

MAS and the future of cereal breeding: how should the genotyping centers fit in ?

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The concept of regional genotyping centers providing marker-assisted selection (MAS) analysis for genetic selection has become ingrained in the U.S. wheat and barley breeding strategies. To remain relevant to the breeding community, the genotyping centers must move past the current paradigm one-gene MAS and toward efficient holistic selection strategies. A chip-based, single nucleotide polymorphism (SNP) marker system applied to genomic breeding is the obvious next step. The transition away from single-gene selection and towards genomic breeding is conceptually easy to understand. The realization of genomic breeding is much more difficult to achieve. To make this leap, the SNPs linked to adaptation, agronomic, and quality traits must be identified for each breeding program. The public U.S. cereal breeding community currently is lacking in genomic information essential to implement the next generation MAS platforms. The USDA genotyping labs, in association with university partners, are currently identifying new SNPs useful in wheat. Identification of SNPs beneficial in specific germplasm also is being developed for PNW programs. Future work will require integrated efforts between genotyping centers and cereal geneticists to discover useful SNPs, identify and implement appropriate marker platforms, and elucidate the association between markers and haplotypes essential in the breeding programs. With the current rate of technological development, now is the time to establish a concerted effort to develop the markers, detection platforms, and the bioinformatics.

SESSION II: APPLICATION OF PHYSICAL MAPS/GENOME SEQUENCE TO BREEDING***The future impact of genomics assisted approaches in maize breeding.***

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The U.S. maize community initiated a huge three-step project in 1998, including the sequencing of the maize genome, to obtain the complete sequence and structure of all maize genes and their locations on both the genetic and physical maps of maize. All the information generated is made available to the community, via the maizegenome.org website, and from the EBI database in Europe. Now the maize genome is almost fully sequenced, which is great news for genomics, and so for maize breeding!

Having access to the genome contributes to crop improvement because comparative genomic approaches make links using the gene information already available on model species, to understand and identify more easily the function of key genes and complex biological mechanisms involved in the agronomic traits of crops. The assembled genome sequence provides a good basis for developing a large number of markers (wet lab or *in silico*) in candidate genes or within gene-rich regions that can be used in genetic studies (QTL and association mapping). Such tools facilitate and stimulate germplasm and allelic diversity characterization and increase breeding efficiency by marker-assisted selection. Traits can then be bred directly (selection of the favorable alleles only). Bioinformatics is an essential component of such studies, because it connects data from very diverse origins (genetic, transcriptomic, phenotypic, and mutants) to the genome sequences, to generate valuable information to be used in applied programs. All this, associated with the new high-throughput and low-cost technologies now available (in sequencing and genotyping), already is speeding up the identification of the most interesting genetic factors involved in agronomic traits, thus improving marker-assisted selection. Breeders need to encourage all the initiatives that aim at sequencing our genomes of interest.