SESSION: 1

KEYNOTE

Barley: a research model for the temperate grasses

Robbie Waugh

The James Hutton Institute and University of Dundee; Robbie.Waugh@hutton.ac.uk

ABSTRACT

As we awaken to the concept that the crop should now also be considered the model, ready access to increasingly powerful research and informational tools complemented by widely available and extensive genetic resources has been driving an resurgence in the use of barley as an experimental system in both applied and fundamental research programs. Crucially, as a major world crop, routes towards testing and translation of discoveries are both immediately relevant and straightforward and can be implemented using a blend of traditional and new breeding technologies. I would argue that this is clearly evidenced in the recent scientific literature. In my presentation I will focus on some of the ways we (and others) have been applying new information and technologies to drive our understanding of how barley has responded to the environmental challenges it has faced in the past as it emerged from its centre of origin and spread throughout the world, and once established, the consequences of intense selection during breeding. I will illustrate and discuss the extensive and worryingly monomorphic tracts present of the current elite barley genome and, time permitting, discuss some of the strategies we are starting to develop to help address this problem.

SESSION: 1

Imidazolinone tolerant barley: an Australian barley breeding success story

David Moody

InterGrain Pty Ltd; dmoody@intergrain.com

Co-authors: M. Materne and C. Pittock

ABSTRACT

In the space of 10 years, imidazolinone tolerant barley in Australia has progressed from the creation of the original imidazolinone tolerant mutant to a national market share exceeding 20%. The popularity of this trait in barley with growers has been (largely) driven by increasing levels of brome grass species (Bromus rigidus and Bromus diandrus) in zero and minimum tillage farming systems, and the ease of control of these weed species using imidazolinone chemistries. Imidazolinone tolerance in barley has also provided growers with a number of additional benefits. Tolerance has allowed barley to be planted into paddocks containing residual imidazolinone herbicides used in the previous crop, with the dry summer and autumn conditions in Australia often resulting in low rates of microbial decomposition. The trait provides growers with the opportunity to achieve higher yields and improve grain quality through earlier sowing into wheat stubbles, due to the ability to remove volunteer wheat in-crop, rather than waiting for the germination and removal of residual wheat by knockdown (non-selective) herbicides. As a result of the combination of advantages the trait provides to barley in Australian farming systems, the relative proportion of imidazolinone tolerant barley to intolerant barley varieties is three-fold higher than the relative proportions of tolerant to intolerant varieties in the other crop species possessing this trait in Australia (canola and wheat).

This paper describes the original development of the trait in barley, the breeding history of the first imidazolinone tolerant barley variety (cv. Scope) and the critical factors that have driven the rapid and successful commercialization of this variety. Further, the paper highlights the future prospects for imidazolinone tolerant variety development and the challenges facing the longevity of this trait in the farming system.

SESSION: 1

From marker-assisted selection (MAS) to genomic selection (GS) - strong support for modern barley breeding

Viktor Korzun

KWS LOCHOW GMBH; viktor.korzun@kws.com

Co-authors: E. Byrne, J. Großer, D. Harrap, J-F. Herbommez, S. Kollers, K. Oldach, M. Schmidt, B. Schinkel, A. Tomerius, N. Wendler, P. Werner, and H. Verstegen

ABSTRACT

Conventional barley breeding is time-consuming and strongly depends on environmental conditions. Therefore, breeders are extremely interested in new technologies that optimize breeding processes. Molecular marker technology offers such a possibility by adopting a wide range of novel approaches to improve selection strategies in breeding. There has been a large and rapid accumulation of genomics tools in the cereal crops during the last decade. These developments have been coupled with the emergence of high throughput technologies, which have allowed advances in molecular marker technology and implementation.

The impact of new molecular tools and technologies available for plant variety development has proven to be essential to optimize and accelerate breeding programs.

Disease resistance and quality are prime targets in practical barley breeding programs. In all cases the breeding process can be accelerated by applying marker-assisted selection (MAS) for developing new material and for improvement of the selection intensity and accuracy. Nevertheless, the recent advance in high density genotyping has opened new possibilities to apply genome-wide markers in Genomic Selection (GS) rather than individual markers as in classical MAS.

Malting quality traits in barley breeding usually has been targeted by using MAS. In this study, the potential to apply genomic selection instead to improve malting quality in two commercial breeding programs of spring and winter barley (Hordeum vulgare L.) was evaluated. Predictive abilities (PA), as derived from cross-validation, for twelve malting quality characters investigated ranged from 0.14 to 0.58 for spring barley and 0.40 to 0.80 for winter barley indicating that Genomic Selection can be successfully applied.

The results of specific applications of molecular markers, potential of genomic selection and practical applications of genomics knowledge in malting barley breeding will be presented and discussed.

SESSION: 2

KEYNOTE

Identification of genes defining culm length in barley

Mats Hansson

Lund University, Department of Biology, Solvegatan 35, 22362 Lund, Sweden;
mats.hansson@biol.lu.se

ABSTRACT

Reduced plant height and culm robustness are quantitative characteristics important for assuring cereal crop yield and quality under adverse weather conditions. A very limited number of short-culm mutant alleles were introduced into commercial crop cultivars during the Green Revolution although more than 1000 different short-culm barley mutants have been isolated and classified in different phenotypic groups according to culm length and additional pleiotropic characters. We are currently employing available short-culm barley mutants in order to identify the genes responsible for regulation of culm length. The mutant lines are from the brachytic, breviaristatum, dense spike, erectoides, semibrachytic, semidwarf, and slender dwarf mutant groups. Our toolbox also includes in-silico gene mapping, a set of near-isogenic lines and various F2-mapping populations. The genes we have identified so far encodes different subunits of heterotrimeric G-proteins as well as brassinosteroid receptors and brassinosteroid biosynthetic enzymes.

References

Braumann, I. and M. Hansson. 2013. “Barley plants with short culm”. Danish Patent Application PA 2013 70363.

Dockter, C., D. Gruszka, I. Braumann, A. Druka, I. Druka, J. Franckowiak, S. P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A. H. Müller, J. Oklestkova, B. Schulz, S. Zakhrabekova and M. Hansson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the “Green Revolution” genetic toolkit. Plant Physiol. 166: 1912-1927.

Zakhrabekova, S., C. Dockter, K. Ahmann, I. Braumann, S. P. Gough, T. Wendt, U. Lundqvist, M. Mascher, N. Stein and M. Hansson. 2015. Genetic linkage facilitates cloning of Ert-m regulating plant architecture in barley and identified a strong candidate of Ant1 involved in anthocyanin biosynthesis. Plant Mol. Biol. 88: 609-626.

SESSION: 2

Story of barley domestication

Mohammad Pourkheirandish

The University of Sydney; mohammad.pourkheirandish@sydney.edu.au

Co-authors: T. Komatsuda

ABSTRACT

Barley is one of the first crops used by ancient farmers during Neolithic agriculture. The most manifest event during its domestication is the appearance of non-brittle rachis. Grain dispersal systems are designed to enable wild to survive in nature, but loss of natural dispersal was essential for agriculture. btr1 and btr2 are non-brittle rachis genes tightly linked and located on the short arm of chromosome 3H. We isolated them by means of positional cloning. Sequence analysis of wild and cultivated barley accessions revealed that non-brittle rachis was generated twice by independent mutations, first in the South (btr1) and then in the North Levant (btr2). The increase of grain number was deliberately selected during early cultivation as another domestication goal. Emergence of six-rowed spike in barley that increases grain number up to three times goes back to the early agriculture. Six-rowed spike gene, vrs1, is located on the long arm of chromosome 2H. The evolutionary study of the gene showed that it was selected four times independently. A notable feature of these three domestication genes is that all of them were created through a dynamic duplication followed by neofunctionalization. Btr1, Btr2 and Vrs1 became dispensable genes unique to Triticeae, and mutation targeted these genes in the domestication process. Wild barley (Hordeum vulgare ssp. spontaneum) always has brittle rachis, two-rowed spikes whereas cultivated barley (ssp. vulgare) non-brittle rachis and two-rowed or six-rowed spikes. “Agriocrithon” barley, exceptionally, have brittle rachis and six-rowed spikes. Here we will present a conclusive answer to the historic question where, when and how agriocrithon was generated.

SESSION: 2

Global transcriptome profiling of developing leaf and shoot apices reveals distinct genetic and environmental control of floral transition and inflorescence development in barley

Maria von Korff Schmising

University of Düsseldorf, Max Planck Institute for Plant Breeding Research;
korff@mpipz.mpg.de

Co-authors: B. Digel

ABSTRACT

The control of shoot development has a strong impact on yield in temperate cereals. However, the genetic and environmental control of developmental processes underlying differences in yield potential are not well understood. We conducted microscopic phenotyping and RNA-sequencing of the developing barley shoot apical meristem (SAM), leaf and stem growth under different photoperiods and temperatures and in introgression lines (ILs) varying at the photoperiod response gene Ppd-H1.

The daylength sensitivity of SAM development revealed two phases, floret primordia initiated under long and short days, whereas successful inflorescence development occurred only under long days. The number of floret primordia initiated until the beginning of stem elongation largely determined the number of final seeds per spike, while Ppd-H1 increased flower fertility during stem elongation. High temperature delayed floral transition and inflorescence development in a Ppd-H1 dependent manner.

The photoperiod- and Ppd-H1-dependent differences in inflorescence development and flower fertility were associated with the induction of barley FLOWERING LOCUS T orthologs: FT1 in leaves and FT2 in MSAs. FT1 expression was coregulated with transcripts involved in nutrient transport, carbohydrate metabolism, and cell cycle regulation, suggesting that FT1 might alter source-sink relationships. Successful inflorescence development correlated with upregulation of FT2 and transcripts related to floral organ development, phytohormones, and cell cycle regulation. This work provides the basis to better understand the genetic control of flowering and yield formation in response to photoperiod and ambient temperature variation in barley.

SESSION: 2

Exploring phenotypic variation for key agronomic and life history traits in a barley legacy collection

Alessandro Tondelli

Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Genomics Research Centre, 29017 Fiorenzuola d'Arda, Italy; Università degli Studi di Milano – DiSAA, 20133 Milan, Italy; alessandro.tondelli@entecra.it

Co-authors: Stefano Delbono, Davide Guerra, Chiara Biselli, Nadia Faccini, Marcello Baravelli, Ivana Tagliaferri, M˝ria Megyeri, Pétér Mik½, M˝rta Moln˝r-L˝ng, Hakan Özkan, Joanne Russell, Marco Bink, Fred van Eeuwijk, Michael Alaux, Thomas Letellier, Luigi Cattivelli

ABSTRACT

The WHEALBI (Wheat and barley Legacy for Breeding Improvement) project, supported by EU funding, is taking a multidisciplinary approach to identify, understand and utilise the genetic diversity available in a barley legacy collection of cultivars, landraces and wild relatives. In this frame, a standard phenotypic approach based on "common garden" trials across Europe has been established to test the whole collection (512 accessions) for exploring its adaptative capacity. In the 2014/15 growing season, winter and spring nurseries have been sown in 4 locations (North Italy - CREA, Hungary - ATK, Scotland - JHI and Central Anatolia - Univ. Cukurova) selected to represent different environmental conditions (latitudes from 32Γ to 57Γ north, altitudes from sea level to 1250 m, from continental to arid climatic conditions), following augmented experimental designs and considering a two-rows plot as the experimental unit. The following adaptive traits have been recorded on a plot basis: growth habit, winter survival, flowering time, plant height, (thousand) grain weight, fruiting efficiency. Morphological traits such as awn length and roughness, leaf length and width and peduncle length have been also evaluated in few trials. Such information is providing the phenotypic information required to complement the genomics data generated by exome sequencing the same accessions and to help deciphering the genetic basis of barley adaptation to contrasting environments.

SESSION: 3

KEYNOTE

The barley genome

Nils Stein

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany; stein@ipk-gatersleben.de

Co-authors: Nils Stein, on behalf of The International Barley Sequencing Consortium (IBSC)

ABSTRACT

Barley is one of the most important cereal crop species. It is a close relative to wheat and rye. Its haploid genome size exceeds 5 Gigabases (Gbp), almost twice the size of any fully sequenced organism or crop species. The International Barley Sequencing Consortium (IBSC) started in 2006 a project to establish a map-based high quality reference sequence of barley. After reaching important intermediate results like (i) virtual gene order maps based on sorted chromosome survey sequencing, (ii) a whole genome shotgun draft sequence integrated to a genome-wide physical map and (iii) a draft sequence of the barley genome gene space based on pooled BAC sequencing, IBSC has come close to reach its 10 year milestone of a genome-wide BAC-by-BAC based genome sequence of barley. All seven barley chromosomes were sequenced based on short-reads sequencing-by-synthesis technology along their respective minimum tiling path of the physical map. Sequence data of more than 85,000 BAC clones was assembled and integrated with high density genetic marker information and 3D conformation capture sequencing data (HiC). As a result 4.6 Gbp of the 4.8 Gbp non-redundant sequences could be linearly ordered into seven pseudomolecules representing a first version (v1.0) reference sequence of the barley genome. A nano-channel electrophoresis based optical map of fluorescently labeled high molecular weight DNA was used to independently validate the physical integrity of the scaffolds of the pseudomolecules.

SESSION: 3

Genetic diversity in the genome era: a fine-scale map of sequence variation in the barley genome

Martin Mascher

IPK Gatersleben; mascher@ipk-gatersleben.de

ABSTRACT

Dense genome-wide marker datasets constitute the basis for research into demographic processes and patterns of natural selection among barley cultivars, landraces and wild relatives and make it possible to correlate genotypes with phenotypes in genome-wide association studies. In barley, sequence-based methods such as whole-genome resequencing, exome capture and genotyping-by-sequencing have been implemented to detect and genotype single-nucleotide polymorphisms across the genome. Moreover, nanochannel mapping has made it possible to assess large-scale structural variation between barley genotypes. Integrated analyses of these variation datasets will greatly benefit from the positional information provided by the linearly ordered, highly contiguous genome sequence assembly of cv. 'Morex' generated by the International Barley Genome Sequencing Consortium. In this talk, I will give an overview about the genotypic datasets collected in recent years using different resequencing strategies and discuss the genomic distribution of genetic diversity in context of the map-based reference sequence of barley.

SESSION: 3

Alan Schulman

ABSTRACT

SESSION: 3

Genome-wide diversity analysis focused on flowering-related loci sheds light on the history of barley domestication.

Artem Pankin

Max Planck Institute for Plant Breeding Research, Cologne; pankin@mpipz.mpg.de

Co-authors: A. Pankin, B. Kilian, M. von Korff

ABSTRACT

The central focus of evolutionary studies in crops and their wild progenitors is understanding genetic architecture of domestication syndrome and underlying processes modulating diversity in wild and domesticated forms. Recent advances in barley genomics made it feasible to investigate patterns of genetic diversity in a large-genome cereal and its wild relative on an unprecedented scale. In this study, we set out to investigate the genetic basis of barley domestication with the following questions in mind. Did domestication deplete genetic diversity and to what extent? Do patterns of genetic diversity carry signatures that distinguish demographic history from different modes of selection associated with barley domestication? Which regions of the barley genome were subject to selection during domestication? Did domestication target flowering-related loci?

To this end, we interrogated ~330,000 SNPs in a diverse set of 345 wild and 87 domesticated barley genotypes using custom designed reduced representation sequencing. The SNPs originated from ~ 12,800 loci, enriched for homologs of flowering- and domestication-related candidate genes. Diversity analysis identified unexpectedly high rate of admixture in both wild and domesticated forms, with the latter case predominantly restricted to the landraces. We found evidence of a severe domestication bottleneck, resulting in loss of genetic diversity and maintenance of extended haplotype blocks in strong linkage disequilibrium.

Selection scans using a combination of tests identified multiple targets of selection under domestication. Several tests identified a sweep around genes involved in non-brittle rachis phenotype. Detailed analysis of the sweeps and signatures of selection at individual loci narrowed down the selected regions and suggested prospective targets of domestication, which included the homologs of genes implicated in the regulation of flowering and phenology. The characteristics and map of barley genetic variation will inform future evolutionary and genome-wide association studies and support advancement of barley breeding.

SESSION: 4

KEYNOTE

Modelling the genetic architecture of plant development in barley through nested association mapping

Klaus Pillen

University of Halle; klaus.pillen@landw.uni-halle.de

ABSTRACT

Flowering time and plant development are major determinants of agronomic yield potential and yield stability. We developed the first barley nested association mapping (NAM) population, HEB-25, derived from crossing 25 wild barley donors with one elite barley recipient, and used it to dissect the genetic architecture of plant development. Upon cultivation of 1,420 HEB lines in multi-field trials and applying a genome-wide association study (GWAS), a number of major QTL were identified to control flowering time.

Extending the GWAS study to include developmental traits like shooting time, shoot elongation phase, flowering time, ripening phase, maturity, plant height and thousand grain weight resulted in locating 89 stable QTL controlling those agronomic traits. Several exotic QTL alleles caused drastic effects, potentially useful for breeding. For instance, thousand grain weight was increased by 4.5 g and flowering time was reduced by 9.3 days after substituting elite QTL alleles against exotic QTL alleles at the denso/sdw1 and the Ppd-H1 locus, respectively. We also showed that the exotic allele at the semi-dwarf locus denso/sdw1 is a potential target to increase yield since it uncouples the negative correlation between shoot elongation and ripening phase, resulting in a beneficial effect on thousand grain weight.

Our study demonstrates that nested association mapping of HEB-25 can assist to unravel the genetic regulation of plant development and yield formation in barley. Moreover, we propose that the introgression of wild barley alleles into the elite barley gene pool may assist in fine-tuning key developmental phases to maximize yield in the long run. We conclude that nested association mapping is a valuable genetic tool, allowing to dissect the genetic architecture of important agronomic traits and, simultaneous, to expand the genetic diversity of our modern elite barley gene pool.

SESSION: 4

Barley Composite Crosses: Past and Future Value in Barley Breeding and Research

Cal O. Qualset

University of California, Davis; coqualset@ucdavis.edu

Co-authors: F.R. Gabor, P.L. Morrell

ABSTRACT

Harry V. Harlan, a life-long barley researcher, advanced the concept of creating diversity for barley genetic improvement by creating diverse populations based on multiparent mating schemes in the early 1920s. His resulting populations were designated Composite Crosses (CCs). These populations were advanced for many generations at Davis, CA by Coit A. Suneson and were used by barley breeders who selected and released at least 10 varieties from the CCs. Seven CCs have been advanced for up to 57 generations, making these populations among the oldest active experimental populations in agriculture. Suneson popularized the CCs with his classic paper on evolutionary breeding in 1956 and with his introduction of male-sterile-induced recombination in CC XXI, his 'Paul Bunyan' creation. Since the CCs harbor genetic diversity, natural selection was expected to improve fitness, i.e., grain potential, over time. This has not been realized, but the populations have been shown to be valuable sources for desirable traits, such as scald resistance. R. W. Allard and his students and collaborators used the populations extensively for documenting genetic diversity via isozyme analyses. The positive gene conservation role of the CCs was demonstrated as well as changes in gene frequency as the populations were advanced. Breeders can expect to find useful genes in the CCs now. Future DNA research can investigate population structure and trait associations with the CCs. This report will examine past results and lessoned learned that are relevant to construction of genetically diverse and useful multiparent experimental populations. The future of the Harlan/Suneson CCs will be discussed with respect to generation advancement and secure curation.

SESSION: 4

The molecular basis of self-incompatibility in Hordeum bulbosum

Katsuyuki Kakeda

Mie University, Graduate School of Bioresources, Japan; kakeda@bio.mie-u.ac.jp

Co-authors: K. Kakeda, and R. Asahara

ABSTRACT

Self-incompatibility (SI) in the grasses (Poaceae) is gametophytically controlled by a distinct two-locus genetic system. In the genus Hordeum, two SI species of H. bulbosum and H. brachyantherum are known. The genetic control by the multiallelic loci S and Z, which are located on chromosomes 1(1Hb) and 2(2Hb), respectively, has been confirmed in the SI of H. bulbosum. This wild species is most closely related and cross-compatible to cultivated barley (H. vulgare). Thus, if the SI system could be transferred into barley, it would be of great value in utilizing for F1 hybrid breeding. In our previous studies using diploid H. bulbosum to elucidate molecular mechanisms of the SI system, we have identified a promising candidate of the female S gene, named HPS10 (Hordeum pistil S-specific 10). This gene fulfills the requirements for the female S, namely, complete linkage to the S locus, stigma-specific expression and a high degree of allelic sequence polymorphisms. The gene product was predicted to be a small hydrophilic protein of unknown function. Here we show the results of in vitro pollen bioassay to demonstrate that HPS10 is the female S determinant. We also report our current approaches involving comparative genomics and transcriptome analysis to further search for candidate genes encoding the remaining SI determinants in H. bulbosum.

SESSION: 4

A pipeline for rapid development of mapping populations relevant to breeding

Laura Ziems

The University of Queensland, Queensland Alliance for Agriculture and Food Innovation; l.ziems@uq.edu.au

Co-authors: L.A. Ziems, H. Robinson, C.A.I. Richard, J.D. Franckowiak, G.J. Platz, R. Williams, R.F. Park, D. Singh, L.T. Hickey

ABSTRACT

Generating populations for mapping quantitative trait loci (QTL) in pre-breeding programs is typically a lengthy process, requiring five to seven plant generations to make a cross and develop recombinant inbred lines. The resulting populations often lack relevance to elite breeding material and segregation for extreme plant height and maturity makes it difficult to precisely phenotype complex traits, such as drought adaptation or quantitative disease resistance. Here, we outline a novel pipeline for development of mapping populations that addresses these limitations. We applied this strategy to generate the first multi-parent reference nested-association mapping (NAM) population, suitable for dissecting complex agronomic traits in barley. 'Speed breeding', the rapid generation advance (RGA) technique developed at The University of Queensland, was used to generate 1,375 F4-derived NAM lines within only 18 months. Twenty-one elite breeding lines diverse for a range of abiotic and biotic attributes were selected as founders and nested within three common parents: Commander, Compass and La Trobe, which are cultivars preferred by industry. An incomplete factorial crossing design was adopted, producing a total of 32 families. All plant generations were grown in the speed breeding system, with the exception of the F2 generation, which was grown in the field and subject to selection for plant height and maturity similar to the respective common parent. The population was genotyped using the Diversity Array Technology genotype-by-sequencing platform, generating over 30,000 polymorphic markers. We performed NAM for plant height and maturity, plus investigated the effects of selection during line development. Both known and novel genes for plant development were detected, highlighting the power of this genetic resource to dissect complex traits. Our novel strategy for NAM population development incorporating both RGA and field-based selection has established a powerful pre-breeding platform that permits examination of new alleles within a relevant breeding context.

SESSION: 5

KEYNOTE

Genetic characterization of salinity tolerance traits to increase salinity tolerance of crops

Mark Tester

King Abdullah University of Science & Technology; mark.tester@kaust.edu.sa

ABSTRACT

Forty percent of the world's food is produced under irrigation, and this is directly threatened by over-exploitation and changes in the global environment. In this talk, the focus will be on the use of forward genetic approaches for discovery of genes related to salinity tolerance in barley. Rather than studying salinity tolerance as a trait in itself, we dissect salinity tolerance into a series of components that are hypothesised to contribute to overall salinity tolerance. Two consecutive years of field trials were conducted at the International Center for Biosaline Agriculture, a site with sandy soil and very low precipitation. Drip irrigation systems allowed the control of salinity by supplying plots with low (1 dS/m) and high salinity water (17 dS/m). A barley Nested Association Mapping (NAM) population developed by Klaus Pillen has been used to dissect physiologically and genetically complex traits in response to salt stress. Ten traits related to yield and yield components (e.g. days to flowering, harvest index, 100 seed mass) were recorded and five stress-indices were derived from each of these measurements. We have identified two significant loci located on the long arms of chromosomes 1H and 5H, which are both associated with several traits contributing to salinity tolerance, namely days to flowering, days to maturity, harvest index and yield. The application of this approach provides opportunities to significantly increase abiotic stress tolerance of crops, and thus contribute to increasing agricultural production in many regions.

SESSION: 5

Genetic resources for climate change: wild barley and genes for tolerance to waterlogging

Anna Westerbergh

Department of Plant Biology, Uppsala BioCenter, Linnean Centre for Plant Biology in Uppsala, Swedish University of Agricultural Sciences, Uppsala, Sweden; Anna.Westerbergh@slu.se

Co-authors: M. Sameri, E. Lerceteau-Köhler, and G. Bedada

ABSTRACT

Wild relatives of crops are adapted to a wide range of habitats and stresses. Much of the phenotypic and genetic diversity of the wild populations was lost as a result of human and natural selection during domestication. Hordeum spontaneum, as the ancestor of barley, is therefore a potential source of genes and alleles for improvement of tolerance to stresses in barley. Waterlogging (WL) is one abiotic stress which is projected to increase in agricultural fields in some regions due to global climate change. We have screened H. spontaneum accessions from areas with high precipitation as well as a set of diverse cultivars and have identified WL tolerant genotypes. Based on the large variation found among these accessions we distinguished suitable parents for generating QTL mapping populations. In a doubled-haploid (DH) mapping population derived from a cross between a susceptible cultivar and a tolerant H. spontaneum accession, we identified several QTL with large effect and favorable H. spontaneum alleles for waterlogging tolerance. Some QTL were verified using near-isogenic lines with H. spontaneum segments in a barley background. For comparison, another mapping population based on two cultivars with variation in WL tolerance is evaluated. Transcriptome sequencing (RNA-seq) of highly WL tolerant and susceptible parents, and selected DH lines is carried out. The combined use of screening, mapping and gene expression studies will identify genes, genomic variation and genetic resources important for improvement of WL tolerance in barley. Robust cultivars adapted to changes in climate will provide the farmers with high yield stability, increased global food security and a sustainable agriculture.

SESSION: 5

Genetic solution for phosphorus use efficiency (PUE) in barley through candidate genes

Xue Gong

The University of Adelaide; xue.gong@adelaide.edu.au

Co-authors: Glenn McDonald, Willie Shoobridge, Diane Mather, Rob Wheeler

ABSTRACT

Improving phosphorus (P) use efficiency (PUE) is an important breeding goal for barley, but barley breeding for high PUE varieties has been slow due to a lack of knowledge in molecular mechanism of PUE and understanding in yield responses to P. To tackle these issues, we used two methods: (1) PUE = yield at no-added P relative to yield at added P and (2) P responsiveness = difference in yield between added P and no-added P. PUE indicates a variety's ability to use native soil P and P responsiveness assesses a variety's yield response to P independently of its yield potential. Phenotyping of the two traits using a Commander/Fleet population was conducted in five field environments. Variation of both traits was observed, but a low correlation was found. PUE varied from 31% to 124% and lines showed a higher than average response to added P also displayed the highest yield in the population. Again, unique QTLs for PUE were mapped with grain yield (GY) or P uptake at no added P, but unique QTLs for P responsiveness were co-localized with GY or P uptake at added P. A shared QTL was also identified for PUE and P responsiveness, but the phenotypic effect was contributed by different parental alleles. These results demonstrated improving PUE, P responsiveness and P uptake is improving GY. Thus, our work provided experimental evidence to cultivate barley varieties that can not only use native soil P efficiently when P is limited, but also response to P when P is available. Assisted with information of whole genome shotgun sequences of Commander and Fleet, candidate genes underlying the QTLs for PUE and P responsiveness are revealed. Molecular markers derived from candidate genes would decrease the time for farmers to realize on-farm benefits from improved varieties.

SESSION: 5

Influence of temperature on recombination in barley

Mikel Arrieta

James Hutton Institute; mikel.arrieta@hutton.ac.uk

Co-authors: I. Colas, R. Waugh, and L. Ramsay

ABSTRACT

Breeding work relies fundamentally on recombination but the control of this process is not fully understood especially in crop plants. In barley the distribution of meiotic crossover events is highly skewed meaning that, substantial proportions of the chromosomes are inherited together as large linkage blocks, preventing the generation of novel gene combinations and useful variation that could be exploited in breeding programmes. An ability to modify the pattern of recombination in these species could therefore have profound impact on the breeding of the crops.

Historical and more recent work has shown that abiotic stress such as high temperature can affect the distribution of chiasmata and thus could provide the means to manipulate recombination within a breeding programme.

As part of a recently funded Marie Curie ITN entitled Control of Meiotic Recombination: Arabidopsis to Crops (COMREC) co-ordinated by Prof FCH Franklin (University of Birmingham) the effect of temperature on recombination in barley is being undertaken at the James Hutton Institute, (Dundee, Scotland).

The initial experimentation has concentrated on cytogenetics of affected meiocytes and the genetic mapping of progeny from F1 plants that have been subjected to a sustained period of heat stress. This work has confirmed the reported effect of temperature on the distribution of crossovers and recombination in barley (Higgins et al 2012, Phillips et al 2015); showing increases in recombination in peri-centromeric regions in the genetic maps derived from F2 progeny of heat stressed F1 plants compared to those derived from progeny from control F1plantsf.

Research is now focused on performing experiments using SSD trays as a higher throughput working-platform, that allow shorter heat shock treatments to be applied, allowing the dissection of the critical effect on crossovers and recombination.

Results of these and other experiments will be presented.

SESSION: 6

KEYNOTE

Gene-based approaches to durable disease resistance in *Triticeae* cereals

Patrick Schweizer

IPK Gatersleben; schweiz@ipk-gatersleben.de

ABSTRACT

Broad-spectrum, quantiative pathogen resistance is of high importance to plant breeders due to its durability. However, it is usually controlled by multiple quantitative trait loci and therefore, challenging to handle in breeding practice. Knowing about the underlying genes would allow its more targeted utilization by allele introgressions. With the available omics tools and data of barley and one of its major fungal pathogens, the powdery mildew fungus *Blumeria graminis* f.sp. *hordei*, at hand we are now enabled to functionally address genes for defense and attack on both sides of this plant-pathogen interaction at a genome-wide scale. To identify genes that mediate race-nonspecific resistance of barley to *B. graminis* we combined a functional-genomics approach based on genomewide transcript profiling and transient-induced gene silencing (TIGS, 1400 genes) with a genetic approach consisting of association- and Meta-QTL mapping plus analysis of copy-number variation. This guided us to a shortlist of approximately 50 candidates with converging evidence for an important role in race-nonspecific resistance of barley. We have started marker-assisted introgression of potentially valuable alleles of some of these candidate genes in barley, followed by assessment of multiple pathogen resistance. On the pathogen side, host-induced gene silencing (HIGS) can inform us about effectors and other molecular weapons that are critical for successful host invasion.

SESSION: 6

Proteomic Comparison of Flag Leaves from Barley Germplasm Varying at a Major Senescence QTL Identifies Numerous Proteins with Functions in Pathogen Defense

Andreas Fischer

Montana State University; fischer@montana.edu

Co-authors: Katelyn E. Mason, Jonathan K. Hilmer, Walid S. Maaty, Benjamin D. Reeves, Paul A. Grieco, Brian Bothner, and Andreas M. Fischer (presenting author)

ABSTRACT

Recent research has established the importance of leaf and whole-plant senescence for barley yield and quality, pointing to the interdependence of senescence timing, nutrient use efficiency, grain nutrient content and yield. It has been suggested that senescing tissues are particularly vulnerable to plant pathogens, further complicating breeding towards an ideal combination of senescence traits. In this context, we have performed a proteomic comparison of flag leaves of late-senescing barley variety 'Karl' and a near-isogenic early-senescing line, '10_11', differing in the allelic state of a chromosome six locus encompassing the HvNAM-1 gene. Protein samples at 14 and 21 days past anthesis were analyzed using both two-dimensional gel-based and label-free quantitative mass spectrometry-based ('shotgun') proteomic techniques. This approach identified >9,000 barley proteins, and one-third of them were quantified. Analysis focused on proteins that were significantly ($p \leq 0.05$; difference ≥ 1.5-fold) upregulated in early-senescing line '10_11' as compared to 'Karl', as these may be functionally important for senescence. Proteins in this group included several membrane and intracellular receptors, glucanases, enzymes with possible roles in cuticle modification, classical pathogenesis-related proteins, membrane transporters and proteins involved in DNA repair. From the global analysis, a common theme of plant pathogen defense arose. Additionally, several proteases and elements of the ubiquitin-proteasome system were upregulated in line '10_11'; these proteins may be involved in nitrogen remobilization and in the regulation of both senescence and plant defense reactions. Together, our data shed new light, at the protein level, on the importance of plant defense reactions during senescence, on senescence regulation, and possibly on crosstalk between senescence regulation and plant-pathogen interactions.

SESSION: 6

The barley 'nibblerome': defining the set of NB-LRR-type R-genes from a diverse collection of barley

William Jackson

The Sainsbury Laboratory, Norwich, UK; william.jackson@tsl.ac.uk

Co-authors: Inmaculada Hernández-Pinzón, Matthew Moscou

ABSTRACT

Plant pathogens are a major impediment to sustainable food production, particularly in light of an increasing human population. One of the major forms of protection against plant pathogens comes from the plant itself – in the form of resistance genes (R genes) – which defend the plant in a pathogen specific manner, typified by the hypersensitive response (HR). The majority of R genes in plants encode NB-LRRs, which are cytosolic proteins with a nucleotide-binding (NB) domain and several leucine-rich repeat (LRR) domains. NB-LRR encoding genes exist in complex loci, meaning that correct assembly and annotation from next-generation sequencing data is typically an extremely difficult task. Using the Morex whole genome shotgun reference assembly as a starting point, we found that approximately 420 NB-LRRs are present in the annotated Morex genome. The ~420 NB-LRRs are unequally distributed across the genome, with particular enrichment on chromosome arms: 1HS, 2HS, 6HL, and 7HS. Here we describe a substantial extension of the number of annotated NB-LRRs, which was achieved using leaf transcript-based approaches utilising a collection of 38 elite, landrace, and wild barley accessions to assess allelic diversity. We also describe the physical anchoring of many of these R gene candidates to chromosomes and POPSEQ ordered contig assemblies. High expression was observed for many NB-LRR encoding R genes, including Mla and Rpg5. In parallel, we have developed an exome capture method (RenSeq) specifically targeting NB-LRRs from barley. The annotated NB-LRRome will be a critical resource in the rapid identification of disease resistance genes.

SESSION: 6

Modulation of integrated decoy R-genes/transcription factor assembly elicits wheat stem rust resistance responses in barley: rpg4/Rpg5-mediated Ug99 resistance

Shyam Solanki

Department of Plant Pathology, North Dakota State University, Fargo, ND 58108, USA; shyam.solanki@ndsu.edu

Co-authors: Shyam Solanki, Jonathan Richards, Gazala Ameen and Robert Brueggeman

ABSTRACT

The rpg4/Rpg5 locus, harboring three tightly linked genes, Rpg5, HvRga1, and HvAdf3 from barley line Q21861, have been genetically and functionally characterized and shown to provide resistance against many races of the wheat stem rust pathogen Puccinia graminis f. sp. tritici (Pgt) including race TTKSK (Ug99). Predicted RPG5 and HvRGA1 proteins are NLRs and RPG5 has an additional C-terminal kinase domain. Initial qPCR of the three genes and microscopy data suggests that rpg4/Rpg5-mediated resistance engage in an early pathogen recognition event manifested as HvAdf3 down regulation and later invoke a strong ETI response 48 hours post inoculation (HPI). A yeast-two-hybrid prey library developed from RNA of barley line Q21861 48 HPI was screened utilizing the RPG5 kinase domain as bait. The, putative barley one-zinc-finger transcription factor, HvVOZ1, was identified. This is the first ever report of interaction between an R-protein kinase domain and putative transcription factor. To validate the role of HvVOZ1 we are using VIGS to determine if the silencing of HvVOZ1 compromises Pgt resistance. RPG5, HvRGA1, and HvVOZ1 proteins with fluorescent tail are being developed to determine protein localization and interactions in-planta. We hypothesize that the RPG5-PK domain acts as an integrated decoy that HvVOZ1 binds to possibly negatively regulate defense activation or binds after defense activation as part of the signaling complex. As is hypothesized in the integrated decoy systems, the second NLR protein HvRGA1 may be guarding this VOZ1-RPG5 interaction or guarding the RPG5-STPK domain from Pgt rpg4/Rpg5-Avr effector manipulation and detection triggers defense responses. To identify other genes involved in the resistance pathway we are characterizing two independent Q21861 fast neutron induced mutants FN617 and FN618, susceptible to Pgt race TTKSK using Genotype-by-Sequencing of RIL populations and RNA-seq. The characterization of rpg4/Rpg5-mediated resistance will establish this pathosystem as a model to understand cereal host-pathogen interactions.

SESSION: 8

KEYNOTE

Current breeding methodologies and future prospects

William Thomas

The James Hutton Institute; Bill.Thomas@hutton.ac.uk

Co-authors: , Luke Ramsay, Joanne Russell, Isabelle Colas, Robbie Waugh, Hazel Bull, Kelly Houston, Mark Looseley

ABSTRACT

Key issues in barley breeding are cycle time and recombination. For example, the current spring barley breeding cycle within a European company is approximately 3 years as Concerto was first recommended in the UK in 2009, followed by a selection from a Concerto cross (Odyssey) in 2012, and then a selection from an Odyssey cross (Octavia) in 2015. Working with other breeders' germplasm extends the cycle to 5 to 6 years as Quench, a parent of Concerto but bred by a different company, was first recommended in 2007. This rapid cycling is generally being achieved without the use of doubled haploids as it is more likely to lengthen a commercial breeder's cycle in the spring crop rather than shorten it. Doubled haploids are used more routinely in the winter crop where the breeding cycle within a company is approximately 5 years with Saffron, recommended in 2005, being a parent of KWS Cassia (2010), which in turn was a parent of KWS Infinity (2015). We will consider how markers have impacted barley breeding programmes to facilitate such rapid breeding cycles and how the cycle could be further shortened. Genomic selection (GS) could be an option to shorten the cycle by removing phenotyping between crossing cycles. GS has therefore been the subject of much research over the past 5 years but there is little information about how successful it really is when omitting a phenotyping step. We believe that the real barrier to major improvement in the barley crop is the lack of recombination in centromeric regions and that the unlocking of novel centromeric haplotypes could lead to major future improvements.

SESSION: 8

Study of barley maturity with new breeding tools

Anne-Marie BOCHARD

Limagrain Europe; anne-marie.bochard@limagrain.com

Co-authors: Doriane Hamernig, Stéphanie Chauvet, Sophie Capon, Jérémy Derory

ABSTRACT

Barley breeding is challenging, due to the diversity of morphology, phenology and end use of this species: six-row v two-row, spring v winter, malting v feed barley types. In a competitive environment, breeders are always on the look-out for new approaches to improve their breeding programs. They have to combine high-throughput phenotyping data, environment characterization, understanding of gene architecture and prediction of genomic values.
In the field, new traits, such as reflectance or canopy temperature, are measured on a broad scale thanks to drone-based technologies and environments can be described and clustered with abiotic data (temperature, rainfall…). In the lab, recent advances in genome sequencing make gene identification much easier while for complex traits, Genome Wide Association Study (GWAS) and Genomic Selection (GS) have become standard breeding methods.

To illustrate the implementation of new tools in breeding, a study of barley grain maturity (flowering to ripening stages) is presented. In a context of climate variability, breeders have to select varieties adapted to specific environments and a better understanding of these environments and the required maturity are key to this adaptation.

While flowering time is intensely studied - the role of photoperiod response loci PPD-H1 and PPD-H2, and vernalization response loci VRN-H1 and VRN-H2 in flowering time have been recently reviewed by Bentley et al (2013) – maturity is less well-understood. Maturity is a generic term covering grain filling period, physiological maturity, and ripening. Each stage duration influences grain composition, yield, yield stability and adaptation to environmental stresses. These stages can be described with the Zadoks scale (Zadoks et al, 1974) but their duration cannot be easily evaluated on a breeding scale, with thousands of plots.
Visible and near-infrared canopy reflectances (Araus et al, 2001), measured with drone-based technologies, were used to calculate Normalized Difference Vegetation Index (NDVI). These measurements, taken during grain filling and ripening periods, are associated with specific plant characteristics (chlorophyll content, pigments…) and allowed to detect the starting point and duration of senescence, key elements to describe maturity.

Using the method described by Bouffier et al (2015), breeding environments were clustered according to their environmental scenarios i.e. occurrence of environmental limiting factors during key developmental phases.

Once genotypes have been characterized for maturity traits and environments clustered by similarities, GS (Meuwissen et al. 2001) and GWAS (Kang et al, 2010) were performed using medium density SNP array to detect loci involved in maturity and to predict breeding values.
Methods and results are presented and the main advantages and pitfalls of these new tools are discussed.

Araus, J.L., J. Casadesus, and J. Bort. (2001). Recent tools for the screening of physiological traits determining yield. p. 59–77. In M.P. Reynolds et al. (ed.) Application of physiology in wheat breeding. CIMMYT, Mexico, DF.

Bentley AR, Jensen EF, Mackay IJ, Honicka H, Fladung M, Hori K, Yano M, Mullet JE, Armstead IP, Hayes C, Thorogood D, Lovatt A, Morris R, Pullen N, Mutasa-Go_ttgens E, Cockram J (2013) Flowering time. In: Cole C (ed) Genomics and breeding for climate-resilient crops, vol 2. Springer, Berlin, pp 1–67

Bouffier, B., Derory, J., Murigneux, A., Reynolds, M., & Le Gouis, J. (2015). Clustering of Environmental Parameters Discriminates Drought and Heat Stress Bread Wheat Trials. Agronomy Journal, 107(4), 1489-1503.

Kang, H. M., Sul, J. H., Service, S. K., Zaitlen, N. A., Kong, S. Y., Freimer, N. B., ... & Eskin, E. (2010). Variance component model to account for sample structure in genome-wide association studies. Nature genetics, 42(4), 348-354.

Meuwissen TH, Hayes BJ, Goddard ME (2001) Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819–1829

Zadoks, J.C., T.T. Chang, and C.F. Konzak. (1974). A decimal code for the growth stages of cereals. Weed Res. 14(6):415–421. doi:10.1111/j.1365-3180.1974.tb01084.x

SESSION: 8

Genome engineering in barley using customizable endonucleases

Jochen Kumlehn

IPK Gatersleben; kumlehn@ipk-gatersleben.de

Co-authors: J. Kumlehn, S. Hiekel, N. Budhagatapalli, H. Trautwein, K. Zelkowska, M. Gurushidze, and G. Hensel

ABSTRACT

Genome engineering is a breakthrough technology that facilitates site-directed modifications of genomic DNA in planta. It offers versatile novel possibilities for both the experimental elucidation of gene functions and the improvement of crop performance. Aiming to establish site-directed mutagenesis in Triticeae cereals, target gene-specific transcription activator-like effector nucleases (TALENs) were designed and barley mutant plants generated via transfer of a pair of TALEN-coding expression units into haploid cells from which transgenic doubled haploid (DH) plants can be produced. Owing to the haploid founder cells and whole genome duplication taking place in the course of the regeneration process, some of the resultant primary mutants proved instantly homozygous, as was indicated by non-segregating progeny. In a second approach, we produced two types of plant lines each carrying only one of the two required TALEN-units. TALEN cleavage activity was then induced in hybrid progeny derived from crossings of complementary pairs of these lines. By this principle, many independent and heritable mutations can be produced even if only a few TALEN-transgenic lines are available. Whereas primary mutants are typically chimeric, mutant dissolution and genetic fixation was readily achieved by generating doubled haploids. To allow for optimization of nuclease construct design and routine prevalidation of target-specific constructs before embarking on the laborious stable barley transformations, a transient expression test was established which indicates cleavage activity via frame shift reconstitution of a reporter gene. In addition, we exemplified homology-dependent genome editing in barley cells using a customized DNA-repair template, which allows to precisely predefine not only the genomic target locus but also the resultant DNA sequence. More recently, we have also used RNA-guided endonucleases (RGENs), which derive from the bacterial CRISPR/CAS immune system, to generate site-directed mutations in barley plants.

SESSION: 8

MARKER-BASED BREEDING TOOLS INFORM EARLY GENERATION SELEECTION AND CROSSING BLOCK DECISIONS

Tyler Tiede

University of Minnesota; tied0068@umn.edu

Co-authors: A.H. Sallam, A.J. Lorenz, and K.P. Smith

ABSTRACT

Genomic selection (GS) is becoming a routinely used tool in plant breeding. The University of Minnesota barley breeding program has been using and evaluating GS since 2009. We have found that predictions, based on genome-wide markers, can be accurate enough to warrant replacing phenotypic selection at some stages of the breeding program, particularly for traits that are difficult or expensive to measure. For example, we have found that genomic selection for Fusarium head blight resistance and grain yield is equivalent to phenotypic selection, but substantially less expensive and can be implemented earlier in the breeding cycle. In addition, prediction accuracy can be improved through proper optimization and maintenance of the training dataset. In addition to using GS to select lines for advancement and crossing, we have recently evaluated the use of genome-wide markers to select parent combinations to maximize genetic variance (__G^2) in bi-parental breeding populations. Previously, metrics such as the phenotypic, genetic, and kinship-based (estimated from genomewide markers) distances between parents have been tested for their ability to predict __G^2. In general there is little to no correlation between these metrics and __G^2. One explanation for this is the inability of such methods to explicitly model the segregation of associated genetic loci (i.e. QTL). This concern has been addressed by three recently proposed methods that, at varying levels, predict __G^2 by explicitly modeling the segregation of QTL. We evaluated the accuracies of all six __G^2 prediction models using field-based estimates of __G^2 from 40 bi-parental barley breeding populations and found that methods that explicitly model the segregation of QTL were superior. Specifically, a method (PopVar) that uses the genomic estimated breeding values of simulated bi-parental populations most accurately predicted __G^2.

SESSION: 9

KEYNOTE

Chris Swersey

Brewers Association; chris@brewersassociation.org

ABSTRACT

SESSION: 9

Genome editing to validate genes putatively contributing to grain (1,3;1,4)-_-glucan content.

Kelly Houston

The James Hutton Institute; kelly.houston@hutton.ac.uk

Co-authors: Abdellah Barakate a, Matt Tucker b, Miriam Schreiber c, Edwin R. Lampugnani d, Monika Doblin d, Rachel A Burton b, Geoffrey B. Fincher b, Robbie Waugh a

ABSTRACT

a The James Hutton Institute, Dundee, Scotland, UK.
b ARC Centre of Excellence in Plant Cell Walls, School of Agriculture, Food and Wine, University of Adelaide, South Australia 5064.
c University of Dundee at The James Hutton Institute, Dundee, Scotland, UK.
d ARC Centre of Excellence in Plant Cell Walls, Plant Cell Biology Research Centre, School of Botany, The University of Melbourne, Parkville VIC 3010.

The cell wall polysaccharide (1,3;1,4)-_-glucan in cereal grain has been shown to have human health benefits such as reducing the risk of coronary heart disease1. However, high levels of (1,3;1,4)-_-glucan are an undesirable component of grain destined for the brewing and malting industries because it clogs filters and causes haze in beer. While members of the cellulose synthase-like CslF gene family have already been implicated in the synthesis of (1,3;1,4)-_-glucan, such as HvCslF6 and HvCslH2,3 , we are interested in validating candidates which contribute to (1,3;1,4)-_-glucan content in the mature grain identified in a GWAS study of this trait4.
The genome editing technique CRISPR-CAS9 has become increasingly popular in the last couple of years. We generated knockout lines using CRISPR-CAS9 for HvCslF6, and several candidates from a recent GWAS on mature grain (1,3;1,4)-_-glucan content4 . We will characterise these knockout lines for various components of their cell wall biology, including (1,3;1,4)-_-glucan and starch content, in a range of tissues and developmental stages. I will describe our overall strategy and the progress we have made towards clarifying the contribution of these genes towards (1,3;1,4)-_-glucan content in the barley grain.

1. http://www.fda.gov/NewsEvents/Newsroom/PressAnnouncements/2005/ucm108543.htm

2. Burton RA et al., (2006). Science 311: 1940-2.

3. Doblin et al., (2009). PNAS 106: 5996–6001.

4. Houston et al., (2014). BMC Genomics 15:907.

SESSION: 9

Identification of two key genes controlling chill haze stability of beer in barley

Lingzhen Ye

Institute of Crop Science, Zhejiang University, China; mylz1987@163.com

Co-authors: Yuqing Huang, Fei Dai, Huajiang Ning, Chengdao Li, Meixue Zhou, Guoping Zhang

ABSTRACT

In bright beer, haze formation is a serious quality problem, degrading beer quality and reducing its shelf life. The quality of barley (Hordeum vulgare L.) malt, as the main raw material for beer brewing, largely affects the colloidal stability of beer. In this study, the genetic mechanism of the factors affecting beer haze stability in barley was studied. Quantitative trait loci (QTL) analysis of alcohol chill haze (ACH) in beer was carried out using a Franklin/Yerong double haploid (DH) population. One QTL, named as qACH, was detected for ACH, and it was located on the position of about 108cM in chromosome 4H and can explain about 20% of the phenotypic variation. Two key haze active proteins, BATI-CMb and BATI-CMd were identified by proteomics analysis. Bioinformatics analysis showed that BATI-CMb and BATI-CMd had the same position as qACH in the chromosome. It may be deduced that BATI-CMb and BATI-CMd are candidate genes for qACH, controlling colloidal stability of beer. Polymorphism comparison between Yerong and Franklin in the nucleotide and amino acid sequence of BATI-CMb and BATI-CMd detected the corresponding gene specific markers, which could be used in marker-assisted selection for malt barley breeding.

SESSION: 9

Barley contributions to beer flavor I: Impact assessment of variety, location, and genotype x environment interaction on beer flavor

Dustin Herb

Oregon State University; Dustin.Herb@oregonstate.edu

Co-authors: R.C. Graebner, S.P. Fisk, T.P. Nielsen, D. Carey, T. Shellhammer, P.M. Hayes

ABSTRACT

Barley grain contains significant amounts of positive flavor compounds; however the impact of variety and environment on flavor is not well understood. In this study we evaluated the beer flavor potential of three barley varieties (Full Pint; AC Metcalfe; Klages) grown in replication in three environments (Corvallis, OR, USA; St. Paul, MN, USA; Saskatoon, SK, CA). The resulting grain was micromalted by Rahr Malting. Sierra Nevada Brewing Co. and New Glarus Brewing Co. both conducted congress wort sensory assessments. The controls were AC Metcalfe high and low color malts. Gas chromatography and mass spectrometry (CG-MS) at Sierra Nevada revealed that the principle volatile compounds present across samples were dimethylsulfide (759164.8 m/z), 3-methyl butanal (72583.2 m/z), 2-methyl butanal (144753.2 m/z), hexanol (129991.8 m/z), phenylacetaldehyde (393667.1 m/z), ocimene quintoxide (757448.1 m/z), and methyl mercaptan (835.5 m/z) and contributed flavors such as fruity, floral, cooked corn, nutty, potato chips, biscuit, malty, and cereal. There were off-odors as well. Concentrations of dimethylsulfide and trans-2-hexanal were highest in Full Pint, while 2- and 3-methyl butanal and methyl mercaptan was highest in AC Metcalfe, and hexanal in Klages. Principle component analysis (PCA) indicated that variety and environment account for 44% and 21% respectively of the variation in mass-spec abundance analyte concentrations across samples. In a blind sensory assessment, panelists distinguished unique flavors and preferences across the difference varieties and environments, suggesting that barley variety and production environment play a significant role in beer flavor.

SESSION: 10

KEYNOTE

Molecular Genetic Characterization of Key Genes for Utilization of Barley as Human Food and Animal Feed

Shin Taketa

Institute of Plant Science and Resources, Group of Genetic Resources and Functions, Okayama University, 2-20-1 Chuo, Kurashiki, Okayama 710-0046, Japan.; staketa@rib.okayama-u.ac.jp

Co-authors: T. Tonooka2, E. Himi1, and T. Kato3

ABSTRACT

Molecular identification and characterization of key genes that would be suited for barley consumption as human health food are our current major research aims. We briefly summarize the achievements of our Japanese barley genetics and breeding group. Emphases are placed on genes for seed characteristics, including (1) hulled or naked caryopsis (Nud), (2) phenol reaction, syn., polyphenol oxidases (PPOs), (3) (1,3;1,4)-beta-D-glucan synthesis (HvCslF6) and (4) proanthocyanidin less (ant mutants). These genes appear to elevate the values of food barley, in terms of better edibility and functional component properties. Promising morphological genes that may enhance animal preference of whole crop barley will also be briefly presented, with a stress on genes that shorten and soften the stiff and harmful awns (lks2).

SESSION: 10

Effects of agronomic practices and soil and climatic zones on the content and molecular structure of dietary fibre constituents in food barley genotypes

Marta Izydorczyk

Canadian Grain Commission; marta.izydorczyk@grainscanada.gc.ca

Co-authors: T. McMillan, S. Bazin, J. O'Donovan

ABSTRACT

The recently developed food barley genotypes are excellent sources of soluble and insoluble dietary fibres, primarily arabinoxylans and (1_3)(1_4)-_-D-glucans . Barley _-glucans are important against two of the most prevalent diseases in industrialized countries, i.e., cardiovascular disease and diabetes. The health benefits of arabinoxylans are less known, but studies showed their positive effects on cecal fermentation, production of short-chain fatty acids, and reduction of serum cholesterol. The health benefits of barley _-glucans are dose-dependent. In addition, the physiological benefits of _-glucans are associated also with their viscosity building properties linked to the high molecular weight of these polymers. While it is known that food barley genotypes contain relatively high amount of _-glucans, little is known about the effects of environment and agronomic practices on the content and molecular properties of fibre constituents. The objectives of this project were to determine how certain agronomic practices (nitrogen fertilization and seeding rates) and environmental factors affect the level and properties of dietary fibre constituents in two food barley varieties, CDC Rattan and CDC Hilose. Field experiments were conducted for three years at five locations in western Canada. The effects of nitrogen rate (60 and 120 kg/ha), and seeding rate (200, 300 and 400 seeds/m2) were determined. Generally, the increasing nitrogen rates significantly increased the content of protein, but decreased the content of starch in the grain. Increasing rates of nitrogen fertilization had small but statistically significant effect on the content of arabinoxylans and insoluble dietary fibre, but no effect on the content of _-glucans and soluble dietary. The increasing seeding rates significantly decreased the content of _-glucans and soluble fibre, but increased the content of arabinoxylans and insoluble dietary fibre. The results indicated significant effects of genotypes, environments, and seeding rates on the composition, molecular structure and weight of barley dietary fibre constituents.

SESSION: 10

Analysis of miRNA-regulated transcription factors in barley

Marcel Lafos

University of Dundee / Plant Sciences Department; Marcel.Lafos@hutton.ac.uk

Co-authors: S. McKim

ABSTRACT

Plant breeders face the challenge of delivering larger crop yields within the context of climate change. A major route to sustainable increases in productivity is by modifying plant architecture to suit specific environmental conditions. To support this effort, we must understand how developmental pathways and gene expression networks interact to determine important agronomic traits such as seed quality and number. Gene expression networks are driven through the activity of multiple transcription factor (TF) families while the actual network read-out is balanced through a combination of antagonism between different transcription factors, environmental and feedback regulation, miRNA-targeting, hormonal crosstalk and higher-order regulatory mechanisms such as chromatin remodelling and epigenetics.
In cereal crops such as barley, developmental phenotypes important to breeding include plant height and grain density, which are determined by internode elongation in the stem and inflorescence, respectively. A miRNA-regulated APETALA2-like (AP2-like) transcription factor, HvAP2, has been shown to regulate internode length in barley (Houston K. and McKim S. et al., 2013). We are using the miRNA-resistant HvAP2 barley semi-dwarf mutant, Zeo1.b, as a tool to analyse the networks controlling internode elongation by identifying targets of HvAP2 regulation and defining interactions between HvAP2 and hormonal signalling pathways. In other plant systems, AP2-like TFs participate in an antagonistic network with another set of miRNA-regulated transcription factors, the SQUAMOSA PROMOTER BINDING-LIKE (SPL) proteins, to control phase-specific traits and developmental timing. We are using a variety of approaches, including TF-ChIP-seq and the expression of miRNA-resistant transcripts, to identify and manipulate components of the barley AP2-SPL network and to investigate their role in internode growth and other agronomic traits.

SESSION: 10

The INUDFOOD Report

Brigid Meints

Washington State University; brigid.meints@wsu.edu

Co-authors: P. Batlle, L. Cistué, S. Fisk, L. Helgerson, K. Murphy, I. Romagosa, W. Thomas, and P. M. Hayes

ABSTRACT

The INUDFOOD (International hull-less food barley) trial represents the start of an international collaboration directed at the rapid development of diverse food barley germplasm resources. It arose from our goal to increase agronomic performance and provide growers and consumers with a range of grain colors, flavors, textures, and processing attributes. The end-goal of this trial is to release varieties that are best adapted to the regions where the trial is being grown. We produced doubled haploids (using anther culture) from crosses of OSU food germplasm with selected German winter barleys that have excellent agronomic performance and high levels of winter hardiness. After several years of phenotypic selection for agronomic and quality traits, selected lines were advanced to the INUDFOOD trial. There are 30 lines in this trial, 13 selected by OSU, 14 selected by Dr. Cistué and colleagues and three hulled check varieties. The experimental germplasm is all doubled haploid and hull-less and includes waxy and non-waxy starch types with moderately high grain _-glucan content. This project focuses on breeding exclusively hull-less barley for food end-uses due to the additional processing steps that become necessary in the presence of an adhering hull. The INUDFOOD trial was planted in fall 2013 at four locations: Corvallis, OR, USA; Pullman, WA, USA; Lleida, Spain; and Dundee, Scotland. In the fall of 2014, it was planted at the same four locations as well as at Mount Vernon, WA, USA. Agronomic and quality traits and resistance to biotic and abiotic stresses were measured at each location based on regional relevance. Preliminary results look promising; a number of the hull-less entries rival or out-yield the checks and have excellent agronomic and food quality ratings.

SESSION: 11

KEYNOTE

Plant Breeder Training Network: Collaborative approach to training

Jamie Sherman

Montana State University; jsherman@montana.edu

Co-authors: Jamie Sherman, Mary Brakke, Deana Namuth-Covert, Mao Thao, Frances Lawrenze, Gwen Nugent, Ashu Guru and Amy Kohmetscher

ABSTRACT

A national priority for the US is to strengthen capacities for cultivar improvement not only for ongoing food, feed and fiber sufficiency, but also to meet new demands for fuels and challenges from climate change. A supply of well-prepared plant breeders and support personnel is a primary capacity need. A collaborative model of plant breeder training, called the Plant Breeder Training Network (PBTN), was created and assessed, to address issues imposed by the changing landscape of plant breeding in the US. The creation of the PBTN was a primary goal of the Triticeae Coordinated Agricultural Project (TCAP), funded by USDA-NIFA. Through the PBTN more than 100 graduate students were mentored by TCAP PIs. Surveys of TCAP and non-TCAP students indicate that TCAP students had greater levels of independent participation in a number of plant breeding skills, including both technical and personal/professional skills. TCAP students also reported greater confidence in a number of knowledge and skill areas. TCAP students also developed a larger network in part through the online environment, increasing their scope of national collaboration. The PBTN provided online learning materials and courses in which hundreds have participated, including students and professionals from outside the project. By tracking student behavior in the online environment, data were archived, including time spent in a single session, number of sessions spent in the environment, materials accessed and quiz grades. These data will be used to inform online course best learning practices, which can help students gain the most from their online learning experiences and also guide instructional design that best supports self-paced learners. Here we will share strengths and challenges of the PBTN in hopes of improving plant breeder training globally.

SESSION: 11

Barley Breeding in the Public Interest: Perspectives on Integrating Research, Variety Development, Learning Experiences, and Extension in a U.S. Land Grant University

Patrick Hayes

Oregon State University ; patrick.m.hayes@oregonstate.edu

Co-authors: P.M. Hayes, all current and past members of the OSU Barley Project, and our worldwide network of collaborators

ABSTRACT

Barley is one of last major crops in the U.S. where the public sector is still actively engaged in cultivar development. A number of factors have contributed, historically, to this unique status. An additional set of factors could lead, in the near term, to a shift towards greater private sector delivery of varieties and public sector delivery of knowledge and training. A retrospective analysis of the Oregon State University (OSU) Barley Project is useful as an example of the outcomes that can be achieved when a public program receives sufficient support to engage in the Land Grant mission of (i) contributing to the fundamental body of knowledge, (ii) stimulating economic development through variety release, and (iii) assisting in forming an educated citizenry. Keys to the success of the program have been a balance of public (e.g. USDA Collaborative Agricultural Project grants) and industry funds (e.g. American Malting Barley Association); an opportunity to explore challenges and opportunities with no obvious immediate practical application (e.g. facultative growth habit and barley contributions to beer flavor); the integration of research and learning (e.g. graduate and undergraduate student research; the Oregon Wolfe Barleys); and an extensive international network based on unrestricted collaboration and exchange. Considerations for future public sector barley breeding include: shrinking public investment in plant breeding research with applied outcomes; expansions (e.g. the craft sector) and consolidations (e.g. the multinational sector) in the malting and brewing industries; an increased emphasis on innovative undergraduate and graduate teaching and experiential learning (with concomitant increases in time commitments); and the mantra that public sector variety development can generate sufficient revenue to be self-sustaining.

SESSION: 11

Connecting Genotype to Phenotype in 7-12 Classrooms with iTAG Barley

Roger Wise

USDA-ARS / Iowa State University; rpwise@iastate.edu

Co-authors: L. McGhee, N. Hayes, R. Schuck, J. Gonzalez, L. Maffin, T. Hubbard, E. Whigham, and G. Fuerst

ABSTRACT

iTAG "Inheritance of Traits and Genes" is a NSF-sponsored Research Experience for Teachers (RET) to promote understanding of the relationship between genotype and phenotype, which is the core foundation for modern genomics projects. Using the diverse Oregon Wolfe Barley population as the model, we have created a self-sustaining, inquiry-based curriculum comprising lab and classroom activities for high school students to learn concepts in plant development, phenotypic diversity, genetics, and/or genomics. Three key systems are presented; homeotic mutations, domestication, and epistasis. Through inquiry based learning, students become better-informed citizen scientists. iTAG Barley is aligned to the National Science Standards, and thus, can be adapted to any state standards. Teachers and workshop participants conduct pre- and post content-based survey of iTAG concepts. Results of the assessment are incorporated into publications and presented at NSTA and ASPB conferences.

The curriculum for iTAG Barley is available as teacher and student versions [PDF or digital textbook (iTAG for iPAD; https://itunes.apple.com/us/book/itag-barley-9-12-curriculum/id959451733?mt=11)], and includes NSF-funded thermal cyclers, microcentrifuges, gel boxes, transilluminators, pipetteman, and reagents. It has been implemented in >35 high-school classrooms from 2009-2014, impacting >800 students, half of which were underrepresented from urban to rural communities. The project is continuing to expand its reach with the first iTAG Barley workshop hosted by Iowa State University July 28th-31st, 2015. Workshop organizers and participants collectively will use iTAG Barley in 53 classes during the 2015-16 school year, impacting an additional 1,400 high school students. Additional workshops for summer 2016 are already being planned at Iowa State University in Ames, IA and Tuskegee University in Tuskegee, AL.

Supported by the National Science Foundation - Plant Genome grants 09-22746 and 13-39348.

SESSION: 11

Genetic basis of barley adaptation to the southern cone of South America: using GWAS to analize phenology in a wide population

Andres Locatelli

Departamento de Produccion Vegetal, Est. Exp. “Dr. Mario A. Cassinoni”, Facultad de Agronomia, Universidad de la Republica; aloca@fagro.edu.uy

Co-authors: L. Gutierrez, L. Viega, A. Castro

ABSTRACT

Phenology is a determinant factor for the adaptation of any crop, particularly in temperate conditions short growing season. Uruguayan conditions during barley growing season are defined by a relatively mild winter and a sharp increase in temperature during spring, which results in a high risk of heat stress during the grain filling period. In order to understand adaptation and to study novel gene combinations for yield potential increase, knowledge about the genetic factors affecting phenology is essential. In this research we study a wide population in order to confirm the previous work performed in adapted germplasm and to look for novel alleles. We used 297 spring barley genotypes from diverse origins. The population was genotyped with 1096 SNPs from BOPA1. It was phenotyped in four field experiments in Paysandu (Uruguay) during two years and with contrasting planting dates. A total of twelve phenotypes were measured, (lenght of GS00-GS20, GS00-GS30, GS20-GS30, GS30-GS49, GS00-Z49, GS49-GS90 and photoperiod response in all of them). A comprehensive GWAS was performed and QTLs were detected for all traits, with a total of 28 QTL regions associated to phenology traits. Most of the QTL involved more than one linked SNP, more than one trait and more than one environment. The long arms of 1H and 4H and the short arms of 2H, 3H and 5H were the regions of the most important QTLs. Four new QTL regions associated to phenology under our conditions were detected on chromosomes 1H, 6H (2) and 7H. Diversity analysis and LD analysis of detected QTLs suggest that phenology and most precisely photoperiod response may be a key determinant of the population structure. Our results are a contribution to expand the knowledge about genes with potential for breeding use in the region.