Nonparametric tests reveal multiple selection events in the wheat genome.

Eduard Akhunov [1], S. Wang [1], S. Chao [2], S. Stephen [3], E. Huang [3], C. Saintenac [1], D. See [4], A. Carter [5], G. Brown-Guedira [6], K. Forrest [7], D. Wong [7], M. Pumphrey [5], G. Bai [8], R. Bowden [8], PS Baenziger [9], L Talbert [10], JA Anderson [11], S Dreisigacker [12], J Chen [13], K Campbell [14], A. Akhunova [15], V. Korzun [16], M. Sorrells [17], J. Dubcovsky [18], C. Cavanagh [3] and M. Hayden [7].

[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 Tondelli [1], N. Faccini [1], M. Rahimi [1], A. Flavell [2], L. Cattivelli [1], and G. Valè [1].

[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