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17–20 August 2026
Novotel Geelong, Victoria

THE AUSTRALIAN BARLEY INDUSTRY

Pivoting to the future



GRDC

INVESTING IN

THE FUTURE OF AUSTRALIAN BARLEY

As the world's largest barley exporter, Australia relies on ongoing innovation to remain globally competitive. Through the Barley Crop Improvement Plan, GRDC is guiding strategic investment in breeding, genetics and crop improvement research to help growers overcome emerging challenges and capture future opportunities.

“GRDC’s purpose is to invest in a diverse portfolio of RD&E to deliver tangible, on-the-ground impact to growers today and tomorrow. The 2026 Australian Barley Technical Symposium is a key example of GRDC investing in the future of the industry.”

Jessica Hyles

Senior Manager, Genetic Technologies - Cereals



Discover how GRDC is helping shape the next generation of Australian barley:



Welcome from the Chair

On behalf of the organising committee, it is my great pleasure to warmly welcome you to the 22nd Australian Barley Technical Symposium “Pivoting to the Future”, held at the Novotel in the beautiful seaside city of Geelong.

This symposium brings together the full breadth of the barley value chain, with delegates from across Australia and around the world representing research, plant breeding, malting, brewing, distilling, grain trading, marketing, agronomy and production. Over the coming days, the program will showcase world-leading science, innovation, technologies, genetics, breeding advances and industry practices that are addressing key challenges and creating new opportunities for barley in Australia and beyond.



We sincerely thank our sponsors and exhibitors, whose generous support has helped bring this symposium to life. Their contribution enables a vibrant forum for sharing knowledge, building connections and celebrating the passion, expertise and commitment reflected across the program.

The social program has been designed to give all delegates, whether attending for the first time or returning as regular participants, opportunities to reconnect, meet new colleagues, exchange ideas and strengthen networks across the barley value chain.

We hope you enjoy the symposium, feel inspired by the world-leading work on show, and take every opportunity to connect, share ideas and enjoy the company of colleagues throughout the program.

Cheers,

Sally Norton

Symposium Chair



Thank you to the Organising Committee

Sally Norton, DEECA

Chair

Kerrie Forrest, DEECA

Secretary

Blakely Paynter, DPIRD

Treasurer

Committee Members

Allan Loh, Barret Burston

Trevor Perryman, Kardinia Group Consulting Pty Ltd

Laura Ziems, University of Sydney

Silvina Baraibar, InterGrain

Elysia Vassos, Grains Australia

Peter Dracatos, La Trobe University

Samir Alahmad, The University of Queensland

Mark Lewis, Riordan Grain Services

Carolina Garcia, GrainCorp

Mary Raynes, AEGIC

Jon Thelander, Seednet

David Peake, RAGT

Mohammed Pourkheirandish, Melbourne University

Kate Murphy and Jenny Lawler, KAM Events

Conference Secretariat



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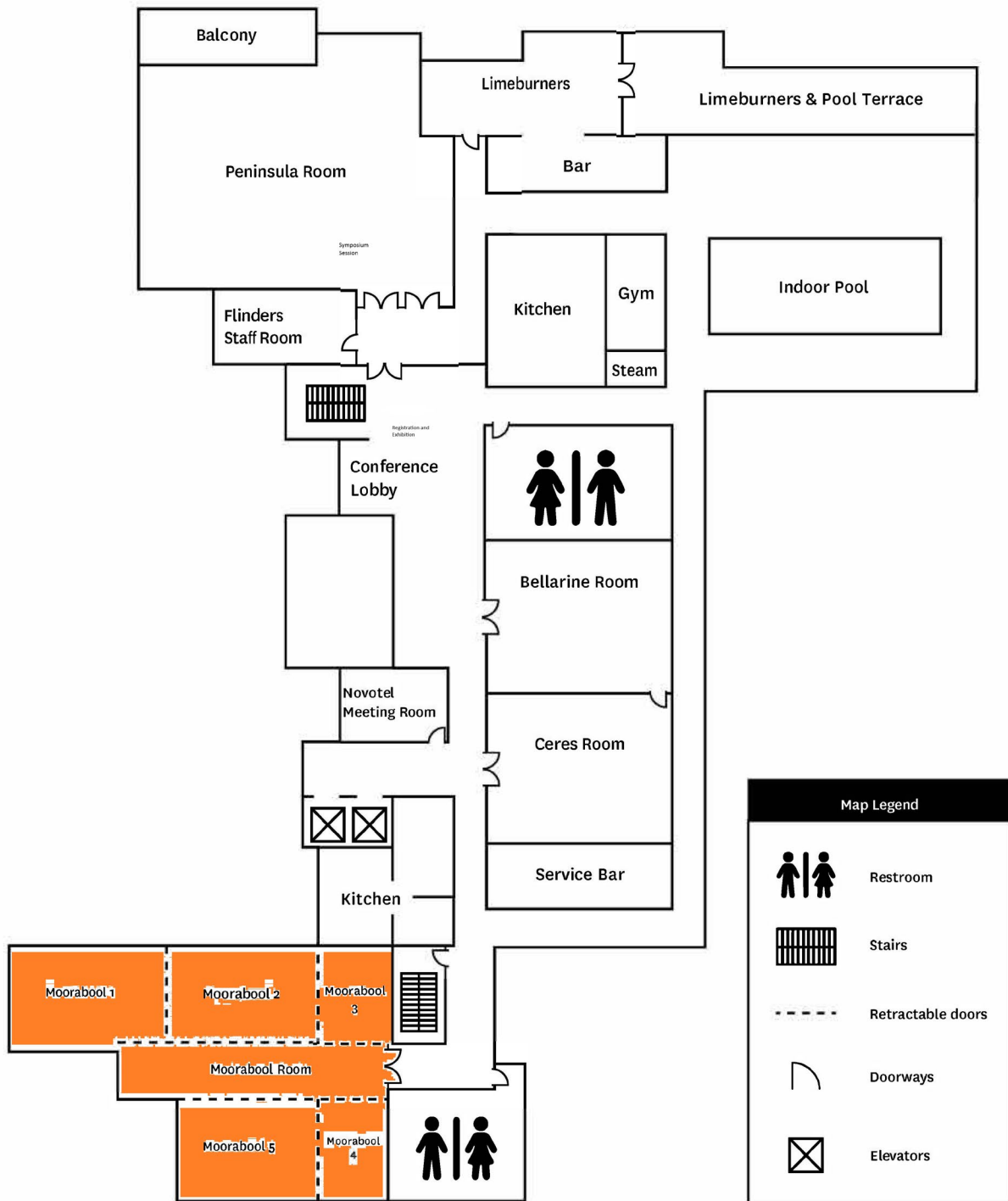


Constantly searching
for better barley
varieties



agtbreeding.com.au

Floor Plan



Moorabool rooms not in use





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AUSTRALIAN
BARLEY
TECHNICAL
SYMPOSIUM

Keynote Speakers



Jia-Wu Feng

Jia-Wu Feng is a Ph.D. candidate specializing in plant genomics and pangenomics, with a focus on the evolutionary and adaptive processes of crop wild relatives. Working primarily with *Hordeum* species, he explores the genetic diversity of wild barley relatives to uncover traits with potential for crop improvement. Feng holds a master's degree in bioinformatics and a bachelor's in biotechnology from Huazhong Agricultural University, where he also developed bioinformatics databases and tools for plant genomics.



Laura Rossini

Laura Rossini received her PhD in Genetics from the University of Milan (Italy). After a postdoctoral appointment in the Department of Plant Sciences at the University of Oxford (UK), she returned to the University of Milan, where she is now Full Professor of Crop Genetics and Head of the Master's Programme in Crops and Plant Sciences. For the past twenty-five years, she and her research team have applied genetic and genomic approaches to investigate the mechanisms underlying barley morphology and development, leveraging the genetic diversity of mutant and germplasm collections. Since 2008, she has also been involved in fruit tree research, contributing to the International Peach Genome Initiative and to the development of genomics-based strategies for dissecting and improving fruit quality and agronomic traits.





Christoph Dockter

Christoph Dockter is Head of Cereal Trait Design at the Carlsberg Research Laboratory, where his team focuses on discovering key cereal breeding traits and the genetics behind them. He bridges fundamental research and practical applications through pan-omics-guided trait development. Christoph helped establish a novel droplet digital PCR approach that accelerates the discovery of targeted genetic variants, significantly speeding up new barley variety development. As PI at AEGIS and leader of the Barley Hub, his work aims to build sustainable, resilient cropping systems under climate change while preserving biodiversity.



Jochen Kumlehn

Dr Jochen Kumlehn is Head of the Division of Cell Biology and Biotechnology at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany, and a leading expert in barley biotechnology and genome editing. His research centres on developing advanced tools such as genome editing, haploid technologies, and plant transformation to accelerate barley improvement.

With a strong focus on barley reproductive biology, grain development, disease resistance, and stress tolerance, his work supports the delivery of higher-yielding, higher-quality, and more resilient barley varieties. Dr Kumlehn has published extensively in top-tier journals and works closely with international breeding and research programs. As a speaker, he brings practical insight into how cutting-edge biotechnology is shaping the future of the global barley industry.





Silvia Pereyra

Dr Silvia A. Pereyra is an internationally recognised plant pathologist and Principal Reference Scientist at Uruguay's National Institute for Agricultural Research (INIA). Her work specialises in the epidemiology and integrated management of barley diseases, with particular expertise in *Fusarium* head blight, *Ramularia* leaf spot and net blotch. She works closely with barley breeding programs and the malting industry to develop disease-resistant varieties and practical management strategies, and has co-authored multiple barley variety releases recognised for improved disease resistance and performance.



Gabriel Keeble-Gagnere

Gabriel Keeble-Gagnere has worked at Agriculture Victoria Research for almost a decade and is currently the Science Program Leader for the Australian Grains Genebank Strategic Partnership. In this role, he leads a multidisciplinary team of researchers and software developers delivering datasets and digital tools that are reshaping how industry accesses and uses genebank resources. His career has centered on technological innovation across genomics, software development and genotyping, with a strong focus on bridging the gap between research and breeding in Australia's major grain crops. He co-developed the widely adopted Infinium Wheat-Barley and Multispecies Pulse SNP arrays, and has contributed to several major international genomics initiatives, including the International Wheat Genome Sequencing Consortium, the 10+ Wheat Genomes project, the Barley Pan Genome Project, The International Pea Pangenome Sequencing Consortium and the Faba Bean Genome Consortium.



Invited Speakers



Paolo Pesaresi

Professor Paolo Pesaresi is Full Professor of Genetics at the University of Milan and head of the PhotoLab research group. His research focuses on the genetic, molecular and physiological regulation of photosynthesis and chloroplast biogenesis, with strong relevance to crop performance and stress resilience. With nearly 30 years of experience working across model plants and crop species, Professor Pesaresi has contributed to key advances in understanding photosynthetic efficiency and environmental adaptation. His current work aims to improve photosynthetic performance and support sustainable strategies for crop productivity, including cereals such as barley.



Roxana Savin

Roxana Savin (Ph.D. in crop physiology at the University of Melbourne, Australia) is currently Professor at the University of Lleida (Spain), where she is also Coordinator of the PhD Programme in Agricultural and Food Science and Technology. Roxana is currently Technical Editor of Crop Science (USA). Her expertise is focused on Physiology of yield and grain quality, carbon and nitrogen relationships, and heat and nitrogen stress. Dr Savin has published more than 90 papers in JCR-indexed journals and 26 Chapters in Scientific books of international publishers (e.g. Elsevier, CAB International, Springer, Academic Press) and has coedited a book and an Encyclopaedia.





Tim George

Tim George is Director of the International Barley Hub and a leading rhizosphere scientist at the James Hutton Institute. His research underpins global barley improvement by revealing how root traits and environmental interactions drive nutrient uptake and stress resilience. Tim coordinates an EU Horizon Europe project developing root phenotyping and genetic strategies to future-proof barley against climate change. With over 150 publications, he is a key voice in advancing barley science and innovation. He also champions plant research globally as President of EPSO and the International Society of Root Research, while holding Honorary Professorships at Aberdeen and Nottingham.



Davide Bulgarelli

Davide Bulgarelli obtained a PhD in Crop Sciences at the University of Milan before leaving his native Italy for Germany, to take a post-doctoral position at the Max Planck Institute of Cologne. This experience represented Davide's first exposure to the plant microbiome, and it was "love at first sight". In 2013 Davide established his own research group at the University of Dundee (UK), where he is currently a Reader and Academic Lead for Public Engagement. The overarching ambition of Davide's team is contributing to sustainable agriculture by dissecting the molecular basis of plant-microbiome interactions and accelerating translational applications.





Kelly Houston

Kelly Houston is Deputy Director of the International Barley Hub and a plant geneticist at the James Hutton Institute. Her work drives barley resilience by identifying genes linked to nutrient uptake and stress tolerance using GWAS and advanced genetic approaches. She combines gene discovery with screening diverse germplasm and applying mutagenesis and gene editing to develop barley lines with improved performance under drought and other abiotic stresses. Kelly leads efforts in major EU projects, Roots2Resilience and BEST-CROP, which aim to enhance drought tolerance and boost photosynthesis, ensuring barley remains productive and sustainable in changing environments.



Hrannar Smári Hilmarsson

Hrannar Smári Hilmarsson is a researcher at the Agricultural University of Iceland. He serves as the Head of Hvanneyri Agronomy Research Center and as the director of VALA the Icelandic plant breeding program. Additionally, he serves on the board of the Nordic gene bank the plant genetic resource institute. His scientific work focuses on adapting cereals to the extreme environment of Iceland. Through his work, he contributes to strengthening Iceland's capacity for domestic cereal production, promoting agricultural resilience in challenging environmental conditions, and supporting sustainable resource management in line with broader environmental and food-security goals.





Shun Sakuma

Shun Sakuma is an Associate Professor at the Faculty of Agriculture, Tottori University, Japan. His team focuses on understanding the genetic basis controlling the inflorescence architecture of cereal crops, such as barley and wheat. He has contributed to identifying several key genes playing pivotal roles in barley/wheat inflorescence development through combining genetics, genomics, and functional analysis. He has also been involved in the international barley/*Hordeum* pan-genome projects. Since 2022, Shun has led efforts in a major project, FOREST, aiming to disruptive innovation through diversity and fusion.



Sarah McKim

Sarah McKim is a developmental geneticist and Deputy Director of the International Barley Hub, with a research focus on the genetic regulation of cereal growth and development. Following her PhD at the University of British Columbia and a fellowship at the University of Oxford, she established her research group at the University of Dundee, where she investigates the developmental processes that underpin barley yield, resilience and grain quality. Her team has identified key regulators of shoot branching, stem growth, floret fertility, cuticular waxes, epidermal patterning and early grain development. Through strong international collaborations, Sarah's research is helping to develop more productive and resilient barley varieties for the future.





Hiroshi Kubota

Dr. Hiroshi Kubota is a Research Scientist in Sustainable Cropping Systems at Agriculture and Agri-Food Canada. Since completing his PhD in Plant Science at the University of Alberta in 2018, his research has focused on developing innovative agronomic practices that improve the productivity, profitability, and sustainability of conventional and organic cropping systems. His work spans cropping system diversity, cropping practice diversity, and integrated crop management. Dr. Kubota currently leads the GROW Barley Projects, advancing barley agronomy and sustainable production practices across Western Canada.

AGRICULTURE VICTORIA

The Australian Barley
Technical Symposium
acknowledges the support
of Agriculture Victoria and
the Victorian Government



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Social Functions

Pre-Symposium Technical Field Tour

16-17 August 2026

Welcome Function

Date: Monday 17th August 2026

Time: 7.00pm – 9.00pm

Venue: Level 1, Novotel Geelong

Sponsored by: GRDC



Networking Function

Date: Tuesday 18th August 2026

Time: 7.00pm – 9.00pm

Venue: Little Creatures

Sponsored by: Lion



Symposium Dinner

Join us for the night of good food, company, and entertainment at the ABTS.

Date: Thursday 20th August 2026

Time: 7.00pm – 11.00pm

Venue: 1915

Dress: Smart Casual

Sponsored by: Asahi



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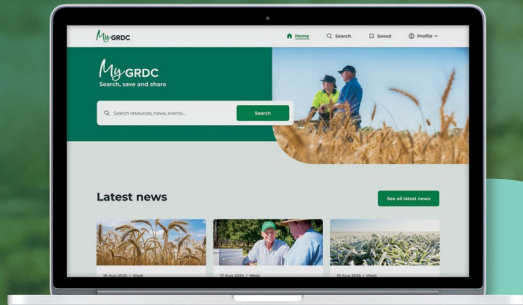


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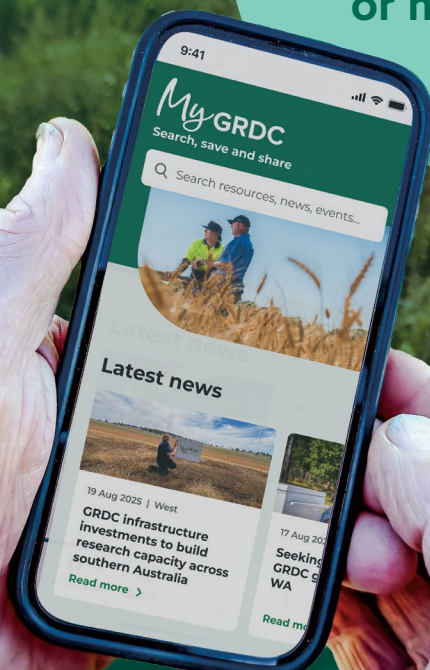
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ABTS 2026 Program

Venue: Novotel Geelong, 10/14 Eastern Beach Rd, Geelong VIC 3220

*Please note this program is subject to change ** All times are in AEST

Sunday 16 – Monday 17 August 2026

Pre Symposium Field Trip

8.45am – departs Novotel Geelong

Returns Mon 17th approx. 4pm

Monday 17 August 2026

3.00pm – 6.30pm	Registration Open	Level 1, Pre-function foyer
4.30pm – 6.30pm	Student and Early Career Forum with Industry Leaders Bellarine Room, Level 1, Novotel Geelong	Sponsored by Meet Geelong and the Bellarine
7.00pm – 9.00pm	Welcome Reception Level 1, Novotel Geelong	Sponsored by GRDC

Tuesday 18 August 2026

7.30am – 5.00pm	Registration Open	Level 1, Pre-function foyer
ABTS Symposium Opening		Peninsula Room
8.30am – 8.40am	Acknowledgement of Country Sally Norton	
8.40am – 8.50am	Opening of Symposium Jessica Hyles, Grains Research and Development Corporation	
8.50am – 9.00am	Shaping the Future of Australian Barley: GRDC's Crop Improvement Priorities Jessica Hyles, Grains Research and Development Corporation	
9.00am – 10.00am	Session 1: Framing the Opportunity Chair: Sally Norton	Sponsored by Riordan
9.00am – 9.20am	To 2035 and beyond: Shaping a sustainable Australian barley industry through market diversification Mary Raynes, Grains Australia	



Tuesday 18 August cont.

9.20am – 9.40am	Malt, Feed, and Food: Insights into how shifting demand is redefining barley markets Sean Hickey, Bendigo Bank Agribusiness
9.40am – 10.00am	The International Barley Hub – Towards sustainable barley production at a global scale Tim George, James Hutton Institute
10.00am – 10.30am	Morning Tea Sponsored by GrainCorp
10.30am – 11.20am	Session 2: Feeding Global Demand Sponsored by Riordan Chair: Mary Raynes
10.30am – 10.45am	Feed Barley and its place in the world Luke O'Connor, GrainCorp
10.45am – 11.00am	Barley strategies for the brewing industry in 2030 Jack King, Riordan Group
11.00am – 11.05am	HB23150: Canada's first black-coloured hulless barley for food Ana Badea, Agriculture and Agri-Food Canada
11.05am – 11.20am	Next generation grain quality varietal assessment: Automation, AI and real-time decision making Ivan Pasmam, ZoomAgri
11.20am – 12.25pm	Session 3: Malting, Brewing and Distilling 1 Sponsored by Malteurop Chair: Trevor Perryman
11.20am – 11.35am	From glass to paddock: How global beer trends are shaping malting – and what they mean for Australian barley Vincent Lauwerier, Malteurop Australia & New Zealand
11.35am – 11.50am	Australian brewing trends, sustainability requirements, and actions Dave Engel, Asahi
11.50am – 12.05pm	Australian whisky industry update Sam Slaney, Starward Distilling
12.05pm v 12.20pm	Regen4real: A sustainability program for the malt barley supply chain Brooke Sauer, Boolah
12.20pm – 1.20pm	Lunch and Poster Session Sponsored by Secobra Recherches SAS
1.20pm – 2:35pm	Session 4: Malting, Brewing and Distilling 2 Sponsored by Malteurop Chair: Doug Stewart
1.20pm – 1.50pm	KEYNOTE: Barley grain germination Christoph Dockter, Carlsberg Research Laboratory
1.50pm – 2.05pm	When good enough isn't good enough: The case for raising Australia's malting barley quality Marcus Williams, Malteurop Australia & New Zealand
2.05pm – 2.20pm	Identification of the molecular drivers of malting performance in <i>Hordeum vulgare</i> Bryan Hau, The University of Western Australia



Tuesday 18 August cont.

2.20pm – 2.35pm	Increasing efficiency of malting by creating a digital twin of malting Infrastructure: Through machine learning and high throughput molecular analysis Owen Duncan, The University of Western Australia
2:35pm – 3:15pm	Panel Session - Barley's place within soft commodity markets: should we be happy where it sits or does it need to Pivot? Facilitator: Mary Raynes Panel members: Luke O'Connor, GrainCorp; Jack King, Riordan; Vincent Lauwerier, MEA; Dave Engel, Asahi; Paul Telfer, AGT
3.15pm – 3.45pm	Afternoon Tea Sponsored by Seednet
3.45pm – 5.00pm	Session 5: Unlocking Crop Performance Sponsored by AGT Chair: Blakely Paynter
3.45pm – 4.05pm	From research gaps to growth opportunities: shaping the future of Canadian barley agronomy through the GROW barley Hiroshi Kubota, Agriculture and Agri-Food
4.05pm – 4.25pm	Optimising canopy photosynthesis in barley: identifying optimal allelic variants within the BEST-CROP project Paolo Pesaresi, University of Milan
4.25pm – 4.40pm	Advancing barley yields: insights from hyper-yielding trials in Tasmanian spring sowing conditions Darcy Warren, FAR Australia
4.40pm – 4.55pm	Setting profitable yield frontiers for barley: yield upside, risk and quality tradeoffs Kenton Porker, CSIRO
4.55pm – 5.00pm	Mitigating climate risk in barley in the Canadian prairies through ultra-early seeding Ana Badea, Agriculture and Agri-Food Canada
5.00pm – 6:15pm	ABTS Inc. Annual General Meeting
7.00pm – 9.00pm	Networking Function Sponsored by Lion Little Creatures - 221 Swanston St, Geelong VIC 3220 Bus boarding: 6:30pm, Bus departs Novotel at 6:45pm



Wednesday 19 August 2026

8.00am – 5.00pm	Registration Open Level 1, Pre-function foyer.
8.30am – 10.08am	Session 6: Next Generation Breeding Tools 1 Chair: Mathew Lewsey Sponsored by Agriculture Victoria
8.30am – 8.45am	The Australian Grains Genebank – Next-gen genebank management for a food secure future Sally Norton, Agriculture Victoria
8.45am – 9.15am	KEYNOTE: From genebanks to breeding: unlocking barley's genetic diversity with data, AI and digital tools Gabriel Keeble-Gagnère, Agriculture Victoria
9.15am – 9.30am	FastStack to accelerate multi-disease resistance breeding in Australian barley: where are we now? Eric Dinglasan, Queensland Alliance for Agriculture and Food Innovation
9.30am – 9.40am	Digital phenotyping of barley foliar disease resistance: Quantitative trait capture across germplasm and mapping populations Eden Tongson, La Trobe University
9.40am – 9.50am	A digital micro-phenotyping pipeline for dissecting net blotch resistance in barley Linda Brain, La Trobe University
9.50am – 10.05am	Whole genebank comparison between two of the largest international barley genebank collections Luisa Teasdale, Agriculture Victoria
10.05am – 10.35am	Morning Tea Sponsored by Boortmalt
10.35am – 12.35pm	Session 7: Developmental Biology Chair: Matt Tucker Sponsored by RAGT
10.35am – 11.05am	KEYNOTE: Unravelling the genetic control of barley shoot architecture traits Laura Rossini, University of Milan
11.05am – 11.25am	Facing forwards: developmental genetics of the epidermis in barley Sarah McKim, University of Dundee
11.25am – 11.40am	How a unique grain retention mechanism evolved in cereals Kelly Rodgers, The University of Melbourne
11.40am – 11.50am	The effect of barley head morphologies on wind-induced stalk failure Muhammad Faizan, Adelaide University
11.50am – 12.05pm	Barley head loss: a farmer's problem and a breeder's challenge Nirmal Rajendran, University of Melbourne / InterGrain
12.05pm – 12.20pm	Towards the grain filling pathway in barley Xiujuan Yang, University of Adelaide



Wednesday 19 August cont.

12.20pm – 12.35pm	Identification of a novel plant height QTL on chromosome 6H and its agronomic effects in field-grown spring barley Hien Minh (Jean) Vu, Adelaide University
12.35pm – 1.30pm	Lunch Sponsored by Coopers
1.30pm – 2.45pm	Session 8: Biotic Stress Tolerance – Net Blotch Focus Sponsored by AGT Chair: Peter Dracatos
1.30pm – 1.45pm	Pathogenic variation of <i>Pyrenophora teres</i> f. <i>teres</i> in Australia between 2020 – 2024 Xuechen Zhang, Queensland Government
1.45pm – 2.00pm	Highresolution mapping and pyramiding of resistance QTLs to achieve durable net form net blotch resistance in barley Xuan Hoan Dinh, Curtin University
2.00pm – 2.10pm	Haplotype-based insights into the genetic architecture of net blotch resistance in barley Dan Liu, The University of Queensland
2.10pm – 2.25pm	Isoform-level resolution of barley and <i>Pyrenophora teres</i> f. <i>teres</i> transcriptomic landscapes during net blotch Jade Davis, Curtin University
2.25pm – 2.35pm	Genome-wide association mapping reveals isolate-specific resistance to Australian pathotypes of <i>Pyrenophora teres</i> f. <i>teres</i> in barley Waleed Khan, University of Southern Queensland
2.35pm – 2.45pm	Host resistance eliminates fungicide reliance for managing net form net blotch in barley Aruni Udugama Vithanage, Department of Energy, Environment and Climate Action
2.45pm – 2.50pm	Gold Sponsor Update Paul Telfer - Australian Grain Technologies
2.50pm – 3.15pm	Afternoon Tea Sponsored by Barrett Burston
3.15pm – 5.10pm	Session 9: Designing Adaptive Crops Sponsored by InterGrain Chair: Tress Walmsley
3.15pm – 3.35pm	Adapting barley to extreme environments of Iceland Hrannar Smári Hilmarsson, Agricultural University of Iceland
3.35pm – 3.50pm	Strigolactones are targets for crop improvement Phil Brewer, La Trobe University
3.50pm – 4.10pm	Rise and fall: a new phenotyping tool to assess canopy traits in barley Francisco Pinera, The Australian National University
4.10pm – 4.25pm	From gene to grain: turning research into commercial impact David Moody, InterGrain
4.25pm – 4.40pm	Barley breeding has contributed to increased resilience across the supply chain - Past wins and future opportunities Paul Telfer, Australian Grain Technologies



Wednesday 19 August cont.

4.40pm – 4.55pm	CAIGE barley project - 12 years of international collaboration Mark Dieters Consulting
4.55pm – 5.05pm	Barley breeding adaptation in global warming climate Dominique Vequaud, SECOBRA Recherches
5.05pm – 5.15pm	Quantifying the contribution of genetics, climate, and agronomy to malting barley yield gains in South America Maximiliano Verocai, Universidad de la República, Uruguay
5:15pm – 6:15pm	Poster Session Sponsored by GRDC
	Free Evening

Thursday 20 August 2026

8.00am – 5.00pm	Registration Open Level 1, Pre-function foyer
8.30am – 10.10am	Session 10: Biotic Stress Tolerance Sponsored by GRDC Chair: Laura Ziems
8.30am – 9.00am	KEYNOTE: Recent advances in managing Ramularia leaf spot in barley: lessons from epidemiology and integrated strategies in South America Silvia Pereyra, National Institute for Agricultural Research
9.00am – 9.15am	RUST-E: a pathology-informed deep learning expert for foliar disease resistance phenotyping Matthew Ulrich, La Trobe University
9.15am – 9.30am	From genebanks to the field: discovery and validation of barley leaf rust resistance loci Shiva Azizinia, Agriculture Victoria
9.30am – 9.45am	Leaf rust and stripe rust of barley: new tools to combat ever-changing pathogens Robert Park, The University of Sydney
9.45am – 10.00am	<i>Rpg1</i> and beyond: Advancing inherited stem rust resistance in Canadian barley Ana Badea, Agriculture and Agri-Food Canada
10.00am – 10.10am	Smart protection: linking barley genetics to fungicide performance Varthini Govindaraju Punithan, Centre for Crop and Disease Management
10.10am – 10.45am	Morning Tea Sponsored by Lion
10.45am – 12.05pm	Session 11: Abiotic Stress Tolerance Sponsored by RAGT Chair: Kenton Porker
10.45am – 11.00am	Variation in HvHMA5 impacts copper transport, photosynthesis and yield Kelly Houston, The James Hutton Institute
11.00am – 11.15am	Assessing the resilience of barley and malt to heat waves Roxana Savin, University of Lleida



Thursday 20 August cont.

11.15am – 11.25am	The SnRK2–SLAC1 module regulates stomatal traits for drought tolerance in barley Zhong-Hua Chen, Adelaide University
11.25am – 11.40am	Envirotyping and historical trends of abiotic stresses affecting barley productivity across Australia Bitá Heidariask, The University of Queensland
11.40am – 11.50am	Expanding the pre-harvest sprouting window in barley: genotype × environment × harvest timing interactions under South African conditions Sandra Hull, Stellenbosch University
11.50am – 12.05pm	Do PPD-H1 alleles affect yield sensitivity to a pre-flowering heat wave? Gustavo Slafer, ICREA and University of Lleida
12.05pm – 12.08pm	Silver Sponsor Update Richard Prusa, RAGT
12.08pm – 1.05pm	Lunch and Poster Session Sponsored by Boolah Pure Network
1.05pm – 2.28pm	Session 12: Decoding Crop Genomes Sponsored by InterGrain Chair: Chengdao Li
1.05pm – 1.35pm	KEYNOTE: Expanding the genomic landscape of barley breeding using wild <i>Hordeum</i> spp. Jia-Wu Feng, IPK
1.35pm – 1.55pm	Genetic basis of barley inflorescence architecture: structure of spikelet and floret Shun Sakuma, Tottori University
1.55pm – 2.10pm	Connecting genebank genomics to the barley pan-genome with Brioche James O'Dwyer, Agriculture Victoria
2.10pm – 2.25pm	OzBarley: a public genome-to-phenome resource for trait discovery Bettina Berger, Adelaide University
2.25pm – 2.28pm	Silver Sponsor Update David Moody, InterGrain
2.28pm – 3.00pm	Afternoon Tea Sponsored by Asahi Group
3.00pm – 4.25pm	Session 13: Next Generation Sponsored by Agriculture Victoria Breeding Tools 2 Chair: Mohammad Pourkheirandish
3.00pm – 3.30pm	KEYNOTE: Genome editing in <i>Triticeae</i> crops Jochen Kumlehn, IPK
3.30pm – 3.50pm	Composition, function and host control of the barley microbiome Davide Bulgarelli, University of Dundee
3.50pm – 4.05pm	Using novel imputation strategies to integrate barley genebank collections genotyped with different technologies Irene Van Den Berg, Agriculture Victoria
4.05pm – 4.10pm	Use of gene-editing to introduce agronomically desirable traits in barley Benjamin Kurya, Adelaide University
4.10pm – 4.25pm	A spatial transcriptome atlas of barley caryopsis development and germination Mathew Lewsey, La Trobe University



Thursday 20 August cont.

4.30pm – 5.15pm	Panel Session 2: Pivoting to the Future – What do we need to do differently? Facilitator: Trevor Perryman Panel Members: Tyson Vivian, Grower/SEABAC; Matthew Tucker, University of Adelaide; Tress Walmsley, InterGrain; Kenton Porker, CSIRO; Jessica Hyles, GRDC; Doug Stewart, Coopers Brewery
5.15pm – 5.30pm	Conference Close Sally Norton
7.00pm – 11.00pm	Gala Dinner Sponsored by Asahi Group 1915 - PH2, 33 ackey St, North Geelong VIC 3215 Bus boarding: 6:30pm, Bus departs Novotel at 6:45pm

Friday 21 August 2026

9.00am – 1.00pm	Post-Conference Digital Tools Workshop Novotel Geelong	Sponsored by Agriculture Victoria
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RAGT'S GLOBAL VIEW ON BARLEY

As a world leader in malting barley, with a global presence in nearly 50 countries, a strong portfolio of varieties, and a recent strategic acquisition that expands its international reach, RAGT has positioned itself well to provide solutions for growers & maltsters across the globe.

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The Grains Research and Development Corporation (GRDC) is responsible for investing in research, development and extension (RD&E) to drive the discovery, development and delivery of world-class innovation for Australian grain growers.



The Australian grains industry plays a vital role in Australia's economy, comprising 27% (\$17.7billion) of the total value of farm production in 2020-21. GRDC invests over \$180 million a year in RD&E on behalf of growers to enhance the productivity, profitability and sustainability of their farm businesses, with benefits to the grains industry and wider community. We partner with leading international experts on innovative RD&E across a diverse portfolio of over 700 projects.

For GRDC, supporting the Australian Barley Technical Symposium contributes to building the expertise and networks that allow the grains RD&E community to continue to deliver world-class, impactful research.

Our purpose is to invest in RD&E to create enduring profitability for Australian grain growers. Our vision is a profitable and sustainable Australian grains industry, valued by the wider community.

For more information about us, our investments, and priorities visit www.grdc.com.au



Gold Sponsors

Australian Grain Technology

Australian Grain Technologies (AGT) is Australia's largest plant breeding company. At AGT, we consider ourselves privileged to be able to serve Australian farmers by developing new barley, wheat, durum, lupin and canola varieties that are more productive, better quality and cost less to grow. We want to see Australian farmers more prosperous, and the global population to be well nourished.



Malteurop: Connecting Growers and Markets Since 1961

Malteurop's story began in 1961 when a group of barley farmers in eastern France came together with a shared vision: to create lasting value from grain to glass.



More than 60 years later, that spirit still guides us.

Today, Malteurop is the world's third-largest maltster, operating 23 malt houses across 14 countries and four continents. We serve more than 900 brewing, distilling and food industry customers in 80 countries. Every second, 2,000 beers made with our malt are enjoyed worldwide.

Yet despite our global reach, our role remains fundamentally the same. We sit at a unique crossroads between growers and the brewing and distilling industries. Every day, we work with farming communities who cultivate our barley and with customers who rely on high-quality malt to create beers, whiskies and spirits enjoyed around the world.

This position gives us a deep understanding of both sides of the value chain. We know the realities growers face in the field, and we understand the evolving needs of malt users and consumers. Our role has always been to help bring those worlds together.

We belong to VIVESCIA, one of France's leading cooperatives with 10,000 farmers.

This is why we also believe the future of malt depends on building a more sustainable value chain. We are expanding regenerative agriculture programs with growers and customers, while continuing to reduce the carbon footprint of our malt houses through targeted decarbonisation initiatives.

In Australia, Malteurop has proudly been part of the Geelong industrial community since 2008. We are delighted to support the 2026 Australian Barley Technical Symposium as a Gold Sponsor and look forward to meeting fellow growers, researchers, breeders and industry partners throughout the event.



Riordan Group

The Riordan Group is a leading Australian family-owned agribusiness delivering grain marketing, storage, transport, bulk commodity handling, and fuel distribution across regional Australia.



Riordan

For 30 years, we have worked alongside growers and customers to move grain efficiently and reliably from paddock to end user. Today, we operate one of Victoria's largest grain handling and marketing programs and continue to invest in the people, relationships and capability that support the long-term success of Australian agriculture.

Barley has always been an important part of our business and remains one of our strongest areas of expertise. Over many years, we have built strong relationships across the brewing and malting industries and developed a deep understanding of what customers value and what it takes to consistently deliver high-quality grain.

We work closely with growers to connect those customer requirements back to production decisions in the paddock. We see real opportunity in bringing the supply chain closer together, creating better alignment between breeding, growing, grain quality and end-use performance.

As the industry continues to evolve, we believe there is more opportunity ahead. Continued innovation in barley breeding, greater focus on functionality and sustainability, and stronger connections across the industry will help support premium barley and world-class brewing outcomes.

We are optimistic about the future of Australian barley and proud to play our part in supporting an industry that continues to adapt, improve and deliver for growers, customers, and consumers.



Silver Sponsors

Agriculture Victoria

Agriculture Victoria, within is the Victorian Government's Department of Energy, Environment and Climate Action is focussed on working with farmers, foresters, industry and communities to support a productive, sustainable and resilient food and fibre sector.



Victoria is Australia's leading food and fibre exporter, generating \$22.1 billion in exports in 2024-25 and accounting for 28 per cent of national food and fibre exports. The sector contributes significantly to the state's economy, with agriculture production and food manufacturing employing more than 154,000 people across Victoria. Victoria is also home to the nation's largest plantation forestry estate, supplying more than a quarter of Australia's plantation-grown timber.

Behind these achievements are the farmers, foresters and regional communities who continue to adapt and innovate despite facing challenges such as drought, bushfires, floods, storms, biosecurity threats and rising input costs. Their efforts helped drive Victoria's gross value of agricultural production to \$22.2 billion in 2023-24 and delivered a fourth consecutive year of record export growth.

Agriculture Victoria plays a key role in supporting this success. We provide scientific research, biosecurity services, emergency response capability, policy advice and practical support that helps producers improve productivity, profitability and sustainability. We work alongside industry to strengthen market access, maintain high standards of food safety and animal welfare, and protect Victoria from pests and diseases that could threaten our environment, economy and way of life.

Agriculture today is far more than farming alone. It is supported by a network of researchers, veterinarians, agronomists, technology specialists, manufacturers, transport operators and exporters who help bring food and fibre from paddock to plate. Through investment in innovation, digital technologies, climate-smart farming and research partnerships, Agriculture Victoria helps ensure producers can respond to changing conditions and emerging opportunities.

Agriculture Victoria also supports thriving regional communities by investing in workforce development, farm safety, wellbeing programs and initiatives that



encourage the next generation of agricultural leaders. Through Victorian Government investment, we help farmers access new technologies, improve business performance and build resilience to climate and market challenges.

By backing farmers and foresters, protecting biosecurity, driving innovation and supporting regional communities, we help ensure Victoria remains a global leader in food and fibre production while delivering economic growth, jobs, food security and environmental stewardship for future generations.

Intergrain

InterGrain is a leading Australian plant breeding company, developing high performing cereal and break crop varieties that help grain growers improve productivity, profitability and sustainability. With successful wheat, barley, oat and emerging faba bean breeding programs, InterGrain services all major broadacre cropping regions across Australia and is widely recognised for delivering varieties that meet both grower needs and end-user market requirements. InterGrain is globally recognised for its proven capability in developing quality malting barley and udon noodle wheat varieties that support both domestic and international grain markets. InterGrain operates a national breeding and evaluation network, employing more than 80 staff and conducting trials across more than 60 breeding sites, with over 300,000 field plots assessed annually. Headquartered in Perth, Western Australia, the company has major breeding and seed facilities in Horsham, Victoria, and representatives located throughout Australia's key grain-growing regions, ensuring strong local connections with growers, advisors and industry partners. Innovation is central to InterGrain's breeding strategy, with investments in genomics, predictive breeding, speed breeding technologies and collaborative research partnerships. The company's breeding programs focus on yield, disease resistance, climate resilience and end-use quality, helping Australian growers adapt to environmental and market conditions. Through continual investment in genetics and research, InterGrain's vision is to strengthen the competitive advantage and long-term sustainability of Australian grain production.



RAGT



think
SOLUTIONS
think RAGT

RAGT Australia is a growing Australian seed breeding and development business focused on delivering high-performing genetics for the nation's broadacre, pasture and forage industries. As part of the global RAGT Group, the company combines Australian research, field evaluation and market knowledge with access to one of the world's leading multi-species plant breeding networks.

Cereals are a major strategic priority for RAGT Australia. The company has strengthened its local wheat capabilities through the acquisition of an established Australian breeding programme, providing locally adapted germplasm, commercial varieties and a continuing pipeline for Australian production environments. Its cereal portfolio also includes winter and spring wheats and internationally recognised barley genetics, including RGT Planet malting barley and RGT Atlantis, developed to provide improved performance under transient waterlogging conditions.

Canola is another core area of investment, with RAGT Australia offering hybrid spring and winter varieties across key Australian growing regions. Its portfolio includes high-yielding Triazine Tolerant spring hybrids and Clearfield® winter canolas suited to longer-season and dual-purpose grazing-and-grain systems. These varieties are selected to provide strong establishment, oil production, yield potential and flexibility within modern crop rotations.

Globally, RAGT is a specialist seed breeder operating across more than 60 countries, with 25 research stations and breeding programmes covering more than 40 agricultural species. This international scale supports RAGT Australia in delivering innovative, resilient and commercially relevant seed solutions adapted to Australian farming conditions.



Bronze Sponsors

Boortmalt

Boortmalt is one of the world's leading malt producers, supplying high-quality malt to brewers, distillers and food manufacturers globally. Headquartered in Belgium and part of the Axéreal Group, Boortmalt operates an extensive network of malthouses spanning Europe, Australia, North America, South America and Asia.



Boortmalt's Australian malthouse Joe White, sources locally grown barley through long-term partnerships with farmers, combining local expertise with global scale to deliver consistent, sustainable malt solutions. Backed by decades of experience, our roasters produce specialty malts renowned for their exceptional performance.

The Joe White Maltings commitment has remained unchanged, delivering premium Australian malt with the consistency, technical expertise and reliability that has earned the trust of brewers for generations.

Barret Burston Malting

Barrett Burston Malting has been at the heart of Australia's malting industry for more than 150 years, producing premium malt for the brewing, distilling, and food industries using quality barley sourced from Australian growers.



With malting plants in Victoria, Queensland, and Western Australia, we maintain a strong national presence, working closely with growers, customers, and industry partners to deliver consistent quality and reliable supply. Our experienced team is driven by a shared commitment to excellence, innovation, and sustainability, ensuring we continue to meet the evolving needs of the industries we serve.

Proud of our heritage and focused on the future, Barrett Burston Malting remains committed to supporting Australian agriculture and producing world-class malt.



GrainCorp

GrainCorp is one of Australia's largest integrated agribusinesses, operating across the food, feed and fuel value chain. The company has a market-leading presence in grain storage, handling and processing, as well as edible oils and feedstocks. With high-quality infrastructure assets and operations across Australia and New Zealand, supported by a global network of offices, GrainCorp has connected regional producers with customers in the nutrition, livestock and energy sectors for more than 100 years.



Symposium Dinner Sponsor

Asahi Beverages

Australia's largest breweries at Yatala, Queensland and Abbotsford, Victoria, are now brewing beer with barley traceable back to its farm of origin as part of groundbreaking deals with Aussie growers.



ASAHI BEVERAGES

The deals means Australian beer lovers can enjoy a VB, Carlton Dry or Pure Blonde knowing it's been brewed entirely with barley sourced direct from select NSW and Victorian farmers.

This allows brewers to work directly with growers to select and perfect barley types.

More than 90% of Asahi Beverages' barley is now purchased direct from Australian farmers.

There are also plans to expand the program for export volumes with Asahi Japan.



Networking Dinner Sponsor

Lion

Lion is a leading beverages company in Australasia, with fast-growing operations in the United States. We produce, market, sell and distribute alcoholic and non-alcoholic drinks. Our portfolio of brands spans beer, cider, wine, spirits, and kombucha.



Our main manufacturing base is in Australia and New Zealand. We operate breweries across the region – XXXX in Brisbane, Tooheys in Sydney, Boags in Launceston, the Pride in Auckland, and Speight's in Dunedin. We also operate craft breweries including Stone & Wood, Malt Shovel, Little Creatures in Fremantle and Geelong, Tiny Mountain in Townsville, and brew pubs in several locations.

Sustainable Nametag and Lanyard Sponsor

Coopers Brewery

Coopers Brewery is family-owned and the largest Australian-owned brewery. We are known for making a variety of beers, but our selection of naturally conditioned, bottle, can and keg-fermented ales and stout are the very reason we've been around for 160 years. Our unique processes, coveted yeasts and love of the craft have proven time and time again why Coopers ales are respected all over the world.



Coffee Cart Sponsor

Secobra Recherches SAS

Founded in 1902 by French brewers and maltsters, SECOBRA Recherches is a small grain cereal breeding company committed to developing varieties adapted to the evolving needs of agriculture, farmers, industry and climate. Headquartered in France, SECOBRA operates five research sites across the world – in France, the United Kingdom, Germany and Australia allowing genetics to be developed for the specific agro-climatic conditions of Europe, Africa, North and South America, and Oceania.



Our breeding programmes focus on winter and spring barley, soft winter and spring wheat, and triticale, with more than 12 active breeding programmes supported by 110 full-time employees and over 50 seasonal staff each year. Each season, our teams observe and score more than 80,000 breeding plots and carry out over 5,500 quality analyses in our internal laboratories, in the continual pursuit of varieties that deliver on yield, agronomic stability and quality.

With more than 100 years of expertise, and a shareholding consisting of maltsters, brewers and commercializers, SECOBRA Recherches remains true to its founding purpose: cereal innovation, committed by the industry, for the industry.

Satchel Sponsor

Boolah Pure Network

We believe that when growers and customers truly understand each other's needs, everyone benefits.



Boolah Pure Network gives growers access to informed, high-value markets while offering buyers a trusted supply chain, backed by sustainability credentials and transparency.

Our Regen4real Program sets measurable goals, supports farmers to meet them, and verifies outcomes with real data.

It captures and validates key indicators across people, soil health, productivity, emissions, biodiversity, and community impact. At its core, Regen4real brings research, technology, and people together to create tangible, verifiable change across the entire supply chain.



PROUD SPONSOR – AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM 2026

Cereals & Innovation – committed by the industry, for the industry.



LAPEROUSE



SPINNAKER

- *More than 100 years of small grain cereal breeding expertise.*

Founded in 1902 by French brewers and maltsters, SECOBRA Recherches develops winter and spring barley, wheat and triticale varieties adapted to the changing demands of farmers, industry, markets and climate. With five research sites across France, UK, Germany and Australia, our teams breed genetics suited to each agro-climatic region we serve — from Europe to Oceania



**SECOBRA
RECHERCHES**

France · UK · Germany · Australia

110

Full-time employees

12+

Breeding programmes

80,000+

Breeding plots observed yearly

5,500+

Quality analyses carried out

FRIENDLY – INNOVATIVE – COMMITTED – EXPERT – DYNAMIC

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EP02	Mitigating Climate Risk in Barley in the Canadian Prairies through Ultra-Early Seeding	Ana Badea
EP03	Use of gene-editing to introduce agronomically desirable traits in barley	Benjamin Kurya



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Abstracts

SESSION 1: FRAMING THE OPPORTUNITY

To 2035 and beyond: Shaping a sustainable Australian barley industry through market diversification

Mary Raynes¹

1. *Grains Australia, Western Australia, Australia*

Market diversity is fundamental to the strength and sustainability of the Australian barley industry. As the world's leading exporter of barley, Australia accounts for around twenty five percent of global trade, and its ability to access, maintain and grow a diverse range of customers and markets will define its long-term competitiveness and prosperity.

Looking towards 2035 and beyond, the global barley market is expected to expand into animal feed, functional foods and distilling while maintaining stable for malting and brewing across key import regions. Australia's ability to position itself at the forefront of this growth will depend on how effectively the industry anticipates market shifts, responds to evolving customer quality requirements and invests in the relationships, technologies and value chains that will underpin its future competitiveness.

Diversifying into new markets while sustaining current customers and market share in a constantly evolving global marketplace is not simply a strategic ambition for the Australian barley industry but a necessity.

With major markets spanning China, the Middle East, Asia and an expanding network of emerging destinations including Latin America and Africa, the industry recognises that over reliance on any single market is a risk. Building and maintaining diverse and resilient markets will be essential in managing that risk to continue to maintain and increase value for growers and industry.

The future of the Australian barley industry is one of considerable opportunity. By embracing market diversity, investing in technologies and working collaboratively across the entire value chain, the industry is well placed to strengthen its global presence and deliver sustainable long-term value for growers and customers around the world.

Malt, feed, and food: Insights into how shifting demand is redefining barley markets

Sean Hickey¹

1. *Bendigo Bank Agribusiness, South Australia, Australia*

This presentation will examine the Australian barley season to date, exploring production expectations across key growing states and the factors shaping regional outcomes. It will assess Australia's export performance, including the record pace of shipments and the potential risks associated with an increasing concentration in major export markets. The discussion will also consider the outlook for barley prices, comparing the domestic influences affecting Australian growers and buyers with the broader global market drivers shaping international demand and trade.



As barley markets continue to evolve, the presentation will explore the growing importance of quality, traceability and sustainability. It will consider how these attributes are creating opportunities for premiums across malting, feed and food markets, while also influencing purchasing decisions throughout the supply chain.

Looking ahead, the presentation will examine how geopolitical uncertainty, changing trade relationships and shifting government policies may affect the future movement of Australian barley. It will also explore the evolution of global feed demand, including changing consumption patterns, competition from alternative feed grains and emerging opportunities for Australian producers and exporters. Together, these insights will provide a practical outlook on how shifting demand is redefining barley markets and what this could mean for the industry's future.

The International Barley Hub – Towards Sustainable Barley Production at a Global Scale

Tim George¹, Isabelle Colas¹

1. *The James Hutton Institute, Invergowrie, Dundee, Scotland, United Kingdom*

Barley is Scotland's most important crop, the UK's second most widely grown cereal, and the fourth most important cereal grown globally, underpinning major food, feed, brewing, distilling, and bioeconomy sectors. However, barley production faces increasing pressures from climate change, declining soil health, input costs, greenhouse gas emissions, and the need to maintain biodiversity. The International Barley Hub (IBH) provides a coordinated research and innovation platform designed to address these challenges by forging strong links with stakeholders in industry, policy and the public, with the aim of supporting sustainable growth across barley value chains.

The IBH integrates advances in genetics, genomics, physiology, soil science, digital technologies, and socioeconomics to deliver resilient barley systems for the future. Core scientific foundations include the exploitation of global barley diversity, multi-omics approaches for trait discovery, and improved understanding of plant-soil-microbe interactions, particularly root traits that enhance nutrient efficiency and stress tolerance. These scientific advances are linked with system-level approaches addressing soil health, nutrient cycling, and carbon sequestration.

Research within the Hub focuses on five strategic targets: improving grain quality and value for food, feed, and drink sectors; developing climate-resilient and regenerative production systems; enabling circular economy approaches through nutrient and carbon recycling; supporting innovation and bioeconomy opportunities; and understanding the social, economic, and policy drivers that influence adoption of sustainable practices.

A key ambition is the development of a Net Zero Barley system, combining improved nitrogen use efficiency, enhanced root systems, and better integration of barley within low-input and regenerative farming systems. Complementing this is a proposed precision barley breeding programme that integrates advanced phenotyping, genomics, and emerging breeding technologies to accelerate the development of climate-resilient varieties.

Together, these activities position the International Barley Hub as a global focal point for sustainable barley research, innovation, and knowledge exchange.



SESSION 2: FEEDING GLOBAL DEMAND

Feed Barley and its place in the world

Luke O'Connor¹

1. *Graincorp, Sydney, New South Wales, Australia*

With the changing global SnD of feed barley we have seen a re-writing of the trade flows in the last decade.

What have been the driver of this and what will be the driver of this over the next decade. From the former feed barley powerhouse consumer of Saudi Arabia to the newly developed almost insatiable appetite of China.

What production trends are we seeing and where will it be consumed?

Barley Strategies for the Brewing Industry in 2030

Jack King¹

1. *Riordan Group, Victoria, Australia*

With beer demand plateauing at best, and declining across much of the globe, the landscape for the brewing industry continues to evolve. In response, we see opportunities for a more focused and efficient barley supply chain, tailored specifically to the requirements of the brewing industry.

This approach involves building stronger connections from paddock to pot, bringing market insight and demand signals further upstream to inform breeding priorities and varietal adoption. Greater emphasis is placed on selecting traits that improve processing efficiency, sustainability, and brewing quality. This helps strengthen the connection between breeding decisions, production systems, malt quality, and brewing performance.

Future competitiveness will depend on supply chains that are quality-focused, responsive to changing market conditions and coordinated across the value chain.

Key areas of focus include:

1. **Varietal Strategy: From Yield to Functional Performance**

Prioritising varieties that deliver measurable value through malt quality, brewing efficiency and processing performance, alongside strong agronomic outcomes.

2. **Climate Risk Management Through Origin Diversification**

Strengthening supply resilience through geographic diversity to improve consistency and reduce exposure to seasonal variability.

3. **Grower-Maltster-Brewer Integration**

Creating stronger commercial and information links across the value chain to better connect production decisions with brewing requirements.

4. **Sustainability as a Market Requirement, not a Bonus**

Embedding sustainability into procurement and operating decisions as a core expectation of customers, markets and investment decisions.



5. **Malting Process Optimisation**

Improving extract, throughput, and resource use to increase conversion and value capture.

6. **Specialty and Identity Barleys for Premium Segments**

Developing differentiated supply chains supported by traceability, identity preservation, and targeted market opportunities.

7. **Risk Management and Commercial Strategy**

Building commercial frameworks that support investment, manage volatility, and improve confidence across the brewing barley value chain.

This presentation will explore how these strategic themes can support a more connected, resilient, and commercially sustainable brewing barley industry through to 2030.

HB23150: Canada's first black-coloured hulless barley for food

Ana Badea¹, Marta Izydorczyk², James Tucker¹

1. Agriculture and Agri-Food Canada Brandon Research and Development Centre, Science and Technology Branch, Brandon, Manitoba, Canada

2. Canadian Grain Commission Grain Research Laboratory, Winnipeg, Manitoba, Canada

Canada is one of the world's leading barley producers and must continually develop new cultivars to meet rising yield demands, adapt to evolving diseases, align with shifting industry quality standards, and respond to emerging markets. Most Canadian barley is grown in western Canada and is used for malting, food, and general-purpose applications.

Anthocyanins are a major class of natural pigments responsible for the colours of many flowers, vegetables, fruits, and cereal grains. These compounds possess antioxidant activity and have been associated with reduced risks of several chronic diseases.

At Agriculture and Agri-Food Canada's Brandon Research and Development Centre (Manitoba, Canada), a new two-row, black-coloured, hulless spring food barley (*Hordeum vulgare* var. *nudum*), HB23150, was developed from the cross H370/HB12322 made in 2015. HB23150 exhibits elevated anthocyanin concentrations, contributing to its distinctive grain colour and potential health-promoting properties.

HB23150 was evaluated in the Western Cooperative Hulless Barley Registration Test (WCHBRT) coordinated by the Prairie Recommending Committee for Oats and Barley (PRCOB), which oversees the testing and assessment of candidate barley and oat cultivars and provides recommendations to the Variety Registration Office of the Canadian Food Inspection Agency.

Across two years of WCHBRT testing (2023–2024), HB23150 demonstrated strong agronomic performance, including yield comparable to the tan-coloured checks, high kernel weight and plumpness, and loose hull adherence. It showed moderate resistance to stem rust, surface smuts, and loose smut, and intermediate resistance to fusarium head blight, spot-form net blotch, and spot blotch.

Quality assessment conducted by the Canadian Grain Commission's Grain Research Laboratory (Winnipeg, Manitoba) indicated that HB23150 has a lower hardness index than all three checks and superior pearling and milling performance.



HB23150 represents the first black-coloured hulless barley for food variety eligible for registration and commercial food use in western Canada. With its rich grain colour and high anthocyanin content, it addresses emerging demands in the food sector and offers potential value to medical and cosmetic industries seeking natural pigment sources.

Next Generation Grain Quality & Varietal Assessment: Automation, AI and Real-Time Decision Making

Ivan Pasman¹

1. Zoomagri, Western Australia, Australia

Grain quality and varietal assessment remain highly manual, labour-intensive and often subjective processes across the grain value chain. Despite advances in digital technologies, many laboratories and receival points still rely on workflows requiring manual sample preparation, visual inspection and delayed results.

This presentation will introduce ZoomAgri's next generation grain assessment technology, combining artificial intelligence, computer vision and automated sample handling to deliver rapid varietal recognition and grain quality analysis in a single workflow.

The newly developed hardware incorporates an automated loading system, eliminating manual grain placement while enabling the analysis of 100g grain samples in under three minutes. In parallel with varietal identification, the system performs grain quality assessment through visual spectrum analysis, including screenings/retention, grain defects and foreign material detection.

The session will explore how these technologies can improve operational efficiency, reduce subjectivity and support faster decision-making for maltsters, grain handlers and breeding programs. It will also discuss the broader direction of digital grain assessment and emerging opportunities for rapid, in-field and laboratory-based quality testing.

This presentation provides a practical view of how automation and AI are beginning to reshape grain quality assessment in the grain industry.



SESSION 3: MALTING, BREWING AND DISTILLING 1

From Glass to Paddock: How Global Beer Trends Are Shaping Malting — and What They Mean for Australian Barley

Vincent Lauwerier¹

1. *Malteurop, Champagne-Ardenne, France*

As Gold Sponsor of the 2026 Australian Barley Technical Symposium, Malteurop is pleased to share a view from the heart of the malt supply chain. The address connects the demand side of our industry — the global beer market — with the manufacturing, sustainability and barley sourcing that sit behind every glass, framing what the next decade may ask of Australian growers and the wider barley sector.

We begin with an update on the global beer market. World beer volumes have entered a period of flat-to-slight decline in mature markets, yet value continues to grow on the back of premiumisation, with consumers paying materially more per litre than in 2019. Low- and no-alcohol beers are among the fastest-growing categories, and Asia-Pacific remains the key engine of volume growth. We unpack what these shifting consumption patterns mean for malt demand and for the quality of barley that brewers ultimately require.

We then turn to Malteurop's manufacturing footprint. As one of the world's leading maltsters, Malteurop operates 23 malthouses across 14 countries with a combined capacity of around 2.4 million tonnes of malt — a network anchored by hubs such as Vitry in France, Great Falls in North America and Geelong malthouse here in Australia. We explain how this global footprint is positioned to serve evolving brewer demand and where Australia fits within it.

Sustainability runs through everything we do. Malteurop is committed to a Science Based Targets initiative (SBTi) pathway, with a target to reduce industrial (Scope 1 and 2) greenhouse gas emissions by 42% - backed by concrete investments such as the new biomass plant at our Seville site and our scope 3 emissions by 29% by 2030 against a 2021 baseline. In Australia, we are determined to carry this momentum forward and to expand our sustainability program, working alongside growers on the on-farm practices, data and shared standards that will keep Australian malting barley both low-carbon and globally competitive.

Finally, we set out Malteurop's malting barley requirement: the volumes, varieties and quality specifications that underpin our supply, and how current and future needs translate into what we are looking for from the paddock. The aim is to give the barley industry a clear, demand-led signal — and to spark an open, whole-of-industry conversation about how Australia secures its position as a premium, sustainable malting barley supplier to the world



Sustainable Barley Production - A Brewers perspective on the Sustainability of Australian Barley

David Engel¹

1. Procurement, Asahi, Melbourne, Victoria, Australia

Industry Context

Consumers and customers are placing increasing pressure on producers to improve sustainability across their supply chains. In response, the global brewing industry is making significant commitments to reduce environmental impact while supporting the safety and prosperity of the communities in which it operates.

Asahi Beverages' Commitment

Asahi Beverages, Australia's largest brewer and part of Asahi Group Holdings in Japan, has committed to reducing its CO2 emissions by 30% by 2030 and to net zero by 2040. Achieving these goals will require close collaboration with upstream suppliers, particularly across the agricultural sector and, most importantly, barley production.

Asahi sources around 100,000 tonnes of malting barley for its Australian and Japanese brewing operations, making barley a critical focus area in its sustainability agenda.

Progress and Opportunity

Over the past two years, Asahi and its partners, Boolah and Riordans, have made strong progress in understanding the sustainability impact of barley production and identifying where further improvement is needed. This work has shown that Australian barley production is already well positioned in terms of sustainability performance.

This position has been strengthened by ongoing yield improvements. It has also been supported by the broad adoption of regenerative agriculture practices.

Together, these factors place Australian barley and malt in a strong position to lead in sustainable barley production today and to help address the next wave of challenges in further improving sustainable production.

Australian Whisky Industry Update

Sam Slaney¹

1. Starwood, Port Melbourne, Victoria, Australia

Australia's whisky industry is emerging as a globally recognised premium category, driven by innovation in barley, malting, and flavour development. This presentation will explore how distillers are increasingly focused on barley variety selection, malt quality, fermentability, spirit yield, and flavour contribution to create distinctive Australian whisky styles.

The session will examine growing demand for provenance-driven grain selection, speciality malts, and production systems that support sustainability and regenerative agriculture. It will also discuss how malt composition influences whisky character, complexity, and consistency, alongside the opportunities this creates for barley breeders, growers, and maltsters as the premium whisky sector continues to expand.



As Australian whisky builds international recognition, collaboration across the grain, malting, and distilling supply chain will be critical to delivering quality, sustainability, and global competitiveness.

Regen4real: A Sustainability program for the Malt Barley supply chain

Brooke Sauer¹

1. Boolah Pure Network, New South Wales, Australia

Regen4real is Boolah's sustainability program comprising the Framework, Trial Farms and Dashboard. It brings together data, people, and research trials to create measurable change for the supply chain. The program identifies clear, measurable indicators for tracking sustainability performance. It manages and reports sustainability-related risks and opportunities across four key pillars, ensuring transparency for growers, partners and end users alike. Regen4real turns complex data into clear insights — helping farmers and partners track performance, demonstrate progress, and meet ESG reporting needs. The commercial-scale regenerative trial farms test and validate new practices and technologies in real farming conditions. It is designed to make sustainability practical - translating research into tools that help growers, partners and end users understand and verify their impact.



SESSION 4: MALTING, BREWING AND DISTILLING 2

Barley grain germination

Christoph Dockter¹

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Barley grain dormancy and germination are central to both crop establishment and high-quality, sustainable malt production. Successful germination depends on precise timing, shaped by environmental conditions and genetic control, and is governed by the balance between key phytohormones—primarily abscisic acid (ABA), which enforces dormancy, and gibberellic acid (GA), which promotes germination.

Although the overall process of barley germination has been studied for decades, the molecular mechanisms that initiate and regulate it remain incompletely understood. Progress has been limited by several challenges: the technical difficulty of accurately measuring low-abundance, unstable phytohormones in complex grain tissues; the dynamic environmental signals influencing dormancy; and the high genetic diversity of barley, only recently captured through long-read sequencing and pangenome approaches.

This complexity has direct implications for breeding. Optimizing dormancy and ensuring uniform and efficient germination remain difficult targets, sometimes necessitating the use of exogenous GA₃ during malting to achieve consistent performance.

In this keynote, we give a general overview on barley grain germination and present new insights into the genetic architecture of germination control from a pangenome perspective, using the GA metabolic pathway as a case study. We highlight how recent advances are reshaping our understanding of dormancy regulation and discuss their implications for breeding strategies aimed at improving malt quality, reducing processing inputs, and enhancing resilience across diverse growing conditions.

When good enough isn't good enough: The case for raising Australia's malting barley quality

Marcus Williams¹

1. Procurement, Malteurop Australia & New Zealand, North Geelong, Victoria, Australia

Beer drinkers want more. Brewers are under pressure to innovate faster, produce more consistently, and do it all with less. That pressure travels up the supply chain — and it lands squarely on malt quality.

As one of the world's leading maltsters, Malteurop sits at the intersection of what brewers need and what farmers grow. And from where we stand, Australian malting barley is at a crossroads.

Australia produces outstanding barley. But a growing share of Australian malting varieties now require processing aids just to meet basic quality thresholds — a workaround that costs time, energy, and money, and that puts Australian malt at a disadvantage against Canadian and European competition.



This talk makes a simple argument: non-additive malting performance shouldn't be a premium trait. It should be the baseline. Getting there won't just benefit maltsters: it will mean better returns for farmers, more reliable quality for brewers, and a stronger position for Australian barley in global export markets.

We'll show you where the gap is, why it matters now more than ever, and what it will take to close it together.

Who is this talk for?

- Barley breeders and seed producers looking to understand where the market is heading and what traits will matter most
- Farmer cooperatives navigating variety choices in an increasingly quality-conscious export market
- Anyone in the Australian grain supply chain who wants to understand how malting and brewing demands are reshaping what "good barley" means

What you'll walk away with:

- A clear picture of the quality gap between Australian malting barley and key global competitors
- An understanding of why non-additive varieties are becoming a commercial necessity, not just a technical preference
- Malteurop's perspective on what the whole supply chain — breeders, farmers, maltsters, brewers — needs to do to close that gap
- A seat at the table for a conversation that will shape the future direction of Australian malting barley

Identification of the molecular drivers of malting performance in *Hordeum vulgare*

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2. The University of Western Australia, WA Proteomics, Perth, Western Australia, Australia

3. The University of Western Australia, Plant Energy Biology, Perth, Western Australia, Australia

Around the world *Hordeum vulgare* (barley) is the most used plant in the malting process for beer brewing, but barley is also bred as a crop that is used for animal feed. Malting is the biological process of efficiently breaking down starches, cell wall components, and storage proteins during grain germination. Malt cultivars are bred to find a balance between producing crop yield and grain malt quality. On the other hand, feed cultivars are not bred to be adept at this malting process but instead focus only on traits for maximising yield in a farmer's field. Although certain enzyme classes are proteins known to play a role in the malting process, at a molecular level it is still ambiguous which specific proteins differentiate the malting process of a high-quality malt cultivar and a feed cultivar. These proteins presumably act directly or indirectly as molecular drivers to produce malt parameters that meet the malt accreditation process. The aim of my research looks to examine the differences in protein profiles between malt and feed cultivars to identify the proteins related to malt quality. The in-lab malting of three Australian malting cultivars and two feed cultivars was performed to acquire samples at multiple timepoints in malting. These samples were analysed with liquid-chromatography mass spectrometry across the five cultivars and over 5000 protein groups were identified.



Bioinformatic analyses shows which types of protein functions are enriched throughout the malting process of these cultivars, protein groups that contain specific protein isoforms and their gene location, and differentially abundant proteins at the different malting timepoints from malt and feed cultivars. It was found that over 250 protein groups were differentially abundant between malt and feed cultivars in at least three of the six timepoints collected. These protein groups were found to be related to grain development, protein transportation, and carbohydrate and storage protein breakdown. By identifying these protein groups and relating them to their respective chromosome position, I aim to further understand the biological process of germination in barley, provide genetic markers to identify malt cultivars, and assist the development of new barley cultivars to achieve malt accreditation.

Increasing Efficiency of Malting by Creating A Digital Twin of Malting Infrastructure Through Machine Learning And High Throughput Molecular Analysis

Owen Duncan¹, Bryan Hau^{2,2,3,4}, Harvey Millar²

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3. The University of Western Australia, WA Proteomics, Perth, Western Australia, Australia
4. The University of Western Australia, Plant Energy Biology, Perth, Western Australia, Australia

This project has built an AI driven digital twin of a major malting facility in Perth, Western Australia. This model is enabled by analytical technology developed by the WAProteomics facility which can measure the biological variation between batches of Barley grain. It was trained on historical cycles of the plant by analysing the input grain from each malting cycle at the UWA lab, adding in data from the plant on how the grain was malted and training the model to predict the outcome of the malting process including certificate of analysis parameters such as diastatic power, free amino nitrogen etc. This is an in silico model of the physical infrastructure at Forrestfield and can be run thousands of times with different malting recipes (times, temperatures, moisture %) to select the optimal recipe for the specific grain batch prior to any physical malting occurring. We believe this capability can offer significant productivity improvements to malting at the plant by optimising the trade off between the use of costly inputs (natural gas, water, power) and the quality of the malt. It can also be used to differentiate between high performing and low or slow performing grain which can reduce the time and money invested in producing malt which fails to meet performance criteria. In essence, the model learns what biological configurations of grain perform well and which perform poorly when paired with the physical plant. For example, by learning the specific metabolic configurations of barley grain which support high endosperm conversion at low moisture percentages, the project can both help select the best available grain to malt and provide data on the minimum moisture percentage required to meet target malt specs, optimising both water usage in rehydration and energy inputs in the kiln drying the grain out again.



SESSION 5: UNLOCKING CROP PERFORMANCE

From Research Gaps to Growth Opportunities: Shaping the Future of Canadian Barley Agronomy through the GROW Barley

Hiroshi Kubota¹

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Barley, which previously ranked second in seeded acreage in Canada, has experienced a 20 to 25% reduction in seeded area between 2000 and 2025 due to increased cultivation of canola and corn. Changing climate conditions in western Canada may improve the adaptability and production potential of corn and soybean in the near future. This trend could further shift acreage from barley to corn or soybean, particularly if barley production continues to generate low net revenue. Recent drought conditions have also reduced producer confidence in barley, as it is perceived as a shallow-rooted and drought-sensitive crop. Commodity prices and weather conditions remain volatile and beyond the control of barley producers. Therefore, increasing barley grain yield while maintaining or reducing production costs is essential to improve net revenue.

Developing a decision-support tool for plant growth regulator applications can reduce unnecessary PGR use and provide economic benefits to producers. Improving the efficiency of adopting newly registered barley varieties is essential for benefiting from their high yield potential. While the adoption of new malting barley varieties depends on factors such as target markets, grain buyers, and end-user requirements, comprehensive agronomy packages can accelerate their adoption. Another important strategy for supporting farmer decision-making under changing climate conditions is to identify the optimal sequence of crop types sown during the limited seeding season. Typically, cereals are seeded first, followed by canola. Pulse crops may be seeded before cereals, between cereals and canola, or after canola, depending on operational considerations, farm location, crop purpose, and other factors. Ultimately, crop seeding order is primarily determined by the likelihood of successful production of high-value crops such as canola and by operational requirements. Although previous studies support early seeding for higher yields in wheat, canola, barley, and some pulses, producers must assess which crop types and seeding orders provide stable revenue across the whole farm. Given rising, unpredictable nitrogen fertilizer prices, incorporating biological nitrification-inhibition traits into Canadian barley germplasm could enhance barley's competitiveness and nitrogen use efficiency, thereby reducing fertilizer input costs.

To keep barley a competitive and profitable crop choice in western Canada, future advancements in barley agronomy should prioritize reducing production costs while increasing net returns. The GROW Barley framework is anticipated to deliver innovative agronomic tools that will improve barley productivity and economic outcomes for producers.



Optimising Canopy Photosynthesis in Barley: Identifying Optimal Allelic Variants within the BEST-CROP Project

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There is an urgent need for transformative technologies capable of increasing crop productivity—both in terms of grain yield and biomass—while enabling their conversion into economically valuable materials. The development of next-generation cereal varieties with enhanced photosynthetic efficiency and improved capacity to assimilate greenhouse gases, such as carbon dioxide and ozone, together with tailored straw characteristics for industrial applications, offers a promising pathway toward a sustainable circular bioeconomy. Within this framework, we outline a strategic vision to improve barley photosynthetic performance through: (i) fine-tuning leaf chlorophyll content and optimizing canopy architecture; (ii) accelerating photosynthetic responses to dynamic light environments; and (iii) implementing metabolic bypasses to mitigate photorespiration. Targeted enhancement of these traits is expected to substantially increase above ground biomass without affecting the harvest index. At the same time, this approach will deliver key sustainability benefits, including improved water and nitrogen use efficiency, and will enable the valorization of straw as a feedstock for high-value bioproducts.

Advancing Barley Yields: Insights From Hyper-Yielding Trials in Tasmanian Spring Sowing Conditions

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The northern Tasmanian cropping zone resembles an environment more similar to NZ, the UK, and Europe than mainland Australia for spring-sown barley production. Increasing spring-sown barley yields has great potential to enhance the productivity of mixed farming rotations in Tasmania, where winter forage crops for livestock offer diverse cropping options prior to sowing spring combinable crops.

Yields achieved in this study underscore the value of photothermal quotient (PTQ) in estimating yield potential in higher production regions where soil water is less limited. With a condensed five month growing season, the critical period for spring sown barley growth occurs later than the traditional window for autumn sown crops and negates the effect of the often light-limited conditions experienced by the longer season autumn



sown crops in high rainfall zones. This allows the crop to exploit increased solar radiation later in the year while capitalising on relatively cooler Tasmanian summer temperatures. New benchmarks have been achieved with spring-sown European and Australian cultivars better suited to Tasmanian conditions under different management regimes across six seasons in both the GRDC Hyper Yielding Crops project (2020/21-2023/24) and FAR Australia's Germplasm Evaluation Network (2023/24- 2025/26). Yields consistently exceeded 10 t/ha across the six seasons, with yields up to 14.66 t/ha achieved in the 2025/26 season. Management regimes have illustrated that crops have lower input requirements than their autumn sown counterparts, making it cheaper to grow with lower emissions. The studies have also revealed that a shorter growing season requires well adapted germplasm (photoperiod sensitivity) with input rates and timings needing adjustment to maximise productivity.

Setting profitable yield frontiers for barley: yield upside, risk and quality trade-offs

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New Australian barley genetics can match or exceed wheat yield, challenging historic water-use efficiency benchmarks. Realising this potential, however, depends on early agronomic decisions made under high input costs and seasonal uncertainty. Using multi-year, multi-site yield frontier experiments, we assessed how early decision-making positions barley to capture seasonal yield upside across diverse environments.

Barley achieved new yield potentials when sown early and aligned with strong radiation interception, adequate soil moisture and appropriate nitrogen status before flowering—the critical period for grain number determination. Across site-years, early-established barley consistently out-yielded wheat, but carried greater downside risk where nitrogen supply or canopy demand exceeded water availability, particularly on ameliorated soils or from delayed emergence, leading to reduced grain size, high protein and malting suitability.

These results highlight opportunities to benchmark barley production and better differentiate feed and malt barley management by sowing date and soil opportunity, enabling high yields with lower nitrogen inputs, reduced emissions intensity and improved whole-farm profitability.



Mitigating Climate Risk in Barley in the Canadian Prairies through Ultra-Early Seeding

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Climate change is increasing the frequency of extreme heat and drought stress during the critical growth stages of barley in the Canadian Prairies. In response to these threats, Agriculture and Agri-Food Canada initiated a four-year study (2024–2028) to evaluate ultra-early seeding (UES) as a mitigation strategy. Initially developed in wheat, the UES protocol identifies the optimal planting window by monitoring the soil temperature at a 5 cm depth. In the case of wheat, an 1–2°C optimum has been established for grain yield protection or improved grain yield stability. This represents a significant shift from the traditional practice of waiting for temperatures to reach 8–10°C or by an arbitrary calendar date. However, it is unknown if barley would exhibit comparable response to this practice. The study's primary objective is to assess how UES impacts the grain yield, yield stability, and quality of barley across western Canada.

A genotype x environment x management framework was designed where barley cultivars representing malt or general commercial purposes, in either spring or winter growth habit, were grown across five Prairie environments in 2024–25. The cultivars were managed with either dormant seeding (DS), UES (0–6°C soil temperature), and conventional seeding (8–10°C), planted at moderate sowing densities (350 m⁻²) or at moderate and high sowing densities (300 vs. 450 seeds m⁻²). Agronomic variables including yield components, and quality parameters such as grain protein concentration were assessed while in-crop and post-harvest disease assessments included leaf disease load and fusarium head blight (FHB) occurrence.

Preliminary results indicate that UES allows barley to better utilize early-season soil moisture and growing degree days, helping the crop avoid heat stress during critical developmental phases. The primary benefit observed was improved grain yield stability, rather than a significant increase in total yield. While UES at 0–5°C proved effective for maintaining quality and advancing maturity, the DS trials faced significant establishment risks without offering additional advantages.

Regarding crop health during 2024–25, leaf spot disease levels remained low at most sites, and natural FHB infection was overall minimal. However, a trend was observed where higher deoxynivalenol (DON) content was associated with warmer seeding temperatures.



SESSION 6: NEXT GENERATION BREEDING TOOLS 1

The Australian Grains Genebank – Next-gen genebank management for a food secure future

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The Australian Grains Genebank (AGG) is one of the world's largest and most diverse genebanks, with over 200,000 accessions of cultivated varieties, landraces, and wild relatives. These genetic resources are essential to global food security and sustainable agriculture, especially amid growing challenges like climate change and emerging threats to crop production. From tropical and temperate cereals to legumes and oilseeds, the sheer scale and complexity of the AGG make efficient genebank management, and strategic use by the grains industry, a formidable task when relying solely on traditional passport data. Finding the right germplasm can often feel like searching for a needle in a haystack.

As pressure on global agricultural systems intensifies, innovative approaches to genebank management have never been more urgent. The AGG Strategic Partnership, a joint investment between Agriculture Victoria and the Grains Research and Development Corporation, is leading the transformation of plant genetic resource management. This future focused initiative is unlocking the full potential of the AGG's barley collection for Australian grain growers by integrating cutting-edge genomic technologies, dynamic curation protocols, and publicly accessible online bioinformatics tools with traditional genebanking practices.

Through dynamic curation, which merges genomic data with passport and characterisation information, the AGG is optimising the conservation, maintenance, and strategic use of its germplasm. The publicly accessible bioinformatics platforms are empowering barley breeders and researchers to make faster, more precise, and more informed decisions about the germplasm best suited to their goals.

Here we report how the AGG's implementation of genomic-informed curation is setting a new standard for accessibility and utilisation of barley resources, and for genebank management. These transformative tools are enabling the barley sector to fully harness biodiversity, accelerate trait discovery, and fast-track the development of climate-resilient, high-performing varieties. In doing so, they offer a powerful path forward to ensure sustainable productivity, economic viability for farmers, and food security in a rapidly changing world.



From Genebanks to Breeding: Unlocking Barley's Genetic Diversity with Data, AI and Digital Tools

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Global genebanks conserve the genetic diversity needed to sustain crop improvement in the face of growing food demand, climate variability and emerging biotic and abiotic threats. As pressures on agricultural systems intensify, the effective use of this diversity is increasingly critical for delivering resilient and productive varieties to growers. Achieving this depends on connecting plant genetic resources to research and breeding knowledge to support practical decision-making.

This presentation will describe how the Australian Grains Genebank (AGG) Strategic Partnership has transformed the AGG into a bio-digital resource that supports germplasm discovery, prioritisation and use. The Partnership has genetically characterised >27,000 barley accessions and established an integrated digital tool ecosystem that addresses the FAIR data challenge for industry. This ecosystem connects genotyped genebank accessions to research and breeding knowledge, enabling integration of AGG resources with pre-breeding and breeding datasets for immediate impact.

Examples will be presented demonstrating how the genotyped barley AGG collection has been integrated with the barley pan-genome and connected across international genebanks using novel imputation methods. Genotypic information is linked to published research, trait associations and comparative analyses, enabling evidence-based germplasm selection. Digital tools such as *Pretzel*, *Genolink* and *Fairybread* allow breeders and researchers to explore haplotypes and structural diversity at the accession level, without specialist bioinformatics expertise. AI-enabled, graph-based approaches further enhance the discoverability and reuse of complex data through natural language queries. These outcomes have positioned the AGG as a critical bio-digital resource for Australia and an active contributor to global efforts to unlock the value of plant genetic resources. By integrating genomic characterisation, interoperable data infrastructure and decision-ready digital tools, the Partnership has established foundations that support climate-resilient crop improvement, informed germplasm exchange and strategic use of genetic diversity at national and international scales.



FastStack to accelerate multi-disease resistance breeding in Australian barley: where are we now?

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12. SECOBRA Recherches, Adelaide, South Australia, Australia

In breeding, combining new genetics from exotic germplasm is challenging that could take many years. Over the past years, we developed FastStack, an AI-guided strategy that selects parents based on optimum haplotype selection to help accelerate crop genetic improvement. As the first implementation of AI-guided strategy in barley in Australia, and through the broader GRDC Net Blotch Consortium, here we present progress from our AI-derived barley populations with stacks of new resistance haplotypes associated with net blotch disease.

FastStack populations were developed from diverse barley accessions sourced from the Australian Grains Genebank following a crossing scheme [(AGG × AGG) × (AGG × AGG)]. Population development was conducted under speed breeding conditions at The University of Queensland in 2020; and the resulting lines genotyped using the 40K Infinium SNP chip were subsequently evaluated in 12 multi-disease nurseries in 2024–2025 coordinated through national partners from QDPI, SARDI and AgVIC.

Across 2 years of disease screening, population exhibited strong resistance to net form of net blotch (NFNB) and spot form of net blotch (SFNB). Cross-year validation demonstrated genomic predictive ability, with correlations between 2024 genomic estimated breeding values and 2025 disease performance of $r = 0.62$ for NFNB and $r = 0.40$ for SFNB. Based on these results, the top 100 lines were further selected to advance to 2026 national field screening. To assess potential trade-offs associated with the introgression of exotic resistance, subsequent selections will be evaluated for agronomic performance through breeder yield nurseries with industry partners in 2027. The FastStack populations represent an important source of novel resistance derived from diverse germplasm that can be deployed within Australian barley breeding programs.

Overall, these results demonstrate the potential of AI-guided haplotype optimisation, combined with coordinated national disease screening, to accelerate crop genetic improvement efforts.



A digital micro-phenotyping pipeline for dissecting net blotch resistance in barley

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Macro-scale resistance screening provides essential rankings for breeding decisions but offers limited insight into the cellular dynamics that underpin those rankings. To address this gap, we have developed a complementary fluorescence microscopy pipeline within a broader digital phenotyping framework to characterise *Pyrenophora teres* colonisation on barley leaves from 24–144 hours post inoculation (hpi).

Using a detached leaf assay, leaf segments from a differential set of barley genotypes are inoculated with net form and spot form net blotch (NFNB & SFNB) isolates. Samples are collected across a time series, stained with a fungal cell wall-specific fluorescent dye and are imaged using an automated slide scanner, capable of processing up to 200 leaf segments per run. Image analysis is performed using a semi-automated QuPath workflow, extracting colony metrics including colony number, area, and morphology without specialist image analysis infrastructure.

Integration of these early micro-phenotypes with macro-scale resistance rankings at both seedling and adult stages reveals a strong alignment for many genotypes, but also discordant cases that may reflect differences in host growth stage or infection progression. We will present data identifying the timepoints and metrics that best discriminate genotype responses and evaluate whether early infection phenotypes can predict, or help explain, disease outcomes observed at later stages.

Ongoing seedling microscopy experiments will expand this dataset ahead of planned genome-wide association studies (GWAS), with the aim of linking micro-phenotypic variation to resistance loci. The pipeline is also being extended to other barley pathosystems such as scald, where differences in pathogen biology present new analytical challenges. This work is designed to integrate with existing screening programs and represents an accessible and transferable approach to high-resolution phenotyping.

Digital phenotyping of barley foliar disease resistance: Quantitative trait capture across germplasm and mapping populations

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Net blotch and scald are among the most economically damaging foliar diseases of barley in Australia, yet phenotyping for disease resistance continues to rely predominantly on



visual scoring, an approach that is labour-intensive, subject to operator biases, and better suited to detecting major gene resistance than to quantifying the continuous variation underpinning quantitative resistance. To address this constraint, a machine learning-based digital phenotyping pipeline was developed for the Compolytics® Macrobot NextGen high-throughput automated imaging platform at La Trobe University AgriBio, as part of the GRDC-funded Net Blotch Consortium. An artificial neural network (ANN) classifier achieved 94.1% pixel classification accuracy across background, necrotic, chlorotic, and healthy tissue classes, quantifying 17 traits per sample including symptom-based measures (% necrosis, % chlorosis, % infection, % green), mean RGB band intensities, and 10 vegetation indices. Assessment of 50 barley differential genotypes against both forms of net blotch (spot form caused by *Pyrenophora teres* f. *maculata* and net form caused by *P. teres* f. *teres*) using detached leaf assay at seedling (GS13) and adult plant (GS55) stages showed substantial phenotypic variation and robust trait heritabilities across RGB-based and symptom measures. For barley scald (caused by *Rhynchosporium commune*), the Yerong × Franklin doubled haploid (DH) mapping population (146 lines) evaluated against two industry-relevant isolates exhibited continuous, transgressive variation in disease response, validating pipeline resolution for QTL mapping. This digital phenotyping approach provides a scalable, objective platform for capturing quantitative resistance variation in diverse germplasm and structured mapping populations, with direct utility for GWAS, QTL mapping, and genomic selection to accelerate breeding for durable barley foliar disease resistance.

Whole genebank comparison between two of the largest international barley genebank collections

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The world's genebanks conserve genetic diversity that is essential for crop improvement, providing breeders with access to traits required to develop resilient, productive and climate-adapted varieties. However, the scale and complexity of large plant genetic resource collections can make it difficult to efficiently identify and access the most useful germplasm. To address this, genebanks are increasingly generating genomic resources to improve collection accessibility. The Australian Grains Genebank (AGG) Strategic Partnership – a joint investment between Agriculture Victoria and the Grains Research and Development Corporation – aims to unlock the genetic potential of crop genetic resources held at the AGG and make them more accessible to the research and breeding community.

The AGG has genotyped its entire domesticated barley collection (>25,000 accessions) using SNP array technology to characterise genetic diversity within the collection. Here, we compare the AGG collection with the IPK barley collection (>20,000 accessions), which was genotyped using genotyping-by-sequencing. By identifying markers common to both datasets and applying novel imputation methods, we enabled comparison of the two collections using a shared set of 3,608 SNP. Despite representing distinct collections with different histories, growth strategies, and servicing contrasting climatic regions, we demonstrate significant overlap that would not have been evident from passport data



alone. Using a novel cluster-based view of the collections, researchers and breeders can now view accessions in the context of all accessions available across both collections. These analyses, made possible by collection-scale genotyping, highlight the power of genomic data to reveal the diversity and composition of germplasm collections, enabling more efficient use, improved access to novel traits, reduced screening of redundant material, and accelerated delivery of improved varieties to growers.



SESSION 7: DEVELOPMENT BIOLOGY

Unravelling the genetic control of barley shoot architecture traits

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Shoot architecture is a key determinant of plant adaptation and crop performance. The deployment of semidwarf varieties during the Green Revolution demonstrated the impact of architectural traits on cereal productivity by improving lodging resistance and harvest index, ultimately driving substantial yield gains. Despite these advances, lodging remains a major constraint in barley production, particularly as climate change increases the frequency and severity of extreme weather events.

Beyond plant height, culm traits such as stem diameter and wall thickness offer additional opportunities to enhance lodging resistance. Likewise, canopy architecture traits, including more erect leaf angles, can improve light penetration through the canopy, increase photosynthetic efficiency, and reduce competition among neighbouring plants, thereby supporting higher planting densities and greater yield potential.

To accelerate the development of productive and climate-resilient barley ideotypes, my research team combines genetic, genomic and phenotypic analyses of mutant resources and diverse germplasm collections to identify genes and favourable alleles controlling culm strength and canopy architecture. Through selected case studies, I will illustrate how the dissection of these traits is generating new knowledge and tools to support the development of next-generation barley varieties adapted to future production environments.

Facing Forwards: Developmental genetics of the epidermis in barley

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How plants grow and reproduce profoundly impacts crop productivity and value. Our research combines genetics with advanced technologies to understand developmental processes important for distinctive features of barley linked to growth, resiliency, yield and quality. My talk will describe our work on the epidermis, the outer tissue surface, and its cuticle, a lipid-rich protective outer barrier. Barley develops two cuticular specialisations: 1) a heavy white-blue "wax bloom" on leaves, stems and spikes, a feature shared with wheat and often associated with improved drought and heat tolerance, and; 2) an adherent barley grain surface which sticks to the floral hulls, leading to covered



(versus naked) grain, a quality trait important for end uses in brewing and distilling. Through studying mutants with defective wax blooms and/or skinning grain which partially sheds the hull, we have identified and characterised conserved cuticular enzymes and regulatory transcription factors which promote both wax bloom deposition as well as covered grain, but also a higher-order signalling pathway controlling of epidermal patterning. In our latest experiments, we applied a combination of genetic, microscopic and single cell approaches which suggests wax bloom deposition is spatially coordinated with specific epidermal cells, revealing a novel mechanistic link between regulation of epidermal cell type and deposition of cuticular wax. We are also expanding our epidermal gene network through reverse and forward genetic approaches, examining the conservation of these coordinating controls in wheat, and assessing the physiological contributions of these epidermal features. Our research provides fundamental insights on the genetic, molecular, and developmental basis of epidermal feature coordination, contributing to future engineering of cereal surfaces for optimal performance.

How a unique grain retention mechanism evolved in cereals

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Grain retention enabled ancient farmers to domesticate cereals that now feed billions of people. This trait allows for the use of harvesting machinery which reduces time, labour, and costs of harvest. Modern agriculture relies on this trait, such that a grain-dispersing crop is unsuitable for commercial use. Moreover, barley and wheat display a unique mechanism of grain retention, which is genetically unrelated to those of other plant species, and is currently poorly understood.

Wild diversity is becoming increasingly utilised in breeding programs to increase crop performance and adaptability. A major risk of introgressing wild traits is the loss of elite traits such as grain retention. This risk is compounded by the current lack of understanding of grain retention in barley. Further, growing interest in de-novo domestication to create new crops is hindered by the lack of grain retention. This trait needs to be understood to be effectively maintained and utilised for crop improvement. We have generated CRISPR-mediated genetic knockout lines which lack the ancestral genes underlying grain retention in barley. Early results indicate a potential function in male fertility. Analysis of these lines aims to further inform our understanding of how this unique trait evolved and, in practice, may aid crop improvement by informing strategies to manipulate grain retention.



The effect of barley head morphologies on wind-induced stalk failure

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Barley head loss is a major form of straw strength failure in the peduncle, or neck, directly adjoining the head (spike). Growing regions with high wind speeds are considered more susceptible to peduncle breakage, although head size and grain weight may also contribute. Despite its importance, limited research has systematically examined the influence of these parameters on head loss. This study focuses on the combined effect of aerodynamic, geometric, and mass properties of barley heads on stalk failure. Various morphological differences were considered, including two-row and six-row cultivars, awned and non-awned heads, kernel angle, awn angle, and scaling ratio. Wind-tunnel experiments were performed under controlled turbulence to measure mean and peak aerodynamic loads. Results indicate that drag forces scale primarily with wind velocity, while turbulence intensity modulates the relative amplification of loading. Among morphological traits, two-row heads are more sensitive to turbulent gusts, whereas six-row spikes exhibit higher absolute wind loads. Awned heads show reduced sensitivity to turbulence compared to non-awned heads, but increased total drag force. In recent work, experimentally derived aerodynamic and mass characteristics were incorporated into a geometrically exact stalk model to assess morphology-driven variation in failure wind conditions. These findings provide a mechanistic framework for guiding breeding and field management strategies to reduce head loss and for interpreting landscape-scale head loss patterns under variable wind conditions.

Barley head loss: a farmer's problem and a breeder's challenge

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Barley head loss is an important but under-recognised problem in Australian grain production, especially under hot, dry and windy conditions near harvest. It occurs when the peduncle, the uppermost stem internode below the spike, breaks and causes the ear to detach before or during harvest. This leads to yield loss and creates a major challenge for both farmers and breeders. Despite its practical importance, head loss has received limited research attention, mainly because reliable phenotyping tools and clear selection strategies have not been available. This study aimed to develop a practical framework for selecting barley genotypes with improved head retention. Field experiments were conducted across multiple environments to capture variation in head loss and related traits. A major outcome of this work was the development of a modified Instron-based mechanical phenotyping platform, designed specifically to test peduncle strength and flexibility under a biologically meaningful loading system. Unlike conventional approaches, this method allowed more realistic assessment of structural failure relevant



to barley head loss. The platform generated repeatable measurements that helped distinguish strong, flexible and susceptible genotypes. Using these mechanical data together with field phenotypes and agronomic traits, a selection model was developed to identify genotypes with lower head loss risk. This model provides a practical way to combine field performance with biomechanical evidence for breeder-oriented decision making. Overall, this work offers a new phenotyping and selection strategy for barley head loss and provides a strong foundation for breeding more resilient cultivars under increasingly variable harvest conditions.

Towards the Grain Filling Pathway in Barley

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In the final stage of barley (*Hordeum vulgare* L.) reproduction, the pistil is pollinated at anthesis, therefrom initiates post-fertilization development to form a grain. Particularly, the germline enclosed in ovule is fertilized and develops into endosperm and embryo, whereas the surrounding somatic tissues become seed coat and pericarp providing essential nutrients and protection. Hence, barley grain is a fruit comprising both maternal and filial tissues.

The maternal tissues exert multi-dimensional control on filial growth, such as establishing transferring path of materials, determining the capacity of endosperm and regulating grain filling, all of which contribute directly to yield and grain quality. Water and essential elements for grain development (e.g., amino acids, sugars) come predominantly from the mother, transported through vascular tissues to the grain. During grain filling, these nutritive components are unloaded from the vascular bundles into a maternal grain tissue called the nucellar projection. These supplies are subsequently released into the adjacent cavity, from which they are absorbed by filial transfer cells, and assimilated by the endosperm. While the tissues involved in grain-filling are known, very little is understood about its regulation.

The use of spatial transcriptome provides a promising approach to discover new genes and even new cell types within a tissue context. By combining this with gene editing technologies, we have established a reverse genetics research pipeline in barley to probe gene function via creating loss-of-function mutants. These insights pave the way for novel gene discovery and future crop improvement strategies.



Identification of a novel plant height QTL on chromosome 6H and its agronomic effects in field-grown spring barley

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Barley (*Hordeum vulgare* L.) is well adapted to Australia's climate but can be prone to mechanical constraints such as lodging, head loss and straw strength issues, which negatively impact yield and crop profitability. Since the Green Revolution, many semi-dwarf genes such as *semidwarf 1* and *ari-e.GP* have been discovered and used in Australian barley breeding, but they can be associated with negative pleiotropic effects. A breeding line showing an ideal phenotype with intermediate height and erect plant architecture was used as a donor parent to develop two biparental mapping populations. From phenotyping the RILs (recombinant inbred lines) across 6 environments, a novel quantitative trait locus (QTL) on chromosome 6H was identified that is stable across multiple environments. This QTL is associated with reduced height, resistance to lodging and tolerance to head loss compared to wild-type, and it does not negatively impact yield nor have any maturity effects. *QTL6H.1* has similar height to *sdw1.d* and an additive effect in reducing height, internode length and spike count. Genes underlying the *QTL6H.1* are being investigated using a candidate approach. This height QTL will be a valuable addition to the breeders' semi-dwarf gene toolkit.



SESSION 8: BIOTIC STRESS TOLERANCE – NET BLOTCH FOCUS

Pathogenic variation of *Pyrenophora teres* f. *teres* in Australia between 2020 - 2024

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Net form net blotch (NFNB), caused by *Pyrenophora teres* f. *teres* (*Ptt*), can cause severe yield losses ranging from 10% to 40% in susceptible barley cultivars under favourable conditions. Deployment of resistant varieties is an economical and environmentally friendly method to control NFNB. Pathogenic variation and virulence groups of *Ptt* can identify the most effective resistance sources in barley that can be utilized in breeding programs to control NFNB. Furthermore, detailed information of *Ptt* pathotyping can provide valuable information to develop host resistance against local pathotypes. In this study, 326 isolates of *Ptt* were collected from six states across Australia between 2020 and 2024. Virulence of these isolates was examined at seedling stage using 30 barley genotypes. Hierarchical cluster analysis was used to evaluate *Ptt* isolates and barley genotypes. *Ptt* isolates were clustered into three distinct groups with three main isolates (NB350, NB73 and NB85) in Queensland representing each group. NB85 was the dominant pathotype in 2020 and 2021. NB73 became the dominant pathotype from 2022 to 2024 across Australia. It is likely that the dominant pathotype change of *Ptt* population resulted from increased cultivation of European barley germplasm in Australia. This study provided essential information for barley breeding programs to develop resistance against NFNB based on the *Ptt* pathogen virulence in different parts of Australia.

High-resolution mapping and pyramiding of resistance QTLs to achieve durable net form net blotch resistance in barley

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Barley net form net blotch (NFNB), caused by *Pyrenophora teres* f. *teres* (*Ptt*), is one of the most destructive barley diseases that reduces both yield and quality of barley grain. Deploying host resistance is the most cost-effective and environmentally friendly approach to protect barley yield. Importantly, combining multiple resistance QTLs can provide strong, durable resistance for effective disease control. Using large mapping populations, we constructed high-resolution maps of two major QTLs conferring NFNB resistance on chromosomes 6H and 3H, significantly narrowing their genomic windows. A major QTL on 6H of barley landrace Eth175, explaining 74.3% of the phenotypic variation, was mapped to a 0.02-cM interval spanning 194 kb. A major QTL on chromosome 3H in the landrace Eth069, accounting for 26.5% of the phenotypic variation, was mapped to a 0.46-cM interval corresponding to 458 kb. To translate these findings into breeding, closely linked PCR-based markers were developed and validated. We have also combined these two major QTLs via conventional crossing and generated homozygous lines that carry both loci. Further efforts focused on pyramiding a third



minor resistance QTL on chromosome 1H from barley landrace Eth210 are in progress. These efforts should produce barley lines with strong resistance to NFNB, suitable for use in various breeding programs.

Haplotype-based insights into the genetic architecture of net blotch resistance in barley

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Net blotch, caused by *Pyrenophora teres*, is a major constraint to barley production worldwide and occurs as two epidemiologically distinct forms: net form net blotch (NFNB) and spot form net blotch (SFNB). Although numerous resistance loci have been reported, their genetic relationships remain poorly understood, and the effective deployment of resistance is constrained by the complex genetic architecture of net blotch resistance. In this study, a diverse panel of 950 barley accessions from the Australian Grains Genebank (AGG) was evaluated for resistance to NFNB and SFNB across 13 experiments conducted in Queensland and Victoria during 2023–2024. Adult plant resistance was assessed in 11 field experiments, while seedling resistance to SFNB was evaluated in two glasshouse experiments. Substantial phenotypic variation was observed for both diseases, with broad-sense heritability ranging from 0.60 to 0.94 for NFNB and from 0.52 to 0.85 for SFNB, indicating high reliability of phenotypic data. Correlation analyses indicated a partial overlap in resistance mechanisms, with approximately 60% of the 4,497 haploblocks showing positive local genetic correlations between NFNB and SFNB. Using a haplotype-based mapping approach, we identified 40 quantitative trait loci (QTL), including 26 associated with NFNB, 29 with SFNB, and 15 common for both diseases. Most loci co-localized with previously reported QTL, while four putative novel blocks highlighted untapped genetic diversity within the AGG collection. Through *in-silico* haplotype stacking simulations, we demonstrated the cumulative genetic potential achievable by combining favourable haplotypes. Dual-disease stacking strategies outperformed single-disease approaches, highlighting the value of prioritising haplotypes with positive pleiotropic effects. Overall, this study provides a comprehensive haplotype-level framework for understanding net blotch resistance and delivers practical insights for breeding barley cultivars with durable and broad-spectrum resistance to both NFNB and SFNB.



Isoform-level resolution of barley and *Pyrenophora teres f. teres* transcriptomic landscapes during net blotch

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Net Form Net Blotch (NFNB), caused by the necrotrophic fungal pathogen *Pyrenophora teres f. teres* (Ptt), is one of the most damaging diseases of barley worldwide. In Western Australia, recent outbreaks have caused significant yield and grain quality losses, driven by the limited availability of resistant barley cultivars and emergence of highly virulent, and in some cases fungicide-resistant, Ptt isolates. A deeper understanding of the molecular mechanisms underlying host-pathogen interactions is therefore essential for developing barley germplasm with durable resistance.

In this work, we combined long- and short-read RNA sequencing technologies to investigate host and pathogen transcriptomes during NFNB. Long-read Oxford Nanopore sequencing enabled improved resolution of full-length transcripts, allowing for the refinement of existing annotations and discovery of novel genes and isoforms associated with disease responses in both barley and Ptt. Building on these refined resources, we performed an isoform-level study of the NFNB pathosystem, revealing extensive gene expression and alternative splicing changes during infection. Several Ptt isolates with varying virulence towards the globally significant RGT Planet barley cultivar were used in the study, facilitating the identification of isolate-specific changes in host gene and transcript expression. These findings provide new insights into the molecular dynamics of NFNB infection and demonstrate the value of integrating long-read sequencing and isoform-level analyses to better understand plant-pathogen interactions in complex crop systems.

Genome-wide association mapping reveals isolate-specific resistance to Australian pathotypes of *Pyrenophora teres f. teres* in barley

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Net form net blotch (NFNB), caused by *Pyrenophora teres f. teres*, is one of the most economically damaging foliar diseases of barley (*Hordeum vulgare*) in Australia. The emergence and persistence of virulent pathogen strains continue to challenge the durability of deployed resistance in commercial cultivars. In this study, genome-wide association mapping was conducted to identify genomic regions associated with NFNB resistance to the three predominant Australian pathotypes, NB73, NB85, and NB350. A diversity panel of 313 barley genotypes collected from European, Japanese, and Australian genebanks was genotyped using 7,989 high-quality SNP markers and phenotyped at the seedling stage under controlled-environment conditions. Population



structure analysis identified four genetic subpopulations, and genome-wide linkage disequilibrium decayed below $r^2 = 0.1$ at approximately 3.0 Mb. For isolate NB73, significant marker-trait associations were detected on chromosomes 1H (LOD = 5.61), 2H (LOD = 7.61), 5H (LOD = 7.34), 6H (LOD = 6.05), and Resistance to NB85 was associated with a SNP on chromosome 1H (LOD = 5.71), and resistance to NB350 with a SNP on chromosome 3H (LOD = 5.42). Co-localisation analysis with previously reported NFNB resistance loci showed that the NB73-associated 5H interval overlapped the APR-QSAT17-8 region. The significant associations were pathotype-specific, with no common QTL detected across NB73, NB85 and NB350. These findings emphasize the pathotype-conditioned nature of NFNB resistance and highlight the need to incorporate diverse pathotypes when identifying and deploying resistance in barley breeding programs.

Host resistance eliminate fungicide reliance for managing net form net blotch in barley

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Net form net blotch (NFNB) is a major disease of barley in Australia and is commonly managed through integrated disease management (IDM) strategies, with a stronger reliance on chemical control. However, emergence of fungicide-resistance strains of *Pyrenophora teres teres*, the causal organism of NFNB, has highlighted the vulnerability of long-term NFNB management strategies that depend heavily on fungicides. As fungicide efficacy declined, host resistance becomes a key strategy for managing NFNB. However, there is limited information on the minimum resistance rating required to effectively manage NFNB and prevent yield loss when fungicide performance is compromised.

To investigate this, two sequential field experiments were conducted at Longerenong, Victoria during 2024 and 2025 using six barley varieties with differing NFNB resistance/susceptibility arranged in six replications. In both seasons, each variety was subjected to two treatments, a minimum control (treated with fungicides) and an untreated control (supplied with 1 Kg of infected stubble to promote infection). During 2025 two foliar fungicide applications at the growth stage (Z31 and Z39) were used whereas in 2024, seed treatment was combined with foliar applications at Z31 and Z39. Disease severity (percent leaf area affected) was measured at key growth stages and grain yield in each variety was measured following harvest.

Both seasons experienced below-average rainfall (decile 1–3), which limited overall disease development. Fungicide applications significantly ($P < 0.001$) reduced early NFNB severity in the highly susceptible variety RGT Planet by 72%, whereas resistant and moderately resistant varieties (Rosalind, Maximus CL, and Neo CL) maintained low disease levels (average disease severity 0–3.7%, $P > 0.05$). Despite the dry conditions, NFNB caused yield losses of up to 11–13% in susceptible varieties in 2024, but not in 2025.



These findings demonstrate that the use of at least a moderately susceptible (MS) or better-rated variety is critical for managing NFNB, particularly where fungicide efficacy is compromised.



SESSION 9: DESIGNING ADAPTIVE CROPS

Adapting barley to the extreme environment of Iceland

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Iceland represents an extreme environment for barley cultivation, characterized by low temperatures, frequent storms, persistent precipitation, and long photoperiods (64-66°N). These challenging conditions often lead to barley being harvested unripe with high grain moisture content (>30%) and poor grain filling (<600g L⁻¹). Consequently, breeding for high dry matter content at harvest and higher test weight are key goals for adaptation of barley to the Icelandic environment. Barley is a novel crop in Iceland, although settlers from Norway and the British Isles brought barley in 874 AD. Cultivation was discontinued in the 15th century due to cooling climate and the plague. Barley was reintroduced in 1923 and barley breeding in Iceland started in the 1980's. However, cultivation didn't gain traction until the turn of the 21st century, with the release of adapted varieties from the breeding program. Breeding efforts successfully improved earliness resulting in breeding lines that were too early, even for Iceland, causing a severe yield penalty. The origin of optimized earliness in the Icelandic two row barley population can be traced back through the pedigree from six row barley. Crossing a two-row Swedish variety with an early six-row breeding line produced Iceland's first registered two row cultivar. Another generation of backcrossing led to a 10% yield increase with the second released variety. The Icelandic barley breeding population is genetically distinct from other early-maturing barley. We identified SNP allele combinations significantly associated with key adaptive traits, distinguishing Icelandic germplasm from other barley groups evaluated under local conditions. Taking advantage of the adapted barley breeding population, we accelerated genetic gain in yield through a recurrent genomic selection program. These advances support the development of a sustainable and novel agricultural sector. As cultivation of barley in Iceland increases, we contribute to self-sufficiency in one of the most demanding agricultural environments of the world.



Strigolactones are targets for crop improvement

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Strigolactones are a novel class of plant hormone. Strigolactones regulate multiple important agronomic traits, including tillering, plant height, grain size, root architecture, nutrient acquisition, stress responses, and interactions with soil microbes. As a result, strigolactones are of considerable interest for crop improvement. We have been progressively isolating and evaluating genetic variation in barley strigolactone pathways to determine how strigolactones may be harnessed for barley improvement. The first generation of alleles showed broad and often strong phenotypic effects. These have been useful for evaluating the extent and impact of strigolactones in crop growth and resilience. In contrast, more recently identified variants confer more targeted benefits on individual traits, with fewer unintended side effects. This has been seen particularly in plants carrying variants of the *LATERAL BRANCHING OXIDOREDUCTASE (LBO)* gene. We will report on our progress, including discussion about why some genetic targets, like *LBO*, have specialised functions, and how such targets may be exploited to deliver customised trait advantages in barley.

Rise and fall: a new phenotyping tool to assess canopy traits in barley

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Visual scores of barley lodging, brackling, and head loss in the field are subjective and limited to conducive years and environments. These plant and canopy phenomena relate to structural architectural characteristics encompassing morphological, biochemical and genetic factors. New phenotyping approaches are required to support accurate characterization and targeted improvement of canopy traits underpinning these production-limiting phenomena. Methods using pushing and pulling forces have been developed for assessing structural architecture but have not been widely adopted for routine use. Here, we developed a mechanistic phenotyping method to assess structural traits at a plant and canopy scale and incorporated this into a portable force gauge device, SpringBack-45, to dynamically characterise canopy strength. Validation of the SpringBack-45 for assessing a range of canopy response traits in controlled environment and field



conditions using the OzBarley elite panel has supported quantification of genetic change and variation in structural stem traits over time. Whilst canopy strength normalized by plant height has increased over time, there has been no genetic progress for viscoelastic response which is an indicator of canopy plasticity. Field assessment of canopy traits with the SpringBack-45 enabled prediction of lodging ($R^2 = 0.73$) providing an accurate means to quantify lodging in non-conductive seasons or environments that could effectively replace the standard visual score. Shorter peduncles reduce head loss, but our results suggest additional potential to address head loss by targeting peduncle diameter, wall width, and dry weight per length. This presentation will provide an overview of the construction of the SpringBack-45 device and demonstrate its utility for quantifying genetic changes in Australian barley canopy traits in OzBarley varieties released or in use between the 1900s to 2022. It will also highlight opportunities to improve the accuracy and precision of canopy trait phenotyping, including improvement of traits that have not yet been targeted through breeding.

From gene to grain: turning research into commercial impact

David Moody¹

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Agricultural R&D funding in Australia is approximately \$3.0billion per annum. Whilst the public sector remains the largest funder, the rate of growth of private sector investment (4.2% per year) is significantly higher than the rate of growth of the public and university sectors. The Australian Government and State Governments are doing less agricultural R&D, with expenditure dropping respectively by 3.0% and 1.9% each year on average since 2005-06. Based on current trends, private sector investment will exceed total investment by the public sector and universities within the next five years.

Given the changes occurring in the funding mix for agricultural R&D, and the decline in investment by State Government Agencies in particular, there needs to be evolution in the model for research translation into commercial impact. Historically the State Government Agencies filled the gap between basic research and industry adoption, through a combination of applied research and extension. Based on current trends, these Agencies will contribute less than 5% of total Agricultural R&D expenditure within the next five years.

This presentation explores the relationship changes needed between public sector research and the private sector to ensure that the public sector investment in core technologies and education is translated into both commercial outcomes and an appropriately trained workforce for the barley industry.



Barley breeding has contributed to increased resilience across the supply chain - Past wins and future opportunities

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Barley breeding, both in Australia and globally, has played a central role in improving resilience across the supply chain, delivering benefits from growers through to end users. Advances in genetics have complemented ongoing improvements in farming systems, together creating a more resilient and sustainable Australian barley industry. This is demonstrated by continued growth in total national production across diverse growing environments, even in the face of challenging and highly variable seasonal conditions.

Genetic improvement through breeding has contributed significantly to efficient use of resources to improve grain yield, improved adaptation to diverse and extreme environments, and adapting to changes in disease virulence. The broad suite of varieties available to growers gives options that suit differing agronomic requirements, management systems and seasonal risks. Improvements in malting quality and processing efficiency have also delivered benefits to end-users. These outcomes highlight the role of breeding in strengthening resilience and sustainability across the entire barley supply chain.

Looking ahead, opportunities exist to further strengthen resilience by harnessing rapidly advancing breeding tools, including genomic selection, modern statistical approaches and predictive modelling. These tools will enable breeders to continue to deliver genetic gain that underpins future productivity gains for the entire barley supply chain. Building on the successes of the past, there are significant opportunities to build for the future.

CAIGE Barley Project - 12 years of international collaboration

Mark Dieters¹

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The CAIGE (CIMMYT Australia ICARDA Germplasm Evaluation) Project (www.caigeproject.org.au) has been funded by the Grains Research and Development Corporation in various forms for over 20 years. Originally, this project focused only on bread wheat from CIMMYT; however, in 2013, the project was expanded to include barley from ICARDA. The project was reviewed externally in 2025, and one more year remains in the current phase. There have been several changes to the structure of the barley CAIGE project over the last 12 years: in the first phase, international nurseries were imported initially from Lebanon (including Winter and Naked types), then moved to the importation of selected breeding lines and seed harvested from resistant plants in resistant landraces, with lines imported annually from 2013-2017; in the second phase, importations from ICARDA focused primarily on breeding lines were selected from across the 2-row breeding trials in Morocco, plus diverse materials from the ICARDA genebank programs (i.e. lines derived from crosses to *H. spontaneum*), with lines imported annually from 2018-2022; and in the third (current) phase, 350 lines imported every second year with 75 coming from wide-crossing and remainder from selections in the Stage 1 and



Stage 2 yield programs, with all lines imported genotyped (SNP) by either InterGrain or the Australian Grains Genebank. Over the life of the project, 2826 lines have been selected and imported into Australia. The final import set of 349 lines is currently in quarantine, but will be released and sown into seed increase plots by the time ABTS26. A total of 2477 lines have been phenotyped for at least foliar diseases (BLR, NFNB, spot-form net-blotch, powdery mildew, and scald), key agronomic traits (plant height, maturity, and lodging), and yield in at least five trials each year (currently, YORK, ROSEWORTHY, PINARRO, BREEZA, and NARRABRI). The accumulated germplasm and phenotypic/genotypic data are available to breeders and researchers in the private and public sectors and represent a very significant resource to support research efforts to identify novel sources of disease resistance(s) in adapted genetic backgrounds, and to support the integration of this diversity into Australian barley breeding programs. The success of this project is underpinned by strong national and international collaboration between ICARDA, the University of Sydney, GRDC, the Australian Grains Genebank, Intergrain, AGT, SECOBRA, Trigall, and the public sector pathology groups in Queensland, New South Wales, and South Australia.

Barley breeding adaptation in global warming climate

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Created in 1902 by French brewers and maltsters, the SECOBRA Association's primary mission is to develop and improve the supply of quality barley to the malting industry. A specialist in malt barley in Europe, SECOBRA Recherches now also develop barley varieties for the United Kingdom, Australia, the Black Sea region and the South America zone (Argentina, Uruguay, Brazil).

With continued global warming, Western European growers have tended to start planting earlier each year. This has led to where today, in some regions, 2 row spring barley types being planted under winter conditions while, only a few decades ago, they were planted at spring time. Consequently, biotic pressures have drastically increased in this sowing window and barley breeders have had to re-align to optimise breeding strategies.

To address this, SECOBRA Recherches is investigating resistance sources and developing breeding strategies in-house as well as participating in collaborative projects, with the intention of identifying and implementing novel genetic diversity into its breeding pipeline. We envisage we will be able to deliver growers and industry, high quality spring barley, with significant improvements in disease resistance and hence agricultural performance.



Quantifying the contribution of genetics, climate, and agronomy to malting barley yield gains in South America

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Accelerating genetic gain in barley yield potential requires understanding how breeding progress interacts with climate and agronomy. Long-term yield trends observed in variety trials networks reflect the combined effect of cultivar substitution, climatic conditions, and agronomic management, making it difficult to isolate and quantify the contribution of genetic improvement. Field studies aimed at quantifying genetic gains in yield often use either direct comparisons of historical cultivars under current environmental conditions or the statistical analysis of extensive long-term multi-environment trials (MET) datasets through mixed linear models. In this study, we used the CERES-Barley crop model as a breeding-support framework to quantify the relative contribution of genetic improvement, climate, and agronomic management to barley yield gains over the last 25 years in Uruguay. The model was calibrated and evaluated with multi-environment field data from the national variety testing networks, including phenology, grain yield, and management records from different production eras. Genotype-specific coefficients were estimated for four cultivars representing two breeding origins (Uruguayan and European) and two release periods, enabling the comparison of historical and more recent germplasm within a common physiological framework. We then implemented a series of counterfactual simulation experiments in which genotype, climate, and agronomic management were modified systematically to partition their individual and combined effects on yield. This approach allowed us to estimate how much of the observed gain in yield potential was attributable to genetic progress. The simulations helped us to interpret how changes in phenology contributed to the higher yield performance of newer cultivars. By separating breeding-driven gains from climate and agronomic management, this study provides a practical basis to support ideotype design in barley breeding programs.



SESSION 10: BIOTIC STRESS TOLERANCE

Recent advances in managing *Ramularia* leaf spot in barley: lessons from epidemiology and integrated strategies in South America

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Ramularia leaf spot (RLS), caused by *Ramularia collo-cygni* (Rcc), has become one of the major constraints to malting barley production in Southern Cone of South America. During severe epidemics, grain yield losses of up to 70% have been recorded in susceptible cultivars, with significant reductions in grain quality. As no commercial barley cultivars are immune to RLS, disease management has relied largely on fungicides, raising concerns about long-term sustainability of this practice.

Over the past 15 years, collaborative research conducted in Argentina and Uruguay has contributed knowledge of RLS epidemiology, pathogen biology, environmental drivers, host responses and best disease management practices under regional production systems. Epidemiological studies confirmed the widespread occurrence of Rcc in commercial seed lots and its transmission to seedlings. Environmental conditions in disease development. Disease development was strongly associated with prolonged leaf wetness during stem elongation and crop stress, highlighting the complex interactions among environmental conditions, host physiology and pathogen activity. Molecular diagnostic tools have also proven essential for pathogen detection and quantification, overcoming the limitations of symptom-based diagnosis and disease surveillance.

Multi-environment field trials have characterized the response of commercial cultivars and breeding material to RLS. Although most currently grown cultivars exhibit intermediate to high susceptibility, advanced breeding lines developed by INIA have shown moderate levels of resistance, supporting the incorporation of host resistance into long-term disease management strategies.

Research has also confirmed reduced sensitivity to the major fungicide groups such as triazoles (DMIs) and carboxamides (SDHIs) and resistance to QoI fungicides in regional Rcc populations, reinforcing the need to optimize fungicide programmes that prioritise product performance and application(s) at disease onset according to risk and crop phenology. The highest of RLS control was achieved with application(s) between late tillering-early elongation stages (ZGS 30-32), with timing adjusted according to early disease pressure, and awns-peeping stage (ZGS 47-49). In parallel, forecasting models incorporating variables such as leaf wetness duration, accumulated rainfall, water availability and water excess have improved the prediction of disease risk and might support more informed fungicide decisions.

Although there are still gaps in RLS research, progress has been made to further understand this pathosystem and optimise management practices. Future perspectives for RLS management will be discussed, including climate-informed decision support,



molecular diagnostics, regional surveillance networks and the deployment of resistant germplasm. Our experience provides valuable insights for the global barley industry and highlights the importance of integrating epidemiology, breeding and disease management to improve resilience against this increasingly important pathogen.

RUST-E: A Pathology-Informed Deep Learning Expert for Foliar Disease Resistance Phenotyping

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Barley leaf rust, caused by *Puccinia hordei*, is a well-characterised biotrophic pathosystem with diverse genetic resistance mechanisms. Distinct host resistance genes produce visually diagnostic phenotypes; however, reliable interpretation of gene-specific responses and quantitative assessment of infection types typically require specialised pathology expertise. Here, we investigate whether a pre-trained deep convolutional neural network (ResNet50) can learn gene-specific resistance signatures directly from leaf images. We evaluate ResNet50 for (i) binary classification of resistant versus susceptible phenotypes and (ii) multiclass classification of five gene- or allele-specific responses and (iii) classification of Stakman infection types. In addition, we perform a feature-level ablation to identify which representation layers are most informative for disease resistance classification. The model achieved 96% balanced accuracy for binary classification and 78% balanced accuracy for multiclass classification and 85% Stakman classification accuracy, demonstrating that gene-specific resistance phenotypes can be reliably inferred from image data. These results highlight the potential for deep learning to capture pathologist-relevant features and support scalable, image-based disease phenotyping.



From Gene Banks to the Field: Discovery and Validation of Barley Leaf Rust Resistance Loci

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Barley leaf rust (BLR), caused by *Puccinia hordei*, remains a major constraint to barley production due to rapid pathogen evolution and the limited durability of deployed resistance genes. Although genetic resistance is the most sustainable control strategy, much diversity in gene bank collections remains underutilised. This study aimed to identify known and novel BLR resistance loci by mining Eastern European barley (EEB) germplasm sourced from the Australian Grains Genebank, using integrated phenotyping and genomic approaches. A panel of 318 EEB accessions was evaluated at the seedling stage with 14 diverse *P. hordei* pathotypes and under field conditions across three seasons using a predominant highly virulent Australian isolate to distinguish all-stage resistance from adult plant resistance (APR). Accessions were genotyped using targeted genotyping-by-sequencing (tGBS) and the Infinium™ wheat-barley 40K SNP array, yielding ~35,000 high-quality SNPs anchored to the Morex v3 genome assembly.

Genome-wide association studies (GWAS) using the FarmCPU model revealed isolate-specific association patterns consistent with virulence/avirulence profiles, indicating that most signals corresponded to known BLR resistance. Of the 14 seedling resistance traits analysed, 10 showed significant marker-trait associations with known resistance genes (*Rph2*, *Rph3*, *Rph12*, and *Rph19*). Novel resistance quantitative trait loci (QTL) were also identified on chromosomes 1H, 2H, 3H, 4H and 6H. BayesR analysis, independently supported these major effect regions and detected additional putative resistance loci. Although no field resistance traits exceeded the Bonferroni threshold, a consistent sub-threshold signal on chromosome 2HL across seasons, suggested genetic components contributing to APR. Biparental population analysis uncovered resistant accessions undetected by GWAS due to low allele frequency, identifying monogenic resistance in the Russian landrace Caspian and digenic resistance in Anska and Athenais. The Caspian resistance gene was mapped to chromosome 4HL and designated *Rph29*, while QTL mapping in an Athenais × Gus population identified a major locus on chromosome 1HS. Overall, this study demonstrates the value of combining dense genomic tools with diverse phenotyping to uncover underutilised BLR resistance loci for future breeding deployment.



Leaf rust and stripe rust of barley: new tools to combat ever-changing pathogens

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This paper is the product of many researchers over many years whose contributions will be duly acknowledged at the conference.

Worldwide, barley is affected by four rusts: crown rust (caused by *P. coronata* var. *hordei*), stem rust (*P. graminis*), stripe rust (*P. striiformis*), and leaf rust (*Puccinia hordei*). In Australia, barley is affected principally by leaf rust and stem rust.

Although sporadic, leaf rust is the most damaging rust in Australian barley crops. Although genetic resistance to leaf rust was estimated to save \$47 million annually, it was also estimated to cause annual losses of \$21 million. Some 28 loci conferring resistance to *P. hordei* have been characterised, 25 all stage resistance (ASR) genes and three adult plant resistance (APR) genes. Ongoing research since 1989 at the University of Sydney has provided a sound understanding of pathogenicity in *P. hordei* and demonstrated widespread occurrence of resistance to DMI fungicides due to increased copy number of the *cyp51* gene. Working with many collaborators, we discovered and designated five new ASR genes, and cloned eight ASR genes. Four of these genes are non-canonical, including a NAC-transcription factor, a protease, and a probable executor gene of unknown function. Three genes conferring additive APR to leaf rust were characterised and codominant markers developed. Genetic studies have identified new sources of APR to leaf rust. A minor gene conferring resistance to leaf rust has also been cloned, it is a recessive allele of a presumed susceptibility gene.

A new variant of the stripe rust pathogen with increased virulence on barley was detected in 2021 ("BGYR+"). It most likely arose via asexual hybridisation between the stripe rust pathogens of wheat and barley grass. The increased virulence of BGYR+ on barley and resistance to DMI fungicides make this an increased threat to the Australian barley industry.

Rpg1 and beyond: Advancing Inherited Stem Rust Resistance in Canadian Barley

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When severe epidemics strike, stem rust, triggered by the fungus *Puccinia graminis* f. sp. *tritici* (Pgt), could result in devastating losses in barley (*Hordeum vulgare* L.). A virulent stem rust race known as Ug99 was initially detected in Uganda in 1998. Since then, it has evolved into over a dozen race variants and expanded across various African countries and into the Middle East and Nepal. Furthermore, recent reports have confirmed the presence of virulent races in Europe, South America, and within the Pacific Northwest region of North America.



In the Canadian agricultural landscape, barley holds a position of high importance, serving as a primary crop for malting, livestock feed, forage, and human consumption. Beyond the thousands of individual farmers whose livelihoods depend on barley cultivation, the crop serves as a cornerstone for the livestock sector, grain handling operations, and diverse value-added sectors including the malting, brewing, and food processing industries.

Although the application of fungicides can manage stem rust outbreaks, the most ecologically and economically sustainable approach to disease control is through genetic resistance. Consequently, there is a vital need to develop barley cultivars with built-in resistance to provide durable crop protection.

The Barley Breeding Program at Agriculture and Agri-Food Canada Brandon Research and Development Centre address this by screening germplasm from gene banks, utilizing doubled haploid production, and employing marker-assisted selection. These efforts also involve rigorous field evaluations in disease nurseries located in Brandon, Manitoba (targeting *Pgt* race QCCJ) and Njoro, Kenya (targeting the Ug99 race complex), alongside detailed genetic mapping. Significant strides have been achieved, resulting in the release of several new barley varieties that feature stem rust resistance, carrying the *Rpg1* gene or a combination of both the *Rpg1* gene and the *rpg4/Rpg5* gene complex. The presentation will provide a comprehensive overview of these strategic endeavours.

Smart protection: Linking barley genetics to fungicide performance

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Optimising fungicide use in cereal crops is essential for delaying resistance development, improving returns to farmers, and extending the lifespan of current fungicide chemistries. Understanding chemical uptake and movement within plants, whether applied as seed, in-furrow, or foliar treatments, is key to refining application strategies.

At Centre for Crop and Disease Management, Curtin University, we investigate fungicide uptake and translocation across barley, canola, and wheat with different chemistries using liquid chromatography-mass spectrometry. The spatial and temporal distribution of seed-applied fluxapyroxad in barley was mapped, revealing predominantly xylem-driven movement for both seed and foliar treatments. Varital differences in uptake patterns were also observed in foliar applications, and temperature was found to influence fungicide uptake dynamics. We also demonstrated that fungicide exposure can reshape the population structure of *Pyrenophora teres* f. *maculata* (*Ptm*), influencing the balance between sensitive and reduced-sensitivity strains.

Building on this, my PhD research explores how barley genotype influences the longevity and protective efficacy of seed-applied fungicides against *Ptm*. We observed synergistic or additive effects among genotypes with differing resistance backgrounds, and identified plant biomass as a major driver of fungicide dilution over time.

To test this relationship under commercial conditions, we established a field trial stratified by plant vigour (low, medium, high) using NDVI data. Results revealed faster



dissipation in high-vigour zones, indicating that physiological traits strongly influence fungicide persistence and may inform optimal timing for subsequent foliar applications. We also detected residual, biologically active fungicide in plants from prior-season applications, highlighting the importance of cumulative field dynamics.

Overall, these findings support a host- and vigour-specific approach to fungicide management. Tailoring application timing and intensity to plant physiological status can help sustain chemical efficacy, reduce resistance risks, and enable more precise, need-based disease control in cereal systems.



SESSION 11: ABIOTIC STRESS TOLERANCE

Variation in HvHMA5 impacts copper transport, photosynthesis and yield

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Copper is a micronutrient that can become toxic at high levels, but too little copper can also be detrimental. Copper (Cu) is an essential co-factor for metalloproteins and participates in key oxidation reactions in both plants and humans. However, in excess this micronutrient has severe physiological implications that result in Cu toxicity. We identified Heavy Metal ATPase-5 (*HvHMA5*) as the likely gene underlying a quantitative trait locus contributing to variation in barley grain Cu accumulation. We observed two distinct haplotypes of *HvHMA5* in cultivated barley associated with contrasting levels of Cu and other grain micronutrients. An analysis of georeferenced genotypic data from more diverse germplasm led to the tentative speculation that the *HvHMA5* allele associated with increased grain Cu is under positive selection in cultivated germplasm. Protein modelling showed that the difference in nutrient accumulation of these alleles can likely be attributed to a single amino acid substitution resulting in differing Cu transport capabilities. We generated mutant resources in several genetic backgrounds using gene editing and screening two large mutant populations. The characterisation of these mutant resources will be discussed.

Assessing the resilience of barley and malt to heat waves

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The detrimental effects of chronic high temperatures during grain filling on yield and quality are well established. High temperatures directly limit the capacity of the grains to grow, reducing final grain weight, decreasing starch accumulation, and increasing grain protein concentration. They also alter carbohydrate and protein composition, although these responses vary depending on genotype and the severity of heat stress. Climate change is not only chronically raising mean temperatures but also increasing the frequency and intensity of short-term heat waves. These episodic events have received far less attention than chronic high temperatures despite potentially causing greater



damage. Most studies have been conducted under controlled-environment conditions allowing more precise heat treatments but are difficult to extrapolate to field conditions. In malting barley, an additional limitation is the insufficient yield produced for comprehensive malting quality analyses. Consequently, field studies investigating the effects of heat waves on yield and quality are urgently needed.

To address this gap, we developed a field-based approach using portable chambers to increase daily maximum temperatures by 5–8 °C over irrigated plots, thereby isolating heat stress from water deficit. Despite some limitations, this method provides a realistic framework for assessing heat waves under agronomically relevant conditions.

Across multiple experiments, years, and genotypes, heat waves during the linear phase of grain filling consistently reduced grain weight (2–30%) and malt extract (0.5–5%), while producing variable effects on other malting quality traits. Grain weight reductions appear to reflect a direct limitation of potential grain size rather than decreased source strength associated with accelerated senescence, and they seem larger than expected under chronic high temperatures. Although declines in malt extract were smaller than those in grain weight, they remain economically significant for the malting and brewing industries. Because malt extract reflects the interaction of multiple grain quality traits, the underlying mechanisms remain poorly understood. Elucidating these mechanisms is important for developing agronomic and breeding strategies to enhance barley resilience to heat waves.

The SnRK2-SLAC1 Module Regulates Stomatal Traits for Drought Tolerance in Barley

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Drought is a major abiotic stress that threatens crop productivity, and stomatal regulation plays a central role in plant drought response. Grass stomata are among the fastest in opening and closing, yet it remains unclear whether slow-type anion channels (SLAC/SLAHs) in grasses such as barley (*Hordeum vulgare*) are specialized to support rapid stomatal responses under water deficit. Here, we investigated the functions of barley anion channels HvSLAC1 and HvSLAH3 and their interactions with SnRK2 protein kinases. Heterologous expression assays in *Xenopus laevis* oocytes, yeast, and barley protoplasts showed that HvSLAC1 interacts with HvOST1.1 and HvOST1.5, whereas HvSLAH3 specifically interacts with HvOST1.5. CRISPR-Cas9 knockout of *HvSLAC1*, but not *HvSLAH3*, resulted in significantly impaired drought-induced stomatal closure and, unexpectedly, reduced stomatal density and stomatal index in *hvslac1* compared with the wild-type. By contrast, *HvSLAC1* overexpression significantly enhanced barley drought tolerance. Transcriptomic and physiological analyses further revealed that *HvSLAC1* contributes to drought responses by maintaining guard cell ion homeostasis and guard cell wall structural stability, rather than by accelerating stomatal movement. Together, we demonstrated that the SnRK2-HvSLAC1 module plays a key role in regulating stomatal function and drought tolerance in barley and highlight a non-canonical role of SLAC-type anion channels in guard cells.



Envirotyping and historical trends of abiotic stresses affecting barley productivity across Australia

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Barley is the fourth most widely cultivated cereal crop globally and the second most important crop in Australia. However, climate change poses major challenges to barley production, with rising temperatures, increased variability in rainfall, and more frequent extreme weather events intensifying abiotic stresses. These stresses threaten yield stability and increase the need for climate resilient cultivars. A robust understanding of genotype by environment (G×E) interactions requires accurate characterisation of the environments experienced by crops within the target population of environments (TPE). This study applied advanced crop modelling and envirotyping approaches to characterise abiotic stress patterns across Australian barley-growing regions. Long-term simulations were conducted using the APSIM (Agricultural Production Systems sIMulator) model across 60 representative sites over a 60-year period (1965–2024). Key environmental factors, including water stress index, vapour pressure deficit, and maximum temperature were analysed both singly, and in combination. Simulations incorporated regionally representative management practices and three barley cultivars differing in maturity. Multivariate clustering identified four main environment types (ETs), while univariate analyses identified four main ETs for water stress index and vapour pressure deficit, and three ETs for maximum temperature. ET frequency varied across regions and cultivars, with the slow maturing cultivar consistently exposed to higher drought and heat stress levels. Comparisons between historical (1965–1994) and recent (1995–2024) decades revealed a 7–14% increase in the frequency of the most stressful ETs, reflecting a substantial impact of realised climate change. Further analysis of the 60-year simulations for the mid-maturing cultivar quantified significant temporal shifts in key climatic drivers and associated drought, heat, and frost stresses, revealing their changing implications for barley productivity across Australian regions. Overall, this study provides a comprehensive assessment of abiotic stress dynamics and offers valuable insights to support targeted selection for the development of climate-resilient barley cultivars adapted to increasingly variable and challenging environments.

Expanding the Pre-Harvest Sprouting Window in Barley: Genotype × Environment × Harvest Timing Interactions under South African Conditions

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Increasing climatic variability has intensified pre-harvest sprouting (PHS) risk, the premature germination of grain before harvest. In barley, PHS threatens yield and malting quality under PHS conditions. In South Africa's barley systems, rainfall may occur well before, during, or after physiological maturity. While cultivar differences are recognised, rainfall timing and genotype × environment (G×E) interactions remain poorly



understood. Addressing this gap is critical for improving crop resilience to abiotic stress. This study evaluated the combined influence of G×E interactions and harvest timing on PHS risk across South African barley environments.

Multi-environment field trials were conducted across 20 sites in five provinces in South Africa during the 2024–2025 seasons under rainfed and irrigation conditions using randomized complete block designs. PHS response was assessed using visual sprouting scores, Hagberg Falling Number, and alpha-amylase activity. G×E interactions were analysed using additive main effects and multiplicative interaction (AMMI) models, while site and harvest date effects were evaluated using mixed-effects models.

Strong G×E interactions confirmed that environment plays a dominant role in modulating PHS expression. Across genotypes, delayed harvest consistently increased sprouting severity. Critically, rainfall up to two weeks prior to harvest significantly elevated PHS risk, revealing a previously unrecognised pre-harvest window of abiotic stress sensitivity. This response varied between sites, with high-risk environments showing disproportionate increases in sprouting under delayed harvest. These findings highlight a pronounced genotype × environment × harvest date interaction, demonstrating that rainfall timing and local environment are key determinants of PHS outcomes.

PHS risk in South African barley is governed by interactions between genotype, environment, and harvest timing, with rainfall as a key abiotic stressor. Rainfall up to two weeks before harvest expands the critical sprouting window. These findings emphasise proactive, site-specific risk assessment and adaptive harvest strategies to enhance resilience under increasing climatic variability.

Do PPD-H1 alleles affect yield sensitivity to a pre-flowering heat wave?

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Rising temperatures associated with climate change increasingly threaten cereal yields. Most previous studies have focused on chronic high temperatures, which primarily affect yield indirectly through modifications of crop phenology. In contrast, the effects of short-term heat waves on reproductive development and yield formation remain poorly understood. In barley, development and reproduction are tightly regulated by photoperiod sensitivity, mainly controlled by the *PPD-H1* gene, which may modulate plant responses to thermal stress. Here, we quantified the impact of a pre-flowering heat wave on yield formation and spike fertility in near-isogenic lines differing at the *PPD-H1* locus, across four contrasting environmental backgrounds. Heat waves were imposed for 10 d at the flag leaf stage under field and outdoor conditions, increasing daily maximum temperatures with minimal effects on mean temperature and phenology. Across environments, the heat wave consistently reduced grain yield. Yield losses were primarily driven by reductions in grain number rather than grain weight and were markedly greater in the photoperiod-insensitive (*ppd-H1*) line than in the photoperiod-sensitive (*Ppd-H1*) line. Differences in flowering time between near-isogenic lines were small or absent, indicating that the contrasting heat wave responses were largely independent of phenological escape and instead reflected direct effects on reproductive development. The lower resilience of *ppd-H1* was associated with both reduced floret fertility at flowering and increased grain abortion, particularly in apical spikelets, whereas spike



fertility in *Ppd-H1* plants was largely preserved. In conclusion, the wild-type *Ppd-H1* allele seemed to confer enhanced tolerance to short-term heat stress immediately before flowering by stabilizing spike fertility and grain set. This study highlights the importance of photoperiod genes not only in shaping phenology but also in conferring intrinsic resilience of reproductive processes to heat waves, providing insights for breeding barley cultivars adapted to climate change.



SESSION 12: DECODING CROP GENOMES

Expanding the Genomic Landscape of Barley Breeding Using Wild *Hordeum* spp.

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The barley gene pool comprises cultivated barley (*Hordeum vulgare*), its wild progenitor, and diverse wild *Hordeum* species that represent an underutilized reservoir of genetic variation for breeding. To expand the genomic landscape for barley improvement, we established two pangenomic frameworks incorporating wild *Hordeum* spp. from the secondary and tertiary gene pools. Extending beyond the crop, a haplotype-resolved pangenome of *H. bulbosum* reveals extensive genome restructuring driven by polyploidization, transposable element activity, and enables precise characterization of crop-wild introgressions. Dissection of the resistance locus *Ryd4^{Hb}* demonstrates the translational value of wild germplasm for barley breeding. Notably, mosaic haplotypes observed in introgression lines indicate the potential to exploit existing introgression populations through recurrent backcrossing to recover and recombine additional wild haplotypes. At the genus level, comparative pangenomic analyses uncover ancient interspecific segment exchange and pervasive structural variation, coupled with rapid turnover of regulatory sequences. These insights provide a framework for understanding *Hordeum* speciation and reveal opportunities for leveraging interspecific variation in barley improvement. Collectively, these results demonstrate how integrating wild *Hordeum* genomic diversity expands the breeding-relevant genomic landscape and provides a foundation for accelerating barley improvement.

Genetic basis of barley inflorescence architecture: structure of spikelet and floret

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Grass inflorescences produce many flowers (florets), which are directly connected to the grain number. Grain number and weight mainly affect final grain yield; thus, understanding inflorescence shape is crucially important for cereal crop breeding. Barley (*Hordeum vulgare* L.) inflorescence, called "spike" is divided into two-rowed and six-rowed spikes based on the grain setting in the lateral spikelets. Interestingly, unlike two-rowed spike-types, six-rowed cultivars distributed in East Asia have sizeable genetic diversity in awn length, classified as long awn, short awn, and awnless. The lemma-derived awns in barley are structurally directly attached to each floret or grain while fulfilling important dispersal and protective functions, e.g., against predatory animal behaviour, or for assimilate supply, e.g., during grain fill. A dominant allele at the *Awnless 1* locus, *Lks1*, on chromosome 2H has been reported to severely shorten awn development, but the molecular mechanism remains elusive. In this study, the genetic basis of awn suppression has been elucidated. Map-based cloning revealed that the *Lks1* locus is confined to a 1.1-



Mbp region that includes 20 high-confidence (HC) genes. Long-read sequencing revealed that the inversion of the 1.1-Mbp region occurred in the awnless genotype. The oligo-FISH analysis of meiotic leptotene chromosomes further confirmed the inversion. Whole-genome shotgun sequencing analysis revealed no significant mutation within the inverted region. Expression analysis of key developmental genes located in the neighbouring region and border of the inversion revealed the specific mRNA accumulation in lemma tips, where awn development and differentiation are facilitated. Using RNAi knockdown of the candidate gene in the awnless genotype background recovered the elongation of awns, suggesting that the underlying gene is a suppressor of awn development. These results demonstrate that this pericentromeric inversion causes long-distance expression changes and provides morphological inflorescence diversity.

Connecting genebank genomics to the barley pan-genome with *Brioche*

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Genebanks safeguard vast reservoirs of genetic diversity essential for future barley improvement, yet the full value of these resources is often unrealised because genebank accessions are rarely linked in a scalable and consistent manner to the structural and functional variation captured in modern pan-genomic resources. Bridging this gap is critical for translating genebank diversity into actionable information for breeders and researchers.

The Australian Grains Genebank (AGG) Strategic Partnership – a \$30 million joint investment between the Agriculture Victoria and the Grains Research and Development Corporation – is transforming the AGG into a bio digital resource centre by genetically characterising its collection and deploying digital and genomic tools to improve access and utility. As part of this effort, we developed *Brioche*, a platform that connects genebank scale diversity data directly to whole genome and pan genomic information.

Using *Brioche*, we generated in silico genome representations of 76 barley genomes from the latest barley pan genome (Jayakodi et al. 2024) and integrated these with genotype data from 27,000+ barley accessions conserved within the AGG. This enabled projection of key pan genomic features, including gene level presence-absence variation and large structural deletions, onto individual genebank accessions. As a result, users can interrogate accession level structural and functional variation at loci associated with important agronomic traits, identify highly diverged accessions, and visualise local genomic context using the AGG digital tool ecosystem.

We demonstrate the utility of *Brioche* through rapid identification of accessions carrying deletions associated with the non-glycosidic nitrile (non GN) trait relevant to the whisky industry, and with the naked grain phenotype at NUD. By linking genebank diversity to the barley pan genome, *Brioche* provides a scalable and practical pathway to unlock the breeding value of barley plant genetic resources.



OzBarley: a public genome-to-phenome resource for trait discovery

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OzBarley was established as a publicly available resource, bringing together genotypic and phenotypic data. The resource is centred around a panel of ~220 barley lines representing the Australian barley breeding history, including international founder lines all the way to modern cultivars. Genotypic data was created through SNP genotyping and RNA sequencing of samples from young barley seedlings. Phenotypic data was acquired during a controlled environment growth study, including growth rates and water use traits. New phenotypic data is being collected by users of the OzBarley resource. Researchers had the opportunity to measure their trait of interest in open-access field trials across multiple years and locations to study traits such as spike morphology or head loss. Others have accessed OzBarley seed to run independent phenotyping experiments, such as the assessment of root angle in barley seedlings. The trait could be mapped to a novel locus controlling root angle, independent of previously described loci.

We will present an overview of the OzBarley data asset and first results of forward genetic studies making use of OzBarley to identify novel loci for important phenotypic traits.



SESSION 13: NEXT GENERATION BREEDING TOOLS 2

Genome editing in Triticeae crops

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The establishment of Cas endonucleases as genome editing tools has expanded the possibilities of plant biotechnology in ways previously thought scarcely possible. We demonstrated the power of this technology by generating gene-specific mutants with agriculturally relevant traits in cereals and other crops. For example, hulled barley was modified to form naked, edible grains through mutagenesis of *NUDUM 1*, and two-rowed barley was converted into the 6-rowed type via knockout of *VULGARE SIX-ROWED SPIKE 1*. Genome editing also facilitates the advancement of other plant breeding technologies. By targeted knockout of *PHOSPHOLIPASE A1*, haploidy-inducing barley lines were developed that, when used as pollinators, lead to the generation of genetically fixed maternal recombinants. The employment of such doubled haploids has proved to be extremely effective in plant breeding. A key challenge of further technological advancement in genome editing is to go beyond targeted mutagenesis by developing more precise methods at an applicable level. For instance, we used base-editing Cas9 derivatives to precisely mimic specific, still functional barley *eIF4E* alleles that confer resistance to bymoviruses. In another example, the heavy metal transporter HEAVY METAL ATPase 3, that had undergone loss-of-function through spontaneous mutagenesis in the context of durum wheat domestication, was functionally restored via Cas9-triggered DNA cleavage followed by repair through the precisely predictable homology-mediated end joining. The deletion of a mutative 17-bp duplication achieved in this approach is expected to result in a significant reduction of the comparatively high accumulation of cadmium in the grains.

Composition, function and host control of the barley microbiome

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The interface between soil and plant roots hosts distinct microbial communities collectively referred to as the rhizosphere microbiome. In analogy with the microbial communities inhabiting the digestive tract of vertebrates, the rhizosphere microbiome may promote the growth, development and health of their host plants. My team uses barley, a staple crop and a superb genetic model, to elucidate the molecular basis regulating the assembly and function of the rhizosphere microbiome. In this presentation I will draw from a decade of investigations in my laboratory to:

- introduce the “rules of engagement” of the rhizosphere microbiome
- delve into genetics to illustrate how plants, akin to an orchestra conductor, shape the rhizosphere microbiome
- take a tour from the lab to the field, illustrating how modulating interactions in the rhizosphere impact on crop production



I will close reflecting on future research directions and the potential for impact, in barley production and beyond.

Using novel imputation strategies to integrate barley genebank collections genotyped with different technologies

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The Australian Grains Genebank (AGG) and the Federal Ex situ Gene Bank for Agricultural and Horticultural Crop Species (IPK genebank) conserve two of the world's largest barley plant genetic resource collections. Recent genotypic characterisation of these collections provides an unprecedented opportunity to unlock their genetic potential for barley improvement. However, each genebank used a different genotyping technology – genotyping-by-sequencing (GBS) at IPK and the Illumina wheat-barley 40K SNP array at AGG – resulting in limited marker overlap and restricting direct integration and comparison of datasets.

Here, we present a genotype imputation pipeline designed to integrate poorly overlapping genotyping platforms, and apply it to barley accessions from the AGG and IPK genebanks. The approach leverages linkage disequilibrium (LD) and haplotype structure to infer untyped variants using a high-density reference panel. Whole-genome sequence data from 1,315 diverse barley accessions (Jayakodi *et al.*, 2024) were used to construct a high-quality haplotype reference. Variants in strong LD ($R^2 > 0.9$) within 500kb of 40K SNP or GBS markers were identified, enabling reciprocal imputation of 40K-tagged variants into GBS datasets and GBS-tagged variants into 40K datasets.

Imputation performance was evaluated using repeated 10-fold cross-validation, achieving high accuracy (average, 0.99) across variants and accessions. Applying this approach enabled imputation of GBS variants into the full AGG barley collection (>27,000 accessions), supporting, for the first time, a comprehensive comparison of genetic diversity between the complete AGG and IPK barley genebank collections.



Use of gene-editing to introduce agronomically desirable traits in barley

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In Australia, soil fertility and weed infestation are major yield limiting factors. A cost efficient and environmentally aware solution is to use gene technology and introduce smart cultivars that can survive with less fertiliser and tolerate herbicides application. My PhD research uses gene-editing technique regarded as non-GMO to precisely edit two important genes in barley with the aim of introducing herbicide tolerance and nitrogen use efficiency (NUE). To introduce herbicide tolerant in barley, we targeted a known sensitive genomic location in the Acetyl CoA Carboxylase (ACCase) gene in barley and generated more than 40 ACCase mutants using CRIPR/Cas9 gene-editing technique. About half of the mutants generated have no phenotypic fitness cost in terms of growth and development making them suitable candidates for herbicide screening. Screening of these candidates using a commercial Group 1 herbicide (Aggressor CoAxiom) will determine their level of tolerance or sensitivity. To improve NUE, genes involved in the production of the plant hormone, Strigolactone (SL), were targeted by gene editing to alter their expression. We found SL-mutants can tolerate low nitrogen conditions better than the un-edited barley parent suggesting they poses better NUE. Further assessments using RNA sequencing revealed that these SL-mutants are highly enriched in genes that are associated with nitrogen metabolism and adaptation to stress under low nitrogen conditions. All together my PhD research is aiming to deliver fast alternative in developing herbicide tolerant varieties and cheaper varieties fit for fertiliser management

A spatial transcriptome atlas of barley caryopsis development and germination

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We have constructed a four-dimensional spatial gene expression atlas of *Hordeum vulgare* (barley) grain development and germination by spatial transcriptomic analysis of serial sections, with which we have reconstructed transcript abundance in three physical dimensions and with temporal kinetics. Using energy biology as an example, we investigated the sub-tissue localisations of processes from starch synthesis to degradation, sugar transport and mitochondrial and chloroplast activity. The atlas revealed different patterns in gene expression across tissues and developmental stages. Heterogeneity in gene expression was observed between cell-types and within domains of individual cell-types, across two-dimensional (xy, 55 µm resolution) and three-dimensional (xyz, 8 µm resolution in z-plane) axes. Expression of several genes matched



previous gene specific studies in different barley varieties verifying the robustness of the approach, and indicating that patterns of gene expression are conserved at least for some categories of genes between varieties. Trajectory analysis of aleurone tissue spanning from early development to the completion of germination, provided a comprehensive roadmap of processes involved in tissue development and identified known and novel transcription factors, with spatial specification, that play roles in seed development and germination. A public visualization browser is available to view two- and three-dimensional transcription abundance profiles at <https://barley-4d.latrobe.edu.au/>. Our study demonstrates the utility of spatial transcriptomics as a tool for high resolution gene discovery.



POSTERS

#01

Assessment of maximum freezing tolerance following cold acclimation in barley under controlled conditions

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Freezing injury is a major constraint to overwintering survival and yield stability in winter and facultative barley (*Hordeum vulgare* L.) as well as a concern for spring types when grown under ultra-early seeding management practices. To ensure survival, barley may cold acclimate to enhance freezing tolerance by sensing declining temperature and photoperiod cues. In this study, the differences in the maximum attainable freezing tolerance of cold acclimated spring, facultative, and winter type barley genotypes, along with winter wheat (*Triticum aestivum* L.) as a reference, were evaluated.

Two sets of experiments were conducted at Agriculture and Agri-Food Canada's Brandon and Kentville Research and Development Center, respectively. The first experiment at Brandon included 186 genotypes (3×3 replicates), followed by a second experiment at Kentville with 73 genotypes (5×4 replicates). Freezing tolerance was measured using a controlled freeze-thaw test after cold acclimation, with a minimum temperature of -10°C. Plant recovery was assessed as regrowth after three weeks under optimal conditions.

There was clear variation among genotypes, with recovery ranging from 0 to 100% and an average of about 20%. As expected, winter and facultative types tolerated the stress better, but some spring genotypes also showed moderate levels of tolerance. Results from the two screening cycles were consistent, showing a moderate positive association and indicating good repeatability of this method. The most tolerant checks, including winter wheat, performed consistently well in both datasets.

Overall, this screening method captured differences in freezing tolerance and can be used as a reliable and scalable approach for screening barley. It provides useful information for identifying tolerant genotypes and supporting breeding efforts aimed at improving freezing tolerance and development of climate-smart barley cultivars.



#02

Enhancing Barley Breeding Efficiency Through Data-Driven Trait Prediction

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Each year, plant breeders face the challenge of screening large breeding populations to identify desired phenotypic traits. Traditional manual phenotyping remains a bottleneck, but high throughput technologies are enabling more efficient and scalable data collection.

To address this, Agriculture and Agri-food Canada conducted a three-year project (2023-2025) to develop and adapt high throughput phenomics pipelines for various crops including barley. This project integrated a user-friendly image analysis platform with Unmanned Aerial Vehicle (UAV)-based data collection. Specifically, multispectral data from a MicaSense RedEdge-MX sensor mounted on a DJI Matrice 210 UAV were used to monitor crop traits during the growing season. The objective was to evaluate how UAV-derived trait and predictive models can identify optimal growth stages for various trait predictions in early-generation breeding material.

Field data were collected weekly over three growing seasons at Brandon, Manitoba, Canada. Plot Vision software was used to process imagery, including stitching images and plot segmentation, enable trait extraction and identification of optimal mission dates. To predict grain yield and other traits, the study employed several machine learning models, including linear regression, Random Forest (RF), Extreme Gradient Boosting, and support vector machines. Ground-truth field measurements were used for model training and validation.

In 2025, the best performance was achieved using a RF model that combined UAV-collected data from the stem elongation, heading, and grain-filling stages with environmental weather data. This model achieved a coefficient of determination (R^2) of 0.39 and a Root Mean Square Error (RMSE) of 482.29, outperforming the linear model (Elastic Net, R^2 = 0.31; RMSE = 515.51).

Overall, results across all three years indicate that UAV-based prediction can serve as a reliable supplemental tool for early-generation selection. While prediction accuracy is moderate, consistent trends suggest that combining multi-stage data and advanced models can improve performance and support barley breeding efforts.



#03

The Paul Johnston Memorial Award: Supporting Future Leaders

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The Paul Johnston Memorial Award was created to perpetuate the memory of Dr Paul Johnston, an eminent barley breeder, astute administrator, devoted disciple of the barley industry and good friend to all, who passed away unexpectedly in 2001. Paul was an enthusiastic supporter of young scientists, and so The Paul Johnston Memorial Award was established to provide opportunities for young researchers under the age of 35. Since 2005 there have been 9 awardees that as a direct consequence of the award, have had the opportunity to present their research findings at conferences in the United States of America, France, Czech Republic, Morocco, Italy, and Latvia. They have also gained invaluable networking experiences by travelling and meeting with other scientists in a wide range of countries including Mexico, Finland, and Germany. Most recipients are still working in agriculture and many are directly or indirectly involved in supporting the barley industry.

#04

Why rate isn't everything: fungicides inside barley

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Seed and foliar applied fungicides are critical for managing barley diseases such as spot form net blotch (*Pyrenophora teres* f. *maculata*). A lot of work has been done in this area during the last 50 years, and yet, their in planta behaviour and interaction with host genotype remain poorly understood. Under the new precision agriculture paradigm and advances in molecular sciences, our group aims to generate the knowledge allowing to transform generic fungicide strategies into farmer-tailored programs that improve return on investment, protect current and future fungicide chemistries, and reduce fungicide resistance development. Using barley as a model, our work studies fungicide dynamics across seed and foliar applications to improve our understanding of uptake, distribution, and efficacy.

Relying on a very sensitive analytical technique, liquid chromatography-high resolution mass spectrometry, we have been measuring fungicide active ingredients inside barley tissue. Here we summarise our results of the last two years of the Fungicide Dynamics project



at the Centre for Crop and Disease Management, Curtin University focusing on the uptake and translocation patterns of a representative group of foliar fungicides and the high-resolution mapping of seed-applied fluxapyroxad. We uncover a complex dynamic that establishes a heterogeneous fungicidal environment within the plant, with spatial and temporal gradients that shape crop protection and selection for pathogen genotypes with differing fungicide resistance/sensitivity ratings.

Fungicide efficacy is not just about the applied rate but relies heavily on the dynamics inside the plant. Together, our findings demonstrate that fungicide efficacy is governed by interactions among chemical properties, plant physiology, and crop traits/genotype. Current work is now geared to understand how these different factors play together aiming to accurately model fungicide behaviour to inform fungicide programs specifically designed for individual paddocks.

#05

An ecosystem of digital tools to solve the FAIR data problem in the pan-genome era

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Barley genetics research in the pan-genomics and big-data era has unprecedented potential to deliver major advances in short timeframes. New genetic, genomic and pan-genomic resources are being published at a rapid pace, with public repositories growing exponentially. However, key challenges remain in how to incorporate these resources effectively – not only in terms of access to specialist bioinformaticians, data scientists and computing infrastructure, but also in knowing how to extract value from the sheer volume and diversity of data available.

The Australian Grains Genebank Strategic Partnership has developed an ecosystem of digital tools designed to address these challenges in novel and practical ways. These include Pretzel, for visualisation and interactive exploration of genetic and genomic data; Brioche, which focuses on solving data interoperability; Genolink, for integrating and working with genebank passport data; and additional tools with complementary capabilities. While each tool was created for a specific purpose, they have been designed to interoperate, enabling users to connect information and functionality across multiple data types.

Although FAIR (Findable, Accessible, Interoperable, Reusable) data principles guided development, the tools are particularly powerful in addressing interoperability, one of the most difficult FAIR components to implement effectively. They enable genotype data to be re-phased onto new reference genomes, integration of datasets from diverse genotyping platforms, comparative analyses across genomes and pan-genomes, and linkage to research and breeder knowledge. Together, these tools lower the barrier to working with large-scale data – supporting tasks ranging from basic data access for



non-bioinformaticians to complex biological queries requiring multi-layered data integration.

This presentation will demonstrate how this digital tool ecosystem has been applied to real-world questions in barley research connected to the Australian Grains Genebank, highlighting its value for accelerating discovery and breeding outcomes.

#06

Towards heat-tolerant barley: Genomic modelling for designing breeding targets and strategies

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Heat stress is a major constraint on Australian barley production causing yield losses of up to 15% annually and up to 30% loss of grower profit through malt to feed downgrading. Heat tolerance is a highly polygenic, quantitative trait controlled by numerous loci of small effects, meaning genetic gain depends on combining the favourable alleles across the genome through haplotype stacking. Since favourable alleles for heat tolerance may be absent or rare in Australian breeding germplasm, we looked into the genetic diversity from a worldwide diversity panel of barley. In previous studies, a panel of 500 worldwide diversity panel was phenotyped across field and glasshouse environments over two years for 18 traits spanning phenology, spikelet fertility, and yield components. Heat stress was imposed at the flowering stage and the grain filling stage. With 15,022 SNPs, we performed genomic prediction modelling across five models: rrBLUP (linear model), random forest, XGBoost (machine learning models), MLP and CNN (deep learning models). Deep learning model MLP achieved the highest prediction accuracies for a majority of the traits, followed by XGBoost and rrBLUP, with the largest gains observed for field evaluated and genetically complex traits like thousand kernel weight and spike weight. Interestingly the SNP effects from MLP and rrBLUP were concordant (Spearman's $\rho = 0.64$), indicating partial overlap in captured genetic signal. Haploblock effects were subsequently derived from rrBLUP marker effects. This method could recover several known development and heat related loci, including *sdw1*, *VRN-H1*, *VRN-H3*, and *DEP1* among the top 50 high effect haploblocks. Also, there were numerous high effect regions without characterised candidate genes. Diversity analyses at these loci revealed that non-Australian germplasm carries higher haplotype diversity and a higher frequency of superior haplotypes than Australian varieties, identifying specific introgression targets and showing potential for improvement. Next steps include in-silico haplotype stacking and optimal parent selection to guide crossing design, with field validation planned as the next stage. This pipeline offers a route to accelerate genetic gain for heat tolerance while reducing the cost, time and resource burden of conventional breeding programs.



#07

Linking AGG Barley Genotypes to Breeding Knowledge Using Pretzel: New Tools for Haplotype-Based Germplasm Selection

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The increasing availability of genomic data for plant genetic resources presents significant opportunities to accelerate research and breeding outcomes in barley. However, for many researchers and breeders, challenges remain in accessing, integrating and interrogating these data – particularly where genotypic data must be interpreted alongside existing research knowledge and genebank information. Pretzel is an established web-based visualisation and exploration tool being developed by the Australian Grains Genebank (AGG) Strategic Partnership, a \$30M joint investment between Agriculture Victoria and the Grains Research and Development Corporation (GRDC). Pretzel was designed to make genotype data generated by the Partnership accessible to non-technical users and to provide a means to connect accession genotypes with research and breeding knowledge. Here, we present recently developed functionality in Pretzel that extends its utility for applied barley research and breeding. First, Pretzel now supports explicit visualisation of null alleles, allowing users to distinguish true biological absence from missing or uncalled data. Second, users can define and apply custom haplotype filters, including haplotypes that incorporate null alleles, to select and refine sets of genotyped AGG accessions. Third, Pretzel has been directly integrated with Genolink – another tool developed by the AGG Strategic Partnership – enabling seamless access to passport and characterisation data for selected accessions within the same workflow. These power of these new features are exemplified using a barley use-case focused on identifying AGG accessions likely to carry the non-Glycosidic Nitrile (non-GN) trait. Building on markers previously associated with non-GN and reported at ABTS 2022, Pretzel is used to search for accessions that carry null alleles across the relevant interval and immediately review associated passport information via Genolink. This example illustrates how Pretzel can be used to connect accessions to prior research and breeding knowledge to support targeted discovery and selection of candidate germplasm. Pretzel can be accessed at <https://agg.plantinformatics.io/>.



#08

Bakery-Genebank: Transforming genebank accessibility through Graph-RAG and natural language

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The Australian Grains Genebank (AGG) Strategic Partnership – a \$30 million joint investment between Agriculture Victoria and the Grains Research and Development Corporation – is transforming the AGG into a bio-digital resource centre through large-scale genetic characterisation of its collection and the development of digital tools to improve data accessibility and utility for industry. For barley, the more than 27,000 plant genetic resources conserved within the AGG have been genetically characterized and made available to industry through an integrated digital tool ecosystem. A key challenge is enabling complex analyses and discovery tasks to be performed on these datasets without requiring advanced technical or bioinformatics expertise. In practice, genebank users may not know what data or resources exist, or how best to interrogate them, highlighting the need for interfaces that allow users to focus on their scientific question rather than the underlying data structure or analysis steps. Modern AI-enabled techniques provide a means to address this challenge.

Here we present *Bakery-Genebank*, an exploration tool that integrates global genebank passport data from Genesys-PGR with genetic distances derived from the genetic characterisation of the AGG collection. The system combines these data within a knowledge graph that captures the high degree of relatedness both among accessions and between genebank collections. Building on this structure, *Bakery-Genebank* employs a Graph Retrieval-Augmented Generation (Graph-RAG) approach, allowing natural-language queries to be translated by a Large Language Model into constrained graph queries that accurately retrieve and contextualise relevant accessions, relationships and genetic similarity information. This approach exploits the relational nature of genebank data to unlock information that is otherwise difficult to access.

Bakery-Genebank transforms how users can query and use the wealth of available genebank information. Tasks that previously required specialist skills – such as identifying genetically similar accessions across collections or navigating linked passport and genotype data – can now be addressed through simple natural-language questions. *Bakery-Genebank* demonstrates how the AGG Strategic Partnership is delivering digital and genomic innovation that enhances the discovery and practical use of conserved barley diversity for breeding and research.



#09

Closing the yield gap: Comparative genomics uncovers candidate grain yield genes in barley

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Barley plays a major role in Australian agriculture and generates significant returns annually. However, its grain yield (GY) potential remains under-realised. Australian barley GY lags the global average and also falls behind leading producers such as Germany and France. Also, since the green revolution, the GY of other cereals such as wheat, rice, and maize has improved massively, but that of barley has not risen nearly as much. GY is a complex, environment-dependent trait shaped by the plant's full life cycle and by component traits such as plant height, days to flowering, grain weight, grain number, tiller number, and many more. Much of the genetic architecture around these traits in barley is unclear or unknown. This study uses a comparative genomics approach to identify candidate genes for GY and contributing traits in barley by leveraging the knowledge of functionally characterised GY related genes in rice, wheat and maize. We assembled a comprehensive database of 1,826 functionally characterised genes for GY and related traits (plant height, tiller number, grain size, grain shape, grain weight, grain number, spike length, spikelet number, kernel rows) from rice (1430 genes), maize (227 genes), wheat (130 genes) and barley (39 genes). Protein sequence similarity was assessed across all twelve pairwise crop combinations, followed by synteny and orthogroup analysis. This yielded 89 high-confidence candidate orthologous genes in barley with evidence coming from two or more crops. Mining for genomic variation in these genes across the barley pangenome revealed complex structural variations (SVs), insertions and deletions (InDels), and copy number variations (CNVs). Key candidate genes include nitrate transporters, aquaporins and Zinc finger and MADS box transcription factors. Further studies are underway to dissect the roles of these genes and their potential for barley GY improvement.



#10

Integrating grain morphometry and protein content to improve early selection for malting quality in barley

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Malting quality is a key target in barley breeding programs, and improving selection efficiency requires a better understanding of the relationships between grain physical traits and malting performance. This study evaluated the association between barley grain physical and morphological traits and malt fine extract, a key indicator of malting quality, to assess their value as early predictors in breeding pipelines.

Seed samples from Preliminary and Advanced Yield Trials of the INIA Uruguay Barley Breeding Program were analyzed over two growing seasons, capturing a wide range of genotypes and environmental conditions. Samples were characterized for thousand-grain weight, grain protein concentration, and grain plumpness (percentage retained above a 2.5 mm screen), as well as morphometric traits including grain width, grain length, length-to-width ratio, perimeter, area, and color. A subset of samples was further evaluated for malting quality using micro-malting.

Results revealed strong genotypic effects for thousand-grain weight, grain plumpness, and morphometric traits, highlighting their potential relevance for selection. The best predictive model for malt fine extract included grain width as a positive predictor, and grain protein concentration and grain length as negative predictors, explaining a substantial proportion of the observed variation. These findings suggest that combining simple high-throughput grain morphometric measurements with protein analysis can support early-generation selection in a malting barley breeding program. This approach provides a practical, scalable, and cost-effective strategy for characterizing lines before resource-intensive malting evaluations, thereby contributing to selection efficiency.



#12

Development and validation of KASP markers for powdery mildew resistance in Korean naked barley using QTL-seq

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Powdery mildew (PM), caused by *Blumeria graminis* f. sp. *hordei*, is a destructive fungal disease affecting barley (*Hordeum vulgare* L.), particularly under warm and humid conditions. Developing resistant cultivars through molecular marker-assisted selection (MAS) represents an eco-friendly and sustainable strategy for disease control. However, validated molecular markers for PM resistance in naked barley remain limited. In this study, quantitative trait locus-sequencing (QTL-seq) was conducted using two independent parental combinations, Nurichal (susceptible) and Jeonju144 (resistant), to identify genomic regions associated with PM resistance in Korean naked barley. A consistent QTL region was detected on chromosome 1H, within which 40 Kompetitive Allele-Specific PCR (KASP) markers were developed based on gene-associated sequence variants. Stepwise validation using an F₂ segregating population (n = 244) identified two markers, NPM32 and NPM43, that showed strong and consistent associations with PM resistance. Among them, NPM43 exhibited complete concordance between genotype and phenotype in the evaluated population, indicating its high diagnostic reliability. The associated sequence variant was located within an uncharacterized gene in the barley reference genome. Validation of the KASP marker NPM43 revealed stable performance and a strong association with PM resistance, highlighting its potential utility for MAS in breeding PM-resistant naked barley. This study provides useful genomic resources for marker-based breeding and supports the development of precision breeding strategies for disease resistance in barley.



#13

CM72 as a novel source of tolerance: is it relevant for Australian Barley Breeding?

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Identifying untapped sources of tolerance is important if we are to diversify Australian germplasm, especially to adapt to climate change. One variety that serves as both a reference for Barley salinity tolerance and a source of QTL discovery is California Marinout 72 (CM72) – a tolerant variety sourced from North America. Despite its well-known status as a tolerant variety, CM72 is not particularly relevant in Australian breeding. Australia is ranked 9th in the world for the percentage of landmass affected by salinity, but contains the most hectares of saline land – for this reason, it is of strategic interest to adopt modern approaches to saline conditions. Within the Australian germplasm, we identified that CM72 is unique and not clustered with other Australian varieties. However, overlapping genotypes have been introduced into the Australian germplasm, most likely from Yagan. Indeed, there are relatively modern varieties like Mundah and Litmus, which share substantial genomic haplotypes through Yagan. The outcome of this is that CM72 is not wholly novel but is still unique among Australian barley germplasm. To identify potential underlying sources of tolerance, we mapped twenty one markers for fifteen distinct QTL traits related to salinity. Of these markers we found two contained rare alleles, which we believe could explain the observed differences in tolerance between CM72 and Gairdner and are shared by fewer than 5% of the 140 varieties sequenced. From these two markers, we confirmed five genes with experimentally validated polymorphisms. These variants were exclusively screened to infer missense, in-frame deletions, early stop, and/or frameshift mutations that may alter gene function. If we are to develop new varieties to overcome the challenges of climate change and localisation, we need to broaden our sources of tolerance, and we believe CM72 could be a source of that adaptation.



#14

Genolink: Seamlessly Connecting Passport and Genotype Data to Enable Discovery of AGG Barley Germplasm

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Despite having access to rich genotypic datasets, the separation of passport and genotype information across different databases creates a significant barrier for genebank users to utilise these genomic resources effectively. In barley, passport data describing accession identity, origin and provenance are available through the *Genesys-PGR* database, while genotype data for genebank collections are distributed across specialised genomic platforms with differing structures, interfaces and update cycles. This fragmentation makes it difficult for users to efficiently locate, access and work with genotype data, often requiring manual data integration or advanced technical skills, and limiting the practical use of large, fully genotyped collections.

Genolink addresses this challenge by providing an intuitive interface that directly links passport data from *Genesys-PGR* with genotype data generated through the genetic characterisation of the complete Australian Grains Genebank (AGG) barley collection of >27,000 accessions. Users can discover accessions using passport-based filters and then seamlessly access the corresponding genotype data within a single, coherent workflow. Passport information is retrieved dynamically from *Genesys-PGR*, ensuring alignment with authoritative, up-to-date records while avoiding data duplication.

Genolink forms part of a broader digital ecosystem of interoperable tools being delivered through the AGG Strategic Partnership that is transforming the AGG into a bio-digital resource centre. Within this ecosystem, *Genolink* provides the foundational link between passport and genotype data, enabling innovative functionality in downstream tools such as *Pretzel*, which connects genebank genotypes to research and breeding knowledge, and *Fairybread*, which supports visual exploration of genetic diversity using passport-based filtering.

By lowering technical barriers and unifying passport-led discovery with direct access to genotype data, *Genolink* enables users to more easily find, access and use genomic information from the AGG, while providing a scalable foundation for seamless integration across international genebanks. It can be freely accessed at <https://genolink.plantinformatics.io/>.



#15

Population genomics of the barley pathogen *Pyrenophora teres f. teres* across Australia using DArTseq

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Net form net blotch (NFNB), caused by the fungal pathogen *Pyrenophora teres f. teres* (Ptt), is one of the most economically damaging foliar diseases of barley production in Australia and globally. The pathogen's capacity to overcome host resistance and adapt to diverse environments underscores the need for a comprehensive understanding of its genetic diversity and population dynamics to support durable disease management.

To address this, 470 Ptt isolates were collected over two consecutive growing seasons (2023 and 2024) from major barley-growing regions across eastern and southern Australia. In 2023, 282 isolates were collected from Grafton (NSW, n=44), Streaky Bay (SA, n=43), Wallup (VIC, n=19), Gnarwarre (VIC, n=112), Wagga Wagga (NSW, n=22), and UniSQ Toowoomba (QLD, n=42). In 2024, an additional 188 isolates were collected from Horsham (VIC, n=29), Field Applied Research (VIC, n=23), Wagga (NSW, n=20), Grafton (NSW, n=18), Hermitage Research Facility, Warwick (QLD, n=36), UniSQ Toowoomba (QLD, n=25), South Australia (n=23), Tummaville (QLD, n=5), Devon Park (QLD, n=1), and Bowenville (QLD, n=3).

Genotyping was performed using Diversity Arrays Technology sequencing (DArTseq). Population structure will be examined using multivariate and model-based approaches, including Principal Component Analysis (PCA), Discriminant Analysis of Principal Components (DAPC), and Bayesian clustering implemented in STRUCTURE. These analyses will enable the assessment of genetic diversity, population differentiation, gene flow, and both spatial and temporal structuring among Ptt populations.

This study will provide insights into the genetic structure and connectivity of Australian Ptt populations, supporting improved disease prediction, resistance breeding, and management strategies.

#16

The effect of split nitrogen fertilization on yield quality and nitrogen use efficiency of spring barley grown in Iceland

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Efficient nitrogen (N) management has become increasingly important in crop cultivation with environmental protection and economic considerations in mind. Split N application is a fertilizer strategy that aligns fertilization timing with plant nutrient demand to maximize nitrogen use efficiency (NUE) and reduce environmental impacts, such as gas emissions and runoff. NUE is relatively low in Icelandic barley cultivation, thus it is



important to optimize N application with the potential to increase yield. Protein crops are not grown in Iceland and increasing protein in barley could help offset protein import dependency. Trials were conducted at two different soil types (high fertility vs low fertility) in Iceland using two spring barley varieties to study the effects of split applications of N (NH_4^+ and NO_3^-) on growth, yield, grain protein content (GPC), and NUE. Treatments included a single application at sowing (drilled in the seeding row), early booting (Zadoks 42), and/or late anthesis (Zadoks ~70) with varying N rates. Split N applications decreased yield and GPC compared to a single application at sowing. Yield was primarily influenced by high N rate at sowing and GPC by grain size, with smaller grains containing higher GPC. Soil type had a stronger effect on yield and grain size than split N fertilization. A single application at sowing had the highest NUE across soil types and varieties, but the 67/16.5/16.5% N split resulted in the highest total N uptake and the lowest unaccounted N. Under wet and cold conditions, splitting N at early booting and/or late anthesis did not improve yield, GPC, and NUE in spring barley cultivation. In conclusion, barley farmers in Iceland are recommended to apply the total N at sowing, with the option to add around 15% at early booting and/or late anthesis.

#17

Using epigenetics to uncover missing sources of disease resistance in barley

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Traditional breeding approaches have faced considerable challenges in developing durable resistance to endemic fungal pathogens including *Pyrenophora teres*. The capacity of *P. teres* populations to evolve through sexual reproduction enables the continual emergence of new virulence profiles, undermining resistance genes deployed in cultivars. This highlights the need to identify and exploit novel sources of resistance within the barley germplasm and to understand the genetic and molecular basis of these traits to support more durable and broad-spectrum resistance.

Beyond genetic variation, epigenetic regulation has emerged as a potentially important contributor to phenotypic diversity and adaptation. Epigenetic mechanisms including DNA methylation, have been proposed to partially explain “missing heritability” in complex traits, where the observed phenotypic variation cannot be fully accounted for by genetic variation alone. While evidence from other cereal crops have demonstrated that epigenetic modifications can influence disease resistance, its role in barley remains largely unexplored, representing a key knowledge gap.

This research aims to address this gap by investigating if DNA methylation states change in response to net blotch infection using a diverse barley coreset. It will identify critical sampling time points and characterise epigenetic responses using novel approaches that improve upon existing methods such as whole genome bisulfite sequencing (WGBS). Building on this, additional work will investigate how minor and major effect epigenetic



alleles (epi-alleles) are inherited together as epigenetic haploblocks (epi-blocks) and estimate their effect. Additionally, a multi-omics framework integrating genomics, phenomics, and epigenomics will be applied to advance the understanding of disease resistance mechanisms. This approach will also uncover previously underexplored sources of variation contributing to “missing heritability” that is inadequately explained by traditional genomic approaches.

#18

Bakery Research Transforming barley research and genebank knowledge through Graph RAG and connected genomic resources

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Advances in genomics have generated unprecedented volumes of research knowledge relevant to barley improvement. However, this information remains fragmented across publications, datasets, online resources and genebank records, limiting its efficient use. While large language models can improve access to literature, their full value for breeding is realised when advanced retrieval methods are tightly integrated with structured datasets and genebank knowledge.

Here, we present Bakery-Research, an AI-powered Graph Retrieval Augmented Generation (Graph-RAG) system that integrates literature-derived knowledge graphs with curated genomic metadata from the Pretzel web visualisation platform and Australian Grains Genebank (AGG) accession passport data. Rather than treating literature search, dataset discovery and germplasm exploration as separate workflows, Bakery-Research unifies them within a single natural language interface that explicitly links published evidence to underlying genomic resources and AGG accessions. The system integrates three tightly connected graph-based knowledge sources: a Literature Graph constructed from research publications; a Metadata Graph capturing genome assemblies, genetic maps, QTL studies, VCF files and datasets available in Pretzel; and AGG accession passport information enriched with genetic distance data.

We demonstrate the utility of Bakery-Research through a case study on barley scald resistance. Twenty-two publications (from 1991-2025) were processed alongside QTL and marker information curated in Pretzel and ingested into the graph. The system enables rapid identification of relevant AGG germplasm and associated genomic regions previously reported to confer scald resistance. Through natural language queries (e.g. “What are the main sources of barley scald resistance?”), users can navigate complex evidence streams and translate literature insights into research and breeding decisions.

By connecting advanced Graph-RAG methods with genomic datasets and AGG genebank knowledge, Bakery-Research shifts AI from a literature summarisation tool to a decision-enabling discovery platform, reducing time from question to data or accession and improving the accessibility and utilisation of genebank resources for barley research and breeding.



#19

Multi-Environment Validation and Genomic Characterization of Wild Barley Alleles for Dry Biomass and Grains per Ear Improvement in Australian Barley

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Domestication has narrowed the genetic base of cultivated barley (*Hordeum vulgare* L.), limiting further yield improvement. Wild barley (*H. vulgare* ssp. *spontaneum*) harbours beneficial alleles for yield-determining traits, yet their deployment in elite backgrounds is often impeded by linkage drag. A previous GRDC project identified two wild barley loci introgressed into Compass: a grains per ear enhancing (GPE) QTL on chromosome 4H (UAB-27 lineage) and a dry biomass promoting QTL on chromosome 3H (UAB-70 lineage). This project aims to validate their effects in advanced backcross near-isogenic lines (NILs) across multiple environments over two years. In 2025, forty-three BC₃F₄ NILs with eight controls were evaluated at Northam (WA), Narrabri (NSW) and Roseworthy (SA). The 4H GPE QTL effect was confirmed across environments: wild allele lines produced significantly more grains per ear than all five commercial controls at Roseworthy (+2.74 grains/ear, $p < 0.001$) and Northam (+1.31 grains/ear, $p < 0.05$). UAB_27_354 and UAB_27_56 exceeded all five controls at Roseworthy (up to +6.9% over Compass), though yield was constrained by later flowering-driven spike loss. UAB_27_56 showed consistently higher GPE across all three sites (+2.1%, +5.4% and +9.8% at Northam, Roseworthy and Narrabri), with a yield advantage of +4.7% and +1.3% above Beast and Compass, respectively at Northam, where UAB_27_205 also yielded 5.89 t/ha (+6.3 to +9.9% above Compass and Beast) in the highest rainfall environment. For the 3H dry biomass QTL, UAB_70_20 produced 1,032 g/m² at Narrabri (+17.3% above Compass, exceeding all five controls), with UAB_70_1057 and UAB_70_685 yielding 5.95 and 5.86 t/ha (+5.8 to +11.0% above Compass and Beast). At Northam, UAB_70_685 yielded 5.67 t/ha (+0.2 to +2.8% above Compass, Beast, Maximus and Cyclops). Wild 3H lines also showed significantly higher GPE at Roseworthy (+2.88 grains/ear, $p < 0.001$) and Narrabri (+2.44 grains/ear, $p < 0.001$), longer spikes ($p < 0.01$) and higher TGW than controls at Roseworthy (+3.35 g, $p < 0.01$). UAB_70_162, classified as Compass allele but still segregating, was the highest-yielding NIL at Narrabri (5.95 t/ha, +7.4% over Compass, +11.0% over Beast) with GPE exceeding all five controls at Roseworthy (+2.8 to +14.5%), a priority for KASP genotyping in 2026. In parallel, whole-genome sequencing of Compass, 8 UAB series lines and 3 BHEB wild donor lines identified 859 diagnostic SNPs through haplotype analysis at the 4H GPE QTL. KASP markers are under development for 10 priority candidate genes at Chr4H:25.2–26.7 Mb, including a stop-gained mutation (4HG0230900) and 12 missense variants (4HG0230770), for fine-mapping and breeder delivery in 2026.



#20

Fairybread: Accelerating germplasm discovery by integrating genetic diversity and passport data in a unified interface

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Effective utilisation of plant genetic resources conserved in genebanks requires the ability to jointly interrogate genomic diversity alongside accession-level passport information. However, common approaches for exploring population structure – typically based on principal component analysis (PCA) of genome-wide marker data – are often disconnected from passport data describing geographic origin, taxonomy and provenance. This separation limits the ability of genebank users, particularly non-specialists, to rapidly identify and compare genetically meaningful germplasm subsets, and often necessitates manual data retrieval, integration and visualisation before meaningful exploration can occur.

The Australian Grains Genebank (AGG) Strategic Partnership is a \$30 million joint investment by the Agriculture Victoria and the Grains Research and Development Corporation (GRDC) that is transforming the AGG into a bio-digital resource centre. As part of this initiative, more than 27,000 barley accessions conserved within the AGG have been genotyped and made accessible through an integrated digital tool ecosystem, including *Genolink* (<https://genolink.plantinformatics.io/>), which links accession-level passport data sourced from *Genesys-PGR* with genotype datasets generated by the Partnership.

Here we present *Fairybread*, an open-source, browser-based visualisation platform that integrates PCA-based representations of genetic diversity within the AGG barley collection with live passport data served via *Genolink*. *Fairybread* provides bidirectional linking between an interactive PCA plot and a dynamically updated passport data table, enabling users to select accessions in genetic space to immediately view associated passport metadata, or to filter accessions by passport fields and visualise the resulting subsets within the genetic diversity landscape. Flexible grouping, colour-coding and automatic binning support clear visualisation at the genebank scale.

By unifying genetic structure and passport information in a single interactive interface, *Fairybread* enables efficient discovery, comparison and utilisation of germplasm for research and crop improvement. *Fairybread* is freely accessible at <https://fairybread.plantinformatics.io>.



Notes



Acknowledgement of Code of Conduct for the 2026 Australian Barley Technical Symposium

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You must not be in the possession of or under the influence of alcohol or illegal drugs while attending Symposium sessions. Alcohol provided by the relevant venue/s may be consumed in a responsible manner at social functions.

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