

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.