Two row-Spring barley Association Panel - A resource for fine-mapping saccharification yield and crop biofuel-related traits

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Introduction

Whole genome association scans are a powerful approach to associate small genomic intervals to traits of interest. If synteny with sequenced organisms is good it provides the framework to identify a set of genes as putative candidates influencing the trait of interest. With the genes in hand, there is potential for identifying strategies to improve the target traits, in this case saccharification yield, crop biofuel-related traits and nutrient value.

Background. Association studies do not rely on having as much genetic diversity as possible because this would introduce large population structure effects, dilute genuine genetic effects by having allelic series and effects might be estimated in genetic backgrounds not related to actual breeding pools. Artificial out-crossing in barley breeding procedures has created genetic clusters of high genetic diversity and low population structure such as UK two row springs / UK 2 row winter barley elite cultivars.

Use of whole genome association scans within clusters is attractive because this minimizes population structure effects and marker:trait associations are identified in a "common" genetic background representative of the germplasm used by the breeding companies.
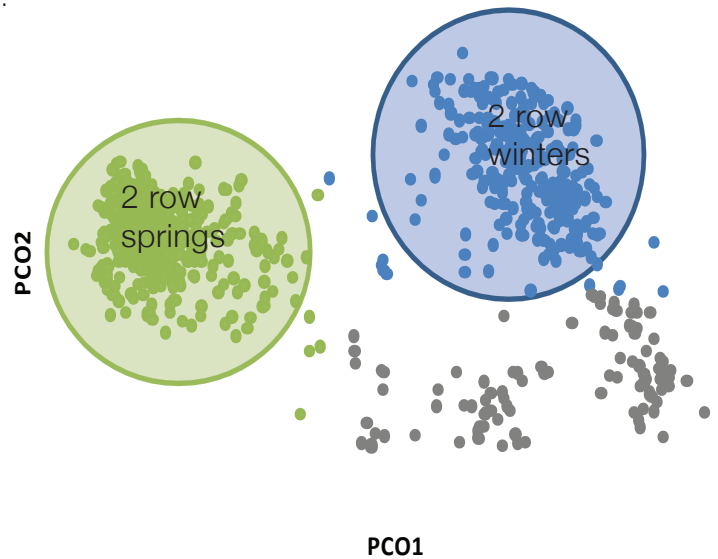
Materials & Methods

1700 barley lines have been recently genotyped at SCRI with 2780 SNP markers. The dataset was used to identify 650 genetically distinct/unique two rowed spring lines with 1309 SNP markers that had minimum allele frequencies (MAF) higher than 0.1.

Allelic frequencies correlation measures between loci pairs (Linkage Disequilibrium) were used to: 1. Explore residual population structure present in the sample and 2. Asses the mapping resolution by treating each polymorphic SNP as a binary trait and use the remaining SNP markers -mapping it by LD.
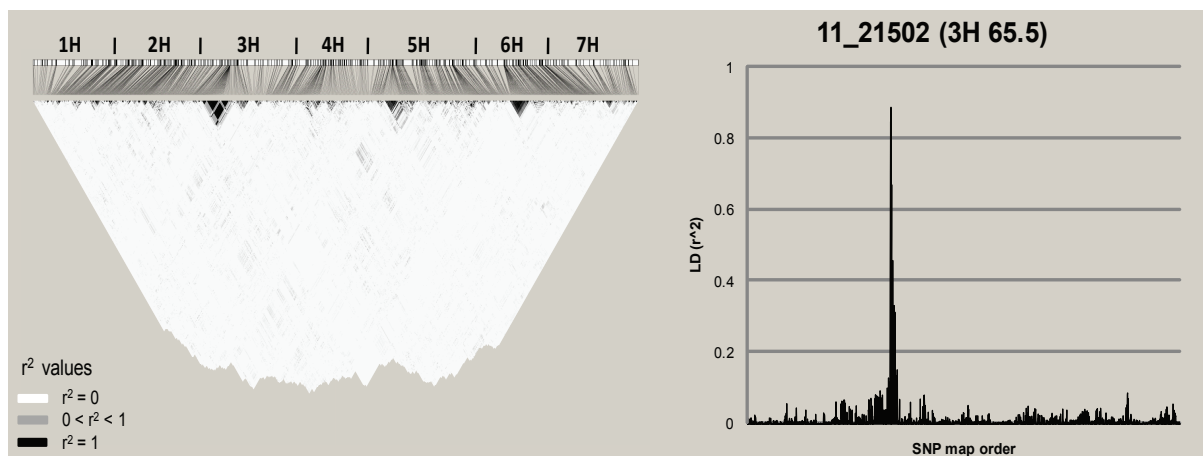
Results and Conclusions

LD heatmap shows a clean background of long distance SNPxSNP correlations, which often arise from uncorrected population structure. Moreover, by re-mapping 98% of 1309 markers with MAF>0.10 (63% of them fine-mapped to less than 1 cM) we show that this panel of lines is suitable for fine-mapping traits to small genomic intervals.

In the BSBEC project we intend to use this resource to identify genomic regions linked to crop biofuel production related traits such as saccharification yield, lignin properties and cell wall related traits. A targeted approach by re-sequencing known genes involved in the lignin pathway / cell wall characteristics will complement the results obtained from GWAs to identify the loci, genes, and alleles that correspond to good biofuel production capacity of barley straw.

Acknowledgements