Steptoe x Morex – the weakest link?

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Introduction

Whilst many single cross QTL studies have been conducted, there are few examples that have compared the results from two different crosses grown in the same environment and with the same marker assay. Two of the most widely studied barley crosses in QTL analyses are DH populations from Steptoe x Morex (SxM), representing adapted North West American germplasm, and Derkado x B83-12/21/5 (DxB), representing adapted North West European germplasm.

The advent of the Illumina SNP genotyping platform means that we can now readily generate marker maps from the same platform and, given trials grown in the same environment, compare results.

Materials & Methods

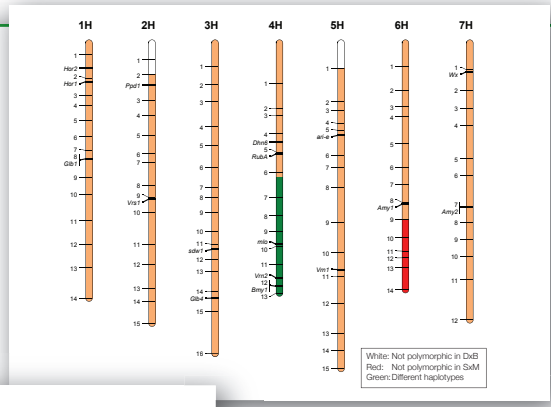
DH populations from SxM and DxB were grown at SCRI in each of harvest years 2002-4 inclusive, with each being sown on the same date and given the same management regime. Plots were scored for heading date and height and harvested when ripe to assess plot yield.

Cleaned and sieved samples were used to measure thousand grain weight (TGW by MARVIN digital analyzer) and hardness (by Comparamill). The DxB population was genotyped with the Illumina BOPA1 SNPs and a fresh marker map constructed that included several key major genes. The SxM population had been genotyped with pilot OPA1 and 2, data from which was used to construct BOPA1. We therefore extracted the BOPA1 equivalent SNP polymorphisms from the pilot OPA1 & 2 data to construct a new SxM map that was directly comparable to the DxB map.

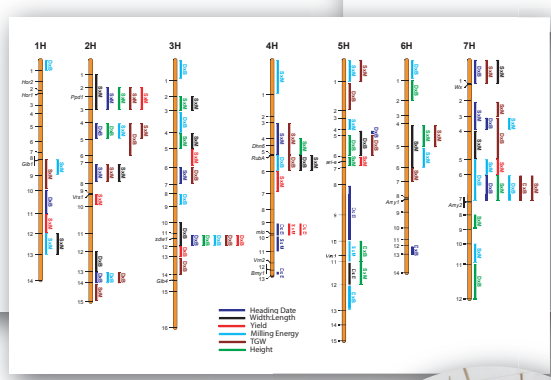
Little spatial variation was apparent in the trials and so the unadjusted scores from each trial in each year were used in QTL detection. QTL locations were then referenced to the SxM bin map to compare locations.

Results

A third of the BOPA1 SNPs were polymorphic in DxB compared to just over a half in SxM. Nevertheless, the DxB data enabled the location of just over a third of the previously unmapped BOPA1 SNPs. In general, both populations spanned similar genomic regions – DxB lacked coverage of the first 2 bins and the first bin on chromosomes 2H and 5H respectively. SxM lacked coverage on the last 7 bins of chromosome 6H and DxB had a completely different haplotype on the long arm of 4H (Figure 1).



Over 100 bin x trait locations were detected over the two crosses but there were only six instances of the same trait being located in the same bin for both crosses, although there were some in adjacent bins (Figure 2). The co-locations were for TGW in bin 5 and bin 7 on chromosomes 2 and 7H respectively, for yield in bin 10 on 4H, for heading date and milling energy in bins 4 and 6 respectively on 7H and for grain width:length ratio in bin 6 of 4H.



Conclusions

Despite the major genes segregating in both crosses, we were able to detect some evidence of co-location of QTLs for the same trait in the different crosses but, despite the common environments and marker assays, most of the locations are cross-specific. Indeed, for yield in SxM, many of the QTLs are associated with various parameters of harvest loss (see photographs), which emphasise the need to work with the right germplasm for the target environment.

Acknowledgements

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