




WHEAT BREEDING ASSEMBLY

NARRABRI 2022
PROGRAM HANDBOOK

28-31 August 2022 | The Crossing Theatre
www.wheatbreedingassembly.com.au



A close-up photograph of a person's hand holding a wheat ear. The person is wearing a blue, ribbed, long-sleeved shirt. The background is a blurred green field. The image is framed by a yellow vertical bar on the right and a multi-colored horizontal bar at the top.

Constantly searching for
better field crop varieties.



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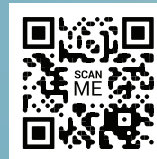
Wheat Breeding Assembly is the biennial conference of the Wheat Breeding Society of Australia.
www.wheatbreedingassembly.com.au

Disclaimer: The opinions and statements of facts expressed in the papers presented at the 2022 Wheat Breeding Assembly are those of the authors and do not necessarily represent those of the Wheat Breeding Society of Australia, the editors, the organising committee or the sponsors of this conference. No responsibility can be accepted by the Society or the conference organisers for errors or omissions in the program, proceedings or individual papers.

WHERE SHOULD GRDC FOCUS ITS INVESTMENT?

CONTRIBUTE NOW TO HELP SHAPE THE 2023-28 RD&E PLAN

We want to understand what is challenging you, what excites you, the issues facing the grain industry and where you believe grains research and development should be focused to deliver greatest impact.




WHAT WILL WE SEE TOWARDS 2040


 **30.6m** people living in Australia¹


 **1.4b** extra mouths to feed globally¹

 **39%** global population growth in Asia¹

Additional **13.7m** tonnes of wheat demand across Indonesia, Philippines, Thailand and Vietnam¹ by 2030 

Carbon intensity of ships to be cut by **40% by 2030**¹ 
(International Maritime Organisation)

More people will die prematurely from over-consumption than perish from starvation¹ 

India will import between **6-11m** tonnes of pulses p.a. by 2030 

Electric vehicles to represent **32%** new passenger vehicle sales globally by 2030²


Additional **2.9m + 0.8m** tonnes stockfeed + tonnes grain for food required domestically¹ 

HOW TO CONTRIBUTE

You are encouraged to contribute to shaping the Plan by visiting:

rdeplan.grdc.com.au/consultation

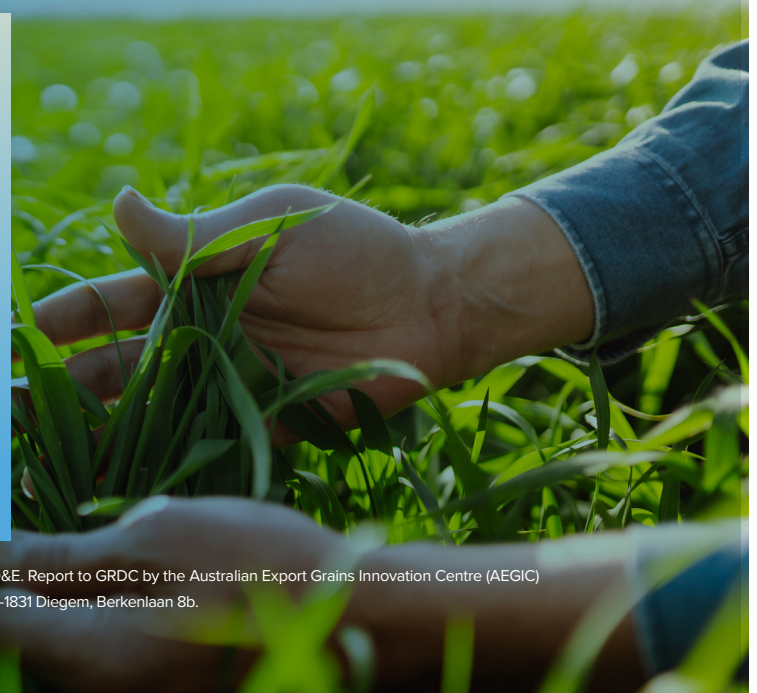
Alternatively, feedback can be provided to us at any stage of the consultation process through:

 rdeplanconsult@grdc.com.au

 [@theGRDC](https://twitter.com/theGRDC)

 <https://www.facebook.com/theGRDC>

We encourage all stakeholders to contribute new ideas and opportunities for investment throughout the life of this Plan by contacting GRDC staff based in our regional offices or Canberra.



1. Kingwell, R. (2021). Grains industry supply/demand drivers and trends: Considerations for Australian grains RD&E. Report to GRDC by the Australian Export Grains Innovation Centre (AEGIC)

2. Deloitte (2020). Deloitte Insights: Electric vehicles. Setting a course for 2030. Deloitte University EMEA CVBA, B-1831 Diegem, Berkenlaan 8b.

WELCOME MESSAGE

On behalf of the organizing committee of the 18th Assembly of the Wheat Breeding Society of Australia, welcome to Narrabri! We acknowledge the Traditional Custodians of the land on which we hold this assembly, the Murri's of the Gomilaroi nation, and recognise their continuing connection to land, water and community. We pay our respects to Elders past, present and emerging and acknowledge their spiritual connection to Country. Our program includes technical talks covering the latest developments in wheat research, an industry update and the opportunity to see wheat research in the field. We trust that you will find the conference both informative and enjoyable.

Local Organising Committee



Prof Richard Trethowan
President, WBA



Dr Lindsay O'Brien
Secretary, WBA



Dr Meiqin Lu
Treasurer, WBA



Dr Philip Davies
Committee member



Dr Jessica Hyles
Committee member



Dr Dan Mullan
Committee member



Dr Rebecca Thistlethwaite
Committee member



Ms Isobella Revell
Committee member

Impossible without you

Many of CSIRO's innovations were once considered impossible.

Fast WiFi, Aerogard insect repellent and the plastic Australian banknote, to name a few.

Until someone, just like you, joined us and took on the challenge.

From researchers to support professionals, see what is possible for your career.

Join Team CSIRO and help make the impossible possible.

csiro.au/careers/impossiblewithoutyou



illumina[®]

The Illumina Wheat Barley 40K v1.0 BeadChip is powered by proven Infinium™ Assay technology, providing excellent call rates and flexible content design. With imputation power across global wheat and barley varieties, this BeadChip is an advanced genotyping solution for crop breeding and research applications.

Learn more at:

<https://ilmnmkt.illumina.com/2016009212>



SPONSORS

Thank you to our Sponsors

The Wheat Breeding Assembly would not be possible without the generous support of our Sponsors.

Platinum Event Partner



Event Partner



Gold Sponsors



Silver Sponsors



GENERAL INFORMATION

Welcome Reception

Date: Sunday 28 August 2022

Location: Club Narrabri

Time: 6.30pm

Gala Dinner

Date: Wednesday 31 August 2022

Location: The Crossing Theatre

Room: The Auditorium

Time: 6.30pm pre-dinner drinks;
7:00pm – 11:00pm Dinner

Other

Speaker Information: Presenters are requested to report to the registration desk on arrival. You will be directed to the AV technician for uploading your presentation to the session room laptop.

Catering and Special Dietary Requirements

All catering breaks will be in the Riverside Room. If you have advised the organisers of a special dietary requirement, this information has been forwarded to the catering staff at The Crossing Theatre, but it is your responsibility to identify yourself to catering staff.

WI-FI

Wi-Fi access is available for delegates. Browse for wireless networks on your device and connect to
NETWORK: WBA2022
PASSWORD: WBA2022



AWARDS

2022 Triticum Award



Presented to: Dr Russell Eastwood

Russell has been involved with wheat improvement for nearly 40 years. He worked in the Victorian wheat breeding program at Horsham as a technical officer from 1982 to 1984 before completing a degree in Agricultural Science at LaTrobe University and later a PhD.

Russell's work with *Triticum tauschii* materials during and after his PhD led to the discovery, transfer and development of a marker for the Cre3 gene for cereal cyst nematode resistance.

His collaboration with CSIRO, in particular Rudi Appels, on the *tauschii* materials was one of the first projects that explored this important source of diversity for wheat improvement. The work subsequently expanded to explore *Triticum tauschii* germplasm as a valuable source of a wide range of resistances and tolerances for both biotic and abiotic traits.

In 1996, Russell moved from being employed as a plant pathologist at the Victorian Institute for Dryland Agriculture in Horsham to wheat breeder. The wheat industry has benefited substantially from this change of career direction.

As a wheat breeder Russell has successfully developed and released new varieties for the full range of quality classes that have been grown in Victoria, southern, northern NSW and Western Australia. One of Russell's first tasks in his new role as the wheat breeder at the Horsham institute was to manage the germplasm in the breeding pipeline, often segregating populations developed by his predecessors through to commercial variety. In this role he managed the Plant Breeders Rights applications for Goldmark and Silverstar and selected and organised the seed production, Plant Breeders rights applications and release of Chara, Mitre, Mira, Annuello, Young, Yenda and Barham.

After the commercialisation of wheat breeding, Russell's first releases with Australian Grain Technologies Pty Ltd were Bolac, Yenda and Barham in 2006 and with the company he has since designed the crosses and produced the populations, selected and managed them through to commercial production of Corack, Wallup and Elmore CL Plus in 2011, Kiora and Condo in 2014, Beckom in 2015, Coolah in 2016, Illabo in 2018, Coota in 2020 and Boree in 2021. His high yielding Australian Hard variety Beckom has excellent disease resistance including Cereal Cyst Nematode and is now making up 20% of wheat production in southern NSW.

The germplasm that Russell developed prior to the decision by the Victorian Department of Agriculture to exit wheat breeding was offered to commercial breeding companies and NuSeed released the Australian Hard varieties Derrimut and Peake from his fixed line materials, while LongReach Plant Breeders Pty Ltd released three varieties from his segregating populations.

Russell has been an excellent mentor to younger breeders and has supervised several PhD students.

Russell has been very supportive of the pre-breeding community and has collaborated with many groups including CSIRO (flowering genes, frost tolerance etc) and was the wheat breeder representative on the council of Wheat Quality Australia from 2016 to 2019.

Presentation and Poster Awards

Two prizes will be awarded:

Best oral presentation by a student
Best poster presentation

Awards will be announced and presented during the dinner on Wednesday 31 August.

KEYNOTE SPEAKERS



Mr Nigel Hart
Managing Director, Grains Research and Development Corporation

Mr Nigel Hart grew up in southern New South Wales and has spent more than 25 years working in executive and leadership positions in large scale infrastructure, port, warehousing and supply chains operations for the grains sector, both within Australian and internationally.

Nigel has worked as an expert consultant on a range of projects in the grain supply chain from international benchmarking of bulk and container supply chains, plant protein manufacturing, hybrid wheat commercialisation, digital strategies for supply chain optimisation and the design and development of a 1.3mmt grain export terminal.

He was previously Global Director (Ports) at Archer Daniels Midland where he led the development of a global port's growth and productivity strategy across Asia, Europe, South America and the USA.

Prior to this he spent 15 years at GrainCorp culminating in his position as Group General Manager – Storage and Logistics where he led the storage and logistics operations, grain accumulation and domestic customer management teams across the east coast of Australia.

Nigel has a bachelor's degree in Agriculture from Western Sydney University, is a Fellow of the Australian Institute of Company Directors and successfully completed the Advanced Management Program at Harvard Business School in 2013.



Dr Alison Bentley
Director, CIMMYT Global Wheat Program

Dr Alison Bentley is the Director of CIMMYT's Global Wheat Program, based in Mexico. Her research combines genetics and genomics to develop and deliver new tools and technology to improve plant breeding, crop production and adaptation to climate change. At CIMMYT, Alison leads a team of scientists using scientific approaches to develop improved wheat germplasm. This germplasm captures packages of traits providing productivity, resilience, and broad adaptation, supporting global wheat improvement and smallholder livelihoods. Prior to joining CIMMYT in November 2020, Alison worked in the UK focused on translation of fundamental scientific breakthroughs into tangible impacts for the agri-food sector. She has a doctorate in agricultural science and PhD in agriculture from The University of Sydney, Australia.

KEYNOTE SPEAKERS



Dr Adam Norman
Wheat Breeder, Australian Grain Technologies

Adam Norman is a Wheat Breeder with Australian Grain Technologies (AGT), currently based in Roseworthy South Australia. Adam completed a PhD at the University of Adelaide in conjunction with AGT on the topic of optimising genomic prediction accuracy, and how to best implement it in a breeding programme. In 2016 he accepted a role with AGT in the Roseworthy wheat breeding programme, and also took on roles around establishing and implementing genomic selection within the various AGT breeding programmes. He is passionate about logical decision making and improving the plant breeding process, and enjoys helping Australian farmers and rural communities through the provision of improved varieties.



Dr Josquin Tibbits
**Research Leader - Plant Functional Genomics,
Agriculture Victoria**

Dr Josquin Tibbits gained his PhD from The University of Melbourne in 2006 working on the genetic dissection of complex traits in forest tree species. In 2009 he joined Agriculture Victoria Molecular Genetics team where he worked on wheat genetics and genomics working in a team utilising next generation sequencing technologies. This opened the door to participation in the international efforts to assemble the wheat and other crop genomes. Josquin is currently the Research Leader for the Plant Functional Genomics group based at Bundoora and is working to accelerate adoption of genomics technologies into plant breeding systems for the benefit of Australian farmers

KEYNOTE SPEAKERS



Dr Felicity Harris
Senior Lecturer, Charles Sturt University

Dr Felicity Harris was previously a Research Scientist at NSW Department of Primary Industries at the Wagga Wagga Agricultural Institute and has recently started a new role as Senior Lecturer in Crop Science at Charles Sturt University, Wagga Wagga. Her research focuses on understanding the drivers of phenology in wheat and barley and using management to adjust timing of crop development to optimise yield and adaptation across variable environments. Felicity is a partner in her family farm at Junee in southern NSW and is passionate about research engagement with grain growers. She was awarded the Australian Society of Agronomy Young Agronomist of the Year in 2017 and GRDC Emerging Leader award in 2019.



Dr Grant Hollaway
Senior Plant Pathologist, Agriculture Victoria

Dr Grant Hollaway is a Senior Plant Pathologist with Agriculture Victoria at Horsham. For the last 30 years he has conducted research and extension into the epidemiology and control of diseases caused by bacteria, nematodes and fungi. During 2003, Grant undertook a sabbatical at CIMMYT with Dr Ravi Sing. He played a pivotal role in the development of what is now the national independent disease rating system that is delivered as part of the GRDC's NVT project. Grant's team are leading providers in the delivery of field based phenotyping services to plant breeders with more than 100,000 rows planted annually across 17 different diseases in 6 different field crops. Grant has published more than 40 scientific papers and was this year's winner of the GRDC's Recognising and Rewarding Excellence Award.

BUSINESS MEETING AGENDA

Business meeting

Tuesday 30 August 2022 at 5:00pm

Location

The Main Work Area of the Plant Breeding Institute, Narrabri

Agenda

1. Welcome by the President, Professor Richard Trethowan
2. Minutes of the last meeting
3. President's report, Professor Richard Trethowan.
4. Treasurer's report, Dr Meiqin Lu
5. Launch of the society's website
6. Year, location and office bearers for the next assembly
7. Any other business
8. Meeting close



A TRIBUTE TO DR FRANK ELLISON

F. W. (Frank) Ellison, 1944-2002.

This year marks the 20th anniversary of the passing of one of the Plant Breeding Institute's most respected and productive staff members Dr Frank Ellison.

Frank started his association with the institute in 1968 when he commenced a Masters degree program under the supervision of Dr Doug Laing, funded by a grant of \$10,500 from Pacific Australia Fertilisers Limited. His thesis "The agronomic response of some wheat varieties" was accepted for the degree in 1971.

Frank then enrolled in a PhD program under the supervision of Nick Derera which he completed in 1975 and then spent a year as postdoctoral fellow at the University of Manitoba before returning to Narrabri in 1977, joining the staff as plant breeder working alongside Nick Derera and Gyatri Bhatt.

Frank was promoted to senior plant breeder in 1984 and in several periods between the appointment of new directors for the institute served as acting director. At the time of his death Frank was Principal Plant Breeder with SunPrime Seeds, the joint venture company between the University of Sydney, GrainCorp Operations Limited and the Grains Research and Development Corporation.

During his career he was associated with or directly bred more than twenty wheat varieties, most of which dominated production in northern NSW and made up a significant proportion of production in Queensland. The varieties covered the full range of quality classes from feed and soft but were mostly eligible for receipt into the Prime Hard grade.



Sunbrook was named and released by the Chancellor of the University Dame Leonie Kramer pictured here with Frank at the release ceremony held at a field day at the Institute.

Frank served the Wheat Breeding Society as president and convened the fifth assembly held in Tamworth in 1990. His contributions to the wheat industry as a breeder, researcher and mentor were recognized with the posthumous award of the Wheat Breeding Society of Australia's Triticum Award for Excellence in Wheat Improvement at the Canberra Assembly in 2004 which was accepted by his widow Anne Ellison.

Frank was an active member of the Narrabri community and a member of the Narrabri Rotary Club and served the club as secretary and was inducted as President in 1999. Newly invested President of the Narrabri Rotary Club Dr Frank Ellison with his wife Anne pictured after the investiture ceremony.

For the entirety of his career Frank's position as wheat breeder and senior wheat breeder was funded by the industry initially by the NSW Wheat Research Committee and after its formation, the Grains Research and Development Corporation, but somehow, he still managed to find time for research and to supervise several postgraduate students.

Frank Ellison was dedicated to wheat improvement and the legacy of his commitment endures through the impact of his varieties and those he mentored.



Program

Monday 29 August 2022

8.30-9.55.	Session 1. Opening ceremony and keynote address. Chair: Professor Richard Trethowan, President of the Wheat Breeding Society of Australia
8.30-8.45.	Welcome to the Assembly by the President of the Wheat Breeding Society and to Narrabri by the Mayor.
8.45-9.15.	Address by the Managing Director of the Grains Research and Development Corporation, Mr Nigel Hart
9.15-9.55.	Assembly Opening Keynote Address Dr Alison Bentley, Global Director of CIMMYT.
9.55-11.35.	Session 2. Genomics and Phenomics. Chair: Dr. Ben Travaskis, CSIRO
9.55-10.10.	OzWheat: A functional genomics platform for wheat breeding. Dr Jessica Hyles, CSIRO
10.10-10.25.	A multi-donor x elite-based populations approach reveals QTL for low-lodging wheat. Dr Fernanda Dreccer, CSIRO
10.25-10.30.	Discussion.
10.30-11.00.	<i>Refreshment break</i>
11.00-11.15.	Wheat improvement through germplasm exchange and omics approach. Professor Guijun Yan, The University of Western Australia
11.15-11.30.	Pan'omics Toolbox - a practical tool for creating and analysing pangenomic datasets. Dr Brendan Boesen, CSIRO
11.30-11.35.	Discussion.
11.35-2.05.	Session 3. Phenotyping, data management and analysis. Chair: Dr. Scott Sydenham, LongReach Plant Breeders
11.35-11.50.	CAIGE (CIMMYT-AUSTRALIA-ICARDA GERMPLASM EXCHANGE): an international model of collaboration for wheat improvement in Australia. Dr Julie Nicol, The University of Sydney
11.50-12.05.	Managing the complex data underpinning the CAIGE collaboration. Dr Amit Singh, The University of Sydney
12.05-12.20.	Applications of multi-scale data to characterise wheat trials and environment interactions Professor Scott Chapman, The University of Queensland
12.20-12.30.	Discussion
12.30-1.30.	<i>Lunch break</i>
1.30-1.45.	Deep Phenotyping - Using AI for Crop Growth Monitoring and Yield Estimation. Dr Dadong Wang, CSIRO
1.45-2.00.	Model-based design for early stage selection experiments using a reduced animal model. Professor Brian Cullis, University of Wollongong
2.00-2.05.	Discussion.



2.05-4.20.	Session 4. Technology for wheat breeding. Chair: Dr Evgeny Glazov, Illumina.
2.05-2.30.	Keynote address: Dr Adam Norman, Australian Grain Technologies Pty Ltd.
2.30-2.45.	Unlocking the future of wheat breeding and research with the Infinium Wheat Barley 40K SNP array. Dr Gabriel Keeble-Gagnère, Agriculture Victoria
2.45-3.00.	Bayesian genomic prediction incorporating with gene expression and environmental data for wheat traits. Dr Shannon Dillon, CSIRO
3.00-3.30.	<i>Refreshment break</i>
3.30-3.45.	Artificial intelligence guided stacking to develop high yielding, highly resistant varieties. Dr Eric Dinglasan, The University of Queensland
3.45-4.00.	Prediction of flowering time in Australian wheat incorporating domain knowledge and machine learning. Dr Hawlader Al-Mamun, CSIRO
4.00-4.20.	Discussion.
4.20-5.30.	Session 5. Breeding for quality and future markets. Chair: Dr. Dan Mullan, InterGrain Pty Ltd.
4.20-4.45.	Keynote address: Dr Josquin Tibbits, Agriculture Victoria.
4.45-5.00.	Spikelet architecture, floret fertility and grain quality: the breeder's trinity of yield traits. Dr Scott Boden, The University of Adelaide
5.00-5.15.	Nicotianamine biofortified wheat as a nutritionally enhanced crop for future markets. Dr Jesse Beasley, University of Melbourne
5.15-5.30.	Discussion.
5.30-6.30.	Happy hour and poster display.



Tuesday 30 August 2022

8.30-10.30. Session 6. Breeding for abiotic constraints on yield.

Chair: Dr. Russell Eastwood, Australian Grain Technologies Pty Ltd.

8.30-8.55. Keynote address: Dr Felicity Harris, Charles Sturt University

8.55-9.10. Physiology, anatomy and proteomic analysis reveal a metabolic pathway and stress-related root adaptations in bread wheat lines differing in salt tolerance mechanisms.
Dr Bhagya Dissanayake, ARC Centre of Excellence in Plant Energy Biology

9.10-9.25. GWAS, KASP-SNP markers and haplotype-based pre-breeding for improving yield potential on sodic-dispersive soils in wheat (*Triticum aestivum* L.)
Dr Roopali Bhoite, Department of Primary Industries and Regional Development

9.25-9.40. Sodicty tolerant wheat selections, genomic regions and phenotyping improvement in Western Australia.
Dr Mirza Dowla, Department of Primary Industries and Regional Development

9.40-9.55. Dissection of morphological, biochemical and grain formation pattern on fertility for the selection of heat tolerant wheat genotypes.
Dr Anowarul Bokshi, The University of Sydney

9.55-10.10. Ice nucleating bacteria-hosting ability varies among wheat genotypes.
Dr Amanuel Bekuma, Department of Primary Industries and Regional Development

10.10-10.30. Discussion.

10.30-11.00. *Refreshment break.*

11.00-12.00. Session 7. Breeding for resistance and tolerance to biotic traits.

Chair: Dr. Maqbool Ahmad, BASF.

11.00-11.25. Keynote address: Dr Grant Hollaway, Agriculture Victoria.

11.25-11.40. A dual role of labile carbohydrates in the algorithm of wheat yield.
Professor Victor Sadras, SARDI

11.40-11.55. Management of *Septoria tritici* blotch (STB) in wheat in the medium and low rainfall zones of southern Australia.
Dr Hari Dadu, Agriculture Victoria

11.55-12.00. Discussion.

12.00-1.45. Board buses to Sunville for field tour and lunch.

1.45-2.00. Board buses to the Plant Breeding Institute for field tour, business meeting and dinner.

9.00pm Board buses back to Narrabri.



Wednesday 31 August 2022

8.30-10.30. Session 8. Breeding for resistance and tolerance to biotic traits (Continued).

Chair: Nick Willey, S and W Seed Company.

8.30-8.45. Identification of novel septoria nodorum blotch resistance of wheat.
Dr Huyen Phan, Curtin University

8.45-9.00. Untangling the 'Gordian knot' – How to unravel a complex fungal disease of wheat by understanding its game of effector hide-and-seek.
Dr Kar-Chun Tan, Curtin University

9.00-9.15. Recent progress in Fusarium crown rot resistance in wheat.
Dr Zhi Zheng CSIRO

9.15-9.30. Intermediate host resistance to new variant of the barley grass stripe rust pathogen in common wheat.
Dr Laura Ziems, The University of Sydney

9.30-9.45. Mitigating the effects of stripe rust on wheat production in south Asia and eastern Africa: Genome wide association mapping of wheat for resistance to Puccinia striiformis f.sp. tritici.
Dr Laura Ziems, The University of Sydney

9.45-10.00. Characterisation of diverse sources of rust resistance from the Watkins Collection of common wheat landraces.
Professor Harbans Bariana, The University of Sydney

10.00-10.30 Discussion Session.

10.30-11.00. Refreshment break

11.00-12.30. Session 9. Breeding for future farming systems.

Chair and moderator: Dr Alison Bentley, CIMMYT.

11.00-11.15. Manipulation of stomata to increase yield potential in wheat.
Dr Abdeljalil El Habti, The University of Adelaide

11.15-11.30. Adapting wheat to heat and drought in current and future climates.
Dr Karine Chenu, The University of Queensland

11.30-11.45. Exploring root-shoot dynamics to enhance yield potential and stability of future wheat cultivars.
Dr Samir Alahmad, The University of Queensland

11.45-12.00. Grain growers' future needs – Northern Cropping region. Ian Gourley, Narrabri.

12.00-12.15. Growers' future needs – Central west region. Mark Swift, Parkes District

12.15-12.30. Discussion and ideas for breeding for future farming systems.

12.30-1.30. Lunch break

1.30-3.00. Session 10. Emerging researchers and the breeders of the future.

Chair: Professor Brent Kaiser, Sydney Institute of Agriculture.

1.30-1.36. Genomic prediction of APSIM Next Gen phenology model parameters in wheat using machine learning.
Cordelia Dravitzki, La Trobe University

1.36-1.42. Spatial Models for Colocated Trials
Monique Jordan, University of Wollongong



1.42-1.48.	QTL Mapping for Nitrogen Use Efficiency (NUE) Based on A High-Density Consensus Map of Wheat. Hang Liu, Murdoch University
1.48-1.54.	Do adult plant rust resistance genes in wheat interact with each other to fight against their rust enemies? Dr Sambasivam Periyannan, CSIRO
1.54-2.00.	Variations in genotypic responses to heat stress on grain size and quality in wheat. Muhammad Yahya, The University of Queensland
2.00-2.06.	Is lipid metabolism in leaf and pollen tissue altered by heat stress, and does this affect pollen viability in wheat (<i>Triticum aestivum</i>)? Yifeng Lyu, The University of Sydney
2.06-2.12.	From lab to field: a major QTL to modify root system architecture in elite durum wheat. Yichen Kang, The University of Queensland
2.12-2.18.	Post anthesis mild water stress can accentuate differences in late deep root development between wheat genotypes. Kanwal Shazadi, The University of Queensland
2.18-2.24.	100-day Wheats for Adaptation to a Changing Australian Climate. Timothy Green, Charles Sturt University
2.24-2.30.	Adaption of Australian wheat to warmer growth environments. Mitchell Clifton, The University of Sydney
2.30-2.36.	Rotational intervals and tillage methods required to reduce yellow leaf spot inoculum. Melissa Cook, Agriculture Victoria
2.36-2.42.	On the use of factor analysis and iClasses to assess genotype by environment interactions in falling number across Australia. David Hughes, University of Wollongong
2.42-2.48.	Late Maturity α -Amylase (LMA) and its implications for wheat breeding. William Fairlie, Australian Grain Technologies
2.48-3.00.	Discussion.
3.00-3.30.	<i>Refreshment break</i>
3.30-5.00.	Session 11. Changes in the grains industry and current issues. Chair: Peter Graham, Managing Director of Cotton Seeds Distributors and Director Australian Grain Technologies Pty Ltd.
3.30-3.45.	A new era for the Australian Grains Industry. Rebecca Reardon. Board Member, Grains Australia Limited.
3.45-4.00.	Australia wheat breeding: celebrating success and future opportunities Ms Tress Walmsley, Director, Australian Crop Breeders Dr Haydn Kuchel, Director, Australian Crop Breeders
4.00-4.15.	Growing soft wheat in the northwest of NSW. James Kahl and Sam Kahl, Merced Farming Pty Ltd.
4.15-4.30.	Support Australian breeding programs to meet soft wheat quality requirements in Asia. Dr Siem Siah, Australian Export Grains Innovation Centre.
4.30-4.45.	Are there barriers to profitable soft wheat production? Dr Lindsay O'Brien, Solheimar Pty Ltd.
4.45-5.00.	General discussion and meeting close by the President Professor Richard Trethowan.
6.30-11.00.	Pre-dinner drinks, Riverside Room; Gala Dinner, Auditorium at The Crossing Theatre Including the Presentation of the Triticum Award for Excellence in Wheat Improvement and the Triticum Address.



POSTERS

#	POSTERS
1	NSW Dpi Post-Entry Quarantine Glasshouses - Open for Business Brett Lobsey, NSW Department of Primary Industries
2	DMSO enhances wheat doubled haploid production via anther culture Dr Marieclaire Castello, DPIRD
3	Symmetric response to neighbour in binary mixed cultivars associate with genetic gain in wheat yield over the last five decades C. Mariano Cossani, Sardi
4	Deep-sown wheat (<i>Triticum aestivum</i> L.): The influence of semi-dwarfing genes and the Lcol-A1 QTL on its coleoptile, seedling vigour, and establishment Jordan Bathgate, Department of Primary Industries
5	The effect of pot size on timing of important developmental stages of wheat Cordelia Dravitzki, La Trobe University
6	Pollen lipids in wheat (<i>Triticum aestivum</i>) varieties are affected by heat stress. Yunlong Bai, USYD
7	Influence of salinity stress on wheat leaf metabolism through its developmental gradient Samalka Wijeweera, University of Western Australia
8	A three-tiered phenotyping approach to effectively improving the heat tolerance of wheat. Dr Rebecca Thistlethwaite, University of Sydney
9	Rapid non-destructive method to phenotype stomatal traits Dr Abdeljalil El Habti, The University of Adelaide
10	Cytological characterisation of wheat- <i>Thinopyrum ponticum</i> translocations carrying leaf rust and stem rust resistance genes Lr24 and Sr24 Dr Jianbo Li, The University of Sydney
11	Improving crown rot phenotyping strategies Dr Philip Davies, Australian Grain Technologies
12	The Effect of Durum Wheat (<i>Triticum turgidum</i> var. Durum) Varieties Westcourt, Bitalli and Zulu on Pasta Production Zoe Taggart Kirbyshire, University of Sydney
13	Connecting wheat breeding and pan-genomics with Pretzel Mr Gabriel Keeble-Gagnère, Agriculture Victoria Research
14	Leveraging from the Vavilov wheat collection for new sources of stripe rust (<i>Puccinia striiformis</i> f.sp. <i>tritici</i>) resistance in Ethiopia Mr Zerihun Tadesse, The University of Queensland





Abstracts

MONDAY 29 AUGUST 2022

New horizons for global wheat breeding

Dr Alison Bentley

International Maize and Wheat Improvement Center (CIMMYT), México-Veracruz, El Batán Km. 45, 56237 Méx., Mexico

For over 50 years the Global Wheat Program at the International Maize and Wheat Improvement Center (CIMMYT) has developed and delivered improved wheat germplasm globally. The impacts of global breeding have been well documented and CIMMYT remains one of the largest providers of publicly available spring, durum, and winter wheat germplasm. Breeding progress is supported by enabling tools and technologies, including growing genomics and phenomics capacity, aligned pest and pathogen screening and research, rigorous quality and baking assessment and pre-breeding to understand and introduce novel variation for complex physiological traits. Combined, this allows the CIMMYT Global Wheat Program to improve wheat for a large range and diversity of production environments worldwide. This talk will summarize recent analyses of the progress of wheat breeding, the increasing use of new breeding methods to accelerate breeding and the value of complex trait pre-breeding. It will also address some of the global and societal challenges facing wheat production and supply, highlighting opportunities for new research to integrate genetics, breeding and agronomy with seed systems, value chains, system-level climate adaptation and mitigation strategies and policy and market interventions.



OzWheat: A functional genomics platform for wheat breeding

Dr Jessica Hyles^{1,2}, Dr Shannon Dillon², Ms Tina Rathjen², Dr Rad Suchecki², Dr Meredith McNeil², Dr Louise Ord³, Ms Lauren Stevens⁴, Mr Brint Gardner⁴, Ms Kerrie Ramm², Ms May Sun², Ms Bjorg Sherman², Dr Gonzallo Estavillo², Dr Steve Jobling², Dr Donna Glassop², Ms Dhara Bhatt², Dr James Broadbent², Dr Haydn Kuchel⁵, Dr Adam Norman⁵, Dr Tristan Coram⁵, Dr Russell Eastwood⁵, Associate Professor Urmil Bansal¹, Professor Richard Trethowan¹, Dr Ben Trevaskis²

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We are in an unprecedented era of technology development for crop breeding. With high-throughput genomics and phenomics, spatial-temporal data are now collected at a population-scale previously not achieved. To integrate and extract meaningful biological information that can inform decision making from these big data, we require new platforms, analytical methods, and visualization tools. We have established the OzWheat genome-to-phenome platform to address these needs as a powerful functional genomics tool to understand the genetic architecture of important agronomic traits in wheat. The OzWheat platform comprises 283 lines representing the genetic diversity of existing Australian cultivars, and novel diversity currently missing from Australian breeding programs. During multiple years, specialized, multi-level phenotyping tools for controlled and field conditions have been deployed to extract multi-trait information from the OzWheat population. The OzWheat data platform has been utilized widely to understand plant biology, investigate yield components, predict crop performance, and characterize the interplay between genomics and the environment. We have also developed new analyses and visualization tools to explore multi-omic data layers (genomic, transcriptomic, proteomic, phenotypic) to identify new sources of genetic diversity and design targets for gene editing. Our goal is to deliver new data-driven breeding technologies to design future crops for different farming systems and environments.

A multi-donor x elite-based populations approach reveals QTL for low-lodging wheat

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Low-lodging high-yielding wheat germplasm and SNP-tagged novel alleles for lodging were identified by combining (a) donor selection through functional phenotyping for underlying traits with a designed phenotypic screen, and (b) a crossing strategy involving multiple-donor x elite populations.

Firstly, local and imported germplasm was screened to identify consistently higher-yielding genotypes with low lodging for NE Australia. Using fertilisation and tactical irrigation to simulate lodging scenarios, lodging rankings were highly reproducible in multi-environment experiments. In separate field experiments, selected genotypes were phenotyped for traits underpinning stem, shoot and root type lodging. Multi-environment and phenotyping experiments ranked genotypes similarly for lodging score. Root plate spread from field grown plants consistently discriminated low lodging, high yielding germplasm from a multi-trait analysis quantifying genotypic correlations. When the root plate spread was greater than or equal to 5.5 cm, the lodging scores were small, and yield was high. Root plate spread was highly heritable (above 0.80), with a high genotypic correlation (0.80) across environments.

Secondly, populations were developed crossing 4 low-lodging high-yielding donors based on lodging related traits, with EGA Gregory, LPB Spitfire and Suntop. Lodging was evaluated in single rows in an early generation and subsequently in plots in 2 years contrasting for lodging. A large number of lines lodged less than their recurrent parents. Heritability for lodging was high, but the genetic correlation between contrasting environments was intermediate-low. Lodging genotypic rankings in single rows did not correlate well with plots.

Finally, lines from the highest lodging background, EGA Gregory, were genotyped (90K array). Fourteen markers on 9 chromosomes were associated with lodging, differing under high vs. low lodging conditions. From those, 10 co-located with previously identified QTL for lodging-related traits or at homoeologous locations, while the remaining 4 (in chromosomes 2D, 4D, 7B and 7D) appear to map to novel QTL for lodging. Lines with more favourable markers lodged less, suggesting value in these markers as a selection tool. Our work shows that the combination of donor functional phenotyping, screen design and crossing strategy can help identify novel alleles in a complex trait without requiring expensive phenotyping in extensive bi-parental populations.




Wheat improvement through germplasm exchange and omics approach

Dr Helen Liu¹, **Dr Dan Mullan²**, **Professor Guijun Yan³**

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Field trials of 150 wheat lines (including 120 Australian and 30 exchanged Chinese cultivars) were conducted at UWA Shenton Park Field Station in 2019, and at Brocklesby (NSW), Cunderdin (WA), Lock (SA), and Kalkee (VIC) in 2020 and yield data collected. The wheat lines were genotyped by double digest restriction-site associated DNA (ddRAD) sequencing. A genome wide association study (GWAS) was conducted using a mixed linear model, simultaneously accounting for population structure and kinship. A total of 223 significant marker-trait associations (MTAs) for yield traits were identified, with 39 of them showing major or consistent effect, explaining up to 20% phenotypic variation. Forty-six candidate genes were identified for the major and/or consistent MTAs. Recombinant inbred lines (RILs), in total of around 1,500 lines, were developed through crosses between high-performance Australian and the exchanged Chinese cultivars. Near isogenic lines (NILs) targeting major loci for drought tolerance and heat tolerance were developed and characterized. Omics profiling of the NILs revealed candidate genes with major effects for the traits. Six differently expressed genes were identified for the drought tolerance locus using RNA sequencing method, and seven candidate genes were identified for the heat tolerance locus using wheat 90K Infinium iSelect SNP array genotyping. Molecular markers based on these candidate genes were developed.




Pan'omics Toolbox - a practical tool for creating and analysing pangenomic datasets

Mr Brendan Boesen¹, Dr Rad Suchecki¹, Mr Sean Li¹, Mr Bertrand Dungan¹, Mrs Nicola Cowen¹, Dr Alex Whan¹
¹*Commonwealth Scientific and Industrial Research Organisation,*

The growing availability of multiple, contiguous, and close-to-complete genome references opens-up new possibilities for pangenome-driven gene discovery and breeding. The method used to store and encode a pangenome has a significant impact on its utility. Some approaches sample a pangenome, others try to represent it in its entirety. Some use individual nucleotides as their lowest level of information, others use sequences of nucleotides that capture exons, genes, and the like. Some are well-suited to comparative analyses, and others to functional analyses, though no representation is well-suited to both.

CSIRO is building a pangenome focused on functionally-relevant sequences of nucleotides, encoding commonality and variation at multiple scales. Such a pangenome for 11 wheat accessions can be rapidly constructed, updated, and queried in minutes, in contrast to existing approaches that struggle with genomes of this size and complexity. It supports arbitrary multi-way comparisons which enable the discovery of conserved haploblocks and structural variants.

A suite of tools has been developed to allow the pangenome to be used for practical tasks and include facilities to partition genomes to identify common/variant sequences, categorise the sequences, identify larger-scale commonality and variation, and query and visualise the pangenome.



CAIGE (CIMMYT-AUSTRALIA-ICARDA GERMPLASM EXCHANGE): an international model of collaboration for wheat improvement in Australia

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The CIMMYT-Australia-ICARDA Germplasm Evaluation (CAIGE) program was established in 2006 to better exploit genetic diversity in wheat (bread and durum) and barley sourced from the Consultative Group on International Agricultural Research (CGIAR). This collaborative program coordinates the selection, importation, quarantine, multiplication and national assessment of the international crop germplasm, and manages and disseminates the information generated. CAIGE aims to extract as much value of relevance to local scientists and farmers as possible to optimize decisions on germplasm choice and use. Partners include universities, government organizations, commercial entities and wheat breeders of the CGIAR, and is supported by the Australian Grains Research and Development Corporation (GRDC).

All CGIAR data linked to the imported germplasm and data captured on the same materials in Australia are available to all partners via the CAIGE website and database. The CGIAR data is used to hone selections made by Australian crop breeders at each of the centres in alternate years. Original seeds delivered to Australia are grown and screened for pest and disease by the Australian Grains Genebank (AGG) and then multiplied post-quarantine at Narrabri before being distributed nationally in multi-environment yield trials. The materials are concurrently screened for disease resistance and some grain quality traits by Australian collaborators.

In partnership with CBADS-SPI (Centre for Biometrics and Data Science for Sustainable Primary Industries) at the University of Wollongong, recent advances in statistical methodology are used to both design and analyse yield trials. Currently, a rolling multi-environment (four year) pedigree-based Factor Analytic Model is used for all three crops. The incorporation of iClass and CAIGE SHINY APP (an interactive data visualisation tool) in data analysis has enhanced breeder decision making.

Underpinning all of these, and in collaboration with the International Breeding Platform (IBP), the CAIGE pedigree and phenotypic data are stored in an application of the Breeding Management (BMS) system, which enables collaborators to search and extract relevant data. BMS also provides a platform for GIGWA which stores relevant genotypic data. The CAIGE program has successfully improved the uptake and use of these globally important materials for the benefit of Australian grain growers.



Managing the complex data underpinning the CAIGE collaboration


Dr Amit Singh¹, Robin Wilson², Clarissa Pimentel³, William Eusebio³, Rowena Tulod³, Sandra Micallef⁴, Dr Julie M Nicol¹, Dr Mark Dieters⁴, Professor Richard Trethowan¹

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Database management is a key factor under modern crop improvement program. The GRDC funded CIMMYT Australia ICARDA Germplasm Evaluation (CAIGE) program is an effective international collaboration that enables Australian grain industry to derive maximum benefit from the significant investment in international bread wheat, durum wheat and barley breeding. The collaborative program offers local stakeholders and stakeholders from two international centres: CIMMYT and ICARDA, to generate and exchange large amounts of pedigree, phenotypic and genotypic data for the benefit of Australian grain growers.

Approximately 700 genotypes of bread wheat, durum and barley from the international centres enter annual multi-environment trials (MET) across three primary grain growing regions of Australia with concurrent screening for diseases of economic importance. An extensive dataset provided by the international centres is pivotal to the selection of candidates for Australian trials and testing. The ensuing yield data are analysed independently by the CBADS-SPI at the University of Wollongong, to produce single year and rolling pedigree MET results. Trial design and analysis is optimized by the inclusion of carefully curated pedigrees and coefficient of parentage (COP) calculations. Pedigrees provide a level of connectivity among lines that would not otherwise be available as new materials are imported each year. These statistical results are supplemented with disease data to optimise information for collaborators, thus assisting the selection of materials for inclusion in breeding programs.

CAIGE-data is managed using the Breeding Management System (BMS) platform of IBP. The diverse data are loaded and stored in BMS, in appropriate formats for end-users. The BMS can also be used for data transformation, analysis, curation, and interrogation using breeder-friendly search tools. Data files and related CAIGE resources are also periodically updated on the project website to keep stakeholders informed. Breeders will be able to generate their own data compilations on germplasm of interest in the upcoming version of BMS. The public and private databases of each crop are maintained separately, with restricted access to data provided by Australian commercial entities. BMS is also an access point for connection to other databases such as GIGWA (dedicated to genotypic data storage). Thus, BMS provides a robust platform for the storage and rapid dissemination of data and related information to the breeding community.



Applications of multi-scale data to characterise wheat trials and environment interactions

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Over the last 10 to 15 years, high-throughput phenotyping supported by digital technologies and UAVs, and improved environmental characterisation through satellites, sensors and crop models have been proposed to improve breeding experiment outcomes. However, there are challenges in processing and utilising these data to improve prediction and/or understanding of genotype x environment interactions. Across several research projects, we are utilising digital and model technologies to remotely monitor trial progress and interpret seasonal impacts on wheat yield in National Variety Trials. This paper reports on progress in using these technologies to interpret early season trial variability and how it relates to spatial patterns of final yield, and how GxE effects can be related to environmental covariates derived from weather and crop model analyses. (The paper will include multiple authors from UQ, CSIRO and WUR).



Deep Phenotyping - Using AI for Crop Growth Monitoring and Yield Estimation

Dr Dadong Wang¹


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Phenomics is the study of the physical and biochemical traits of an organism as they change in response to variation in genomes or the environment. Sensor technology advances mean that climate and certain types of phenotype data are now readily available, however, some critical phenotypes related to yield prediction still rely on manual collection which is expensive and error prone.

In this presentation, we will show our AI-based video phenomics platform developed by utilising machine learning methods, aimed at automating the detection and quantification of plants, spikes and spikelets for plant growth monitoring and yield estimation.

Image and video data was acquired for three cereal crops at different life cycle stages across five trial locations. Repeat data was collected using sensors mounted on UAV and a mobile ground-based platform, PhenoMobile, including RGB videos, depth videos, thermal videos and LiDAR point clouds. Coinciding with this collection, we used mobile devices to collect data to aid in the development decision tools on alternative deployment platforms. Ground truth trait data was collected by processing sample plants across the plant life cycle. Using the ground truth data, we have assessed our AI algorithms for two different densities of wheats for different traits including rate of establishment rate, plant height, number of spikes and average number of spikelets per spike in a plot. Our assessment results show that the AI algorithms performed well and achieved a Root Mean Square Error (RMSE) of 7.93%, and a coefficient of determination (R²) of 0.9383 for the germination detection, an average precision of 85.7% for the spike detection, an average accuracy of 87.04% for spikelet counting, and coefficients of determination (R²) of 0.86, 0.82, 0.77 and 0.65 respectively for UAV flight height 12m, 15m, 20m and 30m. The assessment results show that our deep phenotyping platform can be potentially used for the automatic phenotype quantification during the plant growth, which can greatly facilitate the genotype to phenotype studies.

We will also demonstrate our video phenomics platform with use cases for automated estimation of crop emergence, and automated counting of spikes using videos captured from UAVs.



Model-based design for early stage selection experiments using a reduced animal model

Professor Brian Cullis¹, Dr David Butler, Dr Alison Smith, Dr Calum Watt, Dr Daniel Mullan

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The success of a plant breeding program is based on its ability to maintain high levels of genetic gain. From a statistical perspective, genetic gain will be maintained (or increased) through the use of novel methods of experimental design and analysis, leading to accurate prediction of the genetic value of genotypes. Selection for the key trait, grain yield, is based on information derived from the analysis of multi-environment trial (MET) datasets. The focus of statistical methodologies for METs has been in the development of appropriate tools which incorporate genetic relatedness into the analysis via for example use of a factor analytic linear mixed model. There has been little attention given to the design of METs, particularly those associated with the early stages of the advanced selection phase. For stage 0 and 1 METs (S0 and S1 respectively), trials usually involve growing a large number of genetically related genotypes at as many sites as possible which ensures adequate sampling of the target set of environments (TPEs). Limited seed supplies and budgetary constraints pose a complex problem for constructing an optimal experimental design for METs involving S0/S1 trials. Recently Cullis et al (unpublished) developed a new class of MET designs called Incomplete MET (IMET) designs and these designs have been in use for several years by a number of breeding programs based in Australia and overseas. The construction of these designs has evolved as superior methods and computing tools have been developed. In this talk we present an extended IMET design which resolves computational challenges when the number of test lines exceeds 10,000. A comprehensive account of these methods is in preparation. All designs have been generated using the R package ODW which is freely available from <https://mmade.org>.




Plant breeding technologies: current fit and future opportunities

Adam Norman

Australian Grain Technologies

Wheat breeding has benefited from multiple technological advancements including the advent of molecular markers and high-density genotyping, digital phenotyping, advanced computational tools, and robotics and automation. The application of these technologies has allowed for greater genetic gain to be made for multiple important traits. New and emerging technologies have the potential to further improve our ability to make genetic gain for target traits through, for example, uncovering deeper genetic knowledge, creating new efficiencies, measuring complex phenotypes at scale, and the analysis of complex and disparate datasets to gain insights. The state of implementation of new technologies will be discussed in the context of a commercial breeding programme, as well as a look to what may be possible in the future.



Unlocking the future of wheat breeding and research with the Infinium Wheat Barley 40K SNP array

Mr Gabriel Keeble-Gagnère¹, Raj Pasam¹, Kerrie Forrest¹, Debbie Wong¹, Hannah Robinson², Jayfred Godoy², Allan Rattey², David Moody², Daniel Mullan², Tresslyn Walmsley², Hans Daetwyler^{1,3}, Josquin Tibbits¹, Matthew Hayden^{1,3}

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The Illumina Infinium Wheat Barley 40K SNP array is a new genotyping platform. It implements a novel design approach which aims to simultaneously provide highly accurate genotype data and capture global germplasm diversity while minimising ascertainment bias, as well as enabling dual hybridisation of wheat and barley samples in the same assay. It has been specifically designed to cater for large-scale deployment such as in breeding programs. The array comprises mostly biallelic markers that were designed to be species-specific and single-copy, permitting highly accurate imputation in diverse germplasm to improve the statistical power of genome-wide association studies (GWAS) and genomic selection. The SNP content captures tetraploid wheat (A- and B-genome) and *Aegilops tauschii* Coss. (D-genome) diversity and delineates synthetic and tetraploid wheat from other wheat, as well as tetraploid species and subgroups. An overview of the design methodology will be presented together with examples of how the web-based tool Pretzel can be used to integrate results from the array with other platforms. The array is now available directly from Illumina for use by the international wheat and barley communities.



Bayesian genomic prediction incorporating with gene expression and environmental data for wheat traits

Dr Jia Liu^{1,2}, Mr Andrew Gock³, Ms Kerrie Ramm¹, **Dr Shannon Dillon¹**

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The adoption of novel molecular strategies such as genomic prediction (GP) in crop breeding has been key to maintaining rates of genetic gain, because of its lower cost and increased efficiency compared to conventional breeding selection, including wheat breeding. In the search for improved methodologies to better incorporate novel sources of variation for assessment of genetic merit, GP remains a focus of crop breeding research globally. In this work we integrate multiple-‘omics data including ca. 40K single nucleotide polymorphisms (SNPs) and ca. 50K transcripts as well as non-genetic drivers, categorical environmental data, to conduct genomic prediction on multiple wheat yield-component traits in the OzWheat diversity panel. We evaluated the predictive ability of twelve different predictive models including linear (GBLUP) and nonlinear (RKHS) kernel in the Bayesian regression framework, incorporating epistasis, genotype x environment interactions (GxE), and ‘omic transcriptome data with genomic SNP additive effects. We tested their predictive ability for 10 wheat yield component traits, including flowering time and height, measured on ~300 varieties from the OzWheat diversity panel grown under contrasting daylength environments. In general, gene expression from transcriptome data shows a strong link to phenotype; whereas the benefit of further including environmental data is limited in this context. The GBLUP model showed better performance compared with the Gaussian kernel here. For flowering time, using SNP data combined with transcriptome data and using SNPs plus epistasis effects in the predictive models provide equally best predictive ability (up to 0.804); While the model considering additive and epistasis genomic effects plus transcriptome data performs among the best for height prediction (0.764). These models suggest an advantage to inclusion of additional ‘omic data types for genomic evaluation of flowering and height for breeding selection. For both traits the categorical environments did not play a critical role in the prediction when transcript data were included.



Artificial intelligence guided stacking to develop high yielding, highly resistant varieties

Dr Eric Dinglasan¹, Associate Professor Lee Hickey¹, Dr Bertus Jacobs², Professor Ben Hayes¹, Professor Dr Kai Voss-Fels^{1,3}

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Conventionally, parents are selected based on their performance per se or their breeding value which limits the inference that can be made about the probability for maximising the number of favourable chromosome segments in the offspring of a given cross. This is particularly challenging when a combination of quantitative traits (yield) and mono- or oligogenic traits (e.g. disease resistance, quality) are considered simultaneously. This problem is well suited to evolutionary computation approaches, where algorithms inspired by biological evolution, such as reproduction, mutation, recombination, and selection are employed to find solutions to complex problems. In this ongoing study, we use evolutionary computing in a large commercial data set comprising more than 40,000 genotyped breeding lines which have been tested over multiple years and locations across Australia. The algorithms predict optimal crosses that most efficiently stack complementary alleles for quality, disease resistance and yield. A digital twin simulation of the breeding program suggests these varieties have considerably better yield than existing varieties, as well as strong disease resistance to a number of pathogens. Generated offspring from those crosses is advanced through speed breeding which allows a rapid turnaround of several generations and breeding cycles per year.




Prediction of flowering time in Australian wheat incorporating domain knowledge and machine learning

Dr Hawlader Al-Mamun¹, Dr Jessica Hyles², Dr Ben Trevaskis², Dr Bill Bovill², Dr Howard Eagles, Dr Shannon Dillon²

¹CSIRO, Dutton Park, Australia, ²CSIRO, Black Mountain, Australia

Flowering time is an important phenological trait of wheat determined by a combination of genetic and environmental effects, and their interactions. Understanding phenology informs selection of varieties and sowing times that match flowering time to the optimal flowering window, which is crucial to maximising yield potential in the targeted environment. In this study, we used genotypic data from 285 Australian wheat lines and twenty years of field-based assessments of flowering behaviour and environmental data to predict heading date in Australian wheat. We compared accuracy of forecasted flowering time using different machine learning algorithms that integrate genomic SNP and environmental data up to 120 days after sowing (DAS). We show that by aggregating weather data based on our knowledge of important growth stages of wheat, in growing degree days (GDD), we can achieve prediction accuracies of 95% (RMSE within 5.89 days). This represents a 2-3% improvement over models that apply daily minimum, maximum and average weather data for the period. For example, it requires 100 GDD for seedlings to emerge and a further 200 GDD to reach first tiller. Rather than applying the daily average of weather data over the growing season, we averaged weather observations within the defined GDD intervals. As the current growing season weather data is not available at time of sowing, in order to forecast flowering time for a variety in that season, we used historical observations to approximate weather data at different GDD intervals up to 120 DAS. We demonstrated that, by averaging the historical weather data for different GDD stages, we can forecast flowering time with high accuracy in the current growing season based on sowing date. We also compared prediction accuracy between different data sources (genotype data only, weather data only, combined genotype and weather data). Our finding suggests that combining data sources results in improved prediction accuracy. Our study indicates that, taking a data driven approach by combining data at scale from multiple sources, coupled with machine learning algorithms and domain knowledge can provide robust forecasting of flowering time in Australian wheat. This approach could be incorporated into grower and wheat breeder's toolkits to accurately inform flowering for improved crop management and breeding selection across the landscape.




Predicting wheat quality - practice and implications for wheat breeding (and the broader wheat industry).

Dr Josquin Tibbits

Agriculture Victoria

Wheat quality is a strong determinant of end-use performance, whether it is for flour milling, breads, noodles, cereals, pasta or animal feed. Developing and applying quality standards has been a key to the Australian grain industry securing and maintaining advantage in markets. Currently Australian wheat quality is determined through a classification process to ensure every variety of wheat in a class meets the requirements needed for specific use. As quality is determined by both genetic and environmental factors well accepted wheat classification zones as well as of methods for assessing wheat quality attributes at receipt have been established. While meeting wheat quality standards is a requirement for new variety release, breeding to manipulate wheat quality attributes represents an ongoing challenge as many quality traits are difficult to directly breed for as the standard end-use assays used in varietal proving tests, such as baking tests, mostly require flour quantities only obtainable late in the breeding cycle. While there are exceptions, these assays are also often expensive making the assembly of large reference populations challenging. Large reference collections are required for accurate genomic based prediction approaches. These limitations have spurred efforts to develop methods that take advantage of high throughput, non-destructive and low sample input technologies, such as near infra-red (NIR), that can predict end-product quality traits with high accuracy. Phenotypic predictions from these methods can then be combined with genomic data, and in a best-case scenario, these can be used to predict genetic breeding values before grain is even produced from a new plant. These approaches have been under intense research development and are now being applied in commercial breeding programs. This talk will cover some of the work we have undertaken in this space and touch on how this work is finding application in breeding programs. Ultimately the goal is to open new ways of producing high performance grains that are super fit-for-purpose driving profitability throughout the value chain and protecting/enhancing the quality reputation of the Australian wheat industry.



Spikelet architecture, floret fertility and grain quality: the breeder's trinity of yield traits.

Dr Scott Boden¹, Dr Marianna Pasquariello², Dr Laura Dixon³, Ms Roshani Badgami², Dr Gernot Poschet⁴, Dr Pei Qin Ng¹, Associate Professor Iain Searle¹, Professor Cristobal Uauy²

¹University Of Adelaide, Urrbrae, Australia, ²John Innes Centre, Norwich, United Kingdom, ³University of Leeds, Leeds, United Kingdom, ⁴University of Heidelberg, Heidelberg, Germany

Inflorescence architecture is a major determinant of crop yield potential, with spikelet number and floret fertility contributing significantly to grain production. Breeders have harnessed natural diversity for inflorescence development to improve yields, and induced genetic variation has potential to provide further productivity gains. While wheat provides a fifth of the world's protein and calories, very little is known about the genes that regulate spikelet and floret development. Here, I will discuss our current understanding of the genes and processes that influence spikelet number and floret fertility in wheat, including work showing that induced genetic variation can produce novel variation for inflorescence architecture. This research includes the identification of semi-dominant alleles for a class III homeodomain/leucine zipper transcription factor, HOMEODOMAIN-2 (HB-2), on the A and D sub-genomes of common wheat, which generate more flower-bearing spikelets and enhance grain protein content. These alleles increase HB-2 expression by disrupting a microRNA 165/166 complementary site with conserved roles in plants; higher HB-2 expression is associated with modified leaf and vascular development, and increased supply of amino acids to the inflorescence during grain development. These findings enhance our understanding of the genes that control wheat inflorescence development and offer a new approach to improve the nutritional quality of grain.

Nicotianamine biofortified wheat as a nutritionally enhanced crop for future markets

Dr Jesse Beasley¹, Associate Professor Alexander AT Johnson¹

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Nicotianamine (NA) is an important chelator of iron (Fe) and zinc (Zn) in all higher plants and serves as the biosynthetic precursor to Fe-chelating phytosiderophores such as 2'-deoxymugenic acid (DMA) in graminaceous plants. Both NA and DMA are enhancers of Fe bioavailability and our research suggests that NA is the strongest enhancer of in vitro Fe bioavailability identified to date¹. We have employed constitutive expression (CE) of the rice nicotianamine synthase 2 (OsNAS2) gene to upregulate NA and DMA biosynthesis in bread wheat, resulting in higher concentrations of grain NA, DMA, Fe and Zn². Multi-location confined field trials of a low-copy transgenic CE-OsNAS2 wheat event (CE-1) over 3 consecutive years has demonstrated that CE-1 wholemeal flour, white flour, and white bread contains higher concentrations of NA, DMA, Fe and Zn, and that CE-1 white flour has higher Fe bioavailability relative to a null segregant (NS) control³. Multi-environment models of agronomic and grain nutrition traits in CE-1, NS and wild type plants revealed a negative correlation between grain yield and grain Fe and total protein concentrations, yet no correlation between grain yield and grain NA and DMA concentrations. The same models indicated that white flour Fe bioavailability was positively correlated with white flour NA concentration. These three complementary studies have caused a shift in our understanding of cereal Fe biofortification and suggest that NA itself should be targeted in wheat Fe biofortification efforts.

¹Beasley JT, Hart JJ, Tako E, Glahn RP, Johnson AAT (2019) Investigation of nicotianamine and 2' deoxymugenic acid as enhancers of iron bioavailability in Caco-2 cells. *Nutrients*, 11, 1502

²Beasley JT, Bonneau JP, Sanchez-Palacios JT, Moreno-Moyano LT, Callahan DL, Tako E, Glahn RP, Lombi E, Johnson AAT (2019) Metabolic engineering of bread wheat improves grain iron concentration and bioavailability. *Plant Biotechnology Journal* 17: 1514-1526

³Beasley JT, Bonneau JP, Moreno-Moyano LT, Callahan DL, Howell KS, Tako E, Taylor J, Glahn RP, Appels R, Johnson AAT (2022) Multi-year field evaluation of nicotianamine biofortified bread wheat. *The Plant Journal* 109: 1168-1182



TUESDAY 30 AUGUST 2022

Integrating genetics and agronomy for climate-adapted wheat

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Optimising phenology is critical to the adaptation of wheat to different growing environments across Australia. Research has highlighted the importance of an optimal flowering period, to ensure the critical period for yield development coincides with favourable seasonal conditions, whereby the risk of frost, heat and drought is minimised, and grain yield potential is optimised. Whilst this concept provides useful targets for growers to mitigate risk of abiotic stresses, they remain a major limitation to advancing wheat yields across Australia under a changing climate. Declining rainfall, seasonal variability and the increased likelihood of severe temperature events have increased the complexity associated with cultivar selection and sowing decisions. This presents a challenge for breeders, to release new cultivars which combine improved adaptation and stress tolerance, and for growers, to improve farming systems and agronomic practices to optimise genetic gains. This presentation will summarise recent research whereby integrating genotype × environment × management synergies have enabled growers to adapt to climate variability and maximise yield.

Physiology, anatomy and proteomic analysis reveal a metabolic pathway and stress-related root adaptations in bread wheat lines differing in salt tolerance mechanisms

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Salinity is one of the major abiotic stress constraints that affect crops globally. Salt tolerance in wheat can be obtained through combining shoot Na⁺ exclusion and tissue tolerance traits. The contribution of wheat root physiology and biochemistry to enhance salt tolerance is not well understood. We quantitatively compared root proteomic responses of 3784 proteins in bread wheat varieties Mocho de Espiga Branca (exhibiting tissue tolerance), Gladius (exhibiting salt exclusion) and Westonia Nax1 and Westonia Nax2 (exhibiting enhanced salt exclusion) alongside physiological analysis of root growth, function and ionic content. Analysis of 157 and 139 differentially abundant proteins obtained after 3 and 6 days of exposure to salt treatment showed that many stress-related proteins increased in abundance whereas a number of proteins involved in metabolism decreased in abundance across all genotypes. Westonia Nax1 and Westonia Nax2 lines, that express specific root Na⁺ transporters, increased glycolytic and oxidative phosphorylation machinery; fulfilling the energy demand required to exclude Na⁺ from the shoot. A metabolic bottleneck in the final steps of glycolysis during salt exposure was observed which altered pyruvate metabolism and its products in different ways between the wheat lines. Mocho de Espiga Branca and the Westonia Nax lines had constitutively higher levels of phenylpropanoid pathway (PPP) enzymes that utilise glycolytic products to synthesise lignin and increased them further during salt exposure. This was confirmed by histochemical staining of lignification observed in the central cylinder of the root. In contrast, Gladius reconfigured pyruvate metabolism to maintain glycolysis rather than induce PPP enzymes and accumulate lignin. Several proteins involved in the shikimate pathway and PPP including 3-dehydroquinate synthase, p-coumarate 3-hydroxylase (C3H), cinnamate 4-hydroxylase (C4H), and cinnamyl alcohol dehydrogenase (CAD) were identified as putative protein biomarkers, correlated with physiological traits, and could be used to screen wheat breeding populations for this salt stress metabolic adaptation of roots.

GWAS, KASP-SNP markers and haplotype-based pre-breeding for improving yield potential on sodic-dispersive soils in wheat (*Triticum aestivum* L.)

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Sodic-dispersive soils have multiple subsoil constraints including poor soil structure, high pH (>7), salinity, high subsoil toxic elemental ion concentration (boron, aluminium), and water-logging, affecting growth and development in wheat. Dispersive soils are common in the Australian agricultural landscapes and wheat growing regions around the world. Recent estimates show about 8-10% soils in Western Australian grain belt to be dispersive leading to heavy losses in production and grower income. Tolerance is required at all developmental stages to enhance wheat yield potential on such soils. An in-depth investigation of genome-wide associations was conducted using a two-year field phenotypic data of 206 diverse Focused Identification of Germplasm Strategy (FIGS) wheat lines from different sodic and non-sodic plots and the exome targeted genotyping by sequencing (tGBS) assay. A total of 39 quantitative trait SNPs (QTs), including 18 haplotypes were identified on chromosome 1A, 1B, 1D, 2A, 2B, 2D, 3A, 3B, 5A, 5D, 6B, 7A, 7B, 7D for yield and yield-components' tolerance to soil sodicity. Among these, three QTs had common associations for multiple traits, indicating pleiotropism and four QTs had close associations for multiple traits, within 32.38 Mb. The overlapping metal ion binding (Mn, Ca, Zn and Al) and photosynthesis genes, and transcription factors (PHD-, Dof-, HTH myb-, BHLH-, PDZ_6-domain) identified are known to be highly regulated during germination, maximum stem elongation, anthesis, and grain development stages. The homozygous/biallelic SNPs were identified for yield and crop establishment/plants m⁻². These SNPs correspond to HTH myb-type and BHLH transcription factors, brassinosteroid signaling pathway, kinase activity, ATP, and chitin binding activity (Published, 10.1007/s00122-021-04021-8). Further, the variants (SNPs and InDel) identified are functionally annotated and characterized using snpEff pipeline. The characterized variants are analyzed for their effects on protein based on type of impact (high, low, moderate and modifier) using the wheat genome binary database. The functional SNPs having higher phenotypic variation and allele frequency greater than five percent is now being converted to KASP-SNP markers and the rapid KASP-SNP assay will be validated in FIGS and double-haploid populations. These resources are valuable in haplotype-based breeding and genome editing to improve yield potential on sodic-dispersive soils.



Sodicity tolerant wheat selections, genomic regions and phenotyping improvement in Western Australia


Dr. Mirza Dowla¹, Dr. Roopali Bhoite¹, Mrs. Rosemary Smith¹, Dr. Karyn Reeves, Dr. Darshan Sharma¹
¹DPIRD,

Dispersive soils due to sodicity and alkalinity adversely affect crop production by its multiple soil constraints like poor soil structure, high pH, accumulation of different salt at toxic levels, soil crusting, waterlogging, etc. Breeding wheat, tolerant to sodicity is often limited by this complex nature of this constraint and difficulties in identifying sources of tolerance due to seasonal variability and high yield per se of the modern cultivars. We researched on phenotyping improvement and genomic exploration.

Phenotyping improvement: To identify lines carrying real tolerance, we compared three selection indices namely, simple ratio of yield (REI), ratio of genotypic effects (TI) after excluding site effects, and incremental crop tolerance (ICT) reflected as deviation from regression on two times sowing yield data. We found i) ICT is more efficient than the other two approaches in discriminating the tolerant lines from the intolerant lines, and ii) multiple times sowing data increases its efficiency further.

GWAS: To understand the genetics and mechanism of tolerance, we carried out genome-wide association studies (GWAS) on 206 Focused Identification of Germplasm Strategy (FIGS) wheat lines grown for two consecutive years at sodic and non-sodic sites. Among the identified 39 quantitative trait SNPs (QTSs), two QTS were associated with increased yield-ICT by 11.3% and 79.5% on the sodic site. Likewise, two QTS were found to increase the plant establishment-ICT by 24.2% and 37.6%, on sodic soil.

Germplasm development: Yield trials of F9 selected lines revealed seven selections outperforming or similar to scepter on sodic sites. These lines can be made available to breeding companies and research organisations.



Dissection of morphological, biochemical and grain formation pattern on fertility for the selection of heat tolerant wheat genotypes

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Heat stress is becoming increasingly common and a major threat to wheat production throughout the wheat belt. Plants use a variety of mechanisms to regulate reproduction and maximize plant fitness. Heat stress during the early reproductive development of wheat can severely affect floral development causing infertility and reduced grain formation due to damage in cellular structure from instability of membrane thermotolerance. This can affect various metabolic activities due to changes in photosynthesis or starch synthesis related to pollen development. It is hypothesised that identification of various traits contributing to heat stress tolerance and analysing their interactive effects would provide enhanced data for the selection of heat tolerant wheat genotypes. A study was conducted with four wheat genotypes of different level of heat tolerance in controlled greenhouse conditions to dissect the heat stress effects during meiosis on morphological and biochemical changes in pollen tissue to assess wheat fertility and grain formation. The data indicated that heat tolerant wheat genotypes can maintain a high number of viable pollen and sustain grain formation and yield potential under heat stress. Heat-tolerance in wheat genotypes is related to the level of decrease of unsaturated fatty acids in the pollen tissue rather than in the leaf. Changes in the lipids may have reduced anther size leading to pollen deformation which could have induced infertility. Pollen viability and grain formation within the spike were reduced in the florets due to heat stress. While adapting to heat stress, plants may compromise the sink in supplying the limited metabolites resulting in reduced grain formation. A dissection of all the parameters of pollen fertility, physical deformation, lipid metabolism, and grain formation pattern in response to high temperature can reveal an additional method for the selection of heat tolerant wheat genotypes.



Ice nucleating bacteria-hosting ability varies among wheat genotypes

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Grain frost seems to favour INB colonization on the seed surface but the number of INB populations varies depending on wheat genotypes and the severity of the frost damage. When exposed to a moderate level of frost damage, frost susceptible wheat genotype (Wyalkatchem) showed significantly higher (>100-fold) INB present on the grain compared to Young which is less susceptible. However, the variations were masked when either severe or very mild frost conditions prevail during grain filling. An increased level of sugars in frosted grains and plant tissue in response to cold exposure might hold the key to understand the link between INB colonization and genetic tolerance. At present, the correlation between INB population and percentage of frosted grain is not understood. For instance, it is not clear if the presence of INB on the seed caused the frost or if frost affected seeds provide favourable conditions for opportunistic INB to flourish. The cause and effect of the presence of INB on frosted grains needs to be investigated further to harness untapped opportunities to complement efforts to breed frost resistant cereal varieties which already proved elusive. The role of seed borne INB in repopulating the subsequent crop and sustaining the frost cycle for the next crop also remains to be investigated. In the meantime, growers are advised to avoid keeping frosted grain for seeding purposes to reduce frost risk. The use of qPCR and plate counting techniques have proven to be a powerful tool in detection and quantifying seed borne INB population with prospects for these techniques to be used in other environmental samples.



Current and emerging biotic threats

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Of the more than 25 root, foliar and head diseases of wheat in Australia, most are effectively managed through one or a combination of tools including host plant resistance, fungicides and/or cultural control. Diseases currently impacting wheat production, or difficult to manage, due to inadequate management options include: crown rot (national), stripe rust (north and south region), *Rhizoctonia* (south and west), *Septoria tritici* blotch (STB) and powdery mildew (south) and *Septoria nodorum* blotch (west).

Further to these current threats, emergence of new biotic threats is a perpetual risk. Unfortunately, it is often difficult to predict from where new threats will emerge. New threats can arise from pathogen evolution/introduction, changes in the farming system, re-emergence of previously controlled threats and loss of chemical control options.

Pathogens will continue to evolve due to sexual recombination and/or mutation and/or exotic introduction. These will have an impacts on currently effective strategies such as host plant resistance or fungicide control. Technological changes in the farming system, often in response to a changing climate, can result in emergence of new biotic threats. For example, stubble retention favoured stubble borne diseases such as crown rot. Another threat to wheat production is an inadvertent lack of attention to currently managed diseases, which can result in their re-emergence. An example in Victoria is the re-emergence of STB after ~40 years of effective control with partially resistant cultivars. It's re-emergence follows a change in the farming system, where wheat production has expanded in high rainfall zones, and a reduced emphasis by breeders who focused on more pressing diseases such as stripe rust.

With increasing reliance on fungicides, the development of resistance in pathogen populations or their loss through regulation is a significant threat. Recent Australian examples in wheat include the detection of resistance to Group 11 fungicides (QoI) and reduced sensitivity in Group 3 (DMI) in both powdery mildew and STB. The industry needs to avoid situations where fungicides are the only management tool available and use integrated management. The use resistant cultivars are an important component in protecting the longevity of fungicides.

To address these evolving threats plant breeders, pathologists and growers must collaboratively develop new management strategies fit for on-farm adoption using both traditional and novel approaches.




A dual role of labile carbohydrates in the algorithm of wheat yield

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Wheat accommodates environmental variation through grain number; correlations between yield and grain number in the range from crop failure to yield potential have typical $r^2 \sim 0.8$. Historically, this correlation was misinterpreted as cause-and-effect. Addressing this issue, we advanced an evolutionary perspective of Charles Edwards algorithm relating resources, grain number and grain size, and our conceptual model has more recently incorporated hierarchies in plasticity of yield components and genomic conflict between mother and offspring. Water-soluble carbohydrates (WSC) remain a gap in our model because WSC may buffer grain size but are largely unrelated to yield and involve trade-offs with grain number and root growth. In this paper, we ask if labile carbohydrates might have a hidden role beyond the trophic. We propose that high concentration of labile carbohydrates in wheat may challenge the osmotic homeostasis of aphids thus providing a working hypothesis that connects WSC with aphid resistance in cereals. Selecting against susceptibility to aphids and viruses may indirectly favour phenotypes with high concentration of WSC. The amount and concentration of labile carbohydrates should be regarded as functionally different traits, with amount relevant to the carbon economy of the crop, and concentration playing an osmotic role in plant defence against aphids and viruses.



Management of *Septoria tritici* blotch (STB) in wheat in the medium and low rainfall zones of southern Australia

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Septoria tritici blotch (STB) is a major foliar disease of wheat that can cause grain yield losses of up to 50% in susceptible varieties in conducive years. STB caused by *Zymoseptoria tritici* is increasing in incidence and distribution prevalence in the medium (MRZ) and low rainfall zones (LRZ) of southern Australia. This has been largely due to intensive cultivation of wheat, with no-till and stubble retention, leading to inoculum build-up. While the epidemiology of STB is well-understood in the HRZ, information on the disease factors leading to epidemics and potential losses in the medium and low rainfall zones (MRZ & LRZ) is limited. This fundamental information is required to allow for the development of integrated disease management (IDM) strategies that are specific for the regions.


To determine the impact of STB in Vic and SA's medium and low rainfall cropping zones, Agriculture Victoria in partnership with the South Australia Research and Development Institute conducted thirteen field experiments during 2021 investigating epidemiology, yield loss and management of *Septoria tritici* blotch (STB) in wheat. These experiments demonstrated that the potential for yield loss was mainly dependent on seasonal conditions, with high rainfall, low maximum temperatures, longer periods of leaf wetness were more conducive for STB development, spread and more likely to cause economic damage. Significant grain yield loss of up to 8% was recorded in Vic MRZ only. No significant loss was measured in the SA MRZ or LRZ in either SA or Vic. Significant yield losses occurred in the highly susceptible cultivars with those rated better than susceptible (S) showing no yield loss. This demonstrated that growing better rated varieties would likely be adequate to manage STB, however further research is required from growing seasons with more favourable conditions that increase the risk of disease. Fungicides for STB control demonstrated effective suppression during 2021 in both the MRZ and LRZ regions of southern Australia.

Identification of novel septoria nodorum blotch resistance of wheat

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One of the most economically important necrotrophic fungal disease of wheat is septoria nodorum blotch (SNB) which is caused by the Dothideomycete fungal pathogen *Parastagonospora nodorum* (*P. nodorum*). The majority of the disease incidence could be explained by multiple components of interactions between necrotrophic effectors (NEs) produced by the pathogen and matching dominant susceptibility genes carried by the host. To date, five of such interactions have been characterised including SnToxA-Tsn1, SnTox1-Snn1, SnTox3-Snn3, Tox5-Snn5 and Tox267-Snn2/6/7 and no resistance mechanism has been reported in this pathosystem. In this study, a broad SNB resistance wheat line was identified from CAIGE collection and QTL mapping was used for 22 SNB related traits including different pathotypes, different plant stages, for both invitro and planta. Results obtained have revealed 1) QTL consistently detected with different isolates and conditions such as those found on 2A, 2B, 5B and 7B; 2) 10 and 7 QTL detected where low disease alleles were derived from resistance and susceptible parents, respectively; 3) Six and four QTL that only found associated with culture filtrates or whole plant infection assays, respectively. This will help to determine which QTL will be focused in the future for gene cloning and resistance mechanism investigation. Implication of this findings for future research activities and molecular SNB resistance breeding will be discussed.




Untangling the ‘Gordian knot’ – How to unravel a complex fungal disease of wheat by understanding its game of effector hide-and-seek

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Breeding for durable resistance to fungal diseases is a continual challenge for crop breeders as fungal pathogens have developed many ways to overcome host resistance. Association studies (AM) using mapping populations infected with pathogen mixtures, is frequently used to seek out novel sources of genetic resistance. However, QTL linked to disease resistance detected through AM are often minor or inconsistent. This is a particular problem with septoria nodorum blotch (SNB) of wheat caused by *Parastagonospora nodorum*. *P. nodorum* uses a suite of proteinaceous necrotrophic effectors (NEs) to cause necrosis on wheat carrying a matching dominant susceptibility gene (*Tsn/Snn*). Interactions between these NEs are complex during infection. Once thought to quantitatively contribute to SNB, we now know that NEs suppresses each other's contribution to disease through complex epistatic interactions. Alluding to the title, the Gordian Knot has often been used as a metaphoric representation of a difficult problem that can be solved using an unconventional approach. We liken the complexity of effector epistasis to the Gordian knot of SNB that impedes progress in resistance breeding. In our study, a genetic element called PE401 was discovered in the promoter of the *Tox1* NE gene (John et al. 2022 PLOS Pathog.). PE401 functions as a transcriptional repressor of *Tox1* and suppresses the contribution of *Tox2A-Snn2A* interaction in SNB. *P. nodorum* isolates in Australia generally lacked PE401 and favour the *Tox1-Snn1* interaction in SNB, as opposed to most other wheat-growing regions of the world where *P. nodorum* isolates predominantly harbour PE401. In the context of crop protection, constant surveillance of the pathogen population for the frequency of PE401 in conjunction with NE diversity will enable agronomists to provide the best advice to growers on which wheat varieties can be tailored to provide optimal SNB resistance to regional pathogen population genotypes. Furthermore, we advocate for the removal of *Snn1* and *Snn2A* in wheat to further minimise the impact of SNB. So, did we manage to cut the Gordian knot? Not completely, but at least a substantial nick was made where *Tox1-Snn1* is.



Recent progress in Fusarium crown rot resistance in wheat

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Fusarium crown rot (FCR), caused by various Fusarium pathogens, is a chronic disease to wheat and barley production worldwide. This disease has become more prevalent in recently years likely due to the wide adoption of minimum tillage and stubble retention. Several loci conferring FCR resistance have been reported in wheat. However, previous studies found FCR assessment could be affected by other characteristics including plant height, growth rate as well as drought stress. For removing the interference of these characteristics and accurately assessing effects of these loci, near isogenic lines (NILs) have then been generated for several of them. Facilitated by transcriptome profiling, markers tightly linked several of these loci have been obtained by analysing NIL-derived populations. These markers and populations form solid foundation for cloning genes underlying each of these resistance loci. With the assistance of the diagnostic markers developed, these loci were pyramided, and the results showed gene pyramiding could be effective in enhancing resistance to this disease in wheat. However, only limited number of loci have been identified and additional resistant sources are required. In our current GRDC project, we aimed to introduce a new gene Fhb7 into Australian wheat. Different from Fhb1 which confers resistance to Fusarium head blight but not to FCR, our initial results showed that Fhb7 seems to provide resistance to both Fusarium head blight and FCR. Effects of Fhb7 against different Fusarium pathogens under field conditions in different environments and interactions between it and other resistance loci are being evaluated.

Intermediate host resistance to new variant of the barley grass stripe rust pathogen in common wheat

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Wheat is considered a near-non or intermediate host to the barley grass stripe rust pathogen (*Puccinia striiformis* f. sp. *pseudo-hordei*, Psph) based on low frequency susceptibility observed in commercial cultivars and wheat landraces. Recently, Psph has acquired new virulence that renders a high susceptibility response in wheat genotype Morocco.

It was previously reported that the Australian cultivar Teal was susceptible to Psph (isolate 981549) and Avocet (carrying genes Yr73 and Yr74 that act in a complementary manner to confer resistance to the wheat stripe rust pathogen *P. striiformis* f. sp. *tritici*) was resistant. A Teal x Avocet (T/A) doubled haploid (DH) population was developed and used to map resistance to Psph isolate 981549. Key resistance regions were mapped to chromosomes 3D (Yr73) and 5B (Yr74). DH lines carrying both Yr73 and Yr74 were consistently resistant, suggesting that these genes also confer complementary resistance against Psph. Fewer DH lines were susceptible than expected if resistance was reliant on these genes alone, suggesting the resistance was more complex and additional regions were contributing resistance.

The detection of a new isolate of Psph in 2021 (isolate 20211524; Park RF unpublished) allowed us to further dissect the genetics underlying this relationship. The T/A population was assessed for disease response to isolate 20211524 and QTL analysis was conducted with the 9053 DArT-Seq markers. Key resistance mapped to chromosomes 2B and 5B (Yr74). Lines identified as carrying both Yr73 and Yr74 by molecular markers remained resistant suggesting the Yr73+Yr74 complementary resistance maintained its effectiveness against the new Psph isolate.

The region on chromosome 2B was identified through genetic mapping of disease response to both isolates of Psph and should be further investigated. Several populations based on Avocet and Morocco are under development to allow identification of the gene/s defeated by the new Psph isolate and to map their location/s. This study highlights the importance of monitoring pathogen populations for the emergence of new virulence, even in pathogens that are considered to be non-adapted to important crop species.

Mitigating the effects of stripe rust on wheat production in south Asia and eastern Africa: Genome wide association mapping of wheat for resistance to *Puccinia striiformis* f.sp. *tritici*

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This project is systematically reducing vulnerability to wheat stripe/yellow rust (WYR) in south Asia and eastern Africa by establishing, equipping and mobilising a collaborative network of key cereal improvement centres and a knowledge base to enable research and development. Stripe rust has caused devastating epidemics in south Asia, is a serious problem in the highlands in eastern Africa and recently has become more severe in many regions, extending its footprint into warmer areas where historically it had not been a problem.

A collection of 250 lines comprised of 50 lines from 5 geographic regions; Australia, Ethiopia, India, Nepal, Pakistan to create a genetically diverse collection. Infinium genotyping data analysis was conducted by AgriBio returning 48,180 SNPs with 38,871 chromosome and target SNP position (Mbp) in Chinese Spring IWGSC assembly v1.0. Genotypic data did not strongly cluster by origin indicating historic germplasm exchange. Australian and Indian varieties clusters were most disparate from each other. Phenotyping under the environments of Ethiopia, India and Nepal, revealed a strong genetic relationship.

The collection was screened for response to WYR disease caused by *Puccinia striiformis* f. sp. *tritici* (Pst) and 31 field data sets were recorded from different environments during the 2017 – 2020 crop seasons. Six field screens were conducted in Australia with four in NSW and two in WA. Phenotypic data were recorded, each from Ethiopia (Bekoji, Debre Zeyit, Kulumsa and Meraro), India (Jammu and Karnal), Nepal (Kabre and Khumaltar) and Pakistan (Attock, Faisalabad, Islamabad, Narrowal and Nowshera). Two disease response nurseries were also established in Kenya.


Phenotypic correlations between resistance levels expressed between environments within and across countries indicated that plant performance across all regions was strongly correlated with the exception of Ethiopia. Of the five Ethiopian sites Kulumsa was the only site correlated with the other areas, therefore, recommendations relevant to other sites cannot be applied to Bekoji, Debre Zeyit, and Meraro.

Multipathotype testings were conducted in the greenhouse at the Plant Breeding Institute, allowing the postulations of ASR (all stage resistance) genes. Individuals were also screened with molecular markers targeted for Yr18, Yr36 and Yr46. Eighteen lines were considered candidates for uncharacterised all stage resistance (UASR), showing resistance at the seedling stage not consistent with any known ASR. Fifty lines were susceptible to all the pathotypes at the seedling stage and resistant as adult plants in the field. Eleven lines showed the presence of Yr18 marker and one with Yr46 and the rest, 38 were negative for molecular markers that identify known adult plant resistance (APR) and hence carry uncharacterised APR. Lines carrying Yr18 or Yr46 marker showed high levels of APR in comparison to the near isogenic lines of Yr18 and Yr46, indicating the presence of uncharacterised APR as well.

Genome wide association analysis was conducted on field scores of APR, and 20 QTL were detected.

The QTL of the highest frequency was located on 3A in Pakistan. Two regions were detected across the environments, one QTL at the top of 2A was detected in Australia and Pakistan and one QTL at the top of 1B was detected in both Australia and Nepal. There were no QTL detected on the D genome.

This study contributes to the knowledge of Pst resistance in south Asia and eastern Africa wheat germplasm and our ability to identify adapted wheat germplasm carrying diverse sources of resistance to WYR, and the development of molecular markers linked to APR genes.



Characterisation of diverse sources of rust resistance from the Watkins Collection of common wheat landraces

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We tested a set of pre-Green Revolution tall wheat genotypes, collected by an English botanist Arthur Watkins during the 1920s to 1930s, and identified candidates for detailed genetic analysis of rust resistance. Resistance to rust diseases is categorised into two types: all-stage resistance (ASR) and adult plant resistance (APR). The genes that condition ASR impart resistance throughout the life of a plant against avirulent isolates of the target pathogen and APR genes are effective at the post-seedling stages only. While ASR is vulnerable to breakdown due to evolution in pathogen populations, APR is assumed to be long-lasting. However, combination of more than two APR genes is essential to achieve commercially acceptable level of resistance. ASR genes Yr47, Yr51, Yr57, Yr63, Yr72, Yr81, Yr82, Lr52, LrAW2 and Sr49 have been already named in genotypes belonging to this collection. Yr80 is the only APR locus formally named so far from this collection; however, characterisation of several APR loci is in progress. The identified genotypes carry pleiotropic loci Yr29/Lr46/Sr58/Pm39 and/or Yr46/Lr67/Sr55/Pm46 in addition to at least one putatively new rust resistance locus. We developed large recombinant inbred line (RIL) populations and differentiated these populations into single known APR gene (Yr29/Lr46/Sr58/Pm39 or Yr46/Lr67/Sr55/Pm46), combination of both genes and those lacking these genes using markers linked with these loci. The RILs that lacked Yr29/Lr46/Sr58/Pm39 and Yr46/Lr67/Sr55/Pm46 allowed us to conduct genetic analysis of stripe rust and leaf rust resistance, whereas the remaining two categories facilitated understanding of interaction of known APR loci (Yr29/Lr46/Sr58/Pm39 and Yr46/Lr67/Sr55/Pm46) with the yet uncharacterised gene(s). This presentation will cover progress of characterisation of genetically diverse sources of rust resistance from pre-Green Revolution tall wheat landraces.



Manipulation of stomata to increase yield potential in wheat

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Plant water use is a fundamental component of plant growth and productivity and is mainly controlled by stomata. In wheat-growing regions, water is increasingly scarce due to dryer and warmer climates, reducing plant growth and final grain yield. The negative impact of water scarcity on crop production can be mitigated by developing wheat varieties with efficient use of available water that maximise yield. As part of a collaboration with the International Yield Partnership Program, the aim of this work is to develop and characterise new wheat germplasm with altered stomatal phenotypes to improve yield and yield stability under the impacts of climate change. Using a reverse genetics approach, we screened TILLING Cadenza mutants for mutations in five genes involved in stomatal development and function (MUTE; OST1; SLAC1; YDA1; YDA2). 44 lines with the desired mutations were identified. Mutant lines were grown in a glasshouse under well-watered and drought conditions and were characterised for stomatal phenotype, daily plant water use and water-use efficiency. We identified mutant lines with up to 20% increase and up to 80% decrease in water-use efficiency. Lines contrasting for water-use efficiency will be further tested in field conditions to assess yield.



Adapting wheat to heat and drought in current and future climates

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Heat and drought stress limit wheat production in major production regions worldwide. With climate change, increases in CO₂ concentration, temperature, evaporative demand and rainfall variability are projected to impact different crop processes and their interactions. Here, we used a modelling approach to characterise the type of abiotic stresses that wheat crops are currently and will experience in projected climate scenarios across the Australian wheatbelt. Over the last 30 years, wheat crops (when considering at the same genotype and management, e.g. Janz sown on May 15) have been increasingly affected by post-flowering heat stress, drought and frost. To best tune crop development with environmental variability, genotype and management adaptations were assessed in terms of crop maturity type and sowing date for current and future climate scenarios. Overall, for the future climate scenarios tested, results highlighted a shift towards earlier optimum sowing windows or earlier maturing genotypes by 2050. Heat and its interaction with drought appeared as the dominant sources of yield loss across the Australian wheatbelt in the future climate scenarios. The results, as well limitations relative to future projections and advance in possible physiological adaptations will be discussed to promote increasing yield across the Australian wheatbelt.

Exploring root-shoot dynamics to enhance yield potential and stability of future wheat cultivars

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In theory, root systems of future wheat cultivars could be optimised to enhance soil resource capture and improve both productivity and sustainable production. However, most breeding programs are reluctant to select for root traits due to several reasons: direct selection is laborious; there is a lack of reliable and robust markers and a high degree of plasticity under complex genetic and environmental control. Furthermore, despite considerable phenotypic diversity for root traits identified using phenotyping under controlled conditions, the role of these traits to support yield in different environments is yet to be quantified. To explore the value of specific root traits, we developed introgression lines with different configurations of root angle and root biomass in four elite wheat backgrounds using an innovative single plant selection technique. Importantly, the lines were selected for divergent root traits while maintaining similar above-ground characteristics, such as flowering time and plant height, which influence the timing of water-use and carbon partitioning. In 2021, the lines were evaluated in a field experiment at Gatton, Queensland. Integrated root and shoot phenotyping were performed to 1) validate and characterise changes to root distribution, and 2) gain new insights into the relationships between above- and below-ground development. Extensive root coring of the introgression lines identified lines with significantly altered root distributions in each genetic background. Notably, several introgression lines in each of the backgrounds displayed significantly different root distributions but maintained similar above-ground development. This highlights the opportunity to tailor root-shoot trait combinations for specific environments. Results also highlight the potential for breeders and researchers to target UAV-derived canopy traits as 'proxy traits' to support indirect selection for root traits. Finally, we explored the value associated with the root traits by yield testing the introgression lines at 12 sites across the Australian wheat-belt in partnership with LongReach Plant Breeders. Our multi-environment trial analyses provide new insights into genotype by environment interactions for yield and the potential of root traits to improve yield potential and stability. The introgression lines provide valuable genetic resources for the wheat community to further study the value of root systems in different production scenarios.



Genomic prediction of APSIM Next Gen phenology model parameters in wheat using machine learning

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Accurate prediction of flowering time of wheat (*Triticum aestivum*) cultivars grown in the field helps growers minimise yield reductions due to abiotic stress. To maximise yield, the cultivar choice and sowing date must ensure flowering of the crop coincides with optimal seasonal conditions. Currently flowering time prediction is achieved using APSIM Next Gen (Agricultural Production Systems Simulator). The current model relies on parameters derived from phenotypic data, which involves measuring development stages of genotypes in four different environments: vernalised and unvernalsed, in both long and short days. The data is used to derive parameters which form the basis for the current mechanistic APSIM Next Gen model. The collection of this data for each new cultivar released is time consuming, laborious, and expensive. Advances in genomics such as the development of the Infinium XT 40K SNP array have provided researchers with new methods to acquire high quality whole-genome data. If this data can be used to predict APSIM Next Gen model parameters, flowering time estimates could be available upon cultivar release. We phenotyped 262 genotypes from the OzWheat Diversity Panel in four different environments, and are using these results in combination with existing genetic data to train a machine learning algorithm that can predict phenology parameters in APSIM Next Gen. The model will be validated using previously collected field data of the same genotypes. With this new genetically defined method of parameterisation, both breeders and growers of wheat will be able to access flowering time predictions and therefore optimal sowing date for a given environment faster and more affordably.




Spatial Models for Colocated Trials

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Breeding programs evaluate varieties using trials conducted at various locations and years with the combination of the two often being termed an environment. An early stage plant breeding trial conducted in a particular year and location is often very large, phenotypically evaluating a large number of cultivars. A large trial such as this is often split into several smaller trials/management blocks, the smaller trials may even correspond to different stages of the program. Furthermore these smaller trials are usually conducted in the same field with; (i) very similar management practices, (ii) sowing dates and (ii) harvesting dates. In this instance they are referred to as colocated trials and are considered to be in one environment. In contrast if trials in a particular year and location do not satisfy (i), (ii), (iii) they will not be considered to be colocated and would be considered to be in different environments. In the literature there is limited information on appropriate statistical models for the analysis of such colocated trials. Thus we aim to address this by investigating several statistical models used to analyse such colocated trials and recommend which one should be used in different scenarios. Each method used assumes a different spatial process is occurring on the field and are extensions of the baseline model used in Gilmour et al. (1997) for single trials to colocated trials. Of course there are limitations to which spatial process can be assumed if information is not known about the layout or configuration of trials and thus information pertaining to the distances between plots in different trials. We conducted an in silico experiment designed to compare and assess the performance of the approaches over various scenarios. We present the results of that simulation study and final recommendations on which models should be used to analyse colocated trials.

Gilmour, A. R., Cullis, B. R. & Verbyla, A. (1997). Accounting for Natural and Extraneous Variation in the Analysis of Field Experiments, vol. 2.




QTL Mapping for Nitrogen Use Efficiency (NUE) Based on A High-Density Consensus Map of Wheat

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Nitrogen is not only an essential element for wheat growth but also a major determinant for wheat yield and protein quality. Nitrogen use efficiency (NUE) is a key factor in wheat production profit, either through enhancing grain yields (GY) and grain protein content (GPC) or reducing fertilizer costs. NUE is defined as $GY \cdot GPC / N$ supply thus both GY and GPC are targeted. So far, researchers have carried out QTL mapping on the NUE related traits using recombinant inbred lines (RIL) and doubled haploid (DH) populations under different nitrogen levels. Since most of the QTL mapping is based solely on a single mapping population with limited genetic background, genetic regions identified are less abundant and have lower effects. Compared with a single linkage map from one population, a consensus map generated from multiple genetic populations with better genetic coverage will be more efficient in QTL mapping analysis for important traits. The Murdoch University wheat research group has developed six DH populations. Based on these six populations and 90K SNP array analysis, a high-density consensus map was constructed containing 11,643 markers. Combined with field trials, six major QTL clusters for NUE and related traits were detected on six chromosomes, explaining 4.7 – 20.8% of the phenotypic variances across environments. Two major QTL clusters (CI-2D and CI-4D) showed a favourable relationship between GY and GPC, suggesting it is feasible to improve the grain yield and NUE simultaneously. A total of 176 potential candidate genes were associated with these six major QTL clusters. The use of consensus map from six genetic populations in NUE QTL mapping analysis is unprecedented, meanwhile, further identification and validation of candidate genes, target alleles and gene-based SNP haplotypes in those QTL clusters can accelerate the improvement of NUE in wheat breeding programs.




Do adult plant rust resistance genes in wheat interact with each other to fight against their rust enemies?

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Wheat plants defend themselves against rust pathogens in two different ways. All stage resistance where the crop is protected throughout its lifespan however only against selected rust pathotypes. On the other hand, adult plant resistance (APR) genes are functional only at the later stages of crop growth, some of which have proven to be effective against almost all pathotypes of a single or multiple rusts and mildew pathogens. Furthermore, some APRs are durable as their presence still allows the pathogen to infect and proliferate, albeit at a slow phase. One of the interesting questions is, do they interact with each other to provide stronger resistance? We have generated different APR gene combination lines in Thatcher wheat background and tested them in natural field conditions. Furthermore, transcriptomic analysis is being used to predict any cross-talk between APRs that shows enhanced resistance when present together.



Variations in genotypic responses to heat stress on grain size and quality in wheat

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In Australian cropping systems, heat waves during grain filling adversely impact grain yield and grain quality of wheat. The influence of critical post-anthesis heat stress on grain size and grain composition was investigated both (i) in controlled environments for sister lines SB003 and SB062 which have contrasting heat tolerance, and (ii) in irrigated field trials with 28 or more genotypes. Field trials were conducted at three locations across southern Queensland, Australia, for three consecutive years in 2018, 2019 and 2020, with conventional and late sowing dates. To focus on plants that were subjected to heat stress at the same developmental stage irrespective of the maturity types of the genotypes, field trials were conducted not only with conventional plots but also using artificial lighting to extend the photoperiod.

The greatest impacts of heat stress on grain size as well as protein and starch concentrations were observed when heat stress occurred early to mid-grain filling. In controlled environments as in the field, genotypes which retained green leaf area longer after anthesis (stay-green phenotype) tended to exhibit less impact on grain size and yield. By contrast to its sister line SB003, the heat-tolerant line SB062 had a stay-green phenotype and exhibited no significant impact of some heat treatments on grain size. SB062 was also impacted for grain protein and starch contents. Genotype x environment interactions were observed for grain size and grain quality. Late-sown crops, which experienced more heat shocks during the early to mid-grain filling period, had significantly reduced protein and starch contents.

The findings of this study will help to develop screening methods to identify genotypes that maintain grain quality in the presence of late-season heat stress.

Keywords: grain filling, field trials, genotypes, grain size, protein and starch concentrations.

Is lipid metabolism in leaf and pollen tissue altered by heat stress, and does this affect pollen viability in wheat (*Triticum aestivum*)?

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Global warming has been the most discussed environmental issue for the past decade. With the global mean temperature rising, the heat stress affecting wheat (*Triticum aestivum*) production, a major grain crop in Australia. Heat stress disrupt plant growth, reduce pollen fertility, and lower grain yield. It is essential to breed heat-tolerant wheat varieties that can adapt to higher temperatures. This project aims to investigate the effect of heat stress on wheat leaf, and pollen tissue lipidome and pollen viability, and the association between these two traits. Four wheat genotypes bred by the Plant Breeding Institute (PBI) of Sydney University were evaluated at PBI, Camden, NSW under control and heat-stressed environments. A total of 40 samples were processed. The decrease in unsaturated fatty acid C18:3 (α -linolenic acid) and C18:2 w6c (linoleic acid) were observed in heat-tolerant genotypes #45 and #245, and susceptible genotype #51 after 10 days of heat stress in leaf tissues. Similar trend was found for pollen tissue, with the same fatty acids mentioned above significantly reduced under heat stress, while genotype #45 were less affected. An increase in saturated fatty acid C16:0 (palmitic acid) due to heat stress was observed in all genotypes. Leaf fatty acid composition was less affected than pollen fatty acid composition under heat stress. Plant heat tolerance is more related to pollen tissue fatty acid alteration than in leaves. Reduced pollen viability after heat stress was found in all genotypes, while pollen of tolerant genotypes was less affected compared with susceptible genotypes. Unsaturated fatty acids in the wheat leaf may be positively associated with pollen viability under heat stress due to the similar leaf and pollen lipidome response under heat stress. However, data analysis suggests a lack of correlation between leaf lipid alteration and pollen viability. More research on other heat tolerant and susceptible varieties could be done to further understand the relationship between leaf tissue fatty acid and heat stress.

From lab to field: a major QTL to modify root system architecture in elite durum wheat

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Root system architecture (RSA) is a representation of the spatial and temporal distribution of root growth in the soil, which is critical for water uptake throughout the season. Root systems are complex in nature and comprise a large number of component traits. In durum wheat, a key trait that influences the direction of root growth is seminal root angle. Recently, we identified a major QTL for seminal root angle on chromosome 6A (i.e. qSRA-6A), which appeared to be independent of root biomass. However, the influence of qSRA-6A on the root architecture of mature plants and its value for yield improvement remained unclear. To evaluate the potential to modify RSA through targeted marker-assisted selection (MAS) for this locus, we implemented a rapid backcrossing strategy to introgress the narrow-angle allele into the durum variety DBA Aurora. Kompetitive Allele-Specific PCR (KASP) markers were developed for the qSRA-6A locus to facilitate MAS. Repeated cycles of backcrossing and selection were accelerated using speed breeding to rapidly generate a set of introgression lines. To validate changes in RSA, the lines were evaluated in a series of root phenotyping experiments performed under both controlled conditions (agar plate and rhizobox) and in the field ('core-break' method). Our results highlight the impact of qSRA-6A from lab to field, as evidenced by dramatic changes in root growth angle in gravitropism experiments and significant differences in root distribution under field conditions. DBA Aurora lines carrying the narrow-angle allele produce more roots in the deepest soil layer, which may be beneficial for accessing moisture in deep soil layers under terminal drought conditions. On the other hand, lines carrying the wide-angle allele produced more roots in the upper soil layer, which could enhance yield potential in environments where soil resources are not limiting. The highly context-dependant value of the qSRA-6A presents both challenges and opportunities to deliver yield benefits on farm. We envisage an exciting opportunity for innovative research into genotype by environment by management interactions to identify optimal trait-management packages that could be adopted to help close the yield gap and maximise grower profitability.

Post anthesis mild water stress can accentuate differences in late deep root development between wheat genotypes

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The root system plays an important role in crop performance particularly under rain fed conditions. Limited crop production under water deficit conditions requires a genetic solution because irrigation and some other management practices are not a viable option in many cropping areas. Narrow and deep roots can help wheat to extract more water at depth late in the season and improve yield and yield stability. Particularly where crops rely for grain yield on stored moisture deep in the soil. The objective of this study was to determine the effect of timing of water stress on wheat root development late in the season. We examined shallow and deep root growth of two wheat cultivars, Mace and Scout, under well-watered and terminal water-stress conditions during late development. Mace is typically cultivated in western Australia while Scout is cultivated in southern Australia. Plants were grown in 1.5m poly vinyl chloride (PVC) tubes under (i) well-watered conditions, (ii) mild water stress, withholding water between early anthesis to early grain filling or (iii) mild water stress, withholding water between mid-grain-filling to maturity or (iv) severe water stress, withholding water from anthesis to maturity. There was little difference in dry root biomass between genotypes under well-watered conditions either at anthesis or at maturity ($p \geq 0.05$). When water was withheld between early anthesis and early grain filling and between mid-grain filling and maturity, Scout had higher dry root biomass at maturity than Mace for both shallow (30-40cm) and deep roots (110-120cm). Under severe water stress, both genotypes were similarly severely affected leading to decreased dry root biomass. These results suggest that mild water stress when applied at selected stages of development can be used to highlight and identify wheat genotypes whose root architecture is better adapted to terminal drought.



100-day Wheats for Adaptation to a Changing Australian Climate

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Climate change is a threat to the Australian wheat industry. The combined effects of declining autumn rainfall, increasing temperatures and carbon dioxide levels, and more severe and unpredictable frost risk sets a future challenge for Australian grain growers. Farming systems need to continue to evolve and adapt to climate change, as well as production risks such as herbicide resistance, pest and disease threats, as well as declining soil fertility. It has been proposed that a '100-day' wheat ideotype, able to be sown later than current commercial wheat varieties in mid-winter, would provide southern Australian growers with an alternative management option. This ideotype would require early vigour under cool temperatures, quick development, and yield potential equivalent to, or greater than current elite varieties. A variety developed based on this ideotype would mitigate the need for the autumn break by being sown later in the season (mid-winter), into seedbed moisture, while reducing the risk of exposure to pests and diseases often associated with longer-season wheats. Mid-winter sowing would also provide more time for targeted weed management prior to sowing, in addition to expanding the opportunities for double cropping. The aim of this PhD research project is to identify the plant traits or characteristics which define the "100-day wheat" ideotype. A preliminary field experiment was conducted in 2021 at Wagga Wagga, evaluating 96 Australian and international wheat lines for early biomass, flowering time, grain yield, and harvest index across two sowing dates (7 June and 12 July.) Lines used in this experiment were all purportedly fast maturing but had not been selected for yield potential. We measured significant differences in time to flowering, biomass at stem elongation, flowering date, and yield amongst the lines. Some of the lines had equivalent and greater yield to elite commercial lines indicating that there is germplasm available which could be adapted for this purpose. Future research will focus on early growth under low temperatures, as experienced during winter sowing, in particular the interactions of flowering genes on early vigour.

Adaption of Australian wheat to warmer growth environments

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Wheat yield is sensitive to high temperatures, particularly during and post-reproductive development. Adaptation to warmer growing seasons in Australia could benefit from exploiting variation of agronomic traits that are key drivers for wheat yield under stress. We investigated yield and yield attributes of 30 elite pre-breeding and commercial wheat lines known to vary in thermotolerance, grain quality, and yield in field-based high temperature experiments. The trials consisted of 17 thermal environments imposed by varying time of sowing across field sites in NSW, Victoria, and WA over three seasons (2017 to 2019). Daily temperature at anthesis in these environments ranged from warm to hot (average 11.4-20.8 °C, and maximum 27.9-37.6 °C). To assess the likelihood of traits adapting to warmer conditions, we estimated broad-sense heritability. Heritability was low to moderate for biomass (0.15-0.76), but high for phenology (0.53-0.92), grain attributes (0.49-0.93) and yield (0.56-0.92). Furthermore, heritability values for some grain attributes (protein and screening percentage) showed positive linear relationships with average seasonal temperatures. These results indicate that some grain attributes and yield are likely to adapt faster to warmer growth environments than biomass. It is unclear if the differences between biomass and yield or grain attributes are due to genetic trade-offs following sustained breeding for improved yield and grain attributes under high temperatures. In this paper, we will explore genetic correlations of traits between and within different times of sowing to better understand genotype performance under different heat profiles (heatwave, warming or both). Additionally, genetic correlations were modelled between yield and other traits across some environments, to further investigate the contribution of these other traits to yield under warmer growing environments.

Rotational intervals and tillage methods required to reduce yellow leaf spot inoculum

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Yellow leaf spot (YLS) is a stubble-borne foliar disease of wheat caused by the fungus *Pyrenophora tritici-repentis*. It is common in south-eastern Australia and can cause significant grain yield and quality loss. The three main factors that contribute to YLS severity and grain yield losses are 1) variety resistance/susceptibility, 2) growing season rainfall, and 3) inoculum load in the form of crop residues. This study was conducted to identify decision rules for growers to inform intervals between crop rotations and stubble management techniques that minimise YLS inoculum before planting a wheat crop. This study used PREDICTA[®]B soil/crop debris testing to monitor YLS inoculum amounts following different tillage methods at various phases of wheat-pea-canola rotations in the Sustainable Cropping Rotations in Mediterranean Environments (SCRIME) experiment at Longerenong, Victoria. The SCRIME experiment, is a long-term study established during 1998 in a medium rainfall (~450 mm annually) zone environment in Victoria to evaluate grain yields and profitability of various crop rotations and tillage treatments.

Soil and crop residues were sampled and PREDICTA[®]B testing undertaken during 2017 and 2018, following a three-year wheat-peas-canola rotation. Three different tillage treatments were sampled: conventional (mechanical) tillage; reduced till (crop debris burning); and no till. All treatments were compared to a continuous wheat treatment.

Seasonal conditions significantly ($P < 0.05$) affected inoculum loads, with higher YLS loads of 4508 kDNA/g in 2017 samples compared to 1831 kDNA/g in 2018 in the continuous wheat treatment. Inoculum loads decreased annually by similar amounts regardless of tillage treatment and inoculum amounts decreased significantly with each season. For 2017 samples, inoculum significantly decreased as number of seasons between wheat plantings increased. Where wheat was grown the previous season, inoculum was 1062 kDNA/g, significantly less than the continuous wheat treatment. A one-year break from wheat significantly decreased inoculum to 186 kDNA/g, and a two year break reduced to 20 kDNA/g. For 2018 samples, there was no significant difference in inoculum between wheat grown the previous season (1083 kDNA/g) and continuous wheat (1831 kDNA/g). Both a one-year break and a two-year break from wheat significantly decreased inoculum to less than 7 kDNA/g. While there were differences in both 2017 and 2018 between the inoculum loads following different tillage methods, they were not significant ($P = 0.05$).

This study showed that at least two seasons between wheat rotations were required to reduce YLS inoculum amounts to levels unlikely to reduce wheat yields. Stubble management methods such as burning and cultivation did not provide any additional reductions in a long term strategy.



On the use of factor analysis and iClasses to assess genotype by environment interactions in falling number across Australia.

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The Hagberg-Perten falling number (FN) test is the industry standard to measure starch degradation cause late maturity α -amylase (LMA) enzyme activity in flour. In a recent study Sjoberg et al (2020) investigated the utility of a factor analytic mixed model to assess overall performance and stability of FN for a set of 129 soft wheat genotypes grown in 35 environments. They concluded that examination of factor loadings enabled the separation of environments and genotypes which were responsive to either pre-harvest sprouting or late maturity alpha amylase.

In this talk we use a multi-environment trial dataset spanning 6 years from 2014-2019, with more than 230 environments and 123 genotypes to examine the extent of genotype by environment interaction (GEI) in the Australian wheat growing regions. We use the so-called iClass approach of Smith et al (2021) to examine the overall performance within environment types with the same or similar GEI. We will also present some preliminary results on the relationship between overall performance within iClasses for FN and the propensity to express LMA based on the laboratory assay of Mrva and Mares (2001).

Late Maturity α -Amylase (LMA) and its implications for wheat breeding

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Late maturity α -amylase (LMA) refers to the synthesis of high isoelectric point (pI) α -amylase during the middle- to late-stages of grain fill, within the aleurone layer of wheat (*Triticum aestivum* L.). The α -amylase accumulates and is retained within harvested grain with little to no impact on starch quality. Alpha-amylase activity from LMA is detected by the Hagberg Falling Number, an international standard of grain quality used by grain traders for grain quality classification. Given this, new Australian wheat varieties must pass two-rounds of LMA screening prior to quality classification to avoid potential losses to wheat growers. This research project was designed to elucidate four important aspects of LMA expression, and its impact on wheat breeding and wheat quality.

Firstly, to evaluate LMA expression at the field level to identify the risk of low Falling Number, and weather conditions that contribute to LMA expression. A total of 34 environments from Australian wheat growing regions between 2019 and 2020 identified genotypes at risk of LMA expression. This allowed the identification of genotype-by-environment interaction (G×E) and weather conditions that were conducive to LMA expression. Secondly, a multi-year, multi-treatment glasshouse and growth room trial assessed temperature conditions to identify those that best reflect LMA expression at the field level. The assessment of G×E would assist in improving phenotypic selection while also reducing cost of pre-classification assessment. A total of 13 experiments were tested across three screening seasons.

Thirdly, twelve F4:F5 derived populations were created to identify and validate genetic markers associated with LMA expression. The identification of loci with a commercially significant impact on LMA expression would allow for reliable early generation selection.

Lastly, a population was used to assess the impact of LMA on end-product quality. Given the limited research that suggests very limited effects of LMA expression on end-product quality, the significant results observed here are an important contribution to the field.

This research suggests that LMA screening could be significantly improved for cost and accuracy and certain genetic factors could be used for early generation selection against LMA. Given the impact of LMA on Falling Number and end-product quality, it is clear that the Australian wheat industry must continue to mitigate the risk of LMA expression.



Positioning Australian soft wheat to maximise market opportunities for the Western Australian grains industry

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Soft wheat is differentiated from hard wheat by its low kernel hardness and suitability for application in cake and biscuit products. Soft white wheat (SWW) is produced in the North American Pacific Northwest region with an average of 6.2mmt per annum (2016-2020), and approximately 80% is exported to Asia. AEGIC has identified that the global cake and biscuit demand will grow by 3mmt in the next decade, with Southeast Asia accounting for 1.1mmt. The Asian markets have expressed interest in the supply of Australian soft wheat to reduce dependency on the US. Also, taking advantage of the combined hard and soft wheat cargo, a shorter shipping duration for faster turnover and lower stock carryover risks, and potentially lower freight costs. However, this is a market that Australia is presently unable to supply. Because of the limited soft wheat availability, with production focussed on the east coast to supply the domestic market. Also, there is a lack of suitable soft wheat varieties, resulting from limited investments in soft wheat breeding programs. Low protein soft wheat attracts higher prices, and regions within Western Australia (WA) are well-suited for producing low protein wheat. Developing new soft wheat exports from WA will diversify supply and address Asian consumer trends for soft wheat products. In addition, the production of low protein wheat with reduced input costs and competitive yields will increase cropping options for WA grain growers.

Australian wheat breeding companies have responded to this opportunity by commencing soft wheat breeding programs targeting production in WA. AEGIC aims to support breeding programs to meet market quality targets and gain market acceptance for Australian soft wheat. This study will address key quality attributes prioritised by Asian millers, including solvent retention capacity (SRC), cookie performance and flour milling efficiency. Collaborative SRC laboratory trials between AEGIC Sydney and two major Indonesian mills demonstrated high correlations between SRC values, ranking samples similarly. SRC water and sodium carbonate helped predict cookie spread. Soft wheat breeding programs are recommended to focus on SRC water and or sodium carbonate in predicting cookie performance, aligning with Indonesian mills' quality requirements. The cookie performance of Australian soft wheat varieties harvested in 2020 from Katanning, WA, was comparable to those of US SWW. However, their milling performance was not consistent. AEGIC will continue to build connections between growers, wheat breeders and southeast Asian markets to create a sustainable Australian soft wheat export market.



Are there barriers to the profitable production of soft wheat?

Dr Lindsay O'Brien

Solheimar Pty Ltd, Narrabri, NSW

Soft wheat used in the production of sweet biscuits and cakes is a specialty class of wheat characterised by low grain protein content, low water absorption and weak and extensible dough properties. A small domestic contract production exists in eastern Australia largely through an arrangement between Allied Mills and Arnotts. Exports of soft wheat from Western Australia to Malaysia and South Korea reached tonnages of 300,000 to 400,000 tonnes through markets developed by the Australian Wheat Board during the 1980's and up to the 1990's after which exports dropped to 100,000 tonnes by 2000 to 2001 and no longer occur, despite market analysis suggesting there remains demand for this class of wheat. Some of the factors contributing to this situation are related to market access such as where are they and is it economic to accumulate and market grain for them, cliff-face pricing affecting grower returns, the grain yield and price per tonne for soft wheat in the international market, the yield competitiveness of available soft versus hard wheat varieties. These factors pose the questions of whether business cases would justify the investment of breeding resources to bridge the yield gap and to establish the grower/accumulator/marketer linkages to establish an export quantity of soft wheat to meet the apparent market opportunity.



POSTERS

P1.

NSW DPI POST-ENTRY QUARANTINE GLASSHOUSES - OPEN FOR BUSINESS

Mr Brett Lobsey¹

¹*NSW Department of Primary Industries, TAMWORTH, Australia*

The importation of cereals into Australia for research purposes must first undergo a quarantine screening process that is required to take place in an Australian Department of Agriculture Approved Arrangement Biosecurity Containment Facility.

Against all odds due to the restrictions of the pandemic, in February 2022 the Tamworth NSW DPI post-entry quarantine team were granted permission to operate two biosecurity containment level 5.2 glasshouses by the Australian Department of Agriculture following the required audits and biosecurity containment checks.

When importing seed into Australia and after customs inspection, each individual imported genotype must first be planted, grown and harvested to allow for a complete growth cycle as a way of identifying any exotic pests and diseases prior to the harvested seed being released to the end user.

With 15 years' experience in post-entry quarantine, the team at Tamworth Agricultural Institute are well equipped to process all types of cereal seeds subject to biosecurity.

Our two Approved Arrangement Biosecurity Containment facilities have the capacity to screen several consignments throughout the year. Approved Arrangement Glasshouse 1 has a capacity of 1300 lines and Approved Arrangement Glasshouse 2 has a capacity of 500 lines, with an average of 1.5 growth cycles per glasshouse per year.

Chiefly our facility screens breeding lines for seed companies, which is a great way for businesses here in Australia to collaborate with overseas seed breeding organisations.

Certain restricted species are permitted to be grown in our facility, which provides an opportunity for cereal geneticists to search for unique and generational genes in cereal crop wild relatives while upholding Australia's strict biosecurity guidelines.

Our knowledge in the field of crop improvement and our expertise in biosecurity requirements combine to allow us to assist you with your importation needs.



P2.

DMSO enhances wheat doubled haploid production via anther culture

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Abstract

The production of doubled haploid (DH) lines is an excellent tool for the rapid generation of fixed lines in breeding and research. Fully homozygous lines can be achieved in a single step from heterozygous parents. The Western Australian Department of Primary Industries and Regional Development (DPIRD) supports a Cereal Doubled Haploid Program that provides wheat and barley DHs on a fee for service basis. We have also recently developed several canola DH populations for DPIRD staff. Over 85-90% of our DHs are destined for breeding while 10-15% are used for research. In 2021, the DPIRD DH program delivered over 19,500 DH lines across Australia.

All wheat and barley DHs are produced using anther culture, while canola DHs are produced using microspore culture. In wheat, genotypic variability in i) green plant production and ii) the frequency of chromosome doubling are key challenges. For wheat DH production, we rely on 'spontaneous' chromosome doubling which has advantages over traditional colchicine root-dipping immersion treatments (greater seed volume, no delays after colchicine treatment = faster time to harvest). However, the frequency of spontaneous doubling in wheat can vary widely and, in our program, we have observed frequencies from 14 to 80%.

To improve the frequency of chromosome doubling in wheat, the anti-microtubule agent trifluralin was applied in vitro, during the early stages of androgenesis. While trifluralin significantly improved chromosome doubling, it drastically reduced green plant production. Interestingly, the dimethyl sulfoxide (DMSO) solvent used for trifluralin, when tested as a negative control, yielded significantly more green plants than the control treatment (over 100% increase in green plants). Since then, a DMSO treatment has been applied to large numbers of wheat crosses in the program with positive results observed in terms of green plant production and chromosome doubling. In experiments involving four crosses in 2021, DMSO significantly improved green plant production. DMSO treatment also significantly improved chromosome doubling, by approximately 15%, in two of the four crosses. Further refinement with DMSO treatments may yield greater improvements, especially regarding chromosome doubling.



P3.

Symmetric response to neighbour in binary mixed cultivars associate with genetic gain in wheat yield over the last five decades

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¹SARDI, URRBRAE, AUSTRALIA, ²The University of Adelaide, School of Agriculture, Food and Wine, URRBRAE, Australia

The evolution in the definition of crop yield — from the ratio of seed harvested to seed sown to the contemporary measure of mass of seed per unit land area — has favoured less competitive phenotypes. Here we use binary mixtures of cultivars spanning five decades of selection for yield and agronomic adaptation to ask three questions. First, what is the degree of symmetry in the response of yield to neighbour; this is, if an older, more competitive cultivar increases yield by 10% with a less competitive neighbour in comparison to pure stands, would the newer, less competitive cultivar reduce yield by 10% when grown with older neighbour. Lack of symmetry would indicate factors other than competitive ability underlying yield improvement. Second, what are the yield components underlying competitive interactions. Third, to what extent are the responses to neighbour mediated by radiation, water and nitrogen. A focus on yield components and resources can help the interpretation of shifts in the crop phenotype in response to selection for yield. The rate of genetic gain in yield over five decades was 24 kg ha⁻¹ yr⁻¹ or 0.59% yr⁻¹. A strongly symmetrical yield response to neighbour indicates that a reduction in competitive ability has been the primary driver of yield improvement. Response to neighbour was larger for grain number and biomass than for grain weight and allocation of biomass to grain. Under our experimental conditions, competition for radiation was dominant compared to competition of water and nitrogen. High yielding phenotypes had lower competitive ability for radiation but compensated with higher radiation use efficiency, a measure of canopy photosynthetic efficiency. Genetic and agronomic manipulation of the crop phenotype to reduce competitive ability could further improve wheat yield to meet the challenge of global food security.

P4.

Deep-sown wheat (*Triticum aestivum* L.): The influence of semi-dwarfing genes and the Lcol-A1 QTL on its coleoptile, seedling vigour, and establishment

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Deep sowing of wheat (*Triticum aestivum* L.) is an opportunistic technique used by some growers to access deep soil moisture. This technique is used to ensure the crop establishes within an optimal sowing period and attempts to provide the best chance of attaining yield potential. However, deep sowing has been associated with low plant establishment rates in commercial wheat crops. The coleoptile, an organ found in monocot seedlings, has been shown to be closely associated with establishment from deep sowing. Current commercial wheats have relatively short coleoptiles due to semi-dwarfing genes Rht1 and Rht2. In this honours study, a sample of 108 diverse wheat genotypes containing various semi-dwarfing genes, tall lines, and a novel QTL, Lcol-A1, were evaluated in a temperature-controlled growth chamber experiment to determine genetic effects on coleoptile morphology, specifically length and diameter. Additionally, a subset of 67 genotypes were sown in field experiments in 2020 at Collingullie (southern NSW) and Narrabri (northern NSW) under shallow (4-5cm) and deep (11-15cm) sowing conditions to determine how semi-dwarfing genes and the Lcol-A1 QTL affect seedling establishment. We found semi-dwarfing genes Rht1, Rht2, Rht13, Rht18, and the Lcol-A1 QTL all significantly ($P < 0.05$) affected coleoptile length and diameter, with genotypes containing Rht13, Rht18 dwarfing genes, and the Lcol-A1 QTL producing plants with the longest coleoptiles. Coleoptile length was found to have a strong correlation ($rP=0.87$, $P < 0.01$) with establishment from deep sowing, whilst diameter had a weak correlation ($rP=-0.31$, $P < 0.01$). The Rht1 and Rht2 dwarfing genes were associated with significantly reduced seedling vigour as determined by seedling above-ground biomass, leaf area, and crown depth. The Rht13, Rht18, and tall wheats had similar seedling vigour, except for first leaf area, which was largest in the Rht18 wheat group with an 8% increase compared to tall wheats. Coleoptile tiller frequency in this study was not associated with dwarfing genes or the Lcol-A1 QTL. This study provides evidence that the alternative dwarfing genes Rht13, Rht18, and the novel Lcol-A1 QTL increase coleoptile length to increase establishment under deep sowing conditions. Furthermore, genotypes with increased coleoptile length had similar establishment rates when sown shallow into good soil moisture when compared to elite commercial lines, indicating that these alternative dwarfing genes may provide some sowing insurance for growers in the future.



The effect of pot size on timing of important developmental stages of wheat

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Phenotyping is a crucial part of wheat (*Triticum aestivum*) research, and with the increase in use of high-throughput technologies for phenotypic analysis, experiments are using larger numbers of plants. When this is coupled with the use of controlled environment rooms which have a limited area, there has been a shift towards using smaller pots. Although pot size is known to increase, decrease, or leave unchanged the flowering times of vegetables, trees and flowers, the effect on wheat and other cereals is unknown. To investigate this, 10 near-isogenic lines of wheat with known diversity in alleles of major flowering time genes were grown in four different pot sizes (800 mL, 550 mL, 200 mL, 110 mL). Leaf appearance rate, heading date, anthesis date and plant height were recorded and analysed. Despite the expected change in plant size, it was found that pot size had no significant effect on development rate for any of the wheat genotypes assessed. This enables future research focused on development of wheat to use smaller pots and increase population sizes or replication with confidence, knowing that pot size will not affect timing of important developmental stages such as flowering time.



P6.

Pollen lipids in wheat (*Triticum aestivum*) varieties are affected by heat stress.

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Increasing global temperatures affect the growth and development of wheat plants, especially pollen development and ultimately reduce grain yield. At high temperatures, the reduction of wheat pollen viability may be related to the change in its lipid composition. This research aimed to study the viable pollen count and lipid content of wheat in response to heat stress. Four wheat cultivars of known heat tolerance (Flanker- heat tolerant, Suntop-moderately heat tolerant, Sunchaser-moderately heat sensitive and Cobra-heat sensitive) were selected for this experiment. Plants were treated with heat stress at 35°C/22°C or 40°C/25°C (day/night) for three days during meiosis; the control plants were maintained at 22°C/15°C (day/night) through the growing period. Pollen viability at anthesis was analysed by Ampha cytometer. Lipids from pollen tissue were analysed by Gas chromatography–mass spectrometry (GC-MS) after acid catalyzed transesterification extraction. Saturated fatty acid C18:0 (Stearic acid and unsaturated fatty acid C18:3 (Alpha-Linolenic acid) may contribute to the heat tolerance of wheat, while C20:0 (Arachidic acid) may contribute to the heat sensitivity of wheat. The high heat tolerance of Flanker is worth further investigation. Heat treatment at 35°C did not inhibit pollen development of Flanker, while heat treatment at 40°C directly led to the death of pollen in all cultivars.

P7.

Influence of salinity stress on wheat leaf metabolism through its developmental gradient

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Soil salinity is a major constraint on agricultural production as it causes large yield losses in many important crop varieties. Wheat is a major staple crop for human nutrition and most of its commercial varieties are highly salt-sensitive. Salinity stress in wheat is a quantitative trait, affecting plant development at both physiological and biochemical levels. Within wheat plants, shoot tissues are the most sensitive to salinity and accumulate salt over time through the transpiration stream. To build on past studies, we are quantitatively analysing how molecular phenotypes establish in wheat plants over the course of monocot leaf development.

We exposed wheat cv. Wylkatchem to 150mM NaCl for 8 days through gradual increment of salt and assessed fresh and dry biomass, photosynthetic parameters and chlorophyll content in the 4th leaf. Na⁺/K⁺ measurements and proteomic analysis were performed after dividing the leaf into sections across the leaf developmental gradient. In monocot leaves, the organization of the growth processes is spatially regulated with dividing cells at the base of the leaf, followed by expanding cells and finally mature cells at the tip.

Wheat leaves showed a significant reduction in physiological parameters such as biomass, chlorophyll content and photosynthesis, under NaCl treatment. A significant decrease in K⁺ content and an increase in Na⁺ content and K⁺/Na⁺ ratio were observed under the salt treatment, varying from the base to the tip of the leaf. Shotgun proteomic analysis in leaf sections identified the specific spatial arrangements of 1783 proteins and their salinity response, showing significant reductions in protein synthesis and upregulation of protein degradation machinery under salinity stress.

The results highlight the impact of salt stress on plants at the physiological level and in different spatial contexts and suggest a development pattern in the role of protein metabolism in shoot responses to salinity. Overall, this research will improve fundamental knowledge of the effect of salinity on the establishment of vital cellular functions across the monocot leaf using proteomic and metabolomic techniques. Studying these developmental gradients in breeding populations differing in salinity tolerance molecular mechanisms will aid in the development of salt-tolerant wheat varieties which will bring significant benefits to global wheat production.

P8.

A three-tiered phenotyping approach to effectively improving the heat tolerance of wheat.

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The frequency of high temperature stress events is projected to increase in the coming years due to a changing climate. Wheat yield is significantly reduced when a high temperature event occurs during flowering and/or grain filling, negatively impacting grain size and processing quality. This research implemented a three-tiered phenotyping approach to develop new heat tolerant wheat germplasm for use by commercial breeding companies. Phenotypic analysis was performed, and genomic predictions were validated having been trained at Narrabri for accuracy at other sites. Genotype-by-environment (GxE) genomic selection models which make use of Environmental Covariates (ECs) were used to substantially increase the prediction accuracies for yield, screenings and other traits. This approach provides a method to predict a lines sensitivity to heat during all development stages including anthesis and grain fill, providing additional insight into the mechanisms of heat sensitivity by observing which ECs are most influential on predictions. The heat response of selected lines was then confirmed in the following year on optimally sown materials subjected to short-term heat stress at flowering and grain-filling imposed using field-based heat chambers. Lines with confirmed heat tolerance based on heat chamber responses were then tested in the third year in glasshouses under controlled conditions to determine mechanisms of heat tolerance. In-field controlled environment chambers significantly impacted the yield and kernel weight of most lines evaluated when a heat shock was applied at anthesis and during grain fill. CIMMYT breeding line (CMSA08Y00613S-050Y-050ZTM-050Y-59BMX-010Y-0B) significantly outperformed all current varieties for yield (56% better than Suntop) and kernel weight under control and heat treatments.



P9.

Rapid non-destructive method to phenotype stomatal traits

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Drought is a major limiting factor for plant growth and production. The predicted effects of global warming will increase the frequency and severity of drought events. Plants adapt to drought stress by using specific mechanisms for drought tolerance, one of which is stomatal regulation. Stomata are central to transpiration and therefore yield. Approximately 70% of water is lost through transpiration and 98% of CO₂ is fixed for photosynthesis occur via stomata. The number, size, ratio and stomata aperture on the leaf epidermis affect plant transpiration and the effectiveness of CO₂ uptake through the stomatal aperture, making stomatal traits primary targets to improve water use efficiency. Current methods to screen for stomatal phenotype are time consuming and costly, which prevents advancing knowledge on stomatal physiology and its application at a large scale to identify drought-tolerant crops. We developed a rapid non-destructive method to phenotype stomatal traits at a large scale. Stomata images are taken directly on the leaf using a handheld microscope as an alternative to the conventional methods that use nail polish, which significantly accelerates image capture from minutes to seconds. Images are analysed using a machine-learning program that automatically detects stomata and provides information on stomata number and size quickly and accurately. We developed this method for wheat, rice, tomato and Arabidopsis. The accuracy of the machine-learning model ranged from 96% to 89%, respectively. The proposed method can be readily used in the field and in controlled environments.

P10.

Cytological characterisation of wheat-*Thinopyrum ponticum* translocations carrying leaf rust and stem rust resistance genes Lr24 and Sr24


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The hard red winter wheat cultivar Agent carrying a spontaneous wheat-*Thinopyrum ponticum* translocation T3DS.3DL-3AgL was released by the Oklahoma Agricultural Experiment Station in 1967. At that time, Agent was resistant to all known *Puccinia triticina* (Pt) races and was moderately resistant to stem rust caused by *P. graminis tritici*. The leaf rust and stem rust resistances in Agent were derived from *Th. ponticum*, and were later designated Lr24 and Sr24, respectively. Because of leaf rust resistance, the translocation was incorporated into wheat cultivars, and the Agent source of Lr24 and Sr24 was exploited in the Americas and South Africa. However, attempts to use the resistance in Australia failed because all derivatives had red seed colour. ER Sears used induced homoeologous recombination to produce several 3D/3Ag translocation lines carrying Lr24 and Sr24 in Chinese Spring (CS) wheat. Again, all were red-seeded, having allele R1 from CS or Rag from chromosome 3Ag. Following crosses to Australian cultivars, McIntosh and Partridge obtained white-seeded recombinants from translocation lines CS 3D/3Ag#3 and CS 3D/3Ag#14, which Sears had predicted to carry the smallest alien segments based on chromosome pairing studies, and the first Australian cultivar with Lr24/Sr24, Torres, was released in Queensland in 1983. Subsequently, more than 30 cultivars with Lr24/Sr24 were released and widely grown throughout Australia. Lr24 was effective for almost 20 years until the virulent Pt race 104-1,2,3,(6),(7),11 was detected in 2000. Sr24 continues to be effective and remains an important source of stem rust resistance despite its early failure against race Ug99 in Eastern Africa and earlier failure in South Africa in 1987. Here, we used non-denaturing fluorescence in situ hybridization (ND-FISH) and genomic in situ hybridization (GISH) to visualise the alien segments in cv. Agent and Australian cultivars, Janz and Sunco carrying the 3D/3Ag#3 and 3D/3Ag#14 translocations, respectively. The fraction length (FL) of the translocation in Agent was 0.70-1.00 and those in Janz and Sunco were similar and smaller, at FL 0.85-1.00. It can be deduced that the alien gene encoding for red grain colour was in the *Thinopyrum* segment with FL 0.70-0.85. Lack of recombination between wheat chromosomes and alien segments causes all genes within those segments to be inherited as a linkage block.

North American researchers found that some plants in cv. Amigo with a T1AL.1RS Robertsonian translocation carrying stem rust resistance also carried a 3Ag chromosome segment, but in that case the segment was transferred to the terminal region of chromosome arm 1BS. Later work showed that the segment also lacked the Rag allele.

D11



Improving crown rot phenotyping strategies

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Crown rot, caused by the stubble borne pathogen *Fusarium pseudograminearum*, remains a major limiting factor for winter cereal production in many of the grain growing regions of Australia. Access to highly effective genetics has limited the ability of breeders to deliver varieties with improved resistance and tolerance to this disease. Delivery of improved genetic solutions to growers is further hampered by the lack of reliable and high throughput phenotyping strategies to allow breeders to identify superior germplasm from within their breeding programs.

To address this, a research project has been established to identify alternative strategies to phenotype crown rot. This project seeks to develop high throughput methodologies to identify both resistant and tolerant germplasm using novel technologies. This includes using multispectral, hyperspectral and thermal infrared sensors both in-crop and post-harvest. Further, the project aims to understand the relationship between resistance, tolerance and yield loss to this disease, to allow breeders to prioritise selection pressure ensuring the most effective breeding objectives are targeted. Preliminary thermal imagery and hyperspectral results from trials conducted in 2021 will be presented.



P12.

The Effect of Durum Wheat (*Triticum turgidum* var. durum) Varieties Westcourt, Bitalli and Zulu on Pasta Production

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This research evaluated the quality of the grain, semolina and pasta produced from durum wheat (*Triticum turgidum* var. durum) varieties Westcourt, Bitalli and Zulu. Grain quality tests included Test and Thousand Kernel Weight, Protein, Falling number, Screenings and Grain Moisture. Semolina was tested for moisture, protein, colour and particle size index. Pasta quality tests included dried and cooked colour, firmness and optimum cooking time. Two different water additions (31.5% and 32.5%) were trialled for pasta dough. Oven positioning for the drying process was compared. Results from this research found that the quality of Westcourt durum grain, semolina and pasta were significantly greater than Bitalli and Zulu for protein content, yellowness and firmness. Results were also impacted by water addition and oven positioning. Future studies comparing Westcourt durum wheat to other high performing durum wheat varieties grown in other countries could be useful for increasing Australia's competitiveness in the global market.



P13.

Connecting wheat breeding and pan-genomics with Pretzel

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Numerous opportunities to accelerate wheat improvement exist if new information resources can be effectively exploited. The scale and types of wheat genomics resources have exploded following significant advances in DNA sequencing technology and computing power. There is an opportunity to expand the scope of end users for these resources by making them available in a web-based platform that incorporates curated data together with integrated search, analysis, and visualization features. Pretzel is a visual, interactive tool being developed by Agriculture Victoria, accessible at <https://plantinformatics.io>, enabling the integration and analysis of genomes, genetic maps and QTLs, giving users without bioinformatics skills the power to answer key questions in research and breeding. It is built on modern web technologies and is highly extensible. Here we demonstrate recent Pretzel functionality advances which include the display of QTL information and ontologies, high density SNP data, real-time sequence-based searching and curation of legacy data. Together these provide researchers and breeders a powerful toolbox to connect wheat breeding with pan-genomics and to answer tomorrow's questions today.

P14.

Leveraging from the Vavilov wheat collection for new sources of stripe rust (*Puccinia striiformis* f.sp. *tritici*) resistance in Ethiopia

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Stripe rust caused by *Puccinia striiformis* f.sp. *tritici* (*Pst*) is one of the economically important diseases of bread wheat (*Triticum aestivum* L.) in Ethiopia. In the last two decades, several stripe rust epidemics have occurred in the country and caused up to 90% yield losses in the severely affected farmer's fields. Rapid rust evolution, fast spread of new virulent races, and limited durable resistance coupled with frequent susceptibility of newly released wheat varieties demands that the genetic bases of wheat rust resistance genes be broadened. Assessing sources of resistance from a new genetic pool is one of the most economical and viable strategies to broaden the genetic bases of rust resistance and to protect the small-scale wheat farmer's fields from deadly rust diseases. In this study, a diversity panel of 388 bread wheat genotypes (n=200 from N. I. Vavilov Institute of Plant Genetic Resources and n=188 from the Ethiopian national wheat research program) were evaluated to identify new sources of loci conferring resistance to the predominant *Pst* races in Ethiopia. The panel included landraces, old and newly released cultivars, and breeding lines. Field phenotyping was conducted at three locations (Kulumsa=2200 m.a.s.l), Bekoji=2780 m.a.s.l and Meraro=3031 m.a.s.l) for three years (2017/18, 2018/19, 2020/21) in a partially replicated design under natural infestation. The phenotype response showed a wide variability for stripe rust resistance across locations and years. The field severity response ranged from 0 to 95 and the reaction response ranged from immune to susceptible. The overall coefficient of infection revealed 19.5%, 25.5%, 21.1% and 33.7% of the panel to be resistant, moderately resistant, moderately susceptible, and susceptible, respectively. To identify the source of stripe rust resistance, a genome-wide association study between stripe rust response and DArT-seq marker data analysis is underway. The results of this study will directly contribute to the Ethiopian wheat breeding program's effort to improve rust resistance breeding to meet the country's goals of increasing wheat production and self-sufficiency.

Integrating crop modelling, physiology, genetics and breeding to aid crop improvement for changing environments – How to produce more crops per drops?

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Following advances in genetics, genomics, and phenotyping, trait selection in breeding is limited by our ability to understand interactions within the plant and with the environment, and to identify traits of most relevance to the target population of environments. We propose an integrated approach that combines insights from crop modelling, physiology, genetics, and breeding to characterize traits valuable for yield gain in the target population of environments, develop relevant high-throughput phenotyping platforms, and identify genetic controls and their value in production environments. This presentation will use transpiration efficiency (biomass produced per unit of water used) in wheat as an example of a complex trait of interest to illustrate how the approach can guide modelling, phenotyping, and selection in a breeding programme. Transpiration efficiency was identified as a valuable target to improve crops in major producing regions. Phenotyping platforms were built to study the physiology and genetics of transpiration efficiency. Genetic variations for this trait were partly correlated to water saving at high evaporative demand. Associated molecular markers were identified repetitively across trials and in different genetic backgrounds. Promising genotypes with higher transpiration efficiency than modern varieties were also identified as potential parents for further crossing and selection to produce more crop per drop.

We anticipate that the proposed approach, by integrating insights from diverse disciplines, can increase the resource use efficiency of breeding programmes for improving yield gains in target populations of environments in current and future climates.

Combining genetic variability in the Australian germplasm for yellow spot resistance through MAGIC

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Under the national yellow spot project DAW00247, co-funded by Grains Research and Development Corporation (GRDC) and led by the Department of Primary Industries and Regional Development (DPIRD), a large multi-parent advanced generation inter-cross (MAGIC) population of 1503 wheat lines was developed from a complex cross involving different sources of yellow spot resistance. The four parents included Australian wheat varieties GBA Ruby, H45, King Rock and Magenta. This population provided a unique opportunity to maximise genetic recombination and generate potential parental stocks enriched for yellow spot resistance. The population was phenotyped at the seedling stage at DPIRD, DJPR and USQ in three batches against mixtures of contemporary isolates in 2015, 2016 and 2017 respectively and 135 lines with high levels of seedling resistance were identified. The population showed continuous distribution and transgressive segregation for disease severity in all trials with a few lines showing higher resistance than all parents (Fig.1). Correlations between assessments made at various national sites were moderate ($r = 0.4$ to 0.6). The population was genotyped by University of Adelaide and several QTL for seedling resistance were identified of which the ones on 4A, 5A, 5B, 7B and 4D were of significance ($LOD > 3$) and accounted for 10 to 28% of variation.

In a follow-up project funded by DPIRD, the set of 135 lines with high levels of seedling resistance were tested at various growth stages and environments against a mixture of contemporary isolates at South Perth in 2021 with the aim to identify lines with broad-spectrum adult plant resistance. There were moderate correlations between assessments made in different environments ($r = 0.5$) and at different growth stages ($r = 0.6$). The lines showed continuous distribution and transgressive segregation for disease severity in all trials with a few lines showing higher levels of resistance than all parents (Fig. 2). Of these, 11 lines showed very high levels of broad-spectrum resistance (RMR) effective at various growth stages and environments (Table 1). These lines have been delivered to various breeding companies and are crucial genetic stocks for breeding.

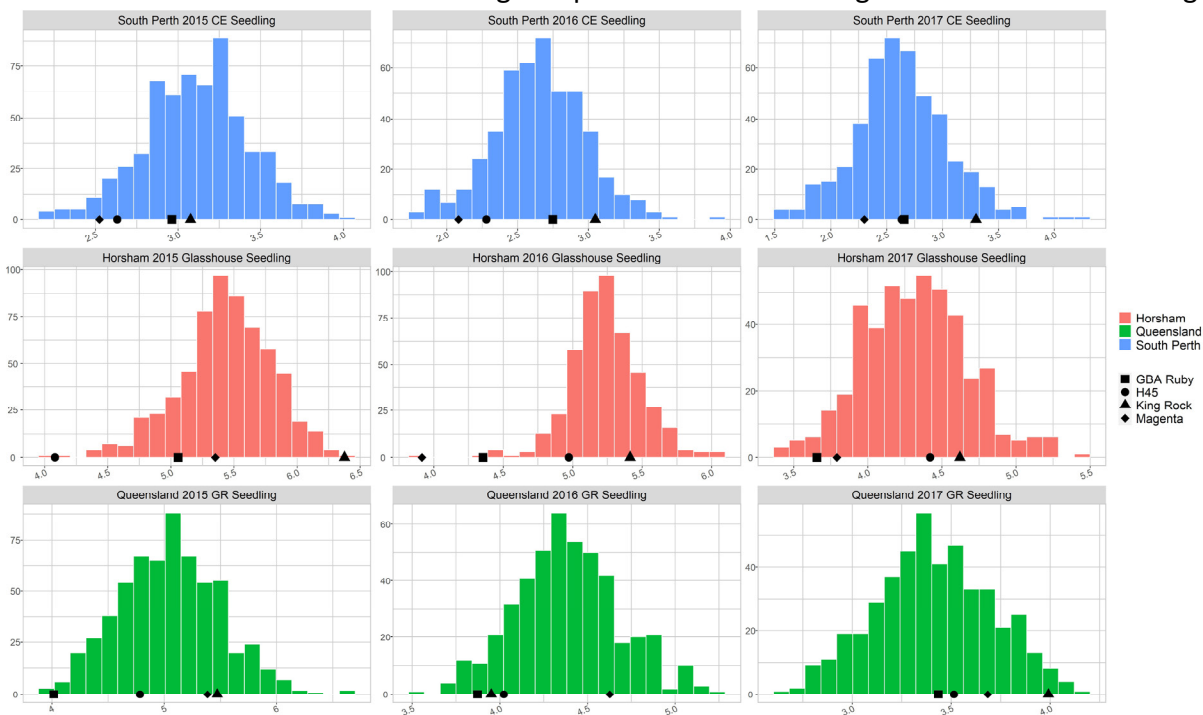


Fig. 1. Frequency distribution of yellow spot severity in the MAGIC population (1503 lines) assessed at the seedling stage at various national sites in 2015, 2016 and 2017.

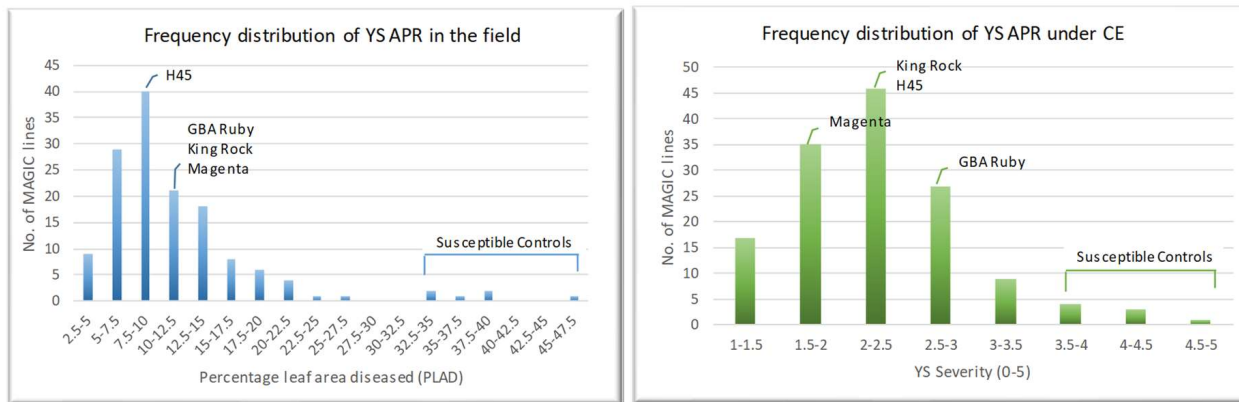


Fig. 2. Frequency distribution of yellow spot severity in selected MAGIC lines (135 lines) assessed at the adult plant stage in the field and controlled environment at South Perth in 2021.

Table 1. List of eleven MAGIC lines showing very high levels of broad-spectrum resistance (RMR) effective at various growth stages and environments as compared to the parents and controls.

Entry	Description	Pedigree	Field				Controlled Environment (CE)			Field APR	CE APR	Seedling Resistance
			PLAD Mean	PLAD Flag	PLAD Flag-1	Days to Head	Seedling (0-5)	Adult (0-5)	Days to Head			
12MS001 HG12-05-1	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	5	4	6	86	0.7	1.0	61	RMR	RMR	RMR
12MS001 HG48-07-2	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	5	3	6	79	1.2	1.7	51	RMR	RMR	RMR
12MS001 HG51-18-1	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	5	3	7	80	1.2	1.7	73	RMR	RMR	RMR
12MS001 HG52-01-1	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	6	3	9	80	1.0	1.7	48	RMR	RMR	RMR
13MS001 DF11-03-02	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	5	4	5	78	0.7	1.3	52	RMR	RMR	RMR
13MS001 DJ07-07-02	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	4	3	5	91	0.7	1.0	74	RMR	RMR	RMR
13MS001 DJ10-04-01	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	4	3	5	97	1.0	1.7	74	RMR	RMR	RMR
13MS001 DJ10-04-02	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	5	3	7	81	0.5	1.7	42	RMR	RMR	RMR
13MS001 DJ14-10-02	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	6	4	9	76	1.2	1.7	51	RMR	RMR	RMR
13MS001 HG08-05-01	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	7	4	10	78	0.7	1.5	56	RMR	RMR	RMR
13MS001 HG16-07-02	MAGIC Line	GBA Ruby/H45//King Rock/Magenta	4	3	4	78	0.8	1.7	66	RMR	RMR	RMR
Annuello	YS Control		24	14	33	70	2.8	2.5	35	MS	MRMS	MRMS
Banks	YS Control		35	27	44	70	4.3	3.7	41	S	MSS	S
Calingiri	YS Control		22	13	31	87	2.3	2.2	62	MS	MR	MR
Correll	YS Control		46	28	64	79	3.3	4.8	48	VS	SVS	MS
Cunderdin	YS Control		14	11	18	79	2.0	2.8	62	MRMS	MRMS	MR
GBA Ruby	MAGIC Parent		11	8	14	77	1.3	2.8	51	MR	MRMS	RMR
Gutha	YS Control		39	27	51	70	5.0	4.3	38	SVS	S	VS
H45	MAGIC Parent		10	8	12	71	1.7	2.2	38	MR	MR	MR
Hartog	YS Control		34	29	39	72	3.5	4.2	40	S	S	MSS
King Rock	MAGIC Parent		11	9	13	74	2.3	2.5	48	MR	MRMS	MR
Leichardt	YS Control		19	16	22	77	1.5	2.7	43	MRMS	MRMS	RMR
Mace	YS Control		22	14	29	78	1.7	2.3	54	MS	MRMS	MR
Magenta	MAGIC Parent		11	5	17	88	1.7	1.8	70	MR	MR	MR
Suntop	YS Control		22	15	29	73	3.3	2.3	40	MS	MRMS	MS
Wyalkatchem	YS Control		17	11	23	81	0.8	2.0	59	MRMS	MR	RMR
Yitpi	YS Control		35	17	53	94	4.0	3.5	78	S	MSS	S

R = Resistant, RMR = Resistant–moderately resistant, MR = Moderately resistant, MRMS = Moderately resistant–moderately susceptible, MS = Moderately susceptible, MSS = Moderately susceptible–susceptible, S = Susceptible, SVS = Susceptible–very susceptible, VS = Very susceptible



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2022
HORIZON WHEAT

