

Association Genetics of UK Elite Barley (AGOUEB)



L Ramsay¹, J Comadran¹, W Thomas¹, D Marshall¹, M Kearsey², D O'Sullivan³, J Cockram³, C Tapsell⁴, S Klose⁵, P Bury⁶, R Habgood⁷, P Gymer⁸, T Christerson⁹, B Allvin¹⁰, N Davies¹¹, T Bringhurst¹², C Boorer¹³ & R Waugh¹.

- ¹Scri, Invergowrie, Dundee DD2 5DA, UK;
- ²School of Biosciences, University of Birmingham, Edgbaston, Birmingham, B15 2TT, UK;
- ³NIAB, Huntingdon Road, Cambridge CB3 0LE, UK;
- ⁴KWS UK, 56 Church Street, Thriplow, Nr Royston, Herts SG8 7RE, UK;
- ⁵LS Plant Breeding, North Barn, Manor Farm, Milton Road, Cambridge CB24 9NG, UK;
- ⁶Syngenta Seeds Ltd, Market Stainton, Market Rasen, Lincs LN8 5LJ, UK;
- ⁷Nickerson-Advanta Ltd, Joseph Nickerson Research Centre, Rothwell, Market Rasen, Lincs LN7 6DT, UK;
- ⁸Secobra/Dalgety, Throws Farm, Stebbing, Great Dunmow, Essex CM6 3AQ, UK;
- ⁹SW Seed, Svalöf Weibull AB, SE-268 81 Svalöv, Sweden;
- ¹⁰Perten Instruments AB, P.O. Box 5101, SE-141 05 Huddinge, Sweden;
- ¹¹The Maltsters Association of Great Britain, 31B Castlegate, Newark, Notts NG24 1AZ, UK;
- ¹²The Scotch Whisky Research Institute, The Robertson Trust Building, Research Park North, Riccarton, Edinburgh EH14 4AP, UK;
- ¹³Brewing Research International, Lyttel Hall, Nutfield, Surrey RH11 4HY, UK

(The AGOUEB Consortium, <http://www.agoueb.org>)

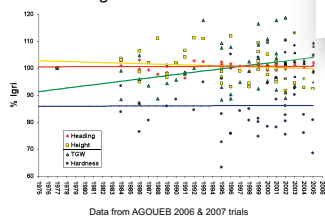
Introduction

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.

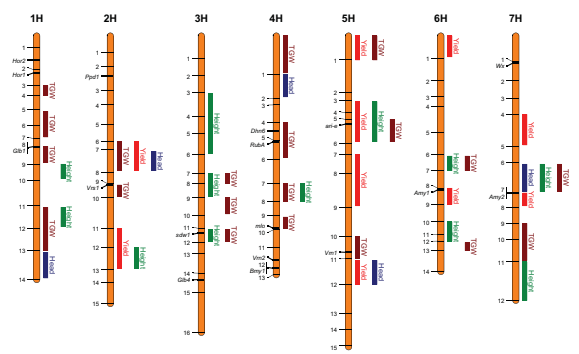
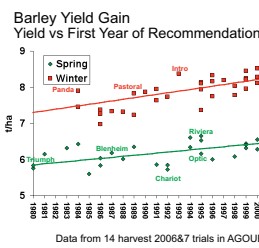
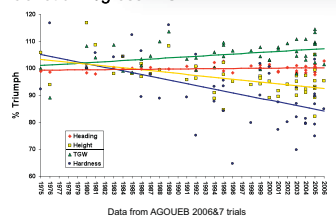
Results

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.

Genetic Progress in WB



Genetic Progress in SB



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 7 on chromosome 2H, 6 on 5H and 7 on 7H.

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. This bodes well for more detailed analysis using over 500 lines that have completed official NL2 trials since 1993.

Acknowledgements

This project was sponsored by Defra and RERAD through the Sustainable Arable LINK programme with the Home Grown Cereals Authority of Great Britain as an additional commercial sponsor.

