



Australian Brassica Conference

July 21st – 23rd 2025

Grains Innovation Park

Horsham, Victoria

Scientific Program Day 2: Tuesday 22nd July 2025

Session	Time	Presenter	Title	Theme
1	Session Chair: Angela Van de Wouw			
	8:30	Angela Van de Wouw and Steve Marcroft	Welcome	
	8:40	1.1 Sarah Clarry (AOF)	Current status of the Australian oilseeds industry in the global setting	Plenary
	9:20	1.2 Kenton Porker (CSIRO)	Canola yield frontiers: from critical periods to system synergies	Plenary
10:00 Morning tea				
2	Session Chair: Willow Liddle			
	10:30	2.1 Rohan Brill (BrillAg)	Hyper-yielding canola research 2020-2023: management factors to push canola yield beyond 5 t/ha	Agronomy
	11:00	2.2 Matthew Nelson (CSIRO)	Genetic solutions for deep sowing: Progress towards long hypocotyl canola	Genetics and breeding
	11:30	2.3 Andrew Fletcher (CSIRO)	Increasing canola establishment through an understanding of sowing depth, soil strength and sowing date responses	Agronomy
	11:45	2.4 Ash Wallace (AgVic)	Stubble trouble for canola establishment	Agronomy
	12:00	2.5 Florence Danila (ANU)	SCAN: an automated phenotyping tool for real-time capture of leaf stomatal traits in canola	Emerging technologies
	12:15	2.6 Steve Marcroft (MGP)	Why did blackleg management in canola actually work?	Crop protection
12:30 Lunch				
3	Session Chair: Kurt Lindbeck			
	1:30	3.1 Michael Nash (UA)	Successful management of invertebrate threats to Canola – comparing contrasting seasons	Crop protection
	2:00	3.2 Chathurika Amarathunga (CSIRO)	Seeing the unseen: Field-scale detection of blackleg crown canker in canola using UAV-mounted hyperspectral sensors	Emerging technologies
	2:30	3.3 Mohamed Zakeel (CSIRO)	Hyperspectral sensing: Advancing non-invasive phenotyping for quantifying canola blackleg resistance	Emerging technologies
	2:45	3.4 Willow Liddle (Advanta)	Agronomic and financial outcomes associated with retaining seed from both Spring and Winter canola hybrids	Agronomy
	3:00	3.5 Sheng Chen (UWA)	Allohexaploid <i>Brassica</i> in canola genetics and breeding	Genetics and breeding
	3:15	3.6 Muhammad Arslan (ANU)	Engineering disease susceptibility genes for durable resistance against blackleg disease in canola	Crop protection
3:30 Afternoon tea				
4	Session Chair: Alex Emerson			

	4:00	4.1 Luke Barrett (CSIRO)	Phenotypic stability in quantitative resistance to blackleg crown canker: Exploring the roles of canola genetics, pathotype, and environment	Crop protection
	4:15	4.2 Andrew Wherrett (LivingFarm)	Improving canola establishment in the medium and low rainfall zones of Western Australia	Agronomy
	4:30	4.3 Saba Rabab (CSIRO)	Quantifying blackleg severity in canola using deep learning and a web-based scoring tool	Emerging technologies
	4:45	4.4 Irene van den Berg (AgVic)	Accelerating durable resistance: AI-augmented speed breeding for blackleg in canola	Genetics and breeding
	5:00	Finish		
6:00-11:00 Conference Dinner (Horsham Town Hall)				

Scientific Program Day 3: Wednesday 23rd July 2025

Session	Time	Presenter	Title	Theme
5	Session Chair: David Pike			
	8:30	5.1 Jeremy Whish (CSIRO)	Pushing the limit of canola productivity in Sth NSW: A 20-year journey	Agronomy
	9:00	5.2 Sheng Chen (UWA)	Pre-breeding for heat and drought tolerant canola	Genetics and breeding
	9:30	5.3 Alexandre Boyer (CSIRO)	Automated canola phenology detection combining UAV imaging and deep learning	Emerging technologies
	9:45	5.4 Alec McCallum (UM)	Detection of SDHI resistance in Australian <i>Leptosphaeria maculans</i> populations	Crop protection
	10:00	5.5 Justin Kudnig (Advanta)	Agronomic and value equation outcomes associated using a treatment matrix of different canola seed sizes by plant populations by seeding depth	Agronomy
	10:15	5.6 Sally Norton (AgVic)	New genomic resources in the Australian Grains Genebank: Delivering transformative impact to the Australian <i>Brassica</i> industry	Genetics and breeding
10:30 Morning tea				
6	Session Chair: Ray Cowley			
	11:00	6.1 Angela Van de Wouw (UM)	The ins and outs of fungicide resistance	Crop protection
	11:30	6.2 Xiaoce Ma (ANU)	Improving pod shatter resistance in canola through gene editing	Genetics and breeding
	11:45	6.3 Susie Sprague (CSIRO)	Towards 2050: Future-proofing pest and disease control in canola	Crop protection
	12:00	6.4 Tao Luo (CSIRO)	Water uptake kinetics of canola seeds	Agronomy
	12:15	6.5 Sadia Majeed (ANU)	Assessing photosynthetic capacity in canola: Integrating leaf and pod photosynthesis	Physiology
	12:30	6.6 Reshma Roy (ANU)	Harnessing genetic transformation and gene-editing technologies to unlock the potential of <i>Brassica carinata</i> as a sustainable cover crop	Emerging technologies
	12:45	6.7 Nay Chi Khim (NSW DPIRD)	Introgression and characterisation of the <i>FUL</i> gene from <i>Brassica carinata</i> for enhanced pod shatter resistance in canola (<i>B. napus</i>)	Genetics and breeding
1:00 Lunch				

Management for Hyperyielding Canola Crops

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ABSTRACT

The Hyperyielding Crops Project included canola research conducted from 2020 to 2025 in high yield potential environments in New South Wales, Victoria, South Australia and Western Australia. At the commencement of the project, it was hypothesised that to achieve > 5 t/ha canola would require an increase in nitrogen (N) and fungicide input, as well as selection of hybrids (such as European winter canola) with higher yield potential than Australian bred spring canola hybrids. However, trials conducted across 12 site year combinations didn't support the hypotheses. The grain yield response to nitrogen plateaued at 75 kg N/ha application rates in 8/12 nutrition trials and the average response to fungicide (seed treatment plus two foliar fungicides compared with nil fungicide) was 0.28 t/ha. The highest yielding variety in 13/15 sites was an Australian bred spring hybrid, with a winter hybrid the highest yielding variety in 2/15 sites (Millicent in South Australia, 2022 & 2023). At 11/15 sites, the application of animal manure (or its inorganic nutrition equivalent) resulted in the highest yield at the site, highlighting the need for fertility beyond fertiliser N input. We conclude that achieving canola yield > 5 t/ha requires a combination of pragmatic agronomic tactics (variety choice, nutrient input and fungicide use) combined with a farming system that builds soil fertility and minimises the risk of crop diseases.

Key words: Manure, nitrogen, hybrid, fungicide, farming systems

Genetic solutions for deep sowing: Progress towards long hypocotyl canola

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ABSTRACT

Canola (*Brassica napus* L.) is Australia's most important oilseed break crop in wheat farming systems, but suffers from poor and inconsistent establishment, particularly with early sowing into hot, dry soils. Deep sowing offers a strategy to access subsoil moisture for establishment in dry autumns to avoid surface extremes. However, Australian varieties are poorly adapted to emergence when sown deeper than 2 cm. Australian canola varieties typically have short hypocotyls while overseas varieties with long hypocotyl emerge more effectively from 5 cm sowing depths.

As part of a GRDC-supported pre-breeding project, we are introgressing the long hypocotyl trait from diverse Canadian, Czech, French, and Japanese varieties using recurrent backcrossing into elite Australian backgrounds. We have developed BC2 generations and have initiated single seed descent to produce recombinant inbred line populations for trait mapping and marker development. Field experiments are planned for 2026 and 2027 to validate the positive impact of long hypocotyls in adapted Australian germplasm on emergence from deeper sowing and to identify correlated traits.

Parallel physiological studies are assessing the impact of soil type, soil strength, temperature, seed size and hypocotyl genetics on hypocotyl growth and emergence. Results will inform trait-marker and physiological associations, and future management strategies. The project aims to deliver germplasm and selection tools for use in commercial breeding to improve establishment under deeper sowing.

Key words: Establishment – Long hypocotyl – Deep sowing – Emergence – Seedling vigour

Increasing canola establishment through an understanding of sowing depth, soil strength and sowing date responses.

Andrew Fletcher¹, Kenton Porker², Jackie Bucat³, Bronte Wackett³, Matthew Nelson¹, Col McMaster⁴, Andrew Ware⁵, Brett Masters⁵, Chloe Rout⁶, Andrew Wherrett⁶, Casey Sim⁷, Thomas Jones⁷, Rohan Brill⁸, Rachel Whitworth⁹, Barry Haskins⁹, Maurie Street¹⁰, John Kirkegaard¹¹

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ABSTRACT

Canola is a high-value crop that plays a crucial role in many crop rotations across Australia. However, it is challenging to establish due to its small seed size and limited seed reserves. This presentation outlines the findings of a collaborative national project aimed at identifying the factors influencing canola emergence and improving establishment.

In early 2023, we conducted an online survey assessing typical canola field establishment rates, identifying causes of poor establishment, and determining grower and consultant research priorities. The survey revealed an average establishment rate of approximately 68%. Key research priorities identified by respondents included sowing depth, moisture requirements, and stubble management.

During the 2023 and 2024 growing seasons, 28 experiments across Australia compared canola emergence from shallow (10–25 mm) and deep (25–50 mm) sowing. While these experiments included various treatments, our primary focus was on the main effect of depth. On average, deep sowing resulted in a 30% reduction in plant numbers ($p < 0.001$), with only one instance showing a minor improvement in emergence. These findings demonstrate that, with current sowing technologies and canola genotypes, deep sowing is not a viable strategy to improve emergence.

High soil strength can also inhibit canola emergence. In several experiments, we examined the effect of reducing or removing press wheel pressure. The results indicate that, particularly when sowing deeper, reducing press wheel pressure can improve establishment in many situations. The presentation will also discuss the influence of sowing date and soil moisture on canola establishment.

Key words: Emergence – Establishment – Sowing depth – Soil strength – Sowing date

Stubble Trouble for Canola Establishment

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ABSTRACT

While stubble retention offers important benefits, high residue levels affect canola establishment and create other farming system challenges. Stubble removal rates increased following recent high production seasons in the Wimmera, particularly before sowing canola. Burning and/or cultivating stubble increases soil erosion and sandblasting risk, and loss of soil moisture, nutrients and organic matter.

Wimmera field surveys of canola establishment revealed inter-paddock variability (average 14-59 plants/m²). Intra-paddock variability ranged from high (CV >40%) to low (CV <10%) but was not always related to stubble management.

To understand optimal management for heavy stubble loads, field trials were conducted in the Wimmera from 2023-2025. Trials compared stubble management (burnt, mulched, baled and standing with various heights) and seeding system (disc versus tyned machines) under 2.8-7.0 t/ha stubble loads.

Results from 2023 and 2024 showed limited impact of stubble management on canola establishment. In some cases, emergence slowed with high stubble loads and low soil disturbance.

Stubble burning reduced seedbed soil moisture and increased seedbed temperature but showed limited impacts on establishment.

In 2024, canola establishment was better when sown with tynes compared with discs; this was likely related to our ability to effectively sow inter-row in plots with differing machines. Grain yield was similar across treatments. A critical plant density of ≥ 20 plants/m² is suggested to achieve yield potential > 3 t/ha in this environment.

Our findings suggest that growers' setup and ability to handle stubble with their individual machine is more important than stubble management or seeder type. In addition to extension undertaken, a guide will be produced to assess stubble loads and sowing practices to optimise canola establishment.

Key words: Stubble burning, Sowing, Seeding systems

SCAN: an automated phenotyping tool for real-time capture of leaf stomatal traits in canola

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ABSTRACT

Canola is an important economic and agronomic crop globally, but its yield is under threat due to climate change. Stomata are a key breeding target because of their importance in carbon capture and water use efficiency. However, screening for elite stomatal traits could be laborious and time-consuming. We developed a new toolkit called Stomatal Comprehensive Automated Neural Network (SCAN) that combines the use of high-resolution portable digital microscopy with machine learning to automate stomatal trait phenotyping in canola. We show that SCAN can rapidly measure stomatal density, size and pore area in canola at 97% to 99% accuracy, and capture real-time stomatal pore status that strongly correlated with leaf porometer measurement in canola. We used SCAN to investigate how leaf stomatal traits vary through a canopy in spring, semi-winter and winter ecotypes of canola grown in field and glasshouse conditions. Stomatal density in canola decreased in more expanded leaves. Stomatal density was 40% higher on the abaxial surface, and the stomatal openings were twice the size compared to the adaxial surface. The patterns of stomatal traits in canola vary between leaf position in the canopy and change with environment in an ecotype-dependent manner. These make SCAN a valuable tool for rapid and accurate stomatal trait screening towards breeding climate-resilient crops.

Key words: Canola – Digital microscopy – High-throughput phenotyping – Leaf development – Stomata

Why did blackleg management in canola actually work?

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ABSTRACT

Blackleg destroyed canola production in 1972, since then Australian growers have produced up to 8 million tonnes in a single season. In 50 years, canola progressed from non-existence to the 2nd most valuable crop in Australia. How?

The answer is by starting with a plant species that:

1. Grows and produces good yields,
2. Can be managed by growers using existing machinery,
3. Can be manipulated by both conventional and molecular breeding and
4. Produces a valuable commodity.

However, none of these factors would mean anything without disease control. Blackleg management in Australia has succeeded by creating a partnership between breeders, agronomists, chemical companies, growers and funding agencies. Any one of these agencies working in isolation would have failed.

Blackleg in 1972 was a common threat to a new industry and created the atmosphere for a unified response.

Blackleg continues to evolve against our genetics, fungicides and even agronomy. New genetics, fungicides and management strategies will be developed but these still must be managed to enable the industry to thrive. The challenge is for academic research, industry researchers, and the canola agronomists / growers to integrate new knowledge to create stable production.

Research findings need to be expressed and measured in production gains in the paddock, researchers working in isolation cannot achieve production gains.

Key words: Blackleg – Management – Genetics– Fungicides

Successful management of invertebrate threats to Canola – comparing contrasting seasons.

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ABSTRACT

Canola crops grown across southern Australia are subject to attack by over forty invertebrate species. This complex of invertebrate pests has changed due to evolving management practices and climate change.

A comparison of pest outbreak reports in broad acre crops from the early 1980's to 2007 from south-eastern Australia highlighted changes in invertebrate threats. The increased area of canola, adoption of conservation tillage systems and intensification, is associated with changing pest threats. The emergence of resident pests, such as slugs, earwigs, millipedes, and weevils, in modern farming systems provides new challenges.

An innovative approach to crop protection is needed where the concept of rigid management strategies is abandoned in favour of understanding pest biology, host plant resistance, reliable predictors based on climatic triggers and agronomic factors, followed by infrequent emergency intervention strategies. This approach needs to be based on developing more stable crop environments that can limit fundamental niches available for exploitation by sporadic pest populations and increasing crop resilience to resident herbivores.

The focus of the presentation will be on invertebrate threats to canola establishment. Data will be presented from 2023 – 2025 pest reports from south-eastern Australia, comparing a decile 9 to a decile 1 season to highlight the need for flexible management approaches.

Key words: Integrated Pest Management – canola – molluscs - production threats

Seeing the Unseen: Field-Scale Detection of Blackleg Crown Canker in Canola Using UAV-Mounted Hyperspectral Sensors

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ABSTRACT

Blackleg crown canker, caused by *Leptosphaeria maculans*, is a major fungal disease affecting canola worldwide, often resulting in significant yield losses. Remote sensing technologies, combined with large-scale surveillance, can enhance disease management by enabling high-throughput phenotyping, early detection of resistance breakdown, and effective crop monitoring. Hyperspectral imaging (HSI) has emerged as a non-invasive, high-resolution technique for capturing subtle physiological changes in plants across a broad spectral range, including responses not visible to the naked eye or standard imaging methods.

In this study, we investigated the potential of UAV-acquired hyperspectral reflectance data for detecting blackleg crown canker infection in canola. Field trials involved a moderately susceptible cultivar grown under two treatments: fungicide-treated and untreated. In addition to yield and disease severity data collected at pod maturation, hyperspectral imagery was acquired using a drone across multiple phenological stages, including pre-flowering, flowering, and pod development. The imagery was converted to reflectance values to enable consistent spatial and temporal comparisons and to assess biological responses. A Random Forest (RF) classifier was applied to distinguish between healthy and diseased subplots based on their spectral signatures.

The RF model classified disease status with over 90% accuracy when differentiating between healthy and infected subplots. Additionally, the spectral signatures showed potential for identifying different phenological stages in canola. These findings highlight the promise of integrating UAV-based HSI with machine learning for in-season disease detection, key phenological stage identification, and precision management. Further multi-environment trials are planned to validate the scalability and robustness of this approach.

Key words: Hyperspectral imaging – Blackleg disease – Canola – UAV remote sensing – Machine learning

Hyperspectral sensing: Advancing non-invasive phenotyping for quantifying canola blackleg resistance

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ABSTRACT

Blackleg crown canker, caused by *Leptosphaeria maculans*, poses a significant threat to canola (*Brassica napus*) production. While genetic resistance underpins current blackleg management strategies, major gene resistance is often rapidly overcome by pathogen adaptation, highlighting the importance of more durable quantitative resistance. Effective genetic mapping and pre-breeding rely on accurate phenotyping, but current visual stem-canker scoring of individual plants is often subjective, labour-intensive, and highly variable, limiting their scalability, accuracy and precision. Hyperspectral imaging offers a promising non-invasive, high-throughput alternative, through its application in detecting vascular diseases in plants remains in the early stages. To test the feasibility of this approach, in the 2024 growing season we conducted a proof-of-concept controlled pot experiment using two canola cultivars with contrasting blackleg susceptibility. Plants were grown under inoculated and non-inoculated conditions, and foliar spectral signatures were collected at four growth stages between 60 and 75 on the BBCH scale using an ASD FieldSpec Spectroradiometer (350 – 2500 nm). Multiple spectral measurements were taken from each plant, yielding over 2200 observations across 2151 wavelengths. Stem-canker severity and plant height were recorded at plant physiological maturity. Spectral data and vegetation indices were compared between plants. Preliminary results revealed significant spectral differences between diseased and healthy plants, notably at wavelengths around 710 nm. Multivariate clustering and variation in vegetation indices by disease severity further supported these findings. Overall, the results indicate the potential of hyperspectral sensing as a non-destructive tool for quantifying blackleg resistance. This proof-of-concept lays the groundwork for high-throughput, remotely sensed field deployment.

Keywords: Canola crown canker, *Leptosphaeria maculans*, Proximal sensing, Spectral analysis, Vegetation indices

Agronomic and financial outcomes associated with retaining seed from both Spring and Winter canola hybrids

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ABSTRACT

Farmers, advisors, and agronomists have been seeking further scientific research on the value of planting F1 hybrid commercial seed compared to blends of F1-F2 or straight F2 seed generations across a wide range of environments throughout Australia.

We found that F1 Spring hybrid seed produced significantly higher effective established plant populations for all varieties compared to the F1:F2 and F2 treatments within the target population of 40 plants/m². F1 Spring hybrids significantly ($p < 0.001$) showed higher yields than the F1-F2 and F2 treatments at most sites. Based on a 'simplified' Gross Margin (GM), F1 Spring hybrid seed produced greater economic returns for most varieties across many growing environments. Regression analysis of GM values shows only at individual low-yielding sites for some varieties does F1-F2 or F2 seed show greater economic returns than F1 seed.

Regression analysis of Winter canola F1 compared to F2 vs F3 treatments over 3 growing environments showed significant decreases in F2 and F3 grain leaf & stem dry matter production and harvested grain yields. The values between F2 and F3 treatments were not significantly different.

Retained F2 seed or a blend of F1-F2 from hybrid Spring canola varieties showed reduced plant establishment, grain yield and gross margins. As the environmental potential yield increases, so does the economic value of F1 hybrid seed. Retaining seed into subsequent F2 or F3 generations from Winter canola hybrids has a significant negative impact on both the crop agronomy and financial outcomes for mixed farming enterprises.

Key words: F1-F2 – Hybrid Canola – Retained Seed – Generations – Gross Margin

Allohexaploid *Brassica* in Canola Genetics and Breeding

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ABSTRACT

In the last two decades, canola researchers are committed to creating allohexaploid *Brassica* to broaden the genetic diversity in *Brassica* and to introduce novel traits for canola breeding with the hope to enhance agricultural productivity. In this study, we will report the polyploidy advantages and genome stability of allohexaploid *Brassica* through continuous self-pollination. Polyploidy advantage was maintained in terms of biomass, protein and glucosinolate content. In advanced selfing-generations, the pollen fertility was significantly improved to more than 95%, and the variation in chromosome number was reduced and gradually approached the expected $2n = 54$. During the selfing process, due to chromosome dosage compensation and partial homeologous exchanges occurred, frequent nullisomic or tetrasomic chromosomal variations (pseudo-euploidy) and large-scale structural variations were identified. The A genome showed the highest mutation frequency and turned to be easier to replace the C genome. The B genome had gradually become complete, and the stability of the allohexaploid had been significantly improved. Based on these findings, the researchers proposed that (1) allohexaploid *Brassica* may have gone through a transition period of pseudo-euploidy or a chromosome number of about 54, (2) in the early stages of polyploid synthesis, the genome composition should be given a certain degree of tolerance and buffering, and (3) offsprings with chromosome numbers of 52 - 56, good fertility, and a complete B genome could all be candidates for allohexaploid *Brassica*, and then strong evolutionary pressure should be exerted to promote its rapid evolution into a stable new species.

Key words: Canola – Allohexaploid *Brassica* – Polyploidy advantage – Advanced self-generation – B genome

Engineering disease susceptibility genes for durable resistance against blackleg disease in canola

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ABSTRACT

Brassica napus (commonly known as Canola or oilseed rape) is a crucial crop globally, providing essential resources such as vegetable oil, livestock feed, and fuel. However, its sustainable production is threatened by the fungal pathogen *Leptosphaeria maculans*, which causes blackleg disease throughout all stages of the plant's life cycle. *Leptosphaeria maculans* is a hemibiotrophic pathogen, initially causing leaf lesions and then stem canker as it penetrates inside the plant which can lead to plant death. Major control measures involve the use of chemicals and the cultivation of varieties containing resistance (*R*) genes. However, disease resistance can be short lived due to the rapid evolution of *L. maculans* and modifications in the effector proteins, enabling evasion by the receptors encoded by *R* genes. Therefore, there is a need to identify an alternative approach to provide durable and broad-spectrum disease-resistance. CRISPR-mediated gene editing of resistance/susceptibility genes present promising avenues for developing disease resistance in plants. By employing site-directed nuclease 1 (SDN-1) techniques, knocking out canola susceptibility (*S*) genes could offer durable and broad-spectrum disease resistance to canola against multiple pathogens including *L. maculans*. We describe a pipeline for modifying *S* genes and developing disease-resistant and non-transgenic canola plants.

Key words: Gene editing – Susceptibility genes – Blackleg disease – Site-directed nuclease 1 (SDN-1) – CRISPR

Phenotypic Stability in Quantitative Resistance to Blackleg Crown Canker: Exploring the Roles of Canola Genetics, Pathotype, and Environment

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ABSTRACT

Quantitative resistance (QR) to blackleg crown canker is an important component of disease management in canola. QR is a complex trait whose underlying genetics remain poorly understood. Reliable phenotyping methods for QR are critical for accurate assessment and breeding. However, the relative contributions of host genetics, pathogen genetics, and environmental factors to phenotypic variation and stability are not well understood or quantified. This study aimed to quantify the relative contributions of host and pathogen genetics, and environment, to phenotypic variation in QR to blackleg. Using a fully factorial design, three canola cultivars with differing resistance profiles were inoculated with three controlled pathogen sources across three environments: Horsham, Wagga Wagga, and Boorowa. Plants were grown to maturity and at harvest, a total of 6,825 plants were scored for crown canker severity. Mixed-effects models were applied to quantify the contributions of main effects and interactions to phenotypic variation. Significant variation was observed in resistance expression, strongly influenced by environmental conditions and canola cultivar. Notably, three-way interactions among cultivar, environment, and pathogen source explained a substantial portion of the phenotypic variation. This study highlights the complex nature of quantitative resistance, the expression of which is shaped by phenotypic plasticity, environmental variation and pathogen genetics. High levels of unexplained variance have potential to complicate future genetic studies and will require further development and refinement of high-throughput, field-based phenotyping methods.

Key words: Pathogen – Host – Disease – Phenotype – Resistance

Improving Canola Establishment in the medium and low rainfall zones of Western Australia

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ABSTRACT

Canola establishment is an ongoing issue for growers in general, but in the medium and low rainfall zones remains a significant hurdle to further adoption. Furthermore, the shift to early sowing in response to favourable conditions often increases the risk of poor establishment.

Two GRDC projects (LIV2112-001SAX, CSP2212-005RTX) have funded over 20 grower focused trials since 2022 conducted through predominantly marginal growing areas of Western Australia. Trial design and preparation was conducted in partnership with grower groups, targeting variables that growers highlighted as influencing factors on canola establishment.

In-person forums and surveys grouped the highest-ranking factors for evaluation; including soil wetters, soil moisture, seed placement, liquid fertilizer placement/rate, seed size, herbicide tolerance and time of sowing. Trials were simple in nature but with a primary aim to foster discussion related to practices limiting poor canola establishment.

Across multiple trials, seeding depth, soil temperature and fertilizer placement consistently contributed to variability in canola establishment, with fertilizer rate also a factor in specific situations. Establishing canola will continue to be an issue into the future, however these projects are providing growers some local guidelines on seeding systems to avoid in marginal production areas.

Key words: Emergence – Establishment – Soil – Fertiliser – Extension

Quantifying Blackleg Severity in Canola Using Deep Learning and a Web-Based Scoring Tool

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ABSTRACT

Phenotyping in agriculture is essential for understanding plant traits that influence yield, resilience and quality. Breeders and agronomists are increasingly able to collect, analyse and apply phenotypic data with improved accuracy and efficiency with the growing availability of digital tools. One key application is disease quantification, where automated tools can support the evaluation of disease severity and inform selection or management decisions. This work presents a deep learning-based phenotyping framework for automating blackleg crown canker disease quantification in canola stems.

The developed pipeline consists of three main components: data acquisition, image segmentation to isolate stem regions and severity prediction based on expert-annotated labels. The system has been developed and validated under controlled imaging conditions which lays a solid foundation for future application in real-world field environments.

The framework supports model interpretability by producing severity scores that closely match expert ratings. This helps users such as agronomists and plant breeders trust the results. The framework can support better decision making and help track disease resistance over time by providing consistent and objective disease measurements.

Future work will focus on applying the framework to field data collected under variable conditions such as changing lighting, different plant orientations and background complexity. More importantly, future work will focus on deploying the model as a real-time tool such as a mobile app or other accessible platform that farmers and breeders can use directly in the field. This will provide immediate disease severity predictions helping them make faster and more informed decisions to manage crop health.

Key words: Disease quantification – Deep learning– Digital tools– Phenotyping – crown canker canola

Accelerating Durable Resistance: AI-Augmented Speed Breeding for Blackleg in Canola

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ABSTRACT

Blackleg is a major fungal disease of canola, causing significant economic losses each year. Traditionally, efforts to improve resistance have focused on introgressing major-effect resistance genes. However, this approach often leads to resistance breakdown over time due to pathogen evolution. Recent studies have highlighted that, alongside these major genes, a substantial proportion of genetic variation in blackleg resistance is attributable to quantitative resistance. Genomic prediction offers a way to estimate genomic estimated breeding values (GEBVs) for blackleg resistance, capturing both major-effect genes and the underlying quantitative resistance. To evaluate the accuracy of GEBVs for blackleg, six field trials were conducted between 2015 and 2023 across multiple locations in Victoria, Australia. Across all trials, 2,118 genotyped lines were tested, which represented a mix of spring lines, winter lines and double haploids. GEBVs were estimated for two traits: survival percentage and average internal infection. These values were used to select candidates for crossing and advancement through eight cycles of an AI-augmented speed breeding pipeline. By the eighth cycle, individuals showed a 10% increase in survival and a 5% reduction in average internal infection compared to the parents from cycle one. Progeny from three speed breeding cycles were included in the 2023 blackleg trial for phenotypic validation, and all showed improved resistance relative to the founder population. These results demonstrate that integrating genomic prediction with speed breeding is an effective strategy for enhancing quantitative resistance to blackleg in canola.

Key words: canola – blackleg resistance – quantitative resistance – genomic prediction – speed breeding

PUSHING THE LIMIT OF CANOLA PRODUCTIVITY IN STH NSW: A 20 YEAR JOURNEY

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ABSTRACT

The productivity of canola in southern NSW has improved dramatically during the last 20 years. Canola water-limited yield was reviewed in 2005 using data from 42 well-managed experiments between 1991 and 2003. Yield potential was best described using an average transpiration efficacy (TE) of 12 kg/ha/mm above an estimated soil evaporative loss of 120mm, with the best earlier-sown crops achieving up to 15 kg/ha/mm. Reflecting industry practice at the time, the crops were dominated by conventional and TT varieties sown from mid-May to mid-June. A subsequent period of experimentation (Optimised Canola Productivity Initiative, 2014 to 2019) focussed on improving canola productivity using earlier sown hybrids (mid-late April), targeting the optimum flowering period with more robust nitrogen supply. These crops achieved a TE of 15 kg/ha/mm more reliably and evaporative loss was reduced to as low as 60 mm, generating a new water-limited yield potential frontier for canola. Subsequent industry-wide trends towards better fallow management, earlier sowing times, increased use of hybrids and higher N rates have been documented. Since 2018, canola has been a pillar crop in a GRDC-funded farming systems initiative in southern NSW involving 4 sites where canola has been grown in farming systems differing in crop sequence, sowing dates and nitrogen strategies. Comprehensive soil water and plant measurements combined with simulation modelling provide an opportunity to once again assess the performance of canola in these current systems, and to explore the major drivers of improved productivity and water-use efficiency in the context of the broader farming system.

Key words: Early sowing, water-use efficiency, optimum flowering period, yield potential, nitrogen

Pre-breeding for Heat and Drought Tolerant Canola

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ABSTRACT

Drought and heat stress is part of life in Australia. Canola is Australia's third largest crop by value and the most important break crop for cereal production. In 2023, national canola yield dropped by 31% (ABARES, 2024) majorly due to confounding heat waves and drought stress at canola reproductive stage. In a GRDC-funded national project, we evaluated the diverse *Brassica napus* population for heat tolerance in multiple years and at multiple sites. Several putative heat tolerant and sensitive lines were identified in the controlled environment at UWA, and then evaluated in the portable heat chambers in the field at NSW DPI. National-wide field trials in Australia validated heat tolerance in several genotypes. Genome-wide association studies identified a number of significant marker-trait associations for heat tolerance, and some showed $\geq 5\%$ phenotypic variance explained for different traits. Each QTL contributed to heat tolerance based on one or more yield-related traits. Candidate genes, once their functions are confirmed, may be used for improving heat tolerance in canola breeding programs. In recent years, we have been investigating the confounding effects of drought stress with heat stress during anthesis, characterizing new heat and drought tolerant genes via multi-omics approaches, and pyramiding multiple heat/drought tolerance genes from different resources through genomic selection. Heat and/or drought tolerant germplasm and molecular markers will be offered to Australian canola breeders with the goal to improve heat and drought tolerance in commercial canola cultivars.

Key words: Canola – *Brassica napus* – Heat stress – Drought stress – Pre-breeding

Automated canola phenology detection combining UAV imaging and deep learning.

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Field-based plant phenotyping is currently conducted manually, making it a costly process for both researchers and breeding companies. Furthermore, the assessment of plants by humans is inherently influenced by personal judgment and varying levels of expertise. Contemporary phenomics leverages drones fitted with high-resolution cameras to swiftly gather trait data at plant, plot, or field scale in agricultural trials. Advanced big data analysis techniques, powered by high-performance computing and deep learning, have demonstrated remarkable success in identifying patterns from images. Our goal was to create a workflow integrating these technologies to streamline and automate canola phenology detection. Over 60,000 drone images were collected across key growth stages of canola, with a structured acquisition and pre-processing workflow ensuring high-quality images and an accurately annotated MS COCO dataset. A detection model was trained to classify nine phenology classes using 19,231 labelled bounding boxes, achieving a mean average precision (mAP) of 0.603.

A separate classification model was trained on paired manual observations and segmented plot images covering several key growth stages of canola. We have developed a phenomics framework that enables automated canola phenology detection across multiple scales, providing a high-throughput alternative to traditional methods that are costly, time-consuming, and susceptible to human error. By integrating high-resolution images, expert-led dataset annotation linked to manual observations of key phenology stages, we demonstrate the effectiveness of deep learning models in detecting canola phenology at both organ and plot levels in field experiments. Such tools will have potential for immediate application in research and commercial settings.

Detection of SDHI resistance in Australian populations of *Leptosphaeria maculans*

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ABSTRACT

The succinate dehydrogenase inhibitor (SDHI) fungicides have, in the last five years, become the most widely used fungicide class for control of blackleg disease (*Leptosphaeria maculans*) in the high canola production areas of Australia. This high use of SDHI fungicides increases the risk of fungicide resistance evolving. In 2024, 110 blackleg populations present on stubble were screened for resistance to nine commercial fungicides (including SDHIs, DMIs, QoIs and mixtures) in a high throughput, high sensitivity *in planta* assay. Fourteen of the 50 populations from the Eyre Peninsula of South Australia exhibited low-high levels of resistance to SDHI fungicides. Resistance to SDHI chemistries has not been previously observed worldwide. Isolates collected from lesions on SDHI-treated plants were screened *in vitro* and *in planta* against four SDHI fungicide actives. This revealed that some isolates had incomplete cross resistance and others had complete resistance across the four SDHI chemistries tested. Resistant and susceptible isolates were crossed and a bulked segregant analysis (BSA) was conducted on the phenotyped progeny. The involvement of two genes was confirmed by Sanger sequencing of *sdhB* and *sdhD*, where three SNPs across the two genes were identified. The confirmation of SDHI resistance is a significant issue for Australian canola growers and has the potential to impact blackleg disease control. Further work is required to determine how SDHI resistance will affect the efficacy of fungicides if it becomes more prevalent.

Key words: *Leptosphaeria maculans* – SDHI fungicides – fungicide resistance

Agronomic and value equation outcomes associated using a treatment matrix of different canola seed sizes by plant populations by seeding depth.

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ABSTRACT

This research examines the environmental differences in canola plant establishment, flowering maturity, grain yield, oil % and economic returns when using one canola hybrid comparing a matrix of different canola seed sizes by plant populations by seeding depths. These 14 trials experienced a range of highly variable establishment conditions which showed a range between 46-91% of the target populations. The faster flowering growth habit was encouraged by larger and mid-size seeds sown at the 40 plants per m² targets, whether they are sown at normal or deeper depths. Some single site environments exhibited better establishment and yields from sowing deeper where subsoil moisture was better than on the surface, irrespective of seed size. The different starting soil moisture profiles and variable rainfall events that subsequently fell at individual trial sites after sowing, had variable influences on continued germination, establishment and growth of both normal and deep sown treatments ultimately may have also affected final yields across some of the environments. Sowing smaller sized canola seeds, especially at depth, can lead to lower plant establishment, later flowering, decreased yields and gross returns to growers and their associated profitability. The larger seed size combined with normal sowing depth and the higher plant population target provided higher effective plant establishment, harvested grain yields and the best value equations. Mid-sized hybrid seeds sown at the higher population target whether sown at the normal or deep levels, provided competitive establishment and grain yields. The smallest seed size only provided moderately competitive yields at normal sowing depth and the higher plant population target. The relative flowering maturity showed the trend of slowing down (later maturing) with the lower plant population target, especially for the smaller seed size at both normal and deep sowing levels.

Key words: Plant populations – Seeding depth – Seed size – Hybrid – Canola

New Genomic Resources in the Australian Grains Genebank: Delivering Transformative Impact to the Australian Brassica Industry.

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The Australian Grains Genebank (AGG) plays a critical role in safeguarding crop diversity essential for global food security and sustainable agriculture. As custodians of one of the world's largest and most diverse grain crop collections, the AGG conserves over 200,000 accessions across tropical and temperate cereals, legumes, and oilseeds—including a significant representation of *Brassica* oilseeds. Genebank management decisions, and utilisation by the grains industry based solely on passport and traditional characterisation data can be challenging – at times like the proverbial needle in the haystack.

The AGG Strategic Partnership, a joint investment between Agriculture Victoria and the Grains Research and Development Corporation (GRDC), has transformed the genebank into a bio-digital resource centre through the implementation of genotyping and innovative work to develop publicly accessible bioinformatic tools. By integrating passport, genomic and bioinformatics tools, the AGG empowers breeders and researchers to navigate the collection with unprecedented precision—helping unlock valuable traits for disease resistance, abiotic tolerances, and yield stability.

With most of the winter crops now genotyped by the AGG, the focus for 2025 is to characterise Brassica germplasm using industry approved genomic assays. Here we report on how the Partnership is planning to genotype 4,500 Brassica accessions, and how the application of these new resources holds transformative potential for the Australian canola industry. By unlocking the genetic potential of crop biodiversity, this work will accelerate trait discovery and support the development of climate-resilient, high-yielding, and profitable varieties—helping farmers manage the growing challenges of climate variability, pests, and diseases.

Key words: germplasm – Brassica – genomics – bioinformatics – breeding

The ins and outs of fungicide resistance

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ABSTRACT

Fungicides have become an integral part of blackleg control in Australia. However, with the increased use of these chemistries comes the increased risk of fungicide resistance. As it stands, we already have resistance to the DMI and SDHI fungicides in regions of Australia. Currently it is not known what management strategies are driving the selection of resistance, what is required for field failure to occur and whether there are any practices that can minimise the impact or slow the evolution of pathogen resistance in the field. Within the current GRDC and ARC-industry fellowship projects we will use a range of field and control environment experiments to investigate these issues to ultimately provide recommendations to growers, industry and researchers. Specifically, the project will: 1- establish if fungicide field failure is occurring, 2- determine the extent of resistance in each canola producing state, 3- determine if current fungicide management strategies influence fungicide resistance and, 4- investigate CropLife recommendations to determine if they can be deployed to successfully stop or reduce fungicide resistance.

Key words: Fungicides – Blackleg – Resistance

Improving pod shatter resistance in canola through gene editing

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ABSTRACT

Brassica napus (canola) is a globally important oilseed crop cultivated for its oil-rich seeds. However, its yield is often damaged by pod shattering, a natural seed dispersal mechanism in several members in Brassicaceae family such as *B. rapa* (genome AA) and *B. napus* (genome AACC). Previous studies have demonstrated that this process is regulated by multiple genes. Therefore, we aim to improve pod shatter resistance of canola through editing the pod shatter related genes.

Candidate genes associated with pod shatter susceptibility will be identified by integrating genetic sequence analysis and pod shatter phenotypes in two *B. rapa* parental lines and their F3 progenies. Previous studies identified Quantitative Trait Loci (QTL) regions that associated with pod shatter so candidate genes can be identified through comparative sequence analysis within these QTL regions. The function of identified candidate genes will be validated through genome editing in *B. napus* using CRISPR/Cas9 and base editing technologies. This research will provide new insights into the genetic and developmental basis of pod shatter and contribute to breeding strategies aimed at improving shatter resistance and reducing harvest losses in canola production.

Key words: *B.rapa* – canola – gene editing – pod shatter

Towards 2050: Future-Proofing Pest and Disease Control in Canola

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ABSTRACT

Effective pest and disease management is vital for sustaining canola productivity and its broader benefits to Australian agriculture. Key threats like Blackleg, Sclerotinia stem rot, aphids, and diamondback moth continue to evolve, challenging genetic and chemical controls. The CSIRO Ag2050 report outlines four future scenarios for Australian agriculture, each with distinct implications for pest and disease control.

1. **Regional Ag Capitals:** A high-tech, production-focused future where precision agriculture, genetic modification, and integrated pest management (IPM) reduce pest and disease risks. Advanced monitoring and predictive tools enable timely, targeted interventions.

2. **Landscape Stewardship:** Emphasizing environmental sustainability, this scenario promotes ecological approaches such as biological control, habitat manipulation, and agroecology. Collaboration between farmers, researchers, and policymakers supports innovation and adoption of sustainable practices.

3. **Climate Survival:** This scenario highlights incremental changes to cope with increasing climate variability. Adaptation through resistant crop varieties, climate-resilient farming, and flexible IPM strategies will be essential with continuous R&D crucial to address emerging threats.

4. **System Decline:** A scenario of limited resources and growing challenges, where pest and disease pressures could worsen due to inadequate responses. Strengthening support systems, farmer education, and community resilience becomes critical.

These scenarios highlight the need for proactive, collaborative strategies to ensure sustainable pest and disease management in Australian canola.

Key words: resistance management – climate adaptation – sustainable production – integrated pest/disease management

Water Uptake Kinetics of Canola Seeds

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ABSTRACT

Seed imbibition is the first critical phase of germination, during which seeds absorb water and initiate metabolic reactivation. In canola (*Brassica napus* L.), understanding imbibition dynamics is essential for improving stand establishment under variable soil moisture conditions in the field. This study aimed to quantify the water uptake kinetics of canola under varying water potentials and to model the imbibition process. Seed water uptake of the canola hybrid Regiment was measured gravimetrically at 0.5, 1, 2, 4, 8, 12, 16, 20, 24, 36, 48, and 72 hours under controlled water potentials (0, -0.5, -1, -1.5, -5, -10, and -20 MPa). These water potentials were achieved using PEG-6000 solutions.

Results showed that seed moisture content increased rapidly during the first 8 hours of imbibition, followed by a plateau phase after 12 hours. The initial water absorption rate and the maximum seed moisture content differed between moisture potentials. The water potential gradient between the seed and the surrounding medium was the primary driver of water influx. The initial water absorption rate, as predicted by the Peleg equation, declined exponentially from 0.32 (% h⁻¹) to 0.05 (% h⁻¹) as water potential decreased from 0 to -20 MPa. A threshold seed moisture content of approximately 0.5 g g⁻¹ fresh weight is required to initiate germination. Even under extremely dry conditions (-20 MPa), there was still a measurable uptake of water by the seed, reaching a moisture content of 8.6%. Although this level is insufficient to trigger germination, it may negatively impact seed vigour. These findings can guide dry sowing strategies and enhance seedling establishment.

Key words: Canola – Imbibition – Seed water content –Water potential

Assessing Photosynthetic Capacity in Canola: Integrating Leaf and Pod Photosynthesis

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ABSTRACT

Photosynthesis is the fundamental process driving crop productivity, directly influencing yield potential and growth efficiency. While leaf photosynthesis has been extensively studied, non-leaf photosynthesis, particularly in reproductive tissues like pods, remains under-explored. Pod photosynthesis may contribute significantly to carbon assimilation during seed development, potentially improving yield potential. This study examines both leaf and pod photosynthesis in canola (*Brassica napus*), focusing on genetic diversity and physiological traits that influence photosynthetic efficiency. For leaf photosynthesis, a diversity panel of 18 canola lines was assessed to identify genetic variation in photosynthetic capacity using gas concurrent measurements of exchange (LI-6800) and chlorophyll fluorescence imaging. For pod photosynthesis, two long pods varieties were selected to track photosynthetic changes in pod wall and embryo over time from 10 to 65 days after flowering. Gas exchange, PAM imaging, chlorophyll content (pod wall and seed), and biochemical analyses (oil, sugar, starch, total carbon, and nitrogen) were conducted to determine the role of pod photosynthesis in seed filling, oil content and yield formation. Preliminary findings suggest that pod photosynthesis serves as an important carbon source for the growing seed, particularly in later reproductive stages. Understanding the interplay between leaf and pod photosynthesis could unlock new breeding strategies for high-yielding, climate-resilient canola varieties.

Key words: Photosynthesis, canola, pod photosynthesis, genetic diversity, crop improvement.

Harnessing Genetic transformation and Gene-Editing Technologies to Unlock the Potential of *Brassica carinata* as a Sustainable Cover Crop

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ABSTRACT

The allotetraploid *Brassica carinata* (BBCC) is a climate-resilient oilseed crop with an unexploited potential for being grown as a cover crop for the production of sustainable aviation fuel. However, its late-maturity and limited breeding has impeded this use in Australian agricultural systems. In this study, we introduce a genotype-adaptable *Agrobacterium*-mediated transformation protocol that facilitates high-frequency shoot regeneration (up to 100%) and achieves stable transformation efficiency of up to 11.5% utilizing cotyledonary petioles from diverse *B. carinata* genotypes. This methodological framework was employed to implement a CRISPR/Cas9 multiplex editing system aimed at targeting loss-of-function mutations into the three *SHORT VEGETATIVE PHASE* (*SVP*) genes of *B. carinata*. *SVP* genes have been shown to be crucial repressors of flowering in closely related *Brassica* species. Among the 30 T₀ transformants analysed, 6 plants exhibited edits across all three *SVP* copies. Importantly, we identified Cas9-free, homozygous triple-edited lines in the T1 generation, that will be progressed for assessment of flowering-time and maturity in T2 progeny. By enabling the development of transgene-free, early flowering lines, this work accelerates the potential application of *B. carinata* as a winter cover crop in Australian agricultural systems. It also supports the crop's deployment as a dual-purpose, climate-smart solution for both cover cropping and sustainable aviation fuel production. Our strategy exemplifies how precision molecular technologies can accelerate the integration of underutilized crops like *B. carinata* into sustainable agricultural systems, thereby yielding agronomic, environmental, and bioenergy co-benefits.

Key words: *Brassica carinata* – Transformation – CRISPR– Early flowering – Cover crops

Introgression and Characterisation of the *FUL* Gene from *Brassica carinata* for Enhanced Pod Shatter Resistance in Canola (*B. napus*)

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ABSTRACT

Pod shatter is a major yield-limiting trait in canola (*Brassica napus*, $2n = 4x = AACC$), with losses reaching up to 70% under adverse weather conditions. Despite ongoing breeding efforts, most commercial cultivars remain susceptible to shattering. In contrast, Ethiopian mustard (*Brassica carinata*, $2n = 4x = BBCC$) displays robust pod shatter resistance (PSR), offering a valuable genetic resource for canola improvement. This study aims to evaluate the potential of *B. carinata* B-genome alleles to enhance PSR traits in a *B. napus* background, expanding the genetic resources available for breeding more resilient canola cultivars. Our recent study identified major quantitative trait loci (QTLs) associated with PSR in *B. carinata*, including a QTL located near the *FRUITFULL* (*FUL*) gene on chromosome B07, which accounted for up to 27.6% of genotypic variation. *FUL*, a MADS-box transcription factor negatively regulated by *APETALA2* (*AP2*), has also been linked to PSR in earlier mapping studies on *Brassica* species.

To functionally validate this QTL and assess its translational potential, we successfully introgressed the *B. carinata* *FUL* allele (*BcFUL.B07*) into two shatter-prone Australian *B. napus* cultivars, Marnoo and Paraplue via *Agrobacterium tumefaciens*-mediated transformation. Transgenic plants were regenerated from petiole-derived calli and have undergone preliminary evaluation for transgene integration. Ongoing work includes determining transgene copy number via droplet digital PCR, quantifying *FUL* expression, and assessing pod shatter resistance, flowering time, and other growth-related traits in the T_0 and subsequent T_1 generations. Pod shatter resistance will be assessed using rupture energy assays and pod anatomical analysis, with comparisons to untransformed controls. We hypothesise that variation in *FUL* expression among regenerants will correlate with differences in rupture energy/pod anatomy, providing insight into its regulatory role in PSR. The resulting introgressed lines can potentially reduce pre-harvest yield losses and improve yield stability under Australian field conditions.

Key words: Pod shatter resistance – *Brassica carinata* – Gene functional validation – Gene introgression – Canola breeding