

SESSION 1: ADDING VALUE – IMPROVING FLAVOUR

Differences in flavour of malt from different barley varieties and growing regions

Sue Stewart¹, Ross Sanders¹, Nat Livanova¹, Kerry Wilkinson¹, Doug Stewart², Evan Evans³, Jason Able¹

1. *University of Adelaide, SA, Urrbrae 5064, SA, Australia*

2. *Coopers Brewery, Adelaide, SA, Australia*

3. *The Tassie Beer Dr Consulting, Hobart, Tasmania, Australia*

It has long been widely appreciated that beer flavour is strongly impacted by malt kilning regimes and the choice of yeast/hops. And, although barley malt is the structural backbone of traditional beers, choice of barley variety has until recently been largely overlooked as a potential supplier of beer flavour compounds, in addition to the products from the Maillard reaction.

Malts from multiple Australian barley varieties grown in several barley growing regions located in South Australia, Western Australia, Tasmania and Victoria were investigated.

Barley malts were infusion mashed (65°C) at laboratory scale (~600mL wort) to produce pre-boiled, post-boiled wort and beer samples. The differences between the flavour profiles observed with sensory assessment and headspace-SPME gas chromatography-mass spectrometry (HS-SPME GC-MS).

HS-SPME GC-MS analysis focused only on compounds that were significantly different between varieties (ANOVA, $P \leq 0.05$). Various flavour compounds and compound groups that influence malt flavour through the brewing process have been identified. Continuing research into malt flavour will provide another tool that barley breeders can use to develop new varieties that are targeted to various growing regions and to the requirements of maltsters and brewers.

Craft malting in the USA: Reviving an old craft in the 21st century

Jesse Bussard¹

1. *North American Craft Maltsters Guild, Todd, PA, United States*

Malting as both a process and trade has been an essential link between agriculture and brewing for eons. In the United States, historically brewers sourced their grain directly from farmers in their area with a large number of those brewers also malting their grains on-site. The Industrial Revolution (late 1700s-late 1800s) and later, Prohibition (1920-1933) would bring about major turning points in this relationship, eventually wiping out the majority of small, independent breweries and consecutively, malting operations that existed to serve their needs. The years following would usher in major consolidation and commercialization in both beer and malting, and in turn, a loss of collective knowledge and expertise in the malting trade. This trend continued well into the 1980s. In time, the rise of American craft beer would revive new interest in both malt as an ingredient, and the trade of malting itself with several craft malthouses coming online in the US and Canada in the early 21st century. This revival was spurred on by the unprecedented growth craft breweries were experiencing thanks to beer drinkers' desire to explore new and exciting flavors and styles. The local food movement was also taking a more prominent role in the conscience of the American consumer. The intersection of these two camps set the stage for a deeper exploration of malt – the soul of beer. Not surprisingly, a similar scenario is also beginning to play out in Australia. Focusing on the role of the maltster, this session will explore the emergence and

evolution of craft malting in America and Australia, offering comparisons and contrasts between the two, as well as the varieties and types grains maltsters are sourcing. Case studies and commentary from the Australian craft maltsters leading the local malt charge will also be shared.

Breeding for barley variety flavour

**Patrick Hayes¹, Maria Munoz Amatriain¹, Harmonie Bettenhausen¹, Scott Fisk¹,
Campbell Morrissy¹**

1. Oregon State University, Corvallis, OR, United States

Barley, via malt, is the base of beer. Barley malt is the ideal source of nutrition for yeast – which in turn produces the essential ethanol many of us are seeking in our beers. But that's only the beginning: barley malts provide color, flavor, aroma, and much, much more. Rigorous testing pipelines ensure that barley varieties produce malts with requisite quality profiles and no off-flavors. Several years ago, research groups around the world began taking things beyond the pale by asking “is there genetic variation for positive contributions of barley genotypes beer flavour?” In this presentation, I'll review our findings regarding flavour contributions from heirlooms to contemporary varieties - and highlight pending questions and directions for further research.

SESSION 2: ADDING VALUE – MALTING AND BREWING

ZoomBarley Varietal Identification 2.0

NICOLAS MARTELLI¹

1. ZoomAgri, Bibra Lake, WA, Australia

Every year 3B tons of grains and oilseeds are produced and for the last 100 years little has changed in determining the physical quality. ZoomAgri's objective is to bring solutions for the pain points our clients suffer: physical limitations, delay in results, subjectivity, fraud and very high cost of analysis.

ZoomAgri provides artificial intelligence (AI), computer vision, and internet of things (IoT)-based cloud solutions that give real-time results of the quality and variety of grains and oilseeds such as wheat, barley, corn, and sunflower. We provide both hardware (laptop and scanner) and software to run our revolutionary convolutional neural network. Our algorithms compare scanned images of samples with preloaded images of samples. We have digitized over 120 million individual images of grains and oilseeds for determining the quality and variety of grains and oilseeds.

ZoomAgri provides the ability to identify varieties (on a single kernel basis) in less than 3 minutes, and at a fraction of traditional costs. This technology allows real-time truck by truck analysis to guarantee maximum varietal purity and therefore the highest quality. Maltsters and handlers are already using our technology to keep the varietal integrity of their stacks. This technology offers the opportunity to add value along all of the supply chain from farm to table.

Malt for craft brewers – Separating wants from needs

Doug Stewart¹

1. Coopers Brewery, Regency Park, SA, Australia

The craft brewing industry in Australia is a small but growing sector, with craft malt demand less than 5% of Australian malt production capacity. The sector however, can punch above its weight in terms of influence as it is dynamic and vibrant part of the industry. Hence it is worth looking at what the craft industry wants in terms of barley and malt, but we must also be mindful of what they actually need.

Wants include interest in heritage barley varieties, barley flavour, terroir, local production and craft maltings. Typically, all of which comes at a price premium. The reality is that what craft brewers really need is good quality malt at a competitive price. This presentation discusses how the craft brewing industry is rationalising wants versus needs.

Adapting hop production to target craft brewers

Simon Whittock¹, George Webster¹, Oliver Hayes¹

1. Hop Products Australia, North Hobart, TASMANIA, Australia

Humulus lupulus L. (hop), along with water, malt, and yeast, has long been a key flavouring ingredient in beer. A diverse suite of plant secondary metabolites accumulates in mature strobili (fruit or cones) of hop. Different beer styles deliberately target specific cohorts of flavour active secondary metabolites from hop. Hop derived alpha acids isomerise during wort boiling to produce iso-alpha acids that produce a bitter character that balances malt sweetness. Terpene derived compounds from hop are responsible for the floral and herbal

hop characters familiar from traditional ale and lager beers. In recent decades the development of the craft beer industry, with its focus on flavour impact and differentiation, has exploited hop terpene derived compounds, and polyfunctional thiols for their distinct fruit-like flavour impact, predominantly through a process known as “dry hopping”. In dry hopping, hops are added to wort at points in the brewing process after boiling has been completed. The increasing beer market share and volume of the craft beer market, combined with a typically higher rate of hop use per litre of beer, has fundamentally altered the global hop market, the variety mix in the hop estate, and driven change in hop production systems and breeding. New hop varieties have been selected and deployed as the reliance of craft beers on flavour for differentiation has elevated the focus on hop quality as it relates to impact in beer. In this context of change, the ability to deploy proprietary cultivars developed in an in-house plant breeding program, along with commitment to variety turnover and market development has seen Australian hops establish global recognition within the craft brewing sector. This presentation provides an overview of the contemporary cycle of adaptation seen in Australian hop production to support the craft brewing community.

Proteomics reveals commitment to germination in barley seeds is marked by loss of stress response proteins and mobilisation of nutrient reservoirs

Sarah K Osama¹, Edward D Kerr¹, Adel M Yousif², Toan K Phung¹, Alison M Kelly¹, Glen P Fox³, Benjamin L Schulz¹

1. University of Queensland, Brisbane, QLD, Australia

2. Tasmanian Institute of Agriculture, College of Science and Engineering, University of Tasmania, Hobart, TAS, Australia

3. Department of Food Science and Technology, University of California Davis, Davis, CA, USA

Germination is a critical process in the reproduction and propagation of flowering plants, and is also the key stage of industrial grain malting. However, when seeds fail to germinate upon steeping this is known as dormancy, and this can result in inefficiencies in industrial malting. We used Sequential Window Acquisition of all Theoretical ions Mass Spectrometry (SWATH-MS) proteomics to measure changes in the barley seed proteome throughout germination. We found a large number of proteins involved in desiccation tolerance and germination inhibition rapidly decreased in abundance after imbibition. This was followed by a decrease in proteins involved in lipid, protein and nutrient reservoir storage, consistent with induction and activation of systems for nutrient mobilisation to provide nutrients to the growing embryo. Dormant seeds that failed to germinate showed substantial biochemical activity distinct from that of seeds undergoing germination, with differences in sulfur metabolic enzymes, endogenous alpha-amylase/trypsin inhibitors, and histone proteins. We verified our findings with analysis of germinating barley seeds from two commercial malting facilities, demonstrating that key features of the dynamic proteome of germinating barley seeds were conserved between laboratory and industrial scales. The results provide a more detailed understanding of the changes in the barley proteome during germination and give possible target proteins for testing or to inform selective breeding to enhance germination or control dormancy.

SESSION 3A: ACHIEVING A SUSTAINABLE BARLEY INDUSTRY

Sustainability, who leads, who pays? A consumer driven take on barley and sustainability

Anne Stephens¹

1. Key Three Data and Investor at Good Living Brew Co, Chobham, United Kingdom

While most consumers want to be “sustainable” – messaging about how to be a sustainable consumer is confusing and personally challenging, with a “never enough” end point.

If we can't explain the benefits of sustainable products and celebrate incremental improvements for behaviour change, then the very consumers that could pay for more-sustainable products are less likely to do so.

Ingredients marketing is a powerful opportunity for a shift in brand power and increased relevance of a sustainable proposition to consumers.

This talk is about why it's an opportunity for Australian malt producers and how it could be brought to life.

Can craft become sustainable?

Glen Fox¹

1. University of California, Davis, CALIFORNIA, United States

The malting and brewing industries are thousands of years old. And since the beginning, both industries have generated various waste streams and used high volumes of water. The last 200 years saw significant innovations through mechanization and the invention of electricity. Over the last few decades the industry has been proactive in exploring options to reduce carbon miles, reduced wastage, reduced water and upcycling waste streams. Life cycle analysis of the malting and brewing industries shows opportunities for reducing waste and energy changes based on scale of the operations with craft maltsters and craft breweries having limited options, compared to large maltings and breweries. With over 100 craft maltings and over 9000 craft breweries in the USA, the issues of sustainability, especially around water and energy costs is part of every companies strategic plan. This presentation will provide a snap shot of how these massive industries are tackling these challenges.

Contribution of malt to the process of a carbon neutral beer

Amy Dennis¹

1. Lion, Sydney Olympic Park, NSW, Australia

More than 80% of the carbon footprint of a beer comes from Scope 3 emissions, meaning they occur upstream or downstream in the value chain and reside with suppliers and customers, with malt supply for beer being one of the top contributors to the overall footprint. Measuring these emissions has historically been a challenge due to the high level of uncertainty and reliance on third-party assumptions to assign emissions factors, however, we see an opportunity to better quantify the carbon impact of malt supply to reflect current practices, improving the overall accuracy of the footprint. Beyond better measurement, there are opportunities to work closely with malt suppliers and farmers to bring about direct emissions reduction.

Transparent Frameworks: a road map to sustainability

Michael Clancy¹, Mark Goldsmith²

1. PURE Grain, Moree, NSW, Australia

2. Asahi Beverages, Melbourne, VIC, Australia

In 2021 Asahi signed an exclusive supply contract with PURE Grain to provide sourcing and accumulation services to deliver “Grower Direct” malt barley for all of the beer produced at the Yatala brewery in Queensland.

Since this announcement Asahi Beverages has unveiled a new sustainability agenda as it uses its significant scale to create a more sustainable future. The agenda introduces new targets while incorporating previously announced ones, to build a more sustainable business.

The agenda covers climate change, sustainable packaging and the circular economy, supporting local farmers and much more. The full list of targets is extensive and includes a reduction of scope 3 CO₂ emissions by 30% by 2030 and to net zero carbon emissions by 2050. In order to deliver on these targets Asahi will engage in projects and initiatives with local growers and the region’s wider community.

Asahi Sustainable Raw Ingredients Goals:

- Review key raw materials across our supply chain to mitigate any climate risks, water risks and management of environmental loads-priority
- Work closely with growers and support farms to drive best practice land, environment & quality management

PURE Grain has been engaged to facilitate and collaborate to help achieve these goals, in addition to sourcing locally produced malt barley. PURE Grain identifies opportunities in which Asahi may provide direct support or benefit from being an active participant in such projects as farm trials, supply chain improvements and production process improvements

SESSION 3B: ACHIEVING A SUSTAINABLE BARLEY INDUSTRY

The economics of sustainability compliance

Andy Barr¹

1. Farmer and Grain Industry Consultant,, Adelaide, SA, 5460

There is a growing push from grain marketers, processors and consumers for evidence that the grain they are buying is produced more sustainably than in the past. The **International Sustainability and Carbon Certification (ISCC)** is a voluntary sustainability certification scheme enabling participants to demonstrate they are producing biomass in a manner which meets community expectations for environmentally, socially and economically sustainable production. Several grain marketers offered barley growers contracts for grain meeting ISCC standards in the 2021 harvest. Such contracts traded at \$2 per tonne above non-ISCC accredited grain. It is a simple and quick matter to claim the ISCC accreditation but growers can be audited at random following delivering grain against the ISCC contracts. The audit requirements are described in detail and the experience of three growers in the lower north of SA is presented. The cost of compliance with the ISCC can be high – with a time commitment of 1, 2 and 5 weeks for the respective farm managers. My estimate for a first time compliance was \$A30,000. Another sustainability system is the “Farm Sustainability Assessment Tool” (FSA) by Sustainable Agriculture Initiative (SAI), which sets even higher standards than ISCC. The suitability and relevance of these two systems for Australian barley production is discussed.

Zero-carbon emissions target for all growers

Simon Wallwork¹

1. AgZero2030, ., WA, Australia

As farmers in the West Australia Wheatbelt, we are adapting to a changing climate with a 20% reduction in growing season rainfall in the last 20 years. Adaptation will be an ongoing process as the climate continues to dry but there are also emerging challenges and opportunities for Agriculture arising from the global decarbonisation of economies. Agriculture is both a contributor to greenhouse gases and can sequester carbon so we have a unique role to play in the solutions and mitigation to climate change. Simon Wallwork and Cindy Stevens, farming at Corrigin have begun baselining on-farm emissions and planning towards carbon neutrality by 2030. Initially this will involve planting trees to offset emissions from crop and livestock enterprises but eventually they hope to be carbon positive as they adopt innovations to reduce emissions. This approach stems from a motivation to be active participants in climate solutions, but also getting ready for the challenges and opportunities of decarbonisation such as sustainability criteria pertaining to market access, finance and insurance. Simon and Cindy were also founding members of the WA Agriculture Sector led movement, AgZero2030. This movement aims to encourage and promote a positive response to the climate challenge by WA Agriculture. This about moving past the debate and focusing more on solutions. Simon will share both his on farm story and the evolution of AgZero2030.

The value of agrichemicals in a sustainable Farming System

Andrew Weidemann AM¹

1. Grain Industry Consultant, Rupanyup, VIC, Australia

Chemical usage is an important strategic facet of modern agriculture in global food production. In Australia farmers are continually seeking new and more strategic ways to grow crops. For the benefit of this Symposium, we will concentrate our discussions around barley growing in the Wimmera Region of Victoria.

Our family farm is based in the central Wimmera region of Victoria at Rupanyup, where a wide variety of crops are grown strategically to achieve a sustainable production system. A typical rotation of crops on the Weidemann Farm would start with a fallow phase followed by canola and/or wheat, then a pulse crop, followed by barley. The diversity of our crop rotation combined with a diversity of chemical control measures are key factors in controlling a wide variety of problem weeds. Like most farms in grain growing regions, ryegrass is the number one enemy in the farming system but other weeds, such as brome grass, have become increasing problems. To conserve both soil health and soil moisture, we minimise the use of cultivation in weed control. Agrichemicals have played a critical role both in improving soil health by reducing the need for cultivation and adapting to a drier environment where soil moisture conservation is critical.

Over the past two decades we have seen the increase of chemical tolerant crops, especially in canola. With the advent of imidazolinone tolerant barley varieties, increased production opportunities for barley have occurred across a range of farming regions. In 2021, Spartacus CL barley was the predominant barley grown given its tolerance of the IMI chemicals which are often residual from use in the previous crop. Chemical usage on malting barley crops designated for malt production requires good stewardship including adoption of appropriate rates to ensure grain Maximum Residue Levels (MRLs) do not exceed customer specifications. Clearly grain residue levels arising from chemical usage should be well understood by the industry prior to commercial use of chemical products on tolerant crop types. The situation of grain residues becoming known only when large quantities of grain

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

are being traded should be avoided at all costs. This situation arose in 2018, when residue levels of imazapyr in 2018 exceeded the listed MRLs for Japan and South Korea. Following this issue, industry came together to facilitate a good outcome with increased MRL's being put in place to allow the technology to be used and grain exported to these regions again.

In our business we have been selling identity preserved barley since 2004 with the growing season data package given to the end user to verify all chemical usage. This provides an example of how farm chemical use can be responsibly incorporated in a farming system with full end user understanding and acceptance. Its an important step for informing end users of our barley the importance of crop rotations utilising break crops which also use different chemicals such as imidazoline Canola, Lentils and Beans.

For the barley purchaser there is also and intrinsic value in knowing the accumulation history of the grain but this is lost in a co-mingled Bulk handler network process. This is why markets are asking for more information around production methods as a way to ensure consumer confidence is satisfied. But this requirement is also facing pressure from growers who see little value in this approach and are concentrating on growing barley for feed markets instead of Malting markets.

With a very close farm cropping rotation between different crops the usage of products like Glyphosate in managing pre sowing weeds including allowing for stubble retention to conserve moisture has been crucial in increased crop yields over the past 3 decades. Combined with chemical tolerant barley varieties such as the Imidazoline group has seen barley average yields increase on our farm from early in the 1990's from around 3.6tha to close to 5tha average in a 300mm growing.

SESSION 4: MARKETING QUALITY AUSTRALIAN BARLEY

Our humble barley

John Stuart¹

1. GrainCorp Ltd, Sydney, NSW, Australia

The physiological traits of barley are impacted by such a vast array of environmental weather events from sowing through to grain filling and harvesting. Malting barley varieties and qualities vary dramatically across so many Australian geographies that impact grain size, proteins, fungal staining, and the internal starch makeup and cell wall structure of kernels. Malting barley is harvested and stored in different storage types and conditions from large bulk handler bunkers, sheds, steel and concrete bins; to large and small diameter on-farm bins and at times, (though not recommended), silo bags. All the while, our industry hopes to maintain a healthy germinative viability during months of deliveries to maltsters.

This paper describes, in layman's terms, the often-forgotten role of the health of the microscopically thin pericarp and testa layers which encase the embryo of barley kernels, and how they play a vitally important role in the storage, handling, malting and brewing successes and challenges our malting barley industry has across different geographies.

Markets for Australian barley beyond 2025

Mary Raynes¹

1. AEGIC, South Perth, WA, Australia

Australia is one of the world's largest exporters of barley, shipping six million metric tonnes annually on average.

Prior to 2019, Australian barley exports represented around 30-40 percent of the global malting barley trade, and 20-30 percent of the global feed barley trade.

Australia remains one of the largest exporters of barley, and market dynamics are continuing to shift. This presentation will explore how export barley markets might continue to change post-2025.

Quality AUSTRALIAN BARLEY – A Strategic Plan for the Barley Industry

Drew Robertson¹, **Megan Sheehy**², **Elysia Vassos**², **Steve Jefferies**³

1. CBH Group, Perth, WA, Australia

2. Grains Australia Limited, Goodwood, SA, Australia

3. Jefferies Ag Solutions Australia, Adelaide, SA, Australia

The Australian Barley Industry has not previously had a collective unifying strategy to direct its future at any point in its history. Strong industry support for a strategic plan led Barley Australia, now merged with Grains Australia Limited, to initiate discussions with a broad cross-section of the barley industry on the concept and content of a strategic plan for the Australian Barley Industry. This included collection and compilation of high-level background information and convening several sector specific focus group sessions to gather initial thoughts on priorities. A S.W.O.T. analysis was conducted in 2022 with a smaller cross section of the industry, and priority ranking carried out on each item from the S.W.O.T analysis. Consultation with the newly inaugurated Grains Australia Barley Council

(formerly the Board of Barley Australia) and key stakeholders of the barley industry has led to further development and refinement of a draft strategic plan.

This presentation will outline high level fundamentals of the draft Strategic Plan for the Australian Barley Industry. This session of the ABTS will be an opportunity for participants to have direct input into shaping key components of the strategy. The focus of the session will be on key elements of most relevance to the R&D and barley breeding sectors. Interactive technologies will be utilised to enable streamlined and engaging participation.

A supply chain digital twin system to improve the performance and efficiency of the Australian grain supply chain

Julius Kotir¹, Adam Komarek¹, Ryan Ko², Jenny Mahuika³, Andries Potgieter³, Pengchen Hu¹, Joshua Scarsbrook², Scott Chapman¹

1. School of Agriculture and Food Sciences, The University of Queensland, St Lucia, QLD, Australia

2. (School of Information Technology and Electrical Engineering, ITEE, The University of Queensland, Brisbane, Queensland, Australia

3. Centre for Crop Science, The Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Brisbane, Queensland, Australia

The grain supply chain in Australia is facing significant challenges, including variability in harvest volumes due to drought; limited storage capacity, transport bottlenecks, fragmentation of receival sites; underutilized and underinvested rail infrastructure; inconsistency of port infrastructure investment. Moreover, the onset of the COVID-19 disruptions and incorrect decisions due to uncertainty has placed additional pressure on the assets of the supply chain, resulting in higher costs in logistics and lower returns on investments for critical supply chain infrastructure. Digital-Twin models have the potential to address these concerns given their ability to integrate data sources to enable real-time monitoring, control, and optimization of the assets; and simulation to produce various supply chain scenarios for improved decision-making.

Here, we present a supply chain digital twin (SCDT) model - developed based on system dynamics and discrete-event simulation – and applied to a test case of barley production and distribution from Shire scale (i.e. Moree Shire in Australia), highlighting where gains in logistics efficiency can be gained. The model uses locations, and quantity of barley produced and determines the logistics as well as the costs and revenues associated with harvesting and transporting the quantity of barley from the farm-gate to various storage facilities (silos), ports, and other customer demand points, including feedlots, flour mills, and bulk export ports. We also illustrate how the model can be applied to evaluate the effect of risks associated with disruptive events as well as demand and supply variability to improve the economic sustainability of different stakeholders, including those producers, consumers, and businesses that manage and operate the wheat supply chain, across the model application regions and beyond.

Acknowledgement

This work was supported by the research project funding by the Australian federal COVID-19 strategic funding at the University of Queensland.

1. ABARES (2022). Agricultural Commodities: March quarter 2022, Australian Bureau of Agricultural and Resource Economics and Sciences, Canberra. CC BY 4.0. <https://doi.org/10.25814/9x91-hc32>
2. LEK Consulting (2021). Cropping Brief- International Supply Chain Benchmarking Sectoral Assessment Report for the Department of Infrastructure, Transport, Regional Development and Communications 20 August 2021. Available via: [sectoral-report--cropping.pdf](#) (freightaustralia.gov.au)

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

3. White, P., Carter, C. and Kingwell, R. (2018). Australia's grain supply chains: Costs, risks and opportunities, November 2018. Available from URL: <http://www.aegic.org.au> [accessed 10 Nov 2019].
4. Nguyen, N., Green, R Lawson, K. and Goesch.T. (2015). Australia's wheat supply chains: infrastructure issues and implication. Australian Bureau of Agriculture and Resource Economics and Sciences Research report no. 15.1, Canberra.

SESSION 5: AGRONOMY AND FARMING SYSTEMS

Global synergies in crop development, agronomy and genetics to improve barley productivity

Kenton D Porker¹, Nick Poole¹, Max Bloomfield¹, Darcy Warren¹, James Rollason¹, Aaron Vague¹

1. FAR Australia, Bannockburn, VIC, Australia

There is increasing demand for more sustainable crop production practices. New opportunities to increase productivity will be sought by exploiting future Genotype x Environment x Management synergies in different barley systems globally. The scale of current yield gaps, yield benchmarks, and understanding of agronomy to overcome exploitable yield gaps to complement genetic increases in potential yield are more developed in wheat than for barley. Using diverse Australian production zones as an example, we identify research gaps and opportunities for collaboration among barley producing regions to respond to a changing climate

Historical barley breeding and crop agronomy efforts in Australia have focused on improving grain size and adaptation to frost, heat and drought stress. Optimising reproductive phases and earlier flowering has increased yield in most Australian low rainfall regions. Sowing dates have become earlier, however, our studies indicate earlier sowing faster developing cultivars in higher rainfall zones is leading to yields below potential based on available sunlight, water and temperature during the critical period for grain number formation. European germplasm with greater vernalisation requirement, and or reduced photoperiod sensitivity can increase profitability and adaptation of barley for seasons of better potential in Australia provided disease and lodging is managed. While many studies focus on Nitrogen management and earlier sowing as the most important factor to close the yield gap, we found other factors such as canopy management (disease, lodging, head loss) were equally as important, more difficult to management and explained yield differences between 3 – 8t/ha. This is an important finding as they are often overlooked in yield gap studies but are under strong genetic and management control that can be exploited. In conclusion this research highlights larger productivity gains are still possible in parts of the medium to high rainfall zone of Australia with systems that improve canopy management.

Agronomic management techniques for reducing barley head loss in Southern Australia

Melissa McCallum¹, Rhiannon K Schilling^{1,2}, Kenton Porker^{1,3}, Matthew R Tucker²

1. Agronomy Program, SARDI - PIRSA, Urrbrae, SA, Australia

2. Waite Research Institute, University of Adelaide, Urrbrae, SA, Australia

3. Field Applied Research Australia, Bannockburn, Victoria, Australia

Barley head-loss occurs after anthesis and prior to harvest, and causes significant yield reductions across many Australian regions. Head-loss typically occurs when harvest is delayed and/or due to windy conditions when a crop is close to maturity and harvest ripe. Management of yield-loss due to head-loss is difficult, as timeliness of harvest is the most practical solution. Variety selection and some in-season management techniques have been suggested as methods to limit losses, but the basis for this variation is unknown, and environmental conditions have a significant influence on total loss. Using a range of current and historical cultivars in multi-site field experiments, we demonstrated that variety selection and the application of a plant growth regulator (PGR) can slow the rate of head loss. Breeding efforts have been able to reduce overall susceptibility of varieties to head loss. This

allows for a wider harvesting time period before head loss causes major yield loss. The use of PGRs can also be effective at improving head retention of more susceptible varieties and making those varieties more competitive in terms of head retention to less susceptible varieties. However, breeder selections also appear to have altered the response of different genotypes to growth regulators that promote yield. Our results suggest that while environment conditions play a major role in determining barley head loss, there are agronomic management levers that can be utilised to limit potential exposure to these events.

Tweaking agronomy for our malt varieties in northern NSW

Matt Gardner¹, Skye Traill¹

1. AMPS Agribusiness, Moree, NSW, Australia

There are a limited number of management levers that growers can utilise during the season to maximise production for a given situation and to meet desired market specifications. Broadly, these management levers available to growers include variety selection, rotation, planting date, nutrition, disease and pest management and canopy manipulation. It is important to understand how each one of these levers will impact the crop at a broad level but also at a variety level to ensure yield potential and grain quality targets can be reached. AMPS Research since 2008 along with many other groups have investigated how barley varieties respond to these management levers and continue to refine variety recommendations. Our data suggests that planting date can still have the biggest impact on yield responses and grain quality throughout our region, particularly in warm dry finishes. Interestingly, of the current varieties grown in our region there is not a large spread in maturity, with approximately 12 days separating flowering dates of the longest and shortest varieties. Reductions of up to 55% yield have been observed where planting date has been delayed from late April to early June, that has coincided with significant reductions in test weight and increases in screenings and protein. There have been large differences between varieties observed and their ability to maintain grain quality as we shift later in the planting window. Alternatively, where cool wet springs have eventuated in years such as 2021 the responses to planting date can be <5%. For this reason, planting date becomes increasingly important as we shift further west into the drier parts of our growing region. Nutrition has been identified to have the next biggest impact grain yield and quality and particularly nitrogen nutrition. It has always been a balancing act of supplying enough nitrogen to achieve yield potential without accumulating excessive protein. Many trials have demonstrated that varieties can vary significantly in their accumulation of protein. For example RGT Planet achieved 1.8% lower protein at a given nitrogen application compared to Commander, while the response curve to increasing nitrogen rates was significantly flatter for Maximus CL compared to RGT Planet. These variations create opportunities to further refine nitrogen strategies for growers throughout the region. Using early planting dates and adequate nitrogen to achieve high yield potential increases our risk of lodging of the crop late in the season. This lodging risk can be further exacerbated by variety selection, especially with varieties that accumulate large quantities of biomass early in the season. Although not widely used across our region growth regulators have been shown to successfully reduce lodging risk and losses associated with lodging. In a preliminary trial in 2021 a lodging susceptible variety Leabrook, showed a 45% reduction in final lodging scores and a significant yield increase of 0.6 t/ha compared to the control where no growth regulators were used. Although many of these trials represent basic agronomy, it is an ongoing process as new varieties are released into the market and from a growers point of view provides important information required to successfully adopt new varieties and realise their full potential.

SESSION 6: ELEVATOR PITCHES (AND POSTERS)

Pre-season soil/crop residue testing can identify barley crops at risk of spot form of net blotch infection

Mark McLean¹, Melissa Cook¹, Grant Hollaway¹

1. Agriculture Victoria, Horsham, VIC, Australia

Spot form of net blotch (SFNB) is a common foliar disease of barley that can cause grain yield losses of up to 44% and reductions to grain quality. Losses vary greatly depending on varietal resistance, seasonal conditions and the amount of infected crop residue present. Spot form of net blotch is caused by the fungal pathogen *Pyrenophora teres* f. *maculata*, which survives from one season to the next on crop residue. PredictaB[®] soil/crop residue testing has been developed by SARDI to quantify inoculum loads and this study was conducted to determine its potential to provide growers with a risk estimate at the start of the growing season. The study consisted of two experiments conducted in the low and medium rainfall zones of south-eastern Australia to determine the relationship between pre-sowing inoculum loads and subsequent SFNB severity and grain yield. In each experiment, different inoculum levels were established during the first year, by sowing either a susceptible or resistant barley variety and adding different amounts of infected barley stubble, or sowing wheat with no infected barley stubble. At the start of the second season, soil/crop residue were sampled, and inoculum loads determined by PredictaB[®]. A susceptible barley variety (var. Dash) was sown during year two and disease severity was visually estimated at early stem elongation, flag emergence and late flowering stages of crop development. Grain yield was measured at the end of the season. In both experiments, pre-sowing inoculum levels correlated to in-season SFNB severity, especially at early stem elongation ($R^2=0.33$ and 0.28). There was less correlation between pre-sowing inoculum loads and SFNB severity later in the season and little correlation to grain yield ($R^2=0.07$ and 0.02). This demonstrated that pre-sowing inoculum loads can be used by barley growers to identify barley crops at greatest risk of loss from SFNB.

Quantitative proteomics of the malt barley proteome: Understanding the impact of genetic variation on water uptake.

Clare E O'Lone^{2, 1}, Angela Juhasz², Mitch Nye-Wood², James A Broadbent³, Jeni Pritchard¹, Hugh Dunn⁴, David Moody⁵, Jean-Philippe Ral¹, Michelle L Colgrave^{2, 3}

1. Agriculture and Food, CSIRO, Black Mountain, Canberra, ACT, Australia

2. ARC Centre of Excellence for Innovations in Peptide and Protein Science, Edith Cowan University, Joondalup, Perth, WA, Australia

3. Agriculture and Food, CSIRO, St Lucia, Queensland, QLD, Australia

4. Pilot Malting Australia, Edith Cowan University, Joondalup, Perth, WA, Australia

5. Barley Breeding, InterGrain, Bibra Lake, Perth, WA, Australia

Malting is the controlled germination of the barley grain in preparation for brewing, distilling, or food manufacturing. Exposure to moisture leads to the activation and synthesis of enzymes that modify the endosperm's physical structure to be suitable for downstream use. Different barley varieties, defined by a distinct genotype, exhibit different malting characteristics in response to water and the abundance of expressed key enzymes. Therefore, identifying the proteins that control this response is important to barley breeders in developing varieties with desirable malting characteristics.

In this analysis, two InterGrain barley genotypes: (1) Flinders, an established premium variety, and (2) IGB1467, a trial breeding line with a unique phenotype of malting at lower

moisture content, were used to uncover differences in the grain proteomes. Data independent acquisition (DIA) mass spectrometry (MS) via Sequential Window Acquisition of all THEoretical fragment-ion (SWATH) was used to achieve an unbiased quantitative characterisation of the malt barley proteomes. Protein abundance patterns were measured at three-time points during water uptake. Subsequent computational biology analysis was performed to define the significant protein abundance differences between the two malt barley genotypes that differ in response to water.

A total of 7,073 unique peptides mapped to 2,316 proteins identified with 1,519 proteins quantified at a minimum of two peptides per protein and a 1% false discovery rate. Unsupervised principal component analysis (PCA) revealed proteome alteration associated with genotype and time points of 24.8% and 15.2%, respectively. Gene Ontology (GO) analysis revealed significant up-regulation of "Hydrolase activity" and down-regulation of "Nutrient reservoir activity" pathways in both genotypes. Malt barley proteome profiling provides insight into how the expression of different protein classes and isoforms differ between genotypes and influences industry-relevant water uptake phenotype.

Identification of QTL for the number of vascular bundles in barley stem

Yanan Nu¹, Tianxiao Chen¹, Chenchen Zhao¹, Meixue Zhou¹

1. University of Tasmania, Prospect, TAS, Australia

The vascular bundle is the transport system that transfers photosynthetic products, mineral nutrients and water from the leaf and root to the panicle, which plays a significant role in determining crop yield and the mechanical strength of the stem. However, the genetic basis for traits associated with vascular bundles has remained largely undiscovered in barley (*Hordeum vulgare* L.). In this study, we performed a quantitative trait locus (QTL) mapping for the number of vascular bundles, stem diameter, and stem wall thickness at the first and third internode of barley stem using 155 DH lines. The number of vascular bundles was mainly by a major QTL on chromosome 2H, accounting for about 20% of the phenotypic variation. The numbers of vascular bundles at both 1st and 3rd internodes showed a minor but significant positive correlation with the stem wall thickness of both the 1st and 3rd internodes and stem diameter of the 3rd internode. Our results provided important insights for understanding the genetic mechanisms of vascular bundle formation in barley stem.

QTL mapping of barley lodging resistance

Tianxiao Chen¹, Yanan Niu¹, Chenchen Zhao¹, Meixue Zhou¹

1. University of Tasmania, Prospect, TAS, Australia

Barley stem lodging is one of the major factors limiting yield potential. Reducing plant height has been the major target for increasing lodging resistance. The purpose of this study is to map QTL for lodging resistance and their relationship with stem length and bending resistance of different internode as well as plant height using 155 double haploid lines generated from a cross between a wild barley accession, SYR01, and a commercial variety, Gairdner. A major QTL for lodging resistance was identified on 4H while the major QTL for plant height was mapped to 3H, indicating that the lodging resistance QTL is independent of plant height, confirmed by a non-significant correlation between lodging resistance and plant height. Bending resistance of the 4th internode contributed the most to the lodging resistance.

Delving into the genetic architecture of early vigour in Australian barley

Samir Alahmad¹, Miguel Plata Fajardo¹, Cameron Van-Lane^{1,2}, Alison Kelly³, Jack Christopher⁴, Ian Godwin¹, Andrew Borrell¹, Ben Hayes¹, Lee Hickey¹, Hannah Robinson^{1,5}

1. Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, St Lucia, QLD, 4072, Australia

2. School of Agriculture and Food Sciences, St Lucia, The University of Queensland, Brisbane, QLD, Australia

3. Department of Agriculture and Fisheries, Leslie Research Facility, Toowoomba, QLD, 4350, Australia

4. Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Toowoomba, QLD, 4350, Australia

5. InterGrain Pty Ltd, Perth, WA, 6163, Australia

Australian rainfall is highly variable with increasing frequency of drought events challenging Australian crop production. To begin tackling this obstacle and better adapt crops to the changing Australian environment, we need to better understand the genetic eco-system modulating drought adaptation. Yet, drought adaptation is complex and is made up of a network of traits and trait-interactions. Early seedling vigour, defined as the rapid development of leaf area, is one such trait and has the potential to improve water-use efficiency and enable drought avoidance. Vigorous early growth in climates which experience late drought reduces evaporative water loss by shading the soil surface from direct solar radiation, allowing more water to be available for crop transpiration. However, if early growth is excessive in a terminal drought, insufficient water may be available to optimise grain-filling. Early vigour also provides other agronomic benefits, such as improved phosphorus and nitrogen uptake as well as enhanced weed competitiveness. This study explored variation for early vigour in barley (*Hordeum vulgare*) and determined its physiological and genetic components. Normalised difference vegetation index (NDVI) was used as an objective, quantitative measure for early vigour across six field trials conducted over two years. Variation for NDVI was explored in a panel of 334 barley individuals, comprised of an Australian relevant doubled haploid population and a subset of a nested association mapping population, and genotyped with 14,984 polymorphic DArT-seqTM markers. Single-marker and haplotype-based genome-wide association analyses were performed, significant QTLs were identified on chromosomes 2H, 3H and 5H and their relationship with proximal key developmental genes was explored. With the current advances in high-throughput phenotyping and genomic modelling, our study delivers insights into how these technologies can be harnessed to improve prediction and breeding for early vigour in barley.

Investigating DNA methylation changes due to crop breeding techniques in barley

Judith Eglitis¹, Peter Crisp¹

1. University of Queensland, Brisbane, QLD, Australia

Studies into epigenetics and specifically DNA methylation have in recent years become much more heavily investigated for its potential use in crop improvements, with new and more accessible technologies such investigations have become feasible. Technology designed by our lab called UMR-seq allows sequencing of the methylome with a twenty-fold decrease in cost. This has opened up the window to look at potential variation in methylation across crop breeding methods to identify new avenues of diversity not found in genes alone.

Barley provides an ideal genome for methylome studies as it is much less complex than other grains due to its diploid state and provides a large genome area for investigation. In this study, we will investigate any variation in methylation produced through speed breeding and tissue culture to determine if and how these techniques may alter methylation profiles and if they are heritable across generations. Research already shows that tissue culture produces somaclonal variation but as speed breeding is such a new method no research has looked into methylation changes due to these conditions. We predict that due to the stressful environments of these methodologies they may induce some changes in methylation but are unlikely to be deleterious but in fact useful sources of variation for breeders and studies.

Protein identifications from hordein-reduced barley and malt

Mahya Bahmani¹, Angela Juhasz¹, Utpal Bose^{1,2}, Mitchell G. Nye-Wood¹, Malcolm J. Blundell³, Crispin Howitt³, Michelle Colgrave^{1,2}

1. Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science, Edith Cowan University, Joondalup, WA, Australia

2. Agriculture and Food, CSIRO, St Lucia, QLD, Australia

3. Agriculture and Food, CSIRO, Canberra, ACT, Australia

Barley (*Hordeum vulgare* L.) is the fourth major cereal being produced globally and is widely used for malting and brewing. Protein content and composition are key determinants of barley grain and malting quality. Hordeins, the major storage proteins in barley are known triggers of Coeliac disease (CD). Here, proteomics was employed to investigate the proteome of both grain and malt from the malting barley cultivar, Sloop, and single-, double- and triple hordein-null lines bred in a Sloop background. The triple-null line is an ultra-low gluten barley cultivar known as Kebari®. Using a discovery proteomics approach, we identified 2,884 proteins in the barley and 3,173 proteins in the malt samples. Comparison between the triple hordein-null line to its corresponding malt showed the presence of 2,228 and 2,240 proteins in barley flour and malt samples, respectively. Among these proteins 44% were common between the grain and malt; there were 869 proteins unique to malt sample and 857 proteins unique to the grain sample. Gene Ontology enrichment analysis showed that unique proteins to malt have catalytic and hydrolase activities and those proteins are involved in metabolic processes such as lipid metabolism, beta-oxidation and acyl-coA synthesis. Future studies will focus on the relative quantitation of the various protein families. The results obtained from this study provide an understanding of the link between protein composition and malting quality in Coeliac-friendly barley varieties.

KEYWORDS: Barley, Malt, Hordein, Proteomics, DDA, LC-MS

Utilising novel genetic diversity to increase barley yields nationally

Anh Tung Pham¹, Jason Able¹, Julian Taylor²

1. University of Adelaide, Glen Osmond, SA, Australia

2. Biometry Hub, University of Adelaide, Waite Campus, Urrbrae SA 5064, Australia

In a previously funded GRDC project (UA00148) several genomic regions were identified in wild barley that were associated with increased biomass, grain number per ear (GPE), and thousand-grain weight (TGW) under drought in controlled conditions. Eight beneficial genomic regions were incorporated into Compass, LaTrobe, and Granger via backcrossing using molecular markers tightly associated with the aforementioned traits. Field trials were

then conducted at 11 locations in two years 2020-2021 with up to 108 experimental lines to examine whether the wild barley genes improved the yield in barley lines with Australian genetic backgrounds. Twelve experimental lines were found to yield 5% or higher than the corresponding parents in at least four tested environments across two years. At the site with the lowest growing season rainfall (GSR), Merredin (WA), Anh-39 was the top-yielding line whose yield was statistically higher than all other lines. It yielded 7% higher than Rosalind and Beast, 15% higher than its parent Compass, and 14% higher than RGT Planet in the 2021 growing season. At the locations with medium and high precipitation, RGT Planet is most often the highest yielding line but there were experimental lines whose yields were not statistically different. Line Anh-27 carried a genomic region from wild barley on chromosome 4H that increased GPE and was shown to have an improvement of 2.5 grain/ear compared to Compass. This line also has the highest GPE in almost all of the tested locations from two year's evaluation and had yield 4-5% higher than Compass in seven out of the 11 tested environments. Selection using the genomic regions from wild barley has shown to improve barley yield and yield components, and has led to the development of germplasm specifically tailored for Australia's variable environments.

Investigating different genomic prediction models in commercial barley breeding programs

Shiva Azizinia¹, David Moody², Hannah Robinson², Daniel Mullan², Jayfred Godoy², Allan Rattey², Gabriel Keeble-Gagnere¹, Kerrie Forrest¹, Mathew J Hayden^{1,3}, Hans D Daetwyler¹, Josquin Tibbits¹

1. Agriculture Victoria, Bundoora, VIC, Australia

2. InterGrain, 19 Ambitious Link, Bibra Lake, 6163, Perth, WA, Australia

3. School of Applied Systems Biology, La Trobe University, Bundoora, VIC 3083, Melbourne, VIC, Australia

Genomic prediction (GP) aims to use the estimated effects of genome-wide distributed markers to estimate breeding values of individual genetic entities. With marker and phenotype information from observed populations, genomic prediction models are trained to estimate genomic breeding values of candidate lines. In this way more comprehensive and reliable selection can be achieved for lines with only genotypic information. A variety of genomic prediction statistical models have been tested in crops for traits with different genetic architectures. The most used genomic prediction models which commonly display high predictive accuracy are linear parametric methods (BLUP) and Bayesian methods.

In this study, we compared genomic prediction models (GBLUP vs Bayesian) to investigate the genomic prediction accuracy of 19 agronomic traits in commercial barley breeding program. Phenotypes from field trials in multiple locations across Australia (2011 to 2020) were corrected for fixed effect in a linear model to generate BLUEs for use in model training. Genotypes were generated Illumina Wheat Barley 40K Infinium assay which was imputed to whole genome level. Prediction accuracy analysis implemented a leave-one-year-out scheme in which lines of a specific year were excluded from the population and considered as validation set. The correlation of estimated GEBV and BLUE phenotypes of the year, represented the prediction accuracy.

Accuracies ranged from 0.4 to 0.6 for the disease traits (e.g. leaf rust, various net blotches, etc.) and 0.2 to 0.55 for the quality traits (e.g. protein, Diastatic power, retention, etc.) in BayesR and similarly for GBLUP models. Overall prediction accuracy of two methods showed that for disease traits Bayesian method performed slightly better than GBLUP which is confirming efficiency of Bayesian methods in estimating GEBVs of traits with simpler genetic architectures and larger SNP effects. For quality traits, where more QTL with small effects are involved, the two methods provided similar results.

Nested association mapping to dissect the genetic architecture of spot blotch resistance in barley

Dipika Roy¹, Eric Dinglasan¹, Kai Voss-Fels^{2,1}, Laura Ziems³, Greg Platz^{1,4}, Reg Lance⁴, Lee Hickey¹

1. QAAFI, The University of Queensland, St Lucia, QLD, Australia

2. Grapevine Breeding, Professor, Hochschule Geisenheim University, Geisenheim, Germany

3. Cereal Molecular Genetics, The University of Sydney, Postdoctoral Research Associate, Sydney, New South Wales, Australia

4. Department of Agriculture and Fisheries Queensland, Principal Pathologist, Warwick, Queensland, Australia

Spot blotch, caused by *Bipolaris sorokiniana*, is a foliar disease of barley (*Hordeum vulgare*). Deployment of resistant cultivars is the most sustainable and economical control strategy. The aim of this study was to dissect the genetic basis of spot blotch resistance and provide potential targets for breeding resistant cultivars. In this study, we evaluated a multi-reference parent nested association mapping (NAM) population for spot blotch disease response, days to flowering and plant height in three field trials. Genome-wide association analyses were performed by combining phenotypic datasets (n=2,445 barley lines) from 2016, 2017 and 2107 experiments and genomic datasets (4,852 high-quality SNP markers) and revealed four key quantitative trait loci (QTL) for spot blotch resistance, namely *q.SB.1H*, *q.SB.3H*, *q.SB.5H* and *q.SB.7H* on chromosomes 1H, 3H, 5H, and 7H respectively. The *q.SB.5H* QTL was considered a potentially new locus, whereas the other three were co-located with previously reported QTL. We demonstrate that pyramiding resistance alleles can achieve significantly higher levels of resistance. Four QTL for days to flowering were detected on chromosomes 1H, 3H, 5H, 7H, along with four QTL for plant height on chromosomes 2H, 3H, 6H, and 7H. Very late, tall genotypes can be differentiated easier in terms of resistance, but importantly resistance alleles are available across the spectrum of plant heights and flowering times. The pre-breeding germplasm and markers identified in this study provide useful tools for barley breeders seeking to develop spot blotch resistant cultivars for the future.

Searching sources of germplasm with multiple disease resistance against barley foliar diseases

Sanjiv Gupta^{2,1}, Simon Rogers²

1. Western Crop Genetics Alliance, College of Science, Health, Engineering and Education (SHEE), Murdoch University, Murdoch, WA, Australia

2. Grains Research and Industry Innovation, Department of Primary Industries and Regional Development, South Perth, WA, Australia

Majority of barley varieties around Australia are deficient in foliar resistances as they are affected by several leaf diseases like net blotches, scald, leaf rust and powdery mildew which impact on their yield and quality and, thus, reduce returns to growers and its marketability in export markets. One out of many key objectives in the breeding programs is to develop varieties holding resistances preferably to more than one disease or rather exhibiting multiple resistances in conjunction with yield, quality and agronomic traits. Under the national barley foliar disease improvement program, more than 300 germplasm lines from various international institutes were phenotyped against net and spot form net blotches, scald, powdery mildew, leaf rust and barley yellow dwarf virus. A summary of results indicated that these lines showed range of responses (resistant through susceptible) to

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

powdery mildew and scald. Over all more than 1500 data points were obtained for this material against three diseases. When screened against net form net blotch, leaf rust and BYDV as well, nearly 50 lines showed additional resistances exhibiting resistances to multiple diseases i.e. two or more diseases. Thirteen lines showed resistance to three or more diseases. A set of lines also exhibited adult plant resistances (APR) against net form net blotch and powdery mildew. Lines like Armelle, Bolivia, Dayton, MSS87, Quinn etc hold great potential to identify genomic regions with multiple disease resistance QTLs in pre-breeding programs.

SESSION 7: NEW OPPORTUNITIES

Genetic approaches to induce novel variation in barley for the control of grain development

Xiujuan Yang¹, Caterina Selva¹, Sarah M McKim², Kelly Houston³, Chao Ma¹, Matthew R Tucker¹

1. University of Adelaide, Urrbrae, SA, Australia

2. Division of Plant Sciences, University of Dundee at the James Hutton Institute, Invergowrie, UK

3. Cell and Molecular Sciences, The James Hutton Institute, Invergowrie, UK

Seed development in barley is dependent upon coordinated inputs from multiple plant organs, floral tissues and the surrounding environment. Understanding how these inputs are integrated is a fundamental requirement to sustain and improve the multi-billion-dollar Australian grains industry, particularly in the face of variable climatic conditions. Knowledge of barley reproductive biology may offer opportunities to improve grain number, size and composition. Advances in this area have historically been hindered by the complexity of floral organs, a lack of mutants, and the large genomes involved. For example, the most prominent tissues in the grain are derived from the ovule, a female reproductive organ that is buried deep within the flower and is difficult to access. The genetic basis for barley ovule development, and how different ovule tissues contribute to grain features, has remained unclear. In recent work we have developed a range of gene editing tools, diversity panels, phenotyping methods and genomic datasets to study cereal ovule and seed development. Using these resources, we've started to address how differences in barley flower development translate into altered grain features. The fundamental knowledge is providing new targets for study that may offer downstream opportunities for application in the barley industry.

Whisky is better with Chips and Pretzels

Gabriel Keeble-Gagnere¹, Don Isdale¹, Kerrie Forrest¹, Debbie Wong¹, Hannah Robinson², Jayfred Godoy², Allan Rattey², David Moody², Daniel Mullan², Tress Walmsley², Hans Daetwyler^{1,3}, Josquin Tibbits¹, Matthew Hayden^{1,3}

1. Agriculture Victoria, Australia, Bundoora, VICTORIA, Australia

2. InterGrain, 19 Ambitious Link, Bibra Lake, WA, Australia

3. School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia

If increased farm gate profits are to be realised by grain growers and future food security challenges are to be met, technological advances in fields such as genomics and bioinformatics need to have clear paths to impact. As variety improvement by breeding is ultimately applied genomics, knowledge gained at the research and pre-breeding end of the breeding spectrum needs to translate seamlessly into the hands of breeders. However, historically this has been difficult to achieve due to the inability to easily link and integrate genomic information generated across time and different technology platforms.

We have developed the Infinium Wheat Barley 40K SNP genotyping array in parallel with the open-source, web-based tool *Pretzel* to harness the growing wealth of genomic information and bridge the divide between research and breeding. The array delivers high quality genotype data for SNP that tag LD blocks in globally diverse germplasm, enabling highly accurate imputation to the exome- or genome scale. It is particularly suited for large-scale deployment in breeding programs. Combined with *Pretzel*, outputs from the SNP array can be seamlessly integrated with existing knowledge, creating a two-way exchange between novel results and the literature, as well as from research to breeding.

This talk will focus on a case study to demonstrate *Pretzel's* ability to integrate genomic data to facilitate the rapid identification and breeder uptake of markers on the Infinium Wheat Barley 40K SNP array for the cyanogenic glucoside epiheterodendrin trait, which is of particular interest to breeders aiming to develop non-glucosidic nitrile (non-GN) barley varieties. This example highlights the emerging challenge of working with multiple complete genomes and relating results from different genotyping platforms to one another.

Development of green (unkilned) barley malt as a brewing raw material

Celina Dugulin¹, Gert De Rouck², David Cook¹

1. *International Centre for Brewing Science, School of Biosciences, , University of Nottingham, Loughborough, LEICESTER, England*

2. *KU Leuven, Bioengineering Technology TC, Ghent and Aalst Technology Campuses, Ghent, Belgium*

Kilning of malt is an energy intensive process which accounts for approximately 78% of energy usage in the malting process. Whilst kilning is important in regulating the colour, flavour, stability and processability of finished malt, green (unkilned) malt already contains the key components of brewing value – extract content and the enzymes with which to digest starch into sugars. Due in particular to this high diastatic enzyme content, green malt is already utilised by some grain whisky distillers.

From a sustainability perspective, the present EU funded project looked at the possibilities to develop a brewing process for lager beers, brewing with 100% green malt. Our key objectives were to demonstrate feasibility and to use advances in brewing technology (e.g. wet milling in the absence of oxygen) to overcome key obstacles such as high levels of S-methyl methionine and lipoxygenase activity in the grist. In the 5 hL pilot brewing study, six pairs of brews were conducted, each of which featured a green malt brew and a kilned pilsener malt brew prepared from the corresponding batch of green malt. Specifications of the finished beers support the hypothesis that acceptable lager beers can be brewed using 100% green malt. Furthermore, storage trial analytical data indicated that green malt beers may be more flavour stable. There is however a need in each case for more detailed sensory studies to support these analytical findings.

Future prospects and possibilities for expanding the use of green malt as a raw material in brewing will be considered. This will be placed within the context of known logistical challenges in the handling and storability of the material.

CRISPR Beer: Gene Editing and the Barleys of the Future

Ian Godwin¹

1. *The University of Queensland, St Lucia, QLD, Australia*

CRISPR? What does it stand for? Gene editing, what does that mean? What the heck is allelic variation? Why do you really, really, really like/hate the flavour of alcoholic beverages? Or perhaps you think beer really doesn't like you?

Do you need to know the answers to these questions? Of course you do, you just don't know it yet. Please join me if you want to understand how the humble barley grain and your beer, whisky and animal feed can benefit from the wonder that is gene editing, particularly in a world of climate change, increasing energy costs and the economic and social drivers of sustainability.

The ability to edit genes gives us the opportunity to create subtle or massive changes to barley – the plant, the grain and the products. This talk will focus on how that can be

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

achieved using CRISPR gene editing, and why it is an important tool in the struggle to ensure that beer maintains its place on the human food pyramid (the top, along with chocolate). CRISPR gene editing is one of the many exciting new breeding tools that can deliver designer barleys for your next pale ale, while achieving better disease resistance, more drought and heat tolerance, better end use and flavour profiles, as well as improving the sustainability of your aspirational circular economy and reduced footprint throughout the life cycle.

You may also gain further insight into your own complex relationship with beer.

SESSION 8: BIOTIC STRESS TOLERANCE / RESISTANCE

Fungicide resistance in the barley foliar pathogen *Pyrenophora teres f. teres* in the southern growing region of Australia

Tara Garrard^{2,1}, Hugh Wallwork², Kejal Dodhia³, Wesley Mair³, Fran Lopez³

1. Agriculture Food and Wine, University of Adelaide, Adelaide, South Australia, Australia

2. SARDI, Urrbrae, SA, Australia

3. CCDM, Curtin University, Perth, Western Australia, Australia

In recent years multiple cases of fungicide resistance have occurred in the Australian grains industry. It is common practice for 2-3 fungicide applications per season to be used in medium and high rainfall zones. Crop rotations and varietal resistance remain a key component of managing disease and a lack of consistency in these practices have led to a rise in cases of fungicide resistance.

In 2019 pathologists at SARDI and fungicide resistance experts from the CCDM were alerted to three paddocks on the southern Yorke Peninsula (YP) in South Australia that were rapidly developing symptoms of net form net blotch (NFNB) caused by the pathogen *Pyrenophora teres f. teres*. The paddocks were sown to the variety Spartacus CL Plus into Spartacus barley stubble and had been treated with a full rate of seed treatment containing the SDHI fluxapyroxad in both years. This put the paddocks at high risk for fungicide resistance and prompted a region wide survey by the CCDM and SARDI pathologists.

Sample analysis conducted at CCDM found that 80% of the 15 paddocks sampled for NFNB across the YP had reduced sensitivity to fluxapyroxad and 60% of those paddocks also contained strains of the pathogen highly resistant to the fungicide. Testing for the DMI tebuconazole was also conducted on the samples and found that 100% of the paddocks contained highly resistant strains of the pathogen.

The pathogen *P. teres f. teres* is sexually reproducing in Australia and has a highly variable pathogen population ranging in virulence patterns and aggressiveness, enabling the pathogen to adapt quickly to changing selection pressures such as varietal resistance and fungicide use.

Since 2019 paddocks across SA and into Vic have been found to contain the SDHI resistance and pathologists are extending management strategies to industry through the Australian Fungicide Resistance Extension Network (AFREN).

Pairing classical techniques and statistical genetics to characterise rust resistance genes

Laura A Ziems¹, Davinder Singh¹, Miguel Sanchez-Garcia², Ahmed Amri², Mark S McLean³, Lisle Snyman⁴, Robert F Park¹, Mark J Dieters⁵

1. School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Sydney, NSW, Australia

2. International Centre for Agriculture Research in Dry Areas (ICARDA), Rabat, Morocco

3. Agriculture Victoria, Horsham, VIC, Australia

4. Hermitage Research Facility, Department of Agriculture and Fisheries, Warwick, QLD, Australia

5. School of Agriculture and Food Sciences, The University of Queensland, Brisbane, QLD, Australia

Utilisation of ICARDA (International Centre for Agricultural Research in the Dry Areas) barley germplasm in Australian breeding programs will be enhanced with knowledge of both known and novel disease resistance genes present in the material. A total of 846 barley lines and landraces imported from ICARDA Morocco through the years 2014-19 were genotyped with

the DArT-seq genotype-by-sequencing platform, returning 90,214 markers. Known barley leaf rust (BLR) all stage resistance (ASR) genes were postulated in this panel through multi-pathotype glasshouse screens identifying; *Rph1*, *Rph2*, *Rph3*, *Rph7*, *Rph9.am*, *Rph12*, *Rph13*, *Rph14*, *Rph19*, *Rph21* and *Rph25*, of which *Rph3* was in the highest frequency. Gene postulations were converted into a binary score for genome wide association analysis (GWAS). GWAS was able to accurately predict genomic location of characterised ASR and identify candidate regions for ASR genes with an unknown location. In addition, minor effects indicated genomic regions (known and novel) interacting with postulated genes. Adult plant field screens were conducted in the years following importation (a total 17 separate screens) with the most virulent pathotype (5457P+) of BLR, to assess resistance across this panel. In 2021 the full panel was screened in a single field environment providing connectivity between screens, allowing prediction of disease response across environments. GWAS of predicted values for adult plant disease response was conducted and identified nine putative QTL. Genomic regions on chromosomes 5H, 7H and two regions on 2H had the largest effect in controlling resistance to *P. hordei*. A total of 79 individuals were susceptible to all pathotypes at the seedling stage, of these 35 showed a resistance response in the field and are considered candidates for uncharacterised adult plant resistance. This study combines classical gene postulation techniques with modern statistical analysis to accelerate the identification and characterisation of both known and previously unknown candidate resistance regions.

Mapping of quantitative trait loci in barley associated with resistance to the stripe rust pathogen *Puccinia striiformis* f. sp. *hordei*

Davinder Singh¹, Laura Ziems¹, Peter Dracatos¹, Kerrie Forrest², Mumta Chhetri¹, Sridhar Bhavani³, Robert Park¹

1. University of Sydney, Cobbitty, NSW, Australia

2. Genomics & Cell Sciences, Agriculture Victoria Research, Bundoora, Victoria, Australia

3. CIMMYT, International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico

Stripe/yellow rust (BYR) caused by the fungus *Puccinia striiformis* f. sp. *hordei* (*Psh*) is one of the most damaging diseases of barley that can cause complete crop loss. Genetic resistance is the most economical and eco-sustainable means to control the disease. *Psh* has not been detected in Australia and the country relies on offshore testing for characterization and mapping of BYR resistance. Offshore testing in Mexico demonstrated that genotypes Baudin, Fumai8, Pompadour, Ricardo and Zug161 carry robust resistance to BYR. To characterize resistance in these genotypes, five mapping populations (Ricardo/Gus, Pompadour/Zhoungdamei, Fumai8/Baronesse, CI9214/Baudin and Zug161/Pompadour) were phenotyped in the field across 2 years and genotyped using >10K DArT-seq markers. QTL mapping detected 15 QTL (two for Ricardo/Gus on chromosomes 3H and 4H; four for Pompadour/Zhoungdamei on 1H, 2H, 5H and 7H; four for Fumai8/Baronesse on 1H, 3H, 4H and 7H; three for CI9214/Baudin on 1H, 4H and 7H; and two for Zug161/Pompadour on 1H and 5H). Among these, four loci (*Rpsh_QRic*, *Rpsh_QPom*, *Rpsh_QFum* and *Rpsh_QBau* contributed by Ricardo, Pompadour, Fumai8 and Baudin, respectively) were the most significant. *Rpsh_QPom* was detected in three populations (Pompadour/Zhoungdamei, CI9214/Baudin and Zug161/Pompadour) on chromosome 1H spanning an area of 1.2-20.2 Mbp with closest marker 3396875 peaking at 8.78 Mbp. *Rpsh_QRic* (595.6-662.6 Mbp) was detected in two populations (Ricardo/Gus and Fumai8/Baronesse) on chromosome 3H with closely associated marker 3255950 positioned at 640.36 Mbp. *Rpsh_QFum* was specific to population Fumai8/Baronesse encompassing an area of 29.4 Mbp with closely linked marker 3260529 at position 8.78Mb on 7H. Among these four QTL, *Rpsh_QPom/Rpsh_QBau* is the

most stable in terms of phenotypic contribution (~35%) and number of associated markers (17-35 depending upon the mapping population). Further fine mapping of *Rpsh_QPom/Rpsh_QBau* is underway to develop simple and robust codominant PCR based markers for use in breeding barley with resistance to BYR.

Is fungicide management of Spot-form net blotch economic in the low rainfall regions of Western Australia?

Andrea A Hills¹, Kylie K Chambers^{1,2}, Jason J Bradley^{1,3}, Geoff G Thomas^{1,3}

1. Dept Primary Industries & Regional Development, WA, Esperance, WA, Australia

2. Dept Primary Industries & Regional Development, WA, Northam, WA, Australia

3. Dept Primary Industries & Regional Development, WA, South Perth, WA, Australia

Spot-form net blotch is the dominant disease of barley in the low rainfall areas of the West Australian grain-belt. While crop rotation and variety choice remain key factors for stubble borne disease control, in parts of WA this is compromised by the ongoing use of susceptible (or worse) rated varieties and high-risk practices such as cropping barley back into retained barley stubble from the previous year. Where SFNB disease levels are considered high or occur early in the growing season during tillering, low rainfall zones (LRZ) growers consider applying fungicides to manage SFNB.

However, in LRZ, management of SFNB by fungicide application may not be worthwhile in many situations. This is due to lower crop yield potentials than those in the medium to high rainfall zones, plus the effect of relatively dry springs in the LRZ environment which can limit disease development on the upper leaves that are critical during the grain filling period to fulfill grain yield and quality potential.

Although few trials investigating SFNB management strategies in LRZ have been conducted, the results of over a dozen trials since 2003 have been compiled to produce this review. The increased understanding of economical SFNB management from this review will provide improved disease management for the LRZ and increase on farm barley productivity and profitability.

KEY BARLEY DISEASES AND THEIR IMPACTS ON YIELD AND QUALITY

Ruth Dill-Macky¹

1. University of Minnesota, Saint Paul, MINNESOTA, United States

Diseases have the capacity to cause significant reductions to the yield and quality of barley in all production environments. The most devastating disease of barley and wheat in the United States is Fusarium Head Blight (FHB or scab), caused primarily by *Fusarium graminearum*. FHB has caused serious losses for more than two decades in the main barley production region, the Upper Great Plains. The pathogens causing FHB produce mycotoxins, esp. deoxynivalenol, that contaminate harvested grain, reducing its marketability and raising food safety concerns for end users. Breeding for resistance to FHB and the reduced accumulation of mycotoxins has been a priority for barley breeding programs in the US. Variety development has been supported through coordinated nurseries and centralized facilities for genotyping and mycotoxin analysis. Varieties with improved resistance to FHB have been developed and now comprise much of the acreage. Research has also enabled the registration of effective fungicides in the U.S. and in the development of prediction models that support a web-based FHB risk assessment tool that is available to growers. In addition to FHB, barley crops in the Upper Great Plains have also suffered losses in recent

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

years due to Bacterial Leaf Streak. Since this disease is caused by a bacterium (*Xanthomonas translucens* pv. *translucens*) that cannot be controlled with fungicides, the deployment of resistant varieties is the only control option for producers. The net-form net blotch (*Pyrenophora teres* f. *teres*) and powdery mildew (*Blumeria graminis* f. sp. *hordei*) can also cause losses in spring-sown and autumn-sown crops, respectively. Pre-emptive resistance breeding efforts have been developed to address these disease threats, in addition to the spot-form net blotch (*P. teres* f. *maculata*), spot blotch (*Cochliobolus sativus*), and the potential threat posed by the Ug99 lineage of stem rust (*Puccinia graminis* f. sp. *tritici*).

SESSION 9: ABIOTIC STRESS TOLERANCE

How to beat the heat: New genetics for breeding fertile and heat-tolerant barley

Camilla B Hill¹, Sharon Westcott², Debbie Wong³, Brett Chapman¹, Xiao-Qi Zhang¹, Gabriel Keeble-Gagnere³, Kerrie Forrest³, Matthew Hayden^{3,4}, Tefera Angessa¹, Chengdao Li^{1,2}

1. Western Crop Genetics Alliance, Agricultural Sciences, , College of Science, Health, Engineering and Education, Murdoch University, Murdoch, WA, Australia

2. Agriculture and Food, Department of Primary Industries and Regional Development, South Perth, WA, Australia

3. Agriculture Victoria Research, Department of Jobs, Precincts and Regions, Bundoora, VIC, Australia

4. School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia

Under the current climate pattern, it is expected that high temperatures and extreme heat events will occur more frequently, much earlier, and will last longer in the future¹. To mitigate the impact of climate change and maintain crop yields in the future, more heat-resistant crop cultivars are urgently needed. The barley flowering stage is very sensitive to high temperatures which significantly decrease fertility, seed-setting rate, and grain quality, leading to severe grain yield losses². Although considerable genetic variation for spikelet fertility has been reported in rice and wheat^{3,4}, such knowledge does not exist for barley and neither candidate genes nor molecular markers currently exist for breeders. We set out to investigate three key research objectives: (i) assess the impact of heat stress at flowering time on spikelet fertility and grain quality traits in key Australian as well as international barleys, (ii) identify barley germplasm with superior genetics to maintain spikelet fertility and grain quality under heat stress, (iii) deliver marker assays for tracking the inheritance of alleles in breeding material. A cost-effective custom target sequencing assay^{5,6} determined the full range of allelic diversity in 132 heat tolerance related genes in 500 global barley varieties. Association mapping and haplotype analyses were performed based on data collected in target field environments as well as combined birdcage and heat chamber experiments. We identified 673 marker-trait associations for spikelet fertility at the flowering stage, including novel associations with heat stress transcription factors. Kompetitive Allele Specific PCR (KASP) markers were developed to distinguish cultivar-specific alleles for superior and inferior haplotypes of candidate spikelet fertility and heat stress tolerance genes. The identified superior haplotypes and the barley varieties carrying these superior haplotypes can be used for haplotype-based breeding to develop next-generation of heat stress-tolerant barley cultivars.

1. King, A.D., Karoly, D.J. and Henley, B.J., 2017. Australian climate extremes at 1.5 C and 2 C of global warming. *Nature Climate Change*, 7(6), 412-416.
2. Dreccer, M.F., Fainges, J., Whish, J., Ogonnaya, F.C. and Sadras, V.O. 2018. Comparison of sensitive stages of wheat, barley, canola, chickpea and fieldpea to temperature and water stress across Australia. *Agricultural and Forest Meteorology* 248, 275-294
3. Park, J.R., Kim, E.G., Jang, Y.H. and Kim, K.M., 2021. Screening and identification of genes affecting grain quality and spikelet fertility during high-temperature treatment in grain filling stage of rice. *BMC Plant Biology*, 21(1), 1-21.
4. Pradhan, S., Babar, M.A., Robbins, K., Bai, G., Mason, R.E., Khan, J., Shahi, D., Avci, M., Guo, J., Maksud Hossain, M. and Bhatta, M., 2019. Understanding the genetic basis of spike fertility to improve grain number, harvest index, and grain yield in wheat under high temperature stress environments. *Frontiers in Plant Science*, 1481.
5. Hill, C.B., Wong, D., Tibbits, J., Forrest, K., Hayden, M., Zhang, X.Q., Westcott, S., Angessa, T.T. and Li, C. 2019. Targeted enrichment by solution-based hybrid capture to identify genetic sequence variants in barley. *Scientific Data*, 6(1), 1-8.

6. Hill, C.B., Angessa, T.T., McFawn, L.A., Wong, D., Tibbits, J., Zhang, X.Q., Forrest, K., Moody, D., Telfer, P., Westcott, S. and Diepeveen, D., 2019. Hybridisation-based target enrichment of phenology genes to dissect the genetic basis of yield and adaptation in barley. *Plant Biotechnology Journal*, 17(5), 932-944.

Digging deeper to improve yield stability: harnessing roots using new breeding technologies

Lee Hickey¹, Kai Voss-Fels², Karine Chenu³, Millicent Smith⁴, Ben Hayes⁵, Ian Godwin⁵, Michael Djordjevic⁶, Allan Rattey⁷, Jayfred Godoy⁷, Hannah Robinson^{5,7}

1. *The University of Queensland, St Lucia, QLD, Australia*

2. *Department of Grapevine Breeding, Hochschule Geisenheim University, Geisenheim, Germany*

3. *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Toowoomba, QLD, Australia*

4. *School of Agriculture and Food Sciences, The University of Queensland, Gatton, QLD, Australia*

5. *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, QLD, Australia*

6. *Division of Plant Sciences, The Australian National University, Canberra, ACT, Australia*

7. *InterGrain Pty Ltd, Perth, WA, Australia*

Australia is a major player in the global barley export market, contributing 30-40% of the malting barley trade and 20% of feed barley. However, barley production in Australia is highly variable and dependant on seasonal rainfall. This has a major impact on farm profits. For example, in a 'typical year' grain growers profit \$230,000, whereas, in a 'dry year' growers suffer average losses of \$125,000. A substantial body of research suggests that optimised plant root systems can improve water acquisition with minimal metabolic cost, which could improve crop yields under both favourable and adverse conditions. However, modern crop improvement programs struggle to incorporate selection for root traits, largely due to the challenges associated with phenotyping root structure, a lack of understanding of the genetic controls of root system architecture, and an inability to assess the value of traits in specific environments.

Through a new ARC Linkage project in partnership with UQ, ANU and InterGrain, we are exploring innovative breeding solutions that harness the 'hidden' part of the plant, roots, to support the development of more productive barley crops in the face of climate variability. The project expects to generate new insights into the biology and genetics of root development in barley by applying cutting-edge genome editing, phenotyping and genomics technologies. Here, we highlight how we are translating knowledge from model plant species to modify the root systems of barley using CRISPR, and present results from field experiments conducted across Queensland and Western Australia. Our results provide new insights of the relationship between root and shoot development in elite barley, and how key root traits support grain yield in diverse environments. We also highlight the opportunity for breeders to apply UAV-based phenotyping methods to efficiently capture canopy traits that indirectly capture root trait variation supporting grain filling and yield potential.

New strategies of the ICARDA Global Barley Breeding Program to breed barley for the Developing World

Miguel Sanchez-Garcia¹, Andrea Visioni¹, Seid-Ahmed Kemal¹, Ahmed Amri¹, Zakaria Kehel¹, Michael Baum¹

1. International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, RABAT, Morocco

To keep the success of the Global Barley Breeding Program of ICARDA (CGIAR) and continue providing highly adapted and performant barley genotypes to collaborators in the Developing World, a new breeding strategy has been deployed. Using product profiles, rapid generation advancement and new genomic and phenotyping tools, the program aims to face the current and future challenges of barley cultivation. In close collaboration with the National Agricultural Research Programs (NARS), new product profiles have been co-designed and grouped in 4 MegaProduct Lines: Feed Barley for Arid and Semi-Arid regions, Food and Fodder Barley, Feed and Forage Barley for Favorable Environments and Malt and Fodder Barley.

Continuing with the traditional use and deployment of the barley genetic diversity hosted at ICARDA genebank the program keeps mining the collection to identify new sources of traits of interest. Both for breeding and pre-breeding purposes, the program makes use of the new ICARDA Speed Breeding Platform in Rabat (Morocco). In this facility with capacity for over 60,000 entries, new protocols allow Disease assisted- and NIR assisted-Speed Breeding strategies.

The strong collaboration with NARS as well as the development of ICARDA research stations in barley hot spots in Morocco, Lebanon and India allow the program to test its germplasm for a wide range of major biotic and abiotic constraints.

Using low-density genotyping, new genomic-assisted sparse multi-environment testing strategies are set in Stage 1 to increase the selection accuracy and intensity. These strategies allow predicting several traits in non-planted entries across testing locations, resulting in prediction abilities for yield using genomic GxE models of up to $r=0.55$.

Coupling the use of advanced technologies, genebank diversity and a strong collaborative approach with the NARS we aim at accelerating genetic gains at farmers' fields while coping with Climate Change.

Proteome responses in barley during short periods of heat stress applied in early grain fill

Catherine Lawn¹, Vijaya Singh², Edward Kerr³, Ben L Schulz³, Glen Fox⁴, Mark Dieters¹

1. School of Agriculture and Food Science, The University of Queensland, Brisbane, QLD, Australia

2. Centre for Crop Science, The Queensland Alliance for Agriculture and Food Innovation, Brisbane, Queensland, Australia

3. School of Chemistry & Molecular Biosciences, The University of Queensland, Brisbane, QLD, Australia

4. Food Science & Technology, The University of California, Davis, California, United States

Incidences of short periods of heat stress are becoming more common in barley growing regions in Australia, and worldwide. Barley quality depends on its molecular composition, particularly the amount, identity, and structures of the starch and protein. A greater understanding of change to protein composition following heat stress will help improve understanding of the impacts on barley, malting, and brewing quality, and potentially identify new opportunities for improving heat tolerance. Barley plants were grown in a temperature-controlled glasshouse: plants in the heat treatment were exposed to five days of higher-than-normal temperatures (4 hours at 45°C) to imitate conditions which may be observed in field.

Tillers were harvested each morning following the 4-hour heat event and again at maturity. Grain samples were analysed to assess the composition of the accumulating proteins with SWATH/DIA-MS proteomics. Peptides were compared to a database of known barley proteins and changes in the composition of the identified proteins were compared across treatments. Differences were observed in the protein response patterns of the two genotypes (La Trobe and RGT Planet) during the heat event, and at maturity. Proteins associated with heat stress were enriched in the heat treatments, and proteins associated with starch biosynthesis were enriched in the control treatments.

Finding the Links between Stomata and Plant Acid Soil (Al toxicity) Tolerance

Chenchen C Zhao¹, Ce C Guo¹, Meixue MX Zhou¹

1. University of Tasmania, Prospect, TAS, Australia

Stomatal activities confer plant tolerance to abiotic stresses. Mechanisms regarding stomatal activities underlying abiotic stresses were broadly studied. However, the links between stomatal activities and heavy metal tolerance were not amply reported. Given the severe effect on agricultural production from acid soil, this review specially aims to highlight the effect of Al exposure on plant stomatal activities. Whether a modification of stomatal physiological or morphological traits favours or decreases Al tolerance was also discussed. Furthermore, by summing the previously reported research cases, it is proposed that Al³⁺ induced stomatal closure may be able to escape from classic ABA stomatal signalling but involves regulations of core and representative stomatal signalling components, typically through regulations of the secondary Ca²⁺ messenger. Through utilising an Al tolerant barley variety under an experimental trial, it was observed that Al exposure decreases stomatal capability in maximum opening within a few hours, indicating a long-term role of Al in regulating stomatal activities. It calls for research focusing on stomatal molecular mechanisms underpinning plant Al tolerance. Therefore, transgenic research modifying stomatal traits and subsequent Al tolerance valuation should be appealed.

SESSION 10: GENETICS AND BREEDING

Barley with tolerance to group 1 herbicides - A weed management tool

Tristan Coram¹, Cathrine Ingvordsen¹, James Walter¹, Stewart Coventry¹, Paul Telfer¹

1. Australian Grains Technologies, Roseworthy, SA, Australia

Grass weeds including annual ryegrass, barley grass, brome grass and wild oats cause average annual losses in winter cereals of over AU\$34M (Llewellyn et al., 2016). Consequently, providing additional tools for the control of grass weeds in barley would have significant benefit to Australian growers. Group 1 herbicides, inhibiting acetyl co-enzyme A carboxylase (ACC'ase inhibitors), are commonly applied in naturally insensitive broadleaf crops to control grass weeds but cannot be utilised in cereal crops due to their sensitivity. Here, we describe the development and characterisation of barley with a modified ACC'ase inhibitor that confers tolerance to multiple group 1 herbicides.

The (non-GMO) mutation responsible for this tolerance occurred naturally in a grower's field and was characterised by the University of Adelaide. Recently, Australian Grain Technologies (AGT) has introduced the mutation into the breeding programme and are assessing the tolerance of barley lines to group 1 herbicides in field trials. Results from three years of field trials demonstrate that yields are maintained after application of some group 1 herbicides at up to twice the recommended label rates. AGT has generated crop tolerance and residue data to support Australian Pesticides and Veterinary Medicines Authority (APVMA) label registration for a group 1 herbicide and expect to commercially launch the technology in the near future, along with stewardship guidelines.

This new technology will provide growers an additional tool for combating grass weeds in their barley crops, particularly where barley grass, brome grass and wild oats are an issue. Additionally, the technology will be valuable for cleaning up volunteer wheat from malt barley crops. Lastly, group 1 herbicides have a short degradation period in the soil, which eliminates any plant back for the following crop.

1. Llewellyn RS, et. al. (2016)

https://grdc.com.au/~media/documents/resources/publications/reports/grdc_weeds_review_r8.pdf

Using artificial intelligence algorithm to rapidly improve multiple disease resistance in barley

Eric G. Dinglasan¹, Lisle Snyman², Tara Garrard³, Hugh Wallwork³, Mark McLean⁴, Lee Hickey¹, Mark Cooper¹, Ben Hayes¹, Kai P. Voss-Fels^{1, 5}

1. Queensland Alliance for Agriculture and Food Innovation, Brisbane, QLD, Australia

2. Queensland Department of Agriculture and Fisheries, Hermitage Research Facility, Warwick, QLD, Australia

3. South Australian Research and Development Institute, Primary Industries and Regions SA, Adelaide, SA, Australia

4. Agriculture Victoria, Department of Jobs, Precincts and Regions, Horsham, Victoria, Australia

5. Department of Grapevine Breeding, Hochschule Geisenheim University, Geisenheim, Germany

Increasing durable resistance against major fungal diseases, including spot form and net form of net blotch and leaf scald, is among the central focus of Australian barley breeding.

This is because pathogens constantly evolve, overcoming genetic resistances deployed in cultivars, thus affecting end-use quality and yield potential. Exotic germplasm serves as a reservoir of undiscovered resistances for targeted introgression into elite backgrounds. However, novel resistance alleles are often hidden in many accessions that are poorly adapted to Australian environments. These accessions are often discarded, making the hidden alleles underutilized. Furthermore, introgression from wild donors to elite germplasm is challenging. The problem becomes identifying the best parent cross combinations that maximises stacks of desirable alleles. To tackle this problem, we propose a new approach that uses artificial intelligence (AI) algorithms designed to solve highly combinatorial problems, coupled with genomic prediction and speed breeding. In partnership with state pathologists from QDAF, SARDI, and AgVic; and linking with broader GRDC investment programs, our novel breeding framework has the potential to shortcut several years of conventional resistance breeding.

A population representing global barley diversity sourced from the Australian Grains Genebank (n = 755) were phenotyped for multiple diseases across Queensland, South Australia, and Victoria in 2020–2021. Combining these phenotypes and 40K XT SNP data, we catalogued resistance alleles using a new haplotype-based approach and applied a genetic algorithm to select the best parents that maximises desirable chromosome segment configurations. A digital twin of different crossing scenarios was created to guide mating design with highest probability of rapidly stacking resistance haplotype. Results showed that resistance alleles can be rapidly stacked into new barley lines. Following the optimal crossing path identified by the digital twin, we are now adopting the AI-guided breeding framework in practice to rapidly develop barley germplasm with improved multiple disease resistance.

Exploring the Genetic Potential to Develop Barley Cultivars with Long Coleoptiles

Hannah M Robinson^{1, 2}, Jayfred Godoy¹, Samir Alahmad², Jonathon Powell², Eric Dinglasan², Kai Voss-Fels², David Moody¹, Lee Hickey²

1. InterGrain Pty Ltd, Perth, WA, Australia

2. Queensland Alliance for Agriculture and Food Innovation, Brisbane, QLD

Climate variability coupled with increased frequency and duration of heat and drought events challenges global crop production. Drought adaptation is complex, made up of several component traits, some interacting, and all influencing crop water-use across the growth cycle. The length of the coleoptile, the protective clear sheath surrounding the emergent leaf, determines sowing depth and is a potential drought avoidance trait of interest to growers. A long coleoptile enables deeper sowing to capture soil moisture at depth. As a result, reducing the reliance on rainfall events and enabling earlier sowing to avoid energy intensive development during periods of increased heat and limited water availability.

Despite the importance, there is limited knowledge of the genetic architecture of coleoptile length in Australian barley germplasm. Further, in previous studies reporting possible genetic controls in global germplasm panels, there has been minimal validation of QTL effects in deep-sowing field trials. In this study, we adopt a two-prong approach to explore the genetic architecture of coleoptile length in an Australian barley breeding population using a traditional single-marker genome-wide association analysis and a haplotype-based approach. Resultant QTL and haplotype effects are compared and then validated for their impact on emergence in a deep sowing trial performed in 2021 at Gatton, Queensland. A significant and novel haplotype on chromosome 5H is described and the relationship with emergence, early vigour, plant height and relevant semi-dwarfing genes is explored. Unravelling the genetic architecture of coleoptile length, specific to Australian germplasm, provides novel insights into opportunities for enhanced and targeted breeding for coleoptile

length as well as prospects for genetic diversity enrichment to extend the current phenotypic variation.

Can vegetative indices from high-throughput phenotyping be used to improve grain yield prediction accuracy for genomic selection in barley?

Silvina Baraibar^{1,2,3}, Diane Mather², Helena Oakey², David Moody³

1. National Institute for Agricultural Research (INIA), Colonia, Uruguay

2. The University of Adelaide, Adelaide, SA, Australia

3. InterGrain, Perth, WA, Australia

Since the introduction of genomic selection, extensive research has been done on evaluating its efficiency for crop breeding. Even though many breeding programs now implement genomic selection, the prediction accuracy achieved for yield is still low. This is partly because genomic selection models must be trained based on measurement of actual yields in trial plots that are subject to spatial variation and complex genotype*environment interactions. For wheat and some other grain crops, vegetative index values obtained by high-throughput sensing have been used in conjunction with plot yield data to improve the prediction accuracy of grain yield. In barley, however, little is known about relationships between vegetative indices and grain yield.

Using drones equipped with multispectral cameras, we collected data at multiple stages of crop development, on more than two thousand barley breeding plots, in several Australian environments. From the images collected, we derived several vegetative indices (NDVI, NDRE, GNDVI, BNDVI). We examined the relationships of these indices with grain yield and investigated how these change during crop development.

Finally, we incorporated the high-throughput phenotypic data into genomic models with the aim of improving the grain yield genomic prediction accuracy in barley. We believe this approach will provide useful insights for the implementation of GS for grain yield in Australian barley breeding programs.

Genome editing to create barley with designer roots

Zachary Aldiss¹, Ian Godwin¹, Andrew Borrell², Hannah Robinson^{1,3}, Peter Crisp⁴, Karen Massel¹, Lee Hickey¹

1. Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, St. Lucia, QLD, Australia

2. Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Warwick, QLD, Australia

3. InterGrain Pty Ltd, Perth, WA, Australia

4. School of Agriculture and Food Sciences, Faculty of Science, The University of Queensland, Gatton, QLD, Australia

Genetic variability has been greatly reduced over the thousands of years of evolution, domestication, and breeding, limiting the capacity to improve many traits that are essential to adapt crops to future environments. New genome editing techniques have the potential to accelerate fundamental research and plant breeding through the rapid, precise, and targeted modifications of genomes. Incorporation of biotechnological tools into breeding programs can expedite the breeding of beneficial traits. Modifying traits in elite varieties can now be done within a single generation, significantly shortening the time from lab to field, and the deleterious traits associated with linkage drag can be avoided, alongside developing novel

trait combinations that are not found in nature. In this study, we used the CRISPR/Cas9 genome editing system to modify the root architecture of Golden Promise barley. By targeting the coding region of a root specific auxin transporter Pin11, gene function was distorted in resulting plants that displayed extreme phenotypic changes in root architecture. The modification resulted in loss of response to gravity, which was root-specific, resulting in a shallower and wider root system. We highlight the potential of genome editing to create novel allelic variations that are unfounded in nature and unlikely to be easily accomplished through conventional breeding. We anticipate that gene editing will likely be a useful toolbox for the modern barley breeder to develop high quality malting varieties with improved climate resilience.

Fun and challenges in barley breeding: complex crosses.

David Moody¹, Cathy Burchell¹, David Watson¹, Simone Tait²

1. *InterGrain, Bibra Lake, WA, Australia*

2. *Biosciences Research, Agriculture Victoria, Horsham, Victoria, Australia*

Rarely do plant breeders adopt crossing designs and selection strategies that allow the simultaneous combination of large numbers of genes. The advent of molecular technology has provided this possibility but, even with this technology, there remain challenges in terms of population size and optimal cross design.

This paper describes the early use of a complex cross design aiming to simultaneously combine seven QTL's for major agronomic and quality traits into a single genetic background. Whilst the strategy ultimately resulted in the release of the variety "Buff", many challenges were faced. These challenges included the lack of suitable molecular markers at the time, organizational changes, pathogen evolution during the time course of the variety development cycle, the wide range of genetic diversity generated, deleterious linkages and pleiotropic effects of major effect QTL and misguided original product design. A retrospective analysis of the variety development was then conducted using current genotyping technologies to assess the effects of complex cross design on genetic recombination events observed in "Buff" compared to its recurrent parent.

Given that "Buff" has now been selected for de novo sequencing assembly as part of the international pangenome project, a description of the historical development of this variety is appropriate. Further, learnings from this early use of marker technology can help inform future breeders in the choice of complex crossing and selection strategies.

Genomic signatures of Australian barley breeding history

Haifei Hu¹, Penghao Wang¹, Tefera Tolera Angessa¹, Ziao-Qi Zhang¹, Kenneth J Chalmers¹, Camilla Beate Hill¹, Yong Jia¹, Craig Simpson¹, John Fuller¹, Alka Saxena¹, Hadi Al Shamaileh¹, Munir Iqbal¹, Brett Chapman¹, Parwinder Kaur¹, Olga Dudchenko¹, Erez Lieberman Aiden¹, Gabriel Keeble-Gagnere¹, Sharon Westcott¹, Josquin F Tibbits¹, Robbie Waugh¹, Peter Langridge¹, Tianhua he¹, Chengdao Li¹

1. *Western Crop Genetics Alliance, Murdoch University, Perth, WA, Australia*

The early barley cultivars grown in Australia were obtained from Europe until Samuel Prior developed the first Australian barley cultivar "Prior" in 1903 from a British variety "Chevalier". Systematic and government-funded barley improvement commenced in 1956 and resulted in the release of several barley cultivars in the late 1960s, all having the pedigree of Prior. The malting barley "Clipper" has been seen as one of the most significant Australian barley cultivars with substantially improving barley yield and production. Since then, new varieties have transformed Australia to one of the largest barley exporters. Using the most advanced

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

sequencing technologies, we assembled the genome of the modern Australian barley varieties: Clipper, Stirling, RGT Planet and Maximus. 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 and yield potential, we have shown that breeders have fundamentally transformed the genomic architecture and landscape of adaptive genes in Australian and North American barley varieties. Genes associated with phenology, development, abiotic and biotic stress tolerance were under strong selection during the early breeding of European germplasm base to adapt to Australian environments. Selection for suitably adapted barley varieties over the past seventy years in Australia has led to the fixation of several key genes in flowering regulatory pathways. Australia's elite barley varieties are dominated by one haplotype of each gene. Identifying these genes and haplotypes provides an understanding of how breeding selections have shaped the genome architecture in Australian barley during its transition from Old World to New World crop. Identifying genes and haplotypes important to current growing conditions also provides insights into breeding for future environments, which may require changing the ideotype of current barley varieties.

SESSION 11: BARLEY A VERSATILE CROP – FOOD, FEED AND FODDER

Barley and Aquaculture: Beer, bugs and sustainability

Megan Edwards¹

1. Australian Export Grains Innovation Centre, South Perth, WA, Australia

Barley has not traditionally been used widely in aquaculture nutrition, however there are increasing opportunities for barley and products derived from barley to contribute directly or indirectly to the nutrient requirements of farmed fish and shrimp. This presentation will explore the current avenues in which barley or products derived from barley are being utilized in the aquaculture industry and how barley can contribute to a more sustainable industry in the future.

Impacts of starch and fibre quality on human/animal nutrition

Mike Gidley¹

1. The University of Queensland, St Lucia, QLD, Australia

Fermentation by gut microbiota underlies many of the nutritional and health benefits of dietary fibre (including resistant starch). In both humans and production animal diets, cereals are often the major source of dietary fibre. Whilst there is a growing knowledge base on the effects of individual dietary fibre components on gut fermentation, there is limited current knowledge on the effects of (i) the organisation of fibre components into plant structures such as cell walls, (ii) the food or feed form that the fibre is consumed in and (iii) variations in the resident gut microbiota due to underlying genetics and diet history. This presentation will explore these effects using wheat as a model, and both (uncontrolled diet) humans and (controlled diet) pigs as sources of inocula for in vitro gut fermentation studies.

POSTERS ONLY

Impact of barley yellow dwarf virus on barley production

Meixue Zhou¹, Chenchen Zhao¹, Peter Johnson¹

1. University of Tasmania, Prospect, TAS, Australia

Barley yellow dwarf virus (BYDV) is one of the most widespread and economically relevant plant viruses affecting a range of cereal crops, mainly barley, wheat, rye, oat and maize. Significant yield losses or reductions of yield components have been reported. A preliminary yield trial on Planet barley in WA showed 15% yield reduction even with no obvious BYDV symptoms. To accurately quantify the impact of BYDV on barley, a specific trial was conducted. RGT Planet was sown in a paddock with a high risk of BYDV infection. Twelve seeds were evenly sown in 1.2 m rows with a 10 cm distance between each seed and 30 cm between rows. All plants were allowed for natural BYDV infection. When severe BYDV symptoms were shown, the neighbouring individuals with contrasting BYDV symptoms (one with no symptom and the other one with different levels of symptom) were labelled. After maturity, plants were harvested for measuring grain yield, plant height, and other yield components. Plant grain yield significantly negatively correlated with BYDV symptoms. The greatest yield reduction was close to 80%, mainly due to reduced tiller number, 1000-grain weight and grain number per spike. The results indicated the importance of BYDV resistance in barley breeding programs.

CAIGE Barley program – A source of diverse germplasm for multiple-disease resistances

Amit Kumar Singh¹, Julie M Nicol¹, Richard M Trethowan¹, Miguel Sanchez-Garcia², Mark Dieters³

1. School Of Life and Environmental Sciences, The University of Sydney, Cobbitty, NSW, Australia

2. Barley Breeder, International Center for Agricultural Research in the Dry Areas, Rabat, Morocco

3. School of Agriculture and Food Sciences, The University of Queensland, Brisbane, Queensland, Australia

The GRDC funded CIMMYT Australia ICARDA Germplasm Evaluation (CAIGE) program is an international collaboration that enables Australian grain industry to derive maximum benefit from significant international investment in wheat and barley breeding. The collaborative program offers both local international stakeholders (CIMMYT and ICARDA) to exchange germplasm along with pedigree information, and phenotypic and genotypic data. In addition to multi-environment yield trials, barley germplasm has been assessed for leaf rust (BLR), scald, spot form of net blotch (SFNB), net form of net blotch (NFNB), powdery mildew (PM), spot blotch (SB) and stem rust resistances.

In total 1831 diverse genotypes belonging to different objective-oriented nurseries (LI; Low Input, HI; High Input, Landraces and Elite breeding lines) have been imported from ICARDA during the period of 2015-to-date. The nurseries under LI conditions are subjected to mild to severe biotic and abiotic stresses, spread across arid and semi-arid regions of the world. Landraces were pre-screened for multiple disease resistances by ICARDA, and landraces showing resistance to one or more disease were imported under the CAIGE project. Many breeding lines from ICARDA are also demonstrating multiple disease resistances, and improved yield potential, agronomic traits and grain quality.

CAIGE barley germplasm imported between 2015 and 2019, and evaluated annually for multiple disease resistance, were reviewed, and lines demonstrating multiple foliar diseases resistances were identified to form a 'disease core set'. Currently, the set constitutes over

20th AUSTRALIAN BARLEY TECHNICAL SYMPOSIUM
QUALITY AUSTRALIA BARLEY: DRIVING OPPORTUNITIES AND VALUE

120 lines with multi-disease resistances. During 2022 this core set will be re-tested for disease resistances, and combined with Genome Wide Association Analyses, to refine the core set. The disease core set will be further updated to include more recent imports of next five years of the CAIGE project. The CAIGE germplasm and database will provide valuable sources of novel genetic resistances to barley foliar diseases, for breeding and research purposes.