

Nonparametric tests reveal multiple selection events in the wheat genome.

Eduard Akhunov¹, S. Wang¹, S. Chao², S. Stephen³, E. Huang³, C. Saintenac¹, D. See⁴, A. Carter⁵, G. Brown-Guedira⁶, K. Forrest⁷, D. Wong⁷, M. Pumphrey⁵, G. Bai⁸, R. Bowden⁸, PS Baenziger⁹, L Talbert¹⁰, JA Anderson¹¹, S Dreisigacker¹², J Chen¹³, K Campbell¹⁴, A. Akhunova¹⁵, V. Korzun¹⁶, M. Sorrells¹⁷, J. Dubcovsky¹⁸, C. Cavanagh³ and M. Hayden⁷.

¹ Department of Plant Pathology, Kansas State University, Manhattan, KS, USA; ² USDA–ARS Biosciences Research Laboratory, Fargo, ND, USA; ³ CSIRO, Food Futures National Research Flagship, Canberra, ACT 2601, Australia; ⁴ USDA Western Regional Small Grains Genotyping Lab, Johnson Hall, WSU, Pullman, WA, USA; ⁵ Department of Crop and Soil Sciences, Washington State University, Pullman, WA, USA; ⁶ USDA–ARS Eastern Regional Small Grains Genotyping Lab, 4114 Williams Hall, NCSU, Raleigh, NC, USA; ⁷ Department of Primary Industries Victoria, Victorian AgriBiosciences Center, 1 Park Drive, Bundoora, VIC 3083, Australia; ⁸ USDA–ARS, Manhattan, KS, USA; ⁹ Plant Science Building, University of Nebraska, Lincoln, NE, USA; ¹⁰ Department of Plant Sciences, Montana State University, Bozeman, MT, USA; ¹¹ Department of Agronomy & Plant Genetics, University of Minnesota, St. Paul, MN, USA; ¹² Genetic Resources and Enhancement Unit, CIMMYT, Mexico, D.F., Mexico; ¹³ University of Idaho Aberdeen Research & Extension Center, Aberdeen ID, USA; ¹⁴ USDA–ARS Wheat Genetics, Quality, Physiology & Disease Research Unit, Washington State University, Pullman WA, USA; ¹⁵ Integrated Genomics Facility, Kansas State University, Manhattan, KS, USA; ¹⁶ KWS LOCHOW GMBH Grimsehlstr. 31, 37574 Einbeck, Germany; ¹⁷ Plant Breeding & Genetics, Cornell University, NY, USA; and ¹⁸ Department of Plant Sciences, University of California, Davis, CA, U.S.A.

Wheat has been subjected to strong human-driven selection aimed at the development of cultivars adapted to local environments. Preferential selection of advantageous alleles changes the patterns of genetic variation and linkage disequilibria around selected loci. To detect such signatures of selection in the wheat genome, we used two nonparametric tests: 1) based on the patterns of genetic differentiation among wheat populations of different geographic origin and 2) based on the extent of haplotype sharing among accessions in wheat populations. A worldwide sample of wheat cultivars and landraces including 2,924 accessions was genotyped using the Illumina 9K iSelect assay. A total of 6,305 high-quality SNP calls were included into the analysis. An integrated genetic map was built using a combination of six bi-parental mapping populations and one MAGIC population. Using the distribution of F_{st} statistics across a sliding window throughout the wheat genome we detected in total 40 selective sweeps events in the populations of spring and winter wheat. Haplotype sharing statistics identified more than 100 genomic regions that showed unusually long identical haplotypes. Some of these genomic regions showed strong differentiation in haplotype frequency among the populations of different geographic origin. An association of selected regions with genes, which are targeted in breeding programs, was used to validate our results. Here we demonstrate that by using the methods of population genetics it is possible to identify genomic regions that have been subjected to selection, providing valuable information for detailed analysis of marker-phenotype associations.

A genome-wide survey of leaf stripe resistance in a low-structured barley association panel.

Alessandro Tondelli¹, N. Faccini¹, M. Rahimi¹, A. Flavell², L. Cattivelli¹, and G. Valè¹.

¹ CRA–Genomics Research Centre, Via San Protaso 302, I-29017 Fiorenzuola D'Arda, PC, Italy, and ² University of Dundee at James Hutton Institute, Invergowrie, Dundee DD2 5DA, UK.

In barley (*Hordeum vulgare*), the application of marker platforms that provide dense genome-wide coverage of molecular polymorphism allows to elucidate the evolutionary history of natural populations and use their biodiversity to dissect traits of agronomic interest, through genome-wide association scan (GWAS) approaches. Here we describe the evaluation of a low-structured collection of ~210 spring, 2-rowed, European barley cultivars for their resistance to leaf stripe, a seed-borne disease caused by the fungal pathogen *Pyrenophora graminea*. For each line, 60 seeds were surface-sterilized and incubated in Petri dishes between two Potato Dextrose Agar layers colonized by an actively growing mycelium of the *P. graminea* isolate Dg5. After 20 days of incubation in the dark at 6°C, the emerged seedlings were transplanted to pots and grown in the greenhouse (20°C, 14 h light and 12°C, 10 h night). Resistance has been assessed as the percentage of plants showing leaf stripes symptoms, and the whole experiment has been repeated during three consecutive years. The same barley collection has been genotyped with a novel set of 7,864 gene-based SNPs incorporated into a single Illumina Infinium™ iSelect assay, in order to investigate: i) trends in the patterning of genetic diversity in European spring

barley cultivars in time and space; and ii) the utility of a low-structured population for discovering significant associations between genetically mapped markers and important agronomic traits. SNP markers mapping on the short arm of barley chromosome 6H (8.6–13.6 cM) showed a significant association with leaf stripe resistance. This genomic region is syntenic with a ~240 Kb of rice chromosome 2, where 42 genes were annotated, that could serve for the identification of candidate genes involved in barley resistance to pathogens or for the development of new SNP markers, in order to increase the resolution of the GWAS.

Haplotype diversity and evolutionary history of the *Lr34* locus of a world wheat germplasm collection.

Abdulsalam Dakouri ^{1,2}, Brent D. McCallum ¹, and Sylvie Cloutier ^{1,2}.

¹ Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, Canada, R3T 2M9, and ² University of Manitoba, Department of Plant Science, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2.

The resistance gene *Lr34* has been a key gene in the genetic management of wheat leaf rust worldwide. However a little is known about the geo-genetic diversity, the history, and the origin of this unique gene. This study was conducted to provide a comprehensive analysis of the genetic diversity at the *Lr34* locus of a world wheat germplasm collection employing ten molecular markers located within the coding sequence of *Lr34* or closely linked to it. A total of 52 alleles were detected for the ten markers. Marker gwm1220 was the most polymorphic with 21 alleles, and the highest PIC value of 0.91. Marker caSNP12 was under positive selection while markers gwm1220 and cam11 were under balancing selection. On the basis of the *Lr34*-specific markers, the world collection was divided into five major haplotypes (H) of which H1 was consistently associated with the resistance phenotype (*Lr34+*). Combined analysis of the ten molecular markers resulted in dividing the major haplotypes into 118 different sub-haplotypes. Structure and clustering analyses grouped these sub-haplotypes into two main clusters and seven sub-clusters. Variance among main clusters represented the largest proportion of the total variation. H4, an *Lr34* haplotype, was hypothesized to be the most ancient haplotype and H1 the most recent, as it likely arose after the advent of hexaploid wheat. Analysis of geographical distribution showed that H1 was more frequent in Asian germplasm, although H4 predominated in European germplasm. *Lr34*, a gain of function mutation, is hypothesized to have originated in Asia.

SESSION IV: GENETICS AND GENOMICS OF IMPORTANT TRAITS

An analysis of variation in the saccharification potential of barley straw.

Robbie Waugh. The James Hutton Institute, Invergowrie, Dundee DD2 5DA, Scotland.

Many people are concerned that using crops as renewable sources of energy/fuel could compete with food production, reducing supply and increasing prices. We have been exploring the potential of using agricultural wastes (straw, grain husks) as feedstocks for energy, fuel, and chemical generation. We are particularly interested in evaluating whether the feedstock can be modified to improve the ease with which fermentable sugars can be extracted, both by breeding through exploiting available natural genetic diversity and/or by transgenesis. Using all parts of a crop will improve the economics and incentive for food production, as well as reducing the overall carbon footprint of the industry. For example, in the United Kingdom, almost one-fifth of the greenhouse gases come from the food chain, with farming accounting for the largest share. Producing more food chain co-products, such as biofuels, has the potential to significantly reduce the carbon balance for each product.

The overall aim of the work I will present is primarily to evaluate the possibility of improving barley straw for next generation biofuel production, thereby producing an optimized raw material for industrial biotechnology while securing sustained grain production. Along with colleagues in the Universities of Dundee (Claire Halpin) and York (Simon McQueen-Mason), we have explored the power of combining GWAS with high-throughput biochemical (functional) phenotyping to identify genes involved in determining straw saccharification potential. We have identified and characterized barley lignin pathway genes and pathway regulators, and used transgenic biology both as a validation tool for the outcomes of GWAS and directly to test of the effect of drastically altering key lignin genes on plant growth and development, and interactions with the environment.