

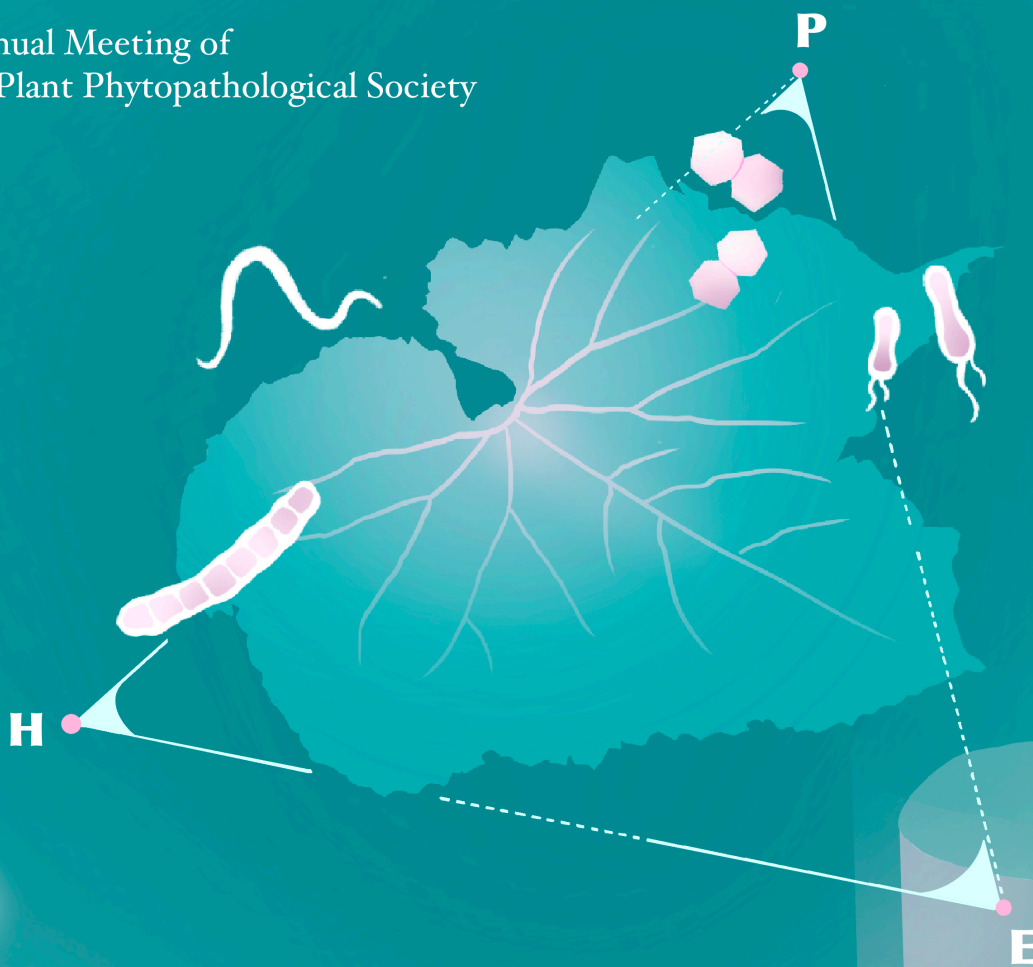
2026 Sat.  
4 / 25

中華民國

# 植物病理學年會

The Annual Meeting of  
Taiwan Plant Phytopathological Society

植物  
病理  
學會



# 2026 中華民國植物病理學會年會

## 議程表及論文摘要

時間：2026 年 4 月 25 日 (週六)

地點：國立中興大學農業環境科學大樓

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# 2026 年中華民國植物病理學會年會暨會員大會 議程

時間：2026 年 4 月 25 日 (六)  
地點：國立中興大學農業環境科學大樓

時間	議程	地點
08:30~09:00	報到及論文宣讀準備	1F 玄關
09:00~12:00	分組論文宣讀 (學生論文宣讀比賽)	1F R1D02 - 05 教室
12:00~13:30	第十九屆第七次理監事會議	2F 院辦 第一會議室
12:00~13:30	會員報到	10F 電梯口
12:30~13:30	工作坊：Application of Digital Twin - Technology in Smart Agriculture 主講人：陳欣正 博士 (台灣海博特技術部經理)	1F 植物教學醫院
13:30~13:40	開幕與理事長致詞	10F 10B05 視聽教室
<b>專題演講 (主持人：鍾嘉綾 主任 (國立台灣大學植物病理與微生物學系))</b>		
13:40~14:10	題目：開啟植物系統性抗病之鑰匙：百合 LsGRP1 蛋白功能解密 主講人：陳昭瑩 教授 (國立台灣大學植物病理與微生物學系/植物醫學碩士學位學程)	10F 10B05 視聽教室
14:10~14:40	題目：由專業實踐邁向創新：植物源保護製劑研發與產業化之歷程 主講人：謝廷芳 研究員兼副所長 (行政院農業部農業試驗所)	
14:40~15:10	題目：亦敵亦友四十年-我與柑橘黃龍病 主講人：洪挺軒 教授兼主任兼副院長 (國立台灣大學植物病理與微生物學系/生物多樣性研究中心/生物資源暨農學院)	
15:10~15:30	<b>大會合照及茶敘</b>	
<b>專題演講 (主持人：鍾文鑫 理事長)</b>		
15:30~16:00	題目：嘉義大學植物醫學系發展歷程—兼論真菌多樣性研究成果 主講人：郭章信 研究員兼特聘教授 (國立中興大學植物醫學暨安全農業碩士學程/循環經濟學院植物保健學位學程)	10F 10B05 視聽教室
16:00~16:30	題目：Mass Spectrometry-Based Multi-Omics Reveals the Roles of Peptides in Plant-Nematode Interactions 主講人：陳盈嵐 副教授 (國立中興大學特用作物及代謝體學位學程)	
<b>中華民國植物病理學會會員大會暨頒獎典禮 (主持人：王智立 祕書長)</b>		
16:30~18:30	終身貢獻獎：陳昭瑩 學術獎：蔣國司、陳盈嵐 事業獎：謝廷芳、洪挺軒、郭章信 優良基層人員：林秀榮、邱燕欣 學生論文宣讀獎	10F 10B05 視聽教室
18:30~	<b>會員聚餐 (阿秋大肥鵝-健康店 402 臺中市南區忠明南路 1118-6 號)</b>	

主辦單位：中華民國植物病理學會、國立中興大學植物病理學系

協辦單位：農業部動植物防疫檢疫署、國立中興大學植物教學醫院、國立中興大學農業推廣中心

# 2026 中華民國植物病理學會年會論文宣讀議程

## 一般宣讀組

A. 線蟲、真菌及卵菌組

地點：R1D03 教室

第一節 主持人：曾昱 助理教授			
時間	編號	報告人	題目
09:15-09:30	A01	蘇俊峯	以根瘤直徑建立南方根瘤線蟲危害之量化指標 Establishing a quantitative index for root-knot nematode damage based on root gall diameter
09:30-09:45	A02	陳俊霖	南方根瘤線蟲族群在兩種辣椒栽培種上的取食差異 Differences in feeding behavior among <i>Meloidogyne incognita</i> populations on two commercial chili pepper cultivars
09:45-10:00	A03	呂昀陞	危害香菇太空包木材腐朽菌之鑑定與病原性分析 Identification and pathogenicity analysis of wood decay fungi from damaging sawdust bag of shiitake
10:00-10:15	A04	林祐楨	臺東地區小米粟熱病病原菌之鑑定與生物特性探討 Identification and Biological Characteristics of the pathogen responsible for foxtail millet blast disease in Taitung
10:15-10:30	中場休息		
第二節 主持人：郭建志 副研究員			
10:30-10:45	A05	薛曉萱	瓜油壺菌 ( <i>Olpidium bornovanus</i> ) 在臺灣之生態初探 Preliminary Study on the Ecology of <i>Olpidium bornovanus</i> in Taiwan
10:45-11:00	A06	黃巧雯	臺灣小花蕙蘭炭疽病菌種類與防治資材感受性評估 Diversity and Control Agent screening of <i>Cymbidium</i> Anthracnose Pathogens in Taiwan
11:00-11:15	A07	張組程	臺灣藍莓病害調查與炭疽病菌之生物學特性及防治研究 Survey of blueberry diseases in Taiwan with a focus on the biological characteristics and control of anthracnose pathogens
11:15-11:30	A08	馮擷安	臺灣辣椒炭疽病原菌族群結構與藥劑感受性之調查與評估 Population structure and fungicide sensitivity of <i>Colletotrichum</i> spp. causing chili anthracnose in Taiwan

第一節 主持人：周浩平 副研究員			
時間	編號	報告人	題目
09:15-09:30	B01	許晴情	萬代蘭花枯病菌之寄主範圍測試及防治資材篩選 Host range test and screening of control materials against flower blight pathogen of <i>Vanda</i> orchid
09:30-09:45	B02	蔡小涵	貝萊斯芽孢桿菌 TNB40 發酵配方優化及防治甜瓜黑點根腐病成效初探 Optimization of fermentation formula for <i>Bacillus velezensis</i> TNB40 and a preliminary study on its efficacy in controlling melon black root rot.
09:45-10:00	B03	高之韋	<i>Pseudomonas mosselii</i> 對青枯病菌之抑菌機制探討 Studies on the antibacterial mechanism of <i>Pseudomonas mosselii</i> against bacterial wilt pathogen
10:00-10:15	B04	林家華	質外體富含甘胺酸蛋白 LsGRP1 介導植物系統獲得抗性之機制與應用 Apoplastic glycine-rich protein LsGRP1 mediates plant systemic acquired resistance and the application
10:15-10:30	中場休息		
第二節 主持人：陳宗祺 教授			
10:30-10:45	B05	劉東憲	苗栗地區橫山梨病毒與黑星病菌複合感染現況及其病徵顯現之初探 Preliminary study on co-infection and symptom expression of viruses and black spot ( <i>Venturia</i> sp.) on 'Hengshen' pear in Miaoli
10:45-11:00	B06	劉雅婷	Multiplex Detection of Major Viral and Bacterial Pathogens in Cucurbits for Improved Disease Diagnosis and Management
11:00-11:15	B07	蕭崇仁	Comparative Analysis of Diagnostic Techniques for Melon yellow spot virus
11:15-11:30	B08	林雨緹	南瓜捲葉中國病毒分子特性分析與寄主範圍之探討 Molecular Characterization and Host Range Determination of squash leaf curl China virus
11:30-11:45	B09	林巧玲	探討 sORF A 與番茄感染性相關聯之關鍵胺基酸序列 The study of the key amino acid sequence of sORF A related to tomato infectivity

## 學生論文宣讀競賽組

學生競賽 SA 組

地點：R1D02 教室

評審老師：沈原民 助理教授、陳以錚 助理教授、吳秉祐 助理教授

第一節			
時間	編號	報告人	題目
08:45-09:00	SA01	陳竑宇	開發紅龍果莖潰瘍病之病害預警系統 Development of a disease warning system for dragon fruit ( <i>Hylocereus</i> spp.) stem canker ( <i>Neoscytalidium dimidiatum</i> )
09:00-09:15	SA02	易昀臻	建立草莓萎凋病菌 ( <i>Fusarium oxysporum</i> f. sp. <i>fragariae</i> ) 於帶菌植株之分子檢測方法 Development of a molecular detection method for <i>Fusarium oxysporum</i> f. sp. <i>fragariae</i> in infected strawberry plants
09:15-09:30	SA03	楊承樺	建立水稻紋枯病病原 <i>Rhizoctonia solani</i> AG1 之快速土壤檢測方法 Development of a rapid soil-based detection method for rice sheath blight caused by <i>Rhizoctonia solani</i> AG1
09:30-09:45	SA04	巫宗錡	以顯微構造解析樹木褐根病菌侵染木質部之策略 Microscopic characterization reveals the infection strategies of <i>Phellinus noxius</i> in tree xylem
09:45-10:00	SA05	陳思妤	探討殺菌劑於正榕木材中對褐根病菌之抑制效力及其擴散性 Investigation of the inhibitory efficacy of fungicides against <i>Phellinus noxius</i> and their diffusion in <i>Ficus microcarpa</i> wood
10:00-10:15	SA06	陳冠宇	How pesticides disrupt top-down control from hyperparasitism
10:15-10:30	中場休息		
第二節			
10:30-10:45	SA07	范綱惟	Possible mechanisms of <i>Fusarium solani</i> species complex (FSSC) from passion fruit showed low sensitivity to QoI fungicides and its characteristics
10:45-11:00	SA08	楊橙宜	Broad and comprehensive Fungicide Efficacy, Resistance Mechanisms, and Biocontrol Potential Against <i>Neopestalotiopsis protearum</i> Causing Fruit Rot and Scab in Guava and Wax Apple in Taiwan
11:00-11:15	SA09	黃信堯	<i>Pseudopestalotiopsis</i> Species Causing Tea Gray Blight: Insights from Comparative Genomics and Nutrient Utilization Assays
11:15-11:30	SA10	Sabnam Rai	Genome-wide comparative genomic analysis of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Tropical race 4 and Race 1 reveals pathogenicity associated accessory regions
11:30-11:45	SA11	陳禹安	Genetic variation, functional validation, pathogenic and evolutionary mechanism of AVR- <i>Pital</i> gene among rice blast fungus population in Taiwan
11:45-12:00	SA12	錢怡安	辣椒炭疽菌 ( <i>Colletotrichum scovillei</i> ) CsBNS 蛋白在辣椒細胞內的定位及分泌 Secretion and localization of <i>Colletotrichum scovillei</i> CsBNS Protein in Chili Pepper Cells
12:00-12:15	SA13	黃思傑	Pathogenicity Assessment for CRISPR-Cpf1 edited <i>Fusarium oxysporum</i> and Development of Microfluidic-Assisted Gene Editing Mutant Isolation Technology

評審老師：林靜宜 副研究員、李淑君 助理教授、黃纓雯 助理教授

第一節			
時間	編號	報告人	題目
08:45-09:00	SB01	林千琪	Foliar transcriptome analysis of quinoa ( <i>Chenopodium quinoa</i> ) to explore the candidate genes involved in cross-protection mediated by attenuated viruses
09:00-09:15	SB02	林湘庭	Functional characterization of the hidden open reading frames in the pathogenesis of tomato yellow leaf curl Thailand virus
09:15-09:30	SB03	林夢欣	馬鈴薯病毒 Y 致病機制探討與馬鈴薯病毒之多重反轉錄聚合酶鏈式反應檢測系統的開發 Investigation of pathogenic mechanisms of potato virus Y and development of a multiplex RT-PCR for the detection of potato viruses
09:30-09:45	SB04	楊婕絲	SUMOylation at K159 of the <i>Begomovirus solanumdelhiense</i> movement protein contributes to chlorosis formation in <i>Nicotiana benthamiana</i>
09:45-10:00	SB05	林恩佑	果膠修飾與 LsGRP1 強化植物免疫之關聯性探討 Investigating the role of pectin modification in LsGRP1-enhanced plant immunity
10:00-10:15	SB06	賴冠廷	篩選有益微生物以緩解非生物逆境對小白菜造成之負面影響 Screening of Beneficial Microorganisms to Mitigate Abiotic Stress-Induced Negative Effects in Bok Choi
10:15-10:30	中場休息		
第二節			
10:30-10:45	SB07	江睿綸	篩選具緩解甜瓜非生物逆境潛力之有益微生物 Screening of Potential Beneficial Microorganisms for Alleviating Abiotic Stresses in Melon
10:45-11:00	SB08	林子傑	Biological control of papaya damping-off and its impact on carbon assimilation by <i>Streptomyces cavourensis</i> strain PES4
11:00-11:15	SB09	巫宣佑	Biological control of papaya Phytophthora damping-off and associated changes in carbon assimilation mediated by <i>Bacillus subtilis</i> WMA1
11:15-11:30	SB10	Kachonsak Iamnok	Two naturally compatible <i>Bacillus</i> strains promote plant growth and suppresses fungal pathogens through cooperative interaction
11:30-11:45	SB11	廖苡辰	運用 RNAi 技術探討褐根病菌 <i>PnCYP51.1</i> 的角色 Using RNAi technology to investigate the role of <i>PnCYP51.1</i> in <i>Phellinus noxius</i>
11:45-12:00	SB12	楊雅芳	Screening and evaluating the potential of endophytes from <i>Corymbia citriodora</i> on inhibition of <i>Bidens pilosa</i>

**2026 中華民國植物病理學會年會論文摘要**

**Abstracts of the 2026 Annual Meeting of  
Taiwan Phytopathological Society**

**專題演講摘要**

**Abstracts of Keynote Speeches**

**KS01- 開啟植物系統性抗病之鑰匙：百合 LsGRP1 蛋白功能解密**  
**Unlocking Plant Systemic Resistance: Deciphering the Function of the Lily**  
**LsGRP1 Protein**

陳昭瑩 (國立臺灣大學植物病理與微生物學系、國立臺灣大學植物醫學碩士學位學程)

Chao-Ying Chen (Department of Plant Pathology and Microbiology, National Taiwan University, Taipei. <sup>2</sup>Master Program for Plant Medicine, National Taiwan University, Taipei.)

Induced resistance in plants can prevent damage from pathogen attacks by augmenting the basic immune response to mitigate disease development. Pre-stimulation with plant immunity inducers strengthens natural defenses, enabling a faster and stronger response that suppresses pathogen multiplication and symptom development through enhanced callose deposition and defense-related protein expression. Salicylic acid (SA) is a plant hormone capable of inducing resistance to pathogens, as demonstrated in *Lilium* against Botrytis leaf blight. Specifically, the SA-induced expression of the LsGRP1 protein (a plant class II glycine-rich protein) enhances pattern-triggered immunity, involving cell wall-associated kinases and pectin modification. The systemic resistance activated by LsGRP1 relies on SA and N-hydroxypipicolinic acid-related signaling pathways. Research shows that drenching with either SA or LsGRP1 increases *Lilium* resistance to Botrytis disease. Furthermore, this glycine-rich protein induces broad-spectrum resistance and can be applied exogenously. Field trials demonstrate that LsGRP1-derived products reduce the incidence of strawberry leaf blight; additionally, treated plants exhibit better growth vigor and reproduction. Plant defense priming keeps plants in a "ready state," allowing them to trigger robust defense responses against subsequent attacks. Harnessing bioproducts to boost plant immunity holds great potential for sustainable agriculture, helping to stabilize crop production and food security in a climate-stressed world.

## **KS02- From Professional Practice to Innovation: A Journey in Developing and Commercializing Plant-Derived Crop Protection Products**

Ting-Fang, Hsieh (Taiwan Agricultural Research Institute, Ministry of Agriculture)

This lecture draws on more than 30 years of hands-on experience in plant pathology, looking back on a journey that spans pathogen identification, ecological studies, and the development and commercialization of plant-derived crop protection products. From the very beginning, the work has been closely tied to the field—starting with disease diagnosis and pathogen identification and building research questions directly from on-site observations. This approach has led to in-depth studies on the epidemiology and management of major diseases affecting lilies, common beans, and a wide range of horticultural crops, laying a solid scientific foundation for integrated disease management. In response to growing concerns about the risks of chemical pesticides and the push toward sustainable agriculture, the research focus has gradually shifted toward non-chemical control methods, especially plant-based protection products. Through screening plant extracts, optimizing formulations, and developing microemulsion technologies, several innovative products have been created, including sunflower oil emulsions, herbal compound formulations, and cinnamon essential oil microemulsions. These products have been patented and shown to be both effective and stable in controlling key plant diseases such as anthracnose, gray mold, powdery mildew, and root-knot nematodes. These technologies have also been successfully commercialized and transferred to industry, helping bring plant-based crop protection products into real-world farming systems and turning research outcomes into practical value. At the same time, by integrating non-chemical materials, monitoring tools, and integrated pest management strategies, reduced-pesticide cultivation models have been developed for crops such as continuously harvested vegetables and passion fruit. These efforts have significantly lowered chemical pesticide use while maintaining productivity and environmental sustainability, earning recognition with the Sustainable Agriculture Award for two consecutive terms. Overall, this journey, from field practice to scientific innovation and real-world application, highlights the important role of plant pathology in advancing safe and sustainable agriculture. It also reflects how research can respond to policy needs and industry challenges. In this talk, I will share key ideas and practical experiences from moving between the lab and the field, and from research to technology transfer, with the hope of offering some insights into the future role of plant pathology in sustainable agriculture.

## **KS03- 亦敵亦友四十年-我與柑橘黃龍病**

### **Overview of the plant doctor act and its related regulations**

洪挺軒 (國立臺灣大學生物資源暨農學院、國立臺灣大學生物多樣性研究中心、國立臺灣大學植物病理與微生物學系)

自 1988 年暑假開始，我正式進入臺大植物病蟲害學系蘇鴻基教授研究室，修習專題研究課程。當時蘇教授給了我一個研究主題：柑橘黃龍病 (citrus huanglongbing, HLB) 新型快速診斷技術之開發，從此便與柑橘黃龍病結下不解之緣，迄今已近 38 年。從病原鑑定、病害快速診斷、媒介昆蟲與發病生態的探討、一直到防治方法的建立與改良等，這個老病害的管理策略歷久彌新，診斷與防治技術也不斷精進，在臺灣達成與病害共存而柑橘產業得以永續發展的目標。黃龍病是我一直要打擊的對象，是長期的敵人，卻也像是我一生的老朋友，伴隨我學術生涯的成長，也賜與我成就感與遍訪世界各柑橘產區的學習契機。黃龍病是臺灣與國際最重要的柑橘病害，由無法培養的韌皮部侷限細菌 (phloem-limited fastidious bacteria, 目前暫定學名為 *Candidatus Liberibacter asiaticus*) 所引起，無法以直接噴灑殺菌劑來加以防治；主要經由帶病種苗來傳播，而在種植後又可經柑橘木蝨媒介傳播，屬於世界性的植物流行病。多年來普遍危害國內外各柑橘品種，使橘株黃化衰弱甚至致死，嚴重影響柑橘產量與品質，成為柑橘生產之限制因子。原本此病僅肆虐於亞洲與非洲的柑橘產區，然而在 2004 年南美洲的巴西開始發現黃龍病，這是美洲地區黃龍病發生的第一次報導；2005 年黃龍病更入侵美國佛羅里達州，美國農業部驚覺該病之嚴重性，紛紛擬定研究計畫與防疫策略，大規模進行黃龍病之相關研究，至此黃龍病也被視為世界農業重大威脅的植物傳染病。黃龍病的防疫工作首重正確的病害診斷與病原追蹤，預防勝於治療。黃龍病潛伏期長，病菌至今無法培養，而在寄主體內含量少且分佈不均，因此不易以傳統的方法進行診斷。本研究室長期建立核酸探針、PCR、qPCR、DNA 檢測晶片、快篩試劑與 iiPCR 等技術，建立一套標準偵測方法，為此病研究之先驅，被世界各國廣泛採用，也協助國內外檢疫工作多年。為實際解決黃龍病的危害問題，進一步將研究觸角伸展至媒介昆蟲的傳病特性研究，找尋田間的中間寄主，且探討病原菌在昆蟲體內的增殖與循環情況，充分瞭解黃龍病的流行病學本質，以精準打擊媒介昆蟲並降低病菌擴散風險。目前針對國內主要的柑橘栽培品種已經建立防治的 SOP，配合健康種苗的使用與媒介昆蟲的妥善防治，可大幅降低黃龍病的田間感染率。最近又改良先前研發的注射防治技術，改變藥劑配方與注射方法，應用到柑橘罹病株的治療工作上，發現治病效果相當顯著。這些黃龍病的診療技術引起各國的重視，長年來成為臺灣農業技術援外與學術外交的強項，亞洲與拉丁美洲多個國家均有實質的合作關係，並展現良好的防治成效，對臺灣國際名聲的提升有所助益。

## **KS04- 嘉義大學植物醫學系發展歷程—兼論真菌多樣性研究成果**

### **Development History of the Department of Plant Medicine at National Chiayi University: Insights into Fungal Diversity Research**

郭章信 (國立中興大學植物醫學暨安全農業碩士學位學程、國立中興大學循環經濟學院植物保健學位學程)

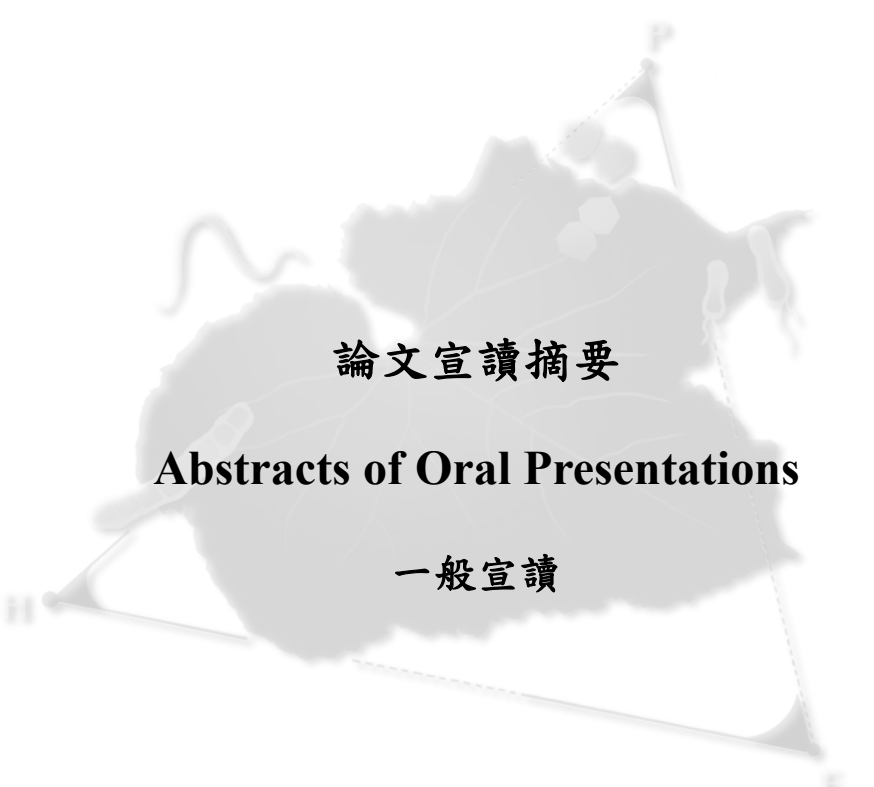
國立嘉義農業專科學校在雲嘉南地區的農業教育中享有盛名，並於 1987 年成立植物保護科。1997 年改制為嘉義技術學院，並於 2000 年升格為嘉義大學。在學校轉型過程中，原有的植物保護科師資為配合校方整體發展政策，整併至生命科學院，成為生物資源學系的主要成員。儘管當時未設置專門的植物醫學系所，具植物醫學專長的師資群仍持續支援農學院植物保護相關課程，並設置植物醫學跨領域學程以培育學生。同時，亦積極投入生物多樣性研究，兼顧教學與學術發展。雖歷程艱辛，仍成功保留了植物醫學發展的基礎與能量。隨著植物醫學領域的逐步發展，經多年佈局規劃與努力，終於在 2012 年自生物資源學系分離，正式成立植物醫學系，致力於配合國家政策，培育具備田間實務經驗的植物病蟲害診斷與植物醫師專業人才。

培訓真菌鑑定之專業能力，有助於提升植物病害診斷及生物多樣性研究之精確性。臺灣高山地區於春夏之際，受溫暖南風與高山低溫交互作用影響，形成暖溫帶氣候，該類區域常年雲霧繚繞且環境高濕，提供真菌多樣化生長之良好條件，亦有利於樣本之採集。高等真菌在生態系中扮演關鍵分解者角色，能將死亡植物組織逐步分解至腐爛狀態，並在植物殘體分解過程中形成重要之真菌演替 (succession) 現象。Garrett (1981) 提出基質上真菌演替理論，指出真菌會依據基質 (substrate) 分解程度而呈現不同階段之族群變化。其中，基質係指自然界中動植物殘體，為真菌腐生提供養分來源。依據該理論，真菌於基質上的演替可分為四個時期：第1a期以弱寄生性真菌 (weak parasites) 為主，如 *Pythium* 與 *Rhizoctonia* 等；第1期以初級腐生真菌及嗜糖真菌 (sugar fungi) 為主，利用單醣類與簡單碳水化合物；第2期主要為纖維素分解者，或與次級腐生菌共享分解產物，多以子囊菌為主；第3期則為可分解纖維素與木質素之真菌，主要為擔子菌類。本研究依據演替理論，透過辨識枯枝落葉之分解程度，鎖定第2期真菌作為主要採集對象，以有效提升野外採集效率並降低非目標菌類之干擾。在演替過程中，真菌會分泌多種酵素與抗生物質，以分解植物殘體或與其他微生物競爭，並逐漸演化出多樣化之次級代謝產物。本研究歷經十餘年採集、鑑定及分析，已於國際期刊發表多項成果，包括：2個新科、13個新屬、96種新種、76種新記錄種及2個新組合種。相關新屬、新種、新紀錄種等模式標本，均典藏於國立自然科學博物館；培養菌種另寄存於食品工業發展研究所，供產業及學界後續研究應用。近年來，真菌次級代謝產物已受到國際高度重視，各國積極整合真菌多樣性、分析化學與生物化學等領域專家，發展跨國與跨學科研究團隊，成為當代真菌研究之重要趨勢。

## **KS05- Mass Spectrometry-Based Multi-Omics Reveals the Roles of Peptides in Plant-Nematode Interactions**

Ying-Lan Chen (Program in Specialty Crops and Metabolomics, Academy of Circular Economy, National Chung Hsing University, Nantou, Taiwan, Department of Plant Pathology, National Chung Hsing University, Taichung, Taiwan)

Plant–nematode interactions pose a major challenge to agriculture, yet the regulatory roles of long-distance mobile peptides remain poorly understood. Here, we applied a mass spectrometry-based multi-omics platform integrating peptidomics, proteomics, metabolomics, and phosphoproteomics to systematically dissect molecular dynamics during *Meloidogyne incognita* infection. Our analyses reveal that nematode infection triggers extensive reprogramming of endogenous peptide landscapes, including multiple classes of long-distance signaling peptides involved in immunity (e.g., CAPE1), as well as the recently identified evolutionarily conserved vascular sap peptide ASAP. In addition, we highlight the role of IDA-related peptides, which are exploited as nematode mimic peptides to hijack host developmental signaling pathways, thereby facilitating parasitism. These peptides exhibit strong spatiotemporal specificity, particularly enriched in nematode-induced feeding structures such as giant cells and their surrounding tissues. By integrating spatial and multi-layered molecular data, we further demonstrate that long-distance peptide signaling is tightly coupled with metabolic reprogramming and phosphorylation-mediated signaling pathways, enabling coordination between local infection sites and systemic responses. Together, our findings highlight long-distance mobile peptides as a critical regulatory layer in plant–nematode interactions and establish a multi-omics framework for uncovering low-abundance systemic signals, providing new opportunities to develop peptide-based strategies for enhancing crop resilience.



論文宣讀摘要

**Abstracts of Oral Presentations**

一般宣讀

## A. 線蟲、真菌及卵菌組

### A01- 以根瘤直徑建立南方根瘤線蟲危害之量化指標

#### Establishing a quantitative index for root-knot nematode damage based on root gall diameter

蘇俊峯、簡蘭懿、李凌雁 (農業部農業試驗所植物病理組)

本研究以 2.5 寸番茄苗接種南方根瘤線蟲 (*Meloidogyne incognita*) 為材料，旨在可控條件下系統性觀察接種二齡幼蟲後植株根部結瘤的變化，並釐清根瘤大小與實質感染率在危害程度上的對應關係。期望建立一套快速、客觀且具可重複性的量化指標，以提升後續防治資材篩選、處理效果驗證與統計分析的效率。試驗於接種後第 5 週量測番茄根系上根瘤直徑，並計算各根瘤內之母蟲數。結果顯示，根瘤直徑與母蟲數呈高度右偏分佈，多數樣本集中於較小直徑，且僅含單一母蟲。迴歸分析結果顯示，四參數邏輯斯迴歸 (4PL) 較簡單線性模型具有更高的判定係數與較低的殘差平方和，能更精準且客觀地反映母蟲數量隨根瘤增大在初期快速增加，並因空間與營養受限而趨於飽和的非線性動態關聯。為優化為害權重評估，本研究依統計檢定結果調整分級標準，提出 <2 mm、2–3 mm 與 >3 mm 的三級分類系統，並分別賦予 1、3、7 的對應為害權重。經 LSD 及 Dunn's test 雙重檢定證實，此三級架構能清楚區分各級距間母蟲數量的顯著差異，成功排除舊有分級模式中大型根瘤排序重疊與小型根瘤鑑別度不足的問題。期望藉由此標準化判讀流程，提供更準確且穩健的根瘤線蟲危害量化評估標準。

## A02- 南方根瘤線蟲族群在兩種辣椒栽培種上的取食差異

### Differences in feeding behavior among *Meloidogyne incognita* populations on two commercial chili pepper cultivars

陳俊霖、陳珮臻 (國立中興大學植物病理學系)

根瘤線蟲 (*Meloidogyne* spp.) 寄主範圍廣包含多種重要作物，其中以南方根瘤線蟲 (*Meloidogyne incognita*) 分佈範圍大及寄主範圍廣泛最具代表性。其寄主之一辣椒 (*Capsicum annuum* L.) 為茄科作物，在許多地區皆為重要的經濟作物，因功能甚多，不僅可做為香料提升食物風味也富含多種維生素，亦可作為消炎用藥緩解疼痛，2025 年統計辣椒與青椒的市場價值約為 13 億美元。本研究即為探討南方根瘤線蟲與辣椒間的作用機制。本研究以 Known-You Seed 公司市售的兩個辣椒栽培種：醉香 (感病)、朱雀 (抗病) 作為寄主進行試驗，使用從台中清水冬瓜植株上採集的南方根瘤線蟲族群 (aQSW) 及從中篩選出可取食抗性朱雀的毒力族群 vQSW 作為主要試驗族群，並加入無法取食朱雀的南方根瘤線蟲族群 YJB 作為對照。侵染測試中，將 50 隻 J2 線蟲接種至四至六片真葉大小的辣椒植株，並在接種後 2、3、5、7 及 10 天時染色觀察線蟲侵染根系情形。染色結果顯示，aQSW 在所有觀察的感性醉香根系中皆可侵入，並能順利發育成長，在抗性朱雀上則僅於第 3 天的兩株根系中發現線少數蟲侵入。vQSW 則在所有的醉香及朱雀根系中皆可觀察到線蟲侵入並成長；無毒力的 YJB 亦僅能侵入醉香根部，在抗性朱雀的根系則無觀察到任何線蟲。因前人研究發現辣椒的抗性，*Me1* 及 *Me3* 基因分別是利用程序性細胞死亡及過敏性反應來進行防禦，但我們在抗病品種辣椒根部組織中未發現線蟲侵入，明顯不同於典型 *Me* 基因之抗性機制，推測朱雀的抗性可能為根系分泌物驅離線蟲或干擾線蟲辨識寄主。因此再進行線蟲對根尖分泌物的趨化性測試，於 1、2、4 及 24 小時區間計算線蟲於放有 1.5cm 根尖培養皿中之分佈數量，並於第 24 小時將根尖組織進行染色，計算侵入線蟲數量。結果顯示，三種南方根瘤線蟲族群對醉香或朱雀皆有隨時間逐漸往根尖移行的現象，並在染色結果中皆有看見線蟲成功進入醉香及朱雀的根尖；故推測朱雀的抗性須由植物持續表現，才能達到阻止線蟲入侵的作用。

### A03- 危害香菇太空包木材腐朽菌之鑑定與病原性分析

## Identification and pathogenicity analysis of wood decay fungi form damaging sawdust bag of shiitake

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香菇 (*Lentinula edodes* (Berk.) Pegler) 為臺灣最重要之食用菇類，年產值約新臺幣 44.8 億元，為國內產值、產量及栽培戶數最高之菇種。其主要生產地為台中市新社區及南投縣埔里鎮、國姓鄉與魚池鄉等地。臺灣香菇主要以太空包模式栽培，但因栽培設施較簡易，栽培期間易受微生物之侵染，導致太空包良率下降。本研究分別於 2025 年 7 月與 11 月發現台中市新社區香菇栽培戶之太空包，出現香菇菌絲生長不良且太空包內木屑出現軟化之情形，因此將罹病之太空包進行病原菌之分離與純化，並獲得 15 株分離株，再將相關菌株進行 ITS 序列分析，經與 National Center for Biotechnology Information (NCBI) 資料庫序列比對，顯示本研究分離到 3 種木材腐朽菌，其中 10 株為 *Phlebia* 屬、4 株為 *Irpex* 屬與 1 株為 *Phanerochaete* 屬，其中兩次採樣之樣本中皆可分離到 *Phlebia* 與 *Irpex* 屬之真菌，顯示此兩類木材腐朽菌之危害最為嚴重。進一步選取 3 株 *Phlebia* 屬菌株、2 株 *Irpex* 屬菌株及 1 株 *Phanerochaete* 屬菌株與香菇菌絲進行之對峙試驗，並量取培養第 7 天之香菇菌絲生長半徑計算抑制率，結果顯示於木屑培養基 (SDM) 上，*Phlebia* 屬及 *Phanerochaete* 屬之分離株對香菇菌絲之生長抑制率介於  $18.2 \pm 0.0\%$  至  $59.0 \pm 3.0\%$  間，且培養至第 12 天時僅會將香菇菌絲鎖死 (deadlock) 在固定範圍，顯示 *Phlebia* 屬及 *Phanerochaete* 屬之分離株具有抑制香菇菌絲生長之能力，而 *Irpex* 屬之分離株抑制率則介於  $50.5 \pm 6.2\%$  至  $57.7 \pm 3.8\%$ ，且培養至第 12 天時，可見 *Irpex* 屬分離株之菌絲覆蓋並取代香菇菌絲之生長位置，顯示其可能具有纏聚或取代香菇菌絲之能力。本研究為國內首次針對木材腐朽菌對太空包香菇栽培影響之研究，未來除將以多基因分析技術對所分離菌株進行鑑定外，並將同時評估防治之策略，以作為後續防範其危害香菇太空包之依據。

## A04- 臺東地區小米粟熱病病原菌之鑑定與生物特性探討

### Identification and Biological Characteristics of the pathogen responsible for foxtail millet blast disease in Taitung

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Chang, F. I. and Lin, Y. C. (Taitung District Agricultural Research and Extension Station, MOA, Taitung)

小米 (*Setaria italica* (L.)) 為一年生禾本科作物，具有耐旱耐瘠的特性，為臺灣原住民傳統重要糧食作物之一。近年於臺東縣小米栽培區，發現病株葉片出現異常壞疽斑，呈橢圓形，中央灰白色，邊緣黃褐色至墨綠色，嚴重者病斑逐漸擴大，造成落葉。本試驗自臺東縣金峰鄉及達仁鄉等地區，蒐集小米病葉進行病原菌分離後，菌株在馬鈴薯葡萄糖瓊脂 (PDA) 上呈現白色至淺灰色之氣生菌絲菌落，經紫外光培養後，可見大量梨形至紡錘形之透明分生孢子，大小為  $44.1-73.4 \times 13.5-18.3 \mu\text{m}$ 、具有 2 個隔膜。分子鑑定方面，以多基因序列 (ITS、ACT、RPB1) 進行親緣演化分析，菌株皆與 *Pyricularia oryzae* 構成單系群，因此將病原菌鑑定為 *P. oryzae*。另以孢子懸浮液對小米葉片進行離葉接種試驗，接種後第 3 日皆可產生與田間相同病徵，後期病斑處亦可見梨形分生孢子。將供試菌株分別於 15、20、25、30 及 35°C 下，於 PDA 培養 7 日後量測菌落直徑，結果顯示以 30°C 生長最為快速，菌落平均直徑為 57.3 mm，而 15°C 下生長最慢 (28.5 mm)。另將分生孢子置於上述不同溫度下培養 48 小時觀察發芽率，結果顯示 20°C 以上各處理組之平均發芽率均高於 95%，而 15°C 下發芽率最低 (平均 77.5%)，顯示該病原菌之菌絲生長與孢子發芽皆偏好約 30°C 之溫暖環境。後續將進一步比較不同小米品種間之感病性差異，並結合田間病害發生生態，作為未來病害防治之參考依據。

## A05- 瓜油壺菌 (*Olpidium bornovanus*) 在台灣之生態初探 Preliminary Study on the Ecology of *Olpidium bornovanus* in Taiwan

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瓜油壺菌 (*Olpidium bornovanus*) 為一種絕對寄生性真菌，且該屬為目前已知唯一可傳播植物病毒之真菌類群。台灣亦於 2023 年首次發現此菌。近年因其在傳播甜瓜壞疽斑點病毒 (Melon necrotic spot virus, MNSV) 中扮演關鍵角色而備受關注。該病毒之感染高度依賴 *Olpidium bornovanus* 之存在，使得此菌之生態特性成為病害發生與防治之重要關鍵。然而，由於其無法以人工培養基培養，相關研究在台灣及國際上仍相對有限。本研究針對台灣 *O. bornovanus* 之生態特性進行初步探討。首先建立接種與繼代系統，結果顯示以田土與泥炭土 (1:1) 作為培養基質可顯著改善瓜類根系發育，並促進 *O. bornovanus* 產孢構造之增殖；相較於殘根繼代需約 1.5–2 個月，游走孢子接種可於 1 個月內觀察到大量產孢構造。此外，本研究建立了一套簡易保存方法，透過乾燥誘導孢子囊轉化為休眠孢子，並於 4°C 條件下陰乾保存，經 2 年後仍可成功活化。在分子偵測方面，初期利用真菌廣效型引子結合 Nanopore 定序，自罹病植株與土壤樣本中篩選出 *O. bornovanus* 相關序列，進而設計專一性引子，建立針對 *O. bornovanus* 之快速檢測系統，並成功應用於田間樣本分析。調查結果顯示，該菌於台灣多數瓜田中普遍存在，且於 MNSV 發病田區中具有較高檢出率，支持其作為病毒媒介之關鍵角色。針對生活史各階段之生理特性，本研究初步測試游走孢子形成靜止子 (cyst) 之條件，結果顯示其不易受機械刺激或溫度變化影響，僅在特定植物組織存在下出現低比例轉換，顯示其感染過程可能高度依賴寄主化學訊號。此外，農藥與非農藥資材測試結果指出，保粒黴素與撲克拉對游走孢子具有顯著抑制效果，但對休眠孢子之致死能力則有限；而中和亞磷酸與苦楝油於盆栽試驗中對休眠孢子形成具有顯著抑制潛力。整體而言，本研究初步建立 *O. bornovanus* 之實驗系統與檢測方法，並揭示其在台灣田間之分布與部分生態特性。研究結果顯示，其生活史關鍵階段 (特別是休眠孢子) 為防治策略之主要限制。

## A06- 臺灣小花蕙蘭炭疽病菌種類與防治資材感受性評估

### Diversity and Control Agent screening of *Cymbidium* Anthracnose Pathogens in Taiwan

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小花蕙蘭 (又稱國蘭或東洋蘭) 為蘭科 (Orchidaceae)、蕙蘭屬 (*Cymbidium* spp.) 多年生草本植物，為蕙蘭屬中的建蘭 (或稱四季蘭)、報歲蘭、春蘭、寒蘭及九華蘭等植物的統稱，為臺灣主要經濟栽種的蘭花之一，炭疽病為限制小花蕙蘭生產中重要的真菌性病害之一。近年來炭疽病菌由多基因鑑定發現許多新種，本研究藉由形態特徵與多基因序列，來釐清目前感染臺灣小花蕙蘭的炭疽病菌種類，並進一步分析來自不同來源寄主的炭疽病菌菌株間是否有交互感染風險，另外進行化學藥劑及友善環境植物保護資材篩選評估。本研究將小花蕙蘭炭疽病菌株以 Internal transcribed spacer (ITS)、 $\beta$ -tubulin 2 (*TUB2*)、Actin (*ACT*) 及 Glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) 基因片段序列進行 4 種基因序列分析，由親緣關係圖得知，以 *C. gloeosporioides* speices complex 中 *C. horii*、*C. psidii* 為主要炭疽病菌種類；其次是 *C. boninense* speices complex 中 *C. cymbidiicola*；零星菌株為其他支序群中 *C. cattleyicola*、*C. cliviicola*，由此得知，感染臺灣小花蕙蘭的炭疽病菌種類有 *C. horii*、*C. psidii*、*C. cymbidiicola*、*C. cattleyicola*、*C. cliviicola* 等 5 種。由不同來源寄主炭疽病菌之病原性評估試驗結果顯示，來自不同來源寄主炭疽病菌菌株間無交互感染問題疑慮。由室內篩選試驗中，在化學藥劑方面，撲克拉錳、撲克拉、快得寧、甲基多保淨、賽普護汰寧、得克利、待克利等 7 種藥劑處理對小花蕙蘭炭疽病菌可有效抑制菌絲生長，四氯異苯腈、百克敏、快得寧、腈硫醃等藥劑則可顯著降低炭疽病菌之分生孢子發芽；在友善環境植物保護資材方面，4-4 式波爾多液與黑修羅製劑對此菌菌株之菌絲生長與孢子發芽抑制效果佳，石灰硫磺合劑其菌絲生長抑制效果不佳，但對孢子發芽之抑制佳，以上防治資材可供田間病害防治之參考。

## A07- 臺灣藍莓病害調查與炭疽病菌之生物學特性及防治研究

### Survey of blueberry diseases in Taiwan with a focus on the biological characteristics and control of anthracnose pathogens

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藍莓 (*Vaccinium* spp.) 為近年於臺灣逐漸發展之新興果樹產業，隨著種植面積與產業規模擴大，其關鍵病蟲害種類及防治技術需求日益受到重視。然而，國內對藍莓病蟲害之發生生態的系統性研究仍相當有限。本研究於 2024 至 2025 年間，針對臺中霧峰、苗栗後龍與西湖、南投南投市及仁愛鄉等主要藍莓產區進行連續性病蟲害田間調查，並就重要病害進行病原分離鑑定、致病性測定、生態特性分析及防治資材之評估，以建立臺灣藍莓病害基礎資料並提供防治管理建議。調查期間共蒐集 305 件有效樣本，其中病害樣本 164 件、蟲害樣本 141 件。病害樣本中以真菌性病害為主，分離結果顯示 *Colletotrichum*、*Alternaria* 及 *Phomopsis* 為主要病原菌屬，其中以 *Colletotrichum* 為最常見之分離屬。於葉片致病性試驗結果顯示，*Colletotrichum* 能於 25 及 30°C 培養下，對兔眼藍莓 (rabbiteye) 及南高叢藍莓 (southern highbush) 等三個品種上穩定形成壞疽病斑，顯示其為藍莓葉部重要致病菌；相較之下，*Alternaria* 與 *Phomopsis* 之致病性則較不穩定。進一步以多基因序列 (ITS、ACT、TUB、CHS-1、GAPDH) 進行 10 株分離株之親緣關係分析，結果顯示臺灣藍莓炭疽病菌隸屬於 *Colletotrichum gloeosporioides* 與 *C. boninense* 複合種，與部分國外藍莓產區之菌系組成有所差異。炭疽病菌之生態試驗結果顯示，其菌絲可於 15 至 30°C 條件下生長，並於 30°C 達到最佳生長表現，顯示高溫環境有利於病原菌生長，亦與臺灣夏季氣候條件相符。防治試驗方面，化學藥劑中以扶吉胺 (fluazinam) 及普克利 (propiconazole) 對炭疽病菌具較佳之菌絲抑制效果，扶吉胺在 0.1ppm 時防治率達 87.0-93.0%，而普克利在 10ppm 時為 94.8-98.9%；在非化學、低風險防治資材中，柑橘精油類資材金桔力具有抑制菌絲生長的潛力，在稀釋 500 倍時具 77.3-91.4% 之防治率、1000 倍時具 68.2-85.8% 之防治率。綜合結果顯示，炭疽病為目前臺灣藍莓生產上之關鍵病害之一，本研究所建立之病害種類、病原特性與低風險防治資訊，可作為未來藍莓病害整合性管理 (Integrated pest management, IPM) 及防治技術建立之重要參考。

## A08- 臺灣辣椒炭疽病原菌族群結構與藥劑感受性之調查與評估

### Population structure and fungicide sensitivity of *Colletotrichum* spp. causing chili anthracnose in Taiwan

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辣椒 (*Capsicum annuum* L.) 為臺灣重要果菜類作物，其生產常受到炭疽病 (Anthracnose) 之嚴重威脅，影響田間栽培與採後貯運品質。本研究旨在調查臺灣主要產區辣椒炭疽病原菌之族群組成，並評估其對現行核准登記防治藥劑之感受性。自彰化、雲林、嘉義、高雄及花蓮等地採集罹病辣椒果實，共取得 15 株具代表性之分離株，經 ITS 序列鑑定結果顯示，*Colletotrichum scovillei* 為目前臺灣辣椒炭疽病之優勢病原，另偵測到 *C. siamense*、*C. fruticola* 及 *C. truncatum* 等種，顯示病原族群具有多樣性與區域性差異。部分菌株呈現 *C. acutatum* / *C. scovillei* 之模糊鑑定，顯示 ITS 於相關種複合群解析度不足，未來需納入多基因座以提升分類準確性。藥劑感受性試驗結果顯示，不同地區菌株對核准登記藥劑之菌絲生長抑制效果存在顯著差異。百克敏於彰化來源菌株中抑制率較高，但在雲林、嘉義與花蓮族群中效果較差；待克利於各地呈現相對穩定之中度抑制；三氟派瑞、氟殺克敏與晴硫醃對多數地區菌株抑制率偏低，顯示敏感性具地理變異。本研究釐清臺灣辣椒炭疽病原之族群結構及其藥劑感受性現況，提供後續抗藥性監測、區域化用藥管理與病害整合防治策略之重要依據，並可作為精準農業下病害管理決策的重要參考。

## B. 細菌及病毒組

### B01- 萬代蘭花枯病菌之寄主範圍測試及防治資材篩選

#### Host range test and screening of control materials against flower blight pathogen of *Vanda orchid*

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萬代蘭為原產於熱帶及亞熱帶亞洲之蘭科植物，兼具盆花與切花利用價值，近年亦為臺灣具發展潛力之蘭花產業作物之一。2020年與2024年於彰化栽培田區陸續傳出一細菌性病害，造成萬代蘭花瓣、萼片及花苞出現水浸狀壞疽及枯萎症狀，其罹病率最高可達50%，經研究已確認其病原為 *Pantoea stewartii* subsp. *indologenes*，為萬代蘭花枯病之首次病害報導，經隔離處置及緊急防治後，後續採集之花苞樣本均未再檢出病原菌，顯示目前臺灣仍維持該病原非疫區狀態。為進一步釐清該病原之寄主範圍並評估可供防治之資材，本研究以自萬代蘭分離之 VB1 菌株進行寄主範圍測試及室內抑菌試驗。研究結果顯示，VB1 菌株可於洋蔥鱗片造成輕微凹陷與褪色病徵，於蝴蝶蘭可造成水浸狀病斑，而於玉米、水稻及小米則未見病徵，顯示其寄主反應可能與已知部分 *P. stewartii* subsp. *indologenes* 病原型並不相同。室內藥劑篩選結果顯示，20% 歐索林酸可濕性粉劑對 *P. stewartii* subsp. *indologenes* 之抑菌效果最佳，10% 鏈四環黴素可溶性粉劑及 68.8% 多保鏈黴素可濕性粉劑亦具有明顯抑菌效果；另次氯酸水、二氧化氯及二氯異氰尿酸鈉於 10-100 ppm 下亦具殺菌效果。綜合而言，本研究係延續萬代蘭花枯病首次報導後之後續工作，進一步獲得該病原之寄主範圍及可用防治資材等基礎資料，所得結果可作為後續監測、緊急防治及栽培衛生管理之參考。

## **B02- 貝萊斯芽孢桿菌 TNB40 發酵配方優化及防治甜瓜黑點根腐病成效初探** **Optimization of fermentation formula for *Bacillus velezensis* TNB40 and a preliminary study on its efficacy in controlling melon black root rot**

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Tsai, H. H., Huang, M. J., and Chen, C. C. (Tainan District Agricultural Research and Extension Station, MOA.)

洋香瓜黑點根腐病為全球性洋香瓜生產之重要限制因子，在臺灣四季皆會發生，常造成重大損失。由於目前病害防治僅登記「脫克松」單一藥劑，長期使用易面臨防治成效遞減問題。為推動化學農藥減量並貫徹 IPM 精神，本研究旨在優化有益微生物貝萊斯芽孢桿菌 (*Bacillus velezensis*) TNB40 菌株之量產技術，並評估其對甜瓜黑點根腐病之田間防治效果。研究結果顯示 TNB40 菌株對於營養源比例具有特定偏好，測試不同碳氮比 (C/N) 配方後發現該菌株偏好較低碳氮比之營養源。在初步通氣量試驗中，當培養液與整體發酵空間體積比維持在約 40% 時，其活菌數產量最高。目前透過液態發酵技術優化，已達成活菌數及內孢子均為  $10^8$  CFU/mL 之發酵條件。在應用性評估與田間確效方面，於嘉義太保進行之田間試驗顯示，以  $10^6$  CFU/mL 濃度稀釋菌液於種植前澆灌瓜苗 1 次，並於種植後每週澆灌 1 次 (連續 4 週)，其採收前 1 週萎凋率可降至 48.8%，顯著優於慣行脫克松防治組之 73.3%。若採 TNB40 與脫克松複合處理，萎凋率可進一步降至 39.8%，顯示生物防治資材加入後之顯著增益效果。綜上所述，貝萊斯芽孢桿菌 TNB40 具備優異之產生內孢子能力與環境抗性，且在田間防治成效上具備取代或輔助化學農藥之潛力。本研究建立之離型配方與發酵製程，將為後續商品化研發與推動農業永續發展奠定重要基礎。

### B03- *Pseudomonas mosselii* 對青枯病菌之抑菌機制探討

## Studies on the antibacterial mechanism of *Pseudomonas mosselii* against bacterial wilt pathogen

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植物青枯病為 *Ralstonia solanacearum* species complex 所造成的植物系統性萎凋病害，其主要以土壤傳播，由植物根部侵入，於木質部繁殖並產生大量多醣體，阻礙水分運輸，造成萎凋徵狀，對番茄等多種重要作物影響甚鉅。青枯病難以防治，目前主要防治手段為結合生物防治等多種方法以進行害物整合管理，然而在臺灣僅一種微生物製劑可用於防治青枯病，因此本研究目的為篩選臺灣可抑制青枯病菌的新菌種。本研究經菌株分離與對峙培養測試，篩選出 5 株分離自番茄與桃樹根圍土之菌株，對青枯病菌之抑制圈皆顯著大於市售菌株，且對其他植物病原細菌亦具抑制能力。以 16S rDNA 與 *gyrB* 序列進行親緣分析，顯示此 5 株菌株皆為 *Pseudomonas mosselii* 物種。透過培養於 King's B 培養基檢測菌株是否產生抑菌物質 pyoverdine (螢光色素鐵載體)，結果顯示 *P. mosselii* 菌株皆可觀察到黃綠色螢光色素，但於富鐵時則不產生此色素，符合產螢光色素 *Pseudomonas* 屬菌株之特徵。於缺鐵與富鐵培養基進行對峙培養測試，結果顯示不論缺鐵或富鐵，*P. mosselii* 菌株的抑制圈皆顯著大於供試產螢光 *Pseudomonas* spp. 菌株；於富鐵時，*Pseudomonas* spp. 菌株無抑菌圈產生 (富鐵時不產生 pyoverdine)，而 *P. mosselii* 菌株相較於缺鐵時產生更大的抑菌圈，顯示尚有其他抑菌物質產生。經檢測生產抑菌物質 pseudoiodinine 基因簇之最終基因 *psdB*，確認 *P. mosselii* 菌株皆具有此基因，故其他抑菌物質可能是 pseudoiodinine，待後續研究確認。此外，進行揮發性拮抗測試，結果顯示 *P. mosselii* 菌株可產生抑制青枯病菌菌落形成的揮發性抑菌物質。經 *hcnBC* 基因引子對檢測，確認 *P. mosselii* 菌株皆具有 *hcnBC* 基因；另以氰化物檢測試紙進行揮發物檢測，結果皆呈現陽性，顯示 *P. mosselii* 菌株可產生 HCN。將 *P. mosselii* 與青枯病菌菌株於液態培養基進行共培養測試，以確認 *P. mosselii* 菌株是否於液態培養時仍具抑菌作用，結果顯示青枯病菌族群量於共培養 12 小時即顯著降低，於 48 小時則降低至檢測極限值 10 CFU/mL 以下。本研究顯示 *P. mosselii* 菌株對青枯病菌具有抑菌效果，其抑菌機制來自可產生多種抑菌物質，如 pyoverdine 與 HCN，以及待確認的 pseudoiodinine。未來將進一步探討 *P. mosselii* 菌株及其抑菌物質對植物青枯病之防治效果，期望本研究能為臺灣在植物青枯病防治上帶來貢獻。

## **B04- 質外體富含甘胺酸蛋白 LsGRP1 介導植物系統獲得抗性之機制與應用 Apoplastic glycine-rich protein LsGRP1 mediates plant systemic acquired resistance and the application**

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系統獲得抗病性是植物權衡生長與防禦間能量分配的適應性策略，被認為是關鍵的化學農藥替代方案之一。位於百合葉部質外體的富含甘胺酸蛋白 LsGRP1 正面調控植物的生長與廣譜病原菌抗性，並因應病原菌攻擊與水楊酸處理而系統性增強表現，暗示其參與誘導性系統抗病的調控。本研究以農桿菌與蛋白浸潤法於莖百合與阿拉伯芥的局部葉片增加 LsGRP1 含量，發現 LsGRP1 能夠系統性地強化植物的抗病性以及免疫活化。分析經 LsGRP1 處理的阿拉伯芥葉片之誘導抗性相關基因表現，確認其機制涉及防禦預警 (defense priming)，改善植物防禦敏感度，針對病原菌攻擊表現更快與更強的防禦反應。透過阿拉伯芥系統獲得抗性相關突變株，確認 LsGRP1 經水楊酸與 *N*-羥基哌啶酸相關傳訊路徑誘發系統獲得抗性。最後透過釐清 LsGRP1 誘導系統獲得抗性相關條件，包括施用濃度、生效與持效時間與可處理植物組織，以及在田間施用 LsGRP1 對作物生長與抗病性的貢獻，闡明 LsGRP1 的應用潛能。這些發現揭示質外體蛋白 LsGRP1 在系統獲得抗性的調控機制以及在植物健康管理的應用價值。

## B05- 苗栗地區橫山梨病毒與黑星病菌複合感染現況及其病徵顯現之初探 Preliminary study on co-infection and symptom expression of viruses and black spot (*Venturia* sp.) on 'Hengshen' pear in Miaoli

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蘋果莖凹陷病毒 (apple stem grooving virus, ASGV)、蘋果黃化葉斑病毒 (apple chlorotic leaf spot virus, ACLSV) 與蘋果莖痘斑病毒 (apple stem pitting virus, ASPV) 為梨穗最常被檢測感染的三種病毒，過去研究指出，橫山梨 (*Pyrus pyrifolia* var. *Hengshen*) 受病毒感染時，葉片可能出現褪綠、黃化、嵌紋、葉畸形、小葉或新梢叢生等病徵，並有可能出現無明顯病徵之潛伏感染。於苗栗三灣鄉梨園發現，2025 年 7 月採收期後的梨成熟老化葉片，葉下表皮陸續發生壞疽病斑，首次採樣自不同棵梨樹具病斑之葉片共 5 樣本，經反轉錄聚合酶連鎖反應 (RT-PCR) 檢測，均檢出 ASPV 感染，其中 3 樣本同時複合感染 ASGV。同年 9 月下旬，進一步於三灣鄉、大湖鄉、卓蘭鎮梨產區進行採樣與檢測，在三灣鄉同一區域，分別自具病斑與無病徵之不同徒長枝採集 3 株樣本，其中僅 1 株檢出相同的 ASPV 和 ACLSV 複合感染，其餘 2 株無論有無病徵，皆至少檢出有 1 種病毒感染。大湖鄉及卓蘭鎮則檢驗具壞疽病斑樣本各 3 株，僅卓蘭有 1 株未檢出病毒，其餘樣本均檢出 1 種以上病毒感染。2 次採樣調查共檢測 17 件樣本，其中 16 件檢出病毒感染。比對日本、韓國梨產區照片上病徵，與本研究調查區之病徵相似；然而，本調查區病徵，葉下表皮褐色壞疽斑多未穿透至葉面。同時，於下表皮病斑處及周圍可分離到黑星病菌 (*Venturia* sp.) 分生孢子。田間觀察顯示，部分梨園之病斑多發生於 9 至 11 月老化梨葉的葉下表皮處；同時期之秋冬梢新葉，以及翌年 (2026 年) 同調查區域春梢均未見類似病徵顯現，亦未檢出黑星病菌孢子。綜上，本研究顯示苗栗調查區橫山梨存在多種病毒局部潛伏感染，而當採收後葉片老化出現壞疽病斑時，病毒感染與黑星病菌之複合感染可能具有密切關聯。

## **B06- Multiplex Detection of Major Viral and Bacterial Pathogens in Cucurbits for Improved Disease Diagnosis and Management**

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A multiplex assay was developed for the simultaneous detection of four important cucurbit pathogens—*Cucumber mosaic virus* (CMV), *Cucumber green mottle mosaic virus* (CGMMV), *Zucchini mosaic virus* (ZYMV), and *Acidovorax citrulli*. The assay integrates multiplex RT-PCR amplification with bead hybridization, enabling the simultaneous identification of multiple pathogens in a single reaction. Pathogen-specific primers and probes were designed to amplify target sequences, and the resulting amplicons were hybridized to color-coded microspheres coated with complementary capture probes. The hybridized beads were subsequently analyzed using a detection system equipped with dual-laser technology for bead classification and signal quantification. The developed assay demonstrated high specificity and sensitivity, with no cross-reactivity among the tested pathogens. In addition, the system successfully detected mixed infections in naturally infected melon and watermelon samples. Compared with conventional PCR, the assay showed improved sensitivity and reliability when analyzing complex plant extracts. This multiplex platform provides a rapid, high-throughput, and accurate diagnostic tool for the simultaneous detection of viral and bacterial pathogens in cucurbit crops, facilitating early disease diagnosis and effective plant disease management.

## **B07- Comparative Analysis of Diagnostic Techniques for Melon yellow spot virus**

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*Melon yellow spot virus* (MYSV), a member of the genus *Orthospovirus*, is an economically important pathogen infecting cucurbit crops in many Asian countries. Infection by MYSV causes chlorotic and necrotic lesions on leaves and fruits, resulting in significant yield losses. Rapid and sensitive detection methods are essential for effective disease management and epidemiological investigations. In this study, a fluorescence-based molecular detection assay was developed for the specific detection of MYSV. Primers and a TaqMan probe were designed based on a conserved region of the nucleocapsid gene to ensure high specificity. The assay showed no cross-reactivity with other common cucurbit viruses. Sensitivity analysis demonstrated that the assay could reliably detect MYSV even at low viral concentrations. Compared with conventional PCR methods, this detection approach provides improved specificity, rapid detection, and real-time monitoring of amplification signals. The developed method was successfully applied to detect MYSV in field-collected melon and cucumber samples. This fluorescence-based molecular detection assay provides a rapid, sensitive, and reliable diagnostic tool for MYSV detection, facilitating early diagnosis and improved disease management strategies in cucurbit production systems.

## B08- 南瓜捲葉中國病毒分子特性分析與寄主範圍之探討

### Molecular Characterization and Host Range Determination of squash leaf curl China virus

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南瓜捲葉中國病毒 (squash leaf curl China virus, SLCCNV) 屬於雙生病毒科 (Geminiviridae) 豆金黃嵌紋病毒屬 (*Begomovirus*)，其基因體由雙單股環狀 DNA (DNA-A 與 DNA-B) 所構成，由媒介昆蟲菸草粉蝨 (*Bemisia tabaci*) 進行傳播。此病毒自 1995 年在中國廣西首次被發現與鑑定，隨後在越南、菲律賓、泰國、印度、巴基斯坦、孟加拉及東帝汶等亞洲國家陸續出現之記錄。受感染植株會出現葉片捲曲、黃化嵌紋及生長遲緩等病徵，嚴重時高達 100% 的產量損失。本研究由香港高華種子公司所提供來自中國田間共 17 個葫蘆科捲葉病乾燥樣品，包含 5 個稜角絲瓜與 12 個南瓜樣品，以 *Begomovirus* 廣效性引子對 PAL1v1978RYNN/PAR1c715H 進行 PCR 反應後共 8 個樣品呈陽性反應，分別為 2 個稜角絲瓜樣品以及 6 個南瓜樣品，後將呈陽性反應之樣品進行全基因體解序，共獲得 6 條 DNA-A 與 6 條 DNA-B 之基因體全長，為 1 個稜角絲瓜及 5 個南瓜樣品。比對分析結果顯示 DNA-A 之序列與來自中國廣州 SLCCNV-GDFS (MW389915) 核酸序列相似度為 99-100%，DNA-B 全基因體序列與同樣來自中國廣州 SLCCNV-FSBG (MW389924) 核酸序列相似度為 94-98%。後續共完成 3 個來自南瓜樣品感染性選植株構築並接種於原寄主，植株則呈現葉片捲曲、嵌紋及節間縮短之病徵與田間病徵相符。後續持續進行寄主範圍測試及目前實驗室抗捲葉病葫蘆科品系之病毒篩選。台灣目前尚無 SLCCNV 發生之正式紀錄，然考量其在鄰近國家與東南亞地區的廣泛傳播，本研究結果可作為台灣未來防疫監測與抗病育種之重要參考。

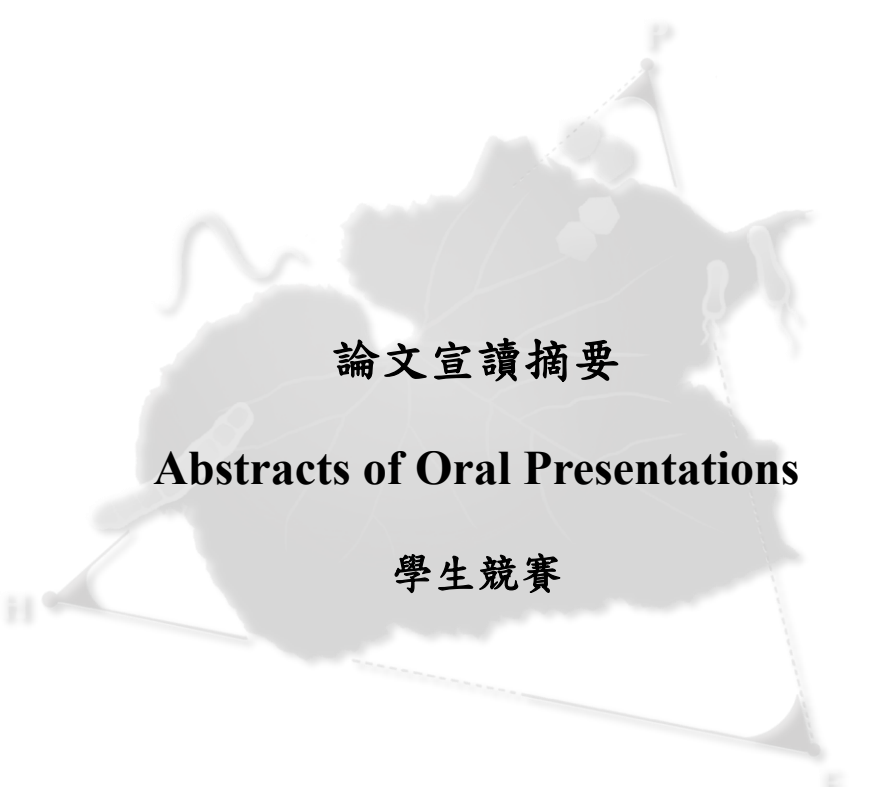
## B09- 探討 sORF A 與番茄感染性相關聯之關鍵胺基酸序列

### The study of the key amino acid sequence of sORF A related to tomato infectivity

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Lin, C.-L. and Tsai, W.-S. (Dept. of Plant Medicine, National Chiayi University, Chiayi)

小開放閱讀框 (sORFs) 定義為編碼 100 個胺基酸以內之 ORF，可編碼功能性胜肽或可調節主要 ORF 的轉錄。sORFs 廣泛存在於真核生物當中，而植物病毒基因體上亦可發現具功能性之 sORF。先前自馬來西亞田間發現的 ToLCNDV-A[MY-BG120-17] 重排病毒株，其基因體組成爲 tomato leaf curl New Delhi virus (ToLCNDV) DNA-A 加上 squash leaf curl China virus (SLCCNV) DNA-B，而此重排病毒株有效感染番茄植株之關鍵因子與 DNA-B 上編碼之 BV1 或 BC1 基因無直接關聯，反而與未曾被報導過的 sORF A (79aa) 有相關。本研究利用點突變，分別將 sORF A N-端起始的第一個甲硫胺酸 (sORF A<sup>ΔM1</sup>)，以及第一與第二個甲硫胺酸 (sORF A<sup>ΔM1ΔM14</sup>) 進行突變，各自形成兩條 N-端截短的 sORF A，另亦將第 45 位胺基酸進行突變 (sORF A<sup>Δ45~</sup>)，形成提前終止的 sORF A，上述點突變 DNA-B 分別與 ToLCNDV-A[MY-BG120-17] DNA-A 共同接種番茄後，雖然引發較輕微病徵，但皆可有效感染番茄，顯示 sORF A 胺基酸序列的 N 端與 C 端可能非是有效感染番茄的關鍵區位。以點突變 sORF A 第 35 個與第 36 個胺基酸，以及 sORF A<sup>ΔM1ΔM14</sup> 與 sORF A<sup>Δ45~</sup> 相對位置之胺基酸，共構築 6 個點突變 DNA-B 組別，將其各別與 ToLCNDV-A[MY-BG120-17] DNA-A 共同接種番茄後，分別計算接種後第 9、12、17、23 與 26 天的罹病率，以及接種後第 17、23 與 26 天的罹病程度。除 ToLCNDV-A[MY-BG120-17] DNA-A 與 sORF A<sup>Δ45~F35C</sup> 共同接種番茄外，其餘組別罹病速度與 ORF A 共同接種番茄時相比，顯著減緩，而 ToLCNDV-A[MY-BG120-17] DNA-A 與 sORF A<sup>Δ45~F35C</sup> 共同接種番茄時，罹病速度及病徵嚴重程度均較與 sORF A<sup>Δ45~</sup> 共同接種番茄時快且嚴重。依上述試驗結果，推測 sORF A 第 35 及 36 個胺基酸改變可能影響病毒感染番茄時與病毒因子或寄主因子之間的交互作用，進而導致番茄產生不同的病徵嚴重程度。透過上述研究有助於釐清重排 ToLCNDV sORF A 在病毒感染番茄時的重要性。



論文宣讀摘要

**Abstracts of Oral Presentations**

學生競賽

## SA 組

### SA01- 開發紅龍果莖潰瘍病之病害預警系統

#### Development of a disease warning system for dragon fruit (*Hylocereus* spp.) stem canker (*Neoscytalidium dimidiatum*)

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紅龍果 (*Hylocereus* spp.) 為台灣重要的經濟果樹之一，由於其生長適應性強且營養價值高，近年來在全球也廣受青睞，栽培面積也不斷增加。然而，隨著栽種面積的提升，病害問題也相繼出現。其中，*Neoscytalidium dimidiatum* (Penz.) Crous & Slippers 造成的莖潰瘍病為臺灣常見的病害之一，嚴重時會造成枝條壞疽潰瘍與果實壞疽，導致產量與品質損失。為了提升紅龍果莖潰瘍病的管理精準度並降低非必要的藥劑投入，本研究已依據積效溫度對於病原菌孢子發芽、溫溼度對於病害潛伏期影響，以及葉狀莖濕度維持時間對於病害潛伏期影響的資料，建立紅龍果莖潰瘍病的風險預警模型，以協助管理者在不同的病害風險時期，判斷可採取的管理措施。研究初步利用 2025 年 2 月至 2026 年 3 月月間，在台中霧峰、彰化二林與南投集集的田間調查資料進行預警模型驗證。根據接收者操作特徵曲線下面積 (area under receiver operating characteristic curve) 的分析結果顯示，中部調查地區的整體風險在觀測窗口為 4 小時的前提下，模型預測的真陽性率達 77.94%，但偽陽性率也達 56.61%，偽陰性率則為 22.06%，是目前最佳的觀測窗口時長；其中，霧峰地區的真陽性率可達 82.86%，偽陽性率略降為 51.91%，偽陰性率則降低至 17.14%。此外，本研究也初步架設預警網站，在網頁上可顯示現有調查地點紅龍果莖潰瘍病的病害風險，隨著中央氣象署每小時的溫濕度更新而持續變動。網頁上亦設計便於閱讀的風險走勢，以及根據近 48 小時的天氣預報結果所預測的紅龍果莖潰瘍病風險。後續可持續進行病害監測、調整預警模型參數，並增加田間操作資訊模組，以提高模型的正確度。並期望本預警系統未來能協助管理者依據不同的病害風險時期進行適當的管理，以降低非必要之藥劑投入並維護環境與食品安全。

## SA02- 建立草莓萎凋病菌 (*Fusarium oxysporum* f. sp. *fragariae*) 於帶菌植株之 分子檢測方法

### Development of a molecular detection method for *Fusarium oxysporum* f. sp. *fragariae* in infected strawberry plants

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草莓為全球廣受歡迎且具高經濟價值之重要作物，惟栽培過程易受多種病蟲害侵襲。其中，由 *Fusarium oxysporum* f. sp. *fragariae* (Fof) 引起之草莓萎凋病，為威脅草莓生產最嚴重的病害之一。該病原菌可藉由厚膜孢子長期存活於土壤或植株殘體中，亦可能經由母株匍匐莖傳播而擴散，顯著提高防治難度並造成產量與品質損失。因此，建立可於育苗與栽培早期偵測帶菌植株之分子檢測技術，對阻斷病原傳播與降低產業風險至關重要。然而，目前用於 Fof 的分子引子仍可能存在專一性不足之問題，且缺乏適用於草莓帶菌根部組織之快速核酸萃取方法，限制了田間與育苗端的即時檢測效率。本研究著重於建立一套適用於 Fof 帶菌組織之核酸快速萃取與分子檢測流程。透過比較不同核酸萃取方法並結合即時定量聚合酶連鎖反應 (real-time quantitative polymerase chain reaction, qPCR)，成功建立一套可快速檢測受 Fof 感染之草莓根部組織的檢測系統。研究結果顯示，本研究篩選出適用於草莓帶菌組織之快速核酸萃取試劑，並證實搭配 qPCR 可於植株尚未出現明顯病徵之感染初期，即有效偵測到 Fof。此外，快速萃取所得之萃取液在不同溫度條件下儲存 30 天後仍維持穩定檢測效果，顯示其具良好保存性與實務應用潛力。綜合而言，本研究建立之快速核酸萃取與 qPCR 檢測流程，可作為草莓萎凋病發生前之早期偵測工具，並可導入育苗與栽培管理流程，以降低帶菌植株進入生產體系之風險。期望藉由此快速且操作簡便之檢測策略，有效降低草莓萎凋病對產業造成之威脅。

## SA03- 建立水稻紋枯病病原 *Rhizoctonia solani* AG1 之快速土壤檢測方法

### Development of a rapid soil-based detection method for rice sheath blight caused by *Rhizoctonia solani* AG1

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水稻紋枯病 (Rice sheath blight, ShB) 主要由立枯絲核菌第一菌絲融合群亞組 (*Rhizoctonia solani* AG1) 引起，為全球水稻重要病害之一，嚴重時可造成高達 70% 的產量損失。由於 *R. solani* 的菌核可於田間植物殘體與土壤中存活數年且仍具致病力，故及早偵測土壤中病原菌對於病害預警與防治決策至關重要。然而，*R. solani* 種內分類複雜；且針對屏東地區 43 株水稻病原菌之評估結果顯示，現有國際上已開發之專一性引子在紋枯病偵測上仍可能存在專一性不足之問題。為克服傳統商業核酸萃取套組耗時且操作繁瑣之限制，本研究在前人研究的流程基礎上加以改良，建立一套快速土壤病原檢測系統。簡要流程為：取 25 mg 土壤樣本破碎後，加入特定緩衝液，經短暫震盪加熱並離心後，即可取得可供後續分子檢測之 DNA。經臺灣 16 縣市共 105 株菌株之專一性測試結果顯示，引子組 RS1F/RS2R 與 SMS RS1-F/SMS RS1-R 表現最佳，其 F 值 (F-measure, F1-score) 分別達 0.986 與 0.923。靈敏度測試顯示，本檢測系統結合快速萃取法後，對每 25 mg 土壤僅含 0.0005 mg 菌核之樣品仍可達 100% 偵測率；在干擾試驗中，即使混入高達 20% 的新鮮水稻組織，其準確度 (Accuracy)、精密度 (Precision) 與召回率 (Recall) 仍皆維持 100%。綜合而言，本研究成功整合高專一性引子組與快速核酸萃取技術，提供一套可靠且高效率之水稻紋枯病土壤檢測方案，可作為田間預警監測與精準病害管理之重要工具，未來具應用於例行田間監測以提升病害預警效能之潛力。

## SA04- 以顯微構造解析樹木褐根病菌侵染木質部之策略

### Microscopic characterization reveals the infection strategies of *Phellinus noxius* in tree xylem

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CODIT 理論 (Compartmentalization of Damage/Dysfunction in Trees) 指出，樹木作為生命週期長的多年生植物，透過組織結構與化學屏障來阻隔木材腐朽菌對韌皮部、形成層，以及邊材中水分輸導組織的侵害。褐根病菌 (*Phellinus noxius*, syn. *Pyrrhoderma noxium*) 具有侵染活體植物組織的能力，對於其如何突破 CODIT 卻仍不清楚。柯 (2023) 於褐根病菌初期侵染植物的石蠟切片中，發現其優先定殖於皮層、形成層與韌皮部，抑制形成層形成 CODIT 中防禦能力最強的第四道壁—阻隔區 (barrier zone)，且病原菌能透過導管與射線薄壁細胞在木質部進行縱向與橫向侵染。本研究進一步利用掃描式電子顯微鏡技術，同樣觀察到褐根病菌菌絲大量佔據導管空腔，顯示以填充體阻擋縱向侵染的第一道壁並未發揮作用。對於由緊密排列的木纖維與縱向薄壁細胞建構的第二道壁，在垂榕、正榕、印度橡膠樹與鳳凰木等具有豐富縱向薄壁細胞的樹種中，褐根病菌較少破壞縱向薄壁細胞，而是透過壁孔與細胞壁穿孔，穿梭於木質部並分解木纖維，使組織產生大量空洞；在楓香與肯氏南洋杉等不具縱向薄壁細胞的木材組織中，也觀察到褐根病菌主要分解木纖維而產生局部空洞。褐根病菌亦可破壞組成第三道壁的射線薄壁細胞以達成徑向擴張，然而在後期腐朽階段，其轉而優先分解木纖維，而留下部分分解之射線薄壁細胞。此外，褐根病菌於木質部定殖過程中會形成多樣結構。在不同的腐朽區域交界處，因木纖維尚未被分解而在木材內產生淡褐色的立體網紋結構。而黑色素沉澱的褐根病菌菌絲會緻密地填充於木質部空腔中形成黑褐色的區隔線 (demarcation lines)，並隨時間發展加粗並完全填滿空腔，這些區隔線在木質部與樹皮交界處形成網紋狀構造。最後褐根病菌菌絲也可在木質部與樹皮之間的空間成束排列形成菌絲索。褐根病菌於木質部中形成的腐朽區域與區隔結構，反映其在感染與腐朽過程中對資源利用與擴張策略的動態調控，亦顯示其能有效突破樹木依賴 CODIT 所建立的空間防禦機制。

## SA05- 探討殺菌劑於正榕木材中對褐根病菌之抑制效力及其擴散性

### Investigation of the inhibitory efficacy of fungicides against *Phellinus noxius* and their diffusion in *Ficus microcarpa* wood

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木材腐朽菌 (wood-decay fungi) 危害是常見的樹木健康問題。目前針對木材腐朽病害的殺菌劑篩選多以含藥培養基進行，能否準確反映木材複雜環境下的抑菌效力值得探討。由於罹病樹木的輸導功能可能受損，且心材無運輸作用，因此殺菌劑於木材內的擴散性，決定其能否有效到達罹病處並發揮藥效。本研究以目前發生嚴重且具破壞性之褐根病 [病原菌 *Phellinus noxius* (syn. *Pyrrhoderma noxium*)] 作為試驗對象。首先以邊長 5 mm 的正榕 (*Ficus macrocarpa*) 立方木塊建立簡便的含藥木塊測定法，並挑選涵蓋 5 類作用機制 (FRAC 3、7、9、11、12) 的 9 種殺菌劑，評估其在木材基質中的抑菌效果。殺菌劑預防性處理木塊的試驗中，得克利 (tebuconazole) 展現出最佳的抑菌效果 ( $EC_{50} = 0.131 \text{ mg kg}^{-1}$ )；而在治療性處理中，則以依普座 (epoxiconazole) 的表現最佳 ( $EC_{50} = 0.256 \text{ mg kg}^{-1}$ )。含藥培養基與含藥木塊兩種測定法所得  $EC_{50}$  值具顯著正相關 ( $r = 0.77-0.79$ )，但木塊法測得之  $EC_{50}$  值為培養基法的 3.6 至 197.5 倍，顯示木材基質會大幅度降低藥劑的效力。為了解殺菌劑於木材內部的擴散性，本研究將殺菌劑 (1.2 mL,  $75 \text{ g L}^{-1}$  有效成分) 注入正榕段木，7 天後以電鑽於注射點上方、下方及右方 2 cm 與 4 cm 處鑽取木屑，並利用液相層析串聯質譜儀 (LC/MS-MS) 進行目標藥劑之定性及濃度定量。百克敏 (pyraclostrobin)、得克利及依普座在縱向 (上下 2 cm) 濃度可達 68.1–132.0  $\text{mg kg}^{-1}$ ，但橫向 (右側 2 cm) 僅有 0.3–1.8  $\text{mg kg}^{-1}$ ，顯示殺菌劑擴散以縱向移動為主，橫向擴散極為有限。此外，滅普寧 (mepronil)、賽普洛 (cyprodinil) 與護汰寧 (fludioxonil) 的整體擴散性極差，推測可能與其水懸劑或水分散性粒劑的理化特性相關。本研究透過量化木材基質效應與藥劑擴散性，建立更符合實際木材環境的評估模式，為樹木醫學篩選木材腐朽病害藥劑及擬定施用策略提供科學依據。

## **SA06- How pesticides disrupt top-down control from hyperparasitism**

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Insect pests are often managed with pesticides to prevent crop loss. However, studies have shown that such practice may lead to pest resurgence, which is often associated with the accidental elimination of natural enemies. On the other hand, while plant pathogens are also often managed with pesticides, the phenomenon of resurgence remains under-explored in plant—pathosystems, representing a critical knowledge gap given that the natural enemies of pathogens (i.e., hyperparasites) function differently compared to those of insect pests. Here, we study whether pathogen resurgence can occur under the top-down pressure from hyperparasites. To this end, we developed a theoretical model to describe the interactions between host plants, pathogens, and hyperparasites, which infect pathogens for a period instead of directly consuming them. We simulated pesticide application by increasing the intrinsic mortality rate of the pathogen, and found that the pathogen equilibrium abundance paradoxically increases with its mortality rate (i.e., pathogen resurgence). This occurs because elevated pathogen mortality reduces hyperparasite abundance, thereby weakening their top-down effect and allowing more pathogens to grow even under a high intrinsic mortality rate. We further explored how the pesticide application altered the dynamics of two competing pathogen strains, characterized by a virulence-to-host and susceptibility-to-hyperparasite trade-off. We found that pathogen resurgence may not occur in the multi-strain system if strains exhibit different pesticide sensitivity. Moreover, we demonstrated that such a multi-strain system exhibits alternative stable states, and varying the top-down control by hyperparasites can generate shifts in the equilibrium plant productivity. Our theoretical model highlights the importance of considering potential species interactions when developing management strategies in the field.

## **SA07- Possible mechanisms of *Fusarium solani* species complex (FSSC) from passion fruit showed low sensitivity to QoI fungicides and its characteristics**

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*Fusarium solani* species complex (FSSC) is one kind of pathogen to attack plants, animals, and humans. As a plant pathogen, FSSC can infect a wide range of economically important crops. In particular, FSSC has severely impacted the passion fruit industries in Taiwan, posing a significant threat to passion fruit productions. Therefore, effective management of diseases caused by FSSC is a critical issue. Chemical control is one of the most common management strategies for passion fruit diseases. This study focused on FSSC isolates associated with passion fruit collar rot and fruit rot and evaluated their sensitivity to Quinone outside inhibitor (QoI) fungicides. The results of fungicide sensitivity assays revealed that FSSC isolates exhibited low sensitivity to QoI fungicides, including Pyraclostrobin, Azoxystrobin, and Trifloxystrobin. To elucidate the mechanisms of QoI-low sensitivity FSSC isolates, the point mutations in the *cytochrome b* (*cyt b*) gene sequences have been analyzed. However, no point mutations were detected in the *cyt b* gene of the low sensitivity FSSC isolates. Therefore, the role of Alternative Oxidase (AOX) activity in QoI resistance was further examined. Salicylhydroxamic acid (SHAM), an AOX inhibitor, was added to the medium in combination with QoI fungicides to determine whether inhibition of AOX could reduce resistance. The results showed that when AOX activity was inhibited, FSSC isolates with low sensitivity to QoI fungicides became more sensitive. These findings suggest that AOX plays an important role in modulating QoI sensitivity in FSSC. Physiological assays demonstrated that QoI-low sensitivity FSSC isolates exhibited slower mycelial growth on PDA and reduced sporulation compared to high sensitive isolates. These results provide valuable insights into the management of QoI-low sensitivity FSSC isolates in passion fruit.

## **SA08- Broad and comprehensive Fungicide Efficacy, Resistance Mechanisms, and Biocontrol Potential Against *Neopestalotiopsis protearum* Causing Fruit Rot and Scab in Guava and Wax Apple in Taiwan**

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*Neopestalotiopsis protearum* was recently identified as an emerging fungal pathogen in Taiwan based on our studies, causing fruit rot and scab in guava (*Psidium guajava*) and wax apple (*Syzygium samarangense*). In particular, *N. protearum* has become the primary causal agent, causing more severe fruit rot than scab symptoms, both during cultivation and post-harvest, resulting in significant economic losses. While several fungicides are currently recommended for guava scab and fruit rot management, their effectiveness against *N. protearum* remains unverified. This study evaluated the efficacy of Ministry of Agriculture (MOA)-recommended fungicides, along with other commercially available chemical and non-chemical agents, through mycelial growth inhibition assays. Among the recommended fungicides, Iminoctadine and Cyprodinil + Fludioxonil effectively inhibited *N. protearum*, whereas Trifloxystrobin and Pyraclostrobin + Boscalid had no inhibitory effect. Screening of 15 additional fungicides revealed that Fluazinam exhibited the highest antifungal activity, followed by Carbendazim + Prochloraz. Several others—including Iprodione, Tebuconazole, Propiconazole, Thiram, and Thiabendazole + Oxine-copper—showed efficacy only at higher concentrations. Fungicides in FRAC groups B (Thiophanate-methyl) and C (Trifloxystrobin + Fluopyram, Azoxystrobin) were ineffective. Further analysis of the  $\beta$ -tubulin and cytochrome b genes revealed that the only difference between resistant and sensitive isolates was a single nucleotide at position 204 of the cytochrome b gene; this single-nucleotide polymorphism resulted in the substitution of glycine with alanine at amino acid position 143, contributing to the emergence of highly resistant strains. Biocontrol potential was also assessed using *Bacillus* strains, including *B. velezensis* GFB08 (from prior studies) and commercial strains *B. velezensis* BF, *B. subtilis* KHY8, and *B. subtilis* Y1336. GFB08 showed the strongest inhibitory effect (34–62%), followed by BF (37–57%), Y1336 (32–57%), and KHY8 (14–54%). Additionally, essential oils (orange, hinoki, luanta-fir), chitosan, and hypochlorite were tested, with orange oil demonstrating the highest inhibition. These findings support the continued use of Iminoctadine for guava scab and the use of Cyprodinil + Fludioxonil for wax apple fruit rot. Fluazinam and Carbendazim + Prochloraz are proposed as alternatives to fungicides showing reduced efficacy. This study also highlights the potential of biocontrol agents and natural products to reduce fungicide reliance and provides a basis for future strategies for managing *Neopestalotiopsis*-associated diseases.

## **SA09- *Pseudopestalotiopsis* Species Causing Tea Gray Blight: Insights from Comparative Genomics and Nutrient Utilization Assays**

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*Camellia sinensis* (tea) is a globally significant crop frequently affected by foliar diseases, including gray blight commonly caused by pestalotioid fungi. In our recent study, we identified *Pseudopestalotiopsis* species as one of the major causative agents of gray blight disease in Taiwan. *Pseudopestalotiopsis chinensis* and *Pseudopestalotiopsis camelliae-sinensis* were identified as the most virulent pathogens, while *P. annellata* and *P. theae* were the least virulent, causing tea gray blight in Taiwan. The present study aimed to investigate the genomic features underlying virulence variation and to assess whether differential nutrient utilization correlates with pathogenic potential. Based on our previous results, two high-virulence strains of *P. chinensis* (YC08) and *P. camelliae-sinensis* (SS17-1), together with two low-virulence strains of *P. theae* (TT15) and *P. annellata* (SL19-1), were selected and subjected to whole genome sequencing and comparative genomic analysis. The assembled genomes ranged from 48.69 Mbp to 51.91 Mbp, with *P. theae* (TT15) possessing the smallest genome. While secretome and effector contents were broadly similar across all strains, profiles of other pathogenicity-related genes, including those annotated by PHI-base, BGCs (secondary metabolite biosynthetic gene clusters), and secreted CAZymes (carbohydrate-active enzymes), exhibited virulence-dependent clustering. All four strains shared 12,391 orthologous proteins, with only 493 orthologs exclusively found within the high-virulence group. Phenotypic assays, including the Biolog FF MicroPlate™, revealed that nutrient utilization variation among strains was strain-specific and independent of fungal virulence. In conclusion, *Pseudopestalotiopsis* species associated with tea gray blight exhibit differences in pathogenicity-related gene composition; however, in vitro nutrient utilization patterns did not correlate with virulence levels. Further transcriptomic or functional studies are warranted to elucidate key regulatory mechanisms driving virulence variation in these species.

## **SA10- Genome-wide comparative genomic analysis of *Fusarium oxysporum* f. sp. *ubense* Tropical race 4 and Race 1 reveals pathogenicity associated accessory regions**

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*Fusarium oxysporum* species complex (FOSC) comprises soil-borne, asexual filamentous fungi classified into host-specific *forma speciales* (ff. spp.). To date, more than 150 ff. spp. have been identified, infecting a wide range of plant hosts and causing diseases like vascular wilt, bulb and root rot, etc. The genomes of these pathogens are organized into conserved core chromosomes and variable accessory chromosomes which are lineage- or pathotype-specific and play a crucial role in pathogenicity. Accessory chromosomes are variable in GC content, enriched with repetitive sequences such as transposable elements, cysteine-rich secreted proteins, pathogenicity genes/effectors, and are often associated with horizontal gene transfer (HGT) events. *Fusarium oxysporum* f. sp. *ubense* (Foc), the causal agent of banana fusarium wilt disease, poses a major threat to banana production worldwide, highlighting the importance of identifying its pathogenic determinants. In our study, we present the chromosomal-level genome assemblies of Foc tropical race 4 (TR4) and race 1 (R1) strains from Taiwan. Comparative genomic analysis was conducted to identify lineage-specific genomic regions and chromosomes in TR4 and R1. These regions were further examined to uncover genes potentially associated with pathogenicity and host specificity. Overall, this study provides insights into genomic architecture and evolutionary dynamics of Foc, contributing to a better understanding of its pathogenic mechanism, host adaptation, and the role of accessory chromosomes in disease development. These findings advance our knowledge of Fusarium wilt and support future efforts in disease management.

## **SA11- Genetic variation, functional validation, pathogenic and evolutionary mechanism of *AVR-Pita1* gene among rice blast fungus population in Taiwan**

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Rice is one of the important crops around the world. Rice blast disease, caused by *Pyricularia oryzae*, reduces rice production and causes 10% to 30% yield loss annually. To manage this disease, breeding and deployment of resistant cultivars have been considered as effective and sustainable strategies. In Taiwan, commercial rice cultivars containing *PtrA* resistance gene have shown good field resistance, however, susceptible lesions have emerged on some cultivars in the fields, particularly in Taitung and Chiayi areas. To evaluate the risk of *PtrA* field resistance breakdown, the genotype, functionality, pathogenic and evolutionary mechanism of cognate *AVR-Pita1* gene among *P. oryzae* population were investigated. Genotyping results revealed that single copy or double alleles of *AVR-Pita1* are present in the genome of *P. oryzae* strains. Nine *AVR-Pita1* genotypes have been identified in Taiwan. *AVR-Pita1* alleles can be categorized into two main types based on the 192<sup>nd</sup> amino acid in the ORF, where change from A to G at the 719<sup>th</sup> nucleotide position led to substitution at the 192<sup>nd</sup> amino acid residue from tyrosine to cysteine. Functional characterization confirmed that A<sup>719</sup> allele is a functional avirulence gene, whereas G<sup>719</sup> allele is nonfunctional. In addition to sequence variation, insertions were detected in both alleles from the strains collected from Taitung, which led to loss of avirulence function, converting the strains virulent toward *PtrA*-containing rice cultivars. Furthermore, most *AVR-Pita1* haplotypes are located in the non-telomeric region of chromosomes, suggesting that various genotypes of *AVR-Pita1* were generated via point mutation and transposon insertion from an ancestor *AVR-Pita1* to avoid being recognized by *PtrA*. Moreover, the expression level of G<sup>719</sup> allele in a wide range of cultivars with varying resistance levels was variable, suggesting that the expression of *AVR-Pita1* was dependent on the host genotype possibly via epigenetic regulation, and contributed to the adaptation of *P. oryzae* to its hosts. In conclusion, *AVR-Pita1* in *P. oryzae* population has quickly evolved through different ways to adapt to its hosts in Taiwan. Understanding the pathogenic and evolutionary mechanisms of *AVR-Pita1* can help provide useful information to sustain the deployment of resistant cultivars and blast disease management.

## SA12- 辣椒炭疽菌 (*Colletotrichum scovillei*) CsBNS 蛋白在辣椒細胞內的定位及分泌

### Secretion and localization of *Colletotrichum scovillei* CsBNS Protein in Chili Pepper Cells

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*Colletotrichum scovillei* is the major causal agent of chili anthracnose, and the biotrophy-necrotrophy switch (BNS) is critical for disease development. CsBNS is a candidate effector protein and is highly expressed during BNS. Previous studies have shown that the loss of *CsBNS* increases virulence, suggesting that CsBNS has a regulatory role in the pathogenic transition. This study aims to (1) characterize the expression pattern and localization of *CsBNS* both *in vitro* and *in planta*, and (2) investigate its role during early pathogenesis. CsBNS-GFP and CsBNS-RFP tagged strains were generated using Golden Gate cloning and PEG-mediated protoplast transformation. In contrast to previous RNA-seq and semi-RT-PCR analyses that failed to detect CsBNS expression during *in vitro* growth, we observed both CsBNS-GFP and CsBNS-RFP signals when the fungus was cultured on PDA media. Further analyses demonstrated that *CsBNS* expression is induced after extended cultivation (3 to 6 days) across three different media, suggesting that medium composition and culture age influence its expression. *In planta* assays demonstrated that CsBNS is significantly expressed in the highly branched penetration structure (HBPS) and is secreted from the HBPS into the cuticle layer of infected chili pepper fruit. This protein primarily accumulated at BNS within the primary hyphae, but not in the secondary hyphae. In addition, RFP-tagged CsBNS was observed filling the infected epidermal cell, indicating its translocation from the primary hyphae to host cell. Furthermore, confocal microscopy detected weak expression of CsBNS in host cell nuclei. Regarding the role of CsBNS during the BNS stage, the *CsBNS* deletion strain consistently initiated secondary hyphae formation earlier than the wild-type strain, supporting the hypothesis that CsBNS may trigger host defense responses to restrict disease progression. We identified several potential host proteins that interact with CsBNS. A Bimolecular Fluorescence Complementation (BiFC) assay confirmed that CsBNS interacts with a specific host protein and co-localizes to the nucleus. This study provides a foundation for understanding the regulation and functional role of *CsBNS* in *C. scovillei* pathogenesis. Future work will include evaluating host defense responses, such as defense gene expression and callose deposition.

## **SA13- Pathogenicity Assessment for CRISPR-Cpf1 edited *Fusarium oxysporum* and Development of Microfluidic-Assisted Gene Editing Mutant Isolation Technology**

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*Fusarium oxysporum* is a soil-borne fungal pathogen characterized by an extensive host range and devastating economic impacts on agriculture. Due to the lack of broad-spectrum control strategies, understanding the molecular mechanisms underlying its virulence is crucial for developing effective control measures. Since conventional mutant recovery becomes extremely challenging when not employing antibiotic resistance selection markers, we established a microfluidic-assisted mutant isolation technology to more effectively obtain and analyze gene-edited strains. This approach integrates CRISPR-Cpf1 gene editing with microfluidic chip-based single-cell isolation, separating individual protoplasts into distinct reaction wells to increase the probability of detecting the edited strains. The single-cell isolation capability was validated using a gene-edited strain (*ura5*-EGFP) of *F. oxysporum*. Meanwhile, we also established a pathogenicity assessment platform to evaluate CRISPR-Cpf1-edited *F. oxysporum*. The assays demonstrated that the *ura5*-EGFP exhibits significantly reduced virulence compared to the wild-type strain. The fluorescence microscopic results also demonstrated the dynamics of *ura5*-EGFP in *Arabidopsis* roots. With the established isolation and gene editing platform, future directions will focus on whole-genome sequencing of *F. oxysporum* f. sp. *conglutinans* to identify target genes, followed by functional studies of key virulence genes. This approach could enhance our understanding of pathogenic mechanisms and inform the development of future control strategies.

## SB 組

### **SB01- Foliar transcriptome analysis of quinoa (*Chenopodium quinoa*) to explore the candidate genes involved in cross-protection mediated by attenuated viruses**

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Quinoa (*Chenopodium quinoa* Willd.), a nutritious and stress-tolerant “golden grain” native to the Andean region, is widely used as an indicator plant for virus isolation. Its local lesion formation reflects a hypersensitive response (HR) that restricts viral spread via localized cell death. Notably, attenuated virus strains that antagonize wild-type (WT) viruses may alter HR in quinoa, suggesting changes in host defense mechanisms associated with viral pathogenicity. Cross-protection, similar to clinical vaccination, is an effective strategy for controlling viral diseases by pre-inoculating plants with mild virus strains to prevent infection by virulent viruses. Previous studies have shown that attenuated strains of two potyviruses, pepper veinal mottle virus (PVMV) and zucchini yellow mosaic virus (ZYMV), can provide effective cross-protection against their WT counterparts in natural host crops. In addition, these WT and attenuated strains elicited distinct responses in quinoa: the virulent strains caused HR, whereas the attenuated strains caused inconspicuous symptoms. In this study, total RNA was extracted from virus-infected quinoa leaves, and RNA-seq transcriptome analysis was performed. The *de novo* assembled contigs were annotated and examined for differential expression using fragments per kilobase of transcript per million mapped fragments (FPKM) values. Selected resistance-related genes showing upregulation in the FPKM analysis were further validated by relative quantitative assays in quinoa leaves infected with PVMV and ZYMV and their attenuated strains. Compared with healthy controls, the transcription factor (TF) homologs *CqWRKY42*, *CqWRKY53*, and *CqWRKY75* and the pathogenesis-related (PR) homologs *CqBG1.2*, *CqCHIB*, *CqPR1*, *CqPR4*, and *CqPRB1* were upregulated in virus-infected leaves and showed significant expression differences between infections caused by WT and attenuated viruses. The results suggested that viral pathogenicity affected the expression levels of WRKY TFs and PR proteins involved in HR-induced quinoa. The functional roles of these genes in the antiviral defense mechanisms will be elucidated in the future.

## **SB02- Functional characterization of the hidden open reading frames in the pathogenesis of tomato yellow leaf curl Thailand virus**

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Plant viruses with compact genomes often use non-canonical translation strategies to expand their coding capacity, making it difficult to define all functional coding regions. Growing evidence indicates that many previously unrecognized hidden open reading frames (ORFs) have been identified in different viruses. Recently, 17 candidate hidden ORFs were identified in tomato yellow leaf curl Thailand virus (TYLCTHV), a bipartite begomovirus; however, their roles in viral pathogenesis remain unknown. Here, we investigated nine hidden ORFs located on DNA-A component, which is important for symptom development. Initial screening showed that disruption of most of hidden ORFs reduced disease severity and viral accumulation in both *Nicotiana benthamiana* and Micro-Tom. Notably, AV2-135 and AV2-189 are two hidden AV2 isoforms identified from the previously annotated AV2 through translation from downstream in-frame start codons. Although previous study showed that AV2-135 likely represents the major isoform, AV2-189 also contributes to viral pathogenicity. We therefore focused on AV2-189 and compared its function to AV2-135. Our results indicated that AV2-189 contributes to viral replication and subsequent systemic infection. Protein–protein interaction assays revealed that, unlike AV2-135, AV2-189, which lacks the N-terminal region, failed to interact with other viral proteins, highlighting the critical role of the N-terminal region. In addition, we found that both AV2-135 and AV2-189 suppress the expression of salicylic acid-responsive gene. Together, these findings demonstrate the functional significance of hidden ORFs in TYLCTHV and provide new insight into the roles of AV2 isoforms in viral infection.

## SB03- 馬鈴薯病毒 Y 致病機制探討與馬鈴薯病毒之多重反轉錄聚合酶鏈式反應 檢測系統的開發

### Investigation of pathogenic mechanisms of potato virus Y and development of a multiplex RT-PCR for the detection of potato viruses

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馬鈴薯 (*Solanum tuberosum*) 是全球第四大糧食作物。然而馬鈴薯易受多種病毒感染，包括 potato virus Y (PVY)、potato leafroll virus (PLRV)、potato virus X (PVX)、potato virus A (PVA)、potato virus S (PVS) 及 potato virus M (PVM)。其中，PVY 在臺灣與國際間皆為危害最嚴重的馬鈴薯病毒之一，在單獨感染或複合感染下皆可造成顯著減產及重大經濟損失。PVY 具有多種系統 (strain)，其所引起之病徵型態與嚴重程度會因病毒系統及寄主品種而異。儘管目前研究多聚焦於抑制寄主植物基因靜默 (RNA silencing) 的能力，但其如何進一步干擾宿主生理代謝或免疫反應，進而造成不同病害嚴重度之分子機制，仍未完全釐清。因此，本研究旨在透過比較強毒與弱毒 PVY 分離株，深入解析 PVY 之分子致病機制；同時開發高效檢測工具，以提升田間病毒檢測效率並篩選 PVY 單獨感染植株，供後續致病機制分析之用。本研究首先針對 PVY、PLRV、PVX、PVA、PVS 及 PVM 等六種主要馬鈴薯病毒開發多重 RT-PCR (multiplex RT-PCR) 檢測平台。經條件最佳化後，其檢測極限為  $10^5$  拷貝數，與單一 RT-PCR 效力相當。經 2023-2026 年臺灣主要馬鈴薯產區田間共 459 個樣本測試，在單一與多重 RT-PCR 中，PVY 感染率分別為 57.73% 和 56.43%，表示多重 RT-PCR 的檢測效力也具有高度田間診斷代表性。此外，PVY 和 PVS 為目前臺灣感染率最高的兩種馬鈴薯病毒。隨後，本研究利用篩選所得之 PVY 單獨感染樣本接種圓葉菸草 (*Nicotiana benthamiana*)，以病徵嚴重程度評估不同病毒株的致病力強弱。結果顯示，強毒株 PVY-33 (PVY<sup>N-Wi</sup> 系統) 會引起嚴重的上位葉捲曲及植株矮化，弱毒株 PVY-96 (PVY<sup>NTNa</sup> 系統) 則幾乎無明顯病徵。進一步進行全基因組序列比對發現，兩者在 5 個蛋白中有 11 個氨基酸差異，分別位於 P1、HC-Pro、P3、NIa 以及 Nib 蛋白。為鑑定與致病性相關之關鍵區域，本研究將上述具有差異之病毒蛋白分別進行交換，並測試其致病力變化。我們首先針對具有最多 (4 個) 氨基酸差異的 P3 蛋白進行交換。實驗結果顯示，當 PVY-33 之 P3 蛋白交換至 PVY-96 中，可使原本弱毒之 PVY-96 引起上位葉捲曲且黃化之病徵，顯示 P3 蛋白或為潛在的致病區域。綜上所述，本研究初步解析了 PVY 之分子致病機制，並建立了高效的分子診斷平台以釐清臺灣馬鈴薯病毒分布現況，為未來馬鈴薯抗病育種與精準防治策略提供了新穎的研究方向與技術支撐。

## **SB04- SUMOylation at K159 of the *Begomovirus solanumdelhiense* movement protein contributes to chlorosis formation in *Nicotiana benthamiana***

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*Begomoviruses*, members of the family *Geminiviridae*, infect a wide range of economically important crops and cause symptoms such as leaf curl, mosaic, chlorosis, yellowing, puckering, and stunting. These viruses are primarily transmitted by the whitefly *Bemisia tabaci*. Previous studies have demonstrated that the movement protein (MP) of *Begomovirus solanumdelhiense* (Tomato leaf curl New Delhi virus, ToLCNDV) can be SUMOylated, and that SUMOylation facilitates the mechanical transmissibility and systemic movement of the virus. However, how host-mediated post-translational modifications regulate viral protein function and contribute to symptom development remains unclear. In this study, we investigated the roles of different SUMOylation sites on ToLCNDV MP in the development of leaf chlorosis. The mutant ToLCNDV-CB<sub>MP(K43A)</sub> slightly reduced the chlorosis, whereas ToLCNDV-CB<sub>MP(K159A)</sub> and ToLCNDV-CB<sub>MP(K43/159A)</sub> almost completely abolished the phenotype, indicating that the residue K159 plays a major role in chlorosis development. Consistently, chlorophyll quantification showed that leaves infected with ToLCNDV-CB<sub>MP(K159A)</sub> and ToLCNDV-CB<sub>MP(K43/159A)</sub> contained higher chlorophyll levels than those infected with ToLCNDV-CB. Transmission electron microscopy (TEM) revealed that ToLCNDV-CB infection reduced chloroplast abundance and caused chloroplasts to become smaller and morphologically abnormal, suggesting that MP<sub>CB</sub> SUMOylation affects chloroplast structure and stability. In addition, quantitative real-time PCR (qPCR) analysis showed that viral accumulation was relatively higher in chlorotic leaf regions. Bioinformatic analysis suggested a potential interaction between MP<sub>CB</sub> and Atg8 proteins, which was subsequently confirmed by BiFC assays. The results showed that Atg8a and Atg8f interacted with both MP<sub>CB</sub> and MP<sub>CB(K43A)</sub>, but not with MP<sub>CB(K159A)</sub> or MP<sub>CB(K43/159A)</sub>. These findings suggest that residue K159 is critical for the interaction of MP<sub>CB</sub> with Atg8a and Atg8f, and further imply that chloroplasts may be degraded through autophagy. Together, our results suggest that SUMOylation of ToLCNDV MP<sub>CB</sub>, particularly at K159, contributes to chlorosis formation by affecting chlorophyll content and chloroplast integrity, providing new insight into how post-translational modification of a viral protein may influence symptom development.

## SB05- 果膠修飾與 LsGRP1 強化植物免疫之關聯性探討

### Investigating the role of pectin modification in LsGRP1-enhanced plant immunity

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植物在面臨生物逆境時會啟動細胞壁重塑，藉由改變其物理結構以增強防禦反應，並透過鈣離子流入促進細胞壁組成分子與細胞壁蛋白 (wall-associated proteins) 之間的交互作用。而經區塊性去甲酯化 (blockwise demethylesterification) 修飾的細胞壁果膠可與細胞質外體 (apoplast) 的二價鈣離子結合，形塑成蛋盒狀 (egg-box) 的果膠結構，進而促進細胞壁連接激酶 (wall-associated kinases, WAKs) 與類受體激酶 (receptor-like kinases, RLKs) 間的連結，引發後續的下游免疫反應。源自百合品種 'Stargazer' 的植物第 II 型富含甘胺酸蛋白 LsGRP1 已被報導可跨物種提升植物抗性，並與百合細胞壁結合。為解析果膠修飾在 LsGRP1 促進植物免疫之作用，於植體 (*in planta*) 與體外 (*in vitro*) 進行共處理試驗。結果顯示部分或完全去甲酯化的果膠可再增強 LsGRP1 促進之 flg22 誘導性癒傷葡聚糖 (callose) 沉積。利用番茄細菌性斑點病菌 *Pseudomonas syringae* pv. tomato DC3000 (*Pst* DC3000) 之致病性試驗顯示，在細胞壁果膠高度去甲基酯化的突變株 *pmei3* 中，LsGRP1 可顯著增強此突變株對 *Pst* DC3000 的抗性；然而在缺乏去甲基酯化作用的突變株 *pme3* 中，LsGRP1 的增強抗病性現象則完全喪失。與部分去甲基酯化之果膠共處理時，LsGRP1 即可造成癒傷葡聚糖沉積增加，但在 *wak2* 突變株明顯減弱。進一步於原位 (*in situ*) 共處理乙二胺四乙酸二鈉二水合物 (EDTA)，LsGRP1 對 flg22 激活癒傷葡聚糖沉積之增強作用減弱；補充氯化鈣則可恢復之，顯示 LsGRP1 增強抗病性與去甲基酯化果膠、鈣離子之間有高度相關性。另一方面，酵素連結免疫吸附分析 (ELISA) 指出 LsGRP1 與部分去甲基酯化果膠之間存在連結關係，後續將以 ELISA 分析 LsGRP1 在此連結關係中的功能性區段，並於植體試驗驗證之。

## SB06- 篩選有益微生物以緩解非生物逆境對小白菜造成之負面影響

### Screening of Beneficial Microorganisms to Mitigate Abiotic Stress-Induced Negative Effects in Bok Choi

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人類活動所引發的溫室效應與其導致的氣候變遷，已對全球農業生產造成深遠且持續的影響。高溫、乾旱及淹水等非生物逆境，已成為造成作物減產的主要因素之一，不僅威脅糧食安全，也對全球經濟發展帶來重大挑戰。隨著氣候變遷持續加劇，作物在生長過程中所面臨的非生物逆境日益嚴峻，傳統農業管理措施已難以全面因應。近年來，許多研究指出，在作物遭受非生物逆境之前施用有益微生物，能有效緩解逆境所帶來的負面影響，有助於維持作物產量與品質。本研究以小白菜 (*Brassica rapa* subsp. *chinensis*) 為材料，進行種子試驗與苗期盆栽試驗，分別施用包含 *Bacillus* spp.、*Streptomyces* sp. 及 *Trichoderma* sp. 等候選有益微生物後，進行乾旱、淹水及高溫等非生物逆境處理。於逆境處理結束後，量測各處理組小白菜之表型變化 (於種子試驗量測小白菜的下胚軸長度、根長度及基部寬度；於苗期盆栽試驗量測小白菜的地上部鮮重、地下部乾重、葉片數、總葉面積及葉片葉綠素含量)，並取苗期盆栽試驗植株之葉片，測定多酚氧化酶 (polyphenol oxidase, PPO)、過氧化物酶 (peroxidase, POD) 及超氧歧化酶 (superoxide dismutase, SOD) 等逆境相關防禦酵素之活性，篩選出可緩解特定非生物逆境對小白菜生長負面影響的有益微生物。試驗結果顯示：在各逆境處理組中，與未處理微生物的小白菜相比，施用特定有益微生物的小白菜部分表型數據有所提升，且從表型數據有所提升的小白菜所測得的各逆境相關防禦酵素活性都有提升，即施用特定有益微生物有助於提升小白菜在極端氣候下的生產穩定性。後續研究將進一步分析經有益微生物處理之小白菜在逆境結束後的韌性基因表現差異，以探討其是否透過調控相關基因來提升小白菜的逆境耐受性。

## SB07- 篩選具緩解甜瓜非生物逆境潛力之有益微生物

### Screening of Potential Beneficial Microorganisms for Alleviating Abiotic Stresses in Melon

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現今極端氣候頻繁發生，植物在其生長過程中經常會遭遇各種非生物逆境，大幅影響作物生長與產量。傳統農園藝措施能在一定程度上緩解非生物逆境，但效果有限。近年來，有益微生物逐漸受到關注，它們可以透過改善根圈環境和調控植物生理來提升作物的抗逆境能力和生產力。本研究透過種子處理和土壤澆灌有益微生物（包括 *Bacillus* spp.、*Streptomyces* sp. 及 *Trichoderma* sp.）懸浮液的方式，評估其在乾旱、淹水及高溫等非生物逆境條件下對甜瓜 (*Cucumis melo* L. ‘Yin Hui’) 生長與生理反應之影響。結果顯示，部分菌株在種子萌發階段對下胚軸、胚根及側根數影響有限，但在幼苗階段可顯著影響葉片數、莖長、地上部鮮重、地下部乾重、全葉面積及葉綠素含量。為了評估甜瓜對非生物逆境之生理反應，本研究進一步測定其抗氧化酵素活性，包括過氧化物酶 (Peroxidase, POD) 與超氧化物歧化酶 (Superoxide dismutase, SOD)；另外，本研究還測定與逆境相關的酵素~多酚氧化酶 (Polyphenol oxidase, PPO)。酵素活性測定結果表明，不同菌株處理下，POD、SOD 及 PPO 活性在各非生物逆境下呈現差異，顯示有益微生物能調控甜瓜生理反應並提升其抗逆境能力。本研究已由生長與生理層面探討有益微生物對甜瓜抗非生物逆境能力之影響，未來將透過基因表現分析探討抗逆境相關基因之調控情形，以進一步釐清有益微生物提升甜瓜抗非生物逆境能力之分子機制。

## **SB08- Biological control of papaya damping-off and its impact on carbon assimilation by *Streptomyces cavourensis* strain PES4**

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Papaya (*Carica papaya* L.) is highly susceptible to *Phytophthora palmivora*, a destructive oomycete pathogen that causes water-soaked, soft or constricted stems at the soil line rapid collapse or death of seedling, ultimately leading to fruit rot. Members of the genus *Streptomyces* are well known for their strong biocontrol potential and plant growth–promoting abilities. *Streptomyces cavourensis* strain PES4, originally isolated from soil of the tea rhizosphere in Taiwan, has previously been reported to enhance tomato seedling growth and suppress diseases caused by *Phytophthora capsici* in solanaceous crops. In this study, the efficacy of damping-off disease control, the effects on plant growth and carbon assimilation in papaya by *S. cavourensis* strain PES4 were assessed. In dual culture assays, *S. cavourensis* strain PES4 significantly inhibited the mycelial growth of three isolates of *P. palmivora*. Application of culture broth at a 100-fold dilution reduced disease incidence and damping-off severity in papaya seedlings by 67% and 61%, respectively, compared with the water-treated control. Furthermore, consecutive application of strain PES4 once per week for three months increased the leaf net photosynthetic rate and total leaf area by 32% and 24%, respectively, compared to the water control, leading to a 63% enhancement in total carbon fixation. Additionally, the culture filtrate of strain PES4 suppressed energy metabolism of *P. palmivora*, suggesting a possible mechanism contributing to its disease control efficacy. In conclusion, *S. cavourensis* strain PES4 exhibited strong antagonistic activity against *P. palmivora*. Application of *S. cavourensis* reduced damping-off disease of papaya and promoted the growth of papaya seedlings. Additionally, it improved photosynthetic efficiency and carbon assimilation. These findings highlight the potential of *S. cavourensis* strain PES4 as an effective biocontrol and plant growth–promoting agent for use in sustainable papaya cultivation.

## **SB09- Biological control of papaya *Phytophthora* damping-off and associated changes in carbon assimilation mediated by *Bacillus subtilis* WMA1**

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Papaya (*Carica papaya* L.) is highly susceptible to *Phytophthora palmivora*, a destructive oomycete pathogen that causes damping off of seedlings, root rot, stem rot, and fruit rot. Members of the genus *Bacillus* are well known for their biocontrol efficacy and their capacity to promote plant growth. *Bacillus subtilis* strain WMA1, was isolated from the natural environment in Taiwan, has previously been reported to enhance seedling growth and suppress diseases caused by *Phytophthora capsici* in sweet pepper. In this study, the efficacy of *B. subtilis* strain WMA1 in controlling damping-off disease, as well as its effects on plant growth and carbon assimilation in papaya, were assessed. In dual culture assays, *B. subtilis* strain WMA1 significantly inhibited the mycelial growth of *P. palmivora* isolate Ph-591. Application of strain WMA1 culture broth at a 100-fold dilution reduced disease incidence and damping-off severity in papaya seedlings by 50% and 79%, respectively, compared with the water control. Additionally, *B. subtilis* WMA1 treatment increased plant height by 34% compared with the water control. Furthermore, weekly application of strain WMA1 culture broth over a 3.5 months significantly enhanced leaf net photosynthetic rate and total leaf area by 31% and 46%, respectively, resulting in an overall 65% increase in total carbon fixation compared with the water control. Our results further demonstrated that, the culture filtrate of strain WMA1 inhibited the energy metabolism of *P. palmivora*, suggesting a potential mechanism underlying its disease suppression. In conclusion, *B. subtilis* strain WMA1 exhibited antagonistic activity against *P. palmivora*. Its application effectively suppressed papaya damping-off while promoting seedling growth. Additionally, it enhanced photosynthetic efficiency and carbon assimilation. These findings suggest the potential of *B. subtilis* strain WMA1 as an effective biocontrol and plant growth-promoting agent for sustainable papaya cultivation.

## **SB10- Two naturally compatible *Bacillus* strains promote plant growth and suppresses fungal pathogens through cooperative interaction**

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Plant-beneficial bacteria, particularly plant-growth-promoting rhizobacteria, are increasingly recognized as essential components of sustainable agriculture. In this study, we investigated the functions and the interaction between two strains *Bacillus velezensis* BV-RGH3 and *Bacillus subtilis* BS-RGH1, which were isolated from the cooked root of the traditional Chinese medicinal herb *Rehmannia glutinosa*. Both bacterial strains demonstrated its broad-spectrum antifungal potential by producing volatile organic compounds that inhibited the mycelial growth of *Fusarium oxysporum* f. sp. *rapae*, and *Colletotrichum truncatum*. These findings were further validated in planta, where co-inoculation of the two strains resulted in the most effective suppression of leaf mustard yellows and soybean anthracnose. Plants treated with the individual strains (BS-RGH1 or BV-RGH3) improved plant growth parameters. Notably, the mixture of BS-RGH1 and BV-RGH3 yielded the greatest mycelial inhibition compared with the individual strains, promote the growth parameters of several plants, and significantly increased chlorophyll content and photosynthetic rate of leaf mustard. Interestingly, we found that these two bacterial strains do not inhibit the growth of each other. In addition, *B. subtilis* BS-RGH1 significantly increasing multicellularity, cell density, surface adhesion, and cellular elongation of BV-RGH3, resembling the features of swarming motility. These results suggest that the two strains are naturally compatible. A comparable effect was observed with commercial surfactin, indicating that surfactin-like compounds may play a central role in this process. Collectively, these results demonstrate that interactions between naturally compatible bacteria can enhances cooperative behaviour, promotes plant growth, and suppresses pathogens. This study therefore supports the application of plant-beneficial bacterial consortia as an effective and sustainable strategy for crop management.

## SB11- 運用 RNAi 技術探討褐根病菌 *PnCYP51.1* 的角色

### Using RNAi technology to investigate the role of *PnCYP51.1* in *Phellinus noxius*

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樹木褐根病 (brown root rot disease, BRRD) 由木材腐朽菌 *Phellinus noxius* (syn. *Pyrrhoderma noxium*) 引起，可感染多種樹木莖基部與根部，造成樹勢衰弱、死亡及倒伏風險。由於 *P. noxius* 具有異核性，且不易人工培養產生子實體及單核擔孢子，因此難以透過同源重組或基因編輯方式獲得同核型突變株，使基因功能分析受到限制。本研究旨在評估 RNA 干擾 (RNA interference, RNAi) 作為替代策略之可行性，並以麥角固醇合成相關基因 *CYP51* 為標靶，解析其在褐根病菌中的角色。基因體分析顯示，*P. noxius* 含有 RNAi 核心因子 Argonaute 與 Dicer 之同源基因，顯示其具備潛在 RNAi 機制。使用螢光標定 dsRNA 及 siRNA 處理褐根病菌節生孢子，以評估 *P. noxius* 對外源 RNA 之吸收性；結果顯示 siRNA 處理 36 小時後於部分菌絲內可觀察到螢光訊號。本研究針對 *P. noxius* 基因體中 *CYP51* 同源基因 *PnCYP51.1* (PNOK\_0784800)，以 *Escherichia coli* 生產 dsRNA (標靶 cDNA 1155–1653 bp 處)，另以化學合成兩條標靶 *PnCYP51.1* 中段 (498–520 bp) 及後段 (1579–1601 bp) 之 siRNA。*PnCYP51.1*-siRNA 可抑制 *P. noxius* 之節生孢子發芽及菌絲生長，且標靶基因中段區域的 siRNA 抑制效果較佳；而 *PnCYP51.1*-dsRNA 僅於高濃度處理下抑制孢子發芽。於毛果楊離莖段接種試驗中，*PnCYP51.1*-siRNA 與 *PnCYP51.1*-dsRNA 處理皆略為降低褐化病斑長度，但與各自非標靶 RNA 對照組間未達顯著差異。Reverse transcription-quantitative PCR (RT-qPCR) 分析顯示，節生孢子經 dsRNA 與 siRNA 處理 72 小時後的菌絲中，*PnCYP51.1* 表現量並未下降，推測與褐根病菌對外源 RNA 吸收效率較低及 RNAi 介導的基因靜默作用時間性相關。本研究初步建立 *P. noxius* 之 RNAi 表型評估平台，藉此驗證 *PnCYP51.1* 為影響褐根病菌生長之關鍵基因，相關成果有助於對 *P. noxius* 生理代謝的瞭解，也為未來基因功能分析及新型防治技術研發建立基礎。

## **SB12- Screening and evaluating the potential of endophytes from *Corymbia citriodora* on inhibition of *Bidens pilosa***

Ya-Fang Yang<sup>1</sup> and Wen-Hsin Chung<sup>1,2</sup> (<sup>1</sup>Department of Plant Pathology, National Chung Hsing University, Taichung, Taiwan. <sup>2</sup>Master Program in Plant Medicine and Good Agricultural Practice, National Chung Hsing University, Taichung, Taiwan)

Weeds greatly affect crop production by competing for nutrients, space, sunlight and other resources, which can reduce yield and quality. They may also serve as alternative hosts for pathogens or habitats for insects, increasing pest and disease pressure. Although chemical herbicides are widely used for weed control, their overuse causes environmental and soil issues and has led to herbicide-resistant weeds. Thus, developing alternative materials to replace chemical herbicides is essential for sustainable crop protection and reducing resistance problems. In this study, endophytic bacteria and fungi were evaluated for their ability against *Bidens pilosa*. A total of 113 strains were obtained from branches, leaves, and rhizosphere soil of *Corymbia citriodora* and used to examine their ability against *B. pilosa* based on seed germination tests. The results of preliminary screening revealed that the herbicidal activity of strain L1 has good ability to inhibit seed germination of *B. pilosa* at 5x and 10x dilution of fermentation broths with 73.7% and 56.7% inhibition rate, respectively. Morphological and multilocus phylogenetic analyses identified strain L1 as *Diaporthe biconispora*. Moreover, strain L1 showed better biomass in the medium containing sucrose as carbon source and cystine as nitrogen source, and these two cultural broths significantly inhibited *B. pilosa* seed germination by 100%. The substrate containing 3% sucrose and 0.3% cystine showed best combination for L1 growth and this broth could inhibit *B. pilosa* seed germination by 100% significantly. Thus, L1 strain has the potential to be agent on control of *B. pilosa*.

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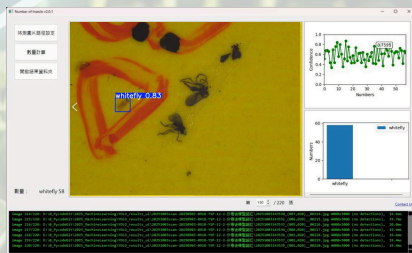
## AI 昆蟲辨識：田間蟲害的即時雷達



## 田間蟲害監測不再靠人工計數

薊馬、粉蟲、蚜蟲等媒介昆蟲的族群動態，往往決定了病毒爆發的時間點。我們自行研發的 AI 昆蟲辨識系統，將回收的黃色黏蟲紙放上設備，即可自動拍攝、AI 即時辨識蟲種與數量，在病害擴散前提供族群密度預警。

訓練過程中由農試所提供已標註影像作為資料，我們負責模型開發與優化，未來可依需求擴充到其他相似昆蟲，監測不再靠人工數蟲，防治介入也能提早一步。



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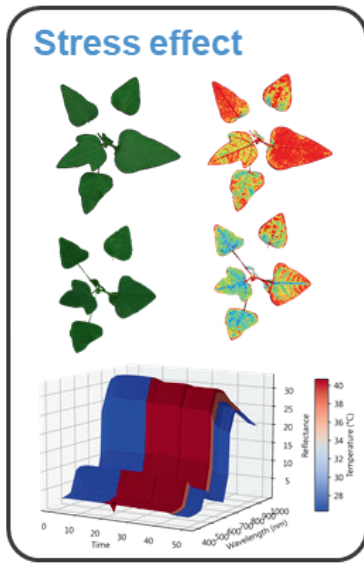
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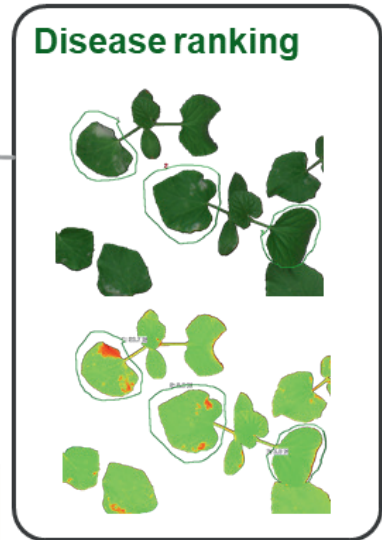
## 長期監測

Long-term tracking



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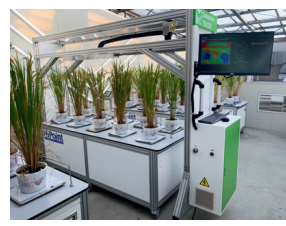
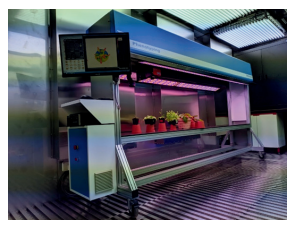
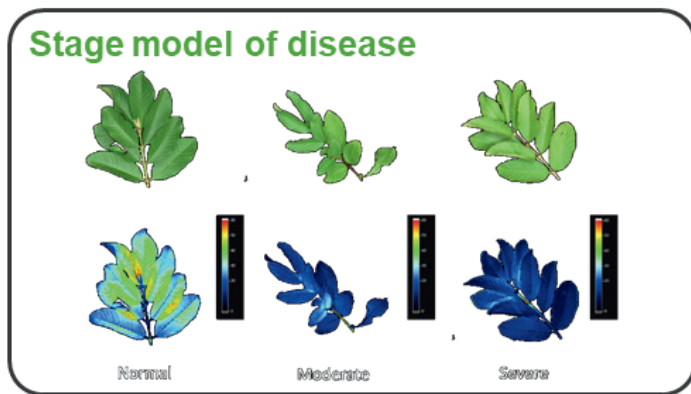


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