Genome resources for bread wheat

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ABSTRACT

The elucidation of genetic factors controlling complex traits in wheat will assist in more accurate breeding selections and assist to increase production and quality attributes. However, to date the genetic resources have provided insufficient resolution to enable fine mapping down to the sub centimorgan level whilst providing a resource for mapping a large number of traits. Therefore, the resources required on a per trait basis, have been large.

The computational and statistical resources are now sufficient to map QTL in complex backgrounds and utilise a much larger diversity of germplasm.

In order to address a number of challenges posed by wheat gene-mapping (such as background specific effects, epistasis, population sub-structure and environmental influences) we have developed two large multi-parent recombinant inbred lines involving four and eight founders respectively. By increasing the number of founders, genetic and phenotypic diversity will be exploited in breeding material from around the world.

The controlled breeding design alleviates difficulties often encountered in association mapping such as population structure. Increasing the number of rounds of meioses increases the resolution available and therefore increases the efficiency of gene identification.

Due to the large number of RIL's in these populations (1500 and 5000) modelling of the environmental influences on a range of traits will be possible without the constraints imposed by traditional approaches. The large number of RILs provides a mechanism to conduct hierarchical phenotyping for expensive to measure traits.

INTEGRATED CROSSES

We are developing two multi-parent recombinant inbred populations. The first ("4-way") population is based on Australian germplasm from four different breeding regions in Australia and include the cultivars Baxter, Chara, Yitpi and Westonia. The progeny (~1500) of these founders will be genotyped and utilised for mapping of production and quality traits which allow characterisation of loci involved in regional adaptation and a variety of end product quality characteristics. This population is currently at F6 and will begin bulking for field trialling in 2009. The second multi-parent population ("8-way") is derived from 8 international lines including three from the "4-way" population and cultivars from China (Xiaoyan54), Canada (AC Barrie), United States (Alsen), CIMMYT (Pastor) and a breeding line from Israel. This population is currently under development with progeny at F3 and field trialling is expected in 2010. Three advanced generation inter-crosses have been carried out on this material which will be utilised for fine mapping QTL identified in early generation material. The early generation material consists of approximately 5000 lines including both spring and winter growth habits.

The large progeny sets in both of these populations allow a unique ability to make informed phenotyping decisions regarding characteristics that are known to impede our ability to localise genes of interest. For example, height and flowering time will be segregating within both populations and have profound effects on many traits. By making early phenotypic/genotypic measures on these traits we will be able to accurately subset the populations so that we can take advantage of the large number of recombinations within the population, without compromising phenotype.

DIVERSITY

Parental lines were selected based on both genetic and phenotypic diversity. Genetic diversity was assessed by surveying 180 international cultivars with Diversity Array Technology (DArT) markers for broad genomic diversity along with selected genetic diversity based around glutenin composition. Figure 1 depicts the principal component analysis based on the DArT markers.

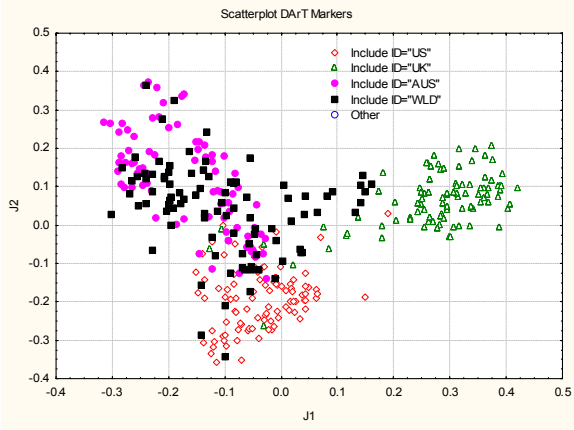

Figure 1: Principal component analysis (PC1-J1 v PC2-J2) of DArT markers for International wheat cultivars used for selection: Key- 'US' (United States), 'UK' (United Kingdom), 'AUS' (Australia) and 'WLD' (final selection group)

Table 1 outlines the high and low molecular weight glutenin composition for the 8-way population highlighting the diversity across the eight founders with 1536 combinations possible.

Table 1: High and low molecular weight glutenin scores for founders of the two RIL populations

	Glu-A1	*Glu-B1*	*Glu-D1*	*Glu-A3*	*Glu-B3*	*Glu-D3*
AC Barrie	b	c	d	e	h	c
Alsen	b	c	d	d	g	a
Baxter	a	f	a	b	h	a
Pastor	a	i	d	c	g	b
Volcani	b	al	d	b	b	b
Westonia	b	i	a	c	h	c
Xiaoyan	a	e	d	d	d	d
Yitpi	a	b	d	c	h	c
Chara	b	al	d	b	b	a

BREEDING DESIGN

The breeding design being implemented in these populations are (1) simplest possible way to combine 4 lines for the 4-way (i.e. making two F1 crosses and then inter-crossing these F1's to create 4-way progeny which were then descended through single seed descent. The 8-way population was created using a more elaborate crossing scheme where all eight lines were inter-crossed but no reciprocal crossing (28 crosses), these F1 progeny were then crossed in a similar manner (i.e. each of the 28 F1 lines were inter-crossed without reciprocal crosses) to create 210 4-way progeny. These 210 4-way lines were then inter-crossed to bring together all 8 founders. Advanced inter-crosses are being conducted for three generations, ensuring that all eight maternal lines are represented in approximately equal proportions. Figure 2, adopted from Cavanagh *et al.* [1] illustrates the breeding design for the 8-way design.

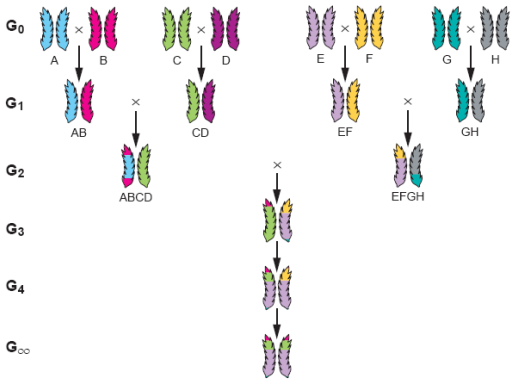

Figure 2: Breeding design for a single RIL after combining the eight founders.

MAPPING RESOLUTION

The large population sizes and the additional rounds of meioses increase the number of recombinations within the progeny and facilitate sub-centimorgan resolution within the 8-way population. The genotypic diversity within the founders will mean that many traits will be segregating; therefore many researchers from multidisciplinary interests will be able to utilise the resource and immediately gain greater resolution than existing populations. We have also made an effort to create a "pipeline" of resources beginning with the 4-way population, extending to the 8-way early generation followed by the advanced generation material from the 8-way. This allows us to move quickly from initial detection to fine mapping and candidate gene identification within the same population.

PHENOTYPING

The large progeny sets in both of these populations allow a unique ability to make informed phenotyping decisions regarding characteristics that are known to impede our ability to localise genes of interest. For example height and flowering time will be segregating within both populations and have profound effects on many traits. By making early phenotypic/genotypic measures on these traits we will be able to accurately subset the populations so that we can take advantage of the large number of recombinations and their diversity without compromising phenotype.

It will also be possible due to the large population sizes to conduct hierarchical phenotyping. For example, quality traits tend to be expensive to measure and time consuming, by phenotyping a subset to gain an understanding of the genetic regions of interest we may then screen the population for lines segregating in these regions and carry out selective phenotyping for fine mapping.

CONCLUSION

Two major genetic resources for gene-trait analysis in bread wheat have been developed which will improve the resolution in mapping for a large number of traits along with the ability to assess the correlations between traits within the same background. The diversity between the parental lines will allow phenotyping across a wide range of environments, contrasting many alleles at each locus and the interactions between genes and the environment. The outcomes from this research will be able to be utilised for whole genome selection based on a large catalogue of phenotypes and a high density marker map.

REFERENCE

1 Cavanagh, C., et al., *From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants.* Current Opinion in Plant Biology, 2008. **11**(2): p. 215-221.