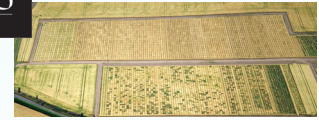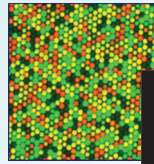# Association Genetics Of UK Elite Barley

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N Davies[11], T Bringhurst[12], C Booer[13] & **W Thomas**[1].

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Introduction

The improvement in the yield potential of UK barley varieties due to plant breeding was estimated at 1% pa up to the 1980s. At that time the varieties Triumph and Igri dominated the spring and winter barley markets respectively and it is now timely to assess the current breeding progress in both crops. The recent development of a SNP based high throughput genome wide assay also means that we can identify genomic regions that are actively being selected in current breeding programmes.

Materials & Methods

Winter and spring barley varieties representing commercial successes and failures spanning the period from 1975 to 2007 were grown in yield trials at a number of sites for harvest years 2006 and 2007.

As well as plot yield, all entries were scored for heading date, height, thousand grain weight and grain hardness. The most appropriate spatial model for each trial was identified and then used in a REML meta analysis to estimate the overall means of each genotype.

Assessment of genetic progress was assessed by regressing genotype means against the year in which they were first recommended.

Genotypic data on the yield trial entries from a high density survey of 1500 SNP loci using Illumina Oligo Pooled Arrays was used in single marker analysis with crop type as a factor to identify genomic regions associated with control of the characters measured.
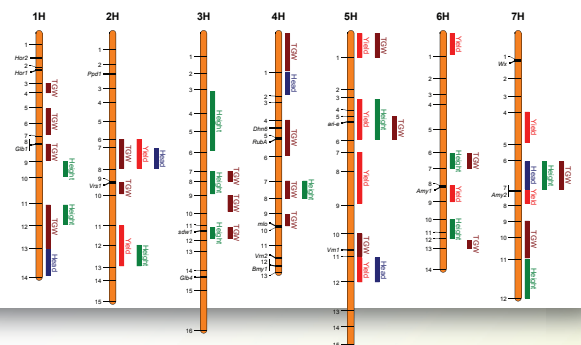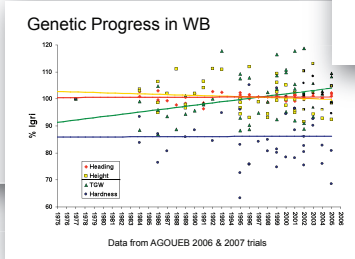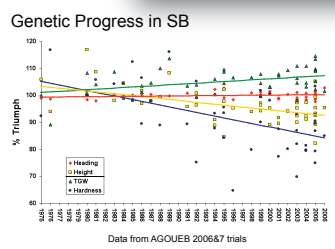
Results

Despite the greater yield potential of the winter crop, there was a significant increase in yield with year of release for both spring and winter barley, accounting for over 40% of the variation in yield. Considering the yield components, there has also been a significant increase in TGW over the same period, suggesting that this component was largely responsible for the yield increase. Over the same period, heading data has not altered in both crop types but height and grain hardness have significantly decreased in the spring crop.
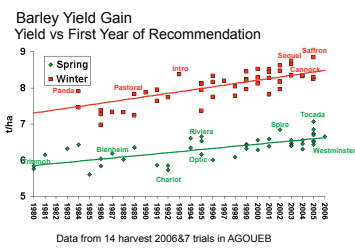
Over 60% of the SNPs were polymorphic amongst the lines assayed and had minor allele frequencies >0.1 and were therefore used to test for associations with the characters measured. Significant associations were detected in a range of genomic regions, the most frequent being bin 8 on chromosome 2H, 6 on 5H and 7 on 7H.

Barley Yield Gain — Yield vs First Year of Recommendation. Data from 14 harvest 2006&7 trials in AGOUEB

Genetic Progress in SB. Data from AGOUEB 2006&7 trials

Genetic Progress in WB. Data from AGOUEB 2006 & 2007 trials

Conclusions

Significant genetic progress due to breeding is still being made in the elite winter and spring barley gene pools.

Genetic regions associated with this progress can be identified from whole genome scans.