Small Cross mapping of Barley Quality Characters

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Introduction

Marker assisted selection (MAS) has had little impact upon commercial barley breeding, apart from for a few major-gene targets. Results of Quantitative Trait Locus (QTL) studies of key characters such as yield and quality have largely been carried out upon the wrong germplasm and failed to identify robust targets. We have developed an alternative strategy based upon the study of a composite population formed from small progenies from several different pair crosses using parents from the contemporary elite UK gene pool.

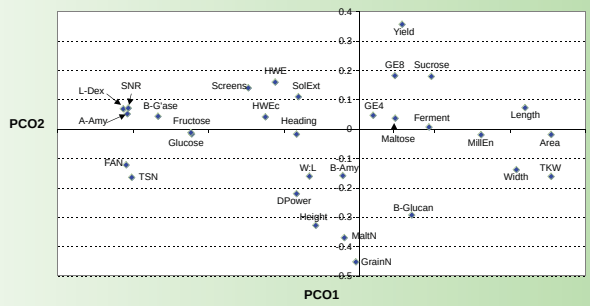
Materials & Methods

Some 200 DH lines from 11 pair crosses were grown in trials at SCRI and NIAB from 2001 to 2003. Grain samples were micro-malted at NIAB and the micro-malts analysed for a range of quality characters. Wort samples from each micro-malt were analysed for their sugar composition and the activities of key malt enzymes. Samples were also scored for a range of dry grain characters.

The DHs were genotyped with a range of previously mapped SSR and S-SAP markers and a composite genetic map formed. A set of binary markers was derived by converting each SSR allele at each locus into an individual binary marker and adding these to the S-SAP markers. The binary markers were then used in multiple regression to detect multi-locus QTL models for each character.

Results

Figure 1



Principal components analysis highlighted the dependence of characters such as fermentability upon wort sugars, principally maltose. It also revealed the close relationships between the activity levels of enzymes in the malting process that are regulated by GA (Figure 1). We detected highly significant amounts of genetic variation for nearly all 31 characters that we measured, despite the fact that the parents were all from the same elite gene pool (Figure 2). A number of markers were significantly associated with Hot Water Extract and whereas some of these associations were also detected in a survey of UK Recommended List cultivars, few were located in regions that were detected by conventional QTL mapping (Figure 3).

Figure 2

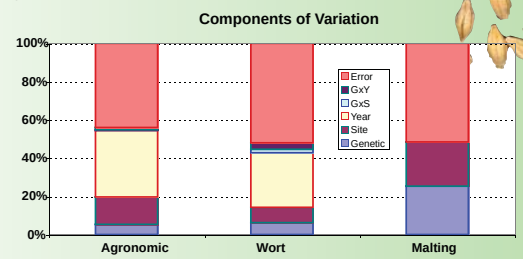
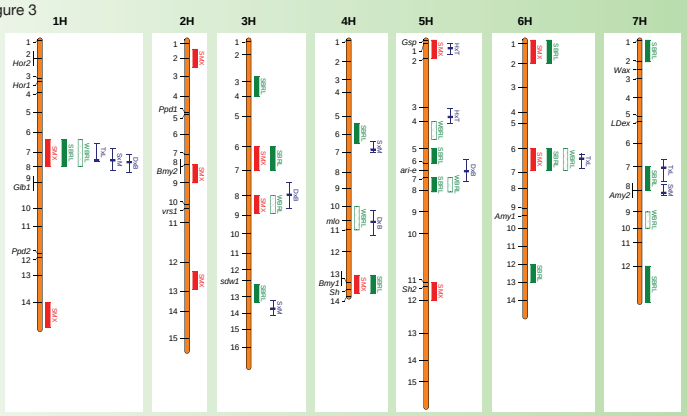


Figure 3



Conclusions

1. Considerable genetic variation for breeders to manipulate still exists in the elite UK gene pool and their problem is identifying superior recombinants.
2. High malt enzyme activity was not highly associated with either hot water extract or fermentability but was highly negatively associated with grain size parameters.
3. Few QTLs detected in the elite gene pool have also been detected in single cross studies.
4. QTL regions centromeric on 1H and 6H were also detected in RL studies and may represent robust targets for MAS

Acknowledgements

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