

The use of genetic mapping to access and understand valuable traits in wild relatives of the cultivated oat

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Introduction

Wild relatives of crop species are a rich source of valuable traits for crop improvement but the challenge is how to successfully access such genetic variation without negative effects on crop production. Diploid, tetraploid and hexaploid relatives of the cultivated oat (*Avena sativa* L.) have been shown to display resistance to a wide range of diseases and possess enhanced grain characteristics such as oil and β -glucan content. The hexaploid nature of cultivated oats (comprising A, C and D genomes), along with its large genome size and limited polymorphism has until recently hindered the production of detailed genetic maps. The reduced complexity of working with a single genome and presence of relatively high levels of polymorphism have been used here to develop a genetic map between two diploid A-genome parents differing for a range of grain and agronomic characteristics.

Materials and methods

- An F_2 mapping population of over 200 individuals was produced from a single F_1 made between an accession of *Avena atlantica* with high β -glucan content in the grain and the cultivated *Avena strigosa*, Cc7651 (table 1).
- A wide range of traits was measured on the glasshouse grown F_2 plants (table 2) and DNA extracted from their leaves using the Nucleon phytopure method.
- 74 polymorphic microsatellite markers were identified from oats (1, 2, 3, 5), barley (4, 6, 9), wheat (7, 8) and ryegrass and used to develop a genetic linkage map of this population.

<i>Avena atlantica</i>	<i>Avena strigosa</i>	Plant stature	Tillering	Flowering time	Retention of greenness	Plant height	Internode lengths	Panicle length	Straw dry weight	No. of spikelets	Floral characteristics	Naked character of grain	Spikelet/floret disarticulation	1000 grain weight	Grain composition
Collected on Atlantic coast of Morocco by M. Leggett	Cultivated; Ceirch Llwyd (Welsh), Corc beag (Gaelic), sand, grey, black or small oat														
Early flowering (primary stem)	Late flowering (primary stem)														
Slow rate of flowering	Fast rate of flowering														
Many productive tillers at harvest	Many productive tillers at harvest														
Seed shed	Seed held														
Covered seed	Naked seed														

Table 1 Characteristics of mapping family parents

Table 2 Traits measured

Results

- The frequency distribution of each trait was approximately normal across the F_2 population (figure 1). Transgressive segregation was apparent for a number of traits.
- Although the plant height of the 2 parents were similar, *A. atlantica* had only 3 internodes whereas *A. strigosa* had 8 internodes (figure 2)

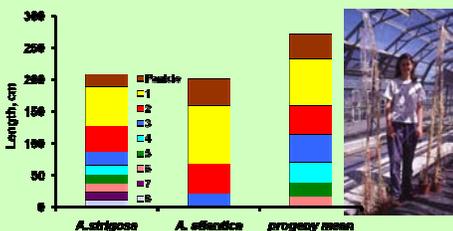
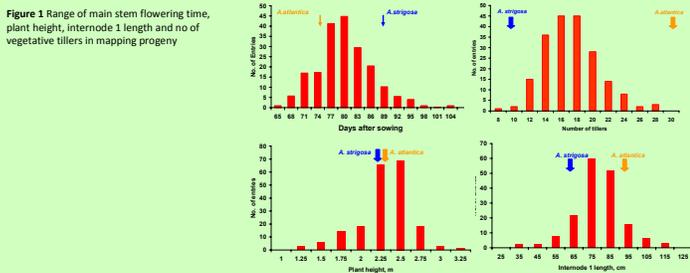


Figure 2 Comparison of plant height, panicle and internode (1-8) lengths of the main stem of mapping population parents and F_2 progeny mean

- A wide range of spikelet types were found in the F_2 progeny including cultivated base and both fatuoid and sterioid disarticulation (figure 3). Seed of approximately 30% of the F_2 progeny were either completely or partly naked (figure 4).

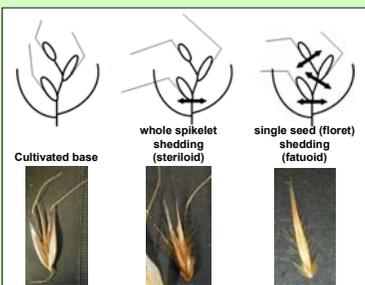


Figure 3 Simplified representation of spikelet types (glumes, peduncles, seeds, and awns). Arrows indicate the presence of abscission cell layers resulting in a sucker mouth scar.

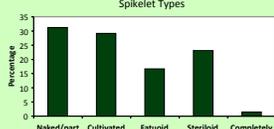


Figure 4 Frequency of different spikelet types

- The secondary and tertiary seed of those individuals with a primary naked seed had a range of disarticulation types including cultivated base, fatuoid and sterioid shedding (figure 5).
- The genetic linkage map currently comprises 85 loci covering 645 cM and 10 linkage groups. 20 loci are currently unlinked. The naked character maps as a major recessive gene on linkage group AS1 (figure 6).



Figure 5 Examples of spikelet types in individuals with a primary naked grain



Figure 6 Genetic linkage map of *Avena strigosa* x *Avena atlantica* mapping population indicating location of naked gene

- 2 QTL associated with seed shedding (and its corollary cultivated base type) were obtained on linkage groups AS4 and AS7. Presence of an *A. atlantica* allele on either AS4 or AS7 (or both) results in seed shedding. Cultivated base is recessive to seed shedding (figure 7).
- The major QTL for the fatuoid trait is found on AS2 but it is the non-shedding *A. strigosa* parent that provides the fatuoid alleles. This fatuoid QTL on AS2 is however suppressed if the QTL region on AS4 and AS7 for cultivated base is homozygous for the *A. strigosa* parent. In other words, the fatuoid trait is only expressed if there are alleles for seed shedding present also (figure 7).

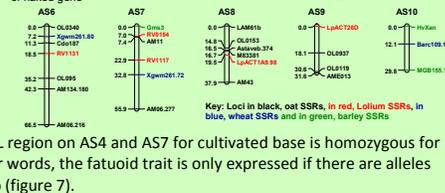


Figure 7 Location of QTL associated with domestication in *Avena strigosa* x *Avena atlantica* mapping population. QTLs on LHS of LG indicate positive allele provided by *A. atlantica*

- The major QTL for the sterioid trait is also found on AS2 but this time the *A. atlantica* parent provides the allele for the sterioid trait (figure 7). Again, if the QTL region on AS4 and AS7 for cultivated base is homozygous for the *A. strigosa* parent then the sterioid trait is not expressed.
- A wide range of QTL associated with the domestication syndrome (Hairy lemma, hairy base, rachilla length, number of vegetative tillers and number of nodes) co-localised with the QTL for seed shedding and spikelet type (figure 7).

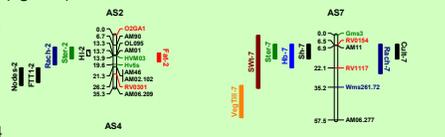


Figure 8 Location of QTL associated with flowering time (FT) and plant height in *Avena strigosa* x *Avena atlantica* mapping population

- 3 major QTL associated with flowering time were obtained (figure 8). For the QTL on AS1 and AS5, the allele from *A. atlantica* enhanced flowering time whereas the alleles from *A. strigosa* on AS3 enhanced flowering time and also co-localised with a QTL for plant height and the number of nodes on the main stem.

Conclusions

- High degree of clustering of QTL associated with domestication
- Clear separation of QTL associated with domestication and those associated with agronomic traits
- Identification of markers to undesirable traits makes possible selection against the simultaneous transfer of adversely linked genes such as shedding grain base, awns and hairy lemmas, which have in the past often reduced the potential of such introgressions in plant breeding programmes.

Further work

- Diploid oats are suitable as a bridge between rice (and other cereals) and hexaploid oats for comparative mapping purposes. Addition of DArT, COS and other markers to this diploid genetic linkage map will enable comparisons with genetic maps of hexaploid oats and other Gramineae.
- A SNP discovery programme is underway for key genes.
- Complete grain composition analysis to identify QTL for the high value trait β -glucan.
- A similar approach is being used to identify QTL and genes associated with increased oil content and grain size from the hexaploid wild relative, *A. sterilis*.

References

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¹In April 2008 IGER-Wales merged with the Institutes² of Biological Sciences and Rural Sciences at Aberystwyth University to form the Institute of Biological, Environmental and Rural Sciences (IBERS).