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GRDC

GROUNDCOVER SUPPLEMENT

PULSE AND OILSEED DISEASES

Suppressing disease to protect break crops

Limiting the impact of disease on pulses and oilseeds requires an integrated approach

By GRDC's Applied RD&E Group and the Genetic and Enabling Technologies Group

■ Commonly used as break crops, oilseeds and pulses provide many rotational benefits to cereal crops and can also be highly profitable in their own right.

The most dominant of these, canola, is the third-largest crop produced in Australia, with about 2.5 million hectares grown each year (Figure 1). Winter and summer pulses, combined, cover a similar area. Limiting the impact of disease is essential to maximise both the rotational benefit and profitability of these crops.

GRDC is targeting profitable disease management through surveillance and diagnostics, pathogen biology, epidemiology (how disease develops in the environment), genetic solutions and the development of integrated disease management packages.

Surveillance and accurate identification are key. Our investment in surveillance provides growers and advisers with intelligence on changes in pathogen population and distribution, virulence and new and emerging threats. It also enables market access by supporting 'area freedom' status.

Advances in DNA testing technology allow disease outbreaks to be detected before symptoms appear, enabling more targeted and timely fungicide application. For example, DNA testing of spores collected by the iMapPESTS sentinel can objectively and accurately track changes in populations to provide timely information on pathogen abundance (page 8).

These tools are particularly useful when studying viruses and have led to more accurate virus identification and, consequently, better understanding about how these viruses spread, which will improve how viruses are managed (page 11). Such technology also plays a crucial role in protecting our industries against new incursions through the quarantine testing of the imported germplasm required by our breeding programs (page 10).

Changing farming systems mean we are seeing changes in host–pathogen interaction. Canola is the perfect example: early sowing has led to the development of upper canopy infection, and stubble retention means spore release may coincide with the time when paddocks are rotated back into canola (page 4). Epidemiology and disease management research need to be revisited to ensure a robust understanding of how they interact under modern and future farming systems, including the effect of climatic variability.

Changes in pathogen virulence and the development of fungicide resistance highlight the need to continue to search for novel sources of genetic resistance to disease. To avoid the 'boom-and-bust' cycles that occur when new resistant varieties are released, GRDC is seeking to broaden its range of resistance genes and to develop markers to speed their progress into breeding programs. The genetic advances reported here include blackleg and Sclerotinia in canola (pages 3 and 6) and Ascochyta in chickpeas (page 12).

To bring it all together for you, GRDC is actively investing in local disease experts who understand their region's agronomic situation and can provide diagnostic services and tailor integrated disease management advice to meet the needs of growers and advisers (pages 14 to 18). One example is the recent update of pulse disease resistance categories to better align with management strategies (page 19). □

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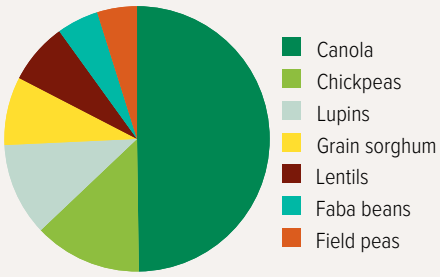
Figure 1: Canola and pulses are significant break crops that provide many rotational benefits to cereal crops and can be highly profitable. Five-year average area grown across Australia (2016/17 to 2020/21).



Source: ABARES

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COVER IMAGE: SARDI's Rohan Kimber demonstrates the iMAP Pests Sentinel 4 prototype at the Hart field site in South Australia. The Sentinel uses spore traps (and an automatic weather station) to capture the airborne spores of 13 pathogens. **PHOTO:** AUSVEG

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Australian approach needed for Sclerotinia

Sclerotinia stem rot research is focusing on genetic resistance and management solutions tailored to Australian conditions

By Dr Lars Kamphuis, Dr Mark Derbyshire, Associate Professor Sarita Bennett

KEY POINTS

- **Research has identified sources of resistance to Sclerotinia stem rot in canola germplasm**
- **A breeding technique called genomic selection can be utilised to introduce Sclerotinia stem rot resistance into canola cultivars**
- **Research has found no correlation between the presence of spores on petals and disease incidence and severity**

■ Successful control of Sclerotinia stem rot – a destructive fungal disease of canola and pulses – is highly dependent on the timing of fungicide application. There are no commercial Australian canola cultivars with resistance to Sclerotinia.

To help growers find more reliable ways to protect canola crops, GRDC investment in the Centre for Crop and Disease Management (CCDM) at Curtin University is targeting improved genetic resistance in canola cultivars and management solutions that are adapted to Australian conditions.

GENETIC RESISTANCE

CCDM researchers have screened a large canola germplasm collection (218 plants) and identified lines with partial resistance. These lines are now a vital resource for Australian breeders seeking to improve Sclerotinia resistance in future canola varieties.

Unlike most other diseases, resistance to Sclerotinia in canola is controlled by multiple minor genes acting together to provide resistance. This means that the classic marker-assisted breeding typically used to screen for major gene resistance for other diseases will not work for Sclerotinia resistance.

Instead, CCDM researchers have been the first in the world to apply genomic selection to estimating Sclerotinia resistance scores in canola. While marker-assisted selection relies on identifying one small section of DNA, genomic selection is based on the identification of much larger sections of DNA. The technique is essential to rapidly and efficiently breed quantitative 'multi-gene' traits into crops.

Such genomic selection can help identify the varieties most likely to carry Sclerotinia resistance for further evaluation and screening.

To progress this Sclerotinia resistance into Australian canola varieties, the CCDM is now providing seeds of resistant canola parent lines to Australian breeding companies, along with statistical and disease expertise.

MANAGEMENT SOLUTIONS

A better understanding of the conditions that lead to Sclerotinia stem rot in canola in Australia is also important to help growers manage the disease.

Current Sclerotinia disease forecasting methods are based on research in Europe and Canada where crops are grown over a summer growing season under cool temperate climatic conditions. This means they may not be appropriate for canola grown in southern Australia during the winter under warm temperate conditions.

To determine the parameters that are required to develop and improve disease modelling for the Australian environment, disease incidence and severity were studied at 25 field sites across the Western Australian grainbelt over four years.

While spores from infected petals are known to be the dominant source of infection, testing of petals collected from the field sites for the presence of Sclerotinia spores showed no correlation between the presence of spores on petals and disease incidence and severity. This means that spore testing of canola petals is not recommended to help determine fungicide spray requirements.

Fungicide treatment at 30 per cent flowering did reduce infection levels compared with unsprayed plots; however, this did not translate into significant differences in yield. Further research is underway to determine what level of Sclerotinia incidence is likely to produce a yield benefit from spraying at the recommended 30 per cent bloom. □

GRDC Code CUR1403-002 (CUR00023-BA-1)

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Photo: Carole Kerr

Ashmita Lamichhane from the Centre for Crop and Disease Management conducting petal tests in the laminar flow cabinet in the laboratory. These tests have shown that the presence of spores on petals does not correlate with disease incidence and severity.

Photo: Yuphin Khentry

Dr Toby Newman and Dr Mark Derbyshire measuring stem lesion length of flowering canola plants that were inoculated with an agar plug containing *Sclerotinia sclerotiorum*.

Keeping canola ahead of evolving blackleg

Staying ahead of this evolving canola pathogen takes constant vigilance

Photo: Dr Angela Van de Wouw

The increased retention of standing stubble means that the release of blackleg spores is now more likely to be delayed until the second year after a canola crop rather than the first. Unfortunately, this is often when canola is sown back into the paddock, putting the crop at greater risk.

By Dr Angela Van de Wouw, Associate Professor Alexander Idnurm, Dr Steve Marcroft, Dr Susie Sprague

KEY POINTS

- Blackleg resistance is influenced by specific farm practices, and regular monitoring of disease severity is essential to determine the risk of disease in your paddock
- While fungicide applied at 30 per cent bloom can reduce blackleg upper canopy infection, the yield benefit depends on many factors
- Changes in stubble management mean that spore release may be delayed to the second year after growing canola

■ New research is developing blackleg management strategies based on a three-pronged approach of genetic resistance, cultural practices and fungicides.

With investment from GRDC, the University of Melbourne, Marcroft Grains Pathology and CSIRO are using molecular and field-based approaches to improve the management of blackleg – a stubble-borne disease that leads to seedling, crown canker and upper canopy infection.

MAJOR GENE RESISTANCE

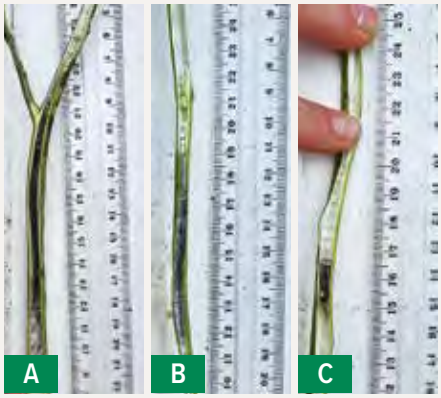
Major gene resistance is an effective way to limit blackleg disease. This resistance is expressed throughout the life of the plant and, when effective, prevents the formation of leaf lesions, subsequent crown canker and upper canopy infection.

However, when varieties with the same major resistance genes are grown in multiple consecutive years, the blackleg fungus can evolve to overcome this form of genetic resistance. In just a few years, resistant individuals will dominate the population.

This research is monitoring the level of blackleg disease at 32 sites across canola-growing regions in association with the National Variety Trials program. Varieties representing each resistance group are monitored to determine regional efficacy of the major resistance genes.

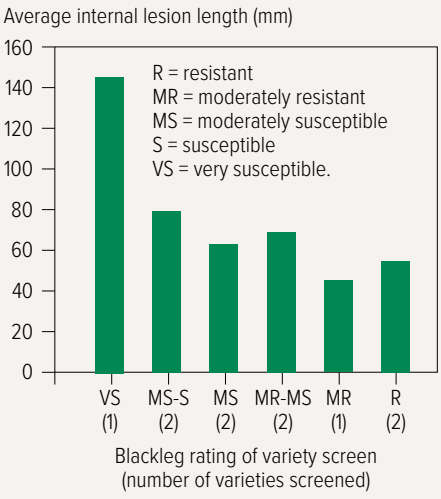
In 2020, monitoring indicated that Group H resistance was being overcome at Hamilton in western Victoria, and this was confirmed by molecular analysis of fungal isolates. The grower had sown Group H varieties for several years as a grain-and-graze option. Monitoring sites showed that the Group H resistance remained effective elsewhere.

Figure 1: Examples of the level of stem infection of a (A) MS-S, (B) MR-MS and (C) an R variety.



Source: Dr Angela Van de Wouw

Figure 2: Preliminary data indicates that the average lesion length for upper canopy infection may be reduced by growing varieties with better resistance ratings.



Source: Dr Angela Van de Wouw

Figure 3: The number of fruiting bodies substantially increases when stubble is lying on the ground (top) compared with standing stubble (bottom).

Source: Dr Angela Van de Wouw

While the monitoring site data indicates which resistance genes are generally effective in a region, it is recommended that growers and advisers monitor the level of disease in their own paddocks.

UPPER CANOPY INFECTION

Upper canopy infection refers to the development of blackleg lesions on the upper stem, branches, flowers and peduncles. Early sowing gets the crop established before winter but means crops are flowering in late July and throughout August, when conditions are ideal for blackleg spore release and they can land directly on the upper canopy.

The 30 per cent bloom fungicide spray timing used to control Sclerotinia stem rot has also been shown to minimise the severity of upper canopy infection. However, while the use of fungicides reliably reduces the level of disease, the likely yield return varies dramatically.

Preliminary data suggests that thermal time, water stress and genetic resistance may all contribute to the ability of a fungicide application to generate a yield response, and these are under further investigation.

When effective, major gene resistance can control upper canopy infection, but initial field observations suggested that all varieties may be equally susceptible without it. To test this, varieties with a range of resistance ratings were inoculated with individual isolates at the same growth stage in glasshouse experiments in Horsham and Canberra in 2020 to remove the variability observed under field conditions due to differing flowering times.

Preliminary results suggest that this initial observation is incorrect. Not all varieties that lack effective major gene resistance are susceptible and there may be some correlation between resistance to upper canopy infection and quantitative resistance – which is indicated by the variety disease rating (Figures 1 and 2).

These potential differences in genetic resistance may contribute to the variability in fungicide yield benefits being observed in trials and growers' paddocks.

CHANGES IN STUBBLE MANAGEMENT

The dramatic shift towards stubble retention over the past 20 years means that stubble now remains standing well into the following growing season, rather than being knocked down and starting to break down. Large visual differences in sexual fruiting bodies on the stubble in the field have been observed and this warranted further investigation (Figure 3).

Stubble was collected from the standing and laying down orientation over the two years following a canola crop and the spore release from the stubble was measured each month. In the year following the canola crop, significantly fewer spores were released from the standing canola stubble than the lying stubble.

When standing canola stubble was knocked down in the second year it produced a significantly higher number of spores than the stubble that had been lying down for two years. The total number of spores released was much higher in year two compared with year one. Unfortunately, this is often when canola is sown back into the paddock, putting the crop at much greater risk.

The impact of this change in spore release on disease severity is undergoing further investigation. □

GRDC Codes UOM1904-004, MGP1905-001, UM00051

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BLACKLEG INCIDENCE

Each year blackleg disease severity will vary between farms depending on rainfall, timing of rainfall, canola intensity in a region, variety resistance, fungicide use and sowing time. However, seasonal climate is also a major driver.

In New South Wales, blackleg levels were very low from 2017 to 2019 and did not cause significant issues. In 2020, blackleg returned and, while mainly well-managed, there was some damage in more susceptible varieties.

In Victoria and South Australia, blackleg has been much more variable between regions as a result of seasonal conditions. Generally, crown canker damage has been low due to early sowing and crops being established prior to cold winter conditions. Upper canopy infection has been very variable, with growers needing to make specific decisions on their individual crop at the 30 per cent bloom spray timing.

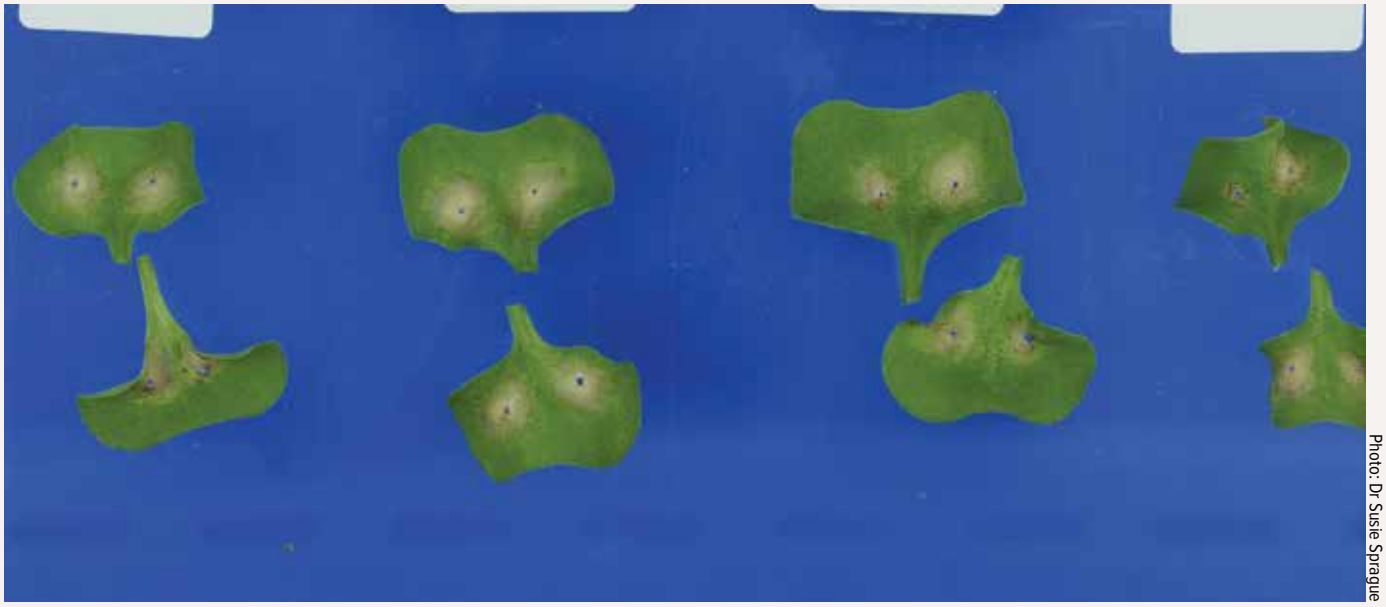

Photo: Dr Susie Sprague

The traditional method of identifying major genes for blackleg resistance involved measuring lesion development on cotyledons after inoculation in the glasshouse. With markers now available for six major genes, this technique can be replaced with a more rapid and reliable screening test of the plant's DNA.

Opportunities to expand blackleg resistance pool

The canola industry depends on effective blackleg resistance, but the highly diverse blackleg fungal population is a moving target

By Dr Susie Sprague, Dr Luke Barrett, Professor Jacqui Batley, Dr Angela Van de Wouw, Dr Steve Marcroft

KEY POINTS

- **Three major genes for blackleg resistance have been identified by the University of Western Australia, doubling the number available to Australian canola breeders**
- **Researchers at CSIRO have developed new techniques to better identify and characterise the more durable minor gene resistance**

■ New research has identified three major genes for blackleg resistance and is working to better understand how minor gene resistance is expressed.

Major gene resistance relies on a single gene to confer resistance, while minor gene or 'quantitative' resistance depends on a cocktail of minor genes that work together. These two forms of resistance act to control blackleg disease in canola in different ways.

The Australian canola industry has, to date, relied on three major genes, but blackleg populations are highly diverse, with the ability to overcome major genes in as few as three years after commercial release. There is now recognition that a combination of major and minor genes will provide a more durable resistance as it is more difficult for blackleg to overcome multiple genes. However, 'quantitative' resistance is difficult to measure in the plant as the effect of each gene on the level of blackleg disease is small and expression is also strongly influenced by the environment, making this a challenging area for development.

Two GRDC investments commenced in 2019 to identify more diverse and effective ranges of blackleg resistance in canola varieties and to develop reliable methods to phenotype quantitative resistance. The University of Western Australia (UWA) is focusing on major gene resistance, while CSIRO is focusing on minor gene resistance.

NEW MAJOR GENES

Since the commencement of this GRDC investment, UWA has doubled the number of major genes identified, which was made possible by combining phenotypic information with state-of-the-art genome-sequencing technologies.

Currently, a range of wild varieties and species are being screened for the identification of novel sources of resistance, while three new genetic sources of resistance are being further characterised.

All current and past Australian varieties were screened to determine and understand which resistance genes they possess. This highlighted

that one gene in particular, *Rlm4*, has been the dominant gene in use by Australian canola-breeding companies.

Increasing the number of major genes available to breeders and growers will help avoid the boom-and-bust cycle that results when new resistance genes are quickly overcome. Molecular markers perfectly linked to all six known genes have been developed and are available and can now be used routinely in breeding programs.

QUANTITATIVE RESISTANCE

Minor gene or quantitative resistance limits the spread of the fungus once it has infected the plant and is provided by numerous genes each with a small effect.

To date, breeders rely on field assessments of blackleg crown canker severity in mature plants to select for quantitative resistance. However, this strategy depends on the development and expression of disease for visual assessment, which has limitations because:

- the blackleg population is dynamic, changing from year to year;
- the presence of effective major genes masks the presence (or absence) of quantitative resistance genes; and
- there are strong environmental effects that influence disease expression.

Better phenotyping of this type of resistance will make it easier for breeders to identify lines with robust resistance to blackleg.

CSIRO has developed a molecular technique to accurately quantify the amount of blackleg fungus in a plant. This method is being used to identify plant tissues, in which minor gene resistance is acting to limit disease, for targeted phenotyping.

A key finding of the project is that quantitative resistance does not provide the same level of resistance to all blackleg isolates, but instead reacts with individual isolates differently in the plant. This interaction requires further characterisation as it has significant implications for the development of a robust phenotyping method. □

GRDC Codes CSP1904-007, UWA1905-006

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Photo courtesy Dr Susie Sprague

Dr Susie Sprague harvesting plants infected with blackleg for visual and molecular characterisation of disease.

Increasing the number of major genes for the management of blackleg disease of canola available to breeders and growers will help avoid the boom-and-bust cycle that results when resistance genes deployed in varieties are quickly overcome.

Photo: Andrew Beveridge

New DNA testing by the South Australian Research and Development Institute (SARDI) will enable better surveillance of disease pathogens collected by spore traps as part of the iMapPESTS project.

DNA tests sharpen decision-making

Accurate identification of fungal disease pests and plant rhizobium will help both researchers and growers make better decisions

By Dr Alan McKay, Dr Rohan Kimber

KEY POINT

- New developments in DNA testing technology are revolutionising research by identifying disease-causing pathogens in situations where traditional approaches fail and by providing an early warning system through the iMapPESTS surveillance program
- The technology is also being adapted to provide a DNA test to confirm the presence of group E and F rhizobia prior to sowing pulses

Every living organism has its own unique genetic code. Now, DNA testing methods are overtaking traditional processes to more accurately identify organisms that impact on agriculture.

Traditional methods of identifying disease-causing pathogens involve detailed visual assessments or time-consuming processes of growing the pathogen to a more identifiable stage in the life cycle.

Researchers at the Department of Primary Industries and Regions research division South Australian Research and Development Institute's (SARDI) Molecular Diagnostic Centre (MDC) are breaking down these barriers with new DNA tests.

This capability is supporting a diverse range of projects from disease identification and monitoring through to the development of a new range of tests to quantify rhizobial populations in soils.

SOIL-BORNE DISEASE IDENTIFICATION

Some important pathogens are difficult to isolate, which is frustrating for both growers and researchers.

A classic example was the identification of the pathogens to explain the severe symptoms associated with several chickpea crop failures in South Australia in 2017. This triggered a series of GRDC and South Australian Grain Industry Trust (SAGIT) projects to investigate soil-borne diseases of pulses and oilseeds nationally.

To support this research, the MDC used next-generation sequencing methods to identify potentially important fungal pathogens including oomycetes (such as *Phytophthora*), and Fusarium species that could be easily missed

using pathogen isolation techniques.

The MDC analysed DNA extracted from diseased chickpea and faba bean crops near where the original crop failures occurred and identified multiple root rot pathogens (*Phytophthora*, *Aphanomyces*, black root rot and a number of *Fusarium* sp.).

Of surprise was a number of major root pathogens reported elsewhere in the world that were already present in Australian pulse crops.

Phytophthora root rot – a serious problem for chickpeas in the northern region – was known to be caused by *Phytophthora medicaginis*. However, this research identified several other disease-causing *Phytophthora* species in chickpea, faba bean, lentil and lupin crops across the country.

While the *Phytophthora* story is interesting, *Fusarium* and possibly *Phoma* species might turn out to be more important in Australia as new information is discovered.

Fusarium species that are pathogenic on faba beans, peas, lentils and chickpeas – *Sclerotinia trifoliorum* on legume crops and *Phytophthora drechsleri* on lupins – have also been found associated with disease. This information brings us closer to finding the causative agent(s) of these root disease observations including the 2017 event and will help inform future research.

EARLY WARNING SYSTEM

SARDI's role in a Rural R&D for Profit project, iMapPESTS, includes developing spore-trapping technology to inform growers when crops are likely to be exposed to infection by specific airborne pathogens. The project's 'sentinels' provide platforms to monitor and report the presence of airborne pests and diseases affecting major agricultural sectors nationwide, including grains, cotton, sugar, horticulture, viticulture and forestry.

The project uses DNA testing to objectively and accurately track changes in spore populations over time, often triggered by seasonal conditions and farming systems.

Once established, timely information on pathogen abundance and spread will improve pest management decision-making, biosecurity responses to exotic pests and diseases, and support surveys and area freedom claims.

DNA testing from spore traps is revealing new information about pathogen behaviour. Deeper analysis of pathogen dispersal events with weather data aims to identify key triggers in the growing season to inform pathogen risk profiles.

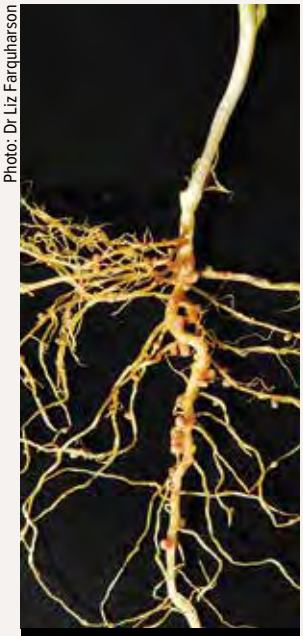
Growers can use the live results from this new-generation surveillance technology (www.imappests.com.au) to guide scouting efforts and pest control action.

Photo: Andrew Beveridge

SARDI's Dr Rohan Kimber says DNA testing from the iMapPESTS spore traps is revealing new information about pathogen behaviour.

Photo: Adam Hancock, Elders

Photo: Dr Liz Farquharson



While traditionally focused on disease testing, the Molecular Diagnostic Centre has now developed a DNA test for group E and F rhizobia, which nodulate field peas, lentils, faba beans and vetch.

Next-generation sequencing methods developed by SARDI's Molecular Diagnosis Centre played a key role in identifying pathogens associated with severe disease in several chickpea crops in SA in 2017.

IDENTIFYING RHIZOBIA

The value of the DNA tools is not just restricted to disease-causing organisms. Growers have long desired a test to determine whether rhizobial inoculants are required when sowing pulses in paddocks with a previous history of the crop. But existing methods used to study rhizobial populations in the field have proved too laborious to use as the basis of a grower service.

The MDC has been working to develop a DNA test since 2013 (DAS00115 and DAS00137), but it took until 2019 to make the breakthrough that led to the successful development of a test for group E and F rhizobia, *Rhizobium leguminosarum* bv. *viciae*. The test is extremely sensitive and, importantly, does not detect the closely related clover rhizobia (*R. leguminosarum* bv. *trifolii*).

The test was released to southern region growers in February 2021 as 'PREDICTA® rNod' and will be delivered nationally from 2022. As much as it will be welcomed by growers, this new technology will have an even greater impact on field research.

Further research is underway to develop tests for the rhizobia associated with chickpeas, lupins and mungbeans. □

GRDC Codes UOA1802-019, UOA1907-004, HIA1805-001, ST16010

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Genome sequencing leaves plant viruses no place to hide

New genome sequencing methods bolster plant quarantine screening through the rapid identification of multiple viruses

By Dr Solomon Maina, Dr Linda Zheng, Professor Brendan Rodoni

KEY POINT

- New genome sequencing techniques will enable faster testing of a broader range of plant viruses to enhance accuracy for quarantine and biosecurity investigations
- Agriculture Victoria is leading the world in developing these new techniques for the grains industry

The 2020 COVID-19 pandemic has taught us much about the potential impact of viruses on humans. Similarly, plant viruses can reduce the yield, quality, competitiveness and marketability of broadacre crops, yet once a crop is infected there is little a grower can do to limit the damage.

While the Australian grains industry has always been at risk from the inadvertent introduction of plant viruses through imported seed, it has a long-standing and rigorous approach to post-entry quarantine and diagnostics.

The potential for this defence to be strengthened further may come from advances being made in the development of high-throughput genome sequencing diagnostics for viruses in grains. This is being developed by researchers at Agriculture Victoria with GRDC investment. If successful, it will allow the detection of new pathogens that could be missed with traditional testing methods.

Genome sequencing methods enable researchers to detect multiple viruses – even those with high genetic variability. These tools are especially valuable when it is not known which pathogens might be present in a grain sample.

Traditional methods, by comparison, rely on the use of antibodies, which are limited by antisera availability, and may not detect viruses with highly variable genomes.

RESEARCHERS AT AGRICULTURE VICTORIA HAVE DEVELOPED AN AUSTRALIAN FIRST – A HIGH-THROUGHPUT GENOME SEQUENCING DIAGNOSTIC METHOD FOR VIRUSES IN GRAINS.

Photo: Dr Piotr Trebecki

Agriculture Victoria's Dr Solomon Maina is working to develop new genome sequencing methods to screen for plant viruses.

SCREENING

The main route for long-distance spread of new viruses is through inadvertent introduction via imported seed. Some may arrive on our shores through illegal importation of plant material or by natural means such as wind. While it might be tempting to close borders to material such as seed, Australian plant breeders and researchers must have access to new germplasm. This is why the onus is on a stringent process of legal importation followed by post-entry quarantine.

Virus screening at the Australian Grains Genebank (AGG) quarantine facility in Horsham, Victoria, enables the legal importation of new germplasm and also supports biosecurity investigations. While the risk of virus introduction can never be completely eliminated, improved testing procedures significantly reduce the risk.

FIRST RUNS

After five years of research, a targeted genome sequencing approach has successfully detected the exotic pea early browning virus and three endemic viruses at the same time and the approach proved substantially more sensitive than traditional methods.

The ability to detect multiple virus targets allows widespread identification of damaging plant viruses across multiple grains, oilseeds and pulse crops, and at a reduced cost.

While genome sequencing tools have been adopted for different crops in the US and parts of Europe as part of their genetic certification programs, Australia is leading this approach for grains.

These new testing regimes may one day provide comprehensive universal pathogen surveillance that will also protect market access for Australia grains. □

GRDC Code DAV1607-011

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New tools reveal more complex virus landscape

Accurate identification of plant viruses is changing our understanding of their incidence and how they impact on pulse crops

By Joop van Leur, Dr Murray Sharman, Dr Benjamin Congdon, Dr Piotr Trebicki

Photo: Dr Murray Sharman

Molecular tools have led to the discovery of phasey bean mild yellows virus, which causes leaf reddening and stunting, as shown in a desi chickpea crop at Kingsthorpe in Queensland.

■ New molecular tools are underpinning dramatic improvements in the ability to identify and study viruses in pulses.

Australian losses affecting one or more pulse species have, to date, been attributed to nine different viruses, but in the past decade research has shown much greater diversity than originally thought. There also appears to be large differences within certain virus species in their harmfulness to different host species.

However, symptoms in the field may be the same for different virus species, making effective diagnostic tools a necessity for plant-virus research. Accurate identification is a prerequisite to developing effective control strategies for specific virus–host combinations.

A four-year GRDC investment led by the New South Wales Department of Primary Industries is shedding new light on these microbial pests. The project is using new molecular tools to study pulse viruses in collaboration with Western Australian Department of Primary Industries and Regional Development, Queensland Department of Agriculture and Fisheries, the University of Queensland, Agriculture Victoria and the International Center for Agricultural Research in the Dry Areas.

WHAT'S IN A NAME?

In 2014, widespread virus damage to canola and pulse crops in south-eastern Australia was attributed to beet western yellows virus (BWYV), diagnosed using the antibody assays available at the time. More recently, research using molecular diagnostic tools and whole genome characterisation has revealed that BWYV is actually not present in Australia. Rather, a complex of genetically distinct turnip yellows virus (TuYV) strains was behind the outbreak and preliminary data suggests they may also have biological differences that could affect management and resistance breeding.

Molecular tools have also led to the discovery of two new viruses, also previously misidentified as BWYV – phasey bean mild yellows virus (PBMYV) and faba bean polerovirus 1 (FBPV-1).

Two distinct strains of PBMYV were detected from 11 field host species from across Australia, including seven important grain legume crops. This suggests that its importance in agriculture may have gone unrecognised due to the inability to correctly identify the virus. PBMYV is transmitted by cowpea aphids, not by the green peach aphid – the main vector of TuYV.

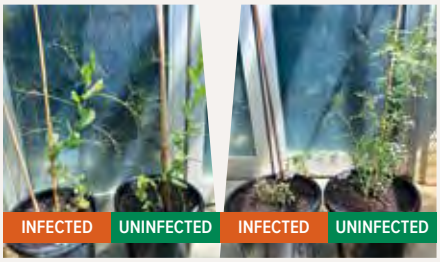
FBPV-1 was found in four grain legume species across northern NSW, but as yet there is limited data on its importance in disease outbreaks and the aphid vector remains unknown.

KEY DIFFERENCES

We now know that TuYV and PBMYV have quite distinct biological traits, but the genetic diversity within these species may also translate to differences in vectors, pathogenicity and genetic resistances. Preliminary experiments are only just beginning to investigate these differences.

There is still much to learn about the impact of viruses on crops and the factors that will lead to infection, disease or yield loss. Recent research has shown that up to 40 per cent of yield losses in field peas and lentils may result from TuYV infection, despite no visible symptoms.

Figure 1: Kaspa$^{\Phi}$ field peas (left) are highly susceptible to soybean dwarf virus infection but relatively tolerant, producing very little disease, while PBA HatTrick$^{\Phi}$ chickpeas (right) are relatively resistant but highly sensitive once infected.



Source: Dr Benjamin Congdon

Crop susceptibility and sensitivity to a particular virus can vary depending on the environmental conditions, growth stage and even the specific crop variety. For instance, the chickpea variety PBA HatTrick$^{\Phi}$ is relatively resistant to soybean dwarf virus infection, but once infected it is highly sensitive, resulting in severe disease that often leads to plant death (Figure 1). In contrast, the field pea Kaspa$^{\Phi}$ becomes infected easily but is relatively tolerant, incurring very little yield loss. □

GRDC Code DAN1504-009 (DAN00202)

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Griffith University's Dr Prabhakaran Sambasivam scoring Ascochyta blight on chickpea plants in growth chambers.

Photo: Justin Ma

Plan of attack for aggressive Ascochyta isolates

Work is underway to limit the increasing aggressiveness of Ascochyta blight in chickpeas

By Professor Rebecca Ford, Dr Prabhakaran Sambasivam, Yasir Mehmood, Melody Christie, Dr Niloofar Vaghefi, Associate Professor Adam Sparks, Dr Ido Bar

KEY POINT

- Ascochyta blight in chickpeas has become more aggressive over the past five years
- The proportion of isolates collected annually from all major growing regions across Australia where Ascochyta epidemics have occurred are able to cause severe disease is as high as 70 per cent for PBA HatTrick$^{\phi}$
- Researchers are targeting pathogen biology and genetics to identify future opportunities to overcome this aggressiveness

■ Ascochyta blight pathogen in chickpeas is becoming more aggressive against commonly grown varieties. Caused by the fungus *Ascochyta rabiei*, it arrived in Australia in the 1970s, most likely on infected seed. Ascochyta has since established across all Australian chickpeas growing regions and has rapidly evolved to become highly pathogenic – meaning it has overcome resistance in many varieties.

To develop more-resistant varieties and provide useful advice for growers, we need to understand the mechanisms that enable the pathogen to overcome both genetic resistance and our best management practices.

RESISTANT ISOLATES ON THE RISE

As part of a six-year GRDC investment (2013–19) researchers from Griffith University and collaborators from NSW Department of Primary Industries, South Australian Research and Development Institute (SARDI) and Agriculture Victoria collected *A. rabiei* isolates annually from all growing regions where Ascochyta epidemics occurred. Surprisingly, extremely low levels of molecular diversity were detected, irrespective of the source region or chickpea variety.

The ability of these isolates to cause severe disease on a set of resistant lines was measured in plant growth chambers.

Despite the lack of diversity, subsets of these isolates caused severe disease on some of the industry's most resistant varieties, including PBA HatTrick$^{\phi}$, Genesis™ 090 and PBA Seamer$^{\phi}$.

In fact, the proportion of highly aggressive isolates in the background population has increased since 2015 (Figure 1). In 2020, the percentage of isolates

sampled from the field that were highly damaging to PBA HatTrick(ϕ) was 70 per cent, 64 per cent were highly damaging to Genesis™ 090 and 62 per cent were highly damaging to PBA Seamer(ϕ).

Isolates able to cause severe disease on ICC3996, which is commonly used as a resistance source within the Australian chickpea breeding program, had also increased to 33 per cent in 2020.

The most damaging isolates have been supplied annually to breeders for use in selecting the most resistant lines to bring forward for commercialisation.

The increase in isolate aggressiveness observed in this long-term study has likely occurred through pathogen adaptation, whereby the fungus has evolved to make more highly aggressive isolates in response to selection pressure applied through environmental factors and farming practices.

While external environmental factors cannot be controlled, changes in the pathogen population towards evolving isolates with increased aggressiveness can be reduced by adhering to recommendations for crop rotation and fungicide use.

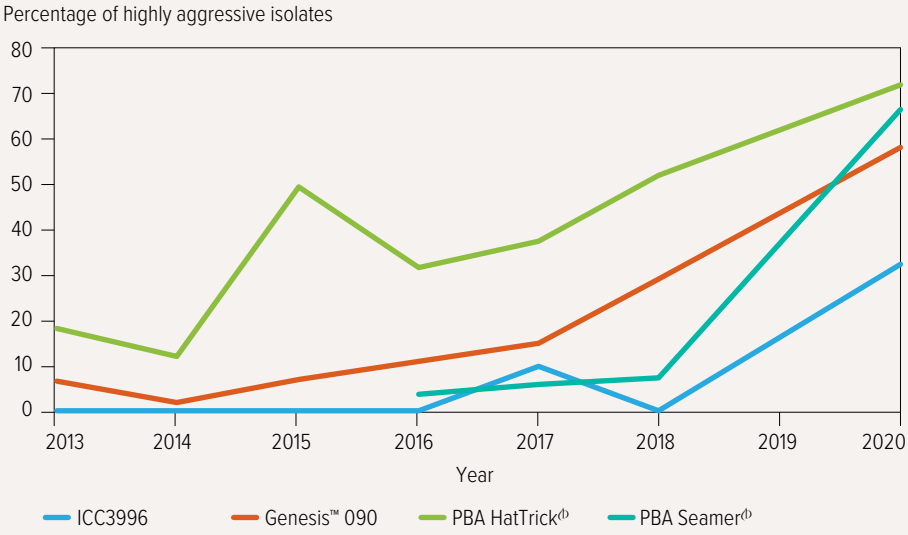
To understand the ability of the pathogen to evolve to overcome current management recommendations, work at Griffith University is focusing on better understanding of the biology, population dynamics and epidemiology of the disease. This is part of the new GRDC investment in collaboration with SARDI, Agriculture Victoria, University of Southern Queensland and Western Australian Department of Primary Industries and Regional Development.

GENETIC TOOLS

In their previous work, researchers at Griffith University found that isolates of different aggressiveness levels behave differently on different chickpea cultivars. Some grow and cause severe disease very fast, especially without proper management.

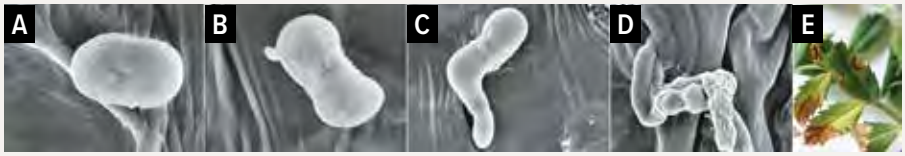
The new work aims to identify the genetic basis of isolate aggressiveness. Researchers are looking for molecular sequences that correlate with the ability of an isolate to cause disease on a chickpea variety that contains a particular resistance gene combination.

Figure 1: In recent years there has been an increase in the frequency of isolates of *Ascochyta rabiei* that are highly aggressive against common chickpea varieties. The proportion of isolates aggressive against ICC3996 – the breeding line commonly used as a resistance source within the Australian chickpea breeding program – has also increased.



Source: Professor Rebecca Ford

Figure 2: Microscope images of the process of *Ascochyta rabiei* infection of a chickpea leaf. A) the *A. rabiei* fungal spore lands on the chickpea leaf; B) the spore germinates (6 to 12 hours); C) the spore grows a germination tube (12 to 16 hrs); D) the germination tube penetrates the chickpea leaf through a stomata opening and colonises the internal tissues (16 to 24 hrs); and E) disease symptoms appear on the chickpea leaves (4 to 7 days).



Source: Yasir Mehmood, Griffith University

The aim is to develop a method to 'pathotype' an isolate and determine its level of risk to the chickpea industry. A 'pathotyping tool' that will quickly and accurately inform growers, pathologists and breeders on the isolate population present at a particular chickpea-growing location would help with variety selection and chemical and cultural disease management decisions.

To develop the pathotyping tool, researchers will investigate *A. rabiei* isolates collected from across all chickpea-growing regions to identify genome sequences that are significantly correlated with severe disease incidence. This will also uncover the genetic controls of isolate aggressiveness.

It will provide a detailed understanding of the behaviour of *A. rabiei* and the governing molecular sequences expressed by the pathogen during the infection and chickpea colonisation processes that lead to disease and crop loss (Figure 2).

Together with the 'pathotyping tool', this will inform the screening for resistance breeding material and disease management packages that are locally relevant.

This research is one of five new four-year research programs invested by GRDC to develop better genetic and management solutions for Ascochyta in chickpeas. The other programs will be led by the University of Adelaide, Agriculture Victoria, CSIRO and the International Center for Agriculture Research in Dry Areas (ICARDA) in Egypt. □

GRDC Code UM00052, GRI2007-001

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Photo: Lisa Kelly

Fusarium wilt symptoms on a Jade-AU® mungbean crop in southern Queensland in March 2020. Infected plants develop wilting symptoms, root rot, stunting and vascular discolouration.

Photo: Murray Sharman, DAF

Grafting of phytoplasma-infected plant tissue on to healthy peanut plants was shown to cause phytoplasma, which is also closely associated with the development of peanut kernel syndrome.

Summer crop disease breakthroughs

By Lisa Kelly, Dr Kirsty Owen, Dr Murray Sharman, Dr Peter Vukovic, Dr Dante Adorada

KEY POINT

- Sorghum, cotton, barley, chickpeas and soybeans have been identified as alternative hosts for Fusarium wilt in mungbeans, but as sorghum is only a poor host it may be a suitable break crop
- Brown leafhopper was confirmed as a vector of phytoplasma to peanuts and pigeon peas

■ Research into summer crop diseases in the northern region has shed new light on Fusarium wilt in mungbeans and phytoplasma infection in grain legumes.

The GRDC-invested research improves the knowledge of summer crop diseases and their management while providing essential pathology support for other GRDC programs. It has been led by the University of Southern Queensland in collaboration with the Queensland Department of Agriculture and Fisheries (DAF).

FUSARIUM WILT IN MUNGBEANS

Fusarium wilt has become an increasing challenge for mungbean growers and can cause substantial losses when associated with other stresses such as waterlogging.

While mungbeans are the only crop that demonstrates typical Fusarium wilt symptoms, researchers have now identified a much broader potential host range.

They have isolated Fusarium pathogens from the roots of asymptomatic hosts – sorghum, cotton, barley, chickpeas and soybeans – indicating that these crops may contribute to survival of the pathogens between mungbean crops.

Of the crops tested, sorghum may offer a more suitable crop rotation choice in paddocks with a history of the disease, as pathogens were only isolated from 20 per cent of sorghum plants in pot trials compared with 60 per cent or more in other crops tested.

Potential interaction between mungbean Fusarium wilt pathogens and the root lesion nematode *Pratylenchus thornei* was also characterised in controlled glasshouse experiments.

For the first time brown leafhopper was confirmed as a vector of phytoplasma to peanut and pigeon peas.

While both cause disease by themselves, the symptoms of wilt were more severe in the presence of *P. thornei*. The dry weight of mungbeans and pod numbers decreased as the rate of Fusarium and *P. thornei* inoculum increased.

As both *P. thornei* and Fusarium are widespread, a PREDICTA® B test may help growers to weigh up disease risk prior to sowing.

PHYTOPLASMA

The research also identified the phytoplasma species causing disease in grain legumes and identified a new vector.

Phytoplasma infection in grain legumes, such as puffy pod in mungbeans and peanut kernel shrivel in peanut, has caused sporadic but serious yield losses in recent years. Leafhoppers were commonly reported vectors of phytoplasma, but no species had been confirmed previously as capable of transmitting phytoplasma to grain legumes in Australia.

A real-time polymerase chain reaction (rt-PCR) was developed to provide rapid identification of phytoplasma species infecting plants and insects. This allows researchers to amplify segments of DNA, making them easier to detect.

For the first time, brown leafhopper (*Orosius orientalis*) was confirmed as a vector of phytoplasma to peanut and pigeon peas. The rt-PCR technique was able to detect phytoplasma directly from infected brown leafhoppers in a manner that may enable potential vector species to be inferred without the need for time-consuming transmission tests.

When plant tissue infected with phytoplasma was grafted on to infection-free peanut plants, about 66 per cent developed typical little-leaf symptoms. In infected plants, 62 per cent of kernels developed kernel shrivel compared with none in healthy plants.

Growers should monitor weeds and surrounding crops for phytoplasma infection and outbreaks of leafhoppers and maintain good farm hygiene to minimise the risk of infected weeds acting as a source of infection to nearby crops. □

GRDC Code USQ1907-001

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Broadleaf rise adds to disease profile

A changing crop mix has seen the rise of viruses and Sclerotinia in broadleaf crops

By Joop van Leur, Dr Kevin Moore, Dr Kurt Lindbeck

■ Viruses and Sclerotinia stem rot are two disease threats that have come under increased scrutiny in New South Wales in recent years. The rise in these diseases has resulted from an increasing frequency of broadleaf crops grown in continuous cropping programs. Pulse and oilseed viruses can easily fly under the radar with symptoms that are often indistinguishable from those caused by abiotic stress factors and herbicides.

A virus diagnostics laboratory was established at the Department of Primary Industries' Tamworth Agricultural Institute with GRDC investment in 2015. The main virus diagnostic tool used is tissue-blot immunoassay, which is a quick and economic method used to process large numbers of individual plant samples.

In 2020, more than 7000 pulse samples, either submitted by growers and agronomists or collected by researchers during surveys or from on-farm field trials, were tested for up to eight viruses or virus groups (Table 1).

The results showed that a severe virus epidemic in faba bean crops in northern NSW, characterised by a wide range of symptoms, was mainly caused by bean yellow mosaic virus (BYMV) with localised co-infections by alfalfa mosaic virus (AMV). High levels of cucumber mosaic virus (CMV) were also detected in narrow-leafed lupins and lentils.

A seed testing program has been initiated for CMV in narrow-leafed lupins and BYMV in faba beans.

Results showed that in-crop CMV infection levels in narrow-leafed lupins were strongly related to seed-transmitted virus and growers should not use seed from CMV-infected paddocks.

While testing showed that seed transmission of BYMV is not of importance in commercial faba bean crops, growers are advised to avoid using seed from severely-infected paddocks as seedling vigour may be reduced, making the crop more vulnerable to aphid-driven viral infection.

SCLEROTINIA

The Sclerotinia fungus is a good example of how the increasing frequency of broadleaf crops has made it easier for the fungus to persist and damage crops when conditions are favourable.

Pulse crop surveys undertaken during the dry seasons of 2018 and 2019 across southern and central NSW detected the disease as discreet infections of the upper taproot and stem base within mainly chickpea and narrow-leafed lupin crops. These symptoms could have been easily missed or mistaken for drought stress.

With more favourable conditions in 2020, surveys detected Sclerotinia in 62 per cent of the 45 pulse crops tested, including narrow-leafed and albus lupins, field peas, chickpeas, faba beans and lentils. The highly favourable conditions in the spring of 2020 meant even low levels of fungal inoculum caused significant levels of disease.

The sclerotia (survival structures of the fungus) produced in 2020 present a significant risk to broadleaf crops in 2021 and beyond. Sclerotia can readily survive in soils for five years – and sometimes up to 10 years. This presents a high disease risk for growers following double-break rotations where canola is sown after a pulse crop, especially in medium to high-rainfall districts. In these situations, growers will need to budget for foliar fungicide applications to manage Sclerotinia disease or opt for a non-host crop.

The NSW Department of Primary Industries provides diagnostics for pulse and oilseed diseases to NSW growers and advisers, as well as research into disease behaviour and management, with GRDC co-investment, through the Grains Agronomy and Pathology Partnership (GAPP). □

GRDC Code DPI1507-002 (DAN00213)

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Photo: Jeb Jackson, NSW DPI

Sclerotinia infection of lupins (albus is shown) was common in central and southern NSW in 2020.

Table 1: The main viruses detected in collected and submitted samples of pulses grown in NSW in 2020. Detection rates greater than 10 per cent are highlighted. Viruses detected in less than five plants (subclover stunt virus and clover yellow vein virus) are not included.

Crop	Number of plants tested	Percentage of positive plants as determined by tissue-blot immunoassay				
		Bean leaf roll virus (BLRV)	Luteoviruses other than BLRV	Bean yellow mosaic virus (BYMV)	Alfalfa mosaic virus (AMV)	Cucumber mosaic virus (CMV)
Faba beans	2236	2	5	62	12	0
Chickpeas	2008	0	1	0	6	1
Lentils	1794	2	1	1	28	31
Lupins	576	1	1	13	17	59
Medics	335	5	15	15	8	0
Vetches	108	0	0	9	4	0
Lucerne	70	1	0	0	27	0
Other pasture legume species	68	0	2	0	0	0

Source: Joop van Leur

Surveys measure the disease challenge

Disease build-up in 2020, due to wetter conditions across many areas, highlights risks for 2021

Photo: Ciara Beard

DPIRD's Geoff Thomas inspects an albus lupin crop for disease. Surveys of commercial pulse crops enable researchers to detect emerging threats and help inform disease advice to growers and advisers.

■ Crop surveys enable the early detection of diseases in commercial crops and ensure that timely messages are provided to help growers and advisers protect crops.

The surveys allow pathologists to identify any new or emerging threats and keep track of the level of control being achieved in the field, which may be associated with changes in disease pathotypes.

The information collected during disease surveillance is also critical for both investment and research priorities, and samples collected may directly contribute to GRDC research programs.

GRDC's national surveillance program for pulses was undertaken in 2019 and 2020 by the Western Australian Department of Primary Industries and Regional Development (DPIRD), NSW Department of Primary Industries (DPI), South Australian Research and Development Institute (SARDI), Agriculture Victoria and Queensland Department of Agriculture and Fisheries. Canola survey results are included for WA and NSW with additional comment provided by Marcroft Grains Pathology (see page 4).

No exotic diseases were detected, supporting Australia's export market access and 'area freedom' status for diseases not present in Australia.

WESTERN AUSTRALIA

In WA, 29 lupin, five chickpea, nine lentil and two faba bean paddocks were sampled across 2019 and 2020. The timing of rain in 2020 favoured Sclerotinia in lupins and canola.

Lupin diseases found in 2020 were Sclerotinia stem rot, Phomopsis and a low level of anthracnose. Anthracnose and brown spot incidence were higher in 2019 than 2020.

Disease in other pulses was minimal due to fungicide application but included Ascochyta blight in chickpeas in 2020 and Botrytis grey mould in lentils in 2019.

There were 68 canola paddocks surveyed across 2019 and 2020. Sclerotinia stem rot was the most common disease and incidence was five times greater in 2020. There was more upper canopy blackleg infection in 2020. Powdery mildew was only found in 2020.

NSW AND QUEENSLAND

In southern and central NSW, 32 narrow-leaf and 13 albus lupin, 14 chickpea, seven lentil, 15 field pea, 14 faba bean and 30 canola crops were sampled across 2019 and 2020. In 2019, the development of Sclerotinia in pulses was higher than expected under dry conditions. In pulses, Ascochyta blight (in field peas and chickpeas) and virus diseases were found frequently.

The wetter conditions in 2020 favoured Sclerotinia infection, with the disease found in 62 per cent of all pulses. Virus and Botrytis diseases were also frequently detected. Blackleg leaf lesions and/or stem canker were found in every canola crop surveyed.

Given the level of disease build-up in 2020, paddocks in medium to high-rainfall areas will be at greater risk of disease in 2021, especially those identified with Sclerotinia.

In northern NSW and southern Queensland, 210 chickpea and lentil paddocks and 50 faba bean paddocks were sampled across 2019 and 2020. Viruses were the most common diseases found in both years, although less so in drier conditions in Queensland in 2020.

While there were few crops showing symptoms of fungal diseases, PREDICTA® B testing in 2019 detected Botrytis, Ascochyta and charcoal rot in chickpeas and in faba beans. Despite being known to be widespread in the region, Aphanomyces root rot and black root rot were not detected in the dry conditions in 2019.

In Queensland, 18 peanut, 36 mungbean and 10 soybean crops were surveyed in 2020. The most common diseases in mungbeans were tobacco streak virus, Fusarium wilt and powdery mildew. In peanuts, Fusarium root rot was common and, to a lesser extent, phytoplasma. In soybeans, the warm temperatures and high rainfall in northern Queensland in early 2020 led to major outbreaks of anthracnose and target spot.

SOUTH AUSTRALIA

In SA, 11 chickpea, 10 lentil, 10 field pea and nine faba bean crops were inspected in 2020. At least one foliar disease was observed in 73 per cent of the samples. However, disease levels were generally low, likely due to fungicide applications and the dry June–July.

All field pea plants showed blackspot at varying levels. Levels of Ascochyta blight in chickpeas, faba beans and lentils were low, with some crops free of disease. Downy mildew was detected at low levels, but chocolate spot was moderately high in some south-eastern crops.

VICTORIA

In Victoria, 35 chickpea, 70 lentil, two field pea, 23 faba bean, six lupin and four vetch paddocks were sampled across 2019 and 2020, with disease severity generally low. Ascochyta blight was common in chickpeas and faba beans and, to a lesser extent, lentils. Cercospora leaf spot and chocolate spot were found in all faba bean paddocks. Disease levels in lupins, vetch and field peas were low. Virus testing found turnip yellows virus in chickpeas, lentils and faba beans; cucumber mosaic virus in lentils; and bean leafroll virus in lentils and faba beans were the most prevalent viruses. PREDICTA® B testing found root lesion nematode, *Pratylenchus neglectus*, in the majority of paddocks, and the pathogens that cause Pythium root rot, charcoal rot and Rhizoctonia were also detected frequently. □

GRDC Codes DAW1907-002, DPI1507-002 (DAN00213), DAQ1907-001, UOA2007-006, DJP1907-004

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Photo: Lisa Kelly

Warm temperatures and large amounts of rainfall in early 2020 in northern Queensland led to major outbreaks of anthracnose and target spot in soybeans in association with soybean stem fly.

Photo courtesy Kevin Moore

NSW DPI's Dr Kevin Moore inspecting Ascochyta infection in chickpeas in northern New South Wales.

Disease services support pulse management

Timely information about spore release, disease incidence and shifting pathotypes has enabled South Australian growers to manage pulse diseases

By Dr Jenny Davidson

KEY POINT

- Disease monitoring and diagnostic services have provided decision-making support for South Australian growers
- Spore traps have demonstrated the conditions that lead to increased disease risk for pulses
- Monitoring of changes to disease pathotypes has informed disease management advice

Growers are increasingly taking advantage of disease diagnostic services for making timely decisions about preventive fungicide applications in pulses, cereals and oilseeds. In South Australia, this service, which includes up-to-date information on disease threats and pathotype changes, is provided through GRDC investment in the South Australian Research and Development Institute (SARDI).

This involves deploying spore traps. In 2018 and 2019, traps set up at eight sites across SA captured the airborne spores of 13 pathogens, including Ascochyta blight of chickpeas, lentils and field peas, Botrytis diseases of pulses (chocolate spot and Botrytis grey mould) and Sclerotinia. No spores of chickpea Ascochyta blight were detected, confirming that this disease is primarily seed and stubble-borne.

Botrytis grey mould spores were regularly detected, demonstrating that this disease is entirely dependent on weather conditions and is favoured by high humidity and temperatures above 10°C. Growers need to apply fungicide sprays to susceptible crops under these conditions.

Sclerotinia stem rot was detected when the average air temperature was below 10°C and the relative humidity was 70 to 100 per cent, or it was raining. Further research is investigating the potential of predicting spore showers to further help growers with fungicide decisions.

Correct disease identification is vital to ensure appropriate disease management strategies and efficacious fungicides. In 2018 and 2019, the SARDI diagnostics service analysed 292 pulse crop samples, detecting Ascochyta blight, Stemphylium blight, Botrytis diseases, Sclerotinia and a range of root diseases.

Another 165 samples were forwarded to Agriculture Victoria in Horsham for virus testing, detecting a low level of turnip yellows virus (previously reported as beet western yellows virus), pea seed-borne mosaic virus and cucumber mosaic virus. These viruses are readily detected in pulse crops and can rapidly escalate in seasons with high aphid populations. Pea seed-borne mosaic virus and cucumber mosaic virus are seed-borne and growers are advised to regularly test seed lots to ensure infection levels are kept below the recommended 0.5 per cent.

PATHOGENICITY CHANGES

The project monitored pathotype changes to help growers, advisers and breeding programs to improve crop type, variety and fungicide selection.

The majority of *Ascochyta fabae* isolates were the widespread Pathotype 2, able to cause significant lesions on Farah$^{\Phi}$, PBA Zahra$^{\Phi}$ and PBA Rana$^{\Phi}$ faba beans. This information meant that disease management recommendations for these varieties were updated to include foliar fungicide sprays for Ascochyta blight. For the first time, a possible third pathotype, aggressive on PBA Samira$^{\Phi}$, is emerging and appropriate isolates have been included in the resistance breeding program at the University of Adelaide. Continued monitoring will be critical to confirm this shift.

Isolates of *A. lentis* that can infect PBA Hurricane XT$^{\Phi}$ lentils are regularly monitored through separate GRDC investment. This research has shown they are likely to spread through the environment. Stubble from lentil crops sprayed with fungicide to control Ascochyta blight still remains a source of infection for the following year's crops and growers should rotate and isolate similar crops from last year's stubble to prevent disease being carried over. □

GRDC Code UOA1807-012

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Photo: Dr Rohan Kimber, SARDI

SARDI's Sara Blake, Jamus Stonor and Michelle Russ test faba bean varieties for reaction to different isolates of *Ascochyta fabae*.

Photo: Jamus Stonor, SARDI

Spore trap and associated automatic weather station at Bordertown in 2018.

Robust disease ratings for pulses now available

By Dr Joshua Fanning, Dr Jenny Davison

A new national pulse disease rating system has been implemented to provide consistent and independent disease ratings across the country, following the expansion of GRDC's National Variety Trials (NVT) disease-rating program to pulse crops in 2019. The independent disease ratings for pulses (Table 1) were developed using processes adapted from those established and proven for wheat and barley.

DISEASE RATINGS

The definitions for each pulse disease rating category have been updated to reflect the appropriate disease management strategy, which is more informative for growers and advisers. There may be some changes to the previous pulse disease ratings in the update, but there will be better alignment between crops and diseases nationally.

KEY RATING DEFINITIONS INCLUDE:

- **resistant (R):** No symptoms are visible and no fungicides are required;
- **moderately resistant (MR):** The disease may be visible but will not cause significant plant damage or loss. However, under high disease pressure or highly favourable environments or conditions, fungicide applications may be required, for example to prevent seed staining;
- **moderately resistant to moderately susceptible (MRMS):** The disease symptoms are moderate and may cause some yield and/or seed quality losses in conducive conditions. Fungicide applications, if applicable, may be required to prevent yield loss and seed staining;
- **moderately susceptible (MS):** Disease symptoms are moderate to severe and will cause significant yield and seed quality loss in the absence of fungicides in conducive seasons, but not complete crop loss; and
- **susceptible (S):** The disease is severe and will cause significant yield and seed quality loss, including complete crop loss in the absence of fungicides, in conducive conditions.

SCREENING PROCESS

Each year 51 disease screenings are conducted across Australia by plant pathologists. These are done in either the field and/or glasshouse to maximise disease expression. In glasshouse conditions, industry-relevant isolates are chosen to infect test plants. Changes in pathogenicity (harmfulness) for some diseases are regularly monitored through separate GRDC investments, and this information influences the choice of isolate used in the NVT tests. This ensures a field-relevant disease rating is obtained. Due to shifts in the pathogenicity, it is important that growers use up-to-date variety ratings to make variety and disease management decisions appropriate for their situation. At the end of the season, data collected nationally via the NVT program is collated and disease ratings assigned by experts for each disease. The disease ratings are updated annually and made available in state-based disease guides and on the NVT website. This information can lead to a change in variety selection where disease risk is high, and it will support effective disease management decisions for the selected variety. □

GRDC Codes DAS1905-013, DJP1905-002, DAN1907, USQ1907-002, WAA1905-001

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Photo: Luise Fanning

Agriculture Victoria's Dr Joshua Fanning says robust disease ratings for pulses were developed using processes adapted from those that were established for wheat and barley.

Table 1: The crops and diseases included in the new National Variety Trials screening that commenced during 2019, and the states where they will be screened.

Crop	Disease	Screening state
Chickpeas	Ascochyta blight	SA, Victoria, NSW
	Botrytis grey mould	NSW
	Phytophthora root rot	NSW
	Pratylenchus neglectus (resistance)	Victoria, Queensland
	Pratylenchus neglectus (tolerance)	Queensland
	Pratylenchus thornei (resistance)	Victoria, NSW, Queensland
	Pratylenchus thornei (tolerance)	Queensland
Faba beans	Ascochyta blight	SA, Victoria
	Cercospora leaf spot	SA
	Chocolate spot	SA
	Pratylenchus neglectus (resistance)	Victoria, Queensland
	Pratylenchus thornei (resistance)	Victoria, NSW, Queensland
	Rust	NSW
Field Peas	Ascochyta blight (synonym: black spot)	WA, SA, Victoria
	Bacterial blight	NSW
	Downy mildew	SA
	Powdery mildew	SA
	Pratylenchus neglectus (resistance)	Victoria, Queensland
	Pratylenchus thornei (resistance)	Victoria, Queensland
Lentisl	Ascochyta blight	SA, Victoria
	Botrytis grey mould	SA, NSW
	Pratylenchus neglectus (resistance)	Victoria
	Pratylenchus thornei (resistance)	Victoria
Lupins	Anthracnose	WA
	Brown spot	WA
	Cucumber mosaic virus	WA
	Phomopsis	WA
	Pleiochaeta root rot	WA
	Sclerotinia	WA

Source: Dr Joshua Fanning

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