側大顎來儲存能量，以快速彈擊敵人；前人透過每秒四萬幀的高速攝影，估計此動作最快可達 67 m/s，是最高速的生物運動之一。另一具不對稱型大顎的歪白蟻類群則有明顯歪斜的左大顎，會受右大顎按壓而彎折，提供彈動所需的能量，前人提出此型能產生更佳的彈擊功效，本研究透過探討具不對稱型大顎之新渡戶歪白蟻 (*Pericapritermes nitobei* (Shiraki, 1909))，提供此說的首度實驗佐證。因受限於現有高速攝影機的拍攝速度，我們運用能量守恆原理，透過計算兵蟻大顎彈擊金屬球後的總動能 (包含金屬球的移動動能，以及白蟻的移動與轉動動能)，來估計彈擊當下左大顎運動端的最快速率。結果顯示，六個受試歪白蟻的大顎運動平均速率為 56±18 m/s，其中有四隻的最高速率超過 70 m/s，最快甚至可達 102 m/s，支持不對稱型大顎在彈擊速率上較對稱型大顎更具優勢。此外，本研究揭示歪白蟻不對稱型大顎的彈動是當今記錄中最快的生物運動，完整過程需每秒至少一百二十萬幀的拍攝速率才得以記錄。透過比較兩型大顎的彈動力學，可進一步探討不同類群兵蟻的防禦策略，及其在生態與演化意義。

關鍵詞 (Key words): 生物力學 (biomechanics)、新渡戶歪白蟻 (*Pericapritermes nitobei*)、彈擊型大顎 (snapping type mandible)、防禦行為 (defensive behavior)

BPSA06_「榕果與榕小蜂的共生關係」行動展示盒開發與教學成效之研究

Loan box development and teaching practice of “mutualism between figs and fig wasps”

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為了使博物館的豐富內容更廣泛地進入社會中，許多博物館正在開發「行動展示盒」計畫。透過行動展示盒整理及呈現博物館的收藏品，行動展示盒計畫演示了一個博物館作為教育資源的巨大潛力。榕屬植物的繁殖依賴於榕小蜂授粉。為了傳播種子，每個榕果至少需要一隻榕小蜂的合作，榕屬植物和榕小蜂發展出一個親密的共生的關係，它們就這樣共同進化了約九十萬年的時間，這樣的關係在本質上非常的獨特和有趣。我們打算使用「榕果和榕小蜂的共生關係」為主題，開發行動展示盒，並評估其在教學應用中的成效。行動展示盒將包含一個教師手冊、教具、遊戲活動教具、學習工作表。行動展示盒將有望達到「激發學習興趣」、「激勵使用者去思考」、「豐富學習體驗」、「具自我糾正和自我學習」等目標。行動展示盒旨在促進教學活動、提高學生關於主題和相關知識的理解。新開發的行動展示盒將會選定一所在臺北市的小學使用。而行動展示盒的有效性將藉由使用調查表、學生在課程前後的心得以及教師教學使用意見反饋進行評價。我將通過從使用者的學習反饋了解此行動展示盒的優點和缺點。該行動展示盒將促進教學活動，並且更有效地提供專題知識。

關鍵詞 (Key words)：榕果 (figs)、榕小蜂 (fig wasps)、行動展示盒 (loan box)、博物館 (museum)、共生關係 (mutualism)

BPSA07_應用 WSN 技術對積穀害蟲之監測及回報機制

Application of monitoring and feedback system of stored grain pests based on wireless sensor networks

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稻穀在儲存的過程中，若遭受害蟲侵害，將導致經濟損失，嚴重甚至造成糧食缺乏。為有效防治害蟲危害，穀倉的監控系統扮演重要的角色。本試驗結合無線感測器網路技術 (WSN) 與 LED 燈光誘引器作為監控系統，此系統能誘引主要積穀害蟲穀蠹，並定時計算蟲數、偵測微氣候等資訊，進一步掌握害蟲行為，得以及時實施防制措施，達到降低損害的目的。目前已在冬山、龍潭、伸港、南投等 11 個倉設置監測點，進行長期害蟲族群與環境因子監測。監測結果顯示，在蟲害的部分，穀蠹發生的時間多在下午 3 至 6 點期間，以 8 至 10 月為危害之高峰期，依儲存地點及儲存環境差異，穀倉蟲害發生以南部危害較嚴重；在溫度部分，全年倉內最低溫約 20 °C、最高溫約 35 °C，由於臺灣濕度較高且穩定，倉內相對溼度多在 50 至 70%，當蟲害發生時，稻穀袋內溫度會高於袋外溫度，顯示害蟲活動使稻穀內溫度升高，溫度升高將導致害蟲危害速度增快。未來將此套系統與預警系統結合，以提供農會或穀倉之應用，預警系統設定穀蠹蟲害發生每日高於 1 萬隻、稻穀袋內溫度超過 35 °C 時。透過簡訊告知穀倉管理者，適時提供蟲害資訊，可有效降低因害蟲危害的儲穀損失，並彙整多年數據後，比較貯藏時間環境因子與害蟲發生之相關資料，可提供未來防治積穀害蟲之參考依據。

關鍵詞 (Key words)：無線感測網路 (wireless sensor network, WSN)、積穀害蟲 (stored-product insect pests)、穀蠹 (*Rhyzopertha dominica*)

BPSA08_應用蜂巢內影像監測系統於蜜蜂運動行為分析

Honey bee movement behavior analysis using an image monitoring system in the beehive

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本研究應用蜂巢內影像監測系統搭配文字標籤標記欲觀察的蜜蜂，紀錄蜜蜂於巢內的活動影像，並使用影像處理技術自動計算影像中帶有標籤蜜蜂的巢內活動軌跡，將該軌跡對應至不同之蜜蜂運動行為，以分析蜜蜂群體以及個別蜜蜂之行為差異。研究中設計兩項實驗分別探討不同分工的蜜蜂以及不同日齡的蜜蜂於巢內的行為模式差異。第一項實驗為箱內蜂與外勤蜂的行為比較，由實驗結果分析得知外勤蜂於巢內的平均移動速度較快且具有週期性，並且在陰雨天的天氣狀況下其行為模式與箱內蜂行為模式較為接近。第二項實驗為比較不同日齡的蜜蜂隨日齡增長的行為模式差異，隨日齡增長可觀察到蜜蜂於巢內的移動速度逐漸提高，而在巢內靜止與徘徊的動作則逐漸減少。此現象推測可能為隨日齡增長而改變蜜蜂的群體分工，進而導致蜜蜂巢內運動行為的差異。

關鍵詞 (Key words)：蜜蜂運動行為 (honey bee movement behavior)、蜜蜂標記 (honey bee labeling)、軌跡分析 (trajectory analysis)、年齡行為多態型 (age polyethism)

IGC01_年積温差與胡麻斑星天牛的表現型相關的探討

Phenotypic variation on elytra maculation pattern of *Anoplophora macularia* (Thomson) in Taipei Basin: from 1966 to 2016

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自 1999 年起逐年在：關渡，竹圍，八里三地紅樹林所收集到胡麻斑星天牛棲群聚集資料顯示：星天牛棲群週年出現羽化峯的數目；時間；跨距；年度間，峯與峯的間距皆呈現多樣性。此多樣性的表現會隨當年的氣相因子 (短期的温度效應) 及常年的氣候因子 (長期的温度效應) 不同而有所改變。且確認到，年來的快速增温；各年天牛世代期間的年積温；各生長期逐日的劇熱，對生物物种產生衝擊効應，可以反應在星天牛翅鞘斑型劇化的表現型上；且其表現型上的改變是可逆的。文中也探討天牛發育温度的上下限與其他相關的影響因素。

關鍵詞 (Key words) : 胡麻斑星天牛 (*Anoplophora macularia* (Thomson)、翅鞘斑型 (elytra maculation pattern)、表現型 (phenotypic expression)、可逆變異 (reversible variation)、年積温 (annual accumulated temperature)

IGC02_胡麻斑星天牛棲群因應日高温的衝擊所呈現外在行為和內在適應的反應機制

Behavioral and autonomic thermoregulation of *Anoplophora macularia* (Thomason) induced by stress of high daily temperature

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北台灣淡水河紅樹林沿岸着生的胡麻斑星天牛棲群應對天侯及天氣的增温呈現諸適應机制如下：1. 提早整個成蟲羽化季的時間，或縮短整個羽化季期間；2. 與此相應的是，短化了交尾的頻率；3. 同一羽比季中，成蟲羽化梯次數量的增減的趨勢；4. 減少了日閒由棲地來往取食及交尾其寄主植物間的移動，增加了其在寄主植物由樹冠到根部的垂直移動；5. 天牛個体間的摩擦在時間/空間及高温的壓力下減到最少；6. 寄主植物或因天牛攝取水分而倍增其落葉，或因天牛攝取養分而大量產生啃食後所溢出的樹汁；7. 棲群的增減及雌雄性比率差異变化。文中討論昇温可能導致寄主植物間接受害的影響。

關鍵詞(Keywords)：胡麻斑星天牛 (*Anoplophora macularia*) (Thomason)、昇温 (temperature increasing)、行為改變 (behavioral modification)、內在熱遷應 (autonomic thermo regulation)

IGC03_人工光害對黃緣螢幼蟲基因表現之影響

Impacts of artificial light pollution on the transcriptome of *Aquatica ficta* larvae

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The artificial light pollution is considered as one of the factors cause declines in firefly population. To elucidate the effect of light pollution on firefly larvae from molecular perspective, we used NGS (Next Generation Sequencing) method to profile the transcriptome of firefly larvae, *Aquatica ficta*, under artificial light pollution. More than 2G of RNA-seq reads were generated from artificial light exposed as well as regular light/dark cycle firefly larvae for transcriptome assembly. Approximately 208,672 transcripts (unigenes) were obtained, and 60,410 unigenes were annotated. Comparing to the control, we identified 1,450 DEGs (Differentially Expressed Genes) from the larvae with the artificial light treatment during the dark cycle. From them, 58 and 1392 unigenes were activated / up-regulated or inactivated / down-regulated, respectively. We then performed GO (Gene Ontology) analysis and found that activated / up-regulated unigenes are enriched in terms relative to regulation of hormone levels and oxidation-reduction process, while inactivated / down-regulated are enriched in terms relative to ribonucleoprotein complex biogenesis, primary metabolic process, macromolecule metabolic process, cellular biosynthetic process, organic substance biosynthetic process, and response to osmotic stress. More research is needed to confirm whether the effect could continue to adult stage.

關鍵詞 (Key words): 黃緣螢 (*Aquatica ficta*)、光害 (light pollution)、轉錄組 (transcriptome)

IGC04_初羽化蜜蜂頭部基因差異表現繼幼蟲時期接觸低致死劑量益達胺

Differential gene expression in honey bee head after exposure to sublethal dose of imidacloprid during larval stage

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Imidacloprid affects honey bee neural development at sublethal doses. Here, we performed transcriptome sequencing and investigated the global gene expression in the heads of newly *emerged* adult honey bees totally *exposed to* imidacloprid at 2 ng per bee during the larval stage. Approximately 10 million qualified reads were obtained from nontreated and imidacloprid-treated bees individually, which were then assembled and aligned to form a differentially expressed gene (DEG) library of 15,314 unigenes. In this DEG library, 578 genes showed more than 2-fold change in gene expression after imidacloprid exposure. Of the 578 genes, 329 had clear functional annotations, which were further classified into 11 groups based on their physiological roles, whereas the functionality of 249 genes remained uncharacterized. Our results indicated that imidacloprid alters the multifaceted honey bee physiology; this gene information may aid in understanding the effects of pesticides on the health of pollinators. For example, genes encoding major royal jelly proteins (MRJPs), comprising a group of multifunctional proteins with major roles in the sustainable development of bee colonies, were strongly downregulated. These downregulation patterns were further validated using quantitative reverse transcription-polymerase chain reaction (qRT-PCR) analysis on the heads of 6-day old nurse bees; the analysis confirmed that imidacloprid exposure significantly downregulates *mrjp1*, *mrjp2*, *mrjp3*, *mrjp4*, and *mrjp6* expression. To the best of our knowledge, this is the first study to conclude that imidacloprid at sublethal doses affects *mrjp* expression and probably weakens bee colonies.

關鍵字 (Key words)：益達胺 (imidacloprid)、低致死劑量 (sublethal dose)、蜂王漿蛋白質 (major royal jelly proteins)

IGC05_氣候變遷如何影響北加州溪流大型無脊椎動物對農藥汙染之反應

Influences of climate change on the response of stream macroinvertebrates to pesticide contamination in Northern California

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Climate change can directly and indirectly influence pesticide pollution through field run-off or spray drift and has impacted river ecosystems worldwide. We used reported pesticide use data as input to a hydrological fate and transport model (Soil and Water Assessment Tool) and climate-change scenarios to simulate spatiotemporal dynamics of pesticides mixtures in the Sacramento River watershed of California. Using a model describing the relationship between macroinvertebrate communities and pesticide dynamics, we found that compared to the base period during 1970-1999: (1) almost of all climate-change scenarios predicted annual rainfall enrichment and warming across the watershed; (2) increasing pesticide contamination and increased impact on macroinvertebrates will likely occur in almost the entire watershed by 2070-2099. Future efforts on practical adaptation and mitigation strategies can be improved by awareness of altered threats of pesticide mixtures under future climate change.

關鍵詞 (Key words)：氣候變遷 (climate change)、群聚 (community)、生態毒性 (ecotoxicity)、極端天氣 (extreme weather)、暖化 (warming)

IGC06_暖化對台灣不同地區小菜蛾之影響

Effects of warming on *Plutella xylostella* in different regions (north, central, and south) of Taiwan

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小菜蛾 (*Plutella xylostella*) 幼蟲以咀嚼式口器啃食植物，是十字花科重要害蟲之一。面臨未來全球暖化的趨勢，台灣低緯度的環境下可能已經達到小菜蛾所能接受的最高溫度範圍。以往溫度影響生物的研究大部分是以定溫的方式進行，但與野外的溫度變化有所誤差，因此本研究將以日溫周期性變化來設定，模擬野外實際的溫度變化，評估現今夏季平均氣溫 (參考台中霧峰農業試驗所 2010 年 7 月之平均溫度 28.6℃) 及 21 世紀末三個不同暖化層級的溫度 (+1.4, 3.9, and 6.4℃)，對台灣不同地區小菜蛾的影響。結果顯示各發育階段的存活、壽命及繁殖受暖化影響，北部及南部小菜蛾幼蟲期隨暖化上升而存活率下降，但中部小菜蛾不受影響：隨暖化上升而小菜蛾壽命下降；輕度造成小菜蛾蛹之死亡率上升，但若能成功羽化為成蟲，北部及中部繁殖率沒有下降，但南部繁殖率則明顯降低；中度 (+3.9℃) 暖化下，小菜蛾存活率為 16%之下，且繁殖率明顯降低；重度 (+6.4℃) 暖化下，沒有任何族群成長到成蟲期以繁衍下一代。暖化下可能有利於中部小菜蛾卵之孵化。

關鍵詞 (Key words)：暖化 (warming)、小菜蛾 (*Plutella xylostella*)、生活史特徵 (life-history traits)

IGC07_暖化對台灣不同地區桃蚜之影響

Effects of warming on *Myzus persicae* (Sulzer) in different regions (north, central, and south) of Taiwan

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桃蚜 (*Myzus persicae* (Sulzer))是危害台灣農業蔬果花木重要的刺吸性害蟲之一，而面臨未來全球暖化的趨勢，台灣低緯度的環境下可能已經達到桃蚜所能接受的最高溫度範圍。以往溫度影響生物的研究大部分是以定溫的方式進行，但與野外的溫度變化有所誤差，因此本研究將以日溫周期性變化來設定，模擬野外實際的溫度變化，評估現今夏季平均氣溫 (參考台中霧峰農業試驗所 2010 年 7 月之平均溫度 28.6℃) 及 21 世紀末三個不同暖化層級的溫度 (+1.4, 3.9, and 6.4℃)，對台灣不同地區桃蚜的影響。結果顯示對不同地區蚜蟲的生活史特徵例如發育時間、繁殖率、若蟲存活率影響不同。北部蚜蟲無法承受不同層級的暖化，僅存的個體存活率為 10%以下，且無法繁殖。輕微暖化 (+1.4℃) 對中部蚜蟲的發育縮短 1 天，但對南部蚜蟲的發育時間平均延長 3.3 天。中度 (+3.9℃) 及重度 (+6.4℃) 暖化下蚜蟲死亡率上升，且繁殖率降低。暖化對於不同地區蚜蟲的影響，輕微暖化下可能有利於中部蚜蟲發育，反之對南部蚜蟲則不利，且對北部蚜蟲可能導致滅種；中度及重度暖化皆對蚜蟲有不利影響。

關鍵詞 (Key words)：暖化 (warming)、桃蚜 (*Myzus persicae* (Sulzer))、生活史特徵 (life-history traits)

IGC08_暖化對基因轉殖東方果實蠅之影響

Effects of warming on transgenic *Bactrocera dorsalis* (Hendel)

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東方果實蠅 (*Bactrocera dorsalis* (Hendel)) 是危害台灣果樹之重要害蟲，使果實受損腐爛，造成經濟損失。以顯微注射轉基因子 *piggyBac*，嵌入東方果實蠅卵內，進行細胞轉型作用，作為具研究價值的基因轉殖東方果實蠅。面臨未來全球暖化的趨勢，本研究模擬野外實際的溫度變化，評估現今夏季平均氣溫 (參考台中霧峰農業試驗所 2010 年 7 月之平均溫度 28.6℃) 及 21 世紀末三個不同暖化層級的暖化 (+1.4℃輕度、+3.9℃中度、+6.4℃重度) 對基因轉殖東方果實蠅的影響。結果顯示重度暖化情境下東方果實蠅無法羽化為成蟲，死亡率高達 100%。幼期發育、性比不受輕度、中度暖化影響，但基因轉殖東方果實蠅雌性比較低。由族群介量結果可得知輕度及中度暖化處理下東方果實蠅族群皆可增長，輕度暖化增長變快，中度則漸下降。轉殖族群隨暖化溫度增加而增長變慢，平均世代時間 30~32 天。暖化越明顯，對轉殖族群的不利影響大於正常族群，若將轉殖族群釋放至田間，其競爭力較野生族群弱，因此若要釋放於田間則須加以考量未來暖化的趨勢。

關鍵詞 (Key words)：暖化 (warming)、基因轉殖 (transgenesis)、東方果實蠅 (*Bactrocera dorsalis* (Hendel))、生活史特徵 (life-history traits)

BE01_Worker reproduction in the invasive yellow crazy ant *Anoplolepis gracilipes* (Hymenoptera: Formicidae)

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Among social Hymenoptera, queens are adapted for colony reproduction while workers are adapted for foraging and nest maintenance. However, in many ant species, workers always retain functional ovaries and can produce trophic eggs or unfertilized male eggs. Previous lab observation indicated the presence of physogastric workers with well-developed ovaries in both queenright and queenless colonies of yellow crazy ant *Anoplolepis gracilipes*, raising the question of the role worker reproduction plays in the colony. The present study showed that physogastric workers from artificially-orphaned colonies possess significantly greater reproductive potential than normal workers, as they are generally characterized by higher number of ovarioles, yolky oocytes per ovariole and total number of yolky oocytes. Reproduction of physogastric workers is further confirmed by production of trophic (sub-spherical) and viable eggs (elongated oval). A small proportion of viable eggs successfully developed into adult males 6 months after orphaned. Lack of spermatheca in physogastric workers, along with ploidy level assessed by microsatellite genotyping, is consistent to arrhenotoky origin of the males. Worker-produced males appear to share similar morphological characteristics with those from queenright colony, with an exception that body size of worker-produced males tends to be greater. In conclusion, we argue that physogastric workers likely represent a ‘‘caste’ specializing in storage and redistribution of protein food as eggs among colony members as most of worker-produced eggs are consumed by other nestmates. This trophic specialist may enable *A. gracilipes* colonies to survive through periods of food shortage and partially contribute to the invasion success of this invasive pest ant.

關鍵詞 (Key words)：*Anoplolepis gracilipes*、arrhenotokous parthenogenesis、invasive species、trophic eggs、worker reproduction

BE02_台灣土白蟻的多王多后初始族群在適存度及族群成長上的優勢

Advantages of multiple kings and queens in colony-founding stage of *Odontotermes formosanus* (Isoptera: Termitidae)

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白蟻的蟻巢通常具有一隻蟻王及蟻后，但在物種分布的邊界地區，多蟻王、多蟻后的蟻巢密度會增加，因此過去的研究推測多王多后的蟻巢較能適應惡劣環境，但機制仍不清楚。根據我們在台灣採集台灣土白蟻 (*Odontotermes formosanus* Shiraki) 蟻巢的紀錄，9 個蟻巢中只有 3 個是單王單后，其餘的蟻巢皆有複數的蟻王或蟻后，顯示台灣土白蟻的多王多后蟻巢相當普遍，甚至可能多於單王單后蟻巢。為瞭解多王多后蟻巢的優勢，本研究嘗試將不同數量的台灣土白蟻蟻王及蟻后在實驗室內配對、建立族群並觀察。根據 244 個 1 王 1 后蟻巢、185 個 2 王2 后蟻巢及 135 個 3 王 3 后蟻巢在13週內的觀察紀錄，2 王 2 后的蟻巢能最快產生出工蟻並具有最高的生存率 (~14%)，且其產生的工蟻及幼蟲的數量顯著高於 1 王 1 后的蟻巢，而 3 王 3 后蟻巢存活率則相當低 (~2%)。我們藉由測量白蟻屍體的體重瞭解其營養存量，並檢查屍體上觸角及足的完整性以量化個體衝突造成的傷害，發現多王多后蟻巢的個體體重下降速度較慢，在 13 週時體重顯著高於 1 王 1 后，而觸角節數減少的數量及肢體殘破的個體數量則在多王多后蟻巢較多，3 王 3 后的蟻巢顯著高於 1 王 1 后的蟻巢。統合以上結果，多王多后蟻巢能增加存活率高且產生更多子代，提升族群適存度，但過多的蟻王蟻后反而會使存活率下降，推測多王多后蟻巢總營養存量大，且能藉由合作養育幼蟲降低能量消耗，但過多的蟻王蟻后可能會增加個體之間的衝突，造成死亡。

關鍵詞 (Key words)：台灣土白蟻 (*Odontotermes formosanus*)、白蟻族群建立 (termite colony-foundation)、多蟻王制 (polyandry)、多蟻后制 (polygyny)

BE03_台灣實例證明榕屬植物可成爲螞蟻共生

Becoming myrmecophyte: revealed evidences of mutualism between ants and figs in Taiwan

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Myrmecophyte plants are extremely common in the tropics: they provide ants with food or shelter and in exchange ants protect them from herbivores. Fig trees (*Ficus*, Moraceae) are not known to belong to the myrmecophyte group. Nevertheless, 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. Moreover, we explore the latest results on fig and ant interactions on Taiwanese fig trees and show that fig trees in Taiwan display key myrmecophytic traits.

關鍵詞 (Key words)：螞蟻 (ant)、共演化 (coevolution)、榕屬植物 (*Ficus*)、榕小蜂 (fig wasp)、三方互利共生 (tripartite mutualism)

BE04_尼泊爾埋葬蟲第二性徵對種內競爭之影響

The influence of secondary sexual characteristics on intraspecific competition of *Nicrophorus nepalensis* Hope (Coleoptera: Silphidae)

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本研究探討尼泊爾埋葬蟲 (*Nicrophorus nepalensis* Hope)對於頭楯處第二性徵色斑的辨識於種內競爭的影響。實驗分為異性辨識與同性競爭，操作方式為塗佈模擬雄性性徵的橘色及雌性性徵的黑色顏料於頭楯性徵處，使存有性徵差異的個體與異性或同性競爭。異性辨識實驗中，初步測試性徵具差異的雌雄個體各15組，從接觸至交配所需的時間，不論雄雌蟲皆無差異 (Wilcoxon rank-sum test: female, $p = 0.336$; male, $p = 0.416$)；以三十秒為一單位累計交配樣本數，雖同性性徵組的時間較異性性徵組長，但尚無顯著差異 (Wilcoxon signed-rank test: female, $p = 0.056$; male, $p = 0.093$; n = 10)；異性辨識時的傷重程度及成功產下子代的比例亦沒有差異 (Wilcoxon rank-sum test: female, $p = 0.631$; male, $p = 0.327$; Fisher’s exact test: female, $p = 1$; male, $p = 1$; n = 15)。此結果顯示與生理性別不符的第二性徵於異性辨識中可能只延長了遭遇時真實性別辨識所需的時間，在較長時間下，並不對辨識的準確性有所影響。同性辨識實驗為將6隻個體同置一容器中，以食物減半的方式來增加競爭強度，經歷4、7、10天候量化統計受傷的程度，初步結果呈現在飢餓4天的狀況下，第二性徵差異產生的傷重程度，於雌、雄蟲組中皆無差異 (Wilcoxon rank-sum test: female, $p = 0.194$; male, $p = 0.195$; n = 15)，可能在短期內性徵辨識對資源競爭的影響程度不大，尚待更長期競爭下的觀察紀錄。

關鍵詞 (Key words)：尼泊爾埋葬蟲 (*Nicrophorus nepalensis*)、第二性徵 (secondary sexual characteristics)、配偶辨識 (mate recognition)、種內競爭 (intraspecific competition)

BE05_直角渫蛲築巢模式對子代發育之影響

The effect on offspring development to nesting mode in *Onthophagus rectecornutus* Lansberge (Coleoptera: Scarabaeidae)

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本研究目的是探討直角渫蛲地下甬道中糞球形成的位置與重量，是否影響子代性別與發育至成蟲所需時間，並探討糞室的深度是否影響糞球重量與發育時間。本研究將野外採集的直角渫蛲於光週期 12/12、溫度 17℃之生長箱馴化一週後，在相同環境條件下將一對直角渫蛲放入含有 100 g 糞便，30 x 15 x 0.8 cm 內部填有 20 cm 高砂土的自製觀察箱，3 日後於暗室紅光下觀察砂土內的築巢模式與糞室位置。一對糞金龜皆構築單一出口之甬道，85.7%的糞室在甬道中有獨立出口，不受其他糞室阻擋。目前初步實驗結果顯示，糞球平均長度為 2.1 ± 0.3 cm、寬度 1.3 ± 0.2 cm、重量 2.2 ± 0.5 g (n = 42)，從中羽化為雌蟲的糞球平均重量 (2.3 ± 0.5 g, n = 15)與雄蟲 (2.0 ± 0.5 g, n = 22)無顯著性差異 (independent sample *t*-test: $p = 0.129$)；糞球距離土表垂直深度為 6.5 ± 2.6 cm (n = 42)，雌蟲糞球的平均深度(5.8 ± 2.3 cm)與雄蟲 (7.1 ± 2.7 cm) 無顯著性差異 (independent sample *t*-test: $p = 0.146$)；發育所需時間則為 27.3 ± 1.4 days (n = 37)，雌蟲 (27.1 ± 1.5 days) 與雄蟲 (27.4 ± 1.4 days)亦無顯著性差異 (independent sample *t*-test: $p = 0.493$)。子代前胸背板寬平均為 4.9 ± 0.2 cm (n = 37)，子代前胸背板寬與糞球重量或發育時間皆呈現顯著相關 ($p < 0.05$)，發育時間與糞球重量亦呈現顯著相關 ($p < 0.001$)，顯示糞球越大，子代發育時間會越長，體型大小也會越大。

關鍵詞 (Key words)：直角渫蛲 (*Onthophagus rectecornutus*)、築巢模式 (nesting mode)、子代發育 (offspring development)

BE06_載卵壓力和聚集效應對於大頭金蠅產卵行為的影響

Egg load and gregarious effects on *Chrysomya megacephala* (Diptera: Calliphoridae) oviposition

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本研究主要探討載卵壓力和聚集效應對於大頭金蠅產卵行為的影響，對於死後間隔時間 (postmortem interval)的估算上能提供參考。首先是連續給予產卵刺激的情況之下，得知正常族群的個體產卵量、壽命及最小產卵間隔時間。其結果為卵量 150~200 顆/每隻、壽命 35~43 天、最小產卵間隔 10~12 天。利用正常族群所得到之生殖週期結果做為對照組，在去除聚集效應的影響下，將單隻交配過的雌蟲給予連續性的產卵刺激，記錄日齡、產卵量及壽命，目的是以日齡作為載卵壓力的量化指標，隨著時間的增加，載卵壓力隨著增大，來測試雌蟲行為反應。結果是一半以上的組別，會在持續的刺激下超過 20 天以上沒有產卵行為，至少超過兩個最小產卵間隔，推測這樣的結果有可能因為載卵壓力的影響不及聚集效應顯著，此外，在單隻雌蟲的情況下給予視覺、聽覺的刺激都有可能促進其產卵，顯示麗蠅的群聚行為才是刺激產卵的關鍵因子。

關鍵字 (Key words)：生殖行為 (oviposition behavior)、載卵壓力 (egg load)、大頭金蠅 (*Chrysomya megacephala*)、聚集效應 (gregarious effect)

BE07_臺灣索鐵線蟲寄主專一性

Host specificity of *Chordodes formosanus* (Nematomorpha: Gordiida)

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寄主專一性通常包含兩個概念：寄生蟲族群的寄主範圍，與其對不同寄主的利用程度。它們決定了寄生蟲所依賴的寄主種類，以及不同寄主對寄生蟲的相對貢獻。鐵線蟲是臺灣常見的水生寄生蟲，成蟲在水中繁殖，幼蟲寄生在水生昆蟲體內後隨其羽化而上陸，並在水生昆蟲成蟲遭到捕食後進入陸生最終寄主體內發育。大多數的鐵線蟲對於其最終寄主具有高度的專一性，僅能寄生在少數或甚至單一的種類，但少有研究探討同一種鐵線蟲對不同寄主在感染程度上的差異。目前我們已知臺灣索鐵線蟲 (*Chordodes formosanus*) 在野外的最終寄主包含臺灣斧螳 (*Hierodula formosana*)、寬腹螳螂 (*H. patellifera*)、日本姬螳 (*Acromantis japonica*) 以及纖畸螽 (*Leptoteratura* sp.) 與日本綠螽 (*Holochlora japonica*)。這些寄主體內的鐵線蟲分別在不同的季節回到水中繁殖。然而在我們針對搖蚊幼蟲的感染調查中，僅九月偵測到一個感染高峰。根據鐵線蟲卵發育的時間去推斷，這個感染高峰應由同年七至八月的繁殖所造成，而這個時間也正好是鐵線蟲離開臺灣斧螳回到水中的時間。因此我們相信，縱使臺灣索鐵線蟲能在不同種類的螳螂及螽蟴體內發育成熟，但其族群延續仍主要依賴臺灣斧螳的貢獻。這個現象可能造成感染其他寄主的臺灣索鐵線蟲在發育成熟後不易找到配偶，長期演化的結果下有可能加強其生理上對臺灣斧螳的寄主專一性。

關鍵詞 (Key words)：寄主專一性 (host specificity)、最終寄主 (definitive host)、保幼寄主 (paratenic host)、線形動物 (Nematomorpha)

BE08_寬腹斧螳性食行為的可能肇因：飢餓與時機

Hunger or timing? The possible causation of sexual cannibalistic behavior in *Hierodula patellifera* (Mantodea: Mantidae)

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性食現象主要發生於無脊椎動物，其中又以蜘蛛和螳螂的例子最廣為熟知。過去科學家以這兩類群的生物為研究材料，發展許多假說以嘗試解釋性食的演化，但眾多假說間的跨物種解釋能力極差，可能是因為假說被提出時並沒有考量各類群的演化歷史。本研究以寬腹斧螳為材料，嘗試從檢測性食的肇因 (causation) 探討斧螳屬性食的可能演化途徑。我們提出三個假說：(一) 若性食乃因雌性無法辨識同種雄性並將之視為食物，則預期雌性之攻擊行為較不受自身飽食程度之影響；(二) 若性食乃雌性辨識同種雄性失敗而將之視為食物，則預期雌性之攻擊行為將因雄性的求偶或接近行為而異，且不受雌性飽食程度之影響；(三) 若性食乃雌性可辨識同種雄性並將其視為食物，則預期雌性之攻擊行為將受雌性飽食程度或交配過與否影響。過去文獻指出雌性的飽食程度與雄性接近雌性的方向會影響性食發生與否，因此我們操控雌性飽食程度與雄性被雌性發現的時間點 (改良接近方向的參數)，觀察此複因子對於交配成功與否及雄性存亡的影響。結果發現雌性的飽食程度在本種中對於性食發生的影響遠低於雄性被發現的時間點，且易遭性食之雄性體型較小，其結果介於我們所提出的前兩個假說之間，但並不符合現有的攻擊性激增 (aggressive spillover)、掠食策略 (foraging strategy) 及致命情人 (femme Fatale) 等假說。

關鍵詞 (key words)：性食 (sexual cannibalism)、性食行為 (sexual cannibalistic behavior)、寬腹斧螳 (*Hierodula patellifera*)

IR01_二化螟乙醯膽鹼酯酶的大量表現與純化

Expression and purification of acetylcholinesterase of *Chilo suppressalis*

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乙醯膽鹼酯酶 (acetylcholinesterase) 是分解與調節乙醯膽鹼傳導系統的重要酵素，因此經常成為有機磷及胺基甲酸鹽類殺蟲劑防治有害生物的首要標的。然而長期使用這些防治藥劑已使得多種害蟲對其產生抗藥性。本實驗室已證實二化螟 (*Chilo suppressalis*) 乙醯膽鹼酯酶之 A314S、R667Q、H668P 點突變與加保扶抗藥性有關。因此，本研究進一步利用昆蟲桿狀病毒表現系統 (baculovirus expressing vector system) 大量表現二化螟乙醯膽鹼酯酶，並以親和性管柱進行純化，再分析其活性及藥劑抑制情形。目前已經順利表現二化螟野生型乙醯膽鹼酯酶，並收集約 60 mg 之蛋白，初步未純化的蛋白液活性約為 1.024 μmol/min/mg；未來將對此表現蛋白進行純化，並檢測純化乙醯膽鹼酯酶的比活性 (specific activity) 與防治藥劑的半抑制濃度 (half inhibition concentration)。

關鍵詞 (Key words)：二化螟 (*Chilo suppressalis*)、乙醯膽鹼酯酶 (acetylcholinesterase)、昆蟲桿狀病毒表現系統 (baculovirus expressing vector system)、純化 (purification)、比活性 (specific activity)、半抑制濃度 (half inhibition concentration)

IR02_小菜蛾代謝相關抗藥性基因之功能性分析

Functional analysis of metabolic related pesticide resistant genes in *Plutella xylostella*

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小菜蛾抗藥性問題為十字花科蔬菜作物栽培管理之重要議題。在先前的研究中，我們以採集自彰化溪湖地區的田間小菜蛾為抗藥性品系篩選的蟲源，接著使用剋胺勃、氟大滅、脫芬瑞與因滅汀四個農藥分別進行藥劑篩選，得到對上述四個藥劑分別產生抗藥性的四個抗性品系。之後我們利用次世代定序技術對這四個抗性品系進行轉錄基因體分析並且和對照組的感性品系與第一代田間蟲源比較，找出差異表現基因。為了瞭解這些差異表現基因的功能性，我們挑選了九個和農藥代謝有關的差異表現基因，希望利用 RNA 干擾的技術使目標基因表現量下降，並且瞭解其表現量的改變是否直接影響到小菜蛾對殺蟲劑的感受性。我們嘗試了餵食與注射兩種方式給予小菜蛾雙股 RNA (dsRNA)，但是經由即時定量 PCR 的分析卻無法觀察到標的基因表現量明顯下降的現象。另一方面，我們利用轉基因的方式於阿拉伯芥表現小菜蛾基因之 dsRNA，希望藉由餵食小菜蛾阿拉伯芥葉片的過程，使 dsRNA 進入小菜蛾蟲體並引起基因靜默的現象。目前我們已經利用北方雜合分析的方法，篩選到有成功表現小菜蛾基因 dsRNA 的阿拉伯芥轉基因植株 (F1)，餵食小菜蛾表現 dsRNA 之阿拉伯芥及後續造成 RNAi 效果並且對基因表現量與藥劑敏感性影響的實驗正在進行中。

關鍵字 (key words)：小菜蛾 (diamond back moth, DBM)、RNA 干擾 (RNA interference)、抗藥性 (insecticide resistance)

IR03_以轉錄基因體探討細胞色素 P450 與東方果實蠅有機磷抗性之關聯

Understanding the relationship of Cytochrome P450 in Organophosphate resistance of *Bactrocera dorsalis* through transcriptome data

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細胞色素 P450 (cytochrome P450, CYP) 是生物體內最重要的代謝酵素之一，除了進行生物體重要的代謝功能外，更是在昆蟲對殺蟲劑產生抗藥性的機制上扮演重要角色。因此，透過實驗室長期以來建立對有機磷類 (organophosphates) 殺蟲劑具有抗藥性的東方果實蠅 (*Bactrocera dorsalis* (Hendel)) 抗性品系以及對殺蟲劑具有高敏感性的感性品系來了解細胞色素 P450 與有機磷類殺蟲劑抗藥性的關聯。利用次世代定序技術 (Next generation sequencing, NGS) 來獲得東方果實蠅抗性和感性體內的 P450 的轉錄體資訊，分析並比較抗性品系與感性品系轉錄體的 RPKM (Reads Per Kilobase per Million mapped reads)，以抗性和感性之間 RPKM 值相差大於 8 倍以上為挑選條件，結果共有 23 條轉錄體符合條件，透過和 NCBI 的資料庫比對，這些轉錄體分別屬於 6 個不同的 P450 基因。利用定量即時聚合酶鏈鎖反應 (Quantitative real time polymerase chain reaction, qPCR) 來比較這 6 個 P450 基因於抗性及感性品系之間的表現量差異。其結果顯示，這 6 個 P450 基因在抗性品系的表現量皆大於感性品系，其中有 4 個基因具有 2 倍以上的表現量差異，而表現量差異最大者可達 18 倍，表示該基因和抗藥性具有高度相關性，往後將會對該基因的功能進行研究。

關鍵詞 (Key words)：東方果實蠅 (*Bactrocera dorsalis*)、代謝抗性 (metabolic resistance)、細胞色素 P450 (cytochrome P450)、NGS (next generation sequencing)

IR04_利用 RNA 干擾探討東方果實蠅 (*Bactrocera dorsalis*) 穀胱甘肽硫轉移酶對有機磷類藥劑抗性相關性

Using RNA interference to study the role of glutathione S-transferase genes in organophosphate resistance in *Bactrocera dorsalis*

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東方果實蠅 (*Bactrocera dorsalis*; Diptera: Tephritidae) 為台灣重要果樹害蟲，目前確認對有機磷類藥劑產生抗性，穀胱甘肽硫轉移酶 (glutathione S-transferase, GST) 與有機磷劑的抗藥性在其他昆蟲中已被證實。但由於東方果實蠅並非模式物種，無基因體序列，因此在分子層次上的研究較難著手。本研究運用次世代定序 (next generation sequencing) 技術，獲得大量有潛在表現的可能序列，並由感性及對不同機磷劑抗性東方果實蠅品系的定序資料中，挑選出在個別抗性品系及感性品系 RPKM (reads per kilobase per million) 比值具有差異的 GST 轉錄子 (transcripts)，利用定量即時聚合酶鏈鎖反應確認差異表現。將有差異表現的 GST 轉錄子以軟體設計 RNA 干擾所需的 dsRNA 片段，以微針注射的方式進行 RNA 干擾功能性分析，同時以定量即時聚合酶鏈鎖反應進行基因表現量分析，並以局部滴定法驗證感受性，以瞭解穀胱甘肽硫轉移酶對有機磷類藥劑的抗性相關性。

關鍵詞 (Key words)：東方果實蠅 (*Bactrocera dorsalis*)、穀胱甘肽硫轉移酶 (glutathione S-transferase)、有機磷劑 (organic phosphates)、次世代定序 (next generation sequencing)、RNA 干擾 (RNA interference)

IR05_台灣地區小菜蛾的抗藥性調查及對因滅汀之抗藥性遺傳研究

Investigation of insecticide resistance and inheritance of emamectin benzoate resistance in diamondback moth, *Plutella xylostella*, in Taiwan

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小菜蛾 (*Plutella xylostella* L.) 為十字花科蔬菜的主要害蟲之一。為了減緩小菜蛾抗性發展的速度與延長防治藥劑的使用年限，目前多以輪用不同作用的機制藥劑作為小菜蛾抗藥性管理的主要策略。了解目前田間小菜蛾對防治藥劑的抗藥性發展趨勢與抗藥性遺傳機制，則是落實抗藥性管理策略的第一步。本研究首先利用先前建立之 SH_{ggt} 感性品系做為對照組，檢測 2013 至 2015 年間採自台灣 6 個十字花科蔬菜產區的小菜蛾對 10 種田間用藥的抗藥性情形。結果顯示田間小菜蛾對因滅汀與芬普尼的抗藥性普遍高於 50 倍;對於剋安勃與美文松的抗藥性則介於 10–20 倍之間；所有調查區小菜蛾對賜諾殺抗藥性皆在 10 倍以下。其次建立抗因滅汀的小菜蛾品系，即以因滅汀篩選草屯品系至千倍抗藥程度，再與 SH_{ggt} 感性品系進行互交、回交與自交，研究異型合子子代對因滅汀的抗藥性遺傳性狀。分析相關結果發現互交子代 F1 (草屯篩選♂ x SH_{ggt}♀) 與 F1’ (草屯篩選♀ x SH_{ggt}♂) 的半致死劑量分別為 14.9 與 12.3 μg/ml，顯性度則為 0.81 及 0.76，顯示小菜蛾對因滅汀的抗藥性是不具母體效應的不完全顯性遺傳性狀。從 F1 與感性親代回交的子代或 F1 自交的 F2 子代之對機數劑量反應曲線 (log concentration - probit) 皆未呈現椅形平台，以及卡方檢測不符合單基因遺傳模型的情況可推知小菜蛾對因滅汀的抗藥性由多個基因控制。而本研究也發現抗因滅汀小菜蛾在沒有藥劑的篩選壓力下，抗藥性下降十分快速，在 10 個世代中抗藥性從 412 倍降至 22 倍。初步以添加協力劑來探討解毒酵素是否參與因滅汀的抗藥性機制，結果發現添加胡椒丁基氧化物 (Piperonyl butoxide) 可使抗因滅汀品系的半致死濃度下降了一半，顯示細胞色素 P450 單氧化酶可能參與部分小菜蛾對因滅汀的抗藥性。

關鍵詞 (Key words)：小菜蛾 (*Plutella xylostella* L.)、因滅汀 (emamectin benzoate)、抗藥性 (resistance)、抗藥性遺傳機制 (inheritance of resistance)

IR06_小菜蛾對美文松抗藥性機制研究

Mechanism of mevinphos resistance in diamondback moth, *Plutella xylostella*

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小菜蛾 (*Plutella xylostella*) 對十字花科蔬菜作物的危害嚴重，在田間常應用化學合成藥劑或微生物製劑防治，但由於生長世代短，抗藥性產生的速度十分快速。抗藥性的機制多樣，除了表皮增厚，藥劑進入蟲體的量降低之外，還包含作用部位不敏感及解毒酵素的作用。本研究探討小菜蛾對美文松抗藥性遺傳特性與抗藥性機制，利用實驗室先前發現與美文松抗藥性相關、具有 A298S、G324A 與 F386V 胺基酸置換的乙醯膽鹼酯酶 (acetylcholinesterase 1, AChE1) 建立攜帶野生型 AChE 的感性 $96C_{ggt}$ 品系與具抗性基因異型合子的 $96C_{NNN}$ 品系，並持續以美文松篩選 $96C_{NNN}$ 品系，再利用此二品系進行生物檢定與突變頻度分析，觀察抗性倍率與基因突變頻度之相關性。另外也進行協力試驗與解毒酵素活性試驗，觀察各個解毒酵素在小菜蛾對美文松抗藥性的參與程度。目前結果發現抗性發展在特定程度與 AChE 基因突變頻度有相關性，而在此特定抗性程度之外則可能與解毒酵素的活性增加有關，因此後續將針對解毒酵素進行研究。

關鍵詞 (Key words)：小菜蛾 (*Plutella xylostella*)、美文松 (mevinphos)、胺基酸置換 (amino acid substitution)

IR07_聖多美普林西比民主共和國岡比亞瘧蚊種群之抗藥性分析

Knockdown resistance (*kdr*) analysis of a new member of *Anopheles gambiae* complex-*Anopheles coluzzii* in Democratic Republic of Sao Tome and Principe

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Democratic Republic of Sao Tome and Principe (DRSTP) is an island nation located in the central west Africa. Malaria transmitted by *Anopheles coluzzii* (formerly named *Anopheles gambiae* M form) has been considered to be the major vector in DRSTP. Following WHO’s recommendations, indoor residual spraying (IRS) and long-lasting insecticidal nets (LLINs) are promoted as the primary vector control strategies in high prevalent area in Africa. According to Tseng et al. (2008), DRSTP had completed a three-year program of IRS with alphacypermethrin at a dosage of 50 mg/m^2 since 2004. Till 2010, alphacypermethrin was continuing applied as a tool for controlling mosquitoes. It is believed that combination of IRS and LLINs would increase frequency of knockdown resistance (*kdr*) which is attributed to mutation in voltage-gated sodium channel gene. However, the information of *kdr* among the malaria vector in DRSTP was lacked. In this study, mosquitoes were collected by human landing catch and light traps at 15 collection sites distributed in 6 provinces of Sao Tome and an autonomous region of Principe from 2010 to 2015. Identification of *Anopheles* species was conducted by morphological and molecular methods. Totally 2,115 *Anopheles* mosquitoes’ DNA were extracted and followed by PCR, sequencing and sequence blast. The frequency of *kdr* mutation was calculated according to the formula “F = 2RR + RS/2n” (RR = resistant homozygotes; RS = heterozygotes; n = sample size). Results showed that the *kdr* mutation of *An. coluzzii* in DRSTP was L1014F (west African *kdr* mutation, *kdr-w*), and the frequency of *kdr* mutation were 0.10, 0.50, 0.52, 0.72, 0.40, 0.32 in the year of 2010, 2011, 2012, 2013, 2014, 2015, respectively. This study represents the importance of monitoring the molecular insecticide resistance while routinely applying IRS and LLINs in DRSTP. Future control strategy should be transformed based on *kdr* data and considered with mosquito density.

關鍵詞 (Key words)：岡比亞瘧蚊種群 (*Anopheles gambiae* complex)、聖多美普林西比民主共和國 (Democratic Republic of Sao Tome and Principe)、室內殘效噴灑 (Indoor residual spraying)、長效型浸藥蚊帳 (Long-lasting insecticidal nets)、抗藥性 (Knockdown resistance)

IR08_褐飛蝨及白背飛蝨族群對不同抗性基因水稻之致害性表現

Virulence of brown planthopper (*Nilaparvata lugens* (Stål)) and whitebacked planthopper (*Sogatella furcifera* Horváth) to rice varieties with different resistant genes

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褐飛蝨及白背飛蝨為台灣重要水稻遷移性害蟲，經常群集吸食水稻植株可迅速造成植株枯萎 (蝨燒)，影響水稻產量甚鉅。抗蟲品種為主要防治方法之一，但長期利用同一抗蟲基因之品種，也容易導致少數能適應之個體，經繁殖而逐漸取代原來之族群，俗稱有害生物小種 (biotype)，致使原有抗性品種失去功效。本研究利用不同抗性基因水稻品種進行褐飛蝨抗性檢定表現，於秧苗期檢定 (SSST, Standard seedbox screening test) 情形，結果表現具有抗級 (5 級以下) 之抗性基因有 *Bph3* (IR60), *bph4* (Babawee), *Bph6* (Swarnalata) 及 *Bph10* (IR65482-4-136-2-2)；另外進行成株期檢定 (MSST, Modified seedbox screening test) 情形，結果表現具有抗級 (5 級以下) 之抗性基因有 *Bph3*, *bph4*, *bph6*, *bph9* (Pokkali) 及 *Bph10*；另外分析具有兩個抗性基因之品種，且對秧苗期抗生性及成株期容忍性檢定均具有良好表現者，分別為 *bph2* + *Bph3* (Ptb33), *Bph3* + *bph17* (Rathu Heenati), *Bph20* + *Bph21* (IR71033-121-15) 及 *bph25* + *Bph26* (ADR52)。於秧苗期及成株期檢定對白背飛蝨抗性檢定之結果，表現具有抗級 (5 級以下) 之抗性基因有 *Wbph2* (ARC 10239), *Wbph3* (ADR 52), *Wbph4* (ARC 6650) 及 *Wbph5* (N‘Diang Marie)。為防範此兩種飛蝨可能帶來之嚴重危害，抗蟲育種研究應朝選用目前尚具抗性之基因進行，同時避免選汰壓力過大，導致適應在抗性品種上之生物小種出現。品種選育應以中等抗性品種或由數量遺傳因子所支配之水平抗性品種，較可持久應用於水稻害蟲綜合防治體系。

關鍵詞 (Key words)：褐飛蝨 (*Nilaparvata lugens*)、白背飛蝨 (*Sogatella furcifera*)、抗性基因 (resistant gene)

PC01_日本與臺灣產白粉蝶 (*Pieris rapae*) 於相同溫度梯度下之生長表現

A comparison of the thermal performance of *Pieris rapae* collected from Japan and Taiwan

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To predict climate change impact on species at large scale, we need to first understand the plasticity and genetic diversity of species across spatial gradients. This intraspecific study is aimed to examine the plasticity and genetic variation in the thermal performance of *Pieris rapae* (cabbage butterfly) across latitude, using populations collected from 2 and 3 sites in Japan (Kyoto area) and Taiwan (Taipei area), respectively, in the first project year (2015). Female *P. rapae* were collected from the field sites and laid eggs in laboratory conditions. The newly hatched larvae were haphazardly assigned into one of six growth chambers (15.5, 18.5, 21.5, 24.5, 27.5, 30.5˚C) with a 12:12 photoperiod. We fed the larvae with common garden cabbages and recorded their performance in both larval and adult stages. The results showed that Japan populations across temperatures generally had a longer larval period, heavier pupa and adult fresh weight, and longer forewing length, suggesting a genetic difference between Japan and Taiwan populations. The results also showed a temperature-latitude (Japan vs. Taiwan) interaction, suggesting a difference in the shape of thermal performance curve (i.e., plasticity) between Japan and Taiwan populations. In addition, Japan populations, but not Taiwan ones, could diapause as pupae at 15.5, 18.5, and 21.5˚C, suggesting a difference in phenology or life history strategy between populations. Our study demonstrates that populations of the same species across latitude may differ plastically and genetically in thermal performance. Therefore, climate change impact assessment may need to treat a population, instead of species, as a single unit.

關鍵詞 (Key words)：climate change、diapause、*Pieris rapae*、spatial gradient、thermal performance

PC02_mir-100 表現量過低的原因及其對果蠅發育所造成的影響

The cause and effects of mir-100 hypo-expression in Drosophila development

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MicroRNAs (miRNAs) are 21~23nt long RNAs, which regulate gene expression at post-transcriptional level by inhibiting the translation of target mRNAs through complementary pairing. Clustered miRNAs, such as let-7-C, are suggested to exhibit coordinate expression via a polycistronic transcription. Let-7-C, consisting of *mir-100*, *let-7*, and *mir-125*, is increasingly expressed at larva-to-pupa transition in *D. melanogaster*. However, the expression level of *mir-100* is found to be lower than that of *let-7* and *mir-125* in Canton S strain as well as that of *mir-100* in other strains in previous study. In this study, we investigated the cause and the effects of low expression level of mir-100 in Canton S from UCI (CS-UCI) by using Oregon R (OR) and Canton S from Pi lab (CS-Pi) as control strains. In qRT-PCR experiments, the expression level of mir-100 was confirmed to be lower in CS-UCI but surprisingly higher in CS-Pi as in OR. A series of PCR experiments in genomic DNA revealed the presence of a flea element"at intergenic region between mir-100 and let-7 in CS-UCI but not in CS-Pi, suggesting the lower expression level of mir-100 may result from this insertion. From our preliminary test, CS-UCI pupae showed significantly lower survival rate at 30℃ in comparison of the other two strains, suggesting mir-100 may be involved in buffering heat stress during pupal development. The detail molecular mechanism on low expression level of mir-100 and its phenotypic effects in Drosophila development are under further investigation.

關鍵詞 (Key words)：微RNA (microRNAs)、集族 (clustered)、*mir-100*、let-7 複合物 (let-7-Complex)、果蠅發育 (*Drosophila* development)

PC03_Walk with butterflies? Evaluating city sidewalks as habitat for *Pieris* butterflies

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Human development rapidly increases the size of urban areas. A number of studies have evaluated urban environment (e.g., parks) as habitat for wildlife; however, few have examined the role of sidewalks. Given that sidewalks are a common component of cities worldwide (e.g., about 900 km long or 1% area in Taipei city), we investigated whether sidewalks in an interactional city (e.g., Taipei) can be suitable habitat for wildlife (e.g., *Pieris* butterflies). Our study included these experiments: 1) To understand the temporal and spatial variation in food resource, we conducted monthly surveys on the host plants of *Pieris* on Taipei sidewalks (N=60). 2) To examine whether *Pieris* would inhabit sidewalks, we conducted daily surveys on *Pieris* density on sidewalks during *Pieris* seasons. 3) To test the quality of sidewalks as *Pieris* habitat, we raised *Pieris* larvae in both sidewalk and natural habitats. Abiotic factors in both habitats were recorded to examine their impact on *Pieris* performance. 4) To understand the factors contributing to *Pieris* mortality, we placed *Pieris* eggs and artificial *Pieris* larvae in sidewalk and natural habitats. The first year results showed that *Pieris* actually inhabited sidewalks in April and May (Exp 2). *Pieris* egg density was higher in natural than sidewalk habitat. However, *Pieris* population peaked earlier in sidewalk than natural habitats, which will be further verified by our second year study. Consistently, *Pieris* larvae developed faster in sidewalk than natural habitats (Exp 3), likely due to the higher temperature on sidewalks. In addition, *Pieris* eggs seemed to face a lower mortality in one sidewalk than its adjacent natural habitat (Exp 4), although more replicates will be needed. Our results suggest that sidewalks may serve as an underappreciated habitat for wildlife such as *Pieris* butterflies.

關鍵詞 (Key words)：herbivory, *Pieris*, urban ecology

PC04_入侵植物（大花咸豐草）如何在不同海拔影響本土植物（葶藶）和相關蝴蝶?

How does an invasive plant (*Bidens pilosa* var. *Radiata*) affect a native plant (*Rorippa indica*) and associated butterflies (*Pieris* spp.) across altitude?

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Plant invasion, a global concern, can abruptly change invaded communities. However, little is known about how invasive plants directly and indirectly affect native plants across spatial gradients, and how this might create cascading effects on associated arthropods. To answer these questions, we examined an invasive plant (*Bidens pilosa* var. *Radiata*; hereafter *Bidens*), a native plant (*Rorippa indica*; hereafter *Rorippa*), and associated *Pieris* butterflies across altitude (100 and 1000 m). *Pieris* are pollinators of *Bidens* but herbivores of *Rorippa*. We conducted field and laboratory experiments: 1) To explore the field relationship between *Bidens* and *Rorippa*, we surveyed their plant height vs. distance across altitude. 2) To examine the interaction between *Bidens* and *Rorippa*, we conducted a laboratory competition experiment and measured plant performance in the *Bidens* alone, *Rorippa* alone, and *Bidens-Rorippa* treatments. 3) To identify the direct effect of *Bidens* on *Rorippa*, we performed a shading x root contact experiment in laboratory. Soil chemicals were analyzed. 4) To identify the indirect effect of *Bidens* on *Rorippa*, we examined how the distance between these two plants would affect *Pieris* oviposition on *Rorippa* across altitude. 5) To understand whether the impact of *Bidens* on *Rorippa* would have a cascading effect on *Rorippa*’s herbivores, we raised and monitored *Pieirs canidia* on *Rorippa* with or without *Bidens* competition. Both plants were collected from each altitude. Our preliminary results showed that the invasive *Bidens* suppressed the native *Rorippa* across altitude (Exp.2), contributed by the direct effects of *Bidens* roots on *Rorippa* (Exp.3). There were more *Pieris* eggs on *Rorippa* close to *Bidens* at low altitude (Exp.4), suggesting an indirect effect of *Bidens*. *Bidens* impact on *Rorippa* reduced *P. canidia* performance (Exp.5), indicating a cascading effect of plant invasion. Our upcoming analysis will help better understand the impact of plant invasion on invaded plant-animal communities across altitude.

關鍵詞 (Key words)：altitude, *Bidens pilosa*, invasive plant, oviposition, *Pieris* species

PC05_台灣菌蠹蟲與線蟲族群關係之研究

Nematode population associating with ambrosia beetles in Taiwan

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The purpose of this research is to investigate the ambrosia beetle associating-entomopathogenic nematode populations in their origins, study the pest-host interactions for putative biological control applications. Several ambrosia beetles are causing serious damages in forests and economic crops such as avocado in the United States. Entomopathogenic nematodes have been known for their ability of effective parasitism and could serve as biological control agents against specific ambrosia beetles. In this study, 358 ambrosia beetles of 10 genera in forests and orchards were collected through 18 filed sampling at 11 locations in Taiwan. A total of 12703 nematodes were harvested from beetle cadavers along with their habitat wood, measured and recorded morphologically under compound microscopes, and identified molecularly by sequences of multi-regions of genes. Phylogenetic analysis revealed 4 genera of nematode populations, including *Acrostichus sp.*, *Deladenus sp.*, *Koerneria sp.* and *Sphaerularia sp.*, are specifically associating with 6 genera of ambrosia beetles: *Cnestus sp.*, *Eccoptoterus sp.*, *Euwallacea sp.*, *Scolytoplatypus sp.*, *Xyleborus* sp. and *Xylosandrus sp.* This is the first population study of entomopathogenic nematodes and ambrosia beetles in Taiwan.

關鍵詞 (Key words)：菌蠹蟲 (ambrosia beetle)、蟲生線蟲 (entomopathogenic nematode)

PC06_光敏試劑對多種昆蟲細胞的胞殺影響與其對蚜蟲成蟲的效果之研究

The influence of photosensitizers treated on several insect cells and effects on adult aphids

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光敏試劑，能透過照光激發產生過氧化物，其藉自由基與細胞結合進而誘發細胞凋亡。本研究探討光敏試劑作用於不同昆蟲種類細胞誘發細胞凋亡之程度，並將光敏試劑加入糖水，以膜餵養的方式供蚜蟲吸食，觀察實驗組相較於對照組的死亡數比例，以期光敏試劑未來能作為防治害蟲的方式之一。數種光敏試劑－PC3、PC4 與 BPDZM 在不同濃度 (藥劑/培養液=1/100、1/1000) 下作用於數種昆蟲細胞－Sf21 (斜紋夜蛾，*Spodoptera litura*)、S2 (黃果蠅，*Drosophila melanogaster*) 與 *Culex* (家蚊)，照光處理一小時，並靜置於室溫黑暗環境下 24 小時後，觀察得實驗組的細胞死亡率皆明顯高於對照組，其中又以 1/1000 的死亡率最高。但膜餵養於蚜蟲方面，則以攝入 PC4 的蚜蟲有顯著的死亡率，其餘與對照組相比則無明顯差異。

關鍵詞 (Key words)：細胞凋亡 (apoptosis)、膜餵養(membrane feeding)、光敏試劑 (photosensitizers)

PC07_如何展示後翅眼紋才能獲得最佳的禦敵效果？

How to exhibit the hindwing eyespots to get the best anti-predator defense?

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「眼紋」是一種與環境背景對比強烈的警戒訊號，具有防禦天敵的功能。這個訊號廣泛存在於各動物類群，而鱗翅目昆蟲的眼紋型式與展現方式尤其多樣複雜。過去眼紋相關研究多以日行性蝶類為目標，且鮮少重現不同的眼紋展示方式。夜行性並具有眼紋的天蠶蛾具有兩種眼紋展現方式：(1) 平時便持續展示眼紋；(2) 平時遮蓋眼紋直到受驚擾時才突然展示。此外天蠶蛾眼紋的尺寸、形狀、複雜度都具有高度多樣性，我們認為使用牠們檢測展示警戒訊號對天敵掠食行為的影響，可以得知不同天蠶蛾類群的防禦策略與眼紋多樣性的關聯性。我們擇翅面底色相對簡單的 *Caligula japonica* 為範本製作前翅可人為控制的假餌，以此模擬天蠶蛾受驚擾時的展示眼紋行為。我們將假餌分別呈現給白腰鵲鴝與白尾八哥，藉由比較不同展示行為下，鳥隻當下的反應及再度攻擊假餌的行為，推測不同展示眼紋方式對天敵掠食行為的影響程度。結果以突然展示後翅眼紋效果最強，能造成白尾八哥短時間內不再靠近假餌。而單純展示行為雖然能在當下使兩種鳥類受到驚嚇，但展示後沒有眼紋的狀況下，鳥隻會再度嘗試攻擊。這樣的檢測方式比起使用固定式假餌更能反應真實現況，也較能提供推測眼紋多樣性，以及各類群天蠶蛾防禦策略演化的生態學基礎。

關鍵詞 (Key words)：眼紋 (eyespot)、威嚇效果 (startling effect)、活動式假餌、天蠶蛾 (Saturniidae)、展示行為

PC08_較低的蝶翅摩擦力是否有利逃離掠食者的攻擊？

Does lower friction of butterfly wing help in escaping from predator?

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蝶翅表面為鱗片所覆蓋，而鱗片的形狀、排列密度與型式，與表面微細結構則決定了表面摩擦力的大小。我們預測較高的翅表摩擦力會使得蝴蝶較容易被天敵捕食，而反之則容易逃脫天敵的攻擊。此外，若較小的翅面摩擦力的確可降低天敵攻擊，增進逃脫能力，或許有可能因此對天敵產生警訊，甚至誘發逃脫型擬態的演化。為了檢驗這個概念，我們使用藍紋鋸眼蝶 (*Elymnias hypermnestra hainana*) 為材料。經過長期的田野觀察，我們發現藍紋鋸眼蝶經常被鳥類攻擊，但是通常只有後翅受損而不危及生命。然而藍紋鋸眼蝶缺乏一般眼蝶具有的亞外緣眼斑，因此理論上應該無法誤導天敵攻擊，因此我們懷疑藍紋鋸眼蝶或許具備較佳的逃脫能力，並與翅面磨擦力有關。我們首先度量藍紋鋸眼蝶與其它共棲與近緣蝶種的翅表面摩擦係數；其次使用掠食試驗來檢測鳥類是否會主動選擇翅表磨擦係數較大的蝶種。由於逃脫型擬態這個概念甚少由實驗檢測，而過往的研究也僅著重於獵物的飛行速度，因此這個研究將可提供逃脫型研究是否存在的物理性證據。

關鍵詞 (Key words)：鋸眼蝶屬 (*Elymnias*)、紫斑蝶屬 (*Eupolea*)、掠食行為 (predation)、摩擦力 (friction)、逃脫型擬態 (evasive mimicry)

PC09_組織胺感受性氯離子通道於柑橘鳳蝶視覺系統中的免疫電顯定位

Immunoelectron microscopic localization of histamine-gated chloride channels in the visual system of *Papilio xuthus*

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Histamine is the only neurotransmitter so far identified in insect photoreceptors. Histamine-gated chloride channels have therefore, been assumed to be involved in the hyperpolarization of the second order visual neuron, lamina monopolar cells (LMCs) upon photoreceptor excitation. The present study provides the first anatomical evidence at electron microscopic (EM) level to support such distribution profile. We conducted immunolocalization on two candidates of histamine-gated chloride channels, PxHClA and PxHClB, in the visual system of the butterfly *Papilio xuthus*. In order to confirm that the candidate molecules exist postsynaptic to photoreceptors, we injected Lucifer Yellow (LY) into retina for tracing of photoreceptor axons. We subsequently carried out EM double labeling in which anti-PxHClA or anti-PxHClB was visualized with pre-embedding DAB staining while LY-injected photoreceptors were detected with post-embedding anti-LY immunogold labeling. In the lamina, the anti-PxHClA immunoreactivity is associated with the plasma membrane of non-photoreceptor neurons, suggesting that PxHClA is responsible for synaptic transmission at the photoreceptor-LMC synapse. We also found that photoreceptors are immunopositive to anti-PxHClB, indicating a possible role of this molecule in interphotoreceptor communication.

關鍵詞 (Key words)：蝴蝶 (butterfly)、免疫組織化學 (immunohistochemistry)、視葉 (optic lobe)、突觸 (synapse)、視覺 (vision)

PC10_物聯網技術應用於蟲害管理之研究：以東方果實蠅為例

Application of Internet of Things on pest management: A case study of *Bactrocera dorsalis*

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本研究以物聯網技術開發一套東方果實蠅 (*Bactrocera dorsalis*) 族群調查系統，可同時監測氣溫與相對溼度，每 30 分鐘收集一次資料，再以 GSM (Global system for mobile communications) 技術無線遠端回傳於後端資料庫中。本系統佈建於臺南市南化區一處愛文檬果園中 (N23°03'34.4", E120°29'52.1"，占地面積約 2700 m^2)，監測期間為 2015/6/12 ~ 6/ 24。監測期間內共收集 3197 筆資料，其中具有蟲數據之資料為 867 筆，共計得 6832 隻。根據所得資料顯示，東方果實蠅於檬果園出現的時段，主要為清晨 (4am ~ 8am)，其次為黃昏 (4pm ~ 8pm)、上午 (8am ~ 12pm) 與下午時段 (12pm ~ 4pm)，捕獲之蟲數分別為 5132、1147、315 和 238 隻。東方果實蠅於各出現時段之平均氣溫與相對溼度，清晨、上午、下午與黃昏分別則為 31.77 ± 3.65、38.06 ± 1.95、37.58 ± 2.38 和 34.20 ± 3.03 °C 以及 67.45 ± 13.99、46.94 ± 6.92、50.96 ± 10.22 和 59.51 ± 13.18 %RH。其中，不論是蟲數、氣溫和相對溼度，清晨時段相較於其他時段具有顯著差異($P < 0.05$)，若再進一步分析氣溫與相對溼度是否對於蟲數有交互作用，則發現氣溫對於蟲數之影響具顯著性 ($P < 0.05$)，蟲數則隨氣溫升高而減少。另一方面，相對溼度對於蟲數之影響則不具顯著性 ($P > 0.05$)，而氣溫與相對溼度對於蟲數之交互作用亦不顯著。本研究結果顯示，透過此開發之系統可於果園即時監測東方果實蠅蟲數，配合系統同時收集的微氣候資訊進行統計分析之結果，將可提供農民最佳防治時機之建議與蟲害管理策略擬定之參考。

關鍵詞 (Key words)：物聯網 (Internet of Things)、東方果實蠅 (*Bactrocera dorsalis*)、蟲害管理 (pest management)

PC11_時間稽延神經網路應用於蜂群預測之研究

A time delay neural network on the prediction of honey bee colony activity

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開花植物是目前人類不可或缺的食物來源之一，而大多數的開花植物又需經由蜜蜂協助授粉，除了開花植物之外，自然界中也有許多植物必須依賴蜜蜂進行授粉，因此，蜜蜂無疑是自然界中最重要的授粉者之一。然而，近年來蜜蜂因不明原因消失的情況在世界各地陸續發生，經過調查，證實蜜蜂消失原因為工蜂因無法回巢而死亡，此現象被稱為蜂群崩潰失調症。本研究的主要目的為開發一套估測蜂群每日活動力的預測模型。首先，架構出一即時蜂箱監測系統，記錄蜂群行為與環境溫度。模型部分則採用外部輸入非線性自動回歸模型之時間稽延神經網路進行訓練。此外，本研究之研究時間規劃成五個滑動視窗，每個滑動視窗又各自分為樣本內配適資料 (訓練資料) 及樣本外預測資料 (測試資料) 滑動，時間長度則為四週。研究針對所有樣本內資料配適適當的稽延神經網路預測模型，並評估模型對樣本外資料之預測績效。根據預測誤差及均方誤差比較後，本模型之預測準確率約為85%。本研究旨在開發蜂群的行為預測模型，提供蜂農及研究人員一可靠的預測數據，以利其在蜂群開始凋亡前進行相關的防範及補救措施。

關鍵詞 (Key words)：蜂群出入巢行為 (activities of honey bees entering and leaving the beehive)、時間稽延神經網路 (time delay neural network)、外部輸入自動回歸模型 (NARX model)、蜂群行為監測系統 (honeybee behavior monitoring system)

PD01_二點葉蟎 (*Tetranychus urticae*) 於台灣夏季自然變溫下之族群特性

Population characteristic of *Tetranychus urticae* (Acari: Tetranychidae) under naturally fluctuating temperature in Taiwan's summer

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二點葉蟎 (*Tetranychus urticae* Koch) 為台灣田間常見害蟎之一，全年皆可發現其危害多種重要經濟作物。因其具有孤雌產雄 (arrhenotoky) 及有性生殖 (zoogamy) 兩種繁殖模式，能於短時間內由單一雌蟎建立族群，而其增長速度會受到溫度的影響，面對全球暖化，可能加速害蟲猖獗的議題，本研究擬針對夏季高溫之自然變溫下，二點葉蟎在花豆 (*Phaseolus coccineus* L. var. *albonanus* Bailey) 葉片上之族群增長特性進行分析。同時以兩性生命表為基礎，利用 TwoSex-MSChart 及 Timing-MSChart 比較該族群增長特性於室外變動溫度下與恆溫生長箱內之差異，以探討其田間發生情形及防治時機。結果顯示二點葉蟎在自然變溫 (29.0°C ~36.2°C, 平均 31.7°C) 及定溫 (32 ± 1°C) 時，成蟎前期分別為 6.3 ± 0.07 及 6.4 ± 0.04 日，雌、雄蟎之成蟎壽命分別為 11.7、13.6 日及 11.4、11.1 日。變溫及定溫下二點葉蟎取食花豆葉之內在增殖率 (intrinsic rate of increase) 分別為 0.2590、0.2800，終極增殖率 (finite rate of increase) 為 1.2956、1.3233，淨繁殖率 (net reproduction rate) 均為 12.1，平均世代時間 (mean generation time) 為 9.6 及 8.9 日。因此，相較於恆定高溫條件下，僅自然變溫對二點葉蟎族群之平均世代時間產生顯著延長的效應，其餘無顯著差別之特性，可提供未來田間該害蟎族群發生之預測及研擬防治策略的參考依據。

關鍵詞 (Key words)：二點葉蟎 (*Tetranychus urticae* Koch)、兩性生命表 (two sex life table)、自然變溫、族群特性 (population characteristic)

PD02_入侵紅火蟻成功入侵臺灣之基因體學探討

Exploring the genetic paradox during invasions of red imported fire ant (*Solenopsis invicta*) using genomic approaches

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The red imported fire ant (*Solenopsis invicta*) is a notorious species that has invaded three continents. The success of fire ants has been attributed to several ecological hypotheses, such as release from natural enemies, the bridge-head effect, and the cryptic invasions. However, what is the genetic basis underlying allowing the fire ants to overcome the genetic bottlenecks after each invasion? To test if any genetic locus or loci might have had important impacts on adaptation to new invasive regions, we have begun a population genomics study. We are comparing the genomes of multiple males from Taiwan and the USA (source of Taiwan population) with next generation sequencing (NGS). We sequenced eight independent males from Taoyuan, Taiwan and will compare them to seven independent males from Georgia, USA. Using this data, we are estimating SNP densities, the distribution of minor allele frequencies, the composite likelihood ratio (CLR), and the Tajima’s D statistic to identify potential loci under directional selection. We anticipate that this analysis will uncover important genetic factors underlying the successful invasion of the red imported fire ant.

關鍵詞 (Key words)：入侵紅火蟻 (*Solenopsis invicta*)、單核苷酸多型性 (SNP) 、遺傳悖論 (genetic paradox)、入侵生物學 (invasion biology)

PD03_不同溫度對黑豆蚜 (*Aphis craccivora* Koch) 生活史之影響

The impacts of temperatures on the life cycle of cowpea aphid (*Aphis craccivora* Koch)

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本研究探討不同溫度對取食萊豆 (*Phaseolus limensis*) 之黑豆蚜 (*Aphis craccivora* Koch) 生活史之影響，作為未來防治之基礎資料。黑豆蚜屬於半翅目 (Hemiptera) 常蚜科 (Aphididae)，為多食性昆蟲。本實驗之蟲源係採自嘉義大學農場種植的萊豆上，帶回實驗室，放入25°C恆溫生長箱內飼養一代後，再進行15、20、25 和 30°C 四個溫度的實驗。自蟲源逢機選取初產下之一日齡若蟲分別進行不同溫度之實驗。以一隻為一重複，每個溫度有50重複。每天觀察記錄其發育與成蟲生殖之狀況。利用 Chi (2015) 年齡齡期之兩性生命表進行數據分析。在上述四個溫度的世代長依溫度由低到高分別為 20.3±0.92、20.3±0.9、12.3±0.6、13.7±0.68天。就生活史參數而言，依溫度由低到高，r 值為 0.2234、0.2545、0.3672、0.4024/天；R_0 為 26.67、32.8、32.93、35.63；λ為1.2503、1.2898、1.4438、1.4954；T 為 14.69、13.71、9.51、8.87 天。上述結果顯示，黑豆蚜在萊豆上隨著溫度的升高，完成一個世代的時間也縮短；但 r 值、λ 值及 R_0 會增加。

關鍵詞 (Key words)：黑豆蚜 (*Aphis craccivora* Koch)、生活史 (life cycle)、皇帝豆 (*Phaseolus limensis*)

PD04_昆蟲免疫系統決定桿狀病毒寄主專一性

Insect immune system to determine baculovirus 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. In addition, small RNA has been reported to participant virus-host interaction, and furthermore determines host specificity. Therefore, we screened microRNA induced by AcMNPV infection, then combined with NGS data from cellular gens to predict the possible regulation network. 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.

Key words: Baculoviruses, Next generation sequencing, host specificity

關鍵詞（Key words）: Baculoviruses, host specificity, next generation sequencing

PD05_開發防蚊液的檢測方法

Establishing the mosquito repellents *in vitro* bioassay system

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防蚊液標準化的檢測方法須確認皮膚單位表面積處理忌避劑的劑量、忌避劑保護時間、供試蚊蟲的種類及生理狀況，及試驗結果需具再現性。以人體試驗或動物試驗進行生物檢測，可能有感染病原及測試化學成分傷害的風險，另外也需考慮實驗動物福祉的問題。為快速且大量評估新忌避劑的效果，使用新穎配方的人工代血，混合鹽類、白蛋白、葡萄糖及腺嘌呤核苷三磷酸，以多孔人工餵血裝置建立防蚊液體外檢測系統，可定量防蚊液的忌避效果，是安全、有效的檢測方法。

關鍵詞 (Key words)：防蚊液 (mosquito repellents)、體外檢測系統 (*in vitro* bioassay system)、人工代血 (artificial blood meal)、腺嘌呤核苷三磷酸 (ATP)

PD06_應用生化分析及分子檢測技術探討埃及斑蚊對除蟲菊劑的抗藥性

Biochemical and molecular analyses to determine pyrethroid resistance in *Aedes aegypti*

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台灣地區的登革熱是由蚊子所傳播的病毒性疾病，病媒蚊對殺蟲劑產生的抗藥性嚴重影響對病媒蚊的防治成效，早期偵測病媒蚊對殺蟲劑的抗藥性，得以擬定適當的防治策略。進行埃及斑蚊對殺蟲劑的藥效生物檢定，發現對百滅寧具抗藥性的 LYPR 品系及野外品系的埃及斑蚊對除蟲菊劑具高度抗藥性。本研究使用 TaqMan® probe 進行分子生物檢測，偵測埃及斑蚊體內殺蟲劑標的部位鈉離子通道蛋白的突變情形，發現存在 V1023G 和 D1794Y 的突變。以 96 孔微量盤進行包括麩胱苷肽硫轉基酶、細胞色素 P450 單氧化酶及 β-酯酶等解毒酵素活性之生化分析。經實驗證實其 *kdr* 基因的突變頻率高，解毒酵素活性也提升，台灣地區埃及斑蚊對除蟲菊劑的抗藥性與標的部位的不敏感及解毒酵素代謝的抗藥機制息息相關。

關鍵詞 (Key words)：埃及斑蚊 (*Aedes aegypti*)、抗藥性 (resistance)、解毒酵素活性 (detoxification enzyme activity)、TaqMan® 探針 (TaqMan® probe)、*kdr* 基因突變 (*kdr* gene mutataion)

PD07_利用基因體增幅次世代定序技術完成火蟻共棲蟎類粒線基體

The complete mitochondrial genome of fire ant phoretic mite by PCR-free whole genome amplification and next-generation sequencing

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The mymecophiles are organisms habitually live with ants. The interaction between ants and mymecophiles is relatively unexplored antecedently. The mite *Histiostoma blomquisti* is a microorganism feeder that uses the red imported fire ant (*Solenopsis invicta*) as a phoretic carrier for dispersal. The *H. blomquisti* mite was speculated as the vector which transmits ant pathogens but lack the evidence to demonstrate before. For investigating the interaction between *H. blomquisti* and *S. invicta*, we challenged the limit of tiny DNA acquirement from 100 μm mites by PCR-free whole genome amplification (WGA) and next-generation sequencing (NGS) methods. We successfully sequenced the circular mitogenome of *H. blomquisti* from the start 20 ng DNA. The mitogenome is 15,892 bp and is composed of 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and six >100 bp non-coding regions. Most tRNAs are highly reduced, like those found in other Acariformes. Phylogenetic analysis based on the concatenated nucleotide sequence of the 13 protein-coding genes supports Histiostomatid mites forming the basal-most lineage in Astigmata. In all, we described the comprehensive mitogenome which could be further utilized in the investigation of population structure and epidemiology in ants and mymecophiles.

關鍵詞 (Key words)：粒線體 (mitochondria)、蟻客 (mymecophile)、入侵紅火蟻 (*Solenopsis invicta*)、次世代定序 (next-generation sequencing)

PD08_How to revise the taxonomy of an insect genus with polymorphism, sexual dimorphism and conservative genitalia? A case study of *Elymnias* Hübner, 1818 (Nymphalidae, Satyrinae)

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Elymnias Hübner, 1818 is a species-rich and widespread butterfly genus distributed throughout the Old World tropics. The genus' widespread range and remarkable wing pattern diversity, together with the economic importance of several species, has attracted the attention of taxonomists and agricultural entomologists for centuries. However, the entire group has not been examined systematically in over 100 years, and no studies to date have employed genetic data to substantiate taxonomic hypotheses. In the present study, we review the genus using all available information on nomenclature, type localities, locations of type specimens, and geographical distributions. An integrative taxonomic investigation using external morphology, male and female genital morphology, and a species-level phylogeny based on DNA sequence data affirm the contentious species status of various species which were retained as subspecies. There is little interspecific genitalic variation among species in this group, and previous taxnomists therefore relied almost entirely on with patterns. Our molecular phylogenetic analysis was generated with markers believed to be unrelated to wing patterning, and reveal both polyphyletic and cryptic species resulting from morphological convergence between species and polymorphism within a single species. These results suggest that both ecological and morphological evidences are still important in the age of molecular systematics when the genetic divergences among species are relatively low and speciation rate is relatively high.

關鍵詞 (Key words)：Batesian mimicry, polymorphism, sexual dimorphism, Southeast Asia

PD09_浸水營地區 (屏東縣轄) 特有森林植物之伴生植食性昆蟲調查

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浸水營國家步道與大漢林道，為浸水營野生動物重要棲息地範圍中較容易受到遊憩與非法採集野生動植物的地區。雖然在 2003 年所完成的浸水營國家步道規劃報告中提及該地區常見蝴蝶約有 80 種，但除此之外，目前為止整個地區並無大型脊椎動物以外的動物相調查研究。由於此區域代表中央山脈南段的森林植物相，具有高度的植物特有性，為了瞭解該區特有植物與其伴生昆蟲的關係，以及非法盜採昆蟲標本的行為對此地區生態資源的衝擊，擬以浸水營國家步道加上大漢林道之一部分為範圍進行調查工作，以利教育、經營與管理之決策。目前本研究團隊根據普查以及特定植物伴生昆蟲調查，已鑑定共 7 目 28 科 291 種昆蟲物種，包含模式產地於大漢山或浸水營古道之昆蟲共 3 目 7 科 8 屬 9 種。根據訪談，於大漢林道與浸水營國家步道容易受商業採集之分類群主要為鞘翅目中金龜子科、天牛科、鍬形蟲科與鱗翅目，而黃帶天牛屬中型種類且因其顏色出眾備受青睞。特定植物之伴生昆蟲調查中發現，非開花植物中以樟科、薔薇科與殼斗科植物之伴生昆蟲類群類群較其他科級類群植物多，且不同海拔之同植物物種具有些許差異之伴生昆蟲。目前已知大漢山上之烏心石舅植株尚未發現有任何鱗翅目昆蟲取食，目前仍持續找尋其他烏心石舅植株並確認其是否有特定之植食性昆蟲。

關鍵詞 (Key words)：大漢山、浸水營古道、非法採集、昆蟲群聚、屏東林區管理處

PD10_楠梓仙溪野生動物保護區及其周邊濕地重要資源昆蟲普查及其棲地保育規畫

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為了瞭解風災後棲地受損、物種多樣性現況，與地方政府在管理經營上可發展之方向，本研究於楠梓仙溪野生動物保護區範圍針對：(1) 轄區內陸域與週邊溼地之重要陸生與水生昆蟲進行普查；(2) 評估現有昆蟲資源與森林與溼地品質之間的關係；(3) 挑選在環境監測、科學研究、教育宣導、生態產業重要之指標物種；(4) 評估重要昆蟲棲地之品質以及所受到之威脅；以及 (5) 提供高雄市政府務實的經營管理建議。自開始執行至 8 月 31 日止共採集到昆蟲形態種 202 種，其中包含水生昆蟲 14 種與陸生昆蟲 188 種。根據物種棲地與食性專一性，我們認為陸 1 樣點為三個個陸域樣點中棲地品質較佳之區域，而三條溪流的水域樣點其水質均佳，週遭植被開發程度略同，物種多樣性目前還沒有差異。由目前已知物種中，我們建議挑選短腹幽蟌作為水域環境監測物種、棋石小灰蝶作為日後可持續進行知科學研究物種，而螢火蟲則作為教育宣導與生態產業物種。藉由物種名錄可反應出樣點所包含之區域原始低海拔森林植被並不佳，且有經濟作物害蟲名列其中，因此我們建議應瞭解這個地質不穩定地區之昆蟲與植被組成特色，以利未來監測與評估的進行。

關鍵詞 (Key words)：莫拉克風災、那瑪夏、楠梓仙溪、野生動物保護區、生物指標

PD11_ *Philotrypesis* 屬榕小蜂雄蟲的非典型形態與行為

Atypical morph and behavior in *Philotrypesis* male fig wasps (Chalcidoidea: Pteromalidae)

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Empirical evidences of dishonest signaling in aggressive communication were rarely found in nature, this study aimed to show that dishonesty are common in male fig wasps. A dishonest signal is when the sender is sending out false information to a receiver. We present evidence of such signaling in nonpollinating fig wasp *Philotrypesis* sp. 1 associated with *Ficus benguetensis*. Firstly, morphometric data indicated that there is 7% of individual males within a population presented atypical morph which tends to be larger in body size and has longer mandibles than typical males. Secondly, attackers (individual who escalated to the fight first, either by bitting or hitting) had significantly lower proportion of atypical morph than the receivers. Attackers were larger in body size and had less injured individuals than the receivers. Behavioral observations indicated that larger males have higher fighting ability to expel their contestants from the mating pool. Thirdly, sheltered males had higher proportion of atypical morph and had remarkably smaller body size than the nonsheltered males. Sheltered males also have significantly higher proportion of injured individuals, about 8% were severely injured. Interestingly, mated and unmated males have no differences in their body size, suggesting that both morphs have an equal chance of mating opportunities and there should be an alternative mating tactics for smaller males. Besides, no severely injured individual has been found in mated males, indicating that fighting injuries have a gravely effect on mating success. Atypical morphology exists in several other fig wasp lineages, implying that this micro-hymenopterans could be used as a model system to study dishonest signaling.

關鍵詞 (Key words)：榕小蜂 (fig wasps)、無翅雄蟲 (wingless males)、不誠實信號 (dishonest signal)、隱蔽行為 (sheltering behavior)、豬母乳 (*Ficus benguetensis*)


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