Barley QTL mapping with atypically small populations

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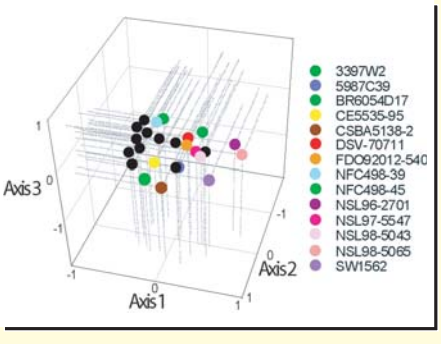
Introduction

Barley malting quality is a complex crop specific trait and therefore a goal for Quantitative Trait Analysis (QTLs) and Marker Assisted Selection (MAS). The construction of reliable meiotic linkage maps enables the analysis of trait to genome (marker) relationships. High recombination maps become mixtures of useful QTL information from the Elite parent in an 'irrelevant' background from the Exotic parent. Our approach is to create Elite x Elite maps that will be reflective of current cultivar breeding. An apparent genomic convergence of the current cultivars, suggest such cross would not reveal sufficient recombination frequencies due to marker homozygosity. Yearly, within the candidates for the UK recommended list sufficient diversity has been identified. Thus whilst no one elite pair cross may adequately sample this diversity, the formation of a composite population from a number of elite pair crosses, each or relatively few individuals provides a good sample. This Small Cross Mapping (SCM) approach has the added advantage of being able to identify QTLs that are robust over several different genetic backgrounds.

Materials & Methods

Eleven Doubled Haploid (DH) populations, from pair crosses between 14 elite parents, were grown in three trials over two seasons. After harvest, cleaned and sieved samples were analysed for grain shape parameters and thousand grain weight. Another sample was micro-malted and, following extraction, wort analysed for mono- and di- saccharide concentrations, enzyme activities and nitrogen levels.

Each DH individual was genotyped using simple sequence repeat (SSR) markers from the SCRI library.

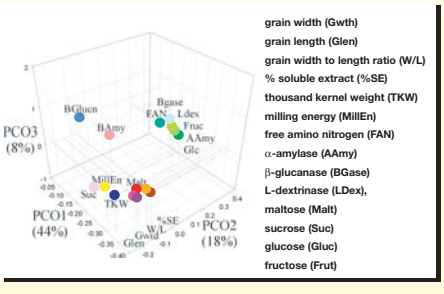


Multi-variate correlation relationships between parental genotypes and the quality variables were revealed by Principal Component Analysis (PCA). The variate means were combined with genotypic data and ANOVA used to identify SSR loci that were associated with significant differences ($P<0.005$) between allelic classes for each character.

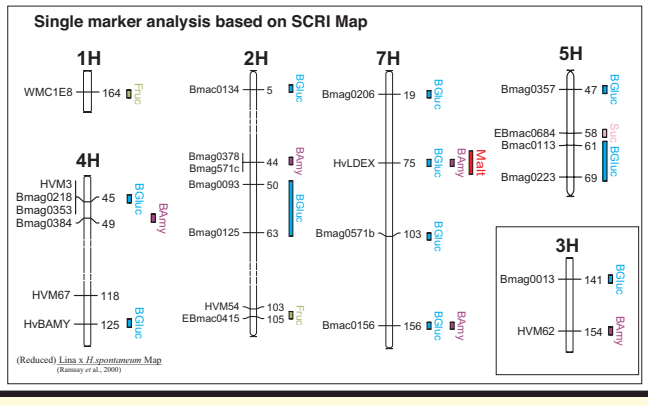
Results

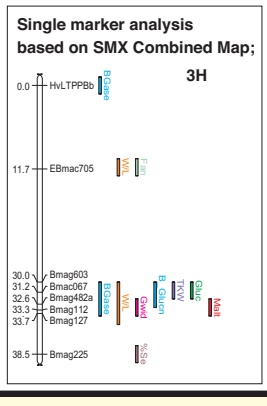
Discluding five monomorphic markers, on average 43% of the SCM populations segregated for each marker.

The PCA of the correlations between the malt quality traits showed that there were two groups with broadly similar partitions on the first three axes.



For ease of presentation we have chosen Maltose and Fructose as single characters to represent each PCA group. We searched for QTL/marker Associations for them, together with β-Glucan and α-Amylase.





We are currently constructing a map so have used the SCRI SSR map (Ramsay et al. (2000). We do not, however, infer maltose or fructose are representative of all the traits in their PCA groupings. Any gaps in the map are largely due to the availability of markers.

Some consistency of trait locations is observed between other maps when comparing chromosome 'Bin' sections, e.g. α-amylase to 2H.8 and 7H.5.

There are few other reports of QTLs for the traits studied here but some of the QTL locations that we have found for β-Glucan and α-Amylase are consistent with other studies. QTL 'hot-spots' could be due to linkage or pleiotropy. in some instances, the latter seems likely as the association of traits could reflect the biochemistry of malting. For example, the association of increased β-glucan with decreased α-amylase and fructose is functionally consistent.

Conclusions

Clearly there is sufficient molecular diversity within these populations and phenotypic variation between malt quality traits of the parents to reveal numerous constant QTLs and to reveal 'novel' loci. There is more than enough polymorphism to construct a composite map from several small populations.

Using the composite map from the SMC populations in an interval mapping approach we expect to provide a credible and consistent QTL map for European malting barley varieties.