Distilling Quality in Winter Wheat

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Introduction

The Scotch Whisky industry used over 550,000t of wheat from harvest 2008 as a starch adjunct in grain whisky production, where the cereal adjunct is cooked prior to mashing with addition of 5-15% high enzyme barley malt in the mash, fermentation and distillation.

The key requirements are a high level of spirit production coupled with a low viscosity of the residue, which are largely the result of carbohydrate and protein respectively and have received little breeding attention.

We used a random inbred population from a cross between Canterbury x Eclipse to study the genetic control of alcohol yield and related characters.





Materials & Methods

The population was grown in replicated field trials under contrasting nitrogen regimes to provide 8 environments, from which yield estimates were obtained.

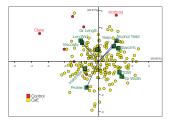
We then utilised NIR to predict alcohol yield, grain protein and starch content and the MARVIN seed analyser to measure grain size parameters from cleaned and graded seed samples and derived overall and environmental means.

Bi-plots were used to study the relationships between the overall means. 201 molecular markers were used to construct a genetic map that we then used in a QTLxE analysis, taking into account the variance/covariance structure between individual environments, to identify genomic regions affecting the genetic control of distilling quality traits.

Results

Variance component analysis showed that the genetic component ranged from 13 (Starch) to 58% (Grain Length:Width) of the sum of the genetic, GxE and error components whilst the GxE component ranged from 9 (grain shape parameters) to 30% (Starch). The bi-plot shows that grain yield, alcohol yield and starch content are highly positively correlated, as are viscosity and grain length:width ratio and thousand grain weight and grain width.

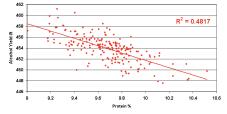
Bi-plot showing relationships between characters and genotypes



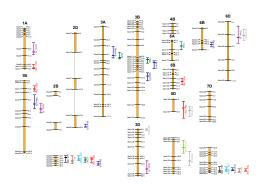
The scatter plot of grain protein and alcohol yield confirms the negative relationship between the two from the bi-plot but indicates that there are considerable deviations at all protein levels.

QTLs were found for all 10 characters; those for viscosity, starch% and TGW were the most numerous. Notable hot spots existed on chromosomes 2B and 7D, where some QTLs reflected the correlations apparent from the bi-plot but some others did not. Useful variation for distilling characters was found in the hard wheat parent.

Relationship between protein content and alcohol yield



Distilling quality QTLs in Canterbury x Eclipse



Conclusions

There is considerable independence between the key distilling quality parameters alcohol yield and viscosity thus both can be improved simultaneously. Although soft wheat is preferred, for ease of processing, useful genetic variation for distilling quality parameters exists in the hard wheat genepool.

Acknowledgments

This project was supported by the LINK Sustainable Arable Programme through sponsorship by BBSRC, RERAD and HGCA and industrial contributions from Syngenta Seeds, The Sochd Wrisky Research Institute, FOSS UK, Wessex Grain, Green Spirit Fuels and Grampian