AUSTRALIAN
BARLEY
TECHNICAL
SYMPOSIUM


Harvesting the Potential of Barley

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ABTS 2024 Abstract Book

SESSION 1: SETTING THE SCENE

A sustainable barley industry: setting the scene.

Stewart Coventry[1], Matthew Tucker[2], Kenton Porker[3], Trevor Perryman[4]
[1]Australian Grain Technologies, [2]The University of Adelaide,
[3]CSIRO (Agriculture & Food), [4]Vice Chair SEABAC

Meeting the sustainability goals for the barley industry is a multifaceted challenge that requires consideration of many stages along the production chain. We must strive to better connect these stages, with an overarching view to enhance industry outcomes. Up to the farm gate, the prevailing focus is directed towards increasing or at least maintaining productivity with more efficient use of inputs and minimal environmental impact. With predicted increased climate variability, current farming methods face significant pressure to remain profitable and sustainable amidst rising input costs, increasing pressure to achieve social license, labour access, and scalability issues. While barley is an important part of the farming system, any new genetics or technology needs to be supported through research agronomy and practical recommendations to the grower, to ensure they can be successfully integrated into profitable and sustainable operations. Development of new “sustainable genetics” requires more research capacity that is fully integrated with the production chain to embrace both on farm and post-farm gate processing efficiency. Growers and advisors are best placed to implement this knowledge within a farming system, to produce sustainable and profitable barley crops that add value to the system while maintaining the quality required by the end user.

Can this vision be realised for barley? If so, a sustainable funding stream for barley research is needed to build the capacity through early research careers to ensure ongoing genetic improvements and farming system integration. Post farm gate, sustainability encompasses various aspects, from grain accumulation and trade logistics to the feed, malting and brewing supply chain. Most stakeholders in the Australian barley supply chain have set a range of sustainability targets to improve operational standards that minimise cost, preserve resources, and meet the expectations of their State, investment, consumer, and staffing partners. Targets include energy use, CO_2 emissions, water and resource use efficiency, gender equality, safety and community engagement. The diversity in targets and stakeholders is challenging to address holistically. In developed economies, sustainability has become a social and moral license to operate, even in the absence of legislative mandates.

It seems clear that we must strive to address these challenges better as an industry, connecting the stages from research to delivery to ensure barley production is a profitable and sustainable feature of current and future farming systems.

SESSION 2: MALTING AND BREWING

KEYNOTE: Overview of ABInBev's global activities with a particular focus on sustainability in the brewing industry

Dr. Nikki Else, ABInBev

AB InBev, established in 2008, is the world's largest beer company, headquartered in Leuven, Belgium, and operating in over 50 countries. The company owns more than 500 brands, including Budweiser, Stella Artois, and Corona, and generates annual revenues exceeding $50 billion. With a global workforce of approximately 170,000 employees, AB InBev's extensive operations highlight its sizeable market presence.

Agriculture is fundamental to AB InBev's supply chain, as the company relies on high-quality inputs such as barley, hops, corn, and rice. Sustainable agriculture practices are crucial for maintaining production quality and meeting global demand. AB InBev is committed to supporting sustainable farming and collaborates with thousands of farmers worldwide. These partnerships provide farmers with resources and training to adopt sustainable practices, ensuring long-term supply chain stability and reducing environmental impact.

This presentation will explore AB InBev's global operations, emphasizing the importance of agriculture and the company's dedication to sustainability. Through innovative practices and strategic partnerships, AB InBev aims to be part of a sustainable brewing industry, championing a resilient and environmentally responsible future for its supply chain.

Total protein content or protein composition: which is best for selecting malting grade barley?

Prof. Glen Fox, University of California

Johan Kjeldahl developed his method to measure total protein content in malt and beer in the 1880s at the Carlsberg Research Laboratory in Denmark. But we moved well beyond protein content and can measure grain, malt and beer composition through methods like electrophoresis and proteomics. Yet industry still uses total protein content to trade grain, and plan malting schedules. From a quality perspective, the endosperm storage proteins (hordeins) have a significant role in influencing endosperm texture and hydration rates. Higher portions of hordein can result in harder grain texture and lower modifications. The range in endosperm storage protein content can vary based on pre-planting nitrogen fertilizer and environmental growing conditions during grain filling. The amount of storage protein was quantified, with this alcohol-soluble protein fraction between 45 and 70% of total protein content. Micromalting data showed barleys with a higher portion of endosperm storage proteins to total protein had lower levels of malt modifications. A near infrared (NIR) calibration was developed to predict endosperm protein content. The NIR calibration was used to screen commercial barleys for endosperm protein content and adjust malting schedules to demonstrate possible steps to improve malting efficiency. Barley samples with the same total protein content but lower endosperm storage protein required shorter steep times to get to the same level of modification. The application of using endosperm protein content compared to total grain protein content will be discussed.

Why Is Malting Barley So Complicated?

John Stuart, GrainCorp Operations Ltd

John Stuart[1], Carolina Garcia[2]
[1]Quality Assurance, GrainCorp Operations Ltd, Australia

A malting barley's commercial essence is varietal purity and its ability to germinate. Yet these two can sometimes cause an abundance of questions, frustration, uncertainty, or praise … of a grain type that is… well, somewhat complicated. But is it really? This paper addresses myths, facts, the science, and the tools we have to reduce its complexity. From 1) understanding germinative shelf-life predictions, to 2) the ZoomAgri technology for varietal purity alongside visual analysis, electrophoresis, and DNA tests we have used or continue to use. Although malting barley was locked away under statutory regulation for a long time, some of these tools used may still not be familiar with many today. (Did you know for example, that looking for long vs short rachilla hairs on barley kernels under magnification is only 1 of at least 15 different areas that can be looked at to help with identification)? What are those 15? And as for germination, our bulk handling system only gets that one chance to assess malting barley at harvest time correctly under time pressure when trucks are lined up at sample stands. How can we do this in a fast, efficient manner to make sure barley is assessed correctly into the right stacks; varietal pure and with minimal chance of early germination loss. And what about optimal malt results needed for repeat business in order to uphold Australia's quality reputation. This paper explores all of the above.

Keywords: Germination, Falling Number, Moisture, ZoomAgri, Rachilla.

Malt Quality Requirements for the Japanese Beer Market

Kenichuiro Haruna, Asahi Beer Malt Co Ltd.

Kenichuiro Haruna[1]
[1] Asahi Beer Malt co., LTD.

The Japanese beer market has been greatly influenced by tax regulations classifying three different beer categories primarily based on malt content, Beer ,Happoshu, and Under happoshu. These categories have differing tax rates, leading to variations in retail prices, significantly impacting consumer purchasing intention and affecting the product strategies as well as the supply and demand of malt. Additionally, the market of functional beers is expanding due to the growing needs of health-conscious products. Quality of malt becomes crucial in the production of functional beers. This paper will explain the beer categories, the history of their introduction, discuss the consumption trends and the impact on malt usage and importantly quality requirements. I would also like to mention other alcoholic beverages such as whiskey and shochu.
Moreover, I discuss the quality requirements that are considered necessary for future barley and malt supply stability.

Understanding and accounting for variation when phenotyping for malting quality in barley breeding
Silvina Baraibar, InterGrain

S. Baraibar[1,2], A.B. Smith[3], H. Oakey[4], B.R. Cullis[3], H. Fenton[1], D.E. Mather[4], D.B. Moody[1]
[1]InterGrain Pty Ltd, Perth, Australia
[2]School of Agriculture, Food and Wine, The University of Adelaide, Australia
[3]Mixed Models and Experimental Design Lab, University of Wollongong, Australia
[4]Adelaide Medical School, The University of Adelaide, Australia

In barley breeding, selection to maintain and improve malting quality is important, but is challenging due to the cost, time, and complexity of phenotyping for quality traits. These factors determine that malting quality is only assessed in advanced stages, and over few genotypes per year. Genomic selection offers an alternative strategy for selection for malting quality. High prediction accuracy using GS is dependent on accurately measuring malting quality parameters in training populations. When phenotyping for quality traits, each stage - from production of grain in the field through to analysis of wort - is subject to its own sources of variation. Despite this, in contrast to what has taken place in selection for field traits, there has been relatively little attention paid to understanding and addressing sources of variation for malting quality traits. Using results from a uniformity trial, we will show the extent to which malting quality results can vary even within a batch of genetically identical micro-malted samples. We will also present results from multi-phase analysis of a set of 622 barley lines, considering sources of variation from the field to the laboratory. Based on the outcomes of that analysis, we will discuss the value of applying advanced statistical methods in experimental design and data analysis for the evaluation of malting quality, especially when results are to be used to train predictive models for genomic selection.

Keywords: Malting quality, breeding, selection accuracy, multi-phase analysis, genomic predictions.

Craft beer industry in Japan – its market trend and technical issues
Dr Kensuke Ogushi, National Research Institute of Brewing

K. Ogushi, H. Fukuda
National Research Institute of Brewing, Japan

The very first beer brewed by Japanese owned breweries was launched in the 1870's. Beer is now one of the most popular alcohol beverages in Japan, with annual production more than 2 million kL.
Although the beer market has been an oligopoly for many years, six craft breweries were established in 1994 following a partial revision of Liquor Tax Law. Craft beers have gradually attracted Japanese customers because of their characteristic flavours thanks to their technical improvement and changes in market trends. We estimate nearly 800 breweries are operating to serve various styles of craft beers now.
Malt purchased by Japanese craft brewers is, on one hand, thought to be mostly imported. Their demand seems to be more focused on stable fermentation and typical colour derived from special malt than detailed specifications on which major brewing companies place importance. On the other hand, some domestic maltsters including whisky distillers are dedicated in malting domestic barley to make full-domestic craft beers as a marketing edge. The National Research Institute of Brewing (NRIB) has made contribution to the craft beer industry in Japan by means of state-of-the-art researches and offering both training courses and quality evaluation of their products. In this paper, the market trend and technical issues that lie in the craft beer industry in Japan is discussed and technical support of NRIB to the industry is described.

Keywords: craft beer, Liquor Tax Law, malt, technical support

Beer, bugs, and sustainability, Pt2

Dr Megan Edwards, Integral Nutrition (S) Pty Ltd

M.V. Edwards[1]
[1]Consultant Nutritionist, Integral Nutrition (S) Pte Ltd, Singapore

Barley occupies a pivotal position in the Australian grains industry, accounting for around 22% of total annual grain production. This is second only to wheat, which further underscores its importance to the Australian economy and agricultural prosperity.

AEGIC, with the support of industry, is committed to increasing value in the Australian barley industry by diversifying markets, identifying new opportunities for Australian barley, and providing technical support and education to customers on the benefits of Australian barley and how to optimise its value. This helps drive demand and reinforces the favourable positioning of Australian barley in global markets.

The ability of Australian barley to positively influence the sustainability of the protein sector continues to grow as the black soldier fly industry evolves to meet the demands of the livestock, aquaculture and petfood sectors. The farming of black soldier fly larvae (BSFL) presents a sustainable and economically attractive opportunity to upcycle the organic waste generated by the brewing industry to generate high quality protein, fats and fertiliser.

Brewers' by-products provide a useful source of fibre, protein and fermentation metabolites that have a favourable water holding capacity which supports ideal growing conditions of BSFL. Larvae can utilise protein or starch to support their energy metabolism for growth (generating protein) and convert either to fat. Brewers' by-products can be further enhanced as the ideal substrate for the cultivation of black soldier fly larvae by additional fermentation, through inoculation with yeast, bacteria and fungi. This additional enrichment provides an opportunity to enhance the sustainability of BSFL cultivation through decreased development time, increased conversion efficiency and increased biomass, at the same time as reducing green house gas emissions and ammonia.

This presentation will provide an update on the evolution of the black soldier fly industry and highlight the ever-growing role barley and brewers' by-products are playing in the sustainability of commercial agriculture.

Keywords: Black soldier fly larvae, brewers' grains, sustainability, livestock nutrition

SESSION 3: BARLEY TRADE

Export markets for quality barley & sustaining a competitive advantage

Mary Raynes, AEGIC

M.C Raynes
[1]Economic & Market Insights Team, Australian Export Grains Innovation Centre, Australia,

Key words: malting barley, market diversity, innovation, malt,

Market diversity ensures the Australian barley industry's resilience and sustainability.

Barley occupies a pivotal position in the Australian grains industry accounting for around twenty-two percent of the total annual grain production second only to wheat further underscoring its importance to the Australian economy and agricultural prosperity.

Diversified domestic and export markets are a catalyst for growth, innovation, and prosperity. requiring concerted effort from all industry stakeholders, including breeders, growers, researchers, trade, marketers, policymakers, and industry leaders. By fostering a culture of collaboration and forward-thinking investment, Australia can position and continue to position itself as a global leader in producing high quality and highly desirable barley, while simultaneously safeguarding the resilience and sustainability for the future.

To optimize opportunities for Australian malting barley while mitigating risks, AEGIC in full collaboration with the Australian grains industry orchestrated a series of technical education events across a diverse array of countries throughout South America, South East and North Asia, and Africa, aimed at stimulating interest and fostering demand. This presentation of findings from these interactions presents up to date market insights from these diverse global markets.

AEGIC with the support of industry remains committed to bolstering investments in the Australian grains industry and sustaining efforts to promote market diversity, thereby driving demand and reinforcing the favourable positioning of Australian malting barley in global markets.

Australia's capacity to harness its geographic diversity will be paramount in safeguarding the industry's sustainability beyond 2030.

SESSION 4: NEW INSIGHTS IN MALTING

Advancing sustainable malting practices: Aquaporins as potential breeding targets for improved water uptake during controlled germination of barley (Hordeum vulgare L.)

Clare O'Lone, Edith Cowan University

C.E. O'Lone[1,4], A. Juhász[1], M. Nye-Wood[1], D. Moody[3], H. Dunn[1,2], J-P. Ral[4] M.L. Colgrave[1,5]*
[1]Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science, Edith Cowan University, School of Science, Joondalup, WA, Australia
[2]Pilot Malting Australia, Edith Cowan University, School of Science, Joondalup, WA, Australia
[3]InterGrain Pty Ltd, Bibra Lake, WA, Australia
[4]Commonwealth Scientific and Industrial Research Organization, Agriculture and Food, Black Mountain, ACT, Australia
[5]Commonwealth Scientific and Industrial Research Organization, Agriculture and Food, St Lucia, QLD, Australia

The conversion of raw barley (*Hordeum vulgare* L.) to malt requires a process of controlled germination, where the grain is submerged in water to raise the moisture content to above 40%. The transmembrane proteins, aquaporins, influence water uptake during the initial stage of controlled germination, yet little is known of their involvement in malting. With the current focus on sustainability, understanding the mechanisms of water uptake and usage during the initial stages of malting has become vital in improving efficient malting practices. In this study, we used quantitative proteomics analysis of two malting barley genotypes, demonstrating differing water-uptake phenotypes in the initial stages of malting. Our study quantified 19 transmembrane proteins from nine families, including seven distinct aquaporin isoforms, including the plasma intrinsic proteins (PIPs): PIP1;1, PIP2;1, PIP2;4, and tonoplast intrinsic proteins (TIPs): TIP1;1, TIP2;3, TIP3;1 and TIP3;2. Our findings suggest that the presence of TIP1;1, TIP3;1 and TIP3;2 in the mature barley grain proteome is essential for facilitating water uptake, influencing cell turgor and the formation of large central lytic vacuoles aiding storage reserve hydrolysis and endosperm modification efficiency. This study proposes that TIP3s mediate water uptake in malting barley grain, offering potential breeding targets for improving sustainable malting practices.

Keywords: aquaporins, water uptake, barley, malting, sustainability

Identification and characterisation of the molecular drivers of malting performance in Hordeum vulgare

Bryan Hau, The University of Western Australia

B. Hau[1], O. Duncan[1], A.H. Millar[1]
[1]ARC Centre of Excellence in Plant Energy Biology, School of Molecular Sciences, The University of Western Australia, Australia

Hordeum vulgare (barley) is used by the malting industry to make malt for food and brewing applications. In this process, the outer aleurone tissue of barley seed releases enzymes that convert its carbohydrates and storage proteins in the starchy endosperm into sugars and free amino nitrogen. In the brewing process, yeast will use these ingredients as nutrients and for alcohol fermentation. The three stages of malting are: steeping, germination, and kilning. A good malt must meet standards such as malt extractability, fermentability, Kolbach Index, and wort viscosity. We have begun an investigation into the biological activities throughout the malting process to determine molecular drivers of specific malting parameters to help in the optimisation of the malting process. To achieve this, we are identifying proteins in each stage of the malting process using mass spectrometry-based proteomics. Determining proteins and enzymes that are differentially abundant throughout the various stages of malting will provide insight into which proteins are important at each stage of the malting process. To supplement this data, various additional experiments measuring protein turnover, protease activity, and tissue-specificity of these processes are planned. These experiments allow for the investigation of which proteins are being synthesised or degraded at high rates, which proteases are most active in the process of storage protein modification, and where enzymes are being synthesised and active. Overall, this work will allow for the short-listing of proteins that are highly related to malt performance and aid in the development of optimal malting barley cultivars and/or altered methods for malt production.

Keywords: Barley, Malting, Proteomics, Protein turnover, Mass spectrometry

SESSION 5: BARLEY AGRONOMY & FARMING SYSTEMS

KEYNOTE: Improving barley adaptation and yield: challenging/supporting assumptions

Prof. Gustavo Slafer, University of Lleida

Gustavo A. Slafer[1,2], Roxana Savin[1]
[1]Department of Agricultural and Forest Sciences and Engineering, University of Lleida – AGROTECNIO-CERCA Center, Av. Rovira Roure 191, 25198 Lleida, Spain
[2]ICREA, Catalonian Institution for Research and Advanced Studies, Barcelona, Spain

Improving barley adaptation and yield of barley has always been, and will continue to be, a central aim of breeding and management. Understanding the crop-physiological basis of barley yield and adaptation is crucial for identifying the traits and genes responsible for yield. A comprehensive consideration of all physiological bases of yield determination would be impractical in the framework of this presentation. Instead, I will focus on a few case studies, noting that much of our knowledge is extrapolated from wheat, which is physiologically similar but not identical to barley. I will evaluate assumptions and ideas from the literature, specifically that (i) barley is more resilient than wheat in stressful environments, (ii) yield components responsible for yield responses differ between 2- and 6-rowed barleys, and (iii) photoperiod-insensitivity (recessive allele *ppd-H1*) has pleiotropic effects on increasing yield. Regarding (i), many claims about barley's higher resilience to stress are unsupported or based on circumstantial evidence. We will discuss the assumption from a re-analysis of experiments from high-standard journals where both cereals were grown side-by-side under field conditions. Regarding (ii), it is generally accepted that 2- and 6-rowed barleys differ in the relevance of the number of grains per spike and spike number, and that the response of 6-rowed barley to environmental and genetic factors mainly involves changes in spike fertility, while 2-rowed barley responds through the number of spikes. We will discuss the assumption from a re-analysis of experiments from high-standard journals where these two types of barley were grown side-by-side under field conditions. Regarding (iii), we tested whether the *PPD-H1* gene, critical for barley adaptation by modifying the crop cycle in response to photoperiod, does actually have a true pleiotropic effect or it simply affects yield as an indirect consequence of changing flowering time.

Keywords: yield components, photoperiod sensitivity, wheat

Redefining flowering times of barley and wheat for future climates

Dr Felicity Harris, Charles Sturt University

Felicity Harris[1]**,** Nectarios Costadopoulos[1], Kenton Porker[2], Pengcheng Hu[3], James Hunt[4], Corinne Celestina[4], Victor Sadras[5,6,7], Rick Graham[8], Blakely Paynter[9], Hammad Khan[9,10], Kelly Angel[11], Matthew Tucker[6], Julian Taylor[6], Max Moldovan[6], Bangyou Zheng[12], Julianne Lilley[3]
[1] Gulbali Institute, School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Wagga Wagga, NSW
[2] CSIRO Agriculture and Food, Urrbrae, SA
[3] CSIRO Agriculture and Food, Canberra, NSW
[4] School of Agriculture, Food and Ecosystem Sciences, University of Melbourne, Melbourne, VIC
[5] South Australia Research and Development Institute, Urrbrae, SA
[6] School of Agriculture, Food and Wine, Faculty of Sciences, Engineering and Technology, The University of Adelaide, Adelaide SA
[7] College of Science and Engineering, Flinders University, Bedford Park, SA
[8] New South Wales Department of Primary Industries, Wagga Wagga, NSW
[9] Department of Primary Industries and Regional Development, Northam, WA
[10] College of Science, Health, Engineering and Education, Murdoch University, Perth, WA

[11]Birchip Cropping Group, Birchip, VIC
[12] CSIRO Agriculture and Food, St Lucia, QLD

The significance of an optimal flowering period to align the critical period for yield development with favourable seasonal conditions has been established. This ensures the combined risk of frost, heat and drought is minimised, therefore maximising grain yield potential for a given location. Whilst this concept provides achievable targets for growers to mitigate risk of abiotic stresses, they remain a major limitation to the advancement of yields of barley and wheat in Australian rainfed cropping systems. A comparative analysis was conducted across 31 diverse locations in NSW, VIC, SA, and WA spanning from 2010–2022. Annual rainfall varied from 117–978 mm and we reported grain yields ranging from 0.5 to 11.8 t/ha across these sites. Grain yield was collected in conjunction with flowering time (phenology) to investigate the relationship between yield and flowering dates in locations where frost, heat and drought are major sources of variation in crop yield, and a significant concern for growers. We consider the importance of integrating genotype (G) × environment (E) × management (M) synergies to rethink our understanding of flowering time in barley and wheat to better enable growers to adapt to climate variability and achieve yield potential.

Keywords: phenology, optimal flowering period, barley, wheat, yield

Developing frost and heat stress damage functions for barley in APSIM Next Generation

Dr Pengcheng Hu, CSIRO

P. Hu[1], B. Leske[2], J. Kirkegaard[1], J. Whish[1], J. Hunt[3], K. Porker[1], B. Zheng[1], J. Lilley[1]
[1]Agriculture and Food, CSIRO, Australia
[2]Department of Primary Industries and Regional Development, Western Australia
[3]School of Agriculture, Food and Ecosystem Sciences, The University of Melbourne, Australia

Barley must flower during its optimal flowering period to maximize grain yield while minimizing the yield reduction induced by frost and heat stresses in a given environment. The optimal flowering period can be identified by using a crop modeling approach, which requires crop models to accurately quantify the yield loss caused by frost and heat events during the sensitive period. In this study, we conceptualized the damage functions by accounting for the potential percentage yield reductions in response to daily minimum temperature (frost stress) and daily maximum temperature (heat stress) as well as sensitivity at different growth stages. These functions were integrated into APSIM Next Generation, and the parameters of the functions were optimized/calibrated using field-measured grain yields of different barley cultivars under contrasting environments, which might experience frost and/or heat stresses during the growing season. These optimized functions will be validated using an independent dataset comprising barley experiments from diverse environments. The primary results indicated that for the calibration dataset, the performance of yield simulations was improved with the optimized damage functions applied ($nRMSE = 17.2\%$) compared to the simulations without the functions applied ($nRMSE = 31.0\%$ $n = 56$). The improved damage functions will be incorporated into APSIM Next Generation and used with agricultural consultants and grain growers to facilitate improved cultivar and sowing date recommendations, to help mitigate climate risk by optimizing flowering and avoiding stress during the critical period of yield formation.

Keywords: frost, heat, yield reduction, APSIM

Yield determinants of spring barley in Western Australian growing environment

Dr Hammad Khan, Department of Primary Industries & Regional Development

H. A. Khan[1,2], H. Shirdelmoghanloo[1], K. Reeves[3], B. Paynter[1,2]
[1]Department of Primary Industries and Regional Development, Northam 6401 WA, Australia
[2]Western Crop Genetics Alliance, College of Science, Health, Engineering and Education, Murdoch University, Perth 6000 WA, Australia
[3]Department of Primary Industries and Regional Development, Perth 6000 WA, Australia

Barley is an important cereal crop in Western Australia; however, yield improvements have been slow over the past decade. A thorough assessment of the contributing factors is essential to enhance yield potential. This study investigated yield formation mechanisms and explored the source-sink balance to unravel the determinants of yield in spring barley. We evaluated eight commercial spring barley varieties (Banks, Beast, Fathom, Laperouse, Maximus CL, RGT Planet, Rosalind, and Vlamingh) in Northam, Western Australia, in 2021 and 2022. The assessments comprised a range of developmental, physiological, and agronomic traits. Also, the source-sink balance was manipulated using canopy shading, spike shading, defoliation, and de-graining techniques. Varieties differed significantly for grain yield ($p = 0.002$), with RGT Planet and Fathom showing the highest (5.3 t/ha) and lowest (4.6 t/ha) yield, respectively. Varieties differed in radiation use efficiency by approximately 20% and showed a contrasting response during the vegetative and reproductive phases. The potential spikelet number spike^{-1} showed a weak relationship with the final grain number spike^{-1} ($p = 0.019$, $R^2 = 0.33$). Notably, grain yield was significantly associated with grain weight ($p < 0.001$, $R^2 = 0.56$) and biomass ($p = 0.002$, $R^2 = 0.50$). Spike length and dry weight were identified as the critical factors for grain yield in barley. As expected, shading and defoliation treatments reduced grain weight by up to 13%, while de-graining increased grain size by up to 7%. Shading of the canopy or spikes resulted in a greater grain weight reduction than defoliation. Varieties varied in their response to the source-sink manipulations. Barley varieties achieved yield through a combination of strategies, with no single component primarily responsible for yield formation. While barley exhibits sink limitations, source limitations may co-occur with sink limitations depending on the season.

Keywords: Barley, radiation use efficiency, yield determinants, source-sink balance.

Increase in Australian barley grain yield aligns to modification in root allocation within the soil profile

Dr Mariano Cossani, SARDI

C. Mariano Cossani [1,2,3], J. Palta [4], and Victor O. Sadras [1,2,3]
[1]. Crop Science, SARDI -South Australian Research and Development Institute, Australia
[2]. School of Agriculture, Food and Wine. The University of Adelaide, Waite Campus
[3]. College of Science and Engineering, Flinders University, Australia
[4]. UWA Institute of Agriculture & School of Agriculture and Environment
The University of Western Australia, Australia

Improved varieties and better agronomy have increased yield of barley in Australia's farms at 21.0 ± 2.3 kg ha^{-1} yr^{-1} between 1961 and 2019. Selection pressure for yield and agronomic adaptation can inadvertently change crop traits. In this work we report how barley breeders have unintentionally modified root distribution and its implications for barley physiology. Six cultivars released between 1942 and 2013 (Prior A, Proctor, Clipper, Schooner, Sloop and Compass) were grown in 1-m deep rhizo-boxes to examine the growth and distribution of the root system. Barley root system was modified significantly in its distribution down the soil profile. Older varieties like Prior A and Proctor allocated an equivalent to 28-38% of their upper roots (top 40 cm) to roots in deeper layers of the soil profile, modern varieties allocated only 16%. Oppositely, the new varieties do have higher proportion of total root length in deeper layers than in the top ones. The proportion of roots allocated to

deeper layers correlated negatively relate with mass of root per shoot. In summary, modern barley lines allocated less root carbon in deeper profile than older ones but explored higher proportion of soil. This indicates a shift in allocating carbon. Our findings indicate that new barley lines do produce higher yields with less C invested per shoot than old ones. This suggests associated changes in water and nutrient use and use efficiency which may imply updates in crop management.

The performance of barley in the farming systems of southern NSW

Dr John Kirkegaard, CSIRO Canberra

J.A. Kirkegaard[1], M. Dunn[2], X. Li[1], T. Swan[1], J. Whish[1], M. Barary[2]
[1]Agriculture and Food, CSIRO, Australia
[2]Agricultural Research Institute, NSWDPI, Australia

The performance of barley, and of cropping sequences involving barley have been evaluated over 6 years (2018 to 2023) at three farming system experimental sites in southern NSW with metrics related to productivity, profitability, risk and aspects of sustainability monitored. Barley was nominated by growers as part of the typical Baseline system (barley-wheat-canola) and this system was compared with other more Intense (canola-wheat) and Diverse (legume-wheat-canola) sequences. Agronomy for all individual crops was optimised in the experiments. Overall, in individual years when compared, barley had higher yields than wheat when similar soil N was available at sowing, and similar yields to wheat despite higher pre-sowing N for wheat. These differences arose because wheat followed canola in the sequences, while barley followed wheat. Average barley yields of 4.2 t/ha, 6.2 t/ha and 6.0 t/ha at Condobolin, Urana and Wagga outperformed wheat at 4.1 t/ha, 4.9 t/ha and 5.1 t/ha at the same sites. Barley performed well in the very dry years (2018, 19) and the wet years (2020, 21, 22). Increased yield was accompanied by higher average gross margins for barley of $818/ha, $1085/ha and $1084/ha compared with $752, $881 and $746 for wheat at the three sites. The differences related mostly to higher grain income as variable costs were similar. The Baseline systems (barley-wheat-canola) ranked 3rd of 9, 5th of 10 and 1st of 16 systems in terms of average annual gross margin at Condobolin ($780/ha), Urana ($820/ha) and Wagga Wagga ($900/ha) respectively. At Condobolin the Baseline system was outperformed by the Intense system (canola-wheat, $826/ha), and at Urana by a range of Diverse systems involving legumes (fababean, chickpea, lentil, $890-$996/ha). In general, the Diverse systems had lower risk (profit:cost ratio), greater return on investment and lower levels of weed and diseases than the Baseline, especially crown rot which proliferated where barley and wheat hosts grew sequentially.

Keywords: crop sequence, farming system, rotation, diversity, profit, risk

Striking the balance: defining the relationship between management, grain yield, and grain quality in barley

Blakely Paynter, Department of Primary Industries and Regional Development

Blakely Paynter[1], Rick Graham[2], Hammad Khan[1], Kelly Angel[3]
[1]Department of Primary Industries and Regional Development, Northam 6401 WA, Australia
[2]New South Wales Department of Primary Industries, Wagga Wagga NSW
[3]Birchip Cropping Group, Birchip, VIC

Barley varieties differ in how they respond to management inputs such as nitrogen application and plant density. This paper revisits a national agronomy study (2010-2016) funded by the GRDC, as reported by Paynter *et al*. at the 18th ABTS held in Hobart, Tasmania, in 2017. It examines the balance between management and variety and their influence on grain yield and quality. What explains most of the variation in yield and grain quality traits – genotype (G), environment (E), or management (M)? Trials from SA have been excluded from the re-analysis, while data gaps were bridged in the initial analysis. The dataset contains 48 trials, 23 from the west (WA) and 25 from the east (NSW and Vic).

A further analysis of the data examines if there is a critical protein concentration at which grain yield is optimised. Unpublished research from WA hypotheses shows a low probability of grain yield being maximised if the grain has a protein concentration below 10.5%. Is this true nationally, and if so, what factors influence the critical protein concentration?

This desktop study is funded through the GRDC project UCS2301-002RTX, “Synthesis of data to optimise yield potential of barley in Australian farming systems”. The study will highlight the importance of different agronomic factors on the performance of barley and opportunities to optimise production. What is the receival trade-off when chasing grain yield in malt barley?

Keywords: Barley, GxExM, grain yield, grain quality, grain protein.

Evaluating barley hay yield and quality to determine its potential role as a dual purpose crop

Mick Faulkner, Agrilink Agricultural Consultants

Mick Faulkner
Agrilink Agricultural Consultants, South Australia

Dual purpose cereals can be cut for hay or harvested grain. There is a large database of grain yield and quality of barley, which are also the primary consideration of plant breeding programs. Fodder plays an important role in nutrition of animal industries and particularly for ruminants. Fodder provides critical soluble and structural carbohydrates for rumen function and nutrient supply for growth and milk production. Hay is a preferred fodder source in many diets, including dairy cows, and the value of Australian fodder is recognised domestically and in key international markets. However, awns present in barley and wheat hay can result in irritation and reduced intake.

Barley, wheat and oat grain and hay attributes can be evaluated in field research. CNCPS near infrared spectroscopy can identify specific hay quality parameters from replicated field experiments, and paired plots can be used for grain yield and quality.

This research shows that barley is a potential dual purpose cereal and that awnless barley has desirable hay characteristics and adequate grain production.

Where have all the barley hectares gone?

Dr Andrew Barr, Farmer and Grain Industry Consultant

Andrew Barr, Farmer and Plant Breeding Consultant, Pinery, South Australia

The area sown to barley in SA exceeded 1.2 m ha four times in the 10 years leading up to 2008. Since then, it has declined to just 800,000 ha for much of the last 15 years. In the lower north, many growers have switched from rotations like wheat-barley-break crop (lentils/peas/canola) to simply wheat – lentils or in the higher rainfall areas, wheat-canola. Why is this ? In this paper, a range of possible causes will be examined. This will include progress in breeding and agronomy compared to competitor crops; challenges in weed and disease control, in head loss and lodging; probability of achieving premium grades; changes in the relative value of crops; local demand and market access

SESSION 6: BARLEY BREEDING

KEYNOTE: Advancing Brewing Science

Adj. Prof. Birgitte Skadhauge, Carlsberg Research Laboratory

At a global scale, food security is challenged by crop productivity stagnations that are aggravated by man-made climate change. This climate emergency calls for collective efforts to lower carbon footprint across the brewing industry, including a boost in sustainable crop production through accelerated genome engineering technologies and their immediate application. The breeding efforts at the Carlsberg Research Laboratory combine decades of expertise in basic and applied barley, hops and yeast research with the latest advances in brewing science to provide novel, sustainable brews with advanced quality. Combining traditional breeding technologies with state-of-the-art genomics and FIND-IT™, our fast and high-throughput trait isolation pipeline, we have now radically shortened the development time of our brewing ingredients allowing us to break new ground in the premiumization of our products. Further, this accelerated breeding approach can easily be applied in advancing the design of other crops, both in developing and matured markets around the globe, and thus help securing a sustainable supply of food and agricultural products.

Barley breeding contribution to barley-malt-beer industry sustainability

Dominique Vequaud, SECOBRA Recherches

D. VEQUAUD[1]; A BOX[2]; G FOUQUIN[3]
[1]GLOBAL SPRING BARLEY BREEDING, SECOBRA Recherches, France
[2]SPRING BARLEY BREEDING, SECOBRA Recherches, Australia
[3]CEO SECOBRA Recherches, France

Created in 1902 by French brewers and maltsters, the SECOBRA Association's primary mission was to develop and improve the supply of quality barley to the industry.
Now a specialist in barley in Europe, SECOBRA Research also develops barley varieties for the United Kingdom, Australia, the Black Sea region and also Argentina.
We continue to support and expand our network of breeding sites located at the heart of the main grain producing areas in the world and this reflects our commitment to agriculture and industry.
Today, SECOBRA Research intends to support the next coming challenge, such as lowering the carbon footprint of the barley-malt-beer industry from the field to the final factory, by exploring and implementing new genetic diversity in its breeding pipeline.

Keywords: Yield, GxE, Disease resistances, Processability.

Fast and Focused: Breeding Better Barley for the Developing World under Climate Change

Dr Miguel Sanchez-Garcia, ICARDA

M. Sanchez-Garcia[1], S. Kemal[1], K. Al-Sham'aa[2], Z. Kehel[1], M. Baum[1]
[1]Biodiversity and Crop Improvement, ICARDA, Morocco
[2] Biodiversity and Crop Improvement, ICARDA, Egypt

Climate Change is making barley cultivation in the Developing World evermore challenging. More prevalent and erratic drought and heat waves and new pest and diseases are forcing the Global Barley Breeding Program of the CGIAR (GBBP) and its partners to accelerate the development of new better adapted cultivars.

For this aim, new technologies like Speed Breeding coupled with selection for traits such as diseases and others have been applied since 2021. The results obtained in the last 2 years show a higher proportion of resistant genotypes among the cohort advanced under disease-assisted Speed Breeding as compared to the field advanced ones. In addition, no significant increase in the proportion of undesired plant types related to plant height, lodging or phenology was observed. Other traits such as number of spikes or grains per spike have also been studied.

Breeding programs often face the dilemma at early testing stages between increasing testing locations or entries tested. This is even more problematic for international breeding programs, generally targeting wider ranges environments. To tackle this problem, the GBBP has since 2021 implemented a genomic-assisted sparse multi-location approach. This way, thousands of entries are tested under multi-location trials having only a fraction of the genotypes present in all environments. Using a selected set of 192SNP, the program has been able to predict traits of interest of thousands of non-planted lines across 8 locations in 4 countries representing relevant growing areas. The results of the 3 years of implementations showed that medium to high cross-validation accuracies (up to r>0.6 for grain yield) have been achieved. In addition to identifying the best adapted genotypes to a wide range of environments, this strategy has also allowed to recover the information of entries planted in trials lost ot extreme climatic events, a recurrent problem under Climate Change.

Keywords: ICARDA, CGIAR, Speed Breeding, Genomic Predictions, Developing World, Genotype by Environment, drought, heat, diseases, insect pests, breeding

Grain yield improvements of barley varieties released in Australia between 1968 and 2022

Dr Paul Telfer, Australian Grain Technologies

P. Telfer[1], C. Ingvordsen[1], J. Walter[1], L. Mazur[1], S. Coventry[1]
[1]Australian Grain Technologies, Australia

Barley production begun in Australia with the first plantings in 1788. By the 1960’s each state had a barley breeding programme funded through government and industry, and later funded by the GRDC (Grain Research & Development Corporation). Since 2013 these programmes have been located within private companies. Today, annual barley production has increased to a 10-year average of 11.3 million tonnes with Australian exports representing up to 30% of the international traded malt barley, and 20% of the barley traded for feed.

In the current study 38 barley varieties released from 1968 to 2022, were grown in eight environments through 2022 and 2023 to explore the historical development in grain yield. The lowest yielding varieties were Clipper, Stirling and Schooner released in 1968, 1981 and 1983 respectively, yielding 3.97-4.05 T/ha on average over the eight environments. The highest yielding variety was Cyclops (5.63 T/ha) released in 2021. The grain yield of conventional (non-herbicide tolerant) barley varieties has grown on average by 0.64% annually from 1968 to 2022, and by 1.02% annually from 2000-2022. Demonstrating significant genetic gain for grain yield with increased productivity for growers, particularly in recent decades.

The advancement in new breeding technologies creates a positive outlook for further improvements in the genetic gain of barley grain yield. The expanded use of genetic markers, genomic sequencing technologies, whole genome selection, advanced statistical methods, as well as tools to rapidly create new genetic variation such as gene editing, are among the tools available to breeders. The application of these tools will enable breeders to deliver varieties with improved grain yield, adaptation to diverse growing environments, disease resistance and tolerance, and improved malt quality, thus providing improved sustainability for growers and industry alike, into the future.

Are breeding programs delivering value for money for the Australian Barley Industry?

David Moody, InterGrain

D. B. Moody[1], C. Lisle[2], S. Baraibar[3]
[1]Senior Barley Breeder, InterGrain Pty Ltd, Australia
[2]Biometrician, InterGrain Pty Ltd, Australia
[3]PhD student/Barley Breeder, InterGrain Pty Ltd, Australia

Australian barley breeding programs are funded through a combination of grower paid End Point Royalties (EPRs) and private company investments. Demonstration of the value of breeding programs is required to maintain support for these investments. Breeding programs can be assessed historically, in terms of genetic gain achieved for various traits, or in terms of investment, which can be used as an indicator of likely future genetic gains. Analysis of historic datasets assessing the rate of genetic gain for grain yield, indicate substantial, genetically driven, yield gains in most production environments. Novel agronomic traits, in particular herbicide tolerance, have also been rapidly adopted by growers. Improvements in disease resistance have been mixed, reflecting the continual evolution of new pathotypes for several of the most important diseases, and a grower focus on yield improvements rather than an interest in high levels of disease resistance. The impact of the new breeding environment on disease resistance breeding will be discussed, including an assessment of obstacles to be overcome in moving forward. Malting quality data indicates the general trends in quality improvements are favourable. Selection for further quality improvements is complicated by the diversity of export markets, ranging from cost and processing efficiency driven markets to those that are driven by customer demand for traceability, sustainability, and lower carbon emissions. Future investments in barley breeding are intimately linked to support of the EPR system. To date, the system has encouraged increased investment, but the reasons for some decline in EPR compliance must be addressed.

Keywords: End Point Royalties, Genetic Gain, Yield, Disease Resistance, Malting Quality.

RAGT creating solutions to barley growers needs

David Leah, RAGT

David Leah1, Meixue Zhou 2
1. RAGT, Shepparton Victoria Australia
2. Tasmanian Institute of Agriculture, University of Tasmania, Launceston Tasmania

Waterlogging is a major abiotic stress that is limiting the expansion of barley in the high rainfall cropping zones of Australia. Barley production losses in Australia due to waterlogging is estimated to be over $20 million per annum (Zhuo et al., 2020). In 2019 RAGT as a solutions-based breeder saw the potential to incorporate the trait into the globally dominant variety RGT Planet PBR in conjunction with University of Tasmania. The partnership set out to develop the world first barley variety that has waterlogging tolerance. In 2025 Australia barley growers will be the first in the world to have access to RGT Atlantis PBR the first barley variety in the world to have waterlogging Tolerance.

Improve genetic gain through the understanding of genotype x environment interactions in spring barley

Maëva Bicard, UniLasalle

M. Bicard[1,2], M.P. Faucon[1], C. Dockter[3], D. Vequaud[4], P. Pin[4], C. Elmerich[1], B. Lange[1]
[1]AGHYLE (SFR Condorcet FR CNRS 3417), Institut Polytechnique UniLaSalle, France
[2]Brasseries Kronenbourg SAS, France
[3]Department of Row Materials, Carlsberg Research Laboratory, Denmark
[4]SECOBRA Recherches, France

Genetic gain is often limited by genotype x environment interactions (GEI) observed in multi-environment trials (METs). Understand and consider these interactions in breeding programs is crucial to develop high-yielding and stable genotypes under a changing climate. Our study aimed to (i) highlight the main eco-climatic factors (EFs) – climatic variables calculated between two growth stages – driving GEI for yield and (ii) define spring barley European Target Population of Environments (TPE) for crop adaptation. Using data from METs comprising 112 genotypes across 121 environments, 91 EFs were calculated at each environment using the CERES-Barley model. Partial Least Squares (PLS) regressions were run to identify the main GEI-drivers. An environmental classification was performed based on the GEI-drivers across 1,450 environments, including tested and untested locations within the European area of production. Elevated temperatures during stem elongation, solar radiation and drought during grain filling shown a high contribution to GEI. Thermal amplitude around anthesis also emerged as influent. From this, three main environment types (ETs) were identified and contrasted in terms of temperatures during vegetative growth, solar radiation intensity, and water stress during grain filling. The ETs varied largely in time and space across the TPE. Our results revealed the need for specific adaptation in regions like North of the United Kingdom and for broad adaptation in Denmark or France. Performances of the existing germplasm across the TPE showed contrasted responses that can be directly used for product positioning. This work will help breeders to cope with GEI for spring barley breeding, especially by weighing trials using MET-TPE alignment, defining more efficient trial networks and designing ideotypes for specific or broad adaptation. Further advancements need to integrate genetic sensitivity to GEI-drivers and environment types in genomics to improve yield prediction accuracy.

Keywords: Multi-Environmental Trials, Crop modeling, Climatic factors, Envirotyping, Target Population of Environments

Using Drones to Predict the Hidden Half of Barley

Dr Samir Alahmad, The University of Queensland

Samir Alahmad[1], Daniel Smith[1], Christina Katsikis[1], Sarah Van Der Meer[1], Lotus Meijer, Karine Chenu[2], Scott Chapman[1, 2], Andries B. Potgieter[3], Anton Wasson[4], Silvina Baraibar[5], Jayfred Godoy[5], David Moody[5], Hannah Robinson[1 5*], Lee T. Hickey[1*]
[1]Centre for Crop Science, Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland (UQ), Brisbane, QLD, Australia
[2] Centre for Crop Science, QAAFI, UQ, Toowoomba, QLD, Australia
[3]Centre for Crop Science, QAAFI, UQ, Gatton, QLD, Australia
[4] Commonwealth Scientific and Industrial Research Organisation, Canberra, ACT, Australia
[5] InterGrain Pty Ltd, Perth, WA 6163, Australia

Barley production in Australia is highly variable and dependant on seasonal rainfall. Research suggests that crop varieties with optimised root systems can improve water acquisition with minimal metabolic cost, which could improve yield stability across seasons. However, selection for root traits in breeding programs is currently not feasible due to the labour-intensive and destructive nature of the current phenotyping approaches. Most importantly, there is a lack of adequate and reliable methods for measuring and predicting root traits at scale in

field conditions and a lack of understanding of the genetic architecture of these traits. In this study, we evaluated 395 Australian barley commercial cultivars, historic and modern breeding lines in a field experiment. Integrated root and shoot phenotyping was performed to 1) characterise root distribution using the 'core break' method and shoot biomass for a diverse subset of 20 genotypes, 2) explore the potential of using drone imagery as a tool to predict canopy and root traits, and 3) gain new insights into the relationships between above- and below-ground development. Data captured from root coring and above-ground biomass partitioning of the 20 genotypes revealed significant variation in root distribution and canopy development. A machine learning approach used the trait dataset along with drone imagery to predict the root and canopy traits for the panel of 395 genotypes. To validate the utility of this prediction model, we employed haplotype-based (local Genomic Estimated Breeding Value; LGEBV) mapping to determine genetic drivers for predicted root distribution and biomass accumulation. Novel haplotypes for both above- and below-ground traits were identified, and haplotypes conferring shared and independent genetic controls were investigated. Our findings highlight the potential to exploit drone imagery and machine learning approaches to facilitate phenotyping and selection for root and canopy traits associated with enhanced yield potential or yield stability.
Keywords: root architecture, drought, drone phenotyping, genomics

Fast-Tracking Access to New Plant Genetic Resources through the Australian Grains Genebank Strategic Partnership

Dr Sally Norton, Australian Grains Genebank, Agriculture Victoria

S. Norton[2], G. Keeble-Gagnere[1], J. Tibbits[1], M. Hayden[1]
[1] Department of Energy, Environment and Climate Action (DEECA), Agriculture Victoria, Australia
[2] Australian Grains Genebank, DEECA, Agriculture Victoria, Australia

The Australian Grains Genebank (AGG) is the national centre for plant genetic resources (PGRs) for grain crops. It is custodian to one of the largest and most diverse collections of grain temperate and tropical crop species globally including cultivated, landrace and wild relative species. The AGG manages its germplasm in accordance with Australia’s obligation under the International Treaty on Plant Genetic Resources for Food and Agriculture and has the mandate to acquire, conserve, maintain and distribute PGRs to plant breeders and researchers to underpin the development of more resilient and productive grain crop varieties for the benefit of the Australian grains industry.

The AGG Strategic Partnership between the Victorian State Government and Grains Research and Development Corporation (GRDC) aims to unlock the genetic potential of plant genetic resources for the benefit of Australian grain growers. To enable more effective, efficient and cost sustainable management and use of its PGR collection, the AGG Strategic Partnership has implemented a new Acquisition policy which will fast-track access and increase the utility of newly deposited germplasm. The policy integrates genomic and passport data to ensure only the most valuable PGRs are acquired, conserved, maintained and made accessible to genebank users to facilitate and accelerate the development of climate resilient, profitable grain crops.

Here we describe the new Policy and explore how it will facilitate widespread access to PGRs for crop improvement and the benefits that will accrue to industry from these changes.

Keywords: Genebank, policy, plant genetic resources

Investigating Australian barley breeding population to identify haplotypes associated with leaf rust resistance

Madhav Pandit, The University of Queensland

Madhav Pandit[1], Sambasivam Periyannan[1,3], Yasmine Lam[1], David Moody[2], Silvina Baraibar[2], Lee Hickey[1], Hannah Robinsons[1,2], & Samir Alahmad[1*]
[1]Centre for Crop Science, Queensland Alliance for Agriculture and Food Innovation (QAAFI),
The University of Queensland (UQ), Brisbane, QLD, Australia
[2]InterGrain Pty Ltd, Perth, WA, Australia
[3]Centre for Crop Health, School of Agriculture and Environmental Science, University of Southern Queensland, Toowoomba, QLD, Australia

Barley leaf rust (BLR) is one of the major diseases contributing to significant yield losses each year in Australia. A continual pipeline and strategy for the deployment of novel and stable sources of genetic resistance is vital for its sustainable management. Exploring genotype by environment (GxE) interactions serves as an important first step toward the development of durable resistance. Further, haplotype-based mapping approaches are emerging as preferred methods for identifying genetic variants associated with traits like BLR resistance. In this study, we explored BLR response of over 16,000 Australian barley breeding lines from InterGrain's commercial breeding program across 10 different environments. A multi-environment trial analysis fitting a factor analytic variance structure to the GxE interaction term under linear mixed model framework was undertaken to assess the level of GxE. Considerable cross-over and scale GxE interaction was observed across environments with genetic correlations ranging from 0.40 to 0.99. The environments were grouped into three interaction classes (iClasses), based on the rotated factor loadings, where crossover GxE was minimal. The Best Linear Unbiased Estimates (BLUEs) for each iClass were used in downstream local GEBV-based haplotype mapping to explore genetic drivers for resistance in the absence of cross-over GxE. Haplotypes, both unique and common to environmental clusters were identified, suggesting the presence of environmentally independent and stable sources of BLR resistance within Australian breeding populations. Furthermore, previously reported all-stage resistance (ASR) and adult plant resistance (APR) genes, such as *Rph20*, were also detected. Finally, an *in-silico* haplotype stacking approach was explored to assess the utility of identified resistance haplotypes in the presence or absence of the major APR gene, *Rph20*. Here, we present the largest study to date exploring haplotypes for BLR resistance and their interaction with the environment and outline breeding prospects to develop Australian barley cultivars with durable leaf rust resistance.

Keywords: Barley, leaf rust resistance, GxE interaction, haplotype mapping

SESSION 7: BIOTIC STRESS TOLERANCE

Exotic incursion of the barley leaf rust pathogen Puccinia hordei carries insensitivity to DMI fungicides

Dr Mumta Chhetri, The University of Sydney

Mumta Chhetri[1], Ding Yi[1], and Robert F. Park[1]

[1] School of Life and Environmental Sciences, Plant Breeding Institute, The University of Sydney, Cobbitty, NSW, Australia.

Since the early 1980s, fungicide use in Australian broadacre farming has significantly affected fungal crop pathogens, leading to the emergence of isolates resistant to many chemicals. Fungicide insensitivity has been extensively observed in various pathogens, including those causing *septoria tritici* blotch, wheat powdery mildew, barley powdery mildew, net form of net blotch, and blackleg in canola. Fortunately, cases of fungicide insensitivity in rust pathogens are much less common, with reports from Brazil indicating a decline in the efficacy of DMIs against the Asian soybean rust pathogen.

Over 800 rust isolates were evaluated for fungicide sensitivity in 2020 using seedling-based assays developed for wheat (P. graminis f. sp. tritici, P. striiformis f. sp. tritici, P. triticina), barley (P. hordei) and oat (P. graminis f. sp. avenae and P. coronata f. sp. avenae) which were collected from across Australia. It clearly indicated resistance to several demethylation inhibitors (DMIs) fungicides in P. hordei, establishing the first clear documentation of a cereal rust pathogen acquiring the ability to circumvent agrochemical control strategies. Additionally, investigation of standard historical rust isolates from our collection revealed that this insensitivity occurs within a clonal lineage of pathotypes that originated from an exotic incursion into Western Australia in 2001. All isolates in this lineage, including the original 2001 isolate, had significant fungicide insensitivity, surpassing recommended high-field treatment rates.

Further testing of samples collected in 2021 and 2022 revealed insensitivity to seven DMIs and one Aza-naphthalenes fungicide. Interestingly, only three fungicides with combined mode of action, namely DMI + quinone outside Inhibitors (QoI) fungicides, DMI + succinate dehydrogenase inhibitors (SDHI) demonstrated efficacy in controlling the insensitive pathotype at recommended high field application rate.

Considering the widespread application of fungicides in broadacre farming internationally, their impact reaches far beyond national borders. The adaptability of fungal diseases to both fungicides and genetic resistance poses a global threat, extending beyond the confines of the Australian barley industry. Vigilant, long-term, monitoring of fungicide insensitivity of rust pathogens globally is crucial for early detection and response to ensure sustainable management practices.

Resistance to Australian foliar pathogens in ICARDA barley breeding germplasm

Dr Laura Ziems, The University of Sydney

L. A. Ziems[1], M. Sanchez-Garcia[2], A. Amri[2], D. Singh[1], H. Wallwork[3], T. Garrard[3], G. J. Platz[4], L. Snyman[4], M. S. McLean[5], M. J. Dieters[6]

[1] The University of Sydney, Plant Breeding Institute, Cobbitty, NSW 2570, Australia
[2] International Centre for the Agriculture Research in the Dry Areas (ICARDA), Rabat, Morocco
[3]South Australian Research and Development Institute, Crop Pathology, Urrbrae, SA 5064, Australia
[4]Department of Agriculture and Fisheries, Hermitage Research Facility, Warwick, QLD 4370, Australia
[5]Agriculture Victoria, Natimuk Road, Horsham, Vic, 3401, Australia
[6]The University of Queensland, School of Agriculture and Food Sciences, St Lucia, QLD 4072, Australia

Resistances for multiple foliar diseases were observed in barley breeding lines and landraces imported from ICARDA (International Centre for Agricultural Research in the Dry Areas), Morocco to Australia through the years 2014-19 as part of the CAIGE (CIMMYT Australia ICARDA Germplasm Evaluation) project. The imported materials were screened for their response to seven significant foliar diseases: leaf rust (LR), net form of net blotch (NFNB), powdery mildew (PM), scald, spot blotch (SB), spot form of net blotch (SFNB) and stem rust (SR) nationally. The investment in this germplasm resulted in an extensive collection of adult plant field disease responses from 83 field screens and DArT-seq genotyping information (90,214 markers) for 846 lines. This is a powerful resource to identify genomic regions controlling pleiotropic resistance. Genome wide association mapping was conducted, and 21 putative quantitative trait loci (QTL) were identified across the 7 barley chromosomes. Nine lines were identified to carry 8 of the QTL, these individuals averaged a moderately resistant disease response across the 7 foliar pathogens. QTL of the strongest effect, located on 3H and 5H, were associated with multiple diseases. Co-location of a QTL for resistance to SR and NFNB was observed on chromosome 5H with a proximal neighbouring region for scald and a distal neighbouring region for PM. A known leaf rust resistance gene *Rph9/12* is located within this 5H region suggesting a non-pathogen specific plant defence enriched region. Resistance regions identified in this study are targets for marker assisted selection and lines carrying multiple resistance regions can be recommend as parental breeding lines. This work shows the benefits of collaboration and supports efforts to breed for more durable resistance in breeding programs. Further research is required to determine if these are novel QTL, and to validate linked markers.

Keywords: GWAS, breeding for resistance, germplasm exchange, genetic resource

Pathogenic variation of Pyrenophora teres f. teres in Australia since 2020

Dr Xuechen Zhang, Queensland Department of Agriculture and Fisheries

Xuechen Zhang[1], Judy McIlroy[1], Peter Thompson [1] Lisle Snyman[1]
[1] Queensland Department of Agriculture and Fisheries, Hermitage Research Facility, Warwick Yangan Rd, Warwick QLD 4370

Net form net blotch (NFNB), caused by *Pyrenophora teres* f. *teres* (*Ptt*), can cause severe yield losses ranging from 10% to 40% in a very susceptible barley cultivar 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 source 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, 90 isolates of *Ptt* were collected from six different states across Australia since 2020. Virulence of these isolates was examined using 30 different barley genotypes at seedling stage. Hierarchical cluster analysis was used to evaluate *Ptt* isolates and barley genotypes. Barley genotypes were clustered into two different groups (relatively resistant and susceptible). *Ptt* isolates were clustered into three distinct groups with three main isolates (NB50, NB73 and NB85) in Queensland representing each group. The composition of groups was distinct in each state in Australia. It is likely that regional evolution of *Ptt* population resulted from cultivation of regionally adapted barley varieties. Results in this study suggested the most effective sources of resistance in Australia. This study also provided essential information for barley breeding programs to develop resistance against NFNB based on the *Ptt* pathogen virulence in different parts of Australia.

Keywords: barley, net form net blotch, pathotype, virulence

Stacking multi-disease resistance haplotypes from a collection of Eastern European barley accessions sourced from the Australian Grains GeneBank

Dr Peter Dracatos, La Trobe University

P.M Dracatos[1,2], Md. Arifuzzaman[2,3], H. Dadu[4], M. McLean[4], B. Ovendon[5], T. Garrard[6], L. Snyman[7]
L. Hickey[8], E. Dinglasan[8]

[1]Department of Animal, Plant and Soil Sciences, La Trobe University, Australia
[2]Plant Breeding Institute, Faculty of Science, The University of Sydney, Cobbitty, NSW 2570, Australia
[3]Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur 5200, Bangladesh
[4]Department of Energy, Environment and Climate Action (DEECA) Horsham, Vic. 3401, Australia.
[5]New South Wales Department of Primary Industries, Wagga Wagga, NSW, Australia
[6]South Australian Research and Development Institute, Adelaide, SA 5064, Australia
[7]Department of Agriculture and Fisheries, Hermitage Research Facility, Warwick, QLD 4370, Australia
[8]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Queensland, Australia

Breeding for the myriad of tolerances, desirable quality traits and yield to enhance our elite barley varieties is challenging especially under Australian environmental conditions. With the aim of simplifying the number of disease resistance breeding targets this study explored the potential of identifying multiple disease resistance (MDR) haplotypes within a largely underutilised gene pool from Eastern Europe (EEBs). The 320 EEBs were phenotyped across national and international field disease nurseries and controlled greenhouse environments (n = 42 traits) spanning three nectrotrophic (Net and Spot form of Net Blotch and Scald) and six biotrophic (leaf rust, stripe rust, stem rust, crown rust, barley grass yellow rust and powdery mildew) diseases. Using high-throughput genotypic data from the 40K XT SNP chip, LD was first calculated and haplotype blocks were defined. Trait variances were estimated for each LD block to highlight genomic regions that are important for disease resistance. This was done based on local genomic estimated breeding values (local GEBVs) of haplotypes associated with resistance to one or more of the 42 disease resistance traits. Generating haplotype-based GEBVs subsequently permitted the development of a disease haplotype catalogue for the EEBs. Pleiotrophic MDR haploblocks were identified in the following categories: 1/ Across both necrotrophic and biotrophic diseases, 2/ Specific to biotrophic disease isolates 3/ Race-specific across both necrotrophic and biotrophic diseases. From 40 specific haplotypes investigated, 14 were isolate specific, whereas 10 haploblocks were pleiotropic conferring resistance to five or more pathogen isolates spanning over more than two different diseases. The most important (MDR) haploblocks were identified on chromosomes 3H, 5H and 7H including a recently reported susceptibility haplotype (3H) that was significant across all diseases traits. The identified haploblock catalogue will be important for introducing novel MDR into Australian barley and also facilitate meaningful haplotype comparisons to determine the haploblocks that already present.

Keywords: Multiple disease resistance, biotic stress, haplotype, biotrophic, necroptrophic

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Development of an international host differential set for spot form net blotch in barley

Dr Ramaharinathreddy Dadu, Agriculture Victoria

Ramaharinathreddy Dadu[1]**,** Tara Garrard[2], Lisle Snyman[3], Sanjiv Gupta[4,5], Ben Ovenden[6], Timothy Friesen[7], Jalli Marja[8], Kelly Turkington[9], Bakonyi József[10], Mark Mclean[1,11]

[1]Grains Innovation Park, Agriculture Victoria, Horsham, VIC, Australia
[2]South Australian Research and Development Institute (SARDI), Adelaide, SA, Australia
[3]Queensland Department of Agriculture and Fisheries (QDAF), Warwick, QLD, Australia

[4]Department of Primary Industries and Regional Development (DPIRD), South Perth, WA, Australia
[5]Western Crop Genetics Alliance, College of Science, Health, Engineering and Education, Murdoch University, Murdoch, WA, Australia
[6]Department of Primary Industries, Wagga Wagga, NSW, Australia
[7]Cereal Crops Research Unit, Edward T. Schaffer Agricultural Research Center, USDA-ARS, Fargo, ND, USA
[8]Natural Resources Institute Finland (Luke), Tietotie 4, Jokioinen, Finland
[9]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Lacombe, Alberta, Canada
[10]Plant Protection Institute, HUN-REN Centre for Agricultural Research, Budapest, Hungary
[11]Project Platypus, Stawell, VIC, Australia

Host differential sets are essential for monitoring the pathotypes in pathogen populations and identification of new virulences of importance to barley production. This study was aimed to develop comprehensive international host diversity set for spot form net blotch (SFNB), which is one of the major foliar diseases affecting barley production in Australia and worldwide. To create an updated international host differential set for SFNB, 43 genotypes including previous host differential sets plus barley germplasm with novel resistance to SFNB were sourced and extensively tested during 2021-22. Testing was done at seedling (in glasshouse) and adult stages (in field), at multiple locations in Australia and internationally. Barley genotypes were sown in replicates and inoculated with locally available virulent pathotypes either on infected stubble (crop residue) or spore suspensions of pure isolates.

Analysis of the resistance responses of the barley genotypes identified different virulence profiles in the SFNB populations within Australia and internationally, confirming diversity in the pathogen populations. Twenty-five barley genotypes including differentials, resistant and susceptible controls were subsequently identified which represented known resistances for SFNB and few other resistance sources that are presumed to be absent in the current commercial cultivars. Genotypes TR03189, Keel, Fathom, Esperance Orge 289 and MXB.468 showed resistance to all isolates both in Australia and internationally, confirming that these resistance sources are still effective, and breeders can continue to access these sources for SFNB resistance. Rest of the genotypes showed differential response to the SFNB populations and demonstrated variable gene structure for SFNB resistance. Overall, 18 genotypes were excluded from future differential set testing on the basis that they showed similar reactions and likely share same resistance genes with other genotypes. The updated differential set will be useful for breeders and pathologists to identify new virulences and novel resistance sources for SFNB.

Keywords: Barley, Spot form net blotch, host differential set, pathotype variation, genetic resistance

Achieving durable resistance to Net Form Net Blotch in barley via gene pyramiding

Dr Xuan Hoan Dinh, Curtin University

X. H. Dinh[1]*, J. Lawrence[1], A. Gilmore[1], N. D'Souza[1], S. Ellwood[1]
[1]Centre for Crop Disease Management, Curtin University, Australia

Barley Net Form Net Blotch (NFNB), caused by *Pyrenophora teres* f. *teres* (*Ptt*), is one of the most destructive barley diseases that reduce both grain yield and quality. Different approaches have been used to control this disease and deploying resistance genes is considered the most effective and environmentally friendly method. However, only a few major QTLs conferring resistance to NFNB have been characterized so far, and such singly deployed genes are usually easily overcome in the field. By using doubled haploid populations derived from the cross between Ethiopian barley lines by Baudin (highly susceptible to NFNB), we detected multiple QTLs that are mapped on different chromosomes, and which confer resistance to NFNB at different growth stages. The phenotypic data using F_1, F_2, and F_3 populations illustrated that these barley lines carry recessive resistance genes at the associated loci. We are interested in combining QTLs on chromosomes 1H, 3H, and 6H of Eth210, Eth69, and Eth175, with the percentage of variance explained (PVE) values being 7.4, 26.5, and 74.4%, respectively. PCR-based markers flanking these QTLs were developed to delimit each QTL of interest within a 1 cM interval. These

will be used to consolidate the three QTLs in an elite barley cultivar via the combination of conventional crossing and developing double-haploid lines. Such an accumulation will help to achieve a strong and durable resistance to NFNB.

Keywords: durable resistance, net form net blotch, gene pyramiding, QTLs

Using AI to rapidly develop disease resistant barley

Dr Eric Dinglasan, The University of Queensland

Eric G. Dinglasan[1], Dilani Jambuthenne Gamaralalage[1], Dan Liu[1], Lisle Snyman[2], Tara Garrard[3],
Hari Dadu[4], Sally Norton[5], Kerrie Forrest[6], Kai P. Voss-Fels[1,7], Lee Hickey[1], Ben Hayes[1]
[1]Queensland Alliance for Agriculture and Food Innovation (QAAFI),
The University of Queensland, St. Lucia, QLD, Australia
[2]Queensland Department of Agriculture and Fisheries (QDAF),
Hermitage Research Facility, Warwick, QLD, Australia
[3]South Australian Research and Development Institute (SARDI),
Primary Industries and Regions SA, Adelaide, SA, Australia
[4]Grains Innovation Park, Agriculture Victoria (AgVic), Department of Energy, Environment and Climate Action (DEECA),
Horsham, VIC, Australia
[5]Australian Grains Genebank (AGG), AgVic, DEECA,
Horsham, VIC, Australia
[6]AgriBio, AgVic, DEECA, Bundoora, VIC, Australia
[1,7]Hochschule Geisenheim University, Department of Plant Breeding,
Geisenheim, Germany

A significant challenge for the Australian barley industry is increasing durable resistance against key fungal diseases including net form and spot form of net blotch, and leaf scald. This is because most high-yielding and good-quality Australian varieties are susceptible. Exotic germplasm serves as a rich source of untapped resistance for introgression into elite backgrounds. However, novel resistances are often hidden in many accessions, making them underutilised. Furthermore, introgression from unadapted donors to elite germplasm is slow and challenging, often involves few resistance factors. The challenges becomes identifying a group of parents, that when combined, will optimise the configuration of stacks of desirable alleles. To address this problem, we propose a new approach that uses artificial intelligence (AI), to solve highly combinatorial problems, coupled with genomic predictions and speed breeding. Linking with broader GRDC programs and in partnership with state pathologists from QDAF, SARDI, and AgVic, our new breeding framework can be applied effectively for barley resistance breeding.

We assembled a barley population representing global diversity sourced from AGG and elite Australian cultivars (n = 3800) and genotyped using 40K XT SNP chip. Combining 14 phenotypic screening data for all the three diseases across Queensland, South Australia, and Victoria in 2020–2023, outputs that barley breeders could benefit from this project include: (1) haplotype catalogue of novel form of resistance, (2) AI-guided framework to select the optimum parent combination for crossing, and (3) newly developed barley populations (n = 2000) with stacks of resistance haploblocks. From these outcomes, for the next phase of the project, we will now transform the haplotype catalogue into an online and public resource to benefit broader community. To deliver the outputs to breeders, we formed a breeders panel and will conduct field testing of the newly developed lines to validate their resistance and influence on yield.

Keywords: Multiple disease resistance, exotic germplasm, resistance catalogue, haplotype stacking, genetic algorit

SESSION 8: ABIOTIC STRESS TOLERANCE

KEYNOTE: The good, the bad, and the ugly: hunting for novel diversity in wild barley

Dr Anna Backhaus, ICARDA

A. E. Backhaus[1], M. Sanchez-Garcia[1], R. P. S. Verma[1], Z. Kehel[1]
1: ICARDA, Rabat, Morocco

The genebank of ICARDA holds the 2nd largest collection of Barley (*Hordeum*) species, storing over thirty-two thousand accessions. Thus, the great opportunity and challenge for pre-breeding lies in the effective identification of useful material and the rapid introgression of novel alleles. While the use of landraces (the Good) is relatively easy, wild Barley (*H. vulgare spontaneum*; The Bad) bears many more challenges, and introgressions from the secondary genepool (*H. Bulbosum L*; The Ugly) are bordering the impossible.

For landraces, a suite of tools that allow for trait-targeted pre-breeding have been developed. The use of FIGS allows for the creation of sub-sets with an increased probability of harbouring useful genes for any trait (Mackay and Street, 2004). Subsequently, the phenotypic evaluation of these sub-sets and crossing of the best landraces can be streamlined to release new pre-breeding lines to breeders within three years. The use of *Spontaneum* is more complex due to the transfer of undesirable traits, such as brittle rachis and lodging. However, *Spontaneum* has been shown to harbour greater genetic diversity than landraces and is a valuable pool of novel alleles for targeted traits, such as drought and salinity tolerance. Most challenging is the utilization of wild relatives, which cannot be evaluated before crossing nor selected via FIGS. Crosses with *Bulbosum* are difficult and have been mainly achieved in the 80s by Pickering (Wendler et al., 2015). By testing the *Bulbosum* derived accessions from Pickering in multi-location field trials across Morocco we discovered that certain introgressions improve performance under drought, heat, and low input soil conditions.

To tackle the future challenges of ever more extreme environmental stresses and novel biotic diseases, we must improve our current methods for identification and use of crop wild relatives. At ICARDA, we are expanding our ability to make wide crosses, incorporate novel breeding tools, and use the available diversity of the CWANA region to accelerate pre-breeding.

Unravelling root growth responses to salt stress in barley

Dr Megan Shelden, The University of Adelaide

M.C. Shelden[1], C. Brien[2], D. Mather[1]
[1]School of Agriculture, Food and Wine, The University of Adelaide, Australia
[2]The Plant Accelerator, The University of Adelaide, Australia

Drought and salinity are major causes of crop yield losses in agriculture significantly impacting on sustainability. Soil salinization is increasing due to the impacts of climate change, reducing the area of arable land for crop production. Plants can alter their root system architecture to acquire nutrients and water for growth and respond to hostile soil environments. Saline soils result in a reduction in primary root growth impacting significantly on growth and yield. The ability of crops to maintain root growth in saline soils is an adaptive mechanism to ensure seedling establishment and maintain water and nutrient uptake for growth. Barley cv. Clipper (malting barley) and Sahara (North African landrace 3771) have been shown to have contrasting root growth responses to salinity stress. To elucidate the genetic basis for these different responses, a Clipper x Sahara double haploid (DH) mapping population was screened for root phenotypic traits under saline and non-saline conditions. This led to the identification of several significant Quantitative Trait Loci (QTL) affecting the roots of barley seedlings, including QTLs for root length and root diameter on chromosome 2H. To identify candidate genes within these loci, bulked segregant RNA-Seq was conducted on the root tips of salt-tolerant and salt-sensitive DH lines. This has resulted in the identification of several differentially expressed genes in these loci, that are potential candidates for root responses in saline conditions. Combining root phenotyping with advances in crop genetics will allow us to uncover root traits that can be incorporated into crop breeding programs for yield stability in saline soils.

Keywords: salinity stress, root growth, barley

Genetic improvement of nitrogen use efficiency in barley via gene editing
Sakura Thennakoon Mudiyanselage, Murdoch University

Sakura Thennakoon Mudiyanselage[1,2], Yong Han[3], Xiao-Qi Zhang[1,2], Chengdao Li[1,2,3]
[1] Centre for Crop and Food Innovation, Murdoch University, 90 South Street, Murdoch, 6150, Australia
[2]State Agricultural Biotechnology Centre, Murdoch University, 90 South Street, Murdoch, 6150, Australia
[3]Department of Primary Industries and Regional Development, 3 Baron-Hay Court, Kensington, WA 6151, Australia

Nitrogen (N) is a main determinant of grain yield and quality. Its excessive application leads to environmental pollution and high production costs. Improving nitrogen use efficiency (NUE) is therefore imperative in sustainable agriculture. The present study aimed at investigating barley tolerance to low N, retrieving candidate genes and developing barley materials with high NUE. Hydroponic screening of barley has identified low to moderate NUE cultivars such as Compass with potential for further NUE improvement. Two independent genome wide association studies of 282 barley accessions and a multiparent advanced generation inter-cross (MAGIC) population pinpointed a number of potential candidate genes which belonged to nitrate transporters, asparagine synthetase, several transcription factor families and protein kinases. High-affinity nitrate transporter 2.7 (*HvNRT2.7*), and abnormal cytokinin response1 repressor 1 (*HvARE1*) on chromosome 7H, protein NRT1/PTR FAMILY 8.3 (*HvNRT1*) gene on 4H and asparagine synthetase 2 (glutamine hydrolyzing) (*HvASN2*) on 1H were identified as promising loci for NUE improvement. Function of *HvARE1* under low N was validated by generating 4 mutant lines from the barley cultivar Golden Promise using Clustered Regularly Inter-Spaced Short Palindromic Repeats (CRISPR)/ CRISPR-associated protein 9 (Cas9). Missense and/or frame shift mutations were identified in T1 and T2 generations and these *are1* mutants exhibited an improvement in NUE related agronomic traits such as plant height, tiller number, grain protein content and yield under both low and optimal N. Some *are1* mutants had 1.5 to 2.8-fold increase in chlorophyl content at the grain filling stage and delayed leaf senescence by 10-14 days than that of the wild type. They also had high N content in shoots under low N conditions. Thus the results of this research can be successfully adopted to improve commercial barley cultivars for high NUE and yield.

Key words: Nitrogen use efficiency, barley, CRISPR/Cas9, yield, mutants

Exploring genetic variation for root architecture in global and Australian barley
Prof. Lee Hickey, The University of Queensland

Lee Hickey[1] Zac Aldiss[1], Yasmine Lam[1], Karen Massel[1], Peter Crisp[2], Ian Godwin[1], Andrew Borrell[3], Hannah Robinson[1,4],
[1]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St. Lucia, QLD, Australia
[2]School of Agriculture and Food Sustainability, The University of Queensland, Brisbane, QLD, Australia
[3]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Warwick, QLD, Australia
[4]InterGrain Pty Ltd, Perth, WA, Australia

Climate variability coupled with increased frequency and duration of drought events is a core challenge for the future of Australian barley production. Drought adaptation is complex, made up of several component traits, some interacting, and all influencing crop water-use across the growth cycle. Research in other cereal crops suggests

that optimising root system architecture can lead to improved water-use efficiency, particularly under marginal production scenarios. However, prior to developing an effective breeding strategy for the selection of root architectural traits for improved adaptation through barley breeding, we first need to better understand the genetic architecture underlying its control. To date, research in Australian barley has focused on bi-parental populations or small breeding populations with constrained diversity that is somewhat unrepresentative of the broader Australian diversity. In this study, we used a multi-experiment approach to explore genetic variation for seminal root angle in a panel of 799 barley lines consisting of wild, landrace, elite Australian breeding lines and commercial cultivars. Seminal root angle was selected as the trait of interest because it is widely regarded as a proxy for mature root system architecture in related cereal crops. Three experiments were conducted to reliably assess seminal root angle performance of the panel and a linear mixed model was used to model the variance-covariance structure across experiments. All individuals were genotyped with 12,562 markers from the Wheat Barley 40K XT SNP chip. Using a haplotype-based mapping approach, key chromosomal regions associated with the trait were identified. Through the exploration of the scaled haplotype variance, five haploblocks were detected on chromosomes 3H, 4H, 5H, and 7H. The haploblocks were compared to previously mapped QTL and inferences were made between diverse and elite breeding lines. Here we present the first comprehensive foundational study exploring the haplotype architecture across globally diverse and Australian germplasm and provide insight into future breeding strategies to improve adaptation of Australian barley.

Keywords: Roots, Development

Unravelling Aluminium Toxicity in Barley: Understanding Physiological and Molecular Insights into Altered Stomatal Kinetics Caused by Guard Cell Aluminium Accumulation

Chenchen Zhao

Chenchen Zhao[1], Ce Guo[1], Meixue Zhu[1]
[1]Tasmanian Institute of Agriculture, University of Tasmania, TAS, Australia

Acidic soil and associated aluminium (Al) toxicity represent a big abiotic threat to global agricultural sustainability. Al accumulation in plants significantly reduced stomatal conductance and crop yield. However, the regulatory networks underlying Al-induced stomatal kinetics changes remain unclear. Here, we investigated stomatal responses of two barley near-isogenic lines (NILs), RGT Planet (acid soil sensitive) and P33-1 (acid soil tolerant), upon long- and short-term Al treatments to dissect aluminium effects on stomatal morphology and physiology. In RGT Planet, excessive Al accumulation in the shoot led to reduced stomata size and enhanced stomatal sensitivity to exogenous abscisic acid (ABA). The introduction of 250 µM Al induced a transient stomatal closure only in Al-sensitive RGT Planet seedlings. Compared to P33-1, seedings of RGT Planet possessed faster stomatal aperture changes under light/dark transitions associated with ABA signalling networks that involve reactive oxygen species (ROS), cytosolic Ca^{2+} signaling and ion channels in guard cells. Our research adds evidence to understand Al-derived stomatal regulations, offering clues in screening germplasm and speeding up the breeding of crops for Al tolerance.

Keywords: Abscisic acid, *Hordeum vulgare* L., acid soil, stomatal conductance, aluminium, reactive oxygen species

Agronomic effects of HvDEP1-V in field-grown barley (Hordeum vulgare)

Hien Minh (Jean) Vu

Hien Minh Vu[1], Matthew Tucker[1], Jason Able[1], Stewart Coventry[2], Tristan Coram[2]

[1]School of Agriculture, Food and Wine, The University of Adelaide, Australia
[2]Australian Grain Technologies, Australia

Barley (Hordeum vulgare L.) is well adapted to Australian extreme conditions such as drought and salinity stress. However, in some high-yielding environments, barley can be prone to stem breakage or lodging, which negatively affects yield and crop profitability. Besides in-season management practices, a genetic solution is preferable. Since the Green Revolution, many semi-dwarf genes have been discovered and are being used in Australian barley breeding to limit mechanical yield constraints, however, some came with negative side effects. One semi-dwarf gene is *HvDEP1*, which encodes an AGG3-type subunit gene, regulating culm elongation, seed size and plant architecture. The *HvDEP1.GP* allele carries a loss of function mutation, showing short stature, and erect leaves but can also have short roots and small grains. The novel *HvDEP1-V* allele was recently identified in the Vlamingh variety, which is associated with grain length, 1000-grain weight and potentially more erect plant stature. In this study, we investigated the novel *HvDEP1-V* allele in field trials by in-depth phenotyping, physiological screening and phenotype-genotype association to evaluate its potential use in barley breeding. The multi-site 2022 and 2023 field trial data indicates that there is a negative trend for grain yield and lodging for *HvDEP1-V* and a positive effect on grain length in some backgrounds. This contradicts the hypothesis that *HvDEP1-V* may contribute to shorter stature and plumper grain. This data will provide information for breeders' decision-making process to solve the barley lodging problem.

Keywords: Semi-dwarf, field, stem, barley, genetics

SESSION 9: GENETICS & GENOMICS

KEYNOTE: The International Barley Pan Genome
Dr Nils Stein, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Nils Stein
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466 Seeland, Germany

The genomic revolution, initiated by the introduction of high-throughput next generation sequencing technology combined with new compute power and algorithms, has made de novo sequencing and assembly a routine task, almost independent of genome complexity. While sequencing of the multigigabase genomes of the Triticeae crop species barley, wheat, rye initially required the collaboration of larger research consortia, sequencing entire Triticeae genomes has just become a routine task and is easily implemented as part of a map-based cloning project. This opens the perspective towards systematically unlocking the crop genome diversity at species scale. Entire genebank collections of are / were genotyped by sequencing, providing global population diversity resolution. This isproviding now foundational information for pangenome sequencing. In frame of an international effort, more than 75 barley genomes, including 23 wild H. vulgare ssp. spontaneum, were assembled into chromosome scale scaffolds using PACBIO Hifi and Hi-C data. This Pangenome is representative for most of the pericentric haplotypes in extant barley germplasm as well as in genetic resources, however, in order to capture rare allelic diversity and especially the highly recombinogenic telomeric ends of barley chromosomes a continued effort of discovery by genome sequencing will be required. In addition, pangenome initiatives working towards a genus-Hordeum-pangenome, will unlock the secondary and tertiary genepools for research and crop improvement.

The genetic basis of malt quality
Dr Christoph Dockter, Carlsberg Research Laboratory

Christoph Dockter[1]-Morten E. Jørgensen[1], Dominique Vequaud[2], Amanda Box[3], Geoffrey B. Fincher[4], Barley pan-genome & pan-transcriptome consortia, Birgitte Skadhauge[1], Eske Willerslev[5], Robbie Waugh[6], Nils Stein[7]
[1]Carlsberg Research Laboratory, Copenhagen, Denmark
[2]SECOBRA Recherches, Maule, France
[3]SECOBRA Research/Seednet, Urrbrae, Australia
[4]School of Agriculture, Food and Wine, Adelaide University, Australia
[5]GeoGenetics Centre, Copenhagen University, Denmark
[6]James Hutton Institute, Dundee, Scotland
[7]Leibniz Institute of Plant Genetics and Crop Plant Research, Seeland, Germany

MKK3 (*Mitogen-activated Protein Kinase Kinase 3*) is a genetic determinant associated with increased post-harvest grain dormancy in East Asian elite malting barley varieties. Grain dormancy modulation is crucial for industrial application and in agricultural production to avoid preharvest sprouting (PHS). PHS is a global problem and is at risk of being further aggravated by climate change. To effectively breed barley varieties with reduced PHS risk, while maintaining malt quality, it is imperative to understand the molecular nature of the loci responsible for high PHS susceptibility. Here, we unravel the complexity of the barley *MKK3* locus through multi-year field trials of *MKK3* near-isogenic lines exposed to PHS-inducing conditions, combined with *in vitro* kinase activity assays and ddPCR-genotyping of contemporary and historical barley accessions. In-depth *MKK3* haplotype and expression analyses in the barley pan-genome and -transcriptome datasets reveal extensive structural variation at the *MKK3* locus including copy-number variation and respective changes in transcript abundance. The presence of variable *MKK3* copy-number and specific hyperactive protein haplotypes coincide with traditional and modern farming practices that are important for yield gain and grain quality. Our results

suggest that *MKK3* gene is the major determinant of grain dormancy selected across the globe to adapt to local climate and agricultural practices and that breeders must carefully choose *MKK3* haplotypes to balance malt quality and the risk of PHS.

Speeding up gene discovery in barley mutants using whole genome shotgun sequencing

Dr Miriam Schreiber, James Hutton Institute, International Barley Hub

Miriam Schreiber[1], Malcolm Macaulay[1], Cong Tan[2], Robbie Waugh[1], Luke Ramsay[1], Micha Bayer[1]
[1]The James Hutton Institute, Invergowrie, Dundee, Scotland, UK
[2]BGI Research, Shenzhen, 518083, China

The development of new resources in the form of pangenomes and the reduction in cost of sequencing technologies have resulted in new approaches to identifying mutations. We have used whole genome shotgun sequencing of multiple mutants to speed up the candidate gene discovery. The mutants were selected from the extensive Bowman near isogenic line (NIL) collection. Most mutants within the collection have been back-crossed multiple times into Bowman, resulting in clearly defined introgressions. One of the examples is the barley mutant *dense spike 9.* Spike architecture is of particular importance for agriculture due to its direct correlation with yield potential and grain quality. In this example we added to the fine mapping and phenotypic characterisation two sets of whole genome shotgun sequencing to identify the underlying locus.

The Australian Barley Pan Genome

Prof. ChengDao Li, Murdoch University

Chengdao Li[1,4] Tianhua He[1], Viet Dang[1], Brett Chapman[1], Yong Jia[1], Haifei Hu[1], Penghao Wang[1], Xiao-Qi Zhang[1], Kenneth J. Chalmers[2], Camilla Beate Hill[1], Gabriel Keeble-Gagnere[3], Sharon Westcott[4], Yong Han[4], Josquin F Tibbits[3], Peter Langridge[2],
[1]Western Crop Genetics Alliance, Agricultural Sciences, College of Science, Health, Engineering and Education, Murdoch University, WA Australia
[2]School of Agriculture, Food and Wine, University of Adelaide, Waite Campus, Glen Osmond, South Australia, Australia
[3]Agriculture Victoria, Department of Jobs, Precincts and Regions, Agribio, 5 Ring Rd, La Trobe University, Bundoora, Victoria 3083 Australia
[4]Agriculture and Food, Department of Primary Industries and Regional Development, South Perth, WA, Australia

Breeders' selections have played a significant role in shaping barley genomes and selecting genes and alleles for adaption to growth conditions. However, the genetic basis of adaptation to distinct agroclimatic conditions remains to be elucidated. Here we assembled the genomes of Australia's modern barley varieties Maximus, RGT Planet, Clipper, Stirling, Vlamingh, Laperouse, Buff and Yeti. With reference quality genomes and population-level re-sequencing data of modern barley varieties from Europe, Australia and North America, and field characterization on their phenology, we show that breeders have fundamentally transformed the genomic architecture and landscape of adaptive genes in Australian and North American barley varieties. Adapting to the Australian environment involves the selection and subsequent enrichment of pre-existing genetic variants within the European barley gene pool, but also later introduces non-European genotypes. Genes associated with photomorphogenesis, circadian rhythm and light response were under strong selection during the early breeding of European germplasm base to adapt to Australian environments. Modern Australian barley harbours dominant haplotypes conferring phenotypes. Our findings will inform the selection from germplasm pools and parental lines when establishing breeding populations to breed new varieties adapted to the novel environments.

Key words: Australia barley, Pan genome, Haplotype, Yield, Adaptation

Trait-Linked Markers in the Genomics Era
Dr Kerrie Forrest, Agriculture Victoria

K. Forrest[1], S. Azizinia[1], D. Wong[1], G. Keeble-Gagnère[1], H. Robinson[2], S. Baraibar[2], D. Moody[2], J. Tibbits[1], M. Hayden[1,3]
[1]Agriculture Victoria, Department of Energy, Environment and Climate Action, Australia
[2]InterGrain Pty Ltd, Australia
[3]School of Applied Systems Biology, La Trobe University, Australia

Marker-assisted selection (MAS) has been applied to plant research and breeding for decades to help make informed decisions, to select lines with beneficial alleles for improved performance, and discard those with undesired alleles. With modern plant breeding practises shifting to incorporate genomic selection using low to medium density genotyping assays to predict the performance of individual lines, trait-linked markers can have a distinct yet complementary role to play.

Historically, vast resources have been invested to develop trait linked markers, both within Australia and worldwide. When new assays are developed, it is possible to convert trait linked markers from one technological platform to another. This enables the outputs from those original investments to be re-cycled, thereby maximising the return on those investments, while improving the utility of genotyping tools for the community.

Cereal cyst nematodes (CCNs) are a significant pest that limits the production of barley globally. Breeding for CCN resistance is a key target in barley variety development. In this case study, we compare the results of genome wide association studies (GWAS) using genotype data of moderate SNP density with and without trait-linked markers for cereal cyst nematode (CCN) resistance in a barley breeding program. Our results show that the use of trait-linked markers amplified signal for CCN resistance.

These results reinforce the continued relevance of high-quality trait linked markers for breeding improved barley varieties, contributing to improved global food security and agricultural sustainability.

Keywords: CCN, cereal cyst nematode, trait linked markers

Rapid domestication - a new approach for accelerating exploitation of wild barley genomes to improve complex traits
Dr Scott Boden, The University of Adelaide

Scott Boden[1], Suong Cu[1], Margie Pallotta[1], Ruth Hamilton[2], Luke Ramsay[2] Joanne Russell[2], Robbie Waugh[2], Peter Langridge[1]
[1]School of Agriculture, Food and Wine, University of Adelaide, Glen Osmond, South Australia, 5064 Australia
[2]James Hutton Institute, Invergowrie, Dundee DD2 5DA, Scotland

A breeder's ability to improve crop performance depends on genetic variation, which has been eroded during domestication and breeding. Depletion of genetic diversity is particularly strong in spring barley, with variation being absent in multiple chromosomes. Wild barleys provide a rich source of genetic diversity that can be introduced into cultivars to improve complex traits, such as yield and stress resilience. However, the process to select accessions and evaluate elite × wild progeny is lengthy and laborious, limiting the number of wild barleys assessed, and target traits are not always maintained in the derived lines. Here, we report an approach to rapidly evaluate multiple accessions of wild barley under breeding-relevant conditions, which involves selection of key domestication loci in genotypes that contain substantial wild genome content. Our unbiased evaluation of these genotypes under controlled environments and field trials has identified 3/12 accessions that confer improvements in complex traits, such as yield and response to drought. Genetic analyses indicates this approach can uncover alleles for key agronomic traits, as preliminary association studies using the elite × wild families has identified loci that confer improved tiller number and yield, including a novel allele for *Vrs1*, as well as new alleles for phenology. Our approach provides an opportunity to harness the genetic variation of wild barleys for improved performance of elite cultivars, and sets a path by which breeders can use genebank collections to improve traits in other crops.

Keywords: re-domestication, genetic variation, yield, drought, breeding

SESSION 10: NEW INSIGHTS IN GENETICS

Developing a next generation of barley scientists

Prof. Robbie Waugh, University of Dundee/James Hutton Institute

Robbie Waugh, Director, The International Barley Hub, Dundee, Scotland.

The International Barley Hub (IBH) and Advanced Plant Growth Centre (APGC) are Innovation Centres established through an Au$120M capital investment from Scottish and UK governments (opening scheduled for July 2024). They are jointly located on the campus of the James Hutton Institute on the outskirts of Dundee, which for the past 20 years has hosted the University of Dundee Division of Plant Sciences. Underpinned by the research excellence of both institutions, the IBH is supported by an expanding number of commercial stakeholders from all along the barley supply and value chain. It aims to assemble a critical mass of barley researchers focused on delivering step changes in barley science that collectively lead to increased barley production and use, resilience across the supply and value chains from primary grower to end user and expansion into new areas such as food and non-food uses. The new infrastructure provides a state-of-the-art discovery/applied/translational research platform that will create opportunities to promote barley science to a wide and diverse audience. Beyond its research, IBH is active in encouraging interactions within the barley research community, increasing awareness of major initiatives/advances in order to avoid duplication, facilitating new collaborations and introducing early career scientists to their peers in the broader international community. It plays an increasingly significant role in mentoring the development of the next generation of barley scientists through its Barley Industrial Training Network PhD program (BARIToNE). In my short presentation I will provide a snap-shot of the new IBH facilities and describe some of the actions we have already taken to meet our stated objectives. I will encourage attendees at ABTS to consider how to engage individually and/or collectively with IBH, and potentially to play a role in influencing how IBH develops.

Harnessing Strigolactones to Improve Barley Architecture and Yield

Jack Kelly, The University of Adelaide

Jack H. Kelly[1], Matthew R. Tucker[1], Philip B. Brewer[2]
[1]School of Agriculture, Food & Wine, The University of Adelaide, SA, Australia
[2]Central Queensland University, QLD, Australia

Strigolactones are a novel class of plant hormone that have a strong impact on a range of important crop traits, in addition to the inhibition of tiller bud outgrowth. We have isolated a series of new barley gene edited mutants that are disrupted in the strigolactone pathway. Each type of strigolactone mutant produces distinctive effects on shoot architecture and other important crop traits, and are helping us understand how hormones regulate crop environmental adaption. Together with synthetic hormones and inhibitors, the mutants provide a tool kit to unravel the effect of strigolactones on various traits, including shoot and root architecture, grain size, senescence, nutrient use efficiency and yield. We report on experiments that further uncover the important impact of strigolactones on crop plants and factors that involve strigolactone function. These factors include sub-optimal conditions, timing of shoot architecture decisions, and the relationship between tiller number and grain size. Moreover, strigolactones show a complex interplay with other plant hormone pathways, in particular with auxin transport. We will describe some of the most interesting aspects of this research and propose a way forward for future research to find ways to utilise strigolactones for enhanced crop performance.

Keywords: Crop tillering, crop yield, plant architecture, strigolactones, sub-optimal conditions

Genome-wide association study for identification of marker-trait association conferring resistance to scald from globally collected barley germplasm

Usman Ijaz, University of Tasmania

<u>Usman Ijaz</u>[1], Chenchen Zhao[1], Sergey Shahbala[2,3], and Meixue Zhou[1]
[1]Tasmanian Institute of Agriculture, University of Tasmania, Launceston, TAS 7250, Australia
[2]School of Biological Science, University of Western Australia, Crawley, WA 6009, Australia
[3]International Research Centre for Environmental Membrane Biology, Foshan University, Foshan 528000, China

Scald is one of the major economically important foliar diseases in barley, causing susceptible varieties up to 40% of yield loss. The identification of quantitative trait loci (QTL) and elite alleles that confer resistance to scald is imperative in reducing the threats to barley production. In this study, genome-wide association studies (GWAS) were conducted using a panel of 697 barley genotypes to identify QTL for scald resistance. Field experiments were conducted over three consecutive years. Among different models used for GWAS analysis, FarmCPU was shown to be the best-suited model. Nineteen significant marker-trait associations (MTAs) related to scald resistance were identified across six different chromosomes. Eleven of these MTAs correspond to previously reported scald resistance genes *Rrs1, Rrs4,* and *Rrs2*, respectively. Eight novel MTAs were identified in this study with the candidate genes encoding a diverse class of proteins including region leucine-rich repeats (LRR), AP2/ERF transcription factor, homeodomain-leucine zipper, and protein kinases family proteins. The combination of identified superior alleles significantly reduces disease severity scores. The results will be valuable for marker-assisted breeding for developing scald-resistant varieties.

Keywords: Marker-trait association, scald, disease resistance, barley, marker-assisted breeding

Genome engineering root systems to drought-proof Australian barley

Richard Dixon, The University of Queensland

<u>R. Dixon</u>[1], H. Robinson[1,3], K. Massel[1], I. Godwin[1], M. Djordjevic[2] L. Hickey[1],
[1] Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Australia.
[2] Research School of Biology, Australian National University, Australia.
[3] InterGrain Pty Ltd, Australia

Optimising barley root systems to attain water and nutrients during adverse growing conditions common to Australia has the potential to significantly improve yield stability. Due to the challenges in visualising and phenotyping root systems, breeding programs have traditionally focused on above-ground traits and yield maximisation. As a result, much of the genetic variation controlling root systems has been inadvertently fixed as a by-product of selection. This is likely particularly true in elite germplasm due to intensive selection over the past century. Clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR associated proteins (Cas), collectively CRISPR-Cas, can be utilised to edit the genome of cereal crops. CRISPR is precise at editing genes of interest as guide RNAs can be designed to recruit CRISPR machinery to a specific location within the genome. Specific CRISPR technologies are now considered not genetically modified and therefore show strong potential for incorporation into barley breeding programs. *C-TERMINALLY ENCODED PEPTIDE RECEPTOR 1 (CEPR1)* has been shown to influence root system architecture in the model species *Arabidopsis* and *Medicago*. We found editing *CEPR1* to generate a loss-of-function *cepr1* barley line produced a novel root system architecture with a steep and compact root system. *cepr1* barley plants also displayed a shoot-penalty and produce less grain per plant. Therefore, our future research aims to optimise both root and shoot traits by targeting *CEPR1's* cis-regulatory elements, other *C-TERMINALLY ENCODED PEPTIDE (CEP)* gene network members, and other genes known to exert control over root systems, for editing.

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

David Chisanga, Agriculture Victoria

J. Tibbits[1, 3], S. Norton[2], G. Keeble-Gagnere[1], K. Forrest[1], D. Wong[1], N. Sawyer[2], E. Barnes[2], M Hayden[1, 3]
[1] Agriculture Victoria, Department of Energy, Environment and Climate Action (DEECA), Australia
[2] Australian Grains Genebank, Agriculture Victoria, Department of Energy, Environment and Climate Action (DEECA), Australia,
[3] School of Applied Systems Biology, La Trobe University, Bundoora, Australia

The Australian Grains Genebank (AGG) is at the forefront of conserving barley's genetic diversity, a crop integral to Australian agriculture and brewing industries. The AGG Strategic Partnership between the Victorian State Government and Grains Research and Development Corporation (GRDC) aims to unlock the genetic potential of plant genetic resources for the benefit of Australian grain growers. The program of works is transforming the AGG from a traditional seedbank facility into a future-oriented bio-digital resource centre whereby passport and genomic data can be integrated and accessed through online bioinformatics tools. A major activity is to genotypically characterise the entire AGG barley collection, which is one of the largest in the world comprising over thirty-five thousand accessions, of which over 90% has now been genotyped. Here we report how this data was generated, and how the Partnership is working to make these genomic resources accessible to the Australian barley research and breeding community. Application of these genomic resources holds transformative potential for industry to address the challenges of climate variability, diseases, and pests, while ensuring stable and enhanced yields for farmers.

Keywords: Genebank, genomics, plant genetic resources

POSTERS

The below Posters will be available for viewing throughout the duration of the ABTS Symposium. An allocated poster session will be held on Wednesday 14 August during the lunch break between 12:25pm – 1:15pm

An integrated modelling and physiological approach to assist breeding for improved yield stability in barley

A/Prof. Karine Chenu, University of Queensland

K. Chenu[1]B. Heidariask[1], S. Ahlmad[1], L.T. Hickey[1], M. Smith[1],
[1]The University of Queensland, Queensland Alliance for Agriculture and Food Innovation (QAAFI), Australia

Barley ranks as the fourth most widely cultivated cereal globally, with primary applications in livestock feed production and in malting for the production of alcoholic beverages. Barley production is highly susceptible to environmental fluctuations, including in seasonal rainfall and heatwaves. The aims of this study are to (i) characterise abiotic stress affecting barley across the Australian grain belt, and (ii) investigate the role of key physiological traits in improving barley yield stability across Australian diverse environments. We propose a modelling approach to characterise broadly (large geographic area, long-term period) and locally (field experiment) drought- and heat-related stresses in order to (i) better understand current and projected stress that barley crops experience across Australian production systems, and (ii) better assess genetic response to specific stress in field trials. This study will leverage phenotypic data acquired in platforms and field trials across the country to estimate the productive value of physiological traits in various environments.

Results from this project will inform breeders about the nature and frequency of key abiotic stressors in major Australian growing regions, as well as changes projected in future climatic scenarios. The project will also provide insights to prioritise adaptive traits of importance for production in targeted environments.

Keywords: Barley, drought, heatwave, trait value, APSIM.

Fee for Service Analysis Providing an Insight into Malt Accreditation and the Future of Barley Breeding

Hayley Lewis, The University of Adelaide

A. Lewis, Hayley1
1School of Agriculture, Food & Wine, The University of Adelaide, Australia

In an ever-changing world, there is an inherent need within each industry to keep up with evolving trends, demands and consumer needs. With Australians consuming on average over 2.5 billion pints of locally produced & sold beer per year with a total retail value of $17 billion , the barley breeding industry is no exception. Australian barley is highly sought after by the malting, brewing and distilling industries worldwide, making up approximately 30% of the world's malt barley trade . In the last 60 years, over 100 barley varieties have been bred and released in Australia , displaying a further need for growth and research in the barley breeding sector. Growers are increasingly seeking varieties that not only produce malt quality grain, but also provide increased yields, disease resistance and optimal growth periods among a changing climate. Meticulous laboratory testing is available to aid in determining whether upcoming barley varieties are suitable for malt classification. The Grain Quality Laboratory at the Waite Campus of the University of Adelaide offers grain and malt analysis tests including Apparent Attenuation Limit (AAL), Hot water extract, Wort β-Glucan, Free α-Amino Nitrogen (FAAN), Diastatic Power, Friability, NIR Analysis and more. These services provide a vital feature of the malt accreditation process and have been attributed to the successful accreditation of many malt barley varieties in Australia.

Keywords: barley, breeding, laboratory, analysis, malt

The three Ds of fungicide dynamics for the stewardship of chemistries and genetic disease resistance.

Jordi Muria Gonzalezm, Curtin University

M.J. Muria-Gonzalez[1], A. Singh[1], V.G. Punithan[1], M. Gibberd[1], J. Mylne[1]
[1] Centre for Crop and Disease Management, Curtin University, Western Australia, Australia 6102

The pressure of fungal diseases on agriculture is rising. Developing new disease-resistant varieties and effective fungicide strategies are at the core of crop protection. However, fungi counteract these measures evolving new virulence and fungicide resistance. Therefore, protecting the fungicide chemistries and the genetic resistance of crops against pathogens is crucial.

To quantitatively determine fungicide **D**istribution, **D**issipation, and **D**egradation, the three Ds of fungicide dynamics, within plant tissue, our project uses relatively simple chromatographic and mass spectrometric analyses using barley as a model crop. Our aim is to understand how plant genetics (traits), environment, and agricultural practices impact on these three D's, and their correlation with disease protection. The generated knowledge will inform new models enabling the next generation of fungicide strategies, aiming to be cultivar and environment specific, to optimise the efficacy of compounds with flow-on benefits for also optimising the life space of new forms of crop genetic resistance. In pursuit of these objectives, we are actively engaging with industry stakeholders, including the agrochemical and breeding sectors, seeking their insights to develop a substantial and impactful program that could foster fruitful collaborations in the future.

In this talk I will present the primal steps of our project and how early results investigating the three Ds of fungicide dynamics for fluxapyroxad, the active compound of Systiva seed treatment, led us to develop a new line of research at the Centre for Crop and Disease Management, Curtin University.

Keywords: Fungicides, Mass spectrometry, Stewardship, Disease resistance

Utilising novel genetic diversity to increase barley yields nationally

Dr Anh Pham, University of Adelaide

Anh-Tung Pham[1], Hue Thi Dang[1], Julian Taylor[1], Jason A. Able[1]
[1] School of Agriculture, Food and Wine, University of Adelaide, Waite Campus, Urrbrae SA 5064, Australia

The genetic analysis employed in a previous GRDC-funded project (UA00148) identified genomic regions in wild barley associated with improved yield components or increased biomass under water-limited conditions. Nine beneficial genomic regions were incorporated into Compass, LaTrobe, and GrangeR via backcrossing using molecular markers tightly associated with the traits. Germplasm carrying those genomic regions was assessed in yield trials across 23 environments in 2020-2022 to examine whether these wild barley genomic regions would improve yield and yield components in the Australian genetic background.

Extensive field trials identified six out of 108 experimental lines that out-yielded their recurrent parents by 5 % across 23 environments. One line with a significantly higher thousand-grain weight, and three lines with consistently higher grain number per ear than those of current commercial varieties were identified. Among nine genomic regions from wild barley evaluated, three were validated to significantly and positively affect yield components in different Australian genetic backgrounds. The research to investigate the effect of these loci to final grain yield enhancement is ongoing, which will help private breeding programs move forward with confidence in utilising such materials.

The Molecular Insights of Barley Response to Waterlogging Stress and the Screening of Key Gene Mutants

Dr Feifei Wang, Yangzhou University

Feifei Wang1, Chao Lv1, Baojian Guo1, Juan Zhu1, Rugen Xu1,
1.Key Laboratory of Plant Functional Genomics of the Ministry of Education /Yangzhou University, Yangzhou 225009, China.

Waterlogging stress is one of the major abiotic stresses affecting the productivity and quality of many crops worldwide. However, the mechanisms of waterlogging tolerance are still elusive in barley. In this study, we identify key differentially expressed genes and differential metabolites that mediate distinct waterlogging tolerance strategies in leaf and root of two barley varieties with contrasting waterlogging tolerance under different waterlogging treatments. Transcriptome profiling revealed that the response of roots was more distinct than that of leaves in both varieties. We also found the number of waterlogging stress-induced upregulated DEGs in the waterlogging tolerant variety was higher than that of the waterlogging sensitive variety in both leaves and roots which suggested the waterlogging tolerant variety may respond more quickly to waterlogging stress. Meanwhile, phenylpropanoid biosynthesis pathway was identified to play critical roles in waterlogging tolerant variety by improving cell wall biogenesis and peroxidase activity. Based on metabolomic and transcriptomic analysis, we found the waterlogging tolerant variety can better alleviate the energy deficiency via higher sugar content, reduced lactate accumulation, and improved ethanol fermentation activity compared to the waterlogging sensitive variety. Through WGCNA of transcriptome data, forty-seven genes were primarily identified as candidate genes. An EMS mutant population of barley was constructed and eleven mutants were screened, including HvRBOHB, HvRBOHE, HvDTX16, HvGLR7.1, HvGLR5.6 gene, by utilizing the TILLING technique. The phenotype of mutants showed HvGLR7.1 gene play important roles in response to waterlogging stress. In summary, our results provide waterlogging tolerance strategies in barley to guide the development of elite genetic resources towards waterlogging-tolerant crop varieties.

Keywords: Barley; Waterlogging stress; Transcriptome; Metabolome; EMS mutant; HvGLR7.

Genome-wide association studies reveal novel essential loci for grain size in two-rowed barley (Hordeum vulgare L.)

Prof. Rugen Xu, Yangzhou University

Rugen Xu[1], Chao Lv[1], Baojian Guo[1], Feifei Wang[1], Juan Zhu[1]
1.Key Laboratory of Plant Functional Genomics of the Ministry of Education /Yangzhou University, Yangzhou 225009, China.

Barley yield and quality are greatly influenced by grain size. Improving barley grain size in breeding programs requires knowledge of genetic loci and alleles in germplasm resources. In this study, a collection of 334 worldwide two-rowed barley accessions with extensive genetic diversity was evaluated for grain size including grain length (GL), grain width (GW), and thousand-grain weight (TGW) across six independent field trials. Significant differences were observed in genotype and environments for all measured traits. SNP- and InDel-based GWAS were applied to dissect the genetic architecture of grain size with an SLAF-seq strategy. Two approaches using the FarmCPU model revealed 38 significant marker-trait associations (MTAs) with PVE ranging from 0.01% to 20.68%.In this study, 334 worldwide two-rowed barley accessions with extensive genetic diversity were genotyped with 233,451 SNPs and 26,453 InDels using SLAF-seq. Markers with MAF (minor allele frequency) ≥ 5% and missing rate ≤ 20% were used to identify markers associated with grain size. Significant phenotypic variations in grain size, including grain length (GL), grain width (GW), and thousand-grain weight (TGW), were observed. SNP- and InDel-based GWAS using the FarmCPU model revealed 38 significant marker-trait associations (MTAs) with PVE ranging from 0.01% to 20.68%. Among these MTAs, 10 five were on genomic regions where no previously reported QTL for grain size. Superior alleles of TGW-associated SNP233060 and GL-associated InDel11006 exhibited significantly higher levels of phenotype. The significant MTAs could be used in marker-assisted selection breeding.

Keywords: Barley; Grain size; GWAS; Marker-trait association; Consensus novel loci

Assessing the Frequency and Impact of the HvHKT1;5 P189 Variant Allele on Barley Grain Sodium Accumulation and Malt Quality.

Harley Young, The University of Adelaide

H.J. Young[1], S.J. Roy[2]
[1]Roy Labs, University of Adelaide, Australia

This research project focuses on exploring a novel salinity tolerance mechanism observed in barley which facilitates the accumulation of high levels of sodium. This mechanism holds the potential to enhance drought tolerance by enabling the plant to lower its leaf water potential, thereby facilitating increased water extraction from the environment. While this salinity tolerance mechanism has been demonstrated to be present in 35% of European barley germplasm, its frequency and impact on salinity and drought tolerance in Australian barley cultivars remains unknown. Leveraging the OzBarley panel at Roseworthy campus, which encompasses both Australian and wild relative barley cultivars, the project aims to assess the frequency of the HvHKT1;5 P189 variant allele in the panel. The resulting lines will be crucial for evaluating the associated phenotype, thus offering valuable insights for enhancing agricultural strategies and improving crop resilience in the Australian context. Barley serves as a primary ingredient in beer production, therefore any alterations in this salinity tolerance mechanism can impact the quality and characteristics of the final product. For this reason, grain analysis will be conducted to determine how the high salt-accumulating lines, resulting from the identified gene, influence salt levels in barley grain. This investigation extends to the brewing process, offering insights into potential changes in flavour profiles and overall beer quality. Understanding the relationship between the salinity tolerance mechanism and brewing parameters will contribute to informed decisions in crop selection for brewing purposes, thus shaping the agricultural practices that support the brewing industry.

Keywords: Salinity, Drought, Malt Quality, OzBarley

Rapid phenotyping of adult plant resistance to net form net blotch in barley

Dr Xuechen Zhang, DAFQueensland

Xuechen Zhang[1], Judy McIlroy[1], Peter Thompson [1], Lisle Snyman[1]
[1] Queensland Department of Agriculture and Fisheries, Hermitage Research Facility, Warwick Yangan Rd, Warwick QLD 4370

Net form net blotch (NFNB), caused by *Pyrenophora teres* f. *teres*, can cause severe yield losses ranging from 10% to 40% in a very susceptible barley cultivar under favourable conditions. Deployment of resistant varieties is an economical and environmentally friendly method to control NFNB. Screening for adult plant resistance in the field is dependent on environmental conditions and limited by low frequency. This study reported a rapid phenotyping method to screen resistance to NFNB at adult plant stage in the glasshouse. A differential set of 30 barley lines and another 10 commercial varieties conferring NFNB adult plant resistance were used in this study. NFNB adult plant resistance can be detected in plants at growth stage Zadoks 31 to 37, (5 to 6 weeks after sowing) under normal temperature conditions (approximately 22°C) in the glasshouse. Disease resistance score of plants at adult plant stage in the glasshouse was highly correlated to adult plant resistance in the field. This method provides the opportunity to identify adult plant resistance to NFNB and to screen large numbers of lines and populations. The method used for screening adult plant resistance in the glasshouse can help accelerate the selection of adult plant resistance in breeding programs and monitoring NFNB pathotypes.

Keywords: barley, net form net blotch, adult plant resistance, disease screening

Service Australian barley industries with an innovative MultiMalter

Dr Qisen Zhang, AEGIC

Qisen Zhang and Jack King
Australian Export Grains Innovation Centre

Barley occupies a pivotal position in the Australian grains industry, accounting for around 22% of total annual grain production. This is second only to wheat, which further underscores its importance to the Australian economy and agricultural prosperity.

AEGIC, with the support of industry, is committed to increasing value in the Australian barley industry by diversifying markets, identifying new opportunities for Australian barley, and providing technical support and education to customers on the benefits of Australian barley and how to optimise its value. This helps drive demand and reinforces the favourable positioning of Australian barley in global markets.

AEGIC developed an innovative micromalter named the MultiMalter, designed to help international brewers and maltsters adopt new Australian barley varieties in a shorter amount of time. Australian barley is well-regarded by international maltsters and brewers, especially in China, but companies have told us that the frequency of the release of new Australian barley varieties can be challenging. Having faster access to information about optimum malting conditions and malting performance would be of great value to customers of Australian barley.

The MultiMalter operates with six malting protocols, compared to the conventional micromalters, with only one protocol. Malting is a time-consuming process, generally taking six days for a single cycle. The MultiMalter can test six different malting protocols on barley samples in a single run, allowing for optimal malting regimes for each sample to be identified.

AEGIC has used our MultiMalter prototype to obtain malting performance information for Spartacus CL, Maximus CL, RGT Planet, Bottler, Alestar and Leabrook. The results showed that each barley sample had unique requirements during the process to achieve suitable malting performance.

After the resumption of barley export to China, the malting performance information for new barley varieties is in high demand by Chinese maltsters and brewers. AEGIC has conducted technical information exchanges with several Chinese malting and brewing companies.

The feedback confirmed that the malting performance information would help them make operational decisions in the adoption of Australian new barley varieties quicker.

Keywords: Barley, malting, quality, malt, variety

Effect of BYDV on barley crop production: A precise assessment of agronomic traits reductions under variable disease severities

Dr Chenchen Zhao, University of Tasmania

Chenchen Zhao[1], Meixue Zhou[1*]
[1]Tasmanian Institute of Agriculture, University of Tasmania, Prospect, TAS, 7250, Australia

Understanding the effects of barley yellow dwarf virus (BYDV) on crop agronomic traits and yield performance helps breeders balance their selection criteria and farmers decide if pesticides should be applied to control aphids that distribute the virus. To precisely assess the deterioration of different agronomic traits and yield components caused by different levels of BYDV infection, seeds of a BYDV-sensitive barley variety cv. RGT Planet were space sown in a field plot with 10 cm between seeds and 20 cm between rows under two consecutive years. When BYDV symptoms were shown, plants with different levels (0 – 5) of BYDV infection were tagged. For accurate comparisons, the neighbouring non/less-infected plants were also tagged. At maturity, different agronomic traits and yield components were measured on those tagged plants. Results showed a strong linear correlation between BYDV severity and the performance of agronomic traits and yield components. The yield reductions ranged from

30% for the least affected (score of 1) to 90% for the severely affected (score of 5). Our research confirmed previous findings that BYDV seriously affects crop yield and the prediction of yield loss due to BYDV infection should use the percentage of plants with different BYDV symptoms.

Keywords: Barley, BYDV, grain yield, agronomic traits

Plant phenotyping: A key to improving plants' stress tolerance
Prof. Meixue Zhou, University of Tasmania

M.X. Zhou, C.C. Zhao
Tasmanian Institute of Agriculture, University of Tasmania, Australia

Phenotyping plays a critical role in plant stress tolerance breeding, which helps to identify and characterise the response of plants to various stresses. Molecular markers have been used to select varieties with different stress tolerances. However, the identification of markers relies heavily on accurate phenotyping. Here we will use salinity and waterlogging stresses as examples to demonstrate the importance of accurate phenotyping for successful breeding.

Keywords: Barley, abiotic stress, phenotyping

The use of fertiliser to mitigate waterlogging damage to barley
Prof. Meixue Zhou, University of Tasmania

J.B. Chen, C.C. Zhao, K. Liu, M. Harrison, P.J. Johnson, M.X. Zhou
Tasmanian Institute of Agriculture, University of Tasmania, Australia

Waterlogging expedites the loss of nitrogen and execrates ion reduction in soil. The cumulative effects of reduced nutrient concentration impact cell permeability, root respiration and activity. Various agronomic strategies have been proposed to mitigate the detrimental effects of waterlogging, with a focus on soil management and crop practices. Here we dissected the interplay between nitrogen fertiliser application timing, method, and subsequent effects on barley growth and development. Our results showed that yield reduction caused by waterlogging mainly due to a marked decrease in spike numbers, while other factors such as grain number per spike and 1000-grain weight remain unaffected across different varieties or fertiliser application under waterlogged conditions. The application of fertiliser during waterlogging can partially mitigate waterlogging damage.

Keywords: Barley, waterlogging, agronomic management

OzBarley: from genome to phenome and back again
Prof. Matthew Tucker, The University of Adelaide

Bettina Berger and Matthew Tucker on behalf of the OzBarley project team
OR
Ute Baumann, Amanda Box, Chris Brien, Kenneth Chalmers, Stewart Coventry, Dini Ganesalingam, Jessica Hyles, Elena Kalashyan, Brett Lobsey, Haoyu Lou, Diane Mather, Sarah Richmond, George Sainsbury, Julian Schwerdt, John Stephen, Ben Trevaskis, Robbie Waugh, Bettina Berger & Matthew Tucker

OzBarley is a public resource capturing the diversity and breeding history of barley in Australia.

The aim is to share genotype-to-phenotype (G2P) data of Australian barley varieties with the research community and provide a platform for future contributions by OzBarley users to grow and expand the database. We want to provide a foundation for researchers to explore and mine the diversity of Australian barley for their respective research projects.

The OzBarley collection was initiated in 2023 and currently contains data for the following resources:

- a recombinant inbred line (RIL) population of Mundah x Keel
- an elite panel of over 200 commercial barley varieties
- a collection of over 500 barley landraces

The vision is to grow OzBarley with further contributions from the barley community.

OzBarley is delivered using the GERMINATE plant genetic resources platform and is hosted at Pawsey. All associated datasets will be linked via the GERMINATE platform.

All datasets contain genotype data, with links provided to the respective access sites for data exploration and download. Pedigree information is also available for the diversity panel, with all seed being deposited in the Australian Grains Genebank. Phenotypic data is available for the Mundah x Keel RIL population and the elite panel.

The Paul Johnston Memorial Award: Supporting Future Leaders

Amanda Box, & Elysia Vassos, Trustees of the Paul Johnston Memorial Trust

Elysia Vassos[1,5], **Amanda Box[2,5]**, Stewart Coventry[3,5], Laura Ziems[4,5], Greg Platz[5]
[1]Grains Australia, Australia
[2]SECOBRA, Australia
[3]AGT, Australia
[4]University of Sydney, Australia
[5]Paul Johnston Memorial Trust

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 to 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.

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