

# Detection and Assessment of Genetic Factors Influencing Quality in a Cross between European and North American Malting Quality Varieties



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## Introduction

Phenotypic assessment of quality has, traditionally, been difficult in crosses between two- and six-rowed barley, due to effects on grain nitrogen associated with ear type. North American and European malting barley germplasm have thus developed independently, so may contain complementary genetic factors, which could be identified and exploited.

An extensive linkage map was developed in a cross between the German variety Triumph and the US variety Morex and QTL analysis has detected genetic factors for a range of quality traits over seasons and over widely different environments.

## Materials And Methods

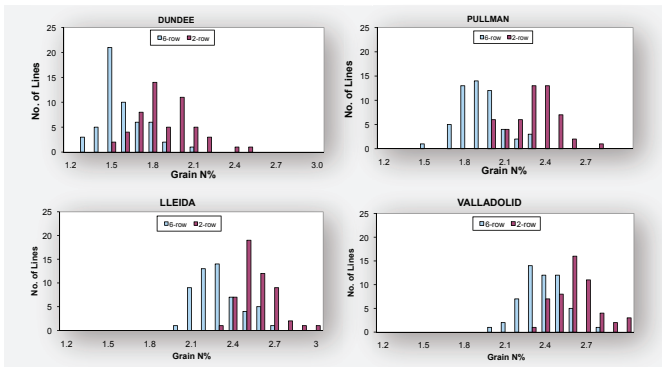
Doubled Haploid (DH) lines from a cross between the 2-rowed, European malting variety, Triumph, and the 6-rowed, N. American malting variety Morex were grown at Pullman, Washington, USA, in 2002. Following harvest grain from the 106 DH lines (54 6-row, 52 2-row) was sent to SCRI, Dundee, Scotland for malting and malt analyses.

Trials were subsequently sown in 2005 at Dundee and at 2 Spanish sites (harvested 2006) Lleida and Valladolid and grain samples were malted. Malt was assessed for Hot Water Extract and Fermentability, using scaled-down versions of Institute of Brewing Recommended methods and the data was used to determine Predicted Spirit Yield (i.e. the volume of alcohol obtainable from a tonne of malted barley). Quantitative loci for these parameters and for Soluble Nitrogen were detected using the PLABQTL programme.

Grain nitrogen content was measured on all samples from all trials by the Dumas combustion method.

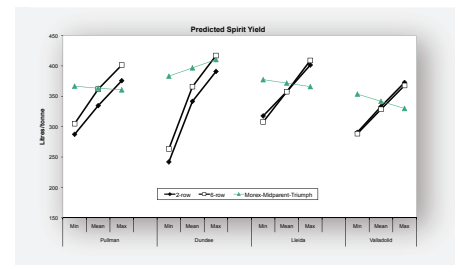
## Grain Nitrogen Content

- There were large differences between sites, with levels highest at the 2 Spanish sites and lowest at Dundee
- Normal distributions were observed amongst both 2-row and 6-row lines, but higher levels, at all sites, were seen in the 2-row lines.



## Predicted Spirit Yield

- Mean values for both 2-row and 6-row lines were generally lower than the mid-parent value.
- There was a substantial amount of transgressive segregation, particularly at the lower end, but lines higher than the better parent were observed at all sites.
- Min., mean and max. values for 6-row lines were higher than those for 2-row at Pullman and Dundee, but not at the 2 Spanish sites



## Location of QTLs

- 2 loci were associated with extract and, consequently, with predicted spirit yield, at 2 or more sites
- Morex provide the 'increasing' allele for the QTL on 1H, while the Triumph allele on 5H increased extract and PSY
- The only genetic effect on fermentability, at more than one site, was due to a factor on 2H, likely associated with the *vrsl* locus
- The Morex allele on 3H that gave an increase in extract at Dundee was also associated with a reduction in fermentability
- A similar association was seen for a factor on 7H at Pullman, so there was no net effect on predicted spirit yield
- The Triumph allele associated with the *vrsl* locus gave an increase in soluble nitrogen, which reduced fermentability and predicted spirit yield

Site/Year*	Chrom	Closest marker	LOD	Position (cM)	Additive effect	Variance explained	
<b>Extract</b>							
P02	1H	HVM43	3.76	48	1.322	15.9	
	2H	<i>vrsl</i>	9.30	86	2.338	34.6	
	7H	bPb5923	5.30	30	2.205	21.7	
D05	1H	bPb9423	8.05	42	3.200	31.0	
	3H	bPb3480	4.63	66	2.634	19.2	
	5H	HVHEMH1	3.37	14	2.220	14.4	
L06	1H	HVM43	5.90	48	1.804	23.8	
	5H	Bmag337	2.91	18	1.401	12.5	
	3H	<i>sdw2</i>	3.39	114	1.691	14.4	
V06	7H	Bmac156	3.31	16	1.223	14.1	
	<b>Ferment</b>						
P02	2H	E39M49_d	3.66	80	0.988	15.5	
	7H	bPb3484	3.23	38	1.479	13.8	
	2H	<i>vrsl</i>	4.51	84	1.168	18.8	
D05	3H	bPb7938	4.28	58	1.248	17.9	
	No QTLs						
	L06	1H	bPb133	4.29	52	0.869	17.9
<b>PSY</b>							
P02	1H	HVM43	3.86	48	7.569	16.3	
	2H	<i>vrsl</i>	8.4	84	14.017	39.5	
	1H	bPb9423	10.91	42	16.178	33.0	
D05	1H	bPb9423	8.70	42	10.746	17.4	
	2H	<i>vrsl</i>	4.04	16	12.521	17.0	
	5H	Bmag337	5.91	48	9.856	23.8	
L06	1H	HVM43	5.91	48	8.627	15.0	
	3H	bPb4616	3.52	108	8.627	15.0	
V06	No QTLs						
	2H	<i>vrsl</i>	2.96	82	0.037	12.8	
	4H	bPb8906	3.04	4	0.045	13.4	
	6H	bPb133	2.99	52	0.025	12.9	

\* P - Pullman, D - Dundee, L - Lleida, V - Valladolid

## Conclusions

- The same population was grown under very contrasting conditions, which clearly affected both grain composition and the relative contribution of different loci
- The *sdw* dwarfing gene only appeared to have an effect at Valladolid, the driest site, with drought stress likely to have an adverse effect on quality
- The *vrsl* locus had a significant effect on quality at 2 of the sites, due, apparently, to the higher levels of grain nitrogen in the 2-row progeny
- Preliminary results suggest that it is possible to bring complementary factors from 2 separate malting gene pools together, to produce lines superior to either parent
- Further data and analysis is necessary and this will be the subject of future publication

## Acknowledgements

The financial support of both the Comisión Interministerial de Ciencia y Tecnología (CICYT) and the Scottish Government Rural and Environmental Research and Analysis Directorate (RERAD) is gratefully acknowledged