Development of markers associated with traits of agronomic importance in winter oats

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Introduction

The breeding of modern oat varieties for specific end uses would be greatly enhanced by the use of marker assisted selection. However this has been restricted in the past due to a lack of appropriate genetic markers. We are using a number of approaches to identify and develop markers associated with traits of interest and to use these markers in the oat breeding programme. In the U.K., the majority of oats grown are sown in the autumn. We have developed a genetic linkage map and conducted detailed phenotyping using a population derived from a cross between two winter oats, Buffalo and Tardis.

In many cereals, the use of dwarfing genes has resulted in a considerable increase in grain yield due to a number of factors including increased spikelet fertility leading to an increase in grain number, a reduction in crop losses due to lodging, and an increase in harvest index due to more effective partitioning of biomass between the grain and straw. In oats however, use of dwarfing genes in commercial oat breeding has been relatively limited. Buffalo is a dwarf oat possessing the dominant dwarfing gene *dw6.* This mapping population will therefore help elucidate the drawbacks often associated with dwarf oats such as poor panicle extrusion (figure 1), low kernel content, late flowering and mildew susceptibility and identify any genetic linkages between the dwarf character and these other traits that have previously limited the use of the dwarfing gene in oat variety development. Analysis of this mapping population indicates that we can we can break these apparent linkages and dissect these traits into their components.

Figure 1 Example of poor panicle extrusion in dwarf plant

Materials and methods

- An F_2 mapping population of over 200 individuals was produced from a single F_1 made between Buffalo and Tardis. Buffalo is a husked dwarf variety with low kernel content, small grains and poor resistance to mildew whereas Tardis is a conventional height variety with excellent kernel content, large grains and high resistance to mildew from PC54 (figure 2).

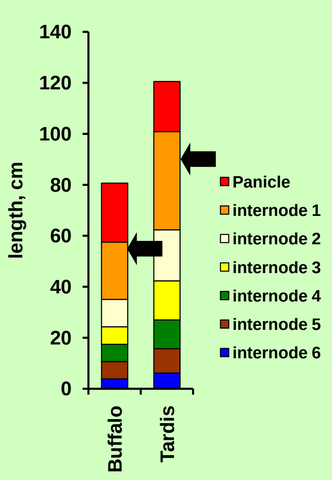

Figure 2 Parents of mapping population indicating difference in height and its components.

Arrow indicates panicle extrusion at harvest

F_2 glasshouse	F_3 Field	F_4 Replicated field trial
Seedling growth	Winter hardiness	Winter hardiness
Flowering time	Flowering time	Growth habit
Plant height	Plant height	Flowering time
Internode lengths	Disease resistance	Plant height
Panicle length	Crown rust	Internode 1 length
Panicle extrusion	Mildew	Panicle length
Tillering		Panicle extrusion
Stem diameter		Kernel content
		Grain yield
		Panicle grain no
		Panicle grain weight
		Thousand grain weight
		Kernel Content
		Disease resistance
		Crown rust
		Mildew

Table 1 Traits scored in the greenhouse and field to date. A second year of replicated trials is in progress

- DNA was extracted from leaves of glasshouse grown F_2 plants.
- 246 polymorphic microsatellite, AFLP and REMAP markers have been identified and used to develop a genetic linkage map of this population.
- DArT genotyping of this population is currently in progress.
- A wide range of traits have been scored on the glasshouse grown F_2 plants and subsequent field grown generations (Table 1) and QTL analysis is currently in progress. In the autumn of 2006 and 2007, 188 mapping population families were sown in the field in a 3 replicated 6 row trial. Phenotyping is still in progress for the 2007 sowing.

Results

- The genetic linkage map currently comprises 157 loci covering 1242 cM and 21 linkage groups (figure 3). Linkage groups range in size from 186.5 cM in length and 27 loci to 4.8 cM and 2 loci. 89 loci are unlinked at present.
- In the F_2 generation, 26% of the plants were tall and 74% dwarf indicating the presence of the major dominant dwarfing gene, *dw6.* In the F_3 generation a 1:2:1 ratio of dwarf, segregating and tall progenies was obtained. *dw6* mapped close to SSR marker OL0256 on linkage group 16 (figure 3).
- For many traits segregation was bimodal and the mapping population could be divided into 2 sub-populations based on height (figures 4, 5). Transgressive segregation was apparent for most traits. Dwarf plants tended to be later flowering, have shorter upper internodes, fewer grain per panicle and poor panicle extrusion. QTL analysis is being conducted both on the complete population as well as separately on the sub-populations.
- Panicle length however displayed unimodal segregation with the dwarf parent possessing a longer panicle length (figure 4). Leaf colour, mildew and crown rust incidence also displayed unimodal segregation.
- A strong correlation between plot grain yield and grain number per panicle was obtained for dwarf plants whereas no correlation between these two traits was found in the tall population (figure 6).
- On linkage group 1, QTL for winter hardinesss, growth habit and early season growth co-located. The allele from the Tardis parent increased winter hardiness whereas the allele from the Buffalo parent increased early season growth and erectness.
- A QTL for panicle grain number was obtained on LG 14 with the Tardis parent providing the positive allele. This QTL co-mapped with one for thousand grain weight in which the Buffalo allele increased grain weight.
- QTL for length of internodes 1, 2 , 3, 4 and 5 length and for panicle extrusion co-mapped with the position of *dw6*. However an additional QTL for panicle extrusion was found on linkage group 21 with the Tardis parent providing the positive allele.
- QTL for flowering time were found on linkage groups 1, 2, 16
- In addition to the major dwarfing gene, QTL for plant height were obtained on linkage groups 1, 5, 11 and 20

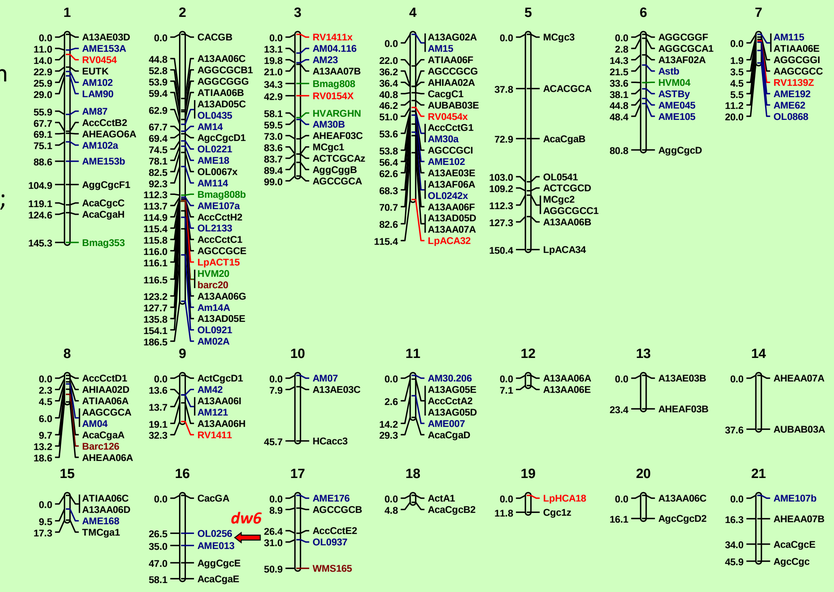

Figure 3 Genetic linkage map of Buffalo *x* Tardis mapping population June 2008 indicating position of *dw6.*
Loci in blue are oat SSRs; red are Lolium SSRs; green are barley SSRs; brown are wheat SSRs; black are AFLPs and REMAPs

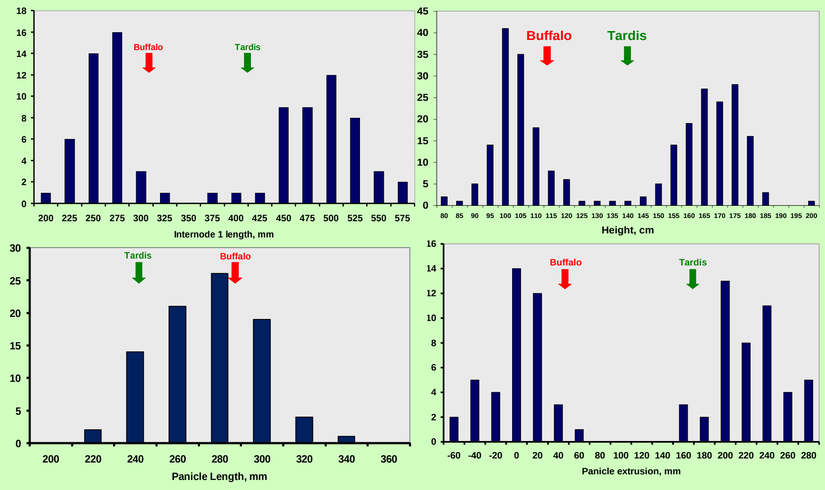

Figure 4 Segregation of plant height, internode 1 length, panicle length and panicle extrusion in Buffalo x Tardis population 2007

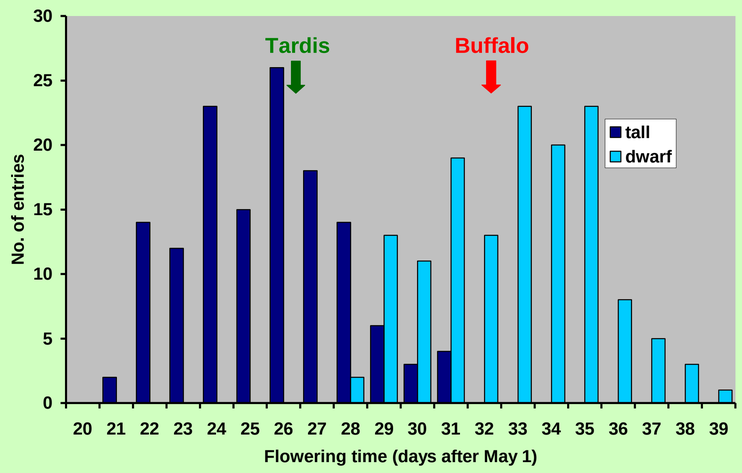

Figure 5 Segregation of flowering time in Buffalo x Tardis population 2007

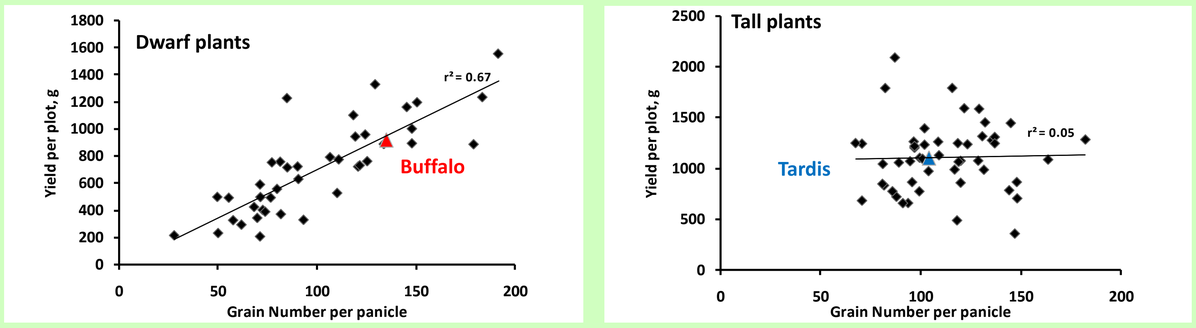

Figure 6 Relationship between grain number per panicle and plot grain yield 2007

Future Work

- Complete analysis of 2007 harvest
- Further phenotyping and QTL analysis of 2007-8 replicated field trial
- Addition of DArT markers to genetic map
- Application of marker- trait associations in applied breeding programme

[1]In April 2008 IGER-Wales merged with the Institutes' of Biological Sciences and Rural Sciences at Aberystwyth University to form the Institute of Biological, Environmental and Rural Sciences (IBERS).

Acknowledgements Participants in this Defra and RERAD sponsored Sustainable Arable LINK project include IGER, the Roslin Institute, Senova Ltd, British Oat and Barley Millers Association, HGCA, Bernard Matthews Foods Ltd, British United Turkeys Ltd, British Poultry Council, Oat Services, GB Seeds Ltd, Svalof-Weibull AB, ADAS and Elm Farm Research Centre.