
中華民國
植物病理學會
2024年會
The Annual Meeting of
Taiwan Phytopathological Society

2024 中華民國植物病理學會年會

議程表及論文摘要

時間：2024 年 5 月 4 日 (週六)

地點：國立臺灣大學共同教學館

2024 年中華民國植物病理學會年會暨會員大會 議程

時間：2024 年 5 月 4 日　　地點：國立臺灣大學共同教學館

時間	議程	地點
08:30~09:00	報到及論文宣讀準備	共同教室三樓
09:00~12:00	分組論文宣讀 (學生論文宣讀比賽)	共同 303~307
	第六次理監事會議暨選舉開票	共同 302
12:30~14:00	職涯午餐座談活動	共同 303
	會員報到	共同 201
14:00~14:10	開幕與來賓致詞	共同 201
	專題演講　(主持人：洪挺軒 理事長)	
14:10~14:40	主講人：鍾文鑫	共 201
	題　目：Fusarium— Plant pathogen vs Human opportunistic pathogen	
14:40~15:10	主講人：黃姿碧	
	題　目：淨零固碳益生菌在農業綠循環的多元應用	
15:10~15:40	主講人：歐海仁	
	題　目：Leaf health matters: Managing foliar diseases of Welsh onion in Sanxing, Taiwan	
15:40~16:00	大會合照及茶敘	
	專題演講　(主持人：鍾光仁 主任)	
16:00~16:25	主講人：王誌偉	共 201
	題　目：洛神葵、薑與釋迦根圈微生物相之研究	
16:25~16:50	主講人：李瑋崧	
	題　目：花臉香蘑高產菌株篩選及其抗非小細胞肺癌活性評估	
	中華民國植物病理學會會員大會暨頒獎典禮	
16:50~17:50	優良基層人員獎：李宗翰、蔡小涵	共 201
	學術獎：鍾文鑫	
	事業獎：黃姿碧、郭建志	
	終身貢獻獎：林益昇、張雅君、劉瑞芬	
	學生論文宣讀獎	
18:15~	**會員聚餐**	品軒樓

2024 中華民國植物病理學會年會論文宣讀議程

一般宣讀組

A. 真菌卵菌組　　地點：303 教室

第一節　主持人：林秀蕊 副研究員			
時間	編號	報告人	題目
08:30-08:45	A01	劉則言	褐根病菌即時定量聚合酶連鎖反應檢測技術之開發
08:45-09:00	A02	劉東憲	紅棗銹病菌致病性與紅棗銹病發生關聯性研究
09:00-09:15	A03	何湧峰	葡萄銹病夏孢子發芽率的影響因素之探討
09:15-09:30	A04	陳錦桐	不同來源菌核病菌株對麥桿菊的致病性與利用有益微生物防治莖腐病
09:30-09:45	A05	袁琴雅	由台灣疫病菌新記錄種在強降雨的環境下引起甜瓜病害之首次報導
09:45-10:00	A06	莊宜芳	Studying the impact of shade avoidance syndrome during *Colletotrichum orbiculare* and *Nicotiana benthamiana* interaction
10:00-10:15	中場休息		
第二節　主持人：　陳以錚 助理教授			
10:15-10:30	A07	陳奐宇	由 *Cladosporium musae* E.W. Mason 引起之香蕉葉黴病初報
10:30-10:45	A08	謝安妮	臺灣香蕉炭疽病菌對苯并咪唑類 (benzimidazoles) 殺菌劑之感受性調查
10:45-11:00	A09	汪倖如	以水稻紋枯病菌之分子檢測平台對罹病水稻進行及早檢測與定量
11:00-11:15	A10	張家丞	利用水解探針技術檢測植株中之香蕉黃葉病菌熱帶第四型生理小種
11:15-11:30	A11	蔡淳昀	分子檢測技術輔助甜瓜萎凋病之生物防治效果評估
11:30-11:45	A12	鄭靜如	應用非熱電漿活化水技術防治番石榴瘡痂病
11:45-12:00	A13	黃家姍	木瓜果疫病分子檢測技術平台開發

B. 細菌病毒組　　地點：304 教室

第一節　主持人：周浩平 副研究員			
時間	**編號**	**報告人**	**題目**
08:45-09:00	B01	林家華	十字花科植物抵抗甘藍黑腐病菌感染之關鍵因子
09:00-09:15	B02	蔡佳欣	在南投縣發現番茄罹染番茄細菌性潰瘍病之研究
09:15-09:30	B03	蔡佳欣	植物菌質體感染嫩莖萵苣之研究
09:30-09:45	B04	蔡佳欣	*Burkholderia* sp. 感染青蔥之研究
09:45-10:00	B05	鄭慈靜	臺灣首次報導由青枯病菌引起的龍鬚菜細菌性萎凋病
10:00-10:15	中場休息		
第二節　主持人：關政平 副研究員			
10:15-10:30	B06	高之韋	臺灣敏豆細菌性萎凋病之初探
10:30-10:45	B07	梁維容	市場潛力柑橘品種對黃龍病的感病性評估
10:45-11:00	B08	黃楹鎣	不同柚類品種對柑橘萎縮病毒柚類莖陷系統的感病性分析
11:00-11:15	B09	陳冠綸	雲林地區蒜頭病毒初步探查
11:15-11:30	B10	謝佳珉	Preliminary study of the Squash leaf curl Philippines virus on chayote in Taiwan
11:30-11:45	B11	林宥均	香蕉芭葉嵌紋病毒之快速檢測技術建立與田間分布調查

C. 病毒組　　地點：305 教室

第一節　主持人：馮雅智 助理研究員			
時間	**編號**	**報告人**	**題目**
08:45-09:00	C01	林靜宜	臺灣海芋微嵌紋病毒 (*Zantedeschia* mild mosaic virus) 發生調查及其分子特性分析
09:00-09:15	C02	林玫珠	蔥科之分蔥潛隱病毒快速檢測技術開發與應用
09:15-09:30	C03	林玫珠	Application of induced resistance microbe for the control of Tomato yellow leaf curl Thailand virus on tomato
09:30-09:45	C04	吳佳宜	宜蘭青蒜產區病毒病罹病情況調查
09:45-10:00	C05	劉雅婷	Innovations in diagnostic tools for accurate detection of Cucumber mosaic virus
10:00-10:15	中場休息		
第二節　主持人：蔡文錫 副教授兼主任			
10:15-10:30	C06	蕭崇仁	Comparative analysis of diagnostic techniques for Squash leaf curl virus
10:30-10:45	C07	馮雅智	瓜類種子甜瓜壞疽斑點病毒檢測技術之建立
10:45-11:00	C08	陳金枝	國內香莢蘭病毒 Ornithogalum mosaic virus 之發生鑑定
11:00-11:15	C09	賴玄春	評估臺灣甜瓜捲葉病抗病性
11:15-11:30	C10	巫宣佑	以有益微生物評估番茄生長及對抗黃化捲葉泰國病毒之能力

學生論文宣讀競賽組

學生競賽 SA 組　　地點：306 教室

評審老師：陳昭瑩 教授、曾昱 助理教授、張道禾 助理教授

第一節			
時間	**編號**	**報告人**	**題目**
08:30-08:45	SA01	朱宜翎	評估高溫對水稻與徒長病菌交互作用之影響
08:45-09:00	SA02	王彥傑	Spatiotemporal population biology of *Phytophthora nicotianae* in Taiwan
09:00-09:15	SA03	郭昱伶	Diversity of fungal pathogens causing different banana leaf diseases in Taiwan
09:15-09:30	SA04	詹皓翔	軸腐相關真菌相及田間衛生措施對台灣香蕉軸腐病發生之影響
09:30-09:45	SA05	黃妤蓁	Physiological factors affecting the incubation period of dragon fruit stem canker
09:45-10:00	SA06	黃育心	以多系品種及基因堆疊策略強化水稻‘高雄 145 號’對稻熱病之持久抗性
10:00-10:15	中場休息		
第二節			
10:15-10:30	SA07	姚儒賓	臺灣中部地區藍莓果樹病害的初步調查
10:30-10:45	SA08	徐源成	Unveiling the diversity of *Pestalotiopsis*-like fungi causing foliar diseases on six precious conifers in Taiwan
10:45-11:00	SA09	李雅真	長春花葉斑病之病原菌鑑定與其寄主範圍初探
11:00-11:15	SA10	武家銘	罹患黃龍病之台灣香檬植株快速衰亡與 *Fusarium* sp.之關聯性
11:15-11:30	SA11	徐佳螢	Characterization of fungal communities associated with leaf blight of invasive Mimosa in Taiwan

學生競賽 SB+SC 組　　地點：307 教室

評審老師：陳賢明 副教授、張賀雄 助理教授、呂依儒 助理教授

第一節			
時間	**編號**	**報告人**	**題目**
08:30-08:45	SB01	鄭鈞澤	The establishment of a CRISPR-Cpf1 ribonucleoprotein delivery system for precision genome editing in *Fusarium oxysporum*
08:45-09:00	SB02	張翾之	Investigating the PR-1La-dependent signaling pathway in *Ustilago maydis*
09:00-09:15	SB03	黃郁珺	Role of transposon methylation in regulating *Termitomyces eurrhizus* fruiting
09:15-09:30	SB04	李湛	Insights into spray-induced gene silencing for controlling plant diseases caused by *Alternaria* spp.
09:30-09:45	SB05	Ahmed Mahrous Mostafa Ramadan	Comparing the methods for screening resistant/tolerant cucumber accessions to anthracnose
09:45-10:00	SB06	徐浥釩	Vascular sap peptidomic profiling of tomato with root-knot nematode infection
10:00-10:15	中場休息		
第二節			
10:15-10:30	SC01	謝家程	利用阿拉伯芥韌性基因開發有益微物之篩選平台
10:30-10:45	SC02	劉勝吉	Fungicide sensitivity and resistance mechanism of *Neopestalotiopsis rosae*
10:45-11:00	SC03	洪瑞辰	Evaluating the efficacy of citrus terpene and *Bacillus mycoides* strain BM103 in managing periwinkle leaf yellowing disease
11:00-11:15	SC04	陳冠廷	Application of wood vinegar in control of plant pests
11:15-11:30	SC05	彭安禮	*Bacillus amyloliquefaciens* PMB05 發酵液之種子包覆與其在洋香瓜果斑病上之防治
11:30-11:45	SC06	趙靚渝	建立反轉錄恆溫環狀擴增法系統及製備廣效性單株抗體來檢測多種可感染蝴蝶蘭之番茄斑萎病毒屬病毒

2024 中華民國植物病理學會年會論文摘要

Abstracts of the 2024 Annual Meeting of Taiwan Phytopathological Society

專題演講摘要

Abstracts of Keynote Speeches

KS01 Fusarium— Plant pathogen vs Human opportunistic pathogen

Chung, Wen-Hsin[1,2]

[1] Department of Plant Pathology, National Chung Hsing University, Taichung; [2]Master Program for Plant Medicine and Good Agricultural Practice, Taichung

Fusarium spp. are commonly present in soil, plant tissues and residues, organic medium, and water. Moreover, *Fusarium* spp. were important agents to cause disease in plant, animal and human. Recently, the *Fusarium* spp. from human have been confirm to cause diseases in plants, such as *F. solani* species complex (FSSC), *F. oxysporum* species complex (FOSC), *F. incarnatum-equiseti* species complex (FIESC), *F. fujikuroi* species complex (FFSC), etc. In Taiwan, members of FSSC, *F. falciforme, F. keratoplasticum, F. petroliphilum* and *F. solani*, have been reported that could cause diseases in plants and human. *Fusarium nirenbergiae* (FOSC member) also has been confirmed to cause diseases in orchids, lisianthus and human. *Fusarium sulawesiense* (FIESC member) from dog skin disease could cause fruit rot in melon. Here, three clinical FOSC isolates (MCC2074, CGMHD0282, CGMHD0413) were studied its characteristics and colonization in tomato and cucumber. For inoculation test, the clinical isolates could not cause wilting symptom in tomato based on root dipping method. Moreover, the specific primers were designed for studying the colonization of clinical isolate in tomato and cucumber. Results indicated that clinical isolate MCC2047 has chance to colonize in root, hypocotyl, cotyledon node and stem with hypocotyl and drenching inoculation methods, especially, root, hypocotyl and cotyledon node. However, the MCC2047 could only colonize in root completely based on infested soil inoculation. For fruit inoculation, MCC2047 has chance to colonize in pericarp wall, locular cavity and columella in tomato and colonize in pericarp wall and locular cavity in cucumber. In this study, interesting phenomenon was observed that the Taiwanese isolates showed higher tolerance to azoxystrobin fungicide than other clinical *F. oxysporum* isolates.

KS02 淨零固碳益生菌在農業綠循環的多元應用

The Diverse Applications of Carbon-Sequestering Probiotics in Agricultural Green Circularity

黃姿碧[1,2]、黃振文[1,2] 、陳郁璇[1,3]、黃文的[4]、林傳順[5]、呂仲倫[6]、高千雅[6]、鍾文鑫[1]

[1]國立中興大學植物病理系、[2]國立中興大學循環經濟研究學院植物保健學程、[3]國立中興大學永續農業創發中心、[4]財團法人農業科技研究院植物科技研究所、[5]財團法人農業科技研究院動物科技研究所、[6]財團法人農業科技研究院水產科技研究所

Huang, T. P. [1,2,3], Huang, J. W. [1,2], Chen, Y. H. [1,3], Huang, W. D [4]., Lin, C. S. [5], Lu, C. L.[6], Kuo, C. Y. [6], and Chung, W. H.[1]

[1]Department of Plant Pathology, National Chung Hsing University, Taichung; [2]Progrm in Plant Heath Care, Academy of Circular Economy, National Chung Hsing University; [3]Innovation and Development Center of Sustainable Agriculture**,** National Chung Hsing University; [4]Plant Technology Laboratories, Agricultural Technology Research Institute; [5]Animal Technology Laboratories, Agricultural Technology Research Institute; [6]Aquatic Technology Laboratories, Agricultural Technology Research Institute)

As global climate change exacerbates its impact on crop cultivation and food security, the Conference of the Parties to the United Nations Framework Convention on Climate Change has set a mission of achieving "net zero emissions" by 2050. In Taiwan, to reach net zero emissions in agriculture, strategies are being implemented through emission reduction, carbon sink enhancement, agriculture by-product recycling, and the promotion of a green economy. Here, we propose Microbial-Based Solutions to reduce the use of chemical fertilizers and pesticides, increase carbon sinks, and add value to agriculture by-products. Our transdisciplinary team has discovered three Bacillus-based probiotics (*Bacillus licheniformis* EC34-01, *Bacillus subtilis* 151B1, and *Bacillus subtilis* WMA1) and demonstrated their high potential for application in crop health care, agricultural pollutant bioremediation, livestock farming, and aquaculture. *B. licheniformis* EC34-01 and *B. subtilis* 151B1 were isolated from plant rhizospheres in Taiwan. The microbial agents of these two strains were developed in liquid and powder formulations and spray-coating granules using pilot plant and industrial-scale facilities to assess their efficacy in multi-industry applications. Our results indicate that both strains can promote the growth of various plants, including strawberries, tea, and cucumber plants, and suppress plant diseases such as *Fusarium* wilt and damping off in cucumber seedlings. They also possess plant growth-promoting traits, including the production of protease, amylase, cellulase, lipase, and IAA, as well as phosphorus-solubilizing activity. *B. subtilis* 151B1 can also produce C14- and C15-family surfactins and C14- and C15-family iturin A to trigger apoptotic-like cell death, reduce mitochondrial membrane potential, and interfere with the energy metabolism of pathogens. *B. subtilis* 151B1 and *B. licheniformis* EC34-01 induce the expression of plant defense genes such as *PAL*, *POX*, and *PR1a* in cucumber seedlings. All three Bacillus strains are excellent

biofilm formers and can colonize plant roots well. They can also enhance the tolerance of plants such as pak-choi to drought and flooding. Additionally, our work demonstrates the beneficial effects of *B. subtilis* and *B. licheniformis* on animals including hogs, chickens, tilapia, milkfish, and whiteleg shrimp. These probiotics serve as good alternatives for improving feed utilization, leading to enhanced growth performance, stress response, immune response, disease resistance, and meat quality. Findings also suggest their potential in improving farm and water quality for sustainable livestock farming and aquaculture. Moreover, both probiotics exhibit activities in degrading pesticides such as malathion and deltamethrin, as well as a fungicide tricyclazole. The influence of introducing these Bacillus-based probiotics on the microbiome of the plant rhizosphere and fish guts was also assessed, indicating an increase in beneficial bacterial and fungal communities but a reduction in pathogenic ones compared to the water control. In conclusion, the Bacillus-based probiotics developed possess multiple functions and could serve as solutions for green circulation and achieving net zero emissions in agriculture.

KS03 Leaf Health Matters: Managing Foliar Diseases of Welsh Onion in Sanxing, Taiwan

Ariyawansa, Hiran Anjana[1], Wang, Chun-Hsiang[1], Yu, Yu-Hsiang[1], Wang, Jian-Yuan[1], Jayasinghe, Himanshi[1], Cho, Yi-Tun[1], and Tsai, Yi-Chen[2]

[1]Department of Plant Pathology and Microbiology, National Taiwan University, Taipei; [2]Crop Environment Section, Hualien District Agricultural Research and Extension Station, MOA, Hualien

The Welsh onion stands as a crucial vegetable crop in Taiwan. However, from 2018 to 2020, the incidence of leaf blight symptoms, somewhat similar to those described for purple blotch caused by *Alternaria porri*, has significantly threatened Welsh onion production in Sanxing, Taiwan. Furthermore, the recommended fungicides by Taiwan Agricultural Chemicals and Toxic Substances Research Institute (TACTRI) and their commercial doses did not effectively control the disease in the field, largely due to their ineffectiveness. Thus, this study aimed to identify the major fungal communities associated with leaf blight and establish integrated management strategies to combat the disease. In total, 80 fungal strains were isolated from diseased leaves, and major causative agents were identified based on multi-locus phylogeny and morphology. The fungal species identified as causing leaf blight of Welsh onion were *Stemphylium vesicarium*, *Colletotrichum spaethianum*, and *C. circinans*. These results were further verified by metagenomic analysis of symptomatic plants, revealing that the leaf blight affecting Welsh onion in Taiwan constitutes a disease complex primarily involving taxa from the *Stemphylium* and *Colletotrichum* genera. In total, 31 fungicides were subjected to testing for their efficacy in reducing the mycelial growth and conidial germination of these three fungal taxa *in vitro*. Notably, Propiconazole, Prochloraz, and Cyprodinil + Fludioxonil were identified as the most effective among the tested fungicides, displaying significant reductions in mycelial growth and spore germination across all three fungal groups. In addition, cultivable endophytic microbes associated with healthy Welsh onion leaves were isolated, and their biocontrol potential against the major fungal taxa identified in this study was evaluated. Among the isolated strains, *Bacillus velezensis* GFB08 exhibited promising results, demonstrating the highest disease control efficacy by reducing the lesion area of Welsh onion leaves by up to 48% in greenhouse assays. Overall, this research will support the sustainable management of foliar diseases in Taiwan, however, further field assessments of the fungicides and *B. velezensis* GFB08 are warranted.

KS04 洛神葵、薑與釋迦根圈微生物相之研究

Investigation into rhizosphere microbiomes of roselle, ginger, and sugar apple

王誌偉[1]、陳穎練[2]、楊姍樺[3]、湯森林[4]

[1]農業部臺東區農業改良場、[2]國立臺灣大學植物病理與微生物學系、[3]國立臺灣大學漁業科學研究所、[4]中央研究院生物多樣性中心

Wang, C. W.[1], Cheng, Y. L.[2], Yang, S. H.[3], and Tang, S. L.[4]

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土壤微生物在農業上對改善作物營養與維持植物健康扮演重要角色，為了找尋對洛神葵、薑與釋迦生長可能的有益微生物或病原菌，以真菌內轉錄區間片段 (ITS) 與細菌核糖體變異片段 (16S rRNA) 增幅定序的方法，研究揭露健康與生病植株根圈或慣行農法轉作有機栽培土壤菌群。在洛神葵的研究發現，真菌赤叢殼菌科族群相對豐度於萎凋病植株根圈相較於健康植株明顯較高，細菌族群的差異受地理位置影響較是否發生病害顯著，但少數細菌族群如枯草桿菌屬等與健康根圈有高度相關。研究發現罹病洛神葵土壤鐮孢菌屬為赤叢殼菌科中最主要族群，因此為進一步病原菌分離的目標。從洛神葵田間共分離出 119 菌株，並以柯霍氏法則驗證部分菌株之病原性。其中茄鐮孢菌 (*Fusarium solani*, FSK1) 被證實可造成洛神葵萎凋和莖髓部壞死，與田間病徵相同。再者，該病原菌序列與微生物相實驗中，真菌 ITS 增幅定序得到的大量序列片段相同，提供茄鐮孢菌為造成洛神葵萎凋病害之重要佐證。臺東縣為臺灣地區薑重要產地之一，因病害與產量因素，大多數薑農不以連作方式進行薑栽培。以薑土壤是否發生病害進行微生物相組成研究，並以經常作為微生物製劑的貝萊斯芽胞桿菌或化學農藥依得利進行處理，觀察薑生長過程中微生物族群變動。本研究發現貝萊斯芽胞桿菌可能以改變土壤微生物組成的方式，增加薑產量。依得利則可能破壞了土壤中有益微生物族群，對薑生長具不良影響，並導致產量下降。為探討有機栽培管理對釋迦果樹土壤微生物菌相之改變，於臺東市慣行農法果園分別進行慣行農法與轉型有機栽培 2 種管理方式處理，每處理每年分別於 2 栽培期結束時採樣土壤進行試驗，已完成 3 年度共 6 個時間點之細菌菌相分析，隨轉型有機栽培時間增加，土壤細菌族群與慣行栽培處理具顯著差異，未來將針對不同栽培農法之優勢微生物種類進行研究。

KS05 花臉香蘑高產菌株篩選及其抗非小細胞肺癌活性評估

Screening of high-yield strains of *Lepista sordida* and evaluation of their anti-non-small cell lung cancer activity

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Li, W. S.[1], Wu, T. Y.[2], Tsai, S. J.[2], Lu, Y. S.[1], Chen, M. H.[1], Lin, C. C.[3], and You, B. J.[4]

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花臉香蘑(*Lepista sordida* (Fr.) Singer)是一紫色及具有薄荷清香的野生食用菇種，因不易栽培至今仍無法規模化量產。本研究發現臺灣本土花臉香蘑菌株以 24-28 ℃菌絲生長最為良好，CEA 為其最佳的培養基。以洋菇高產室內發酵堆肥大量栽培花臉香蘑 LS-2 菌株，覆土後 28.3 日可開始採收，產量達 2.6 kg/筐(15 kg 堆肥)、生物效率 43.5%。LS-2 菌株子實體總多糖含量 13.41%、總多酚含量 10.66 mg/g、總花青素含量 0.49 mg/g。本研究發現花臉香蘑子實體乙醇粗萃物(EE-LS)對 A549 及 CL1-5 肺癌細胞株有毒殺作用，尤其對於高轉移性的肺癌細胞 CL1-5 有更顯著之細胞毒殺作用。EE-LS 引起 A549 及 CL1-5 肺癌細胞死亡是經由調控細胞凋亡相關蛋白，如 Bax、Bcl-2、XIAP 及 Survivin 蛋白的表現，進而降低粒線體膜電位並釋放 cytochrome *c* 至細胞質引起 caspase-9 及其下游之 caspase-3 的活化之內源性細胞凋亡途徑導致肺癌細胞株細胞凋亡。本實驗也以異種移植腫瘤小鼠模式證實 EE-LS 在小鼠體內具有抑制腫瘤生長效果。因此，由本研究得知花臉香蘑菌株子實體乙醇粗萃物中應該含有相當有效的抗癌活性成分。

論文宣讀摘要

Abstracts of Oral Presentations

一般宣讀

A. 真菌卵菌組

A01 褐根病菌即時定量聚合酶連鎖反應檢測技術之開發

劉則言[1,2]、陳昭翰[2]、柯怡君[1]、巫宗錡[1]、廖庭芝[3]、李昕翰[4]、蔡怡陞[4]、張東柱[2]、吳孟玲[2]、蔡志濃[5]、鍾嘉綾[1,3] ([1]國立臺灣大學植物病理與微生物學系、[2]行政院農業部林業試驗所、[3]國立臺灣大學植物醫學碩士學位學程、[4]中央研究院生物多樣性研究中心、[5]行政院農業部農業試驗所)

Development of real-time quantitative PCR assays for *Phellinus noxius* detection

Liu, T. Y.[1,2], Chen, C. H.[2], Ko, Y. C.[1], Wu, Z. C.[1], Liao, T. Z.[3], Lee H. H.[4], Tsai, I. J.[4], Chang, T. T.[2], Wu, M. L.[2], Tsai, J. N.[5], and Chung, C. L.[1,3] ([1]Department of Plant Pathology and Microbiology, National Taiwan University, Taipei; [2]Taiwan Forestry Research Institute, Ministry of Agriculture, Taipei; [3]Master Program for Plant Medicine, National Taiwan University, Taipei; [4]Biodiversity Research Center, Academia Sinica, Taipei; [5]Taiwan Agricultural Research Institute, Ministry of Agriculture, Taichung)

樹木褐根病為熱帶與亞熱帶地區的重要樹木病害，褐根病菌 *Phellinus noxius* 為木材白腐朽真菌，寄主範圍廣泛可危害多種樹木。受褐根病菌感染的樹木根基部腐朽，枝葉黃化及小葉化，嚴重時全株樹勢衰弱枯萎，易受風傾倒。由於褐根病初期的病徵和病兆不明顯，使得病害的早期診斷成為一大挑戰。現有的褐根病菌分子診斷技術，僅基於褐根病菌的 internal transcribed spacer (ITS) 所開發，且缺少對來自全球各地褐根病菌分離株、不同木材腐朽菌和對寄主植物的測試。本研究旨在建立高靈敏度和專一性的褐根病菌即時定量聚合酶連鎖反應 (real-time quantitative PCR, qPCR) 技術。本研究首先依據不同褐根病菌分離株之 ITS 序列比對，新設計引子對 Pn_ITS_F/Pn_ITS_R；此外，透過褐根病菌與 61 種其他真菌的基因體比較分析，篩選出褐根病菌特有的一群同源基因，為 nucleotide-binding-oligomerization-domain-like receptor 基因家族成員，並設計引子對 Pn_NLR_F/Pn_NLR_R。將兩組新設計的引子對和目前常用於一般 PCR 檢測的引子對 G1F/G1R，用於 qPCR 反應條件的優化，並分別測試此三組引子對對 61 株來自世界各地的褐根病菌菌株、5 株 *Phellinus* 屬真菌和 23 株其他木材腐朽菌的專一性。三組引子對在 qPCR 反應中，對褐根病菌基因體核酸 (genomic DNA) 的檢測極限均可低至 100 fg；其中 G1F/G1R 有較佳的專一性，而 Pn_NLR_F/Pn_NLR_R 有較佳的效率。進一步使用人工接種褐根病菌的垂榕 (*Ficus benjamina*) 枝條，以及 6 種野外自然感染褐根病的樹木根部組織、植穴土和根圈土，成功驗證此三組引子對應用於實際樣本檢測的效力。本研究建立的 qPCR 技術，可達到對褐根病菌定量及精確檢測的用途，未來可應用於褐根病發生情形的長期監控，並提升褐根病檢測的效能。

A02 紅棗銹病菌致病性與紅棗銹病發生關聯性研究

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Study of pathogenicity of *Phakopsora zizyphi-vulgaris* in association with occurrence of *Ziziphus jujube*

Liu, T. H.[1] and Chen, G. L.[2] ([1]Miaoli District Agricultural Research and Extension Station, Ministry of Agriculture, Miaoli; [2]Master Program for Plant Medicine, National Taiwan University, Taipei)

紅棗為鼠李科落葉性果樹，主要栽培於苗栗公館鄉及銅鑼鄉兩地，紅棗銹病於 6 月後零星發生在成熟葉，而採收期後 (8 月) 於苗栗公館地區紅棗的成熟葉全面發生，但未發現感染同期營養枝幼葉，結果枝 (棗吊) 葉片以下位葉發病時間早於上位葉，銹病菌產生夏孢子堆先於葉下表皮開裂釋出，大多位於下表皮，以表徵僅感染葉片。比對夏孢子產孢形態及抽取 DNA 以 ITS 序列分析，結果經鑑定為 *Phakopsora zizyphi-vulgaris*。不同於其他種常見銹病菌，該菌夏孢子於無菌水不發芽，經測試添加展著劑、0.1N 氯化鈣、離心清洗方式、添加紅棗葉片萃取液 (16.7%)、或和前列養分物質同置於 WA 培養基等條件下，皆難讓夏孢子發芽 (發芽率<0.1%)，亦無附著器產生。直接將夏孢子離葉接種於紅棗甫成熟葉片上下表皮，室溫自然光照下培養 6 天，無論有無傷口皆無發病情形。由不發芽和接種不發病結果均難逕以認定該菌夏孢子為該病感染源。另於使用 4-4 式波爾多液防治田區，觀察成熟葉片發病率為 100 % 與未使用藥劑發病率相同，顯示該藥劑無顯著控制發病能力。以本研究結果支持該病發生是結果枝葉片轉移果實養分耗盡失去抗病的自然現象論點，為葉齡老化併發症，葉片因老化而易掉落，而難認定該銹病是造成紅棗葉片提早老化掉落的原因。

A03 葡萄銹病夏孢子發芽率的影響因素之探討

何湧峰、許晴情 (農業部臺中區農業改良場植物保護研究室)

Factors affecting the urediniospores germination rate of grape rust

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葡萄銹病 (Grape rust) 為限制臺灣溫室葡萄生產的重要病害之一，主要危害成熟葉片，好發於葡萄座果後，初在葉之表面出現淡黃色斑點，其葉背呈現橘黃色粉狀夏胞子堆，主要藉風傳播。若發病嚴重時，會使葉片提早掉落，進而使果實無法成熟轉色。為了解目前葡萄銹病菌對現行登記藥劑感受性差異，於 2023 年在彰化縣大村鄉葡萄田採集野外發病葉接種源，初步測試其發芽率，發現在 22℃，全黑暗條件下不超過 25%。為提升夏孢子發芽率以確保後續藥劑試驗數據代表性，遂進一步針對夏孢子日齡、發芽溫度、光照有無及基質種類進行探討。在不同夏孢子日齡之發芽率結果發現，在有光線的情況下，以第 9 天發芽率最高並與其他組有顯著差異；在光照有無試驗結果顯示，比較無光照與光週期 (12hr/12hr) 的處理組發芽率，在有光照的條件下發芽率較無光照對照組提高了約 50%，顯示光照有助於促進夏孢子的發芽；再分別針對 20℃、24℃和 28℃的溫度條件進行了實驗。其發芽率分別為 1.3%、13.5%和 53.3%，顯示在有光照的條件下，銹病的發芽率隨著

溫度上升而增加，並以 28℃發芽率最高，顯示在較高的溫度下能促進夏孢子發芽；最後測試在不同洋菜基質種類上夏孢子發芽率，發現兩種廠牌的洋菜基質的發芽率有顯著差異，可提升約 50%發芽率。綜上所述，葡萄銹病夏孢子發芽率受夏孢子日齡、發芽溫度、光照有無及基質種類多種因素影響，經試驗，將以 9 日齡夏孢子、有光線條件 (12hr/12hr)、溫度 28℃，培養於 WA 之狀況下進行後續藥劑抑制夏孢子發芽率試驗。

A04 不同來源菌核病菌株對麥桿菊的致病性與利用有益微生物防治莖腐病

陳錦桐[1]、褚哲維[1]、林玫珠[2]、蔡志濃[2]、吳容儀[1]、戴廷恩[1] ([1]農業部農業試驗所花卉試驗分所、[2]農業部農業試驗所植物病理組)

Assessing the pathogenicity of diverse isolates of *Sclerotinia sclerotiorum* on strawflower and employing beneficial microbes for the biocontrol of stem rot in *Helichrysum bracteatum*

Chen, J. T.[1], Chro, J. W.[1], Lin, M. J.[2], Tsai, J. N.[2], Wu, R. Y.[1], and Tai, T. N.[1] ([1]Floriculture Experiment Branch, Taiwan Agricultural Research Institute, MOA, Yunlin; [2]Plant Pathology Division, Taiwan Agricultural Research Institute, MOA, Taichung)

近年來在中部南投山區麥桿菊的栽培田發現病害，嚴重時造成近 1/2 栽培面積的危害，被害的植株呈現莖腐枯萎死亡，被鑑定為是由 *Sclerotinia sclerotiorum* 所引起的莖腐病。測試由台灣不同地區、作物分離的菌核病菌株對麥桿菊的致病性，結果發現在西螺、雲林、霧峰鄉等地區從萵苣與番茄植株所分離的 4 支菌核病菌株不會感染麥桿菊，由國姓鄉與苗栗的草莓所分離的菌株則可感染麥桿菊，顯示不同來源菌核病菌株對不同作物的致病性有差異。麥桿菊莖腐病為土壤傳播性病害，會用子囊孢子或菌核發芽的菌絲體攻擊宿主植物及行生物營養型和壞死營養型的侵染方式，其菌核可殘存休眠土壤中數年，不易防治。化學農藥 10 年減半是國家重要政策，自 2018 年開始推動，主要管理策略為「強化綜合管理，鼓勵友善農業」，其中開發生物性防治資材保護作物以降低化學農藥使用。本研究由菇類栽培後剩餘物的堆肥中分離微生物菌株，進行麥桿菊莖腐病菌的拮抗測試，在馬鈴薯葡萄糖瓊脂 (PDA) 平板上初步篩選有 B4、B11 與 B34 等 3 支菌株有抑制莖腐病菌菌絲的生長，其中以分離株 B34 效果較佳。將 B34 菌株以 16S rDNA 進行鑑定，證實為 *Bacillus velezensis*，在溫室進行防治試驗，將 B34 菌株以營養培養基在 33℃培養 2 天後的培養液澆灌到播種後 5 週的麥桿菊幼苗上，再接種莖腐病菌。在 3 週後記錄發病率與株高。結果莖腐病發生率從對照組的 83.33%降低到處理 B34 菌株的 28.33%。同時發現這支 B34 菌株有顯著的促進植株生長效果，顯示 B34 菌株具有開發為促進作物生長與防治麥桿菊莖腐病的潛力。

A05 由台灣疫病菌新記錄種在強降雨的環境下引起甜瓜病害之首次報導

黃晉興、袁琴雅 (農業部農業試驗所植物病理組)

First report of the new recorded *Phytophthora* species which caused melon blight under heavy rainfall in Taiwan

Huang, J. H. and Yuan, C. Y. (Plant Pathology Division, Taiwan Agricultural Research Institute,

MOA, Taichung)

台灣在夏秋季易發生連續或短時強降雨，常造成露天栽培甜瓜出現果腐及植株死亡的病害，以前研究報告顯示，主要病原菌為 *Phytophthora melonis* 與 *P. capsici*。2019-2023 年赴新竹新豐鄉、高雄燕巢和岡山等地區，取回因降雨造成田區淹水的罹病果實與植株進行組織分離，可分離得到 3 種疫病菌 (*Phytophthora* spp.)，再將此 3 種疫病菌游走子懸浮液接種於果實上，可得到與田間相同之病徵，並能再分離得原接種的同種疫病菌，完成科霍氏法則，證實其病原性。利用形態外觀及多基因 internal transcribed spacer (ITS)、ß-tubulin (TUB2)、Elongation factor 1 alpha (EF1-α)及 cytochrome c oxidase 1 (cox 1)等序列進行分析，將此 3 種疫病菌鑑定為 *P. melonis*、*P. kelmanii* 及 *P. viriginiana*-like。*P. melonis* 孢囊呈卵圓形或長橢圓形，不具有乳突且不脫落，具有內展增生或內巢增生的特性，大小為 53.9-66.8×38.6-44.3μm (avg. 60.2×41.8) μm，並可產生指狀不規則形的菌絲膨大體，但不產生厚膜孢子，有性世代為異絲型，配對型為 A^1，藏精器為底著，藏卵器表面平滑，大小為 25.6–31.3 (avg. 28.6) μm，卵孢子為非充實性，大小為 20.0–25.6 (avg. 23.2) μm；*P. kelmanii* 孢囊呈現卵圓形，不具乳突，具有內展增生或內巢增生，大小為 43.6–53.1×26.4–33.6 (avg. 48.5×29.4) μm，並可產生球狀之厚膜孢子，菌絲膨大體小球形呈堆聚狀，有性世代為異絲型，配對型為 A^2，藏精器為底著，藏卵器球形，具有波浪的壁，大小為 25.3–32.3 (avg. 29.2) μm，卵孢子為球形，大小為 17.5–26.0 (avg. 23.0) μm；*P. viriginiana*-like 孢囊呈現卵圓形或倒梨形，有時候為檸檬形至橢圓形，不具乳突，但具有內展增生或內巢增生，大小為 55.5–64.0×33.6–42.9 (avg. 59.3×38.7) μm，可產生球形的厚膜孢子，以及花生狀或各種扭曲形狀之菌絲膨大體，有性世代為異絲型，配對型為 A^1，但與不同配對型的菌株對峙培養則自己不產生卵孢子。將此 3 種疫病菌接種於胡瓜、洋香瓜及美濃瓜果實 (離果及著果)，*P. melonis* 及 *P. viriginiana*-like 皆會造成上述 3 種瓜果腐，但 *P. kelmanii* 只會造成洋香瓜及美濃瓜 (離果) 果腐，不會造成胡瓜果腐。進一步接種於上述 3 種瓜盆栽植株上，*P. melonis* 會造成上述 3 種瓜葉枯及根腐，嚴重時植株死亡，*P. viriginiana*-like 會造成上述 3 種瓜葉斑及矮化 (輕微根腐)，但 *P. kelmanii* 在美濃瓜及洋香瓜上僅出現極輕微葉斑及根腐，但對胡瓜植株不產生任何病害。

A06 Studying the impact of shade avoidance syndrome during *Colletotrichum orbiculare* and *Nicotiana benthamiana* interaction

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In nature, plants experiencing shade trigger Shade Avoidance Syndrome (SAS) that prompts a rapid elongation growth of stems and petioles, enabling plants to move away from high-density planting. SAS is initiated by the plant's photoreceptor, phytochrome, detecting a low red to far-red light ratio (low R:FR). Under artificial LED lighting, SAS can be induced by white light supplementing with additional far-red light. SAS's growth-promoting feature has been

applied in the greenhouse to enhance crop yields. However, in some plants, SAS has a negative impact on plant defense against pathogens. Thus, the role of SAS in plant defense remains to be explored. This study aims to investigate how the interaction between *Colletotrichum orbiculare* and *Nicotiana benthamiana* is affected under a SAS condition. Our results indicate that after a 2-week treatment with additional far-red light (WFR), *N. benthamiana* exhibits typical SAS, with significant increases in growth parameters such as plant height, branch length, and fresh weight compared to the white light (W) control treatment. However, flagellin-induced reactive oxygen species (ROS) production in *N. benthamiana*, following a WFR pre-treatment, showed no significant difference compared to W pre-treatment, thus indicating that the basal immunity of *N. benthamiana* is not affected by SAS. In contrast, the fungus is also affected by far-red light. In the case of *C. orbiculare*, there were no significant differences observed between the W and WFR treatments in terms of colony appearance, diameter, conidial production, or colony growth on the PDA medium. The fungal growth between WFR and W conditions remained the same when culturing *C. orbiculare* under different stress conditions. In both the detached leaves and the whole plant inoculation test, *N. benthamiana* treated with WFR light displayed higher resistance to *C. orbiculare* compared to the W control treatment. To further understand the impact of additional far-red light on the early infection of *C. orbiculare*, we investigated spore germination and appressoria formation of *C. orbiculare*. Our results showed that spore germination is delayed under WFR treatment during *C. orbiculare* infection, thus indicating the SAS may regulate fungal development and virulence. Additional experiments are needed to investigate the impact of additional far-red light on the interaction between *N. benthamiana* and *C. orbiculare*.

A07 由 *Cladosporium musae* E.W. Mason 引起之香蕉葉黴病初報

陳奐宇、曾國維、黃昭寰、蕭文琍 (財團法人台灣香蕉研究所技術服務組)

Preliminary study on cladosporium leaf speckle of banana caused by *Cladosporium musae* E.W. Mason

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香蕉屬於熱帶與亞熱帶作物，是許多開發中國家重要糧食，亦是臺灣外銷日本主力果品之一。於 2022 年 9 月首次在嘉義縣民雄鄉有機蕉田區，發現植株下位葉具深褐偏紫色的圓形病斑，葉表病斑顏色較深而葉背顏色則較淡，葉背病斑可見明顯緻密黴狀物，陸續又於高屏香蕉產區進行病害調查，同樣可在環境濕度高與管理較粗放，及通風透光不良之華蕉品種田區的植株上發現此病害，不同的是華蕉品種上的病斑顏色為橘黃色，病斑形狀不局限於圓形，有時可見隨葉脈發展約 2-3×1.5cm 的條紋病斑，感染嚴重者葉片褐化並提早落葉。將罹病葉片取回實驗室，置於解剖顯微鏡下鏡檢，可見病斑密布掃帚狀分生孢子梗，頂端著生卵圓形至長橢圓形分

生孢子，分生孢子不具隔膜，大小約為 8-13×2.5-4μm，此病害不易由常規分離純化方式取得，需製成孢子懸浮液進行單孢分離，經純化後之病原菌在馬鈴薯葡萄糖瓊脂 (potato dextrose agar, PDA) 上呈灰綠色菌落，具有稀疏氣生菌絲體，依據形態特徵輔以引子對 ITS1/ITS4 進行分子鑑定，利用 BLAST 方法針對美國國家生物科技資料中心資料庫中的序列進行比對，將該菌株初步鑑定為 *Cladosporium musae* E.W. Mason (新分類學名為 *Metulocladosporiella musae* (E.W. Mason) Crous *et al.*)，將菌株接種於香蕉幼苗葉片上並套袋保持高濕環境，大約 7-10 日出現與田間相同病徵，並可再分離出相同菌株，完成柯霍氏法則 (Koch's postulates)，證實 *C. musae* E.W. Mason 對香蕉具有致病性，為 *Cladosporium* 屬在臺灣首次危害香蕉之紀錄，中文名暫定為香蕉葉黴病，未來可再深入研究該病原菌之生物特性與藥劑感受性，以建立該病害的田間管理策略。

A08 臺灣香蕉炭疽病菌對苯并咪唑類 (benzimidazoles) 殺菌劑之感受性調查

謝安妮、詹皓翔、陳以錚(國立嘉義大學植物醫學系)

Investigation of sensitivity of *Collectotrichum musae* from banana to benzimidazole fungicides in Taiwan

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香蕉 (banana) 泛指芭蕉屬 (*Musa* L.) 的熱帶或亞熱帶作物，現為世界第四大宗作物，亦是臺灣的重要外銷水果之一，外銷市場以日本為主；2022 年臺灣栽培面積為 15,307 公頃，年產量為 351,480 公噸。香蕉採收後的貯運過程中，常因多種真菌性倉儲病害造成損失，其中以複合感染的軸腐病 (crown rot) 對採收後的蕉果品質最為嚴重。引起軸腐病的病原菌如 *Collectotrichum musae* 、*Lasiodiplodia theobromae* 、*Fusarium* spp. 等，先前調查發現臺灣香蕉軸腐病以 *C. musae* 最為普遍。香蕉軸腐病目前以化學防治為主，在臺灣僅核准登記 methyl benzimidazole carbamate (MBC) 殺菌劑中苯并咪唑類 (benzimidazoles) 的免賴得 (benomyl) 及腐絕 (thiabendazole)；此類殺菌劑主要攻擊真菌有絲分裂過程中 *β*-tubulin 微管蛋白組合，進而影響細胞有絲分裂並阻礙發芽管延長，然已被 Fungicide resistance action committee (FRAC)證實為真菌產生抗藥性風險高之藥劑，因此防治上可能具有高度抗藥性菌株產生風險。為了調查臺灣香蕉炭疽病菌對苯并咪唑類藥劑的感受性，本研究配製含有 1、5、10、50、100、500 及 1,000 μg a.i./mL 等共 7 種不同濃度免賴得、腐絕與貝芬替 (carbendazim) 之馬鈴薯葡萄糖瓊脂培養基 (Potato Dextrose Agar, PDA)，測試其對來自雲林、屏東、南投、台南、彰化及嘉義等地區共 41 株炭疽菌分離株菌絲生長的抑制效果，並計算半數有效抑制濃度 (effective concentration for 50% inhibition, EC_{50})。結果表明來自南投集集'台蕉 5 號'的 TC5JJ21 分離株與雲林古坑'烏龍蕉'的 WLGK07 分離株對藥劑皆感受性低，兩者對免賴得之 EC_{50} 值分別為 272.867 和 229.452 μg a.i./mL；對腐絕為 37.147 和 44.816 μg a.i./mL；對貝分替則皆大於 500 μg a.i./mL；其餘菌株則同時對藥劑呈現高感受性。進一步分析不同菌株 *β*-tubulin 基因序列以探討感

受性降低的可能機制，結果顯示 TC5JJ21 菌株於第 198 密碼子由 GAG 變為 GCG，胺基酸由 glutamic acid 變成 alanine；WLGK07 菌株於第 50 密碼子由 TAC 變為 TCC，胺基酸由 Tyrosine 變成 Serine；抗藥性產生或與 *β*-tubulin 基因點突變有關。臺灣香蕉炭疽病菌已在田間出現抗苯并咪唑類藥劑之菌株，後續應持續關注或調查是否有族群產生。

A09 以水稻紋枯病菌之分子檢測平台對罹病水稻進行及早檢測與定量

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Using early molecular detection and quantification of *Rhizoctonia solani* AG1 in infected rice plants

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水稻紋枯病 (Rice sheath blight, ShB) 是由立枯絲核菌 (*Rhizoctonia solani* AG1) 引起，為水稻生長過程中常見與重要的病害之一，此病原菌能透過菌核 (Sclerotia) 隨灌溉水流進行長距離傳播並感染水稻，藉此擴大感染範圍，進而造成大規模的水稻產量損失。因此，及早偵測此病原菌對於水稻紋枯病的防治管理具有重要意義。本研究分別對溫室及田間罹病水稻檢體，以不同分子檢測系統搭配自動核酸萃取進行檢測，以此評估對罹病水稻檢體早期檢測之可行性，並分析植株罹病程度與檢體內病原菌含量之相關性。試驗結果顯示，於溫室試驗中，帶菌水稻檢體以自動核酸萃取法搭配不同的分子檢測系統進行檢測，皆能夠於接種後第 3 小時之無病徵水稻檢體上達到 88.9% 的檢出率，而這些檢體未能以病原菌分離檢查法 (Plate-out assay) 判斷出帶有病原，此外，以本研究所採用之 qPCR 的檢測系統其檢測的再現性變異率 (Coefficient of variation, CV) 在 15 % 內，顯示利用此 qPCR 技術定量分析水稻檢體內之含菌量具有高度的精準度。而分析於溫室接種後植株紋枯病之病害嚴重程度與病原菌族群量，依斯皮爾曼等級相關係數 (Spearman's rank-order correlation coefficient) 統計值達 0.88，顯示病害嚴重程度與病原族群量呈高度正相關性。此研究也根據兩場田間試驗採樣調查之結果，證實本研究使用之自動核酸萃取法搭配 qPCR 能於田間水稻紋枯病病程開始發展前，及早檢測出田中稻株上之水稻紋枯病菌，且其試驗田中植株的病害嚴重程度也與病原族群量具正相關性，顯示此分子病原檢查法於田間試驗中證實具高度可行性。由於水稻紋枯病能以菌核殘存於土壤中進行傳播，因此本研究後續擬利用此水稻紋枯病之分子檢測系統，於帶菌土壤上建立一套檢測流程並對該流程進行優化，以此檢測出水稻紋枯病菌，達到病害發生之早期預警。

A10 利用水解探針技術檢測植株中之香蕉黃葉病菌熱帶第四型生理小種

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Molecular detection of *Fusarium oxysporum* f. sp. *cubense* tropical race 4 in plants based on TaqMan probe technique

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香蕉 (Banana) 及大蕉 (Plantain) 據聯合國糧農組織年報統計，2022 年食用蕉全產值約 300 億美元，是世界上最重要的果樹作物之一。營養體親合群 (Vegetative compatibility group, VCG) 01213/16 的香蕉黃葉病菌 (*Fusarium oxysporum* f. sp. *cubense*, Foc) 屬於熱帶第四型生理小種 (Tropical race 4, TR4)，同時也是被諸多學者認為是目前世界上造成香蕉栽培損失最嚴重的 VCG；然而這並不代表其餘 VCG 對生產活動毫無威脅，如 VCG 0121、VCG 0122，儘管尚未完全確定此二種 VCG 隸屬於第四型生理小種 (Race 4, R4) 抑或是 TR4，但已有學者對其提出可能具有與 VCG 01213/16 相似危害潛力的說法。在病害管理的策略中，盡早偵知並採取預防手段是相當重要的一環，為了落實此項目的，需要快速且精準的檢測技術來協助栽培管理策略的擬定。本研究參考國際間所發表針對 VCG 01213/16 Foc TR4 的專一性引子對群及另一組針對 VCG 0121、VCG 0122、VCG 01213/16 具選擇性之專一性引子對 (SIX1a_266 系統)，經過專一性測試並利用 F-measure 進行統計分析可以得知，其中 FocTR4-F/FocTR4-R 及 SIX1a_266_F/SIX1a _263_R 兩組引子對，能於眾多 *Fusarium oxysporum* formae speciales 中分別鑑別出 VCG 01213/16 或 VCG 0121、VCG 0122、VCG 01213/16，並獲得 F-score 為 1 的結果，顯示此二組引子在一眾 VCG 01213/16 Foc TR4 之專一性引子對中有極高的精準度。本研究同時希望能利用具有足夠精準度的引子對，開發適用於植物組織檢測之即時聚合酶連鎖反應技術，並透過田間樣本驗證此技術是否能快速且精確的檢測出植物組織中是否帶有 Foc。本研究未來將進一步利用此套檢測技術，應用於田間土壤之診斷檢測實務上，以降低 VCG 0121、VCG 0122、VCG 01213/16 此三種重要的黃葉病菌 VCG 群對香蕉產業之威脅。

A11 分子檢測技術輔助甜瓜萎凋病之生物防治效果評估

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Using molecular detection methods for evaluation of the biocontrol effects against melon *Fusarium* wilt.

Cai, C. Y.[1], Chang, T. D.[1], Wang X. R.[1], Chen, T. Y.[2], and Lin, Y. H.[1] ([1]Department of Plant Medicine, National Pingtung University of Science and Technology, Pingtung、[2]Kaohsiung District Agricultural Research and Extension Station, MOA, Kaohsiung)

甜瓜生長過程中會受到甜瓜萎凋病菌 (*Fusarium oxysporum* f. sp. *melonis*, FOM) 危害，此病原菌可透過厚膜孢子與受汙染的種苗進行傳播，病害危害嚴重時，會導致甜瓜的產量下降，造成嚴重的經濟損失。隨著近年來

永續農業的概念興起，生物防治技術逐漸受到重視，生物防治可減少化學藥劑對人體及環境之危害。本研究擬將分子檢測技術用以評估拮抗菌處理甜瓜萎凋病菌帶菌幼苗後之病原菌抑制效果與拮抗菌之族群數量變化。首先在不同拮抗菌株中，篩選出對 FOM 較具有防治效果之 *Streptomyces* sp. 菌株，將此拮抗菌株施用於甜瓜幼苗確認拮抗菌株可有效降低甜瓜幼苗上萎凋病之發生，後續搭配 FOM 與 *Streptomyces* sp. 兩分子檢測技術進行病原菌與拮抗菌之定量。從結果中得知，使用前述分子檢測系統，可於病原菌接種後的甜瓜幼苗中，測得 FOM 帶菌量為每 μg 甜瓜幼苗 DNA 中含有 6.03 ng 至 625 ng 的 FOM DNA，且病勢發展與病原菌的量呈正相關性；而在生物防治處理組，甜瓜幼苗中的 FOM 帶菌量和萎凋病發病情形，與對照組相比有明顯下降的趨勢。此外，我們也發現經拮抗菌處理後之甜瓜幼苗，該拮抗菌於甜瓜根部定植第 4 天後來到高峰。綜上所述，本研究所使用之分子檢測系統可用以協助評估拮抗菌 *Streptomyces* sp. 處理之帶菌甜瓜幼苗的萎凋病防治效果，並可用於協助評估拮抗菌 *Streptomyces* sp. 於甜瓜幼苗根部的定植情形，未來或可將此套分子檢測系統應用於協助評估幼苗處理 *Streptomyces* sp. 之生物防治效果，進而加速 *Streptomyces* sp. 系列的生物防治劑之開發。

A12 應用非熱電漿活化水技術防治番石榴瘡痂病

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Application of non-thermal plasma-activated water for inhibition of *Pestalotiopsis psidii* on guava

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由 *Pestalotiopsis psidii* 所引起的番石榴瘡痂病 (Guava scabby canker) 嚴重影響採收後的番石榴果實，造成重大經濟損失。番石榴瘡痂病為採收後常見的儲藏性病害，為了降低病害之發生率，通常會以水洗或溫湯處理果實。然而，現行的採後處理方法存在諸多問題，包含可能導致果實失重率增加或成為傳播病害的潛在途徑。因此，近年來許多研究提出使用含有抑菌物質的非熱電漿活化水 (Non-thermal plasma-activated water, PAW) 或可替代現行方法。為驗證此技術對防治番石榴瘡痂病的可行性，本研究探討 PAW 對 *P. psidii* 之抑制效果。首先，由平板抑制試驗及分生孢子發芽情形結果顯示 PAW 可以有效地抑制 *P. psidii*，菌落生成抑制率最高可達 95% 以上，而菌絲體經 PAW 處理後第 1 天抑制率最高可達 60 及 40%，第 2 天後各處理組對於菌絲生長的抑制率皆下降；而從分生孢子發芽情形結果中可以看出，60 分鐘處理組抑制效果最好。此外，以掃描式電子顯微鏡觀察分生孢子形態，也證實 PAW 處理 10 分鐘後之瘡痂病菌分生孢子，外部形態皆會呈現凹陷，且 30 及 60 分鐘處理組的分生

孢子凹陷皺縮的情況會更明顯，附屬絲甚至可能斷裂。經 PAW 處理後之分生孢子於光波長 260 nm 和 280 nm 下的吸光值，與水處理組相比皆較高，顯示處理 60 分鐘時孢子 DNA 滲漏量為水處理組的 1.2~1.8 倍，而蛋白質的滲漏量則為 1.3~1.4 倍；並且經 PAW 處理後之菌絲體電導率會隨著 PAW 處理時間與觀察時間而有所增加，此結果顯示出瘡痂病菌經 PAW 處理後會有細胞滲漏的情形產生。最後，人工接種番石榴瘡痂病菌後進行 PAW 處理，發現不同的處理方式均能有效減緩病勢發展，其中直接處理 PAW 效果最佳，即使在觀察第 6 天時，其病斑直徑僅 0.09±0.07 mm，而未經 PAW 處理的對照組之病斑直徑達 25.79±1.77 mm。綜上所述，PAW 處理能有效抑制 *P. psidii* 的生長，且能有效減緩人工接種番石榴果實上的病斑發展。未來若將此技術應用於番石榴果實的採後處理中，可能提高農產品的倉儲能力。

A13 木瓜果疫病分子檢測技術平台開發

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Development of the molecular methods for detection of *Phytophthora palmivora* in papaya

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由 *Phytophthora palmivora* 所引起的木瓜果疫病是造成番木瓜嚴重的卵菌類病害。木瓜果疫病於幼果至成熟果均會發生，可藉由風雨飛濺及土壤進行傳播。為了減少疫病菌對番木瓜所造成的經濟損失，於番木瓜生長期間進行病原監測可降低病害發生。因此，本研究使用分別對疫病菌 (*Phytophthora* spp.) 或對木瓜疫病菌 (*P. palmivora*) 具有專一性之引子對 Phy1s/Phy2a 與 Pal1s/Pal2a，搭配聚合酶連鎖反應技術 (polymerase chain reaction, 簡稱 PCR) 及即時定量聚合酶鏈鎖反應技術 (quantitative real-time polymerase chain reaction, 簡稱 qPCR)，來建立可用以檢測 *Phytophthora* spp. 或 *P. palmivora* 之分子檢測技術平台。結果顯示，以 qPCR 搭配 Phy1s/Phy2a 或 Pal1s/Pal2a 引子技術，分別能檢測出距離病徵 10.5 公分或 14 公分處之人工接種無病徵番木瓜帶菌果實。此外，qPCR 搭配 Phy1s/Phy2a 或 Pal1s/Pal2a 引子技術，能用以檢測田間番木瓜果疫病罹病果實上無病徵處之 *P. palmivora*，且檢出率達到 100%。這項技術未來或能導入在果實未有病徵前，田間番木瓜疫病發生之即早檢測，並提前防治病害的傳播。

B. 細菌病毒組

B01 十字花科植物抵抗甘藍黑腐病菌感染之關鍵因子

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The key players of crucifers for fighting *Xanthomonas campestris* pv. *campestris*

infection

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半活體營養型細菌 *Xanthomonas campestris* pv. *campestris* (Pammel) Dowson (*Xcc*) 引起的黑腐病 (black rot) 是十字花科作物最嚴重的世界性病害之一，因病原菌經維管束感染寄主植物全株，難以有效防治。本研究透過田間試驗檢測候選根圈細菌菌株對甘藍黑腐病的防治效果，發現菌株 37-1 可高度抑制 *Xcc* 感染維管束所造成的莖腐病徵。全基因體序列分析結果確認菌株 37-1 為 *Bacillus velezensis*，可能產生多種可誘導植物系統抗性的次級代謝物。根圈澆灌菌株 37-1 懸浮液能促進甘藍與阿拉伯芥對黑腐病的系統抗性，並強化抵抗 *Xcc* 所需的防禦相關癒傷葡醣沉積。此外，菌株 37-1 還會影響阿拉伯芥因應 *Xcc* 攻擊所啟動的其他防禦反應，包括類過敏性反應的寄主細胞死亡、活性氧平衡、防禦荷爾蒙訊息路徑活化等。進一步以阿拉伯芥突變株與轉型株探討，則發現主控病原菌誘導性活性氧生成的 RBOHD 酵素有助於 *Xcc* 感染，而水楊酸生合成及其下游訊息路徑活化對 *Xcc* 抗性以及菌株 37-1 誘發系統抗性具有重要貢獻。據此，涉及調控活性氧平衡的 RBOHD 與水楊酸生合成及其訊息路徑應是影響十字花科植物對抗黑腐病菌的關鍵因子。

B02 在南投縣發現番茄罹染番茄細菌性潰瘍病之研究

蔡佳欣[1]、許秀惠[2]、曾獻嫻[3]、許晴情[4] ([1]農業部農業試驗所植物病理組、[2]農業部農業試驗所鳳山熱帶園藝試驗分所 [3]農業部動植物防疫檢疫署植物防疫組、[4]農業部台中區農業改良場植物保護研究室)

The study of bacterial canker of tomato found in Nantou County

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2020 年在南投縣信義鄉 1 處番茄栽培田區，植株出現生長不良、葉片褐化焦枯。縱切罹病植株莖部出現維管束褐化，後期植株莖部空心化、最後萎凋。以光學顯微鏡鏡檢罹病莖組織，可見大量細菌湧出，疑似細菌性病害。從罹病植株莖部可分離出 1 種黃色細菌。該細菌經 Biolog 鑑定系統分析與 *Clavibacter michiganensis* subsp. *michiganensis* 相似度最高，相似值達 0.8 以上。以 *C. michiganesis* 專一性引子對 CMR16F1/CMR16R1 對該細菌可增幅出約 1400 bp 特異性片段。將該 DNA 片段進行定序，在 NCBI 以 blastn 比對結果與 *C. michiganensis* subsp. *michiganensis* strains (GenBank accession number CP047054.1; CP033724.1; AM711867.1)，相似度最高，達 99.9% 以上。進一步將該細菌以 *C. michiganensis* subsp. *michiganensis* 專一性引子對 CMM5/CMM6 可增幅出約 600 bp 特異性片段。由於 *C. michiganensis* subsp. *michiganensis* 在 2018 年經 Li 等人重新分類，將學名改為 *C. michiganensis*，因此將該細菌鑑定為 *C. michiganensis*。將該細菌接種至番茄植株，可造成與田間所見相似之萎凋與維管束褐化病徵，並可再分離出相同細菌，完成

科霍氏法則，證實該細菌為病原菌。由於該細菌為番茄細菌性潰瘍病之病原菌，為我國植物檢疫有害生物，為防治該病害，農業部已公告緊急防治藥劑，該罹病田區經緊急防疫處理及移動管制措施，已完成撲滅，且周邊區域經監測未再發生該病害，亦未擴散至其他區域，屬零星發生，迄今我國仍為該病害之非疫區。

B03 植物菌質體感染嫩莖萵苣之研究

蔡佳欣、黃淑苓、胡馨分 (農業部農業試驗所植物病理組)

The study of phytoplasma infecting *Lactuca sativa* L. var. *asparagina* Bailey

Tsai, C. H., Hwang, S. L., and Hu, S. F. (Plant Pathology Division, Agricultural Research Institute, Taichung)

嫩莖萵苣學名 *Lactuca sativa* L. var. *asparagina* Bailey 屬於菊科一至二年生的草本植物，為台灣常見蔬菜，嫩莖去皮後，可涼拌生食或加熱煮食，加工後可製成醬菜罐頭。2023 年在溪湖 1 處嫩莖萵苣栽植田區，發現部分植株出現矮化、葉片褪色，心葉呈束頂狀，採集田間有病徵及無病徵之植株枝葉，萃取植物總核酸後，以菌質體廣效性引子對 P1/16S-SR 及 R16F2n/R16R2 進行巢式聚合酶連鎖反應測試。具病徵之萵苣植株樣品可增幅出預期之約 1200bp DNA 片段，無病徵之植株樣品則無預期之 DNA 片段產生。將該菌之 16S rDNA 序列選殖定序後，在 *i*Phyclassifier 網站對該菌進行分析，該菌屬於 *Candidatus* Phytoplasma asteris 相關菌株，以虛擬限制酵素片段多型性分析，該菌歸屬於 16SrI-B 亞群。將田間罹病之萵苣組織嫁接至健康萵苣植株，該植株可出現與田間所見之相同病徵，並可再以上述的巢式聚合酶連鎖反應增幅出預期的 DNA 片段，顯示該病害具傳播性。

B04 *Burkholderia* sp. 感染青蔥之研究

蔡佳欣、劉育菁、黃淑苓、林玫珠 (農業部農業試驗所植物病理組)

The study of *Burkholderia* sp. infecting welsh onion

Tsai, C. H., Liu Y. C., Hwang, S. L., and Lin, M. J. (Plant Pathology Division, Taiwan Agricultural Research Institute)

青蔥學名 *Allium fistulosum*，在台灣作為辛香料作物，2023 年在宜蘭地區的青蔥田區，部分植株莖部出現水浸狀褐化的情形，植株有倒伏情形，切取莖部罹病組織於光學顯微鏡下可見細菌大量泳出，疑似細菌性病害，罹病植株於營養培養基 (nutrient agar) 可分離出 1 種黃色細菌，該細菌經測試為革蘭氏陰性菌，可誘導萬國士煙草葉片產生過敏性反應，以 Biolog 細菌鑑定系統測試此菌，結果顯示與 *Burkholderiai cepacia* 相似度最高，以 *B. cepacia* 之專一性引子 CMG-23-1/CM-23-2 進行 PCR，所分離的細菌可增幅出 388 bp 之特異性片段，將該細菌之 16S rDNA、gyrB、recA 序列進行 DNA 片段進行定序，在 NCBI 以 blastn 比對，3 基因之 DNA 序列分析結果均與 *B. cepacia* strain 相似度最高，均達 99% 以上。為了解該細菌之病原性，以細菌懸浮液接種至青蔥莖部，可造成與田間所見相同之病徵，並可再分離出相同細菌，確認該細菌為病原菌。

B05 臺灣首次報導由青枯病菌引起的龍鬚菜細菌性萎凋病

鄭慈靜[1]、高之韋[1]、葉曜誠[2]、林志鴻[1] ([1]國立嘉義大學植物醫學系、[2]臺中市新社區農會)

First report of *Ralstonia pseudosolanacearum* causing bacterial wilt of chayote in Taiwan

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隼人瓜 (*Sechium edule* (Jacq.) Swartz) 又稱佛手瓜，屬葫蘆科梨瓜屬多年生宿根蔓性植物，其果實及嫩梢皆可作為蔬菜食用，而嫩梢部位除嫩葉外，因帶有捲鬚莖蔓，俗稱龍鬚菜，正式名稱為隼人瓜苗。龍鬚菜因低熱量、高纖維、富含維生素及鐵、鋅等多種營養元素，是臺灣優質的夏季蔬菜來源之一。每年4-10月是龍鬚菜的產季，根據農糧署111年度統計年報資料，全臺種植面積約403公頃，主要產地位於中南部及花蓮淺山坡地區，更是花蓮縣吉安鄉的重要經濟作物。於2023年11月在臺中市新社區的一處龍鬚菜生產田區，植株出現萎凋病徵，感染初期的植株，部分葉片出現疑似缺水萎凋徵狀，而萎凋葉片仍維持綠色，但不具光澤，罹病嚴重植株則全株萎凋枯死。切取罹病莖基部組織置於清水中，可觀察到乳白色菌流產生。以NA培養基進行菌株的分離純化，共獲得5株分離株，利用16S rDNA之通用引子對fD1/rP2進行PCR反應，將PCR產物定序後，於NCBI進行相關序列比對，顯示5株分離株皆與青枯病菌菌株*Ralstonia pseudosolanacearum* PLU-6 (Acc. No. KY346977.1) 之序列相似度達100% (1,385/1,385 bp)。進一步就5株分離株進行生物型 (biovar)、演化型 (phylotype)、序列型 (sequevar) 及硝酸還原反應等特性分析，結果顯示5株分離株均屬於臺灣普遍存在的phylotype I、biovar 3菌株，其序列型皆為sequevar 14，亦是臺灣既有之序列型菌株。而硝酸還原反應測試結果，5株分離株皆具有硝酸還原能力，並能夠產生氮氣。將5株分離株各別配製成10^8 CFU/mL細菌懸浮液，再分別澆灌接種龍鬚菜苗，皆可引起萎凋病徵，且與田間罹病株病徵相似，經再分離確認後完成柯霍式準則。此外亦接種茄子、彩椒及番茄等茄科作物，亦會引起萎凋病徵。所有測試結果皆證明*R. pseudosolanacearum*是引起龍鬚菜萎凋的病原菌。過去臺灣青枯病菌的葫蘆科作物寄主有絲瓜、苦瓜及南瓜，並無佛手瓜，故本研究為青枯病菌引起龍鬚菜細菌萎凋病之首次報導。

B06 臺灣敏豆細菌性萎凋病之初探

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Preliminary study on bacterial wilt disease of common bean (*Phaseolus vulgaris* L.) in Taiwan

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菜豆 (common bean, *Phaseolus vulgaris* L.) 屬於豆科菜豆屬的一年生草本植物，臺灣種植的菜豆多為蔓性品種，其中果莢形狀為圓莢型者俗稱敏豆，目前主要栽培品種為白仁敏豆。2022 年臺灣菜豆栽培面積約 1,299

公頃，各縣市均有種植，產區主要分布於南投、高雄與屏東等地，主要提供國內鮮食使用。於 2021 年 9 月在嘉義縣梅山鄉一處敏豆田區，發生部分葉片出現萎凋或褪綠乾枯等徵狀。另於 2023 年 8 月在臺中市新社區一處敏豆田區，同樣發生植株萎凋徵狀。剪取一小段萎凋植株之莖基部，置於水中觀察，皆可發現乳白色菌流產生。經分離純化共獲得 15 株分離株，其中嘉義梅山 11 株，臺中新社 4 株。利用 16S rDNA 序列分析進行初步鑑定，經 NCBI 比對結果，15 株分離株皆與青枯病菌菌株 *Ralstonia pseudosolanacearum* PLU-6 之 16S rDNA 序列 (Acc. No. KY346977.1) 相似度達 100% (1,377/1,377 bp)。進一步對 15 株分離株進行生物型 (biovar)、演化型 (phylotype)、序列型 (sequevar) 及硝酸還原反應等特性分析，結果顯示 15 株分離株均屬於臺灣普遍存在的 phylotype I、biovar 3 菌株，其序列型分別為 sequevar 14 和 sequevar 13，其中分離自嘉義梅山的 11 株菌株屬於 sequevar 14，分離自臺中新社的 4 株菌株屬於 sequevar 13，此兩種序列型皆已存在臺灣。而硝酸還原反應測試結果，顯示 15 株分離株皆可還原硝酸鹽並進一步產生氮氣。利用沾菌穿刺與細菌懸浮液澆灌兩種接種方式，分別接種含 1 至 2 片真葉之敏豆植株，結果顯示兩種接種方式皆可引起敏豆萎凋徵狀，且與田間病徵相似，經回分確認完成柯霍氏準則；另將部分菌株接種於番茄、茄子及番椒等茄科作物，皆會引起供試植株出現萎凋病徵。本研究證明 *R. pseudosolanacearum* 是引起敏豆萎凋的病原菌，此為臺灣第一起敏豆細菌性萎凋病的紀錄。

B07 市場潛力柑橘品種對黃龍病的感病性評估

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Virulence analysis of Huanglongbing on potentially-marketing citrus cultivars

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柑橘作為臺灣產量最大的果樹，其經濟價值不容小覷。產期集中、品種單一化，是臺灣的柑橘產業長期以來的問題，而肆虐全世界的黃龍病一直是柑橘品質與產量的重要限制因子。農業試驗所的嘉義分所保存逾 170 個柑橘品種，並積極進行新品種的選育，其中不乏優良柑橘品種，儘管園藝性狀良好，其抗黃龍病的抗病能力卻是缺乏掌握的。有鑑於此，本研究選擇四種具有市場潛力的柑橘品種─臍橙、黃金茂谷、佛利蒙、與扁實檸檬，進行黃龍病之感病程度的測試，並與主流品種當中已知較感病的椪柑、桶柑還有已知較耐病的文旦、優利加檸檬相互比較。本研究也測試不同的接種條件，對試驗結果的影響。四品種當中，黃金茂谷最感病，感染後葉片強烈黃化斑駁，且植株矮化程度高，臍橙與佛利蒙次之，扁實檸檬較耐病，罹病嚴重度低且菌量低，感病程度近似優利加檸檬。接種條件方面，雖然小植株與大植株在菌量增殖速度相差不大，但是小植株的發病速度普遍較快，此外矮小且分枝多的植株，其菌量分布較均勻。本研究針對上述四個具市場潛力的柑橘品種，提供黃龍病的試驗資料及田間危害現況，有助於未來推廣品種及田間管理能更加精準，因「品種」制宜。

B08 不同柚類品種對柑橘萎縮病毒柚類莖陷系統的感病性分析

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Analyzing Pomelo cultivars for susceptibility to Citrus tristeza virus pomelo stem-pitting strain

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臺灣柚類產業以文旦栽培為主，其採收盛期與銷售盛期均在中秋節，但節後常會出現價格急劇下跌情況。此外，柚類產業面臨著柑橘萎縮病 (*Citrus Tristeza Virus*, CTV) 的威脅。在臺灣，柑橘萎縮病柚類莖陷系統已經分離出兩個不同的系統，分別為柑橘萎縮病強毒系統 (TC1) 和柑橘萎縮病弱毒系統 (TC5)。TC1 是強毒系統，會在柚類引起嚴重病徵，包含生長遲緩、葉片畸形和莖部凹陷。相反地，TC5 是弱毒系統，幾乎不會在柚類莖部引起凹陷。透過即時定量反轉聚合酶連鎖反應 (RT-qPCR) 技術，每月監測 CTV 在柚類植株的病毒累積，第二年開始每兩個月監測一次。接種後一年顯示，具有扁圓形果實且粉紅色果肉特徵的西施柚表現出對 TC1 強毒系統的高抗病性，而具有圓球形果實且淺黃色多汁的白柚對 TC1 強毒系統表現出極度感病。此外，預先接種 TC5 弱毒系統於白柚和西施柚半年後，再接種 TC1 強毒系統。研究顯示預先接種弱毒處理組與單獨接種 TC1 相比，能有效降低 TC1 強毒系統在植株內的病毒累積量。這表明交叉保護效益至少在感染的早期階段提供了柚類保護的效果，有助於對柑橘萎縮病制定有效的預防策略。

B09 雲林地區蒜頭病毒初步探查

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Preliminary investigation of garlic virus in Yunlin county

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蒜頭 (*Allium Sativum* L.)，又可稱為蒜、大蒜，是家家戶戶不可缺少的辛香料，也是料理中的常客。根據取用部位的不同，可區分為食用地上部的青蒜以及食用地下部的蒜頭(garlic bulb)。在台灣，蒜頭的年種植面積大約為五千到六千公頃左右，每年略有波動，其中又以雲林種植最多，占據約九成的生產面積，其次則是彰化地區生產較多。在生產上，因為多數的蒜頭不會產生種子，因此多以營養器官–蒜瓣(garlic clove)進行無性繁殖。長期以營養器官進行繁殖之下，許多的蒜頭都有帶毒的現象。根據前人研究，有多種病毒能夠感染大蒜且對大蒜產量造成一定程度的影響，例如洋蔥黃萎病毒 (*Onion yellow dwarf virus*, OYDV)、韭蔥黃條斑紋病毒(*Leek yellow stripe virus*, LYSV)、大蒜普通潛隱病毒 (*Garlic common latent virus*, GCLV)、分蔥潛隱病毒 (*Shallot latent virus*, SLV) 以及蔥屬 X 病毒屬

(*Allexivirus*) 中的多種病毒等，都對大蒜具有感染力。本研究參考了前人文獻的檢測方法，應用多重聚合酶連鎖反應 (multiplex PCR) 同步檢測多種病毒，成功在雲林地區取得的多個樣本中得到與文獻相似的目標片段，再次證實在雲林地區的蒜頭有多種病毒感染的跡象。

B10 感染佛手瓜之南瓜捲葉菲律賓病毒初探

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Preliminary study of the squash leaf curl Philippines virus on chayote in Taiwan

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佛手瓜是一種多年生植物，屬於葫蘆科 (cucurbitaceae) 刺果瓜屬 (Sicyos) 的瓜菜類，早期從墨西哥南部和中美洲被引入到包括台灣在內的多個國家。在台灣，農民常以發芽的果實直接種植於露天的田區；在栽培過程中，佛手瓜會受到各種病蟲害的危害，其中以病毒感染為大宗。目前台灣僅有南瓜捲葉菲律賓病毒 (Squash leaf curl Philippines virus，簡稱SLCuPV) 被確認能夠感染佛手瓜。然而，儘管佛手瓜在夏季蔬菜中地位重要，台灣對於SLCuPV感染佛手瓜的研究相對稀少，在制定佛手瓜預防SLCuPV感染的整合性栽培管理策略上頻頻遇到困難。本研究的目標是透過優化和標準化SLCuPV的分子檢測技術，以了解發病率、氣候與田間作業之間的關係。此外，我們對於SLCuPV陽性的葉片進行了病徵的分類和計數，也利用qPCR了解不同植物組織、均質方式和萃取方法所得到的病毒量差異。研究結果顯示：新植田的罹病率低於舊植田，且翻耕可以有效降低罹病率，但其長期效果有限。從肉眼觀察來看，春季的罹病率較秋季低，儘管PCR檢測結果顯示罹病率仍然相當高。再者，由qPCR的結果顯示，不同植物組織、均質方法和萃取方法對獲得的病毒量都有顯著影響。令人驚訝的是，在幼苗生長測試中，有22.5%幼苗 (來自感染SLCuPV佛手瓜的果實) 顯示為SLCuPV陽性，即使在種植後8週，仍然可以檢測到非常低量的病毒。然而，還需要進一步的研究來確定這種現象是否在佛手瓜中普遍存在，或僅存在於特定地區與品種中，以及SLCuPV在幼苗中的病毒量是否能夠透過媒介昆蟲傳播至健康植株中並成功建立族群。這是SLCuPV在全球中首次透過種子的傳播紀錄，同時也是台灣首次對於SLCuPV感染佛手瓜進行較深入的研究，這些研究結果將有助於更了解SLCuPV在佛手瓜上的發病情形與可能的傳播途徑，並對佛手瓜的栽培管理提供不同的思考方向。

B11 香蕉苞葉嵌紋病毒之快速檢測技術建立與田間分布調查

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Development of rapid detection system for *Banana bract mosaic virus* (BBrMV) and survey of BBrMV in Taiwan

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香蕉為國內與國際的重要果樹，栽培過程容易遭受香蕉黃葉病與病毒病害的侵害，防疫即成為香蕉產業的成敗關鍵因素之一。香蕉苞葉嵌紋病毒 (*Banana bract mosaic virus*, BBrMV) 為 Potyviridae 科，*Potyvirus* 屬之(+) ssRNA 病毒，會在香蕉苞葉上產生暗紅色紡錘型病斑，於葉子及假莖上則產生褪色紡錘狀嵌紋病斑。該病毒可藉由蕉苗與媒介蚜蟲進行傳播，已在東南亞及南亞地區造成顯著減產。該病毒在國際上被列為重要檢疫病毒，無論香蕉種苗的進口與出口皆需要檢查該項病毒。目前香蕉種苗的外銷成為臺灣香蕉產業的另一項選擇，因此開發出精準且快速的檢測方式至關重要。本研究開發用於檢測該病毒之單株抗體，將應用於 ELISA 檢測技術，以利進出口檢疫使用；除此之外，為確保精準度，也同時建立之反轉錄-聚合酶鏈鎖反應 (Reverse transcription-polymerase chain reaction; RT-PCR) 技術以供選擇。另一方面，BBrMV 在臺灣最早的紀錄為 2006 年於屏東恆春採集到的三尺蕉，但近年來幾乎無相關記錄。國內目前尚未進行針對 BBrMV 的大規模田間調查，該病毒是否於田間存在、分布、以及否存在不同系統仍有待釐清。運用開發出之快速檢測系統，本研究自臺灣各地廣泛針對 BBrMV 進行調查，得知該病害僅在臺灣南部有零星案例出現，現階段對於田間之威脅較小。本研究以快速且精準之檢測技術了解 BBrMV 在臺灣之分布，未來期望開發出之檢測系統能夠協助國內推動「香蕉健康種苗制度」與「蕉苗外銷」。

C. 病毒組

C01 臺灣海芋微嵌紋病毒 (*Zantedeschia* mild mosaic virus) 發生調查及其分子特性分析

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Occurrence and sequence analyses of Zantedeschia mild mosaic virus in Taiwan

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海芋為天南星科 (*Araceae*)、馬蹄蓮屬 (*Zantedeschia*) 的多年生球根花卉，在國內外之花卉市場及國內休閒觀光農業均具有重要地位，然而其栽培過程中易受病毒危害。海芋微嵌紋病毒 (*Zantedeschia* mild mosaic virus, ZaMMV) 首次於 2001 年於臺灣發現，並於 2003-2004 年間之田間調查結果顯示此病毒為廣泛發生於臺灣海芋栽培區之主要病毒。臺灣海芋栽培品種多樣，除了國內育成的海芋新品種之外，亦藉由國際貿易引進國外繁殖種球與新品種，品系及來源複雜、田間管理較為粗放，加上在過去 20 年間並未針對海芋進行病害調查，以至於對於台灣海芋栽培的流行病毒種類更替、病毒菌株變異或特性演化等資訊相對貧乏。本研究於臺灣三個海芋產區包括神岡、后里及竹子湖地區共採集 150 個疑似病毒感染的樣本，以酵素免疫吸附分

析法 (enzyme-linked immunosorbent assay, ELISA) 進行 7 種感染海芋病毒之檢測，結果顯示三個地區疑似病毒感染海芋中，以 ZaMMV 和海芋嵌紋病毒 (*Zantedeschia* mosaic virus, ZaMV) 的檢出比例最高，其中神岡及后里地區之樣品測得複合感染 ZaMMV 與 ZaMV 分別為 25%及 32.4%，竹子湖地區則為 7.4%。根據 NCBI 資料庫序列比對的結果顯示，臺灣過去所分離到的 ZaMMV 病毒株 (NC_011560 及 AY518550) 在鞘蛋白 N 端具有一段特有的重複麩醯胺酸 (glutamine, Q) 序列，因此本研究針對檢出 ZaMMV 之樣品進一步利用 Potyvirus 屬簡併式引子對進行增幅及選殖，將選殖獲得之 12 個 ZaMMV 選殖株進行鞘蛋白核酸序列分析，結果顯示分離株彼此之間的核苷酸相同度為 82.9-100%，其中 9 個病毒分離株與前人發表之臺灣病毒株 ZaMMV-T17Q (AY518550) 核苷酸序列相同度為 99.5-100%，胺基酸序列相同度 99.4-100%，且其鞘蛋白 N 端皆有一段重複麩醯胺酸序列；另外 3 個病毒分離株則與 ZaMMV 紐西蘭病毒株 (EU532065) 較為相似，其核苷酸序列相同度為 91.7-92.2%，胺基酸序列相同度 93.0-94.0%，而鞘蛋白 N 端則未發現重複麩醯胺酸序列。本研究田間調查結果顯示臺灣海芋上存在有 ZaMMV 紐西蘭病毒株，而序列分析結果則顯示鞘蛋白上的重複麩醯胺酸序列為台灣分離株所特有；未來將探討鞘蛋白 N 端胺基酸序列對 ZaMMV 病原性、寄主範圍及傳播特性之影響。

C02 蔥科之分蔥潛隱病毒快速檢測技術開發與應用

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台灣地區種植的青蔥 (*Allium fistulosum* L.) 以四季蔥為大宗，全年栽培面積為 4,460 公頃，主要產區分佈在彰化縣 1,910 公頃、雲林縣 1,476 公頃、宜蘭縣 443 公頃 (110 年農業統計年報)。青蔥一般經濟栽培只能利用分株繁殖，長期分株繁殖，分蔥潛隱病毒(shallot latent carlavirus, SLV) 因無明顯病徵顯現，易隨分株苗潛藏在植株內一代代傳下去，植株生長勢逐漸減弱，經濟產能降低的退化現象，系統性的病毒危害在發病後已沒辦法挽救，因此分蔥潛隱病毒快速檢測技術的開發有助於健康種苗之生產，徹底解決病毒問題。以韭菜和青蔥分離株之抗體進行交金結合測試，結果顯示青蔥分離株之抗體效價較高，因此，以青蔥分離株進行快速檢測試紙的開發。應用於田間青蔥病毒之檢測，本研究發展之分蔥潛隱病毒快速免疫試紙條應用於青蔥病毒檢測，結果顯示 SLV strip 之檢出率高於 ELISA；時效提高，唯檢測成本高出一倍，未來得視需求選擇檢測方式。

C03 Application of induced resistance microbe for the control of tomato yellow leaf curl Thailand virus on tomato

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Tomato Yellow Leaf Curl Thailand Virus (TYLCTHV) is a member of the Begomovirus genus and poses a significant threat to tomato (*Solanum lycopersicum*) cultivation in Thailand and neighboring regions. Characterized by distinct symptoms including yellowing and curling of leaves, TYLCTHV infection leads to reduced plant vigor and fruit yield, causing substantial economic losses to farmers. The virus is primarily transmitted by the whitefly vector, *Bemisia tabaci*, which facilitates its rapid spread within and between tomato fields. In 2022, Taiwan experienced significant agricultural losses due to the outbreak of TYLCTHV, a devastating disease affecting tomato plants. The outbreak underscores the urgent need for enhanced surveillance, research, and proactive measures to safeguard tomato crops against future viral threats and to ensure the resilience of Taiwan's agricultural sector in the face of emerging plant diseases. An induced resistance *Bacillus velezensis* strain JS, was tested for its efficacy in controlling TYLCTHV on tomato. The results showed that for the large-fruited tomato variety 301, the incidence rate in the treated group decreased from 50% in the control group to 10%, with alleviated symptoms. Furthermore, when the JS strain was applied to severely affected fields, compared to those without JS treatment, tomato plants exhibited reduced disease severity, resulting in an increase in final yield of over 30% and improved fruit quality. Detection of five induced resistance-related genes, one of which has a difference in expression between control and treated plant. In the future, the mechanism is to comprehensively understand the metabolic and gene expression changes in tomato plants after the application of JS fertilizer through integrated interdisciplinary analysis.

C04 宜蘭青蒜產區病毒病罹病情況調查

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Investigation on virus disease in Yilan green garlic production areas

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大蒜 (*A. sativum* L) 為蔥科蔥屬 (*Allium*) 之作物，在臺灣之種植與食用方式有採收地下部鱗莖之「蒜頭」，亦有採收地上葉部之「青蒜」。依據我國 111 年農業統計年報，青蒜該年度種植總面積為 343 公頃、總產量 6,312 公噸，宜蘭為青蒜之重要產區，該年度種植面積 92 公頃為全國最高。蒜以鱗莖進行無性繁殖，容易感染並傳播系統性之病毒病，據文獻記載臺灣地區之大蒜病毒多達 9 種，近年因鑑定技術進步與接種試驗後，現存且可能流行者應為洋蔥黃萎病毒 (*Onion yellow dwarf virus*, OYDV)、韭蔥黃條班紋病毒 (*Leek yellow stripe virus*, LYSV)、分蔥潛隱病毒 (*Shallot latent virus*, SLV)與大蒜普通潛隱病毒 (*Garlic common latent virus*, GCLV)。宜蘭青蒜產區已近 20 年未有病毒病之調查，本場為瞭

解青蒜目前之帶毒情況，作為往後蒐集無帶特定病毒的種蒜並推行健康種蒜之重要參考資料，於 112 年起陸續於三星鄉、宜蘭市與五結鄉等產區共 7 個樣點採樣，並以酵素結合免疫吸附分析法 (ELISA) 進行病毒檢測，113 年進一步依照種植總面積約每 3 公頃設 1 採樣點，共調查 21 個樣點約 70 公頃。112 年結果顯示 SLV 檢出率約 30%、OYDV 約 19%、LYSV 約 14%與 GCLV 約 41%；113 年結果顯示 SLV 檢出率達 90%、OYDV 約 76%與 GCLV 約 32%，各產區帶毒種類差異雖大，但 113 年所有樣點 SLV 檢出率皆高，宜蘭市與五結鄉樣本更為 100%檢出。宜蘭地區栽植品種為軟骨蒜，為會抽蒜苔之品種，因蒜苔有較高機率不被病毒侵染，因此從帶毒比率相對低的田區採收蒜瓣與蒜苔，檢測無特定病毒者種植於隔離網室中，後續繁殖並篩選作為健康種蒜之材料。

C05 Innovations in diagnostic tools for accurate detection of Cucumber mosaic virus

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Cucumber mosaic virus (CMV) the type member of the genus Cucumovirus. CMV is considered as one of the most primitive viruses. Unlike other members of the family Bromoviridae, CMV have a very broad, collective host range, infecting more than 1200 plant species in over 100 families, including fruit crops, vegetables and ornamentals, both monocots and eudicots. Seedlings emerged from the infected seeds initially showed mottling and wrinkling of leaves, which further intensified as leaf deformation and stunted appearance compared to healthy ones, and the presence of CMV was confirmed by RT-PCR. CMV is seed-borne in chilli and transmitted from seed to seedlings and the rate of transmission as determined by grow-out test and RT-PCR. The management of the virus in pepper is difficult and expensive in cultivation under a structure and open field production. In the field, peppers are infected frequently with several viruses during a growing season, which leads to reduced yield and seedlings quality. A real-time PCR based assay combined with TaqMan chemistry was developed for detection of the CMV in pepper seedlings. The designed probe for specific to CMV was detected without electrophoresis analysis and effective removal of PCR inhibitors. To evaluate the detection capacity of RT-PCR, and to prove its reliability, a reverse transcription polymerase chain reaction assay was performed for comparison. The assay showed a relative higher sensitivity comparable to the PCR reaction. The assays presented here could assist in the implementation of quarantine measures for CMV on site identification and in routine indexing of CMV for the production of virus-free pepper.

C06 Comparative analysis of diagnostic techniques for Squash leaf curl virus

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A novel TaqMan-based real-time polymerase chain reaction (qPCR) technique has been devised to identify and measure Squash Leaf Curl Virus (SLCV), a member of the Begomovirus genus within the Geminiviridae family. This assay, designed to target the AV1 (coat protein) gene, and has been sequence analyzed to ensure that it is specific for SLCV isolates and not reactive with other melon viruses. Remarkably, the developed assay can detect the virus in total nucleic acid at low concentrations, showcasing its exceptional sensitivity. In comparison to traditional PCR methods, the qPCR assay exhibits approximately 100-fold greater sensitivity and has successfully amplified SLCV from various cucurbit hosts as well as from viruliferous whiteflies. Furthermore, validation of the assay was conducted using melon samples infected with one or more viruses obtained from field collections. The system not only demonstrates high sensitivity but also offers a rapid and efficient means of detecting tomato viruses, thereby presenting a valuable tool for disease surveillance and management in agricultural settings.

C07 瓜類種子甜瓜壞疽斑點病毒檢測技術之建立

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Establishment of detection techniques for *Melon necrotic spot virus* in Cucurbitaceae seeds

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葫蘆科 (Cucurbitaceae) 瓜類作物廣泛分布於熱帶和亞熱帶，為全球重要作物之一，亦為臺灣不可或缺的蔬果，2022 年全球栽培面積共達 849 餘萬公頃，以西瓜佔居首位約 291 餘萬公頃，其次為胡瓜、甜瓜及南瓜 (國際農糧組織 FAO, 2022)。瓜類作物栽培期間容易遭受真菌、細菌、病毒等危害造成植株生長不佳，果品不良甚至減產，影響農民收益甚鉅。近年來因全球農作物貿易跨區栽培及供應，種子銷售到全球各地栽種愈趨頻繁，病毒隨種子跨國長距離傳播之例子愈增，種傳問題已是各國關注的焦點。文獻指出，全球可感染瓜類作物的病毒已超過 50 種，根據臺灣植物病害名彙記錄可感染瓜類作物的病毒有 10 餘種，分屬於 *Cucumovirus*、*Potyvirus*、*Leteovirus*、*Tospovirus*、*Begomovirus*、*Crinivirus* 及 *Tobamovirus* 等。甜瓜壞疽斑點病毒 (*Melon necrotic spot virus*, MNSV) 為 *Tombusviridae* 科 *Carmovirus* 屬之顆粒病毒，單鏈正股核酸病毒 (ssRNA)，基因體 4.3 kb，全球於 1960 年首次紀錄在日本的甜瓜，隨後快速遍及全球各洲，可感染葫蘆科多種瓜類作物包括甜瓜、胡瓜及西瓜等，透過機械工具、種子帶毒及土壤媒介真菌 (*Olpidium* spp.) 等

途徑傳播，受 MNSV 感染之洋香瓜葉片可見密集針狀褐斑或帶黃暈之壞疽斑點，嚴重時於葉柄處呈現褐色壞疽狀，莖部易因壞疽而斷裂，最終整株枯亡。本場依照國際種子檢定通則，建立酵素連結抗體法 (Enzyme-linked immunosorbent assay，ELISA) 及反轉錄聚合酶連鎖反應 (Reverse transcription-PCR，RT-PCR) 檢測方法，協助輸入種子檢查。種子於分樣研磨後，以 MNSV 抗體 (Agdia®) 進行 ELISA 檢測作第一步判讀，若呈陽性反應，再進一步進行 RT-PCR 並解序確認。本試驗為了解種子萃取液對病毒的遮蔽影響，以健康甜瓜種子萃取液為稀釋基質與 MNSV 病組織液做 10 倍依序稀釋進行 Direct ELISA，結果可見含病毒之種子液不影響 ELISA 之檢測。另選用 MNSV1/2 (鞘蛋白基因區域)、MNSV3/4 (移動蛋白區域) 及 MNSV5/6 (RdRp 區域) 引子對分別以罹病葉片及種子萃取液進行 RT-PCR，比較各引子對之適用性，初步結果顯示以 MNSV3/4 引子對用於罹病葉片檢測為佳，若為種子樣本則以 MNSV1/2 引子對較佳。本研究結果可應用於 MNSV 之監測及邊境種子檢疫工作，有助於穩定國內瓜類產量及產能。

C08 國內香莢蘭病毒 Ornithogalum mosaic virus 之發生鑑定

陳金枝、林靜宜、林玫珠、江芬蘭 (農業部農業試驗所植物病理組) First report of Ornithogalum mosaic virus infecting domestic *Vanilla* spp. and virus identification

Chen, C. C., Lin, C. Y., Lin, M. J., and Chiang, F. L. (Plant Pathology Division, Taiwan Agricultural Research Institute, MOA, Taichung)

香莢蘭 (*Vanilla* spp.) 為蘭科 (Orchidaceae) 多年攀緣性的常綠植物；香莢蘭發酵後的果莢，即是有「香料皇后」之稱的香草。香莢蘭種植後約需 3-5 年才會量產果莢。香莢蘭栽培期間有真菌、蟲害及病毒引起的病害，文獻上記載可感染香莢蘭的病毒至少十種。本研究以間接式-酵素連結免疫吸附反應 (Indirect enzyme-linked immunosorbent assay; indirect ELISA) 及反轉錄-聚合酶鏈鎖反應 (Reverse transcription-polymerase chain reaction; RT-PCR)進行國內香莢蘭病毒種類之檢測調查，於 2020 年由后里所採集的香莢蘭植株葉片 (樣品代號 HL-Van1) 出現嵌紋斑駁徵狀，檢出有複合感染蕙蘭嵌紋病毒 (Cymbidium mosaic virus; CymMV)、齒舌蘭輪斑病毒 (odontoglossum ringspot virus; ORSV) 和天鵝絨嵌紋病毒 (Ornithogalum mosaic virus; OrMV)；經由機械傷口接種法將此複合 3 種病毒感染之香莢蘭 HL-Van1 罹病組織液接種於健康的香莢蘭葉片，仍引起複合感染且原始 HL-Van1 病株相類似的病徵，於接種試驗雖無法揭示單獨受 OrMV 感染的香莢蘭病徵型態，但於 RT-PCR 檢測中，分別以 OrMV 專一性引子對、2 組 Potyvirus 廣效性引子對進行檢測，均可由原始 HL-Van1 樣品及接種後的香莢蘭 HL-I5 樣品檢出 OrMV 的產物，且經核甘酸定序後確認為 OrMV。HL-Van1-OrMV 分離株之鞘蛋白核甘酸與胺基酸序列與 NCBI GenBank 上已登錄之印度香莢蘭 OrMV (AY845014) 的相同度分別高達 98.4 及 99.2%；而與天鵝絨、虎眼萬年青、水仙、唐菖蒲和鳶尾花 OrMV 分離株之鞘蛋白核甘酸序列相同度介於 81.3-98.6%，胺基酸序列相同度則介於 90.5-98.8%。OrMV 為 Potyvirus 屬的病毒成員之一，其寄主範圍廣，涵蓋天鵝絨、鳶尾花等花卉植物。以鞘蛋白胺基酸序列進

行香茨蘭 HL-Van1-OrMV 與其他寄主來源 OrMV 分離株之類緣關係,結果顯示本研究之香茨蘭 HL-Van1-OrMV 與同屬香茨蘭來源的印度 OrMV (AY845014) 有更相近的類源關係,但採集自屏東的香茨蘭 OrMV 分離株則與荷蘭鳶尾花 OrMV 的類源較相近,縱觀所分析的 OrMV 分離株之間的類源關係,尚未有明顯受寄主來源或不同地區的影響。文獻上已有 OrMV 感染香茨蘭的報告,而本研究為國內首次發現香茨蘭 OrMV 的病毒病紀錄,並開發可有效檢測香茨蘭 OrMV 之引子對。香茨蘭可以組織培養或扦插法作無性繁殖量化,因此病毒可隨扦插苗而傳播;調查桃園、台中、南投埔里、彰化及屏東等處之香茨蘭 OrMV 發生概況,目前於后里及屏東之香茨蘭檢出有 OrMV,此病毒在國內香茨蘭的發生實況仍持續調查與釐清。

C09 評估臺灣甜瓜捲葉病抗病性

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Evaluation of melon resistance to leaf curl disease

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由於瓜類捲葉病嚴重危害該類作物種植與生長,造成產量損失可達 100%。該病害主要流行於熱帶、亞熱帶地區,並引起瓜類作物葉片捲曲、黃化、嵌紋及矮化等病徵,病原為菸草粉蝨 (*Bemisia tabaci*) 傳播的雙生病毒科豆金黃嵌紋病毒屬 (Begomovirus) 病毒。在亞洲此病害主要由豆金黃嵌紋病毒屬的 Tomato leaf curl New Delhi virus (ToLCNDV)、Squash leaf curl China virus (SLCCNV)、以及 Squash leaf curl Philippine virus (SLCuPV) 等病毒所引起,以上病毒均為雙基因體 (含有基因體 DNA-A 與 DNA-B)。選育抗品種為抗瓜類捲葉病害最有效方式之一,對 22 個甜瓜品系 (M1-M22) 進行抗病性評估,以農桿菌媒介接種 ToLCNDV 後,觀察植株病徵表現,並使用專一性引子對以 PCR 方式檢測病毒,其中 M1 與 M3 品系的接種植株均無病徵表現,且病毒檢測皆呈陰性,後持續評估及純化自交至第 4 世代,其篩選植株均無病徵表現,且病毒檢測皆呈陰性。此外,以農桿菌媒介接種 SLCCNV,進行 M1 與 M3 抗病性評估抗性評估,接種植株亦均無病徵表現,且病毒檢測皆呈陰性。以上顯示 M1 與 M3 對 SLCCNV 與 ToLCNDV 均具有抗病性。此二甜瓜品系與感病親本的雜交一代植株,於接種 SLCCNV 及 ToLCNDV 病毒後均表現病徵,推斷 M1 與 M3 之對 SLCCNV 與 ToLCNDV 之抗病性為隱性抗病性,此二品系未來可用於甜瓜抗病育種之種原,然需持續探討其抗病遺傳特性。此外,對其它可能含有抗病性的甜瓜品系,則尚需進行抗病性純化,以及抗病遺傳特性研究,以為甜瓜捲葉病抗病育種之重要種原。

C10 以有益微生物評估番茄生長及對抗黃化捲葉泰國病毒之能力

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Evaluation of beneficial microbes on tomato growth and their ability to resist Tomato yellow leaf curl Thailand virus

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番茄 (*Solanum lycopersicum*) 是全球重要經濟作物，在種植過程很容易受到病毒感染而影響產量及品質。在台灣，番茄病毒病害主要由 *Begomovirus* 屬的病毒所引起，例如：番茄黃化捲葉泰國病毒 (tomato yellow leaf curl Thailand virus, TYLCTHV)和番茄捲葉台灣病毒 (tomato leaf curl Taiwan virus, ToLCTWV) 等，這些病毒會造成番茄黃化、捲葉、矮化和生長停止。由於目前常用來對抗病毒病害及媒介昆蟲的方法仍存在許多缺點，因此，使用生物製劑誘導植物免疫反應來對抗病毒相對更安全、環保、成本低且容易操作。本試驗利用三種有益微生物來評估是否能增進番茄對抗病毒的能力，同時也偵測植物防禦酵素之表現及植株生長的能力。所測試之菌株包括來自農委會高雄農業改良場之鏈黴菌 *Streptomyces misionesis* KHY26、貝萊斯芽孢桿菌 *Bacillus velezensis* KHH13 及農業試驗所之 *Bacillus* sp.。溫室試驗結果顯示，有澆灌此三種有益微生物之番茄，其種子發芽率皆有顯著提升。而微生物處理後再接種病毒之植株，除了可減緩病毒感染後之病徵表現外，也可誘導多酚氧化酶 (Polyphenol Oxinase, PPO) 表現；而有澆灌微生物之番茄生長勢及地上部鮮重也比對照組增加。另外，在露天栽培番茄的試驗則發現，單純施用微生物來防治番茄病害之效果不明顯，因此建議搭配其他病蟲害管理策略。本試驗初步結果顯示，有益微生物具有促進番茄種子萌芽、誘導番茄免疫反應及減緩病毒病徵表現之能力，此外，也可促進番茄植株之生長。

D. 學生論文宣讀競賽組

SA01 評估高溫對水稻與徒長病菌交互作用之影響

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Assessing the effect of high temperature on the interaction between rice and *Fusarium fujikuroi*

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氣候變遷自 19 世紀以來成為國際關注的議題，其中地表平均氣溫的提升是最受關注的指標之一。1911 至 2020 年間臺灣的平均氣溫已上升 1.6℃，且極端高溫事件 (濕球溫度≧35 ℃) 發生頻率逐漸上升。病害作為植物、病原菌與環境三互動的結果，受到全球暖化極大的衝擊，前人研究中多預測高溫會加劇病害的發展。由 *Fusarium fujikuroi* 引起的水稻徒長病是臺灣重要的水稻病害之一，但高溫對該病害的影響目前仍不清楚。本研究主要區分為兩個部分：首先，以 22 支臺灣徒長病菌田間代表分離株為材料，於 30℃及 35℃下測試人工培養基中的菌絲生長、孢子

發芽、gibberellin A3 (GA_3) 及 fusaric acid 生成量，發現 35℃下菌絲生長、孢子發芽及 GA_3 生成均受到顯著抑制，fusaric acid 生成量則顯著提升。接著，針對感病品種 *Zerawchanica karatals* (ZK) 及抗病品種臺農 67 號於 35/30℃和 30/25℃人工氣候室中進行接種，發現 35/30℃下植株的罹病嚴重度、徒長病菌 DNA 含量顯著降低。值得注意的是，ZK 植體內之 GA_3 含量受到高溫抑制、fusaric acid 不受影響；臺農 67 號中則無論是 GA_3 或 fusaric acid 含量都不受高溫改變。本研究結果顯示，35℃高溫對徒長病菌的 *in vitro* 及 *in planta* 生存皆有負面影響，不利於徒長病發生。未來將進一步分析高溫逆境下的水稻防禦途徑及徒長病菌致病途徑轉錄調控，希望能深入釐清高溫、水稻、徒長病菌間的三方交互作用。

SA02 Spatiotemporal population biology of *Phytophthora nicotianae* in Taiwan

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Phytophthora nicotianae Breda de Haan (*P. parasitica* Dastur) is a phytopathogenic oomycete of worldwide importance. In Taiwan, this pathogen infects approximately 103 plant species across 85 genera, including various economically important fruit trees, vegetables and ornamental crops, making it stand out among *Phytophthora* species. Due to its substantial economic impact, extensive research has been conducted on *P. nicotianae* in the past. Different findings on dispersal, the mode of reproduction, and population structure have been documented in various countries. However, studies on population biology of *P. nicotianae* in Taiwan are still limited. Hence, isolates obtained from different spatiotemporal origins and horticultural crops were genotyped using 9 simple sequence repeat markers to investigate the population structure and mode of reproduction. A total of 121 multilocus genotypes were identified from 181 isolates. Regardless of spatiotemporal or hosts origins, the *P. nicotianae* population displayed both high genotypic diversity and clonality, suggesting a mixed mode of reproduction in Taiwan. In spite of the high genotypic diversity, isolates obtained from the same host had higher similarities based on minimum spanning network and principal coordinate analyses. Pairwise Wright's fixation index, F_{ST}, also indicated higher genetic differentiation between host populations rather than spatiotemporal populations. To further investigate whether *P. nicotianae* populations exhibited host preference, cross-inoculation of six representative isolates collected from eggplant, Welsh onion, passion fruit, strawberry, celosia, and periwinkle on their respective hosts was conducted. Relative treatment effect and area under disease progress stairs revealed that although some of the isolates were able to infect several hosts, the *P. nicotianae* isolates were prone to cause more severe symptoms on their host of origin, suggesting a certain degree of host preference in the pathogen.

SA03 Diversity of fungal pathogens causing different banana leaf diseases in Taiwan

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Musa sp. (Banana) is a crucial food crops in Taiwan. During the plantation, different pathogens can affect the quality and quantity of bananas. In recent years, the diversity of fungal pathogens that cause banana leaf diseases in Taiwan has remained unclear. Between 2021 and 2023, banana leaves with different symptoms were collected from Nantou, Chiayi, Pingtung, and Taitung. In total 175 fungal isolates were cultured and identified based on fungal morphology and internal transcribed spacer, ITS sequencing. *Alternaria* spp. and *Cordana musae* were identified as the predominant pathogens in our collection. *P. fijiensis* and *Guignardia musae* were also found during this investigation. Three isolates including *Corynespora cassiicola*, C*urvularia geniculata*, and *Pyricularia angulata* were not recorded in Taiwan before and are able to cause symptom on the banana leaves. Twenty-one *Alternaria* isolates showed similar morphological characteristics and have close phylogenetic relation. The *Alternaria* isolates all belonged to the *Alternata* section, including *A. burnsii*, *A. jathincicola* and some could not be identified as species based on phylogenetic analysis. Pathogenicity test was conducted on three prevalent cultivars in Taiwan, including Tai-Chiao No.5, Pei-Chiao and Oolong-Chiao. Tai-Chiao No.5 was the most susceptible cultivar in the study compared to Pei-Chiao and Oolong-Chiao. Thin layer chromatography analysis (TLC) was employed to identify the toxins produced by the *Alternaria* isolates. The result showed that the amount of fungal toxins correlated to the virulence on banana leaves. This study provides basic knowledge about the pathogens associated with different banana leaf diseases and various *Alternaria* spp. can cause banana leaf diseases in Taiwan, the toxins of each *Alternaria* isolate are factors that affect their virulence on banana leaf.

SA04 軸腐相關真菌相及田間衛生措施對台灣香蕉軸腐病發生之影響

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The effects of associated fungal flora and field sanitation strategies on banana crown rot progress in Taiwan

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香蕉 (*Musa* spp.) 為全球第一大宗貿易果品，在臺灣為重要熱帶果樹，2022 年栽培面積為 15,307 公頃，出口量 1,542 公噸；主要栽培於中部山區、嘉南平原及高屏溪流域等。香蕉在臺灣生長期約 10–13 個月，果實為更年果，採收後經低溫 (13–15 ℃) 貯運及催熟後上市。香蕉貯運期間常因軸腐病 (crown rot) 造成果軸壞疽或腐爛，後致果指脫落，嚴重影響果品價值。軸腐病為複合病害 (disease complex)，國外許多報告指出常見病原為 *Colletotrichum musae* 、 *Fusarium* spp. 及

Lasiodiplodia theobromae 等；各地病原組成不盡相同。臺灣雖有早期文獻描述軸腐病菌之種類，然完整之調查闕如。除病原菌組成，軸腐病之病勢強度也被指出或與栽培環境有關；故本研究調查臺灣香蕉主要產區軸腐病之發生與其相關真菌相及田間環境的關係，以釐清病因並對後續防治提出參考建議。調查於 2022–2023 年間至中部山區、嘉南平原、屏北及屏南等樣區，採集軸腐樣本並分離得到 266 株真菌，經形態觀察及 internal transcribed spacer (ITS) 序列分析鑑定主要為 *Penicillium*、*Colletotrichum* 及 *Fusarium* 等屬，分離頻率分別為 24.81、22.56 及 13.53%；其中在 4 個樣區分別歸納出 16 屬 (51 分離株)、14 屬 (52 分離株)、22 屬 (107 分離株) 及 19 屬 (57 分離株) 真菌。分析樣點間之真菌多樣性，結果表明各樣區之 Chao 1 及 Shannon Diversity Index 分別為 10.02–18.75 及 1.29–1.49，樣區間兩指數皆無顯著差異 ($p \leq 0.05$)；Bray-Curtis 分析則顯示各樣區之真菌族群組成不同，真菌相相似度與樣區間距離有關。後續依 ITS 鑑定結果之各屬分離株中，依分離比率隨機挑選分離株進行病原性測定。將培養於 PDA 7–14 天之真菌菌絲塊依常溫無傷口、常溫有傷口、低溫 (13–15 ℃) 無傷口及低溫有傷口等 4 種條件接種於青香蕉上，記錄接種後第 7 與第 14 天病斑直徑 (cm) 並再分離病斑處真菌確定與接種者相同。接種結果以主成分分析 (principal component analysis) 可將分離株依毒力強弱分為 1–4 毒力群，第 1 群包含 *C. musae*、*F. proliferatum*、*F. sacchari* 及 *L. theobromae* 等菌種；其中 *C. musae* 在各樣區分離頻率最高，為臺灣香蕉軸腐病主要病原菌之一。進一步於 2023 年 7 月 (夏) 及 2024 年 1 月 (冬) 調查田間雜草覆蓋面積 (WCA)、殘體覆蓋面積 (DCA)、老病葉未割除比率 (RL) 及香蕉活葉指數 (INLL) 等田間衛生或環境條件與採收後軸腐病病害發展曲線面積 (area under disease progress curve, AUDPC) 之相關性；結果指出夏季之 DCA 及 RL 與 AUDPC 呈顯著相關($p \leq 0.05$)；冬季時 AUDPC 則與 WCA 及 INLL 顯著相關 ($p \leq 0.05$)，此結果顯示良好的田間管理模式可降低香蕉軸腐病之嚴重度。

SA05 Physiological factors affecting the incubation period of dragon fruit stem canker

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Dragon fruit stem canker, caused by *Neoscytalidium dimidiatum* (Penz.) Crous & Slippers, is an emerging disease in global dragon fruit production areas. The pathogen can cause yellow sunken spots and necrotic lesions on cladodes and fruits, leading to severe yield losses and a reduction of market value. Based on our field observations, stem canker symptoms could distribute across the entire cladode or be limited in certain sections of infected cladodes. However, the effect of cladode developmental stages and physiological conditions on pathogen invasion or the incubation period remains unexplored. We hypothesize that the distribution of symptoms on the cladode may be associated with epidermal thickness and the age of the cladode sections when weather conditions are conducive. To explore the relationship between the developmental stages of cladodes, the epidermal

thickness, and the incubation period of dragon fruit stem canker, quantitative data were collected after artificial inoculation of cladodes in a controlled environment. The results exhibited a positive association between the incubation period and both epidermal thickness and cladode age. Younger parts of the cladode with thinner epidermis tend to have a shorter incubation period. Additionally, symptoms developed more rapidly in younger parts, while progressing slower in the matured and aged parts of the cladodes. To further investigate the protective effect of the epidermis, the cladodes were inoculated with or without wounds. The results revealed that the incubation period was shortened when the cladodes were wounded compared to unwounded ones. Nevertheless, lesion expansion in matured and aged parts was still slower compared to younger parts, suggesting that in addition to the physical defense provided by the epidermis, ontogenic resistance or other defense responses may also be involved in different developmental stages of the cladodes.

SA06 以多系品種及基因堆疊策略強化水稻‘高雄 145 號’對稻熱病之持久抗性

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Improving blast resistance of the rice cultivar ‘Kaohsiung 145’ using multiline variety and gene pyramiding strategies

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使用抗病品種為最有效、經濟且環保的防治方式，但稻熱病菌演化快速，只帶有單一抗稻熱病基因的品種往往在推出後的數年內就會失效。本研究利用多系品種與基因堆疊策略，改善感病栽培稻‘高雄 145 號’對於稻熱病之抗性。多系品種部分，自 2021 年起進行三年的田間試驗，將高雄 145 號導入系 KHY5508 (*Pi9*)、KHY5496 (*Pik-h*)、KHY5491 (*Ptr*) 以混合栽培模式種植於高雄美濃、大寮；臺東關山及屏東長治等地，田間調查結果顯示混植品系與純系相比對於葉稻熱病及穗稻熱病皆具有良好抗性，且其農藝性狀與米質亦與高雄 145 號相似。基因堆疊品系部分，則建立帶有 *Pi9*、*Pik-h*、*Ptr* 以及帶有 *Pi2*、*Pik-h*、*Ptr* 之三基因堆疊品系。帶有 *Pi9*、*Pik-h* 及 *Ptr* 之堆疊品系 KHY5698 目前已完成一年區域試驗，對葉稻熱病呈現 2-3 級之抗病性，對於穗稻熱病呈現 1-3 級之抗性至中等抗性。而

帶有 *Pi2*、*Ptr* 及 *Pik-h* 之品系目前正在進行初級產量比較試驗。為延長堆疊品系之田間抗性，本研究也將帶有水平抗性基因 *pi21* 之「戰捷」與帶有 *Ptr*、*Pik-h*、*Pi9* 之 KHY5697 進行雜交，將水平抗性基因導入堆疊品系中，同時以分子標誌輔助篩選出帶有抗病基因之品系。期盼透過增加田間抗病基因多樣性，建立不易被病原菌克服之持久抗病栽培體系。

SA07 臺灣中部地區藍莓果樹病害的初步調查

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Preliminary survey of blueberry diseases in central Taiwan

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藍莓為原產於溫帶地區之落葉性果樹，其果實味美且富含多種營養成分與抗氧化物質，因此受到許多民眾的喜好。早期在臺灣試種時，由於藍莓需要經過特定時長的冷涼氣候才能開花，因此商業栽培有限。但近年來的品種在選育及改良後，已有許多低需冷性且適合亞熱帶及熱帶地區種植的品種問世，在臺灣也吸引許多農友嘗試種植。然而，藍莓產業在臺灣仍處於萌芽階段，對於藍莓在調適臺灣的氣候環境以後，栽培期間可能遭遇的病害資訊仍十分有限，因此也限制了產業的發展。此外，進口藍莓可能存在用藥不符合臺灣規定等問題，而產生食品安全的疑慮。本研究的主要目的，在於調查並釐清臺灣藍莓栽培期間面臨的主要病害種類、病害好發時期，並評估不同病害可能造成的損失，以利發展病害管理措施與國產安全藍莓。自 2022 年 7 月起，本研究已於中興大學試驗溫室與臺中霧峰的藍莓農場採集可能的病害樣本，並初步在藍莓的葉部、莖部與根部發現至少 8 種不同的病徵。經由組織分離與純化培養後，已蒐集、鑑定 5 種以上與藍莓病害相關的真菌或細菌，並保存逾 30 株的真菌與細菌菌株。其中，已完成 *Colletotrichum fioriniae*、*Corynespora cassiicola* 以及 *Xanthomonas euvesicatoria* 之科霍氏法則，確認各菌株在藍莓植株上的病原性，並已進行部分細菌菌株的生理生化測試。未來將持續調查臺灣不同地區的藍莓栽培田區中，主要病害的好發時期與其在時空上的變化，期有助瞭解危害臺灣藍莓的病害與病原菌生態，並發展病害管理策略，建立國產安全藍莓產業基礎。

SA08 Unveiling the diversity of *Pestalotiopsis*-like fungi causing foliar diseases on six precious conifers in Taiwan

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Six conifers belonging to order Pinales, namely *Calocedrus formosana*, *Chamaecyparis formosensis*, *Chamaecyparis obtusa* var. *formosana*, *Podocarpus costalis*, *Podocarpus macrophyllus*, and *Podocarpus nakaii*, are

esteemed as some of the most economically and aesthetically valuable native tree species in Taiwan. However, their seedlings are susceptible to various fungal infections, with leaf blight and wither tip diseases caused by *Pestalotiopsis sensu lato* (referred to as pestalotiopsis-like fungi) being major concerns in forestry nurseries and botanical gardens globally. As part of a survey on fungal diseases affecting aerial parts of these precious conifers in Taiwan, 66 pestalotiopsis-like fungal strains were collected and *Neopestalotiopsis brasiliensis*, *N. camelliae-oleiferae*, *N. cubana*, *N. iberica*, *N. pandanicola*, *N. rosicola*, *Pestalotiopsis neolitseae*, *P. parva*, *P. subshorea*, *P. trachycarpicola*, *Pseudopestalotiopsis elaeidis*, *Ps. ixorae*, and ten tentative clades in *Neopestalotiopsis* were identified associated with leaf blight and wither tip diseases of these conifers. Species identification was based on both phenotypic characters and multi-locus phylogenies from ITS (internal transcribed spacer), *tef1-α* (translation elongation factor 1-α), and *tub2* (beta-tubulin). Species limits were determined using the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) principle, Poisson Tree Processes (PTP), Pairwise Homoplasy Index (PHI) test, Automatic Barcode Gap Discovery (ABGD) method, and Average Nucleotide Identity (ANI). Pathogenicity assessments identified *N. camelliae-oleiferae*, *P. parva*, and *P. trachycarpicola* as major pathogens associated with foliar diseases of these conifers. In addition, *N. brasiliensis*, *N. cubana*, *N. iberica*, *N. pandanicola*, *N. rosicola*, *P. subshorea*, *Ps. elaeidis*, were reported for the first time in Taiwan. This study provides the first assessment of pestalotiopsis-like fungi associated with the leaf blight and wither tip diseases on six precious conifers in Taiwan. Future research will focus on testing the efficacy of fungicides on representative strains, enabling the identification and management of foliar diseases caused by pestalotiopsis-like fungi in these conifers.

SA09 長春花葉斑病之病原菌鑑定與其寄主範圍初探

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Periwinkle target spot caused by *Corynespora cassiicola* and its host range

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長春花 (*Catharanthus roseus* (L.) G. Don) 又名日日春、時鐘花，為夾竹桃科長春花屬的多年生草本觀賞作物，因其具有耐旱易栽培的特性，常用於造園，但有時也被視作一種雜草。2021 至 2022 年間，分別在台灣南部與北部的長春花葉片上出現褐斑且略帶輪紋的病徵，病徵周圍有時可以見到黃暈的情形，枝條亦會受害產生黑褐色壞疽病斑，與先前在長春花上報導的病害紀錄皆不相同。將罹病部位進行組織分離後，純化獲得數個真菌菌株。在完成柯霍氏法則後，將代表菌株培養於馬鈴薯葡萄糖瓊脂培養基並觀察其菌落、產孢構造及分生孢子形態，配合多基因位點序列

分析結果，顯示造成長春花葉斑病的菌株均被鑑定為 *Corynespora cassiicola* (Berk. & M. A. Curtis) C. T. Wei ，且屬於 Dixon 等人 2009 年所發表 PL1 分支群。其菌落生長及孢子發芽的最適溫度，皆介於 24-32 ℃。為比較長春花植株的抗感病性，將代表菌株分別接種於相同品種不同花色，以及不同品種的長春花植株後，結果相同菌株接種在不同花色或不同的品種後，不同花色之間與不同品種之間的罹病度皆無顯著差異。由於 *C. cassiicola* 的寄主範圍廣泛，但不同的病原菌族群之間可能存在寄主偏好性，因此進一步將代表菌株接種於多種植物以測試其寄主範圍。初步結果顯示，茄子與甜椒皆可被感染，但兩者的罹病度都較長春花輕微，而其他供試植物在接種後則不一定會出現壞疽病斑。本研究的結果顯示，造成長春花葉斑病的 *C. cassiicola* 可能危害其他作物，若長春花在農業生態系中成為雜草，是否存在作為感染不同作物的 *C. cassiicola* 之替代寄主的風險，未來將值得再深入探討。

SA10 罹患黃龍病之台灣香檬植株快速衰亡與 *Fusarium* sp.之關聯性

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Correlation between the rapid death of *Citrus depressa* plants with Huanglongbing and *Fusarium* sp.

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台灣香檬 (*Citrus depressa*) 又稱扁實檸檬，因其代謝產物具有多種生理特性而廣受消費者喜愛，栽培面積逐漸擴大，為台灣檳榔廢園轉作之推薦作物。2022 年屏東內埔一處台灣香檬果園內發現病害，病徵包含葉片黃化、植株半側或樹冠黃化、全株黃化死亡、莖基部褐化及根部褐化，採病葉進行碘液反應測試，結果未偵測到澱粉累積現象，但以 *Candidatus* Liberibacter asiaticus 專一性引子進行 PCR 結果產生片段大小 228 bp 之產物。由於碘液檢測結果可能受氣候、病葉種類影響，且檢測靈敏度較低，因此診斷結果為植株感染黃龍病 (HLB)。研究中發現感染植株之莖基部及根部罹病組織經表面消毒培養均分離到 *Fusarium* sp.。作者調查田間台灣香檬病害進程，發現黃化及死亡植株逐月攀升，大部分植株發病呈現黃化後 1 至 2 個月即枯死。由於植株發病至死亡時間與其他柑橘類黃龍病之記錄差異過大，且發病植株莖基部及根部組織均存在有 *Fusarium*，因此進一步探討其是否與植株快速衰亡有關。選用可抑制 *Fusarium* 之菌絲生長及孢子發芽之 Difenoconazole (待克利)，施用於半側黃化之植株，與施用水之對照組相比延緩了植株死亡。研究結果顯示，*Fusarium* 可能與罹患黃龍病之台灣香檬快速死亡有關。未來研究可探討台灣香檬 *Fusarium* 分離株之病原性及與其他柑橘類黃龍病之關聯。

SA11 Characterization of fungal communities associated with leaf blight of invasive *Mimosa* in Taiwan

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Three species of *Mimosa*, namely *M. pudica, M. diplotricha,* and *M. pigra*, are recognized as some of the most invasive plant taxa globally. These plant species have recently been reported throughout Taiwan. *Mimosa* species are well-known for their high invasiveness and remarkable adaptability to alien environments, posing a considerable threat to indigenous plants and native habitats. Urgent measures should thus be implemented to eradicate these invasive *Mimosa* species from Taiwan. During recent field observations, severe leaf blight symptoms caused by fungal infections were observed on leaves of certain *Mimosa* plants in Taiwan. This observation suggests the potential for finding environmentally friendly solutions to control the spread of invasive *Mimosa* in agricultural systems and landscapes. Therefore, this study aimed to identify the main fungal taxa associated with three *Mimosa* species in Taiwan and to identify fungal strains for managing the abundance of invasive *Mimosa* plants. In the present study, a total of 96 fungal strains were isolated from three *Mimosa* species showing leaf blight across Taiwan using a culture-dependent approach. Strains were identified based on multi-locus phylogenetic analysis together with phenotypic data. The study identified 14 genera, including *Alternaria, Bartalinia, Corynespora, Curvularia, Diaporthe, Fusarium, Hymenopleella, Neopestalotiopsis, Periconia, Pestalotiopsis, Phaeosphaeria, Pseudopestalotiopsis, Pseudopithomyces,* and *Robillarda*. *Robillarda* was identified as the predominant fungal genus associated with *Mimosa* (36.46%). At the species level, 30 taxa were identified, among which *Bartalinia kevinhydei, Curvularia vietnamensis, C. prasadii, C. panici-maximi, C. verruculosa, Neopestalotiopsis iranensis*, *Robillarda africana, R. australiana,* and *R. sessilis* were reported for the first time in Taiwan. This project represents the first comprehensive study aiming to investigate the hidden fungal diversity of *Mimosa* in Taiwan. In future studies, these fungal strains will be tested for their pathogenicity towards *Mimosa* to fulfill Koch's postulates. By completing this project, we aim to provide insights into developing non-chemical control methods for eradicating invasive *Mimosa* species in Taiwan.

SB01 The establishment of a CRISPR-Cpf1 ribonucleoprotein delivery system for precision genome editing in *Fusarium oxysporum*

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Fusarium wilt is a severe disease affecting crops worldwide, caused by the soil-borne fungal pathogen *Fusarium oxysporum*. Uncovering the pathogenicity of *F. oxysporum* to hosts is important. However, it requires more effective and precise gene editing tools. Our research aims to establish a CRISPR-Cpf1 (or Cas12a, a novel single RNA-guided endonuclease) system for precise gene editing in *F. oxysporum*. CRISPR-Cpf1 has advantages over the widely

used CRISPR/Cas9 system. For example, the staggered digestion sites on the genome generated by Cpf1 demonstrated high efficiency of homology-directed repair. This feature improves the gene knockout by homologous recombination with a shorter flanking sequence than conventional methods. We used the CRISPR-Cpf1 ribonucleoprotein delivery system to integrate the *EGFP* expression cassette with a 20 bp flanking sequence to disrupt the target gene. To optimize our genome editing platform, we improved the protoplast generation process, reducing the consumption of digesting enzymes. Furthermore, the *Arabidopsis thaliana* inoculation system was applied as a rapid virulence assessment platform of virulence-associated genes in *F. oxysporum*. Our research proposes that the application of CRISPR-Cpf1 could precisely and cost-effectively modify the *F. oxysporum* genome. This system can be used to study genes involved in pathogenicity and host-pathogen interaction. In the future, it could be applied to other *F. oxysporum* subspecies and potentially develop disease control strategies.

SB02 Investigating the PR-1La-dependent signaling pathway in *Ustilago maydis*

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Dimorphic filamentous fungi have the capability to respond to environmental cues, transitioning from vegetative to filamentous cells. This transition enables them to initiate the infection process and complete life cycle within hosts. The shift to filamentous growth requires the activation of subsequent events, including environmental sensing, upregulation of specific genes, and involvement of regulatory networks. We have previously demonstrated that the biotrophic fungus *U. maydis* responds to plant phenolics by inducing filamentous growth through its cell wall-associated protein, UmPR-1La. These UmPR-1La-shielded filaments effectively counteract the toxicity of plant phenolics and enhance survival. However, the specific signaling pathway dependent on the perception of phenolics by UmPR-1La remains unexplored. Here, we demonstrate that *U. maydis* perceives signals through the G-protein signaling pathway to trigger the hyphae formation in an UmPR-1La-dependent manner. The deletion of *GPA3* resulted in cells exhibiting distinct morphology and remaining in filamentous form. Conversely, when the active form of Gpa3 was constitutively expressed, cells remained unresponsive to phenolics and retained sporidial morphology. Interestingly, the deletion of *GPA1* in the Δ*pr-1la*_UmPR-1La strain did not induce filamentation, and the cells remained unresponsive to phenolics. Our findings suggest that, in contrast to the negative role of Gpa3, Gpa1 plays a positive role in *U. maydis* filamentous growth in an UmPR-1La-dependent manner. Gpa2 and Gpa4 are dispensable in the UmPR-1La-dependent filament signaling

pathway. Through comparative transcriptomics analysis, we identified upregulation of components of the G-protein signaling pathway (including Gpa2 and GPCR proteins) and the PKA signaling pathway, as well as effector proteins and transcription factors, both in UmPR-1La-dependent and independent manners. Currently, we are actively investigating the components involved in the UmPR-1La pathway to achieve a comprehensive understanding of signal transduction mechanisms.

SB03 Role of transposon methylation in regulating *Termitomyces eurrhizus* fruiting

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In fungi, the expression of genes may be influenced by the transposable elements (TEs) at promoters through their DNA methylation. However, such correlation is weak and largely unclear. In *Tuber melanosporum*, *Pleurotus*, *Laccaria*, and *Neurospora*, genes located near methylated TEs are likely to be less expressed. However, in *Rhizophagus irregularis*, the expression of around 1/3 of genes exhibits a positively correlation with TE methylation, implying the involvement of additional factors in this regulation, such as TE expression. Here, we aimed to clarify the relationship between TE methylation, TE expression, and their neighboring gene expression in basidiomycete *Termitomyces eurrhizu*, and exemplify our model in its fruiting initiation. We identified 45% of TEs located at promoters having the ability to modulate their neighboring gene expression by both methylation and expression. While these TEs are typically lowly expressed, their expression had a stronger impact on the expression of adjacent genes, compared to TE methylation. This regulation is consistent in all 5 developmental stages of *Termitomyces*. At the fruiting initiation stage, primordium, we observed a significant genome-wide increase in DNA methylation level, which was majorly enriched in the TEs, associating with a generally loss in both TE and neighboring gene expression. Specifically, those genes repressed by significantly hypermethylated TEs at primordium were identified to be involved in vegetative growth. We therefore hypothesized that the fruiting initiation in *Termitomyces* may be promoted by repressing the vegetative pathways epigenetically. Overall, our findings revealed that promoter-embedding TEs with lower expression affecting gene expression through both expression and methylation in *T. eurrhizus*. This epigenetic regulation promotes *T. eurrhizus* fruiting initiation by increasing TE methylation and repressing genes relating to vegetative growth, highlighting the relationship between transposon-associated epigenetic regulation and fungal development.

SB04 Insights into spray-induced gene silencing for controlling plant diseases caused by *Alternaria* spp.

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Spray-induced gene silencing (SIGS) emerges as a promising strategy for environmentally friendly management of plant diseases. The application of SIGS for controlling plant diseases caused by *Alternaria* spp. has not previously been established. Thus, this study aimed to use double-stranded RNA (dsRNA) to target ergosterol biosynthetic genes in two *Alternaria* species, *A. alternata* and *A. brassicicola*, causing devastating diseases in banana, citrus, and brassica. We first explored whether the dsRNA uptake capability varies among different *Alternaria* species or isolates. The result of dsRNA uptake assays demonstrated that both *A. alternata* and *A. brassicicola* could absorb dsRNA. Moreover, eight *Alternaria* isolates obtained from bananas exhibited the ability to absorb dsRNA, indicating that dsRNA uptake by *Alternaria* spp. is not dependent on isolate or species specificity. Furthermore, our findings suggested that the uptake capacity of dsRNA varies at different growth stages, with fungi absorbing dsRNA only from their hyphae but not from spores. Notably, the dsRNA uptake assays conducted on detached banana leaves revealed that fungi can absorb dsRNA during the infection. Applying erg2 and erg24 dsRNAs on banana leaves reduced the lesion size caused by *A. alternata* and downregulation of gene expression as assessed by qPCR. In conclusion, this study provides comprehensive evidence that *Alternaria* spp. can absorb dsRNA during infection and highlights the feasibility of SIGS as a management strategy against *Alternaria* diseases in various crops.

SB05 Comparing the methods for screening resistant/tolerant cucumber accessions to anthracnose

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Anthracnose caused by *Colletotrichum* spp. is the one of most serious and economically devastating disease in open-field and under protected cultivation worldwide. Among *Colletotrichum* spp., *C. orbiculare* affects cucurbit crops including cucumber, squash, watermelon, and pumpkins. Several methods have been used to control anthracnose. However, development of anthracnose-resistant varieties is an effective way for controlling this disease. Information on anthracnose resistance levels in cucumber germplasm and molecular markers associated with resistance would be useful for cucumber breeding. The aim of this study is to identify source of resistance and develop molecular markers linked with anthracnose

resistance *Cucumis sativus* accessions obtained from the Word Vegetable Center (WorldVeg). Here, 35 cucumber accessions were tested for its reactions to *C. orbiculare*. Moreover, three screening methods, cotyledon inoculation, true leaf inoculation and stem inoculation, were used to evaluate the reactions of *C. orbiculare* in cucumbers. For true leaf inoculation, one accession was highly resistant with 2% disease severity (DS), eight accessions were resistance with 10% DS and five accessions were moderately resistance with 11-25% DS. In cotyledon inoculation, one accession was highly resistant with 2% DS, 12 accessions were resistance with 10% DS and four accessions were moderately resistance with 11-25% DS. During observing the symptom on true leaf and cotyledon, the stem symptom also was observer. According to the reaction level, 17 accessions were highly resistant with no lesion observed on cotyledon stem, six accessions with disease index 1 and 12 accessions with disease index ranging 2-5. In true leaf stage, 19 accessions were highly resistant with no lesion observed in stem, four accessions with disease index 1 and 12 accessions with disease index ranging 2-5. Based on cotyledon, true leaf and stem lesion observation, six accessions showed highly resistance, especially, accession VI055898 (Bz) is most resistance to anthracnose. For confirming the resistance, the CAPS marker design from *CsSGR* gene was used to check the resistant accession. However, results showed that the maker could not detect these six accessions completely; meanwhile, several susceptible accessions showed positive reaction with CAPS maker. Thus, CAPS maker is not stable to detect resistant cucumber to anthracnose. It is necessary to develop new maker in future.

SB06 Vascular sap peptidomic profiling of tomato with root-knot nematode infection.

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Root-knot nematodes (RKN) are considered as the important pests that cause severe crop losses worldwide. Current strategies for nematode control, including crop rotation, sun exposure, flooding, chemical pesticides, however these strategies are either harmful to the environment or not efficient for continuous cropping. In this study, we would like to understand the molecular mechanism and signaling pathways of the plant-RKN interaction to facilitate the development of an efficient and environmental-friendly way for nematode control. Peptides are known to play the critical roles in regulating plant development and immunity, which can be transported by vascular sap for long-distance signaling. We recently found a long-distance mobile peptide in various clades of angiosperms, named Angiosperm Sap Peptide (ASAP), including magnoliids *Cinnamomum kanehirae*, woody eudicots *Eucalyptus grandis* and *Populus trichocarpa*, herbaceous eudicot Glycine max and herbaceous monocot *Zea mays*. ASAP was known to

regulate lignin biosynthesis that can enhance the strength plant cell wall to prevent the vascular pathogen infection. Here, we collected the vascular sap from Solanum lycopersicum (tomato) with or without RKN infection for peptidomic profiling. In our results, we firstly identified and quantified ASAP in tomato vascular sap and also found the abundance of ASAP was significantly reduced in RKN-infected tomato. In addition, we also firstly identified the novel peptides secreted from RKN. This study not only can identify the novel long-distance mobile peptides from tomato and RKN, but also facilitate our understanding of regulatory mechanism during the plant-nematode interaction.

SC01 利用阿拉伯芥韌性基因開發有益微物之篩選平台

謝家程[1]、張碧芳[1,2]、張道禾[1] ([1]國立中興大學循環經濟學院植物保健碩士學位學程、[2]國立中興大學植物病理學系)

Development of a beneficial microbes screening platform through Arabidopsis thaliana resilience genes

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台灣農業常面臨極端的非生物逆境，對農業生產帶來嚴重的損失。有益微生物 (Beneficial microorganisms) 如內生菌 (Endophyte)、生長促進根際細菌 (Plant growth-promoting rhizobacterium, PGPR) 或是叢枝菌根菌 (Arbuscular mycorrhizal fungi, AMF) 具有促進作物生長和提升作物耐逆境能力，可作為新穎資材提升作物對非生物逆境韌性。然而開發提供植物韌性之有益微生物需耗費大量的空間、時間和人力，為此本研究目的為開發快速並有效預測有益微生物效益的分析平台。初期利用已知具有提升阿拉伯芥韌性的蕈狀芽孢桿菌 BM103 (Bacilius mycoides) 做為主要研究標的，以加權基因共表現網絡分析 (Weighted gene co-expression network analysis, WGCNA) 了解「阿拉伯芥-BM103-逆境」反應下的阿拉伯芥轉錄基因體並取得 19 個與韌性相關之核心基因，其中數個基因與植物代謝途徑 (Metabolic pathway) 和植物光合作用 (Photosynthesis) 有關。進一步比較阿拉伯芥使用其他有益微生物後核心韌性基因之表現，同時分析阿拉伯芥在施用有益微生物於逆境下的生長與生理參數，以此評估有益微生物提升植物韌性之效益。部分有益微生物在乾旱逆境下可提升阿拉伯芥幼苗的根長，並且提升阿拉伯芥成株的葉片數、葉面積與鮮重。另外也有部份有益微生物在乾旱條件下可提高阿拉伯芥過氧化酶 (Peroxidase, POD) 的活性。施用有益微生物對阿拉伯芥韌性基因表現量與提升阿拉伯芥耐旱能力具有關聯性。未來將進一步收集更多不同類型的有益微生物，並整合該些微生物對阿拉伯芥核心韌性基因表現量與阿拉伯芥韌性能力的影響，最終建立一套快速篩選有益微生物並預測其效益的標準分析流程。

SC02 Fungicide sensitivity and resistance mechanism of *Neopestalotiopsis rosae*

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Leaf blight caused by *Neopestalotiopsis rosae* is new emerging disease in strawberry in Taiwan, especially the disease outbreak at 2018. Fungicides have been used as a major strategy on control of strawberry disease for a long time. However, the leaf blight still could not be reduced significantly. Therefore, the objective of this study is to evaluate the sensitivity of *N. rosae* population to current recommended fungicides on strawberry and to explore possible resistance mechanisms of *N. rosae*. Total 158 isolates were collected from Nantou and Miaoli city during 2020 to 2023. According to the morphology and phylogenetic analysis, all isolates were identified as *N. rosae*. For fungicides test, these isolates showed variable reaction to the fungicides. Almost all isolates show low-sensitivity to boscalid, azoxystrobin, kresoxim-methyl and trifloxystrobin. However, all tested isolates showed high-sensitivity to pyraclostrobin, difenoconazole, propiconazole and oxine-copper. Furthermore, the isolates obtained from different areas showed different sensitivities to fungicides. The isolates from Shitan, Miaoli are lower sensitivity to the tested fungicide than the other isolates from different area. In the sensitivity test to the benzimidazoles, most of isolates showed low-sensitivity to the thiabendazole. However, same isolates showed relatively high-sensitivity to the benomyl. In this study, both high- and low-sensitivities isolates carried F200Y mutation in *tub2* gene. It seems that the mutation did not affect the sensitivity of *N. rosae* to benzimidazoles. We also analyzed the codon 143 in *cytb* gene to confirm the relationship between low- and high-sensitive isolates to strobilurins. However, the codon 143 mutation did not affect the reaction of *N. rosae* to the strobilurin fungicides.

SC03 Evaluating the efficacy of citrus terpene and *Bacillus mycoides* strain BM103 in managing periwinkle leaf yellowing disease

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Phytoplasmas are obligate phytopathogenic bacteria belonging to the class Mollicutes. The pathogens, transmitted mainly by insect vectors, were associated with hundreds of plant diseases worldwide. Due to the regulation and limited efficacy of the traditional disease management manners, an eco-friendly alternative is needed. Given that terpene and probiotics may have antibiotic activity and the ability to induce systemic resistance, in this study, the effectiveness of citrus terpene and a *Bacillus mycoides* strain, BM103, was evaluated in potted periwinkle plants infected with periwinkle leaf yellowing (PLY) phytoplasma derived from a shoot-tip tissue culture system. According to the

optimization test, the best application rate of citrus terpene (1,000 ppm) and pre-activation 1/100× BM103 liquid culture were used for comparative tests. By drenching once per week, the treatment of 1,000 ppm citrus terpene emulsification solution or 1/100× BM103 liquid culture exhibited the ability to inhibit PLY accumulation. The expression of the genes associated with plant defense response and flower development was upregulated after treatment. While citrus terpene at 1,000 ppm did not suppress the symptoms, BM103 may benefit diseased plants with its plant growth-promoting characteristics that led to a milder symptom expression. Since the expression of *CrIAA* genes did not exhibit an apparent up-regulation within 72 h, further investigation shall focus on the interaction between BM103 and diseased plant to elucidate its mechanism in phytoplasma disease control. Taken together, this research indicates that citrus terpene and BM103 could potentially be developed as biological control agents.

SC04 Application of wood vinegar in control of plant pests

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Wood vinegar is a byproduct of biomass pyrolysis in anaerobic or anoxic environments and can be used to control plant pathogens, insects, promoting plant growth and suppress weed growth. However, efficacy of wood vinegar are varies depending on different pyrolysis conditions and materials. In this study, agricultural wastes collected from Murcott tangor, space bag of mushroom, and bamboo were used as raw materials to produce wood vinegar at 300, 500 and 700°C, and these wood vinegars were examined its efficacy on control of different plant pests. Antimicrobial experiment showed that wood vinegar made from Murcott tangor has better antimicrobial ability compared with wood vinegars made from space bag of mushroom and bamboo, especially the Murcott tangor wood vinegar produced at 300°C pyrolysis could inhibit fungal and bacterial pathogens more than 93% inhibition rate at 100X dilution. For nematode test, the Murcott tangor wood vinegar prepared at 300°C also showed good inhibition rate (over 82%) of Meloidogyne enterolobii egg hatching rate at a 200X dilution and could also completely kill M. enterolobii Second-stage juveniles nematodes. Moreover, weed seed suppression test revealed that Murcott tangor and space bag of mushroom wood vinegars could inhibit seed gemination of Bidens pilosa over 96% inhibition rate at 100X dilution. In promoting plant growth test, the Murcott tangor wood vinegar could promote the growth of rice seeds when the dilution concentration is over 1000X. Specifically, wood vinegar prepared at 700°C exhibits a Relative Vigor Index (RVI) 46% higher than that of the control group. According to the results, the Murcott tangor wood vinegar has the potential to be a potential agent for controlling plant diseases,

promoting plant growth and suppressing weed seed growth.

SC05 *Bacillus amyloliquefaciens* PMB05 發酵液之種子包覆與其在洋香瓜果斑病上之防治

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Seed coating of *Bacillus amyloliquefaciens* PMB05 fermentation liquid and its effect on controlling bacteria fruit blotch in melon

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由 *Acidovorax citrulli* 造成的細菌性果斑病會在洋香瓜果實上造成危害，進而影響商品價值。此病害最主要的傳染途徑為帶菌之種子在田間成為初次接種源，因此如何解決帶菌種子的問題成為防治此病害最重要的策略。在病害防治上，前人研究指出 *Bacillus amyloliquefaciens* PMB05 能夠藉由強化植物免疫之防禦訊號降低包括西瓜果斑病在內的多種病害的發生。因此，本研究擬利用此菌株探討不同處理方式的應用對防治洋香瓜果斑病之影響。首先透過浸泡 PMB05 細菌懸浮液、發酵液與粉劑處理於洋香瓜種子上，在種植兩周後將病原菌透過葉噴接種，比較對於果斑病之防治效果，結果顯示與對照組比較，將種子浸泡於 PMB05 發酵液能最有效提高種子帶菌量並降低果斑病的發生，相較於對照組 51%之罹病度可降低至 31%。為進一步提升種子上 PMB05 之帶菌量以增加對果斑病的防治效果，本研究利用發酵液添加相同濃度海藻酸鈉、羧甲基纖維素、阿拉伯膠及 Tween 80 進行種子包覆，結果顯示與發酵液浸泡處理相比，不管添加何種黏著劑皆能顯著提升種子帶菌量，其中以海藻酸鈉最佳。進一步分析以海藻酸鈉為資材之最適濃度，以添加 1%的海藻酸鈉能達到最高的種子帶菌量，且帶菌量超過 10^9 CFU/g 仍不會對種子發芽造成不利之影響。在果斑病之防治上，也證明與發酵液浸泡處理比較，添加 1%的海藻酸鈉能顯著提升發酵液之防治效果，罹病度可降低至 24%。綜上所述，本研究證明利用 *Bacillus amyloliquefaciens* PMB05 處理於種子上可以防治洋香瓜果斑病之發生，並且在 PMB05 發酵液中添加 1%海藻酸鈉進行種子包覆具有更好的防治效果。

SC06 建立反轉錄恆溫環狀擴增法系統及製備廣效性單株抗體來檢測多種可感染蝴蝶蘭之番茄斑萎病毒屬病毒

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Establishment of RT-LAMP and production of broad-spectrum monoclonal antibody to detect *Phalaenopsis*-infecting orthotospoviruses

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蝴蝶蘭原生種大部分生長於印尼、菲律賓及馬來西亞等國家，其分類地位屬於蘭科 (*Orchidaceae*)、蝴蝶蘭屬 (*Phalaenopsis*)，花形似其名有如蝴蝶一般，廣受消費者喜愛。蝴

蝶蘭為台灣經濟重要花卉， 2022 年我國蘭花出口總值高達 2 億美元，其中蝴蝶蘭出口值佔約 80%，範圍擴及美國及日本等。病毒病害為蘭花栽培品質之限制因子，且病毒也是國際貿易間關鍵檢疫之病原，因此在發展蘭花產業時，健康種苗的培育及病原檢測技術至關重要。番茄斑萎病毒屬 (*Orthotospovirus*) 之病毒廣泛分布於世界各地，許多重要之農作物、蔬果及花卉均為此病毒屬之寄主，且因該病毒屬可透過薊馬作為媒介昆蟲進行傳播，導致國內外重大經濟損失。番茄斑萎病毒屬病毒在罹病蘭花葉片上會出現黃化輪斑、壞疽等病徵，使得外觀受損，影響我國蘭花外銷之商譽。現今植物病毒檢測技術的多項發展中，除了聚合酶連鎖反應檢定法 (polymerase chain reaction, PCR) 廣為應用外，酵素結合免疫吸附分析法 (enzyme-linked immunosorbent assay, ELISA) 更經常作為出口檢測方法。為有效節省檢測上耗費之時間及成本，改善靈敏度、專一性不足等問題，本研究嘗試 (1) 建立反轉錄恆溫環狀擴增法 (reverse transcription loop-mediated isothermal amplification, RT-LAMP) 之快速病毒檢測系統，針對可感染蝴蝶蘭之番茄斑萎病毒屬病毒，設計出保守序列區之引子對，並檢測出番椒黃化病毒 (*O. capsiciflavi*, CaCV)、鳳仙花壞死斑病毒 (*O. impatiensnecromaculae*, INSV) 及番茄斑點萎凋病毒 (*O. tomatomaculae*, TSWV) 三種病毒，此法特點為耗時短、實驗全程恆溫反應，無須複雜控溫設備、可肉眼觀察結果，無須電泳等；(2) 發展廣效性單株抗體 (monoclonal antibody)，抗原製備為使用 CaCV、INSV 及 TSWV 之非結構性蛋白 (non-structural protein, NSs) 為對象，經序列比對後分別針對保守性高之序列區域設計專一性引子對，以 PCR 方式增幅目標片段，並構築於大腸桿菌中進行蛋白質表現及大量純化。將目標蛋白免疫小鼠以製備單株抗體，藉由 ELISA 方法篩選反應優良之融合瘤細胞，注射細胞至小鼠腹腔產生大量腹水，測試力價。未來進一步將所製備的三種單株抗體混和並生產快速免疫試紙，除了單株抗體具有有專一性高、能進行體外培養及永久繼代外，免疫試紙應用更具有可直接在田間使用之優點。

主辦單位：

中華民國植物病理學會

協辦單位：

農業部動植物防疫檢疫署

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