Overview of Marker-Assisted Selection and its Implementation in a Wheat Breeding Project

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Although QTL mapping has resulted in numerous DNA marker/QTL linkages over the past 12 years, an important pay-off for this research will not be realized until this information is exploited in breeding programs via marker-assisted selection. The benefits and use of such markers can be accelerated by: 1) concentrating marker resources on "major" QTLs and relying on conventional phenotype screening to accumulate relatively minor genes; 2) finding diagnostic, closely linked markers; 3) verifying the QTL effect in breeder-relevant populations; and 4) utilizing high-throughput technologies to reduce costs per datapoint. The wheat breeding and genetics project at the University of Minnesota uses DNA markers for three purposes: i) parental characterization for key genes; ii) backcrossing; and iii) selection in segregating generations to enrich populations. We characterize all of our parental germplasm for one Fusarium head blight (*Fhb1*) QTL and the high molecular weight glutenins. We are currently backcrossing into our elite germplasm these genes, plus those for resistance to leaf rust (*Lr21* and *Lr47*), high grain protein (*Gpc-6B1*), and the barley yellow dwarf virus (*Bdv2*). DNA markers are used in the backcrossing process for most of these genes unless an alternative screening procedure is more efficient. The cost and time needed for DNA extraction and obtaining marker data severely limit the number of samples that can be processed in our lab. With the recent establishment of the USDA-ARS Small Grains Genotyping Centers in the U.S. and the development of high throughput genotyping techniques in the centers, we have increased our efforts in marker-assisted selection (MAS) for FHB resistance. During 2005 we screened more than 5,000 F_2 or F_3 individuals for their genotype at the *Fhb1* (major QTL on chromosome 3BS) locus. This will increase to more than 7,000 individuals in 2006. Because additional loci (e.g. high molecular weight glutenins, leaf rust resistance) are also being subjected to MAS in the same individuals, we are practicing allele enrichment, i.e. selection against the homozygous undesirable types, as a means of maintaining an adequate population size for subsequent selection. In the future, a greater emphasis will be placed on screening BC_1F_1 individuals with markers. Enriched populations will undergo phenotypic selection for FHB resistance, and other yield, disease resistance, and end-use quality testing necessary to produce FHB resistant germplasm and variety candidates. We believe that substantial efforts in phenotypic assessments will still be necessary, even with an increase in MAS for key traits, because there are likely numerous "minor" effect genes that need to be combined with the major QTLs in order to obtain the desired phenotypes.