APVW 2026

16th Australasian Plant Virology Workshop

Rendezvous Perth Scarborough
27 - 29 October 2026

WORKSHOP HANDBOOK

APPS
Plant Health is Earth's Wealth

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WELCOME MESSAGE

From the Chairs

The 16th Australasian Plant Virology Workshop (APVW) acknowledges the Traditional Custodians of Country, the Whadjuk people of the Noongar Nation, and recognizes their enduring connection to the land and waters. APVW acknowledges their continuing cultures and value the contribution they make to the life of our regions. We pay our respects to Elders both past and present and extend that respect to all Aboriginal and Torres Strait Islander people.

On behalf of the organising committee, thank you for joining us. We are delighted to welcome delegates from across Australia, New Zealand and around the world to Perth for three days of scientific exchange, collaboration and networking within the plant virology community. This meeting continues a long tradition of bringing together researchers, students, industry representatives, diagnosticians, biosecurity specialists and policy makers to share the latest advances in the study of plant viruses, viroids, phytoplasmas and other obligate pathogens.

We are especially honoured to host an outstanding group of invited speakers: Santiago F. Elena (Institute for Integrative Systems Biology, Spain); Safaa G. Kumari (ICARDA, Lebanon); Marc Fuchs (Cornell University, USA); Kingsley Dixon (The University of Western Australia, Australia); Robin MacDiarmid (The New Zealand Institute for Plant & Food Research Limited, New Zealand); and Maher Al Rwahnih (University of California, Davis, USA).

We gratefully acknowledge the generous support of our sponsors and partners, whose contributions have made APVW 2026 possible. Our Gold sponsors the Grains Research and Development Corporation, Australian Government: Department of Agriculture, Fisheries and Forestry, Government of Western Australia: Department of Primary Industries and Regional Development. Our Bronze sponsor Qiagen, Travel support thanks to Wine Australia and our Destination Partner: Business Events Perth.

We wish to thank those who have helped us along the way, particularly Tonny Kinene and Asad Prodhan for assisting us with the scientific program and all those who have agreed to chair sessions and participate in the panel discussions. These events only run thanks to their generosity with their time. A special thank you to the team at KAM events, especially Jenny Lawler for flawlessly guiding us through the last two years. We could not have done this without you!

Thank you for being part of APVW 2026. We hope the workshop is informative, inspiring and enjoyable, and that you leave with valuable new insights, strengthened professional relationships and renewed enthusiasm for advancing modern plant virology, plant health research and biosecurity.

Monica Kehoe, Craig Webster, Ben Congdon

COMMITTEE



Ben Congdon
DPIRD WA



Monica Kehoe
DPIRD WA



Craig Webster
DPIRD WA

Conference Managers - Kate Murphy and Jenny Lawler,
KAM Event Management, PO Box 318, Coolangatta Qld 4225.
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SOCIAL FUNCTIONS

Welcome Reception

Where: Mentelle Deck, Rendezvous
Time: Tuesday 27th 1800 - 2100

APVW Dinner

Where: The Sandbar Scarborough Beach, 1 Scarborough Beach Road.
Time: Wednesday 28th 1800 – 2130
Getting There: The Sandbar is across the road from the Rendezvous and a short 2-minute walk.



APVW PROGRAM

Tuesday 27th October	
0800 – 1700	Registration Open — Pre-Function Foyer
0900 – 1000	**Session 1 – Opening** — **Preston BC Room** **Chair:** Monica Kehoe
0900 – 0915	**Welcome and acknowledgement to country**
0915 - 1000	KEYNOTE: Living in a biodiversity hotspot – **Kingsley Dixon**
1000 – 1030	Morning Tea
1030 - 1115	**Session 2 – Diagnostics methods** — **Sponsored by:** DPIRD WA **Chair:** Ben Congdon
1030 – 1045	Unearthing elusive viruses in Australian cereals using high-throughput sequencing **Narelle Nancarrow**
1045 – 1100	Pivoting to manage a potato certification scheme – the DDLS experience - **Craig Webster**
1100 - 1115	Update on the transition of banana germplasm diagnostics to the Post Entry Quarantine Facility (PEQ) at Mickleham - **Candace Elliott**
1115 - 1230	**Session 3 - Plant, virus and vector interactions** — **Sponsored by:** DPIRD WA **Chair:** Ben Congdon
1115 - 1130	Impact of drought and barley yellow dwarf virus infection on wheat physiology and morphology **Brendan Vouadec**
1130 - 1145	Dual RNAi protection against barley yellow dwarf virus in wheat and barley - **Nora Derbal**
1145 - 1200	Improving narrow leafed lupin (*Lupinus angustifolius*) resistance to cucumber mosaic virus **Elaine Gough**
1200 - 1215	Virus diversity in wild Agaricus species in Australia - **Madhav Jatin Chandarana**
1215 - 1230	Modifying plant sterols for resistance to insect pests and insect-transmitted viruses - **Jing Li**
1230– 1330	Lunch
1330 – 1500	**Session 4 - New tools and technologies** **Chair:** Asad Prodhan
1330 – 1400	One Biosecurity BHAG: Understanding plant virus vertical-transmission biology **Robin MacDiarmid (Sponsored by Wine Australia)**
1400 – 1415	Spray-induced gene silencing as a strategy for virus and vector management in horticultural crops **Karl Robinson**
1415 – 1430	Discovery of novel plant antiviral agents against potato virus Y using an integrated screening strategy **Mina Park**
1430 – 1445	Exploring the influence of colour cues on aphid behaviour and barley yellow dwarf virus-PAV movement in wheat - **Piotr Trebicki**
1445 – 1500	Improved vector and pathogen monitoring strategies for insect-borne diseases in horticultural production systems - **Brendan Rodoni**
1500 – 1530	Afternoon Tea
1530 – 1700	**Session 5 - Epidemiology, Ecology and Management** **Chair:** Nazanin Nazeri
1530 – 1545	Investigating novel strategies for grapevine virus management in Australia - **Chongxi Yang**
1545 - 1600	Turnip yellows virus resistance in Brassica napus – will it be durable? - **Benjamin Congdon**
1600 – 1615	Turnip mosaic virus canola resistance-breaking strain: Symptoms, seed and contact transmission, yield losses and seed germination - **Roger Jones**
1615 – 1630	Challenges in virus management for canola and carinata in Queensland's subtropical climate **Fiona Filardo**

1630 – 1700	**Panel discussion –** What does a next gen plant pathologist look like? **Chair:** Monica Kehoe – **Panellists:** Fiona Constable, Robin MacDiarmid, Santiago Elena
1800 – 2100	**Welcome Reception** **Sponsored by: Business Events Perth** Mentelle Balcony, Rendezvous
Wednesday 28th October	
0800 – 1630	Registration Open
0830 – 1000	**Session 6 – Biosecurity** **Preston BC Room** **Chair:** Margaret Uloth **Sponsored by:** Department of Agriculture, Forestry and Fisheries
0830 – 0845	Whole genome informed diagnostics distinguish mild and orange stem pitting RB2 variants of citrus tristeza virus in Australia – **Mark Jackson**
0845 – 0900	TAS-AP: A portable Targeted Amplicon Sequencing Analysis pipeline for rapid plant pathogen detection – **Tonny Kinene**
0900 -0915	MECAR: An accessible metagenomic diagnostic platform - **Asad Prodhan**
0915 – 0920	A new recombinant begomovirus in Indonesian chillies – **Kathleen Crew**
0920 - 0925	Linking viruses found by environmental metagenomics with physical specimens – tobamoviruses in Queensland – **John Thomas**
0925 - 0930	An update from Department of Agriculture, Forestry and Fisheries – **Candace Elliot**
0930 - 1000	**Meeting Part 1**: Outlining options for APVW-APPS alignment
1000– 1030	Morning Tea
1030 - 1115	KEYNOTE: A four-decade journey of monitoring and surveillance of viruses that cause yellowing and stunting of legume crops in the West Asia and North Africa (WANA) region - **Safaa Kumari**
1115 – 1230	**Session 7 - Plant, virus and vector interactions 2** **Sponsored by:** Qiagen **Chair:** Alistair Hall
1115 – 1130	Turnip yellows virus infection increases cucumber mosaic virus disease sensitivity in narrow-leafed lupin - **Nazanin Nazeri**
1130 – 1145	Turnip yellows virus-associated RNAs in crop hosts: prevalence, transmission and development of molecular tools - **Mianmian Wang**
1145 – 1200	Lineage-resolved surveillance of the wheat curl mite-transmitted virus complex in New South Wales **Tobiasz Druciarek**
1200 – 1230	**Panel discussion –** Effective communications to stakeholders **Chair:** Ben Congdon **- Panellists:** Nicole Thompson, Brendan Rodoni; Alan Little
1230 – 1330	Lunch
1330 - 1400	Navigating virus challenges and technological opportunities at foundation plant services **Maher Al Rwanih (Sponsored by Wine Australia)**
1400 – 1500	**Session 8 - Diagnostic methods 2** **Chair:** Tonny Kinene **Sponsored by:** Grains Research Development Corporation
1400 – 1415	From blot to base pairs: Sequencing viral genomes from tissue blot immunoassay membranes - **Tahnee Saunders**
1415 – 1430	Best practice sampling and virus detection in Australian grapevine propagation assets - **Roshni Rohra**
1430 – 1445	Incorporating High Throughput Sequencing into everyday plant virology diagnostics - **Monica Kehoe**
1445 – 1450	Producing synthetic monoclonal antibodies for banana bunchy top virus diagnostics – **Nga Tran**
1450 - 1455	Sampling irrigation water to detect and monitor vegetable plant pathogens – **Addam Corallo**
1455 – 1530	Afternoon Tea

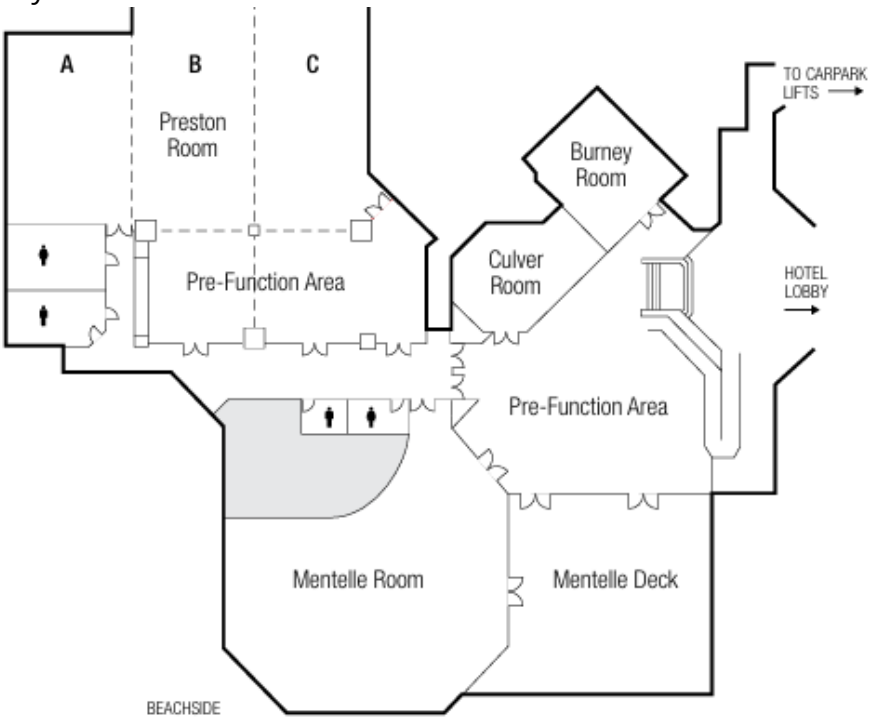
1530 – 1630	**Session 9 - Epidemiology, Ecology and Management 2** **Chair:** Craig Webster **Sponsored by:** Department of Agriculture, Forestry and Fisheries
1530 – 1545	Long-term surveillance of viruses in pulses in western Victoria - **Mohammad Aftab**
1545 – 1600	The epidemiology of canola viruses in Victoria, Australia - **Narelle Nancarrow**
1600 – 1615	Replicative fitness and virulence differences among turnip yellows virus isolates in susceptible and resistant canola - **Sharmin Rahman**
1615 - 1630	Distribution and host range of turnip yellows virus in South Australian weeds: Novel detections in Poaceae and other potential hosts – **Nicole Thompson**
1800 – 2130	APVW Dinner The Sandbar Scarborough Beach
Thursday 29th October	
0800 – 1500	Registration Open
0845 – 1000	**Session 10 – New tools and technologies 2** **Chair:** Chi Cao **Sponsored by:** Grains Research Development Corporation
0845 – 0900	Pathogenic characteristics and molecular mechanisms of tomato spotted wilt virus resistance of *Capsicum annuum* - **Jooeun Kim**
0900 – 0915	Streamlining diagnostics for horticultural seeds imported into Australia - **Anjali Zaveri**
0915 - 0930	What makes a great bioinformatics workflow? - **Bradley Pease**
0930 - 0935	The C4 protein of Papaya leaf curl Guandong virus is essential for symptom induction and RNA silencing suppression - **Ju-Yeon Yoon**
0935 - 0940	Evaluating coloured sticky traps for aphids vector surveillance under semi-field conditions - **Piotr Trebicki**
0940 - 1000	**Meeting Part 2** - Discussion recap and vote on options presented previously
1000 – 1030	Morning Tea
1030 - 1115	KEYNOTE: Host aging, immunosenescence and the evolution of RNA virus' virulence - **Santiago Elena**
1115 – 1230	**Session 11 – Diagnostic methods/Diversity and Evolution** **Chair:** Elaine Gough
1115 – 1130	A probe-based multiplex qRT-PCR assay for viruses infecting Australian and exotic honeybees **Sadia Iqbal**
1130 – 1145	Genetic analysis of bean yellow mosaic virus from Australia: New genomic and biological insights, and evolutionary dynamics - **Solomon Maina**
1145 – 1200	Enhancing diagnostic efficiency and scope in virus surveillance using high throughput sequencing **Chi Cao**
1200 – 1230	**Panel discussion –** Importance of collections **Chair:** Craig Webster **- Panellists:** Safaa Kumari, Maher Al Rwahnih, Candace Elliott
1230 - 1330	Lunch
1330 - 1400	Landscape ecology shapes treehopper-borne disease dynamics **Marc Fuchs (Sponsored by Wine Australia)**
1400 – 1500	**Session 12 – Diagnostic methods/Diversity and Evolution** **Sponsored by:** DPIRD WA **Chair:** Sharmin Rahman
1400 - 1415	An assessment of diagnostic molecular assays for detection of grapevine berry inner necrosis virus detection in Australia - **Sumit Chahal**
1415 – 1430	Rapid, field-deployable diagnostic for plant viruses using microneedle technology - **Nawar Shamaya**
1430 – 1445	Improving plant virus detection from trapped insect vectors - **Flavia Sarti Bonora**
1445 – 1500	**Closing remarks**
1500 - 1530	Afternoon Tea

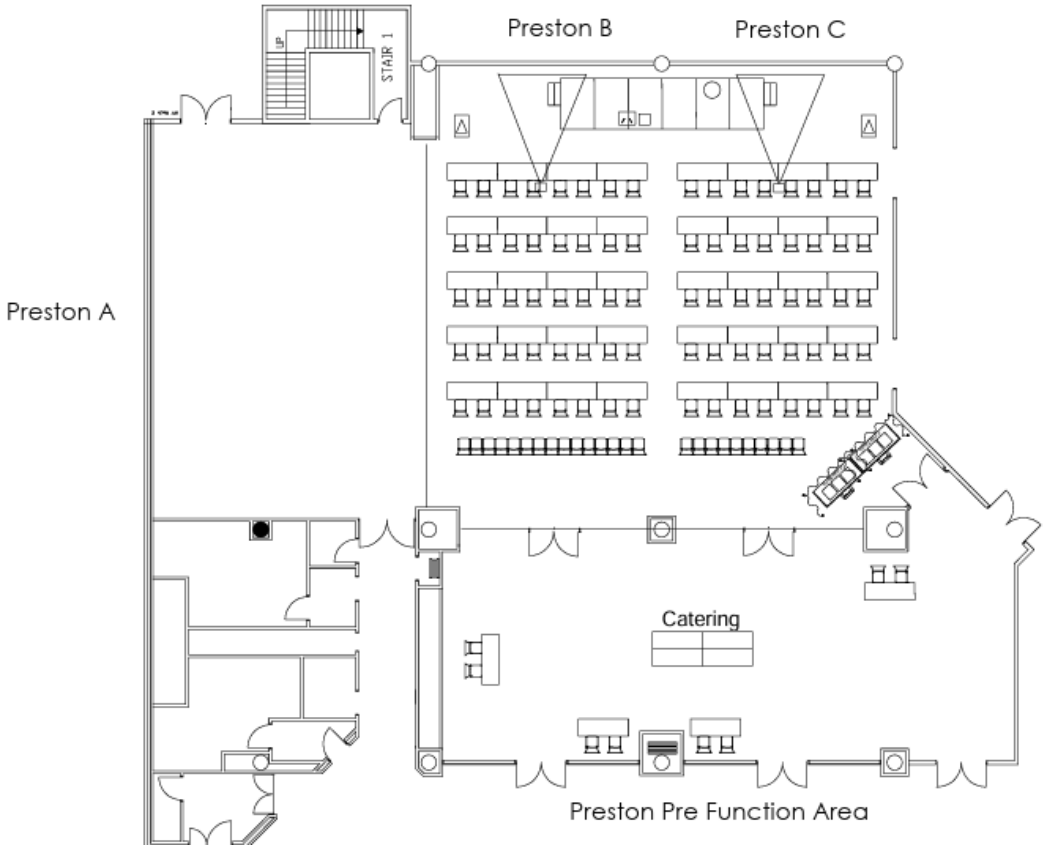
VENUE MAP

Preston BC Room

Located on the ground floor Lobby Level North.

Lobby Level North





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As a sponsor of the Australian Plant Virology Workshop, the department is pleased to support the exchange of scientific expertise, collaboration and innovation that strengthen Australia's plant biosecurity system. The workshop brings together specialists working across plant virology, diagnostics, surveillance, research and biosecurity policy, all of which are central to protecting Australia's plant industries, environment and communities.

The Australian Government Department of Agriculture, Fisheries and Forestry (DAFF) works towards a more sustainable and prosperous Australia through biosecurity, agricultural production and trade. We support productive and internationally competitive industries, maintain and create export opportunities, and manage biosecurity risks that could affect Australia's multi-billion-dollar industries, environment and way of life.

The department focuses on three objectives:

- Sector growth - Support Australia's agricultural sector to be increasingly prosperous and internationally competitive.
- Sector resilience and sustainability - Increase the contribution agriculture, fisheries and forestry make to a healthy, sustainable and low-emissions environment.
- National biosecurity - Strengthen our national biosecurity system to provide a risk-based approach and an appropriate level of protection to Australia's people, our environment and economy.

Science is fundamental to Australia's plant biosecurity system. DAFF scientists work across a range of disciplines, including plant pathology, entomology, molecular biology and epidemiology, with diagnostic capability playing a critical role in detecting and responding to plant pests and diseases. This includes work to identify and characterise plant pests and diseases, develop and validate diagnostic methods, conduct surveillance, and contribute to national and international plant health standards.

Biosecurity is a shared responsibility. DAFF works alongside state and territory government laboratories, research institutions, industry and international partners to understand emerging threats, share knowledge, support diagnostic capability and improve Australia's ability to detect and respond to plant health risks.

Through its scientific expertise and partnerships, DAFF helps ensure Australia is well placed to manage plant health risks now and into the future. This work supports a strong biosecurity system, protects plant industries and contributes to the sustainability and resilience of Australia's agricultural sector.

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The Grains Research and Development Corporation (GRDC) is one of Australia's leading research and development corporations (RDCs), responsible for planning, investing in and overseeing research, development and extension (RD&E) activities that support the nation's grain growers. Its purpose is to invest in RD&E to create enduring profitability for Australian grain growers through innovation, collaboration and the delivery of practical solutions that improve farming outcomes.

Established in 1990 under the Primary Industries Research and Development Act 1989, GRDC is a statutory corporation funded primarily through grain grower levies and matching Australian Government contributions for eligible research and development activities. This unique co-investment model enables GRDC to undertake strategic, long-term investments that benefit growers, industry and the broader Australian community.

GRDC's primary objective is to drive the discovery, development and delivery of world-class innovation that enhances the productivity, profitability and sustainability of Australian grain-growing businesses. The organisation invests upward of $300million across a diverse portfolio of initiatives, including crop breeding, soil and nutrition management, biosecurity, pest and disease control, farming systems, digital agriculture, automation, sustainability, and grower capability development across 27 leviable crops.

A key strength of GRDC is its ability to bring together researchers, growers, advisers, industry organisations, universities, government agencies and commercial partners to address challenges facing the grains sector. Through national and regional investments, GRDC supports the development of new crop varieties, improved farming practices, emerging technologies and decision-support tools that help growers adapt to changing environmental, economic and market conditions.

GRDC also plays an important role in building the future capability of the Australian grains industry. Programs such as the GRDC Research Scholarship (GRS) support the development of highly skilled researchers by funding doctoral studies aligned with industry priorities. These initiatives help ensure the grains sector has access to the expertise and innovation needed to meet future challenges and opportunities.

Guided by its RD&E Plan 2023–28**,** GRDC focuses on delivering measurable impact through investments that improve grower profitability, strengthen industry sustainability and support resilient grain-growing systems. By connecting scientific research with on-farm application, GRDC continues to play a critical role in advancing Australia's grains industry and ensuring it remains globally competitive, innovative and sustainable for future generations.

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The Department of Primary Industries and Regional Development (DPIRD) leads sustainable development of Western Australia's regions and agriculture, aquaculture, food and fisheries sectors.

We unlock and guide economic opportunities for these sectors and regions, balanced with the stewardship of our land and aquatic resources.

Our purpose is to enable enduring prosperity for all Western Australians through our work with regions and primary industries.

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QIAGEN is a global leader in molecular testing, sample preparation, and genomics technologies. We support plant virology research with innovative solutions for nucleic acid extraction, PCR, digital PCR, next-generation sequencing (NGS) and bioinformatics. Our integrated workflows help researchers accelerate discovery, characterize plant pathogens, and advance crop health through reliable molecular insights.

Further information can be found at http://www.qiagen.com.

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Strong research partnerships are critical to addressing emerging and ongoing virus challenges in Australian grain crops.

GRDC invests in research, development and extension that helps deliver practical knowledge, improved management strategies and better outcomes for grain growers. We are proud to support the Australasian Plant Virology Workshop as a Platinum Sponsor.



> *Strong partnerships between researchers, industry and growers are essential to tackling current and emerging virus threats and translating science into practical outcomes on farm.*

Dr Alan Little
GRDC Manager, Diseases

Investing in RD&E to create enduring profitability for Australian grain growers

KEYNOTE SPEAKERS

Professor Santiago Elena



Santiago F Elena is a CSIC Professor and heads the Evolutionary and Systems Virology group at the Institute for Integrative Systems Biology. An external professor at the Santa Fe Institute, he studies how RNA viruses adapt to hosts and manipulate cellular resources, combining experimental evolution, molecular biology, omics, epidemiology and mathematical modelling. He holds a PhD in Evolutionary Genetics of RNA viruses from the University of Valencia and is an elected member of EMBO, the American Academy of Arts and Sciences and Academia Europaea. He has published over 320 papers..

Dr. Safaa Kumari



Safaa G. Kumari heads the Seed Health Laboratory and is a Plant Virologist at ICARDA, Lebanon. Her research focuses on legume and cereal viruses, diagnostics, and managing seed-borne pests and diseases to prevent transboundary spread. Recognised among the BBC's 100 most influential women in 2020, she also joined the MEDNIGHT 2023 Mediterranean Science Team. She served as President of the Arab Society for Plant Protection (2022–2025) and has been Associate Editor of the Arab Journal of Plant Protection since 2003. She has published 133 refereed papers.

Professor Kingsley Dixon AO



Kingsley Dixon is a botanist and conservation biologist who specialises in Australian plants, their biology, ecology and ultimately their conservation. He is widely known for his discovery of smoke from bushfires as the key agent responsible for native seed germination and established the research team at Kings Park and Botanic Garden and now at The University of Western Australia. The presentation will overview why meeting in southwest Western Australia puts you at the heart of one of the most extraordinary floras on earth.

INVITED SPEAKERS

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Professor Marc Fuchs

Marc Fuchs leads research and extension programs on viruses affecting vegetable and fruit crops at Cornell University. His work translates discoveries into practical applications, focusing on disease ecology, virus–host–vector interactions and disease management. He holds a Master's degree and PhD from University Louis Pasteur, Strasbourg, France. A Fellow of the American Phytopathological Society, he is President of the International Council for the Study of Virus and Virus-like Diseases of the Grapevine and chairs the National Clean Plant Network for grapes.



Assoc. Professor Robin MacDiarmid

Robin MacDiarmid is based at The New Zealand Institute for Plant & Food Research Limited where she hosts students from the University of Auckland. She teaches about viruses of plants, fungi and oomycete pathogens of crops or native plants. When not at work Robin enjoys sailing her wooden boat on the Bay of Islands where she lives.



Dr. Maher Al Rwahnih

Maher Al-Rwahnih is the director of Foundation Plant Services at the University of California, Davis, and a plant pathologist specializing in plant health, diagnostics, and graft-transmissible pathogens. His work focuses on strengthening science-based plant quarantine, phytosanitary regulation, and clean plant certification systems. He has played a leading role in the validation and regulatory adoption of High-Throughput Sequencing (HTS) for pathogen detection, supporting the modernization of quarantine and certification programs and the safe international movement of plant material.

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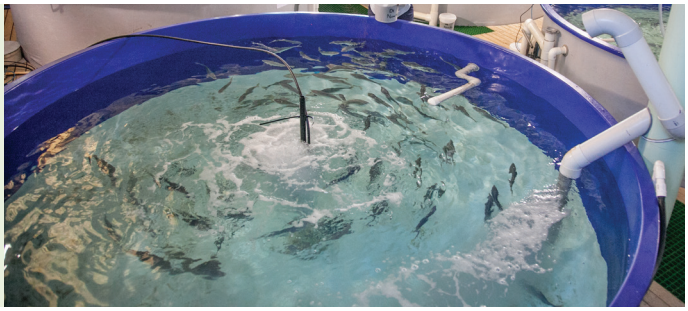
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ABSTRACTS

Session 1 - Opening

Living in a biodiversity hotspot

Kingsley Dixon [1]

1. The University of Western Australia, Western Australia, Australia

The southwest of Australia stands tall as one of the most unique places for plants and ecosystems. Lacking mountains and terrain familiar to most floral rich areas, the southwest has, through a process unparalleled in almost all other regions of the world has developed a flora of extraordinary richness and endemism. One of the few places on the planet with an endemic flowering plant order, the plants are replete with astonishing levels of adaptation to heat and, 'abject plant poverty'.

Unearthing elusive viruses in Australian cereals using high-throughput sequencing

*Avinthika Rajendran [1,2] , **Narelle Nancarrow** [3] , Fiona Constable [1,4] , Brendan Rodoni [1,4] , Tahnee Saunders [1]*

1. Agriculture Victoria, Bundoora, Victoria, Australia
2. RMIT University, School of Science, Bundoora West, Victoria, Australia
3. Agriculture Victoria, Horsham, Victoria, Australia
4. La Trobe University, School of Applied Systems Biology, Bundoora, Victoria, Australia

Yellow dwarf viruses (YDVs) are economically important pathogens that cause significant grain yield losses in cereals such as wheat (*Triticum aestivum*), barley (*Hordeum vulgare*) and oat (*Avena sativa*). To date, seven different YDV species have been reported to infect cereals and grasses in Australia. In a recent study, samples were collected from 1,313 individual cereal and grass plants that displayed typical symptoms of virus-infection. Interestingly, despite displaying obvious virus symptoms, no viruses were detected in 25% of the plant samples assessed by the serological testing method, tissue blot immunoassay (TBIA). To better understand disease aetiology and epidemiology, and improve diagnostics to support disease management, 28 plant samples that had previously tested negative for viruses by TBIA were further analysed using both polymerase chain reaction (PCR) and high-throughput sequencing (HTS). Surprisingly, 13 full-length virus genome sequences were obtained from the 28 samples, and multiple full-length virus genomes were obtained from two plant samples. Additionally, all 28 samples tested positive with at least one YDV PCR assay. These findings demonstrate that molecular approaches can uncover YDV infections that remain undetected by serological assays and suggest that previous estimates of YDV prevalence in Australian cereals have been considerably underestimated. Improved detection of these hidden infections will enhance diagnostic capability and provide a more accurate understanding of YDV epidemiology and disease risk.

Pivoting to manage a potato certification scheme – the DDLS experience

Craig Webster [1]

1. Department of Primary Industries and Regional Development, WA, Australia

Sustainable potato production worldwide relies on seed potatoes being inspected and tested for tuber borne disease, which can rapidly multiply in crops leading to large crop losses. Historically testing in WA has relied on serological (i.e. ELISA) based detection of 5 viruses (potato leafroll virus, potato virus S, potato virus X, potato virus Y and tomato spotted wilt virus) in leaf material collected during crop inspections at defined times to meet an industry led certification process (i.e. the scheme). Annually up-to 25,000 plants are surveyed and tested to meet grower requirements. However, recent changes in the industry (both in WA and internationally) have seen rapid increases to test requirements in the WA seed potato scheme with additional testing now required for both seed potato certification (and export market acceptance). Discovery of additional viruses in Australia (including potato spindle tuber viroid, the NTN strain of potato virus Y and most recently potato mop top virus) has increased the number tests growers are required to test for. Therefore, laboratory testing has had to pivot rapidly to PCR based methods for an increasing list of viruses. Delivering results in a quality assured setting has both helped (and hindered) delivering this service. The challenges and benefits to both DPRID and growers as we've made these changes to testing methods and accreditation will be discussed.

Update on the transition of banana germplasm diagnostics to the Post Entry Quarantine Facility (PEQ) at Mickleham

Candace Elliott [1] , *Ruvini Lelwala* [1] , *Emma McFarlane* [1] , *Pooja Sharma* [1] , *Kathy Crew* [2]

1. Department of Agriculture Fisheries and Forestry, Science and Surveillance, Victoria, Australia
2. Department of Primary Industries, AgriScience Queensland, Dutton Park, Queensland, Australia

The Department of Agriculture Fisheries and Forestry's (DAFF) national post-entry quarantine (PEQ) facility at Mickleham, Victoria, is a purpose-built primary entry point for imported high-risk nursery stock for Australia's agricultural and horticultural industries. PEQ Mickleham hosts 600–800 plants yearly, represented by 60 genera that collectively undergo thousands of tests each year. With the closure of Queensland Department of Primary Industries' (QDPI) dedicated banana PEQ Approved Arrangement sites, greenhouse and diagnostics services are transitioning to DAFF Mickleham. The tissue culture service of *in vitro* multiplication has transitioned to the Crop Hygiene Biosecurity Services group at Agriculture Victoria.

In April 2026, the first consignment of tissue cultures commenced processing by the new service providers following the established banana PEQ process. Following inspection at PEQ Mickleham, clonal tissue culture accessions for each cultivar were established from individual plantlets. While *in vitro*, several accessions per cultivar will undergo preliminary diagnostic virus screening. If no viruses are detected, two accessions per cultivar, with three representative plantlets each, will be grown out in the Mickleham greenhouse and undergo several rounds of pathogen testing, as virus titre in tissue culture can be below detection assay thresholds. QDPI will continue to provide virus diagnostic services while DAFF's diagnosticians undergo further training and verification exercises.

Banana diagnostics conducted by QDPI include immunocapture (RT)-PCR tests for a suite of specific viruses along with immunosorbent electron microscopy for additional species. Diagnosticians at PEQ Mickleham are evaluating the efficacy of their existing high throughput sequencing of small RNA (sRNA-seq) workflow for detecting banana viruses using reference samples from QDPI's collection, which is held under containment with DAFF approval. However, detection of episomal badnaviruses, including exotic banana streak virus species, brings special challenges to the interpretation of sRNA-seq due to endogenous sequences naturally integrated into the host genome.

Impact of drought and barley yellow dwarf virus infection on wheat physiology and morphology

Brendan Vouadec [1] , *Soo Jean Park* [1] , *Manuella van Munster* [2] , *Piotr Trebicki* [1]

1. Macquarie University, Applied Biosciences, Sydney, New South Wales, Australia
2. PHIM, INRAE, Montpellier, Languedoc-Roussillon, France

Yellow dwarf viruses (YDVs) represent one of the most damaging group of viruses affecting cereal production worldwide. In Australia, these viruses infect major grain crops including wheat, barley, and oats, causing significant reductions in yield and grain quality, with consequent economic losses for growers. At the same time, cereal crops are increasingly exposed to drought stress, a major environmental constraint that limits plant growth and productivity. Although both factors independently affect crop performance, their combined influence on plant physiology and plant–virus–vector interaction remains poorly understood.

The interaction between drought stress and barley yellow dwarf virus (BYDV) infection has produced various outcomes across previous studies, suggesting that environmental conditions and drought intensity play critical roles in determining plant responses. The present study investigated the effects of BYDV infection under contrasting water availability scenarios. Wheat plants were exposed to well-watered, constant moderate drought, and terminal drought treatments to evaluate how the level of water stress and timing influence plant development, physiological traits, and viral responses.

The results demonstrated that drought scenario strongly influenced the consequences of BYDV infection. Under constant moderate drought conditions, virus-related effects on plant performance were intensified, whereas terminal drought triggered a different response pattern, indicating that the interaction between water stress and viral infection is highly dependent on the severity of drought.

These findings demonstrate that drought scenario can substantially modify host–virus–vector interactions. Understanding these relationships will be essential for improving disease forecasting, refining management practices, and developing more robust epidemiological models for cereal production systems facing increasing climate variability.

Dual RNAi protection against barley yellow dwarf virus in wheat and barley

Nora Derbal [1] *, Narelle Manzie* [1] *, Eric Dinglasan* [1] *, Neena Mitter* [1] *, Karl E Robinson* [1]

1. The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Queensland, Australia

Barley yellow dwarf virus-PAV (BYDV-PAV) is a major constraint on wheat and barley production, driven by efficient transmission from the aphid *Rhopalosiphum padi*. With increasing pressure to reduce insecticide use, RNA interference (RNAi) has emerged as a promising, targeted and environmentally compatible approach for managing virus infection and vector infestation in plants. This study explores a dual RNAi strategy: stimulating antiviral RNAi responses in planta through foliar dsRNA application, and silencing aphid genes involved in virus transmission.

Foliar-applied dsRNA targeting BYDV-PAV was readily absorbed by wheat and barley leaves and remained detectable for several weeks. Early observations indicate primitive but noticeable differences between dsRNA-treated plants and untreated controls following exposure to viruliferous aphids, suggesting a potential reduction in virus impact. These preliminary outcomes are supporting the feasibility of RNAi-based plant protection and provide a foundation for ongoing challenge assays to quantify antiviral effects.

In parallel, vector-directed RNAi was assessed by targeting two aphid genes associated with BYDV transmission: Eph and ASG. In vitro-synthesised dsRNAs were delivered to *R. padi* via an artificial feeding system. A significant knockdown of the Eph gene was achieved, with qPCR confirming markedly reduced expression in treated aphids compared with controls. ASG knockdown experiments are continuing.

Together, these findings demonstrate the potential of combining plant-directed SIGS with vector-targeted RNAi to reduce both BYDV-PAV infection in cereals and transmission efficiency by aphids. This dual approach represents a promising step toward pesticide-free, RNA-based management strategies for cereal viruses.

Improving narrow leafed lupin (*Lupinus angustifolius*) resistance to cucumber mosaic virus

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Cucumber mosaic virus (CMV) is a seed and aphid transmitted disease that causes stunting, chlorosis and yield loss in narrow leafed lupin (*Lupinus angustifolius*). Transmission to the seed results in damaging infections in subsequent crops[1]. Resistance to seed transmission is poorly understood.

In this study, a recombinant inbred line (RIL) population was developed between Unicrop (susceptible) and Tanjil (resistant) to study resistance to CMV seed transmission. A field trial of 104 F8 RILs with two replications were naturally infected with aphid vectors from CMV infected spreader rows. Main stem and lateral pods were harvested separately, threshed and 100 seeds from each plot were germinated. The radicle was phenotyped for CMV by quantification of infection by ELISA. A QTL analysis was carried out on the RILs using MapQTL6.0. One significant QTL for CMV seed transmission was mapped to Chromosome NLL_02 which could explain 15% of the phenotypic variation. Twenty annotated genes are associated with the QTL region of which four genes are associated with disease resistance.

These results demonstrate the multigenic basis of resistance to CMV in Tanjil. Future research will determine the candidate genes of these QTLs and develop molecular markers for marker-assisted selection or genomic selection in breeding programs.

Reference

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Virus diversity in wild Agaricus species in Australia

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Previous research on farmed *Agaricus bisporus* has shown that cultivated mushrooms host several viruses or associated viral RNAs, most of which appear to be benign. However, three viruses have been associated with disease of commercial importance – La France disease associated with by Agaricus bisporus virus 1 (AbV1), brown cap mushroom disease associated with Agaricus bisporus virus 16 (AbV16), and patch disease associated with Agaricus bisporus virus 6 (AbV6). These viruses are transmitted via anastomosis (hyphal fusion) and through spores and are believed to lack extracellular means of transmission. Due to this inability to spread as free particles, researchers have hypothesised that these viral infections could be a result of ancient infection events and that populations of wild, uncultivated *Agaricus* species could serve as viral reservoirs.

Australia is home to several native and introduced *Agaricus* species. While there is ongoing work documenting the diversity of *Agaricus* species in Australia, the diversity of mycoviruses present in uncultivated and small-scale produced *Agaricus* species remains undocumented. Even on a global level, viral diversity of only farmed *Agaricus bisporus* has been studied. To address this gap, the viromes of eight samples of various wild *Agaricus* species and one sample of commercially purchased *Agaricus subrufescens* spawn were investigated using high throughput RNA sequencing. A bioinformatic pipeline, compliant with the Minimum Information about an Uncultivated Virus Genome (MIUViG) standard, was used to investigate the diversity of viruses in the samples. The taxonomy and phylogeny of the identified viruses is being investigated and will be presented.

Modifying plant sterols for resistance to insect pests and insect-transmitted viruses

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Agricultural crops are severely affected by insect pests and insect-vectored viruses, resulting in global yield losses of 20–40%. As many pest species have developed resistance to chemical insecticides and biological control measures, new strategies for managing insect pests and insect-transmitted viruses are urgently needed. Our novel approach involves modifying plant sterol profiles to enhance insect resistance. Herbivorous insects are unable to synthesise cholesterol, which is essential for their growth and development. Instead, they rely on ingesting phytosterols from host plants and converting them into cholesterol. This conversion requires specific structural features in plant sterols, and many phytosterols are unsuitable for insect growth and reproduction.

The objective of this work is to engineer canola plants to produce sterols that are non-utilisable by insects, thereby conferring insect resistance while maintaining normal plant growth and development. Our research has generated several categories of insect-resistant canola lines, including transgenic (GM) canola, mutant lines from both *Brassica rapa* and *B. napus*, and CRISPR-edited lines. Our studies revealed that aphids, diamondback moths, and common cutworms feeding on some of these canola lines exhibited reduced body weight and lower survival rates, with aphids showing the greatest susceptibility. Aphids also displayed a strong preference for wild-type canola over modified lines. This approach may not only reduce direct insect damage but also limit the spread of aphid-transmitted plant viruses, which contribute substantially to crop losses worldwide.

INVITED SPEAKER

One biosecurity big, hairy audacious goal: Understanding plant virus vertical-transmission biology

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Understanding the biology of vertical transmission (from parent to progeny) of plant viruses is a big, hairy, audacious goal (BHAG). Although not formally from parent to progeny, virus transmission to clonal propagules holds many similarities to vertical transmission. Virus-infected seeds or clonal propagules can insidiously enter a new territory, remaining undetected for months, if not years; a single, untraced source can then lead to epidemics, resulting in regional devastation and global economic loss. Vertical transmission of plant viruses via seeds (or clonal propagules, especially through tissue culture), occurs in hard-to-access plant parts, over time, and usually manifests at low rates, rendering study challenging. Observations are generally destructive, often resulting in orphaned scientific claims, experiments are difficult to repeat; furthermore, meaningful time-course experiments are littered with challenges for creating quantitative data. Different virus–plant systems have nuances making generalisations difficult—highlighted by Australasian-relevant examples. Many terms have been used to describe different aspects of vertical transmission of plant viruses via seeds, resulting in some confusion regarding the mechanisms involved and therefore management of the transmission potential. Understanding the biology of this vertical transmission would enable a paradigm change in management, resulting in advanced regional and global biosecurity, food security, and economic resilience. We outline the impacts of vertical, and horizontal, transmission of plant viruses, summarise transmission mechanisms, provide examples of vertically transmitted plant viruses, explore biological and technological research complexities, discuss confusing historic terminology, and provide a logic for potential future transmission nomenclature. Finally, using the biological knowledge at hand, simple measures and advanced virus detection methods, we provide suggestions on how the management of plant virus vertical transmission may be improved to gain greater biosecurity. This abstract builds on MacDiarmid et al. 2026 (Advances in Virus Research 125: 69-151, DOI 10.1016/bs.aivir.2026.08.001).

Spray-induced gene silencing as a strategy for virus and vector management in horticultural crops

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Insect pests and the viruses they transmit pose a significant threat to horticultural production. Insecticide resistance impacts and the absence of any commercial viricidal spray represent critical gaps in IPM strategies. Spray-induced gene silencing (SIGS) is the foliar application of double-stranded RNA (dsRNA) to trigger RNA interference (RNAi) and offers a precise, non-transgenic approach to address both challenges simultaneously.

Here, we present research characterising SIGS as a holistic three-pronged approach: direct viricidal action in the plant, disruption of vector-mediated virus transmission, and suppression of vector populations.

Direct viricidal action following foliar application of ZYMV CP targeting dsRNA (ZYMV_CP-dsRNA) in zucchini (*Cucurbita pepo*) reduced infection by 60–80% against mechanical inoculation for up to 15 days post-treatment. Plants challenged by viruliferous *Myzus persicae* at day 5 post-spray achieved ~90% reduction in ZYMV infection rate, with significant protection sustained to day 10.

Orally delivered dsRNA targeting *M. persicae* stylet cuticle proteins, implicated as receptors for non-persistent virus retention, significantly disrupted viral transmission. Co-administration of nuclease-targeting dsRNA to overcome midgut endonuclease degradation reduced virus particle retention by 84–90%, translating to a 56–67% reduction in plant infection incidence, decoupling transmission disruption from aphid mortality.

For vector population suppression, artificial diet bioassays targeting eight essential *M. persicae* genes identified Acetylcholinesterase, Aquaporin, and RNA Helicase as the most effective individual targets, inducing mortality of 56%, 46%, and 72%, respectively. Combinatorial strategies achieved 78–85% mortality, and a multi-target stacked construct induced 54% mortality from a single dsRNA molecule, establishing that multi-gene targeting amplifies insecticidal efficacy beyond single-target approaches.

The next phase will address key translation challenges including dsRNA formulation, delivery optimisation, and scalable manufacturing for agricultural deployment, ultimately to develop a commercially viable multi-approach biopesticide application, delivering a first-in-kind viricidal spray and adaptable insecticidal tool for integration into IPM programs in protected vegetable production systems.

Discovery of novel plant antiviral agents against potato virus Y using an integrated screening strategy

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Plant viruses cause substantial crop losses, yet the development of effective antiviral control agents remains constrained by the lack of systematic screening strategies. This study proposes an integrated workflow for screening plant antiviral compounds against potato virus Y (PVY), using 10α-*Allylsulfidylartemisinin* (DHA), a bioactive compound derived from *Artemisia annua*, as a candidate molecule. The proposed strategy was designed as a stepwise pipeline progressing from *in silico* prediction to *in vitro* molecular verification and *ex vivo* biological validation. In the *in-silico* stage, molecular docking was used to evaluate whether DHA could exhibit stable binding affinity (-8.1 kcal/mol) toward PVY NIb, an RNA-dependent RNA polymerase essential for viral genome replication. The predicted binding profile of DHA was compared with those of reference antiviral or defense-related compounds, including ribavirin, ningnanmycin, and salicylic acid. Molecular dynamics simulations were applied to assess the stability of the predicted DHA-NIb binding site using Root-Mean-Square Deviation (RMSD) based analysis.

To support the computational predictions at the molecular level, recombinant PVY NIb protein was expressed and isolated for an *in vitro* verification step. Microscale thermophoresis (MST) analysis was used to evaluate ligand-target binding, thereby providing a molecular bridge between *in silico* prediction and biological antiviral activity. The biological relevance of DHA was examined using *ex vivo* validation systems. Leaf disc and protoplast assays were combined with RT-qPCR and ELISA to quantify PVY accumulation after DHA treatment. DHA reduced viral accumulation in these systems, supporting its potential antiviral activity at both tissue and cellular levels. Taken together, these results demonstrate that DHA suppresses PVY infection and reduces viral accumulation in the proposed validation systems. This integrated workflow provides a reliable strategy for evaluating plant antiviral compounds and identifying promising antiviral control agents against plant viruses.

Exploring the influence of colour cues on aphid behaviour and barley yellow dwarf virus-PAV movement in wheat

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Visual cues play an important role in aphid host-finding and landing behaviour, yet their influence on aphid dispersal within crop environments remains poorly understood. *Rhopalosiphum padi*, the principal vector of barley yellow dwarf virus (BYDV), relies on visual and olfactory signals during host location. This study investigated whether different background colours influence aphid movement from a central source plant and assessed virus movement using sentinel wheat plants under field conditions.

A BYDV-PAV infected wheat plant supporting a colony of viruliferous *R. padi* was positioned centrally and surrounded by healthy wheat seedlings placed in front of coloured backgrounds (yellow, green, blue and red) or a no-background control. Background colours were rotated among positions throughout the experiment to minimise directional effects associated with prevailing winds. Aphid activity on plants and coloured backgrounds was monitored twice daily over six days. Following the experiment, all sentinel plants were tested for BYDV-PAV using tissue blot immunoassay (TBIA).

Preliminary results indicated differences in aphid abundance among colour treatments, with yellow backgrounds generally attracting more aphids than other colours. However, aphids were observed across all treatments, including the no-background control. BYDV-PAV was detected in most sentinel plants, confirming successful movement of viruliferous aphids from the source plant. These findings suggest that background colour may influence aphid landing behaviour, although its effect on subsequent virus spread remains unclear. The widespread detection of BYDV-PAV highlights the capacity for virus movement even when observed aphid dispersal appears limited. Further replicated studies are required to determine the mechanisms underlying colour-associated responses and their epidemiological significance for aphid-transmitted viruses in cereal production systems.

Improved vector and pathogen monitoring strategies for insect-borne diseases in horticultural production systems

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New diagnostic tools are broadening the scope of surveillance programs for insect -borne diseases, making these activities faster, cheaper and more accurate. Here we highlight two case studies focusing on developing and optimising nucleic acid sequencing-based techniques to improve insect monitoring and surveillance while incorporating identification of their vectored viruses and bacteria.

A combination of insect cytochrome c oxidase subunit I (COI) metabarcoding and amplicon sequencing for orthotospoviruses using MinION long read sequencing is being developed to enable nursery staff to monitor thrips levels within and around a production nursery with the goal of implementing early IPM measures to control potential insect and viral disease outbreaks. Amplicon sequencing for orthotospoviruses is being used to screen for viruliferous thrips vectors.

In a second case study, COI barcoding of psyllids DNA was combined with 16S ribosomal RNA metabarcoding of their associated bacterial microbiome collected from citrus growing districts in Australia. These techniques were used to identify psyllid species associated with citrus production in Australia and to determine a better understanding of microbiome profiles in Australian psyllids. This tool has the potential to identify psyllid borne plant pathogenic bacteria, such as liberibacters and phytoplasmas.

Overall, the utility of the DNA sequence-based diagnostic tools to support surveillance activities across industries will be discussed.

Investigating novel strategies for grapevine virus management in Australia

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[1]High-health grapevine planting material is essential for limiting pathogen transmission and maintaining the productivity and sustainability of the grapevine industry. RNA interference (RNAi) serves a significant function in plant antiviral systems to mitigate the detrimental effect of viruses by silencing replication. A previous study demonstrated that RNAi can be employed to reduce the replication of grapevine Pinot gris virus (GPGV; species *Trichovirus pinovitis*; Family *Betaflexiviridae*) in *in vitro* grown grapevine plantlets: a single application of double-stranded RNA (dsRNA) targeting conserved motifs within the GPGV RNA-dependent RNA-polymerase gene resulted in a substantial reduction in titre of an isolate of GPGV strain LT6 (OQ199009) [1]. However, the plantlets were only tested at seven days post application, therefore the durability and long-term effect of the single application was not measured, and the effects of dsRNA on other GPGV strains remain unclear. In addition, the mechanism behind the viral titre reduction was not revealed.

In this study, the efficacy and durability of the RNAi treatment in tissue culture is being investigated. This will be illustrated using examples of virus infected Grüner Veltliner, from which the GPGV LT6 strain originates, that will be treated by dsRNA and then assessed at 7, 14, 30 and 60 days post treatment using RT-qPCR to measure virus titre and assess the persistence of antiviral effects over time. Small RNA sequencing will be employed to detect the accumulation of virus-derived small interfering RNAs associated with dsRNA-mediated antiviral response. The study will provide insight underlying dsRNA-mediated antiviral activity against GPGV and further contribute to the optimization of the application of dsRNA in an *in vitro* system for the production of high-health grapevine germplasm.

Reference

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Turnip yellows virus resistance in *Brassica napus* – will it be durable?

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Turnip yellows virus (TuYV) is a major constraint to canola (*Brassica napus*) production worldwide, and especially in Australia with more than 80% of canola crops infected over the past three years. Due to declining effectiveness of insecticide-based control of its vector, *Myzus persicae*, research has been increasingly focussed on host resistance. All TuYV resistances identified to date are phenotypically quantitative, reducing virus accumulation and transmission efficiency. However, most studies characterising TuYV resistance have challenged it with a single virus isolate, not accounting for the significant diversity of this virus in the field.

To assess their spectrum of resistance, eight *B. napus* varieties with reported quantitative resistance were challenged with three genetically diverse TuYV isolates and tested using ELISA. Resistance responses varied widely, depending primarily on the TuYV isolate. Some varieties exhibited strong resistance across isolates, while others exhibited clear strain-specific resistance.

Next, the evolutionary capacity of one TuYV strain to adapt to a highly resistant *B. napus* variety was tested using serial passaging. After eight passages, the virus had accumulated three non-synonymous mutations in open reading frame 1 (encodes the P1 portion of the P1P2 RdRp) which was associated with an increase in fitness in the resistant variety. However, there was a reciprocal decrease in fitness in the susceptible variety indicating a trade-off. The adapted isolate also showed improved fitness on other resistances, suggesting a shared resistance pathway.

The findings highlight the risk of relying on single-isolate screening, which may select for narrow, strain-specific resistance. This study also demonstrates that TuYV can rapidly gain fitness to quantitative resistance, although at a fitness cost on susceptible hosts. This information will greatly improve TuYV resistance screening protocols. Finding durable resistance will require evaluation against diverse virus populations and an improved understanding of host–virus evolutionary dynamics.

Turnip mosaic virus canola resistance-breaking strain: Symptoms, seed and contact transmission, yield losses and seed germination

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Turnip mosaic virus (TuMV) causes yield-limiting diseases in *Brassica* crops including in canola (*Brassica Napus)*. Further spread of TuMV's canola resistance-breaking (RB) strain poses a threat to canola oilseed production. Isolate phenotyping found that, like isolate 12.1 from canola, isolate BRSB1 from *B. rapa* belongs to this RB strain. New information was obtained on the responses of canola cultivars to infection with isolates BRSB1 and 12.1, including about symptoms they elicit in infected plants, their seed-to-seedling and contact transmission, and, for isolate 12.1, effects on yield limiting parameters and seed germination. In 12/13 canola cultivars with diverse TuMV resistance traits, BRSB1 reached lower virus concentrations and caused milder symptoms than isolate 12.1. However, because isolate BRSB1 overcame TuMV temperature sensitive invasion resistance, it reached higher virus concentrations in cv. Scoop. Late TuMV symptoms in five cultivars included axillary shoot growth proliferation, flower abortion, pod discoloration, deformation and size reduction, and within-pod seed germination sometimes causing pod splitting. TuMV seed-to-seedling transmission was demonstrated in canola. For isolate 12.1, its rate was enhanced from 0.1% after growing infected-mother plants under natural light to 0.5 - 3.3% after growing them under artificial light, and to 2.4 - 3.5% when there was mixed infection with cucumber mosaic virus (CMV). Low rates (0.1-0.9%) of CMV seed-to-seedling transmission occurred following mixed infection. TuMV seed-to-seedling transmission rates of 0.3-1.5% were obtained with seed from isolate BRSB1-infected mother plants under natural light. Both TuMV isolates were contact-transmitted, which occurred more readily with abrasive dusted leaves. Isolate 12.1-infection reduced average pod number/plant, total pod dry weight/plant and individual dry weight/pod by 59%, 84% and 62%, respectively. Seed yield loss/plant was 71% with pregerminated seeds included, but 87% when excluded. When pregerminated seeds were included, yield loss was due to fewer seeds, but, with pregerminated seeds excluded, individual seed weight reduction also contributed. Seed germination decline during storage was faster with seeds from TuMV-infected plants. These findings concerning biological properties of TuMV's canola RB strain emphasise not only its potential to cause major losses to global canola oilseed industries, but also provide important clues towards improving its management.

Challenges in virus management for canola and carinata in Queensland's subtropical climate

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Historically, canola (*Brassica napus)* hasn't been a traditional broadacre crop in Queensland due to the warmer subtropical climate, which adversely impacts seed set and oil content. However, with the development of new fast maturing canola varieties and the emergence of a new market in feedstocks, there has been growing interest in its cultivation as an alternative to traditional crops such as barley, wheat, chickpea, and faba bean in the Darling Downs region in southwest QLD.

Turnip yellows virus (TuYV), a phloem-limited polerovirus transmitted by green peach aphid (*Myzus persicae*), is a significant concern for canola growers Australia wide. As part of the GRDC-funded project DAW2305-003RTX, "Effective Virus Management in Grain Crops," we conducted aphid trapping, crop inspections and TuYV monitoring in canola crops during the 2024 & 2025 season in the Darling Downs region (SW QLD). Results highlight the unique challenges of QLD's weather, and the short, fast-growing season compared to other states. These conditions influence both the epidemiology of TuYV and the development of effective management strategies.

In addition to canola, carinata (*Brassica carinata*), a relative of canola, is being trialled as a potential biofuel crop. To support the emerging industry, carinata plants are being screened for susceptibility to common brassica viruses such as TuYV and turnip mosaic virus (TuMV).

The outcomes of the aphid trapping and TuYV surveys in canola, as well as the canola field trial and carinata virus screening will be presented. These efforts aim to support the sustainable expansion of oilseed production in Queensland.

Whole genome informed diagnostics distinguish mild and orange stem pitting RB2 variants of citrus tristeza virus in Australia

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Citrus tristeza virus (CTV) is a graft-transmissible, aphid-transmitted virus that is widespread in citrus-growing regions of Australia. CTV can cause a range of disease syndromes, including quick decline, seedling yellows, and stem pitting. While quick decline is now largely controlled using resistant or tolerant rootstocks, stem pitting remains a quarantine-sensitive disease phenotype, particularly in Queensland, where orange stem pitting outbreaks have been especially damaging. Previous work on the identification of the CTV isolates responsible for orange stem pitting implicated a variant within the RB2 genotype group of CTV. In this study, we used whole-genome sequencing of CTV isolates, combined with greenhouse pathotyping on citrus indicator hosts, to resolve the genotype–phenotype relationship of Australian RB2 variants. Comparative genome analysis revealed two highly similar RB2 variants, sharing 99.5% nucleotide identity, with contrasting biological phenotypes: one induced orange stem pitting, whereas the other was mild under the same pathotyping conditions. Variant-specific markers were then used to assess the prevalence of these RB2 variants in field samples. Our findings show that orange stem pitting risk in Australia is better explained by strain-level variation within RB2 than by broad genotype assignment alone. Together these findings will improve surveillance, quarantine decision-making, and assist in the development of mild strain cross-protection strategies against orange stem pitting.

TAS-AP: A portable Targeted Amplicon Sequencing Analysis Pipeline for rapid plant pathogen detection

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Targeted amplicon sequencing (TAS) is increasingly being adopted for rapid detection, characterisation, and surveillance of plant pathogens and pests. However, existing analysis workflows often rely on multiple command-line tools, specialised bioinformatics expertise, and complex computational environments, limiting their accessibility for routine diagnostics and biosecurity response activities.

TAS-AP was developed as an integrated, user-friendly, and portable bioinformatics application for analysing nanopore-based targeted amplicon sequencing data. The platform streamlines key analytical steps including quality control, read filtering, consensus generation, phylogenetic analysis, and automated visual reporting within an intuitive graphical user interface (GUI). TAS-AP is packaged for straightforward deployment with version-controlled releases, enabling reproducible analyses across diagnostic and accredited laboratory environments.

The application supports flexible primer schemes and can be readily adapted for multiple plant pathogens and pests, enabling rapid implementation for surveillance, diagnostics, and outbreak investigations. TAS-AP also improves accessibility to genomics-based workflows for laboratories with limited bioinformatics capacity.

In this presentation, TAS-AP is demonstrated through the analysis of different strains of Potato virus Y, highlighting its utility for rapid sequence analysis and phylogenetic interpretation in plant pathogen surveillance workflows.

MECAR: An accessible metagenomic diagnostic platform

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Metagenomics is increasingly used for plant health diagnostics and surveillance. However, routine adoption remains limited by the complexity of bioinformatics workflows and dependence on specialist bioinformatics expertise. Multiple analysis steps, software tools and command-line requirements continue to present challenges for many diagnostic laboratories and researchers.

To address these challenges, we developed MECAR (Metagenomic Contig Assembly and Reporting), an accessible metagenomic diagnostic platform that enables users to progress from raw metagenomic sequencing reads to diagnostic interpretation through a simple point-and-click interface. MECAR integrates read quality control, *de novo* assembly, sequence identification and automated reporting into a single reproducible workflow, eliminating the need to perform individual analytical steps or manage software dependencies.

Designed for users of all computational backgrounds, MECAR delivers rapid and reproducible analyses on Linux, cloud environments and Windows computers through Windows Subsystem for Linux (WSL). Results are automatically organised into biologically meaningful categories including viruses, bacteria, fungi, archaea and host sequences, allowing users to interactively inspect supporting evidence and confirm pathogen detection. Sensible default settings provide a streamlined workflow for routine use, while advanced users retain full control over analytical parameters for optimisation and customisation.

MECAR bridges the gap between sequencing data and actionable biological insights, enabling faster and more accessible diagnostics for routine surveillance, outbreak investigations and biosecurity applications. Its 'click-and-diagnose' approach makes metagenomics accessible to diagnosticians and researchers of all computational backgrounds, not just bioinformaticians.

A new recombinant begomovirus in Indonesian chillies

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Begomoviruses are one of the most important groups of plant viruses affecting solanaceous, cucurbit, legume and fibre crops. South-east and south Asian countries host high levels of begomovirus diversity, and recombination between individual species infecting a single host is common and can give rise to new species with altered host range or symptom severity. Of the five species known in Australia, only tomato yellow leaf curl virus causes significant economic impact to tomato production and is managed mainly through resistant cultivars. Movement of viruliferous whitefly vectors or begomovirus-infected planting material poses a substantial risk to Australian agriculture.

In the early 2000s in Indonesia, an incursion of pepper yellow leaf curl Indonesia virus (PepYLCIV, *Begomovirus capsicumindonesiaense*) spread rapidly throughout the major chilli (*Capsicum* sp.) production areas on Sumatra and Java, and still significantly restricts yield of one of their largest vegetable commodities by 20-100%. To date, efforts to assess chili begomovirus diversity in Indonesia have largely been based on sequencing of PCR amplicons from plants with suggestive symptoms. A recombinant species, pepper yellow leaf curl Aceh virus (PepYLCAV, *Begomovirus capsicumacehense*), related to PYLCIV, is prevalent and causes milder symptoms on chilli.

In our study, RNAseq high throughput sequencing of pooled symptomatic chili samples strongly suggested the presence of unrecognised begomovirus diversity. Rolling circle amplification, restriction and cloning of begomovirus DNA-A components was undertaken and initial sequencing for one sample collected in North Sumatra from a stunted plant with very small distorted chlorotic leaves and leaf mosaic symptoms revealed a novel recombinant sequence with nearest matches to PepYLCIV and Clerodendrum golden mosaic Jiangsu virus (*Begomovirus clerodendrumjiangsuense*). We are currently obtaining the full component sequence and assessing its geographic range in current and historical samples.

Breeding for durable resistance to PepYLCIV in chilli has been difficult, however recent analysis of inheritance patterns has revealed a complex multi-locus system (Wahyono et al., 2026) which offers promising prospects for improved hybrid cultivars. Improved knowledge of chilli begomovirus diversity in neighbouring countries supports programs breeding for begomovirus resistance and Australian diagnostic biosecurity preparedness.

Reference

Wahyono et al., 2026, https://doi.org/10.1007/s40858-026-00788-7

Linking viruses found by environmental metagenomics with physical specimens – tobamoviruses in Queensland

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The advent of high throughput sequencing (HTS) technologies has revolutionized virus discovery and with the avalanche of data biological characterization can get left behind. This report links two tobamovirus sequences identified through environmental metagenomics with respective field hosts.

A surveillance project was undertaken across Australia in 2013-2014 to examine the feasibility of early plant virus detection using pollen via honeybee sampling (Roberts et al., 2019). Ten recognized plant viruses, including youcai mosaic virus (YoMV, *Tobamovirus youcai*), were detected from Queensland from pooled samples collected from Bundaberg to Charters Towers. This tobamovirus, first reported in *Brassica rapa parachinensis* (choy sum/you cai) from China in 1958, has a wide host range, infecting both monocot and dicot species and had not been previously recorded in Australia. Independently, plants of tropical chickweed (*Drymaria cordata*) with vein mosaic symptoms were sampled from two locations in Brisbane in 2024-2025, >250 km from the nearest honeybee sampling site, and shown by HTS, RT-PCR and electron microscopy to be infected with YoMV. Although new host and distribution records for YoMV, this work indicates an established, endemic status for the virus in Queensland.

Another serendipitous connection was made with the discovery of a novel tobamovirus through HTS in the weed, *Alternanthera ficoidea*, showing mild mosaic symptoms in Townsville, Queensland. Independently and concurrently (Maha et al., 2025), a surveillance strategy based on metatranscriptomic sequencing of animal gut contents was undertaken. This latter study identified five tobamoviruses, two of which were previously undescribed. One of these, from a domestic dog rectal swab sample, was designated “Bluey” tobamovirus (PV005935), and shared 98.3% nucleotide identity across the complete coding sequence with the *A. ficoidea* virus. This represents the first in planta record for “Bluey” tobamovirus. The sampling locations for the two isolates are 500km apart, again implying an endemic status for the virus.

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A four-decade journey of monitoring and surveillance of viruses that cause yellowing and stunting of legume crops in the West Asia and North Africa (WANA) region

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Temperate grain legumes (faba bean, chickpea, and lentil) are among the most important pulse crops in WANA, serving as a primary source of protein for farmers with limited resources. Total pulse production in WANA has declined, while imports have increased. This is due to several factors, including outbreaks of viruses that often cause stunted growth, yellowing or sometimes reddening of the leaves, and poor or absent pod formation. When I joined the virology team at ICARDA in 1987, the viruses causing yellowing/stunting (such as chickpea stunt disease) were well-known by their symptoms and, for many years, were thought to be caused by infection with bean leafroll virus (BLRV), and the only diagnostic reagent available at the time was a BLRV polyclonal antiserum. Over the past four decades, numerous surveys have been conducted on legume viruses in most WANA countries in collaboration with national programs. Outbreaks of insect-transmitted viruses causing yellowing/stunting and poor pod setting, leading to significant reduction in crop yield have been documented. In the early 1990s, a severe epidemic of faba bean necrotic yellows virus was observed in Middle Egypt, the Jordan Valley, and the Syrian coast, leading to faba bean yield losses of 70-90%. Similarly, outbreak of chickpea chlorotic dwarf virus was recorded in Iran, Syria, and Sudan. Ten years later, another outbreak of chickpea chlorotic stunt virus was reported in chickpea and faba bean in Ethiopia, Tunisia and Syria. Through molecular diagnostics, developed in collaboration with ICARDA and Australian virologists in Melbourne and Brisbane, and funded by GRDC, new *Nanovirus* species were identified: milk vetch dwarf virus in China and faba bean necrotic stunt virus in Uzbekistan. In addition, five *Polerovirus* species (cucurbit aphid-borne yellows virus, cotton leaf roll dwarf virus, pepper vein yellows virus, pepo aphid-borne yellows virus, and brassica yellows virus) have been identified, which for many years were thought to be caused by beet western yellows virus. This presentation will provide an overview of the current status of yellowing/stunting viruses and their potential impact on the productivity of major legume crops in the WANA region.

Turnip yellows virus infection increases cucumber mosaic virus disease sensitivity in narrow-leafed lupin

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Mixed virus infections can increase disease severity and yield loss in pulse crops; however, interactions between cucumber mosaic virus (CMV) and turnip yellows virus (TuYV) in narrow-leafed lupin remain poorly understood, despite TuYV being commonly detected in lupin crops. This study examined effects of CMV and TuYV single infection and co-infection on virus titre, plant performance, yield components and CMV seed transmission in narrow-leafed lupin cultivar 'Jurien'.

A glasshouse experiment used a randomised block design with five retained treatments: CMV early, CMV mid, TuYV early, TuYV early followed by CMV mid, and an uninoculated control. Early inoculation occurred at the four-leaf stage, with mid inoculation one month later. Virus titre was quantified by qPCR, growth and reproductive traits were assessed at harvest, and CMV seed transmission was evaluated using harvested progeny seed.

TuYV titre was higher in TuYV single-infected plants at the first sampling time, but higher in co-infected plants later. CMV titre tended to be highest in co-infected plants at later sampling times, although the treatment effect was marginal. TuYV single infection had limited effects on harvest traits and was close to the control, whereas CMV early infection reduced plant height, dry weight and yield. The greatest yield loss occurred when TuYV-infected plants were later inoculated with CMV, producing significantly lower seed yield than all other treatments, including CMV early and mid infection alone. This treatment also produced the lowest pod weight, pod length and seed number, while pod number was not significantly affected. CMV seed transmission tended to be highest in co-infected plants but did not differ significantly among treatments.

These findings suggest TuYV single infection may have limited impact on lupin yield, but background TuYV infection could exacerbate losses if CMV is introduced through infected seed. Maintaining low-CMV seed stocks is therefore critical where TuYV is present.

Turnip yellows virus-associated RNAs in crop hosts: prevalence, transmission and development of molecular tools

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Turnip yellows virus (TuYV; genus *Polerovirus*) is an economically important polerovirus infecting a wide range of vegetable and grain crops. Disease outcomes are influenced by virus-host interactions and may also be affected by associated RNAs (aRNAs), which are satellite-like RNAs that depend on the helper virus for transmission. However, aRNAs are capable of self-replicating as they encode their own viral polymerase. The aRNAs found with TuYV have ancestral relationships to the *Tombusviridae*, and two different types of aRNA have been identified in Australia, labelled as ST9-aRNA and Oz-aRNA. Research from the USA suggests that the aRNAs can stimulate virus accumulation of polerovirus and potentially modulate the disease symptoms. Understanding the occurrence and biological significance of aRNAs in Australia is important for improving knowledge of TuYV epidemiology and informing future disease management strategies.

Preliminary results indicate that aRNAs are present in a substantial proportion of TuYV-infected crop samples, including broccoli, cauliflower and wombok. To understand if the incidence of aRNAs differ between plant species and whether the host plant may affect establishment or persistence of the aRNA, aphid transmission tests are being undertaken to test this hypothesis.

Further, to determine the contributions of the aRNAs to the disease syndrome and virus infectivity, it is necessary to compare plants infected with the helper virus alone, or with the helper virus and aRNA. To separate the two components of the infection, infectious clones are being created. Progress on creating these infectious clones will be reported. Together, this work provides foundational resources for dissecting TuYV-aRNA interactions and will support broader studies on the epidemiology of TuYV-associated disease in crop systems.

Lineage-resolved surveillance of the wheat curl mite-transmitted virus complex in New South Wales

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The wheat curl mite complex (WCM; *Aceria tosichella* sensu lato) is an important vector system for cereal viruses, but its diversity, distribution and epidemiological role in Australian grain systems are still poorly understood. In NSW, wheat streak mosaic virus (WSMV, *Tritimovirus tritici*) and possibly High Plains wheat mosaic virus (HPWMoV, *Emaravirus tritici*) are associated with recurring disease problems in early sown wheat crops. However, there is still limited information on which WCM lineages occur in the region, how widely they are distributed, and how mite-associated virus diversity relates to disease outbreaks.

Here, we present recent results from 2025-2026 field surveys of WCM and associated cereal viruses in NSW. Field-collected mites and host plant samples were screened using serological and molecular diagnostics to identify WCM lineages and detect WCM-transmitted viruses, including WSMV, HPWMoV and other cereal virus targets. In addition to testing plant material, we used direct RT-PCR to detect viral RNA from field-collected mite specimens. This allowed mite lineage identity and virus presence to be assessed from the same field-collected vector material, helping to examine associations between WCM lineages and viruses under field conditions.

The survey showed uneven occurrence of WCM and WCM-associated viruses across sampled cereal systems. WSMV was detected in over one-third of the wheat paddocks tested, and the major WCM lineages MT-1 and MT-8 were also identified. These results show that multiple components of the WCM-transmitted virus complex are present in NSW cereal systems.

This work provides a lineage-resolved view of WCM and associated virus diversity in NSW and supports improved surveillance and risk assessment of the WCM-transmitted virus complex in Australian cereal systems.

Navigating virus challenges and technological opportunities at Foundation Plant Services

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UC Davis Foundation Plant Services (FPS) tests, maintains, and distributes plant material of clonally-propagated specialty crops and conducts research to improve and validate novel diagnostic methods. High throughput sequencing (HTS) is the most impactful new technology of the last two decades, allowing the detection and characterization of viruses not detected with traditional methods. HTS contributed to the discovery of grapevine red blotch virus (GRBV), and the virus was deemed economically damaging and prohibited in California's grapevine certification program. Detection and spread of GRBV in FPS's foundation grapevine collection at Russell Ranch Vineyard resulted in its abandonment. FPS actively communicated with industry as GRBV was detected and spread, and in response to this threat, FPS and industry worked together to protect the core collection indoors. Today, the FPS grapevine collection remains productive in the intensively managed Classic Foundation Vineyard, with those selections duplicated in the new indoor collection.

HTS combined with PCR is now used to determine phytosanitary status of quarantined material and authorize its release from FPS. The timeline from HTS proof of concept for plant virus detection to regulatory acceptance in the US was lengthy and required methodical validation of FPS protocols and side-by-side comparison to biological indexing, culminating with interlaboratory validation at United States Department of Agriculture. FPS now uses HTS + PCR to qualify grapes, fruit and nut trees, and roses for release from quarantine and inclusion in state certification programs. Additionally, HTS is being leveraged to develop high-capacity, highly-multiplexed testing technology to screen for multiple viruses and variants in a single reaction: HiPlex. FPS recently completed research projects validating HiPlex assays for strawberry and grapevine viruses and is continuing this research by expanding to blueberry and additional grapevine viruses. Once the assays are tested, the next objective may be to develop a more user-friendly analysis interface.

From blot to base pairs: sequencing viral genomes from tissue blot immunoassay membranes

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As part of the National Grains Surveillance and Diagnostics Initiative, Agriculture Victoria is generating viral genomes from intercepted post entry quarantine (PEQ) specimens to capture global genetic diversity and thus, enable development of robust molecular diagnostics for their detection. PEQ collections of intercepted virus isolates represent an invaluable resource to address this challenge as they comprise of diverse and well-documented exotic virus-host combinations. However, these materials are typically archived in formats not optimised for RNA preservation, potentially limiting complete genome recovery.

Focussing on expanding genomic resources and to capture host-associated diversity for broad bean stain virus (BBSV; family *Secoviridae,* species *Comovirus viciae*), genomes were successfully generated from dried plant material. However, key host species remained underrepresented due to the absence of suitable archived dried plant specimens. To overcome this limitation, approaches adapted from medical genomics workflows for degraded RNA were applied to tissue blot immunoassay (TBIA) membrane.

RNA extracted from TBIA membranes was undetectable by Nanodrop and high-sensitivity Qubit but detected using a high-sensitivity TapeStation. RNA quality was assessed using the DV200 metric, with TBIA-derived RNA often comparable to or higher quality than RNA from dried plant or seed. Library preparation using the NEBNext RNA kit (MGI) was adapted for low RNA input and quality by adjusting fragmentation time, adaptor dilution, and PCR cycles.

Of 12 TBIA membranes processed, 8 yielded full-length BBSV contigs for at least one genomic RNA segment, with 5 producing complete sequences for both. Notably, a complete viral genome was recovered from a TBIA membrane prepared over 14 years ago, demonstrating long-term sample stability.

These results demonstrate that TBIA membranes represent a previously underutilised resource for recovering archival viral genomes, expanding opportunities for retrospective surveillance, incursion analysis, and integration of serological and genomic diagnostics.

Best practice sampling and virus detection in Australian grapevine propagation assets

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Grapevine (*Vitis spp.*) is susceptible to infection from 104 viruses, of which, 20 have been reported in Australia. Grapevine viruses of economic importance to the Australian wine industry are grapevine leafroll-associated virus 1 (GLRaV-1), GLRaV-2, GLRaV-3, GLRaV-4, grapevine virus A (GVA), grapevine Pinot gris virus (GPGV), grapevine berry inner necrosis virus (GINV), and grapevine red blotch virus (GRBV). The management of economically impactful viruses hinges on effective diagnostic processes. Diagnostic success of grapevine viruses can be low due to inconsistencies in sampling, assays, and complexities in viral biology. Guidelines for effective and robust sampling and diagnostic procedures which can be harmonised across laboratories is integral to long term grapevine virus management strategies in Australia.

Assessment of grapevine sampling practices is underway across three vineyards in distinct grape growing climates of Australia (hot, cold, and temperate). Selected grapevines (n = 64) include white-berried varieties (primarily Chardonnay; n = 33) and red-berried varieties (primarily Shiraz and Cabernet Sauvignon; n = 31) with high incidence of priority grapevine viruses. Selected grapevines are sampled every three months (seasonally) across two years (CY25-26 and CY26-27) for three tissue types (two shoots/canes, four shoots/canes, and ten leaf petioles). A next generation of multiplex RT-qPCR (mRT-qPCR) diagnostic assays for grapevine viruses are being developed and validated against contemporary Australian and international viral populations.

Preliminary results from the first timepoint of sampling (spring 2025) suggest high diagnostic success across seven economically significant viruses was achieved using four shoots (95%), compared to two shoots (87%) and 10 petioles (79%); which highlights the impact tissue type can have on diagnostic success. Further timepoints of sampling will build a comprehensive dataset to inform on best practice guidelines for sampling which combined with updated assays will improve Australia's diagnostic capability for grapevine viruses.

Incorporating High Throughput Sequencing into everyday plant virology diagnostics

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High Throughput Sequencing based diagnostic assays are fast becoming incorporated into the day-to-day operations of laboratories around the world. However, the range of complicated workflows and data analyses associated with the testing requires stringent protocols to be established to ensure that the results of HTS based diagnostic assays are robust, reproducible, meaningful and relevant to our stakeholders.

Added to this, ensuring that diagnosticians keep up-to-date with the new and emerging HTS technologies remains a challenge in the face of rapid technological developments across both the sequence data generation and the analysis space.

Here, we will present examples of how these tools are being used within the DPIRD Diagnostics and Laboratory Services specifically for plant virology diagnostics including amplicon vs metagenomic approaches, and the prospects of automation and NATA accreditation. We will discuss the bottlenecks in workflows, identify gaps and future opportunities as well as our responsibilities in sharing the methods and reporting results derived from them to our colleagues in policy and biosecurity settings. The outputs and roles of groups such as the Subcommittee for Plant Health Diagnostics (SPHD) High Throughput Sequencing Working Group, and the Working Group for Biosecurity HTS Diagnostics (WGBHD) in the roll out of these methods into everyday usage is also covered.

Producing synthetic monoclonal antibodies for banana bunchy top virus diagnostics

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Banana bunchy top virus (BBTV) is the most damaging viral pathogen of banana worldwide, and infection results in failure to produce a bunch and hence almost total yield loss. In many banana-growing regions, particularly in resource-poor settings, antibody-based diagnostics such as ELISA remain essential because they are affordable, robust, and require less specialised equipment than molecular methods. The existing commercially available polyclonal and monoclonal antibody (mAb) ELISA reagents for BBTV were developed in the mid-1990s. Unfortunately, the supplies of polyclonal antibodies are almost exhausted, and the original monoclonal hybridoma cell lines have lost viability and thus the ability to replenish these mAb stocks from them is also lost. To address this situation, the variable regions of the two purified mAbs were protein sequenced (outsourced to Biomedicine Discovery Institute, Monash University). Subsequent cloning and expression were outsourced to the National Biologics Facility, The University of Queensland. The derived variable region DNA sequence was synthesised with mouse constant regions and cloned into a constitutive mammalian expression vector. The recombinant monoclonal antibodies were expressed after transient transfection of a mammalian cell expression system. The synthetic mAbs demonstrated binding performance comparable to the original mAbs and reliably detected BBTV in infected banana tissues using ELISA. We have developed new polyclonal antibodies and a panel of 22 new mAbs. To safeguard BBTV diagnostic capability and ensure a reliable supply of high-quality antibodies, the new mAbs have also been subject to the above cloning and expression protocol. All 22 new mAbs showed comparable performance to their conventionally produced counterparts in ELISA.

This technique was shown to effectively immortalise antibodies, allowing long-term accessibility and eliminating the risk of loss through hybridoma contamination, genetic drift, or culture failure. The technique also allows “resurrection” of mAb production originally derived from hybridoma cell lines that are no longer available.

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Sampling irrigation water to detect and monitor vegetable plant pathogens

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Maintaining biosecurity in Australia is essential for protecting our agricultural industry. It requires keen observation and routine surveillance to combat established and emerging pathogens that pose a significant risk to crop health.

However, large-scale monitoring and surveillance methods can be time consuming and costly, both for diagnostic labs and the growers paying for the service. Hundreds of samples are required to effectively characterize a disease outbreak in a greenhouse, increasing strain on labour, slowing response times and mitigating effective intervention strategies.

This project, in collaboration with the ARC Plant Biosecurity Training Centre, will explore an alternative surveillance approach utilising irrigation water as the primary analyte to diagnose pathogens in vegetable production systems. Water sampling has the potential to increase sampling efficiency, requiring fewer samples to characterize entire sites, improving the speed and efficacy of interventions, limiting damages and tightening biosecurity.

The project will explore the potential of this water sampling approach, characterising its benefits and limitations and optimising protocols to maximise its potential. A deployment pipeline will be developed to allow for the implementation of this method in a wide range of greenhouse or open-field scenarios, allowing scalability and flexibility for industry. The development will be done in collaboration with industry partners to deliver a system that is practical and applicable to best support growers.

Early-stage experiments will use cucumber green mottle mosaic virus (Genus: *Tobamovirus;* Species: *Tobamovirus viridimaculae*; CGMMV) as a model pathogen to characterise the flow of tobamoviruses from plants into water reservoirs, using RT-qPCR to quantify virus titres in plants and water over time, from inoculation to symptom expression to evaluate the potential for early detection and risk mitigation. These early experiments will establish the feasibility of irrigation water for surveillance, providing critical guidance for future experiments, including alternative plant pathogens.

Long-term surveillance of viruses in pulses in western Victoria

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Pulses are an important component of dryland farming system in south-eastern Australia, contributing to crop rotation and soil fertility by adding nitrogen through nitrogen fixation. The most important pulse crops grown in southern Australia are chickpea, faba bean, field pea, lentil and lupin. Pulse production is frequently affected by viral diseases that can substantially reduce grain yield and quality. However, long-term studies of viruses in pulses in Australia are limited. To address this knowledge gap, plant samples were randomly collected from 363 pulse fields across western Victoria during ten individual years (2004, 2007, 2009 and 2014-2020). Each plant sample was tested for six common pulse viruses: alfalfa mosaic virus (AMV), bean leaf roll virus (BLRV), bean yellow mosaic virus (BYMV), cucumber mosaic virus (CMV), pea seed-borne mosaic virus (PSbMV) and turnip yellows virus (TuYV); samples were all tested using tissue blot immunoassay. Overall, TuYV and CMV were the most commonly detected viruses in pulses and were detected in 46% and 26% of fields, respectively, while AMV, BLRV, BYMV and PSbMV were less prevalent (2-13%). Mean virus incidence was also highest in TuYV (5%) and CMV (4%) while maximum within-field virus incidence was highest for CMV (100%), PSbMV (69%) and TuYV (24%). Overall, multiple viruses were detected at almost one third of the examined pulse fields. Considerable variation in virus prevalence and mean and maximum virus incidence was observed across pulse species and years, demonstrating the important influence of varying seasonal weather conditions on pulse virus epidemiology. The findings of this extensive long-term survey provide foundational data and will result in a better understanding of pulse viruses and their epidemiology in Australia.

The epidemiology of canola viruses in Victoria, Australia

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Canola (*Brassica napus*) production in Australia is impacted by several viruses, including turnip yellows virus (TuYV), cauliflower mosaic virus (CaMV), and turnip mosaic virus (TuMV). TuYV, which significantly reduces grain yield, grain quality and seed oil content, is considered the most widespread and important canola virus in Australia. TuYV is persistently transmitted by aphids, and its most efficient and important vector is the green peach aphid (GPA, *Myzus persicae*). Virus surveys of canola fields that have been conducted across western Victoria, Australia, over the past ten years were recently collated and analysed to get a better understanding of the occurrence and epidemiology of canola viruses in the region. Overall, 165 canola fields were examined across eight individual years (2015-2020, 2024 and 2025). Plant samples were randomly collected from each field during September-October of each year and tested for the presence of TuYV, CaMV and TuMV using tissue blot immunoassay (TBIA). TuYV was detected in 92% of the canola fields examined over the eight years, while TuMV and CaMV were detected in 8% and 9% of fields, respectively. The maximum within-field virus incidence was also higher for TuYV (100%) than CaMV (9%) and TuMV (8%). Additional intensive surveillance of selected canola fields was also conducted during 2024 and 2025, and the within-field presence of TuYV-infected aphids and field plants were monitored over time. This intensive monitoring suggested that TuYV infection occurred late in the season during both 2024 and 2025 in western Victoria; the lack of early TuYV infection was likely due to relatively dry seasonal conditions in both years. These results, along with information about TuYV outbreaks from other parts of the state and contrasting seasonal conditions during the 2026 canola-growing season, will be discussed and brought together to provide a more detailed picture of TuYV epidemiology in canola in Victoria.

Replicative fitness and virulence differences among turnip yellows virus isolates in susceptible and resistant canola

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Turnip yellows virus (TuYV; Family: *Solemoviridae,* Genus: *Polerovirus*) is a major virus of Australian canola with genetically diverse local populations. However, the implications of this diversity for important biological traits remain poorly understood. Combining genotypic and phenotypic characterisation of diverse TuYV isolates may provide a rationale for a strain classification system for TuYV that can be used for robust resistance-screening protocols. The current study aims to assess the replicative fitness and virulence of TuYV isolates collected during surveillance activities across Australia in susceptible and resistant canola varieties. Twenty-two highly diverse TuYV isolates were collected and cultured in the glasshouse. Each isolate underwent high-throughput sequencing to obtain a consensus sequence, while phenotypic diversity is being assessed using key biological traits, such as virus replication in different host genotypes, ability to overcome host resistance and virulence. These isolates were tested for replicative fitness in one resistant and two susceptible canola varieties. Virus accumulation at 4 and 7 weeks after inoculation was quantified using qPCR and ELISA. Isolates 5414, 5509 and 5594 were included as reference standards. Substantial variation in virus titre was observed across the isolates and host genotypes. Although some variations were observed between detection methods, qPCR and ELISA generally showed similar trends. Three isolates consistently ranked in the top quartile at both time points, indicating high relative replicative fitness, whereas two isolates remained in the lowest quartile, indicating lower replication capacity. The resistant variety was highly effective against eight isolates, partially effective against five and ineffective against three, demonstrating isolate-specific differences in ability to replicate in a host resistance background. Virulence assessment of a subset of isolates is currently underway to assess the relationship between replicative fitness and virulence. These findings highlight significant phenotypic diversity among Australian TuYV isolates and provide a foundation for selecting representative isolates for resistance screening and future research.

Distribution and host range of turnip yellows virus in South Australian weeds: novel detections in Poaceae and other potential hosts

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Turnip yellows virus (TuYV; *Polerovirus TUYV*) is an economically significant aphid-transmitted polerovirus impacting canola and other broadacre crops. This study investigates the role of weeds as reservoirs of TuYV in South Australia, essential for improving disease management and minimizing virus carryover between growing seasons. An extensive survey was conducted, collecting 761 plant samples from diverse weed and volunteer crop species to analyse the distribution and host range of TuYV. Results demonstrated a widespread presence of TuYV across nearly all surveyed regions, though regional incidence varied significantly. No detections occurred in the Upper Eyre Peninsula, likely due to low weed abundance from adverse seasonal conditions. At the same time, irrigated regions such as Urban Adelaide and the Fleurieu Peninsula recorded the highest incidences. Expected hosts within the *Brassicaceae* and *Fabaceae* families were confirmed. However, TuYV was also found in an unexpectedly broad range of plant families, identifying several new potential hosts, including *Chenopodium album*, *Foeniculum vulgare*, and *Asphodelus fistulosus*. Notably, TuYV was detected in multiple grass species, including *Avena fatua* and *Triticum aestivum*. Confirmation of detection by Sanger sequencing and subsequent variant analysis underscored the need for further investigation. To assess the epidemiological importance of these findings, greenhouse transmission experiments are underway to evaluate the potential for TuYV transmission between cereal hosts and canola via aphid vectors. Significantly, the current outbreak of TuYV in South Australia, the first in more than a decade, indicates that weed hosts could maintain TuYV in the environment over prolonged periods of drought. This research significantly expands the known host range of TuYV in Australia and sets a foundation for future inquiries into host competency and virus transmission dynamics.

Pathogenic characteristics and molecular mechanisms of tomato spotted wilt virus resistance of *Capsicum annuum*

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Tomato spotted wilt virus (TSWV) is one of the most destructive viruses affecting chili pepper (*Capsicum annuum*) production. The dominant resistance gene *Tsw*, originally identified in the related species *C. chinense*, has been widely introgressed into commercial *C. annuum* cultivars worldwide. However, the increasing emergence of resistance-breaking TSWV (TSWV-P1) isolates, distinct from the common strain (TSWV-P0), challenges this global defense strategy. The TSWV NSs protein acts as an avirulence determinant recognized by the Tsw resistance protein. Crucially, the host factor *Ca*TCP21 facilitates this NSs–Tsw interaction that is strictly required for triggering Tsw-mediated cell death and viral resistance.

To elucidate the functional divergence between TSWV-P0 and TSWV-P1, we first performed sequence alignments and phylogenetic analyses that highlighted key variations in their amino acid substitutions at the C-terminal regions. Based on these structural insights, we investigated their interactive properties. *In silico* modeling using AlphaFold3 predicted a distinct interaction interface between *Ca*TCP21 and the TSWV NSs proteins (TSWV-P0, P1) that was validated robustly *in vivo* via yeast two-hybrid (Y2H) assays. Finally, to determine the downstream molecular consequences of this interaction, we conducted RNA-seq transcriptome profiling. The data revealed widespread reprograming of genes involved in programmed cell death and signal transduction of phytohormones, and these expression patterns were confirmed independently by RT-qPCR. In conclusion, these findings provide a comprehensive mechanistic framework for Tsw-mediated immunity, offering critical molecular targets for breeding durably resistant crops against emerging TSWV variants.

Streamlining diagnostics for horticultural seeds imported into Australia

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International seed trade is a major pathway for introduction and spread of seed-borne bacteria, fungi, oomycetes, viruses and viroids. This pathway poses significant biosecurity risks to Australia's vegetable industries due to their heavy reliance on imported seeds. Seed testing is used globally to mitigate this biosecurity risk, however, low pathogen prevalence in seed lots can make detection difficult. Additionally, currently used molecular assays can produce false positive results. Therefore, this project is focussing on the development of an accurate high-throughput sequence-based diagnostic pipeline for cucurbit and solanaceous seeds that can screen large sample sizes and detect multiple pathogens simultaneously.

A universal nucleic acid extraction protocol was established to efficiently recover both DNA and RNA from cucurbit and solanaceous seed, enabling downstream compatibility with multiple diagnostic platforms. This was followed by multiplex RT-PCR and MinION amplicon sequencing to allow simultaneous amplification and identification of multiple target pathogens in a single assay. The assays were optimised and validated using sample sizes ranging from 100 to 1000 seeds that were each spiked with a single seed naturally or experimentally contaminated with cucumber green mottle mosaic virus (CGMMV) and melon necrotic spot virus (MNSV). A dedicated bioinformatics workflow enabled rapid pathogen identification, confirmation, and estimation of relative abundance, successfully detecting both viruses and fungus from a single seed across all sample sizes. To further assess assay robustness and reproducibility, samples were also evaluated through inter-laboratory (ring) testing involving independent diagnostic facilities. Evaluation of the workflow is ongoing to expand its application to a broader range of cucurbit pathogens and solanaceous seed pathogens.

This adaptable, sensitive and sequence-informed diagnostic pipeline enhances sample throughput and diagnostic accuracy while reducing processing time and cost, thereby strengthening Australia's diagnostic capacity and mitigating plant biosecurity threats at the border.

What makes a great bioinformatics workflow?

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For years, our community has celebrated faster algorithms, larger reference databases, better classifiers and increasingly sophisticated analytical workflows. We benchmark runtimes, compare accuracy metrics and compete to detect ever fainter biological signals.

But what if we're optimising the wrong outcome?

Perhaps a better measure of a successful pipeline is not what it can calculate, but whether someone can confidently act on its conclusions?

In operational biosecurity, that question matters. Every day, diagnosticians and decision-makers rely on increasingly complex genomic analyses to guide regulatory actions, trade decisions and responses to emerging threats. The science behind those analyses may be exceptional, yet the outputs often remain difficult to interpret, communicate and defend. We frequently treat reporting as the final cosmetic step of a workflow, when in truth it is the critical point where value is either realised or lost.

VIEW (Virus Evaluation Workflow) was developed through a collaboration between the Department of Agriculture, Fisheries and Forestry (DAFF), the Queensland Cyber Infrastructure Foundation (QCIF), the Queensland University of Technology (QUT) and the Queensland Department of Primary Industries (QDPI). Rather than developing yet another virus assembly pipeline, VIEW brings together proven approaches for viral genome assembly, pathogen detection and sequence characterisation within a workflow designed around a single objective: helping users understand the evidence.

The defining feature of VIEW is an interactive report that presents the evidence, interpretation and confidence of every finding in a coherent, accessible format. Reporting is not treated as something that happens after analysis; it is embedded into the workflow itself.

This presentation will showcase the architecture, analytical capabilities and reporting framework underpinning VIEW. In doing so we hope to challenge attendees to reconsider a question rarely asked during pipeline development.

If your users cannot understand the result, what was the point of the analysis?

The C4 protein of Papaya leaf curl Guandong virus is essential for symptom induction and RNA silencing suppression

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Passion fruit is a highly nutritious tropical fruit that grows on climbing vines and is propagated vegetatively, which increases its susceptibility to viral diseases. Papaya leaf curl Guandong virus (PaLCuGdV) is one of the major viruses in passion fruit, a whitefly-transmitted monopartite begomovirus. In the PaLCuGdV genome, the *C4* gene, located on the complementary strand and overlapping a partial *C1* gene, is a known viral symptom determinant and a potent viral suppressor of RNA silencing. Through quasispecies analysis of PaLCuGdV-infected passion fruit, we identified a highly prevalent mutant subpopulation (44.3%) harboring a premature stop codon in the *C4* gene (W59Stop) and a corresponding 17-amino-acid deletion in the *C1* gene. *In silico* analyses utilizing IUPred3 and AlphaFold3 revealed that the wild-type C4 protein is intrinsically disordered, lacking a stable three-dimensional structure. The W59Stop mutation truncates 27 C-terminal amino acids, potentially altering conformational changes in host interactions. To investigate the biological function of C4, we constructed infectious clones of the wild-type (pPaLCuGdV-WT) and C4 mutant (pPaLCuGdV-MT) virus genomes and evaluated their infectivity in *Nicotiana benthamiana*. Plants inoculated with pPaLCuGdV-MT exhibited delayed viral accumulation at 7 days post-inoculation (dpi) but reached WT titer levels by 14–21 dpi. Despite this high viral accumulation, the mutant induced only mild symptoms with significantly reduced stunting and leaf curling at 45 dpi. Notably, co-inoculation with the RNA silencing suppressor p19 restored severe, WT-like symptoms. Our findings demonstrate that the PaLCuGdV C4 protein is a critical virulence factor regulated by a premature stop codon. While its conserved N-terminus supports delayed systemic infection, the C-terminus is indispensable for efficient early viral movement and symptom induction via RNA silencing suppression.

Evaluating coloured sticky traps for aphids vector surveillance under semi-field conditions

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Aphids-transmitted viruses are major limitations to cereal production worldwide. Accurate surveillance of aphid vectors is essential for estimating virus transmission risk and supporting timely disease management. Although sticky traps are widely used to monitor aphids flight activity, their ability to accurately represent vector presence within crops remain uncertain.

Therefore, this study evaluated the performance of coloured sticky traps under semi-field conditions using wheat plants infested with *Rhopalosiphum padi*. Traps were deployed around infested plants, and aphid captures were quantified across multiple experimental repetitions under varying environmental conditions.

Yellow traps recorded the highest overall captures, although captures patterns varied among colours and between repetitions. In several trials, low trap catches were observed despite the confirmed presence of aphids on source plants, indicating that trap captures may not accurately reflect vector abundance.

Overall, sticky traps provide valuable information on aphid flight activity but should be interpreted cautiously when estimating virus transmission risk. Improving vector surveillance will contribute to more reliable epidemiological assessments and better management of aphids-transmitted viruses in cereal production systems.

Host aging, immunosenescence and the evolution of RNA virus' virulence

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Host age plays a crucial role in shaping virus-host interactions, yet its impact on virus evolution remains underexplored. Using turnip mosaic virus (TuMV) in *Arabidopsis thaliana* as a model pathosystem, we investigated how host developmental stage influences infection dynamics, immune responses, and viral evolution. Plants at later developmental stages were more susceptible to TuMV infection, with systemic spread facilitated by downregulation of cell wall biosynthetic genes. However, despite increased susceptibility, infected mature plants exhibited greater reproductive fitness, suggesting a trade-off between viral tolerance and fertility. Experimental evolution of TuMV in hosts populations with different age structures revealed that viruses adapted more rapidly in younger hosts, with distinct mutational patterns depending on the developmental environment and initial viral strain. Host developmental stage emerged as a key determinant of viral evolution, immune modulation, and infection severity. These findings underscore the broader evolutionary implications of host age in virus-host interactions, with relevance for plant models in a changing environment.

Probe-based multiplex qRT-PCR assays for viruses and other diseases affecting honeybees

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Recent invasion of the bee pest and virus vector, varroa mites, in Australia and its rapid spread has necessitated the development of effective molecular diagnostic tools for viruses that may be transmitted to honeybees by the mites. We report on the development of probe-based quantitative Reverse Transcription-PCR assays for honeybee-infecting viruses including DWV, SBPV, SBV, CBPV, KBV, BQCV, IAPV, ABPV, CBPV and LSV and fungal diseases like Nosema species some of which were verified using virus-infected Australian and exotic honeybees. The assays can be useful as a diagnostic tool and an essential part of honeybee virus surveillance programs to ensure the long-term profitability of the Australian honeybee industry.

Genetic analysis of bean yellow mosaic virus from Australia: new genomic and biological insights, and evolutionary dynamics

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Bean yellow mosaic virus (BYMV) infects both dicotyledonous and monocotyledonous plants. It causes substantial disease risks to cultivated plants, particularly grain and pasture legume species. In Australia, cool-season grain legume crops such as faba bean (*Vicia faba*) and lupin (*Lupinus spp.*) are severely affected by BYMV leading to significant yield losses. This study provides an in-depth analysis of both historical BYMV isolates spanning a 73-year period, and recent Australian BYMV isolates, including 73 genomes from GenBank and 40 new ones from this study. High-throughput sequencing and comprehensive bioinformatics approaches revealed further genetic diversity, including expansion of previously monotypic phylogroup VIII, and newly identified phylogroup X. Phylogroup VIII was predominantly composed of sequences from red clover (*Trifolium pratense*) isolates. When faba bean plants were mechanically inoculated with isolates from phylogroup VIII, they exhibited unusually severe symptoms, including systemic foliage necrosis, and eventual plant death. The isolates in phylogroup X showed the highest evolutionary divergence, a difference of 22% nt. The coat protein (CP) gene of BYMV was the most conserved genomic component. Additionally, episodic positive selection was identified primarily in the P3 and CP genes, suggesting selective pressures acting on them. Recombination analysis revealed more than 50 breakpoints. This study offers valuable insights into the complex interplay of mutation, recombination, and selection in shaping BYMV's genetic diversity and ongoing evolution. It also has important practical implications for improving virus disease biosecurity systems and virus resistance breeding efforts.

Enhancing diagnostic efficiency and scope in virus surveillance using high throughput sequencing

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Traditional virus surveillance in broadacre grains typically relies on conventional targeted assays, such as an antibody based assay - ELISA, or species specific molecular assays - PCR and qPCR, which are labour-intensive and often limited by targeted testing. Unlike these targeted methods, High-Throughput Sequencing (HTS) enables the untargeted, simultaneous detection of all co-infecting pathogens. Between 2022 and 2025, we developed and validated a transformative diagnostic protocol utilizing HTS to enable unbiased detection of the grain crop virome in Western Australia. Initial validation was performed on leaf samples from major Australian crops, including canola, cereals, and various pulses (lentil, bean, lupin, and field pea), using Illumina MiSeq and NextSeq platforms.

To evaluate diagnostic sensitivity and scalability, over four years, 85 bulk samples were tested, with each bulk sample comprising a pool of 60 to 100 3mm leaf discs collected from a single sampling site. Total RNA was isolated then sequenced on Illumina NextSeq platform. Bioinformatic pipelines, incorporating Blastdbbuilder, were deployed to filter host reads, assemble viral genomes and identify the virus species using Blastn search. To validate diagnostic accuracy, HTS profiles were directly compared against routine PCR and ELISA screening results and follow up testing of the samples using conventional methods.

The HTS workflow demonstrated exceptional concordance with conventional methods, reliably identifying expected endemic viruses in the bulked samples. Furthermore, the HTS revealed an unexpected virus plant host combination, identified novel viruses previously unreported in its respective plant host in Western Australia, and successfully detected several mycoviruses (fungal viruses). This study provides a robust proof of concept for the validation and integration of HTS into broad-spectrum virus surveillance frameworks, with clear potential for increasing workflow efficiency and diagnostic scope, as well as adaptation to other complex diagnostic sample types such as seeds and insect vectors.

Landscape ecology shapes treehopper-borne disease dynamics

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Grapevine red blotch virus (GRBV, *Grablovirus vitis*, genus *Grablovirus*, family *Geminiviridae*) is the causal agent of red blotch disease of grapevines. GRBV is transmitted by the threecornered alfalfa hopper, *Spissistilus festinus* (Hemiptera: Membracidae), in a circulative and nonpropagative mode, yet some parameters of disease ecology remain poorly characterized. These gaps in knowledge are primarily due to a limited understanding of epidemiological relationships between treehopper dispersal and plant communities at the landscape level. We investigated the connectivity of natural and cultivated plants in vineyard ecosystems for red blotch disease dynamics by characterizing the dietary history of *S. festinus* and its landscape movement. Molecular analysis of the gut content of *S. festinus* specimens caught in more than a hundred vineyard sites and the flora proximal to vineyards in northern California in the USA revealed a total of 171 genera from 60 plant families with a preeminence of Asteraceae, Fabaceae, and Vitaceae over two growing seasons, illustrating dietary profiles composed primarily of natural vegetation. Distinct seasonal feeding trends related to weather patterns were documented with host repertoires unique to some vineyard sites and estimated *S. festinus* travel distances of up to 2 km. This work also identified potential reproductive and overwintering hosts of *S. festinus* in natural habitats and conformed a suspected ecological relatedness between vineyards and free-living vines in riparian corridors for GRBV transmission. Together, our findings on landscape ecology and *S. festinus* dispersal transformed not only our understanding of red blotch disease ecology but also informed disease management options.

An assessment of diagnostic molecular assays for detection of grapevine berry inner necrosis virus detection in Australia

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Grapevine berry inner necrosis virus (GINV; *Betaflexiviridae*, *Trichovirus necroacini*) was detected in Australian table grapes in October 2025. Infection with GINV is associated with reduced vine vigour, shortened internodal distance, reduced berry/cluster size, and compromised fruit quality and taste in susceptible grapevine varieties and poses a threat to the Australian wine and table grape industries, which combined contribute $AUD 52 billion to the Australian economy. Symptoms associated with GINV can be confused with symptoms caused by other viruses or abiotic stress making field-based diagnosis unreliable, necessitating effective lab-based diagnostic strategies which are sensitive and specific.

Several endpoint RT-PCR and real-time RT-PCR (RT-qPCR) assays that have been published or newly designed were established and evaluated to ensure accurate surveillance for GINV in Australian vineyards. The results demonstrated a SYBR based RT-qPCR, newly designed by Italian researchers, had improved sensitivity, specificity and reproducibility compared to endpoint assays making it a valuable tool for accurate diagnostics of GINV. Detection results were also supported by high throughput sequencing (HTS) data confirming the reliability of the assay. A probe-based RT-qPCR assay targeting a conserved region of the RdRp/MP gene has also been developed and is currently undergoing validation and the results will be presented.

An analysis of the grapevine virus testing done for industry by Crop Health Services indicates that GINV occurs in several states and as of May 2026 the virus has been detected in 188/708 (26.6%) of samples tested. Further molecular characterisation studies are required to assess the genetic variability of the different strains and isolates of GINV present in Australia to develop more robust diagnostic assays for GINV, understand transmission and plant host interaction to inform varietal susceptibility and to improve management of this virus.

Rapid, field-deployable diagnostic for plant viruses using microneedle technology

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Early and accurate detection of plant viruses is critical for biosecurity, crop protection, and rapid incursion response. Conventional diagnostic methods such as ELISA and PCR-based assays are sensitive and reliable but remain constrained by the need for laboratory-based nucleic acid extraction, specialised expertise, and time-intensive workflows. Microneedle (MN) patches enable direct sampling of plant sap without destructive tissue processing or hazardous reagents. The aim of this project was to simplify the isolation of nucleic acids from plant leaves using MN array patches.

In this study, nucleic acid was isolated from virus infected plants using MN array patches and compared against conventional methods (Maxwell extraction robot). Two economically significant strawberry viruses, Strawberry mild yellow edge virus (SMYEV) and Strawberry vein banding virus (SVBV), were investigated using *Fragaria × ananassa* (Albion) plants grown under glasshouse conditions. Our results showed that the MN-based extraction successfully recovered nucleic acids suitable for downstream molecular assays, although yields remain lower than conventional Maxwell methods. However, pooling MN samples and purification using RNA-binding magnetic beads significantly improved viral detection compared to individual MN extractions, resulting in an increased sensitivity. Overall, the findings of this study, demonstrated the feasibility of MN-based extraction for virus diagnostics while identifying key optimisation strategies. With further refinement, MN technology could enable rapid, non-destructive, and field-based plant virus surveillance.

Improving plant virus detection from trapped insect vectors

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Early detection of endemic and exotic plant viruses is critical for protecting Australia's plant industries. As insect vectors transmit many important grain viruses, surveillance approaches that target trapped insects have the potential to provide earlier and more sensitive detection than traditional crop-based monitoring. A major objective of the National Grains Diagnostic and Surveillance Initiative (NGDSI) is to develop and validate methodologies to reliably detect vector-borne viruses in trapped insects under operational field conditions.

Preservation of trapped insects was initially focused on maintaining morphological traits and, more recently, insect DNA for species identification through barcoding. However, understanding the longevity of RNA plant viruses within trapped insects is essential for interpreting negative diagnostic results. This is particularly important for small vectors such as thrips and aphids, where extended trapping periods under tropical environmental conditions may compromise virus detection during surveillance for exotic plant viruses.

Our current work focuses on determining how trapping conditions affect virus detection over time and identifying trap preservatives that extend the virus detection window. As downstream diagnostics increasingly rely on high-throughput sequencing rather than targeted PCR assays, maintaining viral RNA integrity over time is a key consideration. The outcomes will strengthen Australia's capacity to detect emerging virus incursions and improve confidence in negative detections obtained through insect-based virus surveillance programs for the grains industry.