Lessons from barley recommended lists

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The UK barley market requires high-yielding cultivars with good agronomic characteristics and, especially for spring barley, good malting quality. Barley breeding in the UK is very competitive with over 35 spring and winter barley entries, derived from many European as well as UK breeding programmes, submitted to National List Trials yearly. Since 1993, 125 spring and winter barleys have been evaluated in the HGCA/CEL funded Recommended List Trial (RLT) system for the UK leading to 64 new recommendations. As new recommendations have to show improvement in at least one character over existing cultivars, the average of over 6 new recommendations each year demonstrates that real breeding progress is being made. The pedigrees of recommended cultivars clearly demonstrate that commercial breeders are achieving this progress largely by working with crosses between elite genotypes. Moreover, Marker Assisted Selection (MAS) has, to date, not been widely deployed by commercial breeders. We have used the RLT yield and Hot Water Extract (HWE) data collected over the period 1993 to 2003 to highlight the advances that are being made through conventional phenotypic selection as this sets the standard that MAS must be judged against. We have combined the HWE phenotypic data with genotypic and pedigree data to trace the advance in winter malting quality since the introduction of Maris Otter and thereby illustrate a potential means of deploying MAS for HWE in winter barley.

Since 1992, 72 spring and 82 winter barley genotypes have been grown in fungicide-treated RLTs at sites throughout England, Scotland and Northern Ireland, resulting in yield ($t\ ha^{-1}$) data from a total of 228 spring and 237 winter trials. A more restricted set of malting quality data was available for 50 spring and 50 winter cultivars from five selected sites each year from 1995 to 2002 inclusive. From each site, the mean grain nitrogen (GN) content and hot water extract (HWE) were used to derive a hot water extract corrected to 1.5% grain nitrogen content (HWEc) using the formula HWEc=HWE+11(GN-1.5) following Bishop[1] as this gives a more accurate representation of varietal performance over contrasting seasons. These data were used to estimate overall mean plot yields (PY) and HWEc for each entry. For both spring and winter barley, the PYs of the highest yielding cultivars on the 2003 recommended list (Doyen and Colossus respectively) were over $0.6t\ ha^{-1}$ greater than those of the highest yielding cultivars on the 1993 list (Fig. 1). Improvements in HWEc of at least 3 Linter° kg^{-1} were also apparent in comparisons of the cultivars on the 2003 and 1993 recommended lists. We tested the significance of the breeding progress by regressing the means of each cultivar placed on the recommended list from 1993 onwards against the year that it was first recommended. This showed that the genetic improvement in PY was 0.8 and 0.9% *per annum*, accounting for 58 and 34% of the variation amongst the cultivar means for spring and winter barley respectively (Fig. 1). Whilst malting data was available for a wider range of RLT entries, we restricted our analysis of breeding progress to those that had at least been provisionally recommended by the Institute of Brewing for use by UK maltsters. Despite this restriction, we found evidence of significant genetic improvement in HWEc for spring barley that accounted for 43% of the phenotypic variation in the character. We did not, however, find any significant genetic improvement in HWEc for winter barley, largely because newly recommended cultivars do not

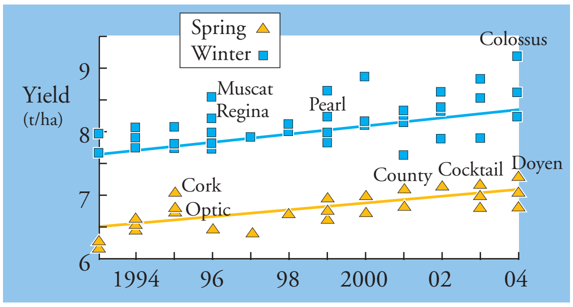


Figure 1 Recommended list treated yield against year of first recommendation.

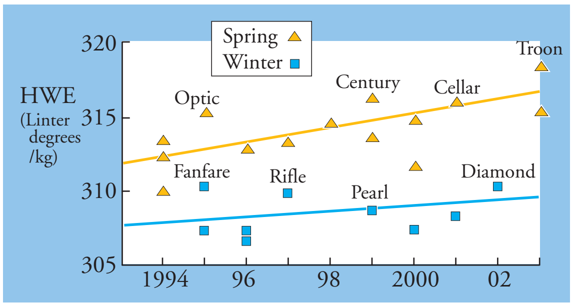


Figure 2 Recommended list hot water extract corrected to 1.5% grain nitrogen against year of first recommendation.

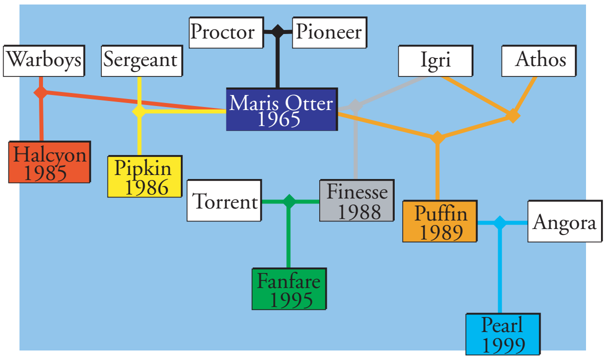
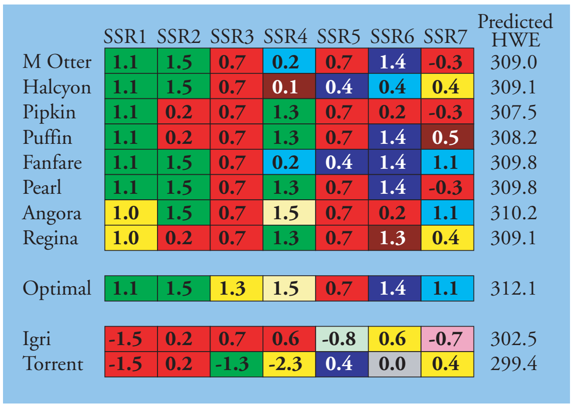


Figure 3 Pedigree tree of UK bred recommended winter barley malting cultivars and year of first recommendation.

exceed Fanfare, which was first recommended in 1995 (Fig. 2).

We have genotyped most of the RLT entries using 48 previously mapped SSR markers and the fragment sizes associated with each allele converted into frequencies and coded accordingly. We combined these genotypic data with the overall mean HWEc from our analysis of the winter barley data and used analysis of variance to test for differences in the SSR allele group means for winter barley HWEc at each locus. This detected significant associations of 10 SSR loci with HWEc but, as the map locations of the SSR loci were known, we discarded three because neighbouring loci had similar but more significant effects.

Pedigree analysis of the UK-bred winter cultivars reveals that they are all derived from Maris Otter which was introduced in 1965 (Fig. 3) and they exhibit considerable similarity in their alleles at the seven SSR loci associated with HWEc (Fig. 4). For instance, they all have the same alleles at SSR1 and SSR3, both of which appear to have been transmitted from Maris Otter. Furthermore, the Maris Otter allele is found in three of the UK cultivars for SSR2 and SSR6. By contrast, two other ancestors in the pedigrees of the UK cultivars share few alleles at these loci and also possess at least one allele with a marked detrimental effect upon HWEc. Whilst Angora and Regina have also been placed on the UK recommended list, they were both derived from the Breun breeding programme in Germany and their pedigrees cannot be traced in such detail as they contain breeders' codes. Whilst Angora and Regina have a different allele at SSR1 from the UK-bred cultivars, at least one of them shares an allele at the other six SSR loci. These data suggest that several of the seven SSR loci associated with HWEc could be used in MAS for assembling an elite malting quality gene pool and then using phenotypic selection to pick out the best. Intriguingly, none of the cultivars possesses the best allele at all seven loci. Assuming that effects are estimated accurately and the loci act in an additive manner, assembling optimal alleles at all seven loci would increase HWEc by nearly 2 Lintner° kg^{-1}.



	SSR1	SSR2	SSR3	SSR4	SSR5	SSR6	SSR7	Predicted HWE
M Otter	1.1	1.5	0.7	0.2	0.7	1.4	-0.3	309.0
Halcyon	1.1	1.5	0.7	0.1	0.4	0.4	0.4	309.1
Pipkin	1.1	0.2	0.7	1.3	0.7	0.2	-0.3	307.5
Puffin	1.1	0.2	0.7	1.3	0.7	1.4	0.5	308.2
Fanfare	1.1	1.5	0.7	0.2	0.4	1.4	1.1	309.8
Pearl	1.1	1.5	0.7	1.3	0.7	1.4	-0.3	309.8
Angora	1.0	1.5	0.7	1.5	0.7	0.2	1.1	310.2
Regina	1.0	0.2	0.7	1.3	0.7	1.3	0.4	309.1
Optimal	1.1	1.5	1.3	1.5	0.7	1.4	1.1	312.1
Igri	-1.5	0.2	0.7	0.6	-0.8	0.6	-0.7	302.5
Torrent	-1.5	0.2	-1.3	-2.3	0.4	0.0	0.4	299.4

Figure 4 Graphical representation of allelic diversity of UK winter barley malting cultivars and some parents at seven loci significantly associated with hot water extract and estimates of allelic effects.

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References

[1]Bishop,L.R. (1948) *Journal of the Institute of Brewing*, **54**: 330-333