Association analysis and complex trait dissection can be integrated into conventional breeding programs using molecular tools and information to facilitate marker-assisted selection of parents and segregating populations. Breeding programs are dynamic, complex genetic entities that require frequent evaluation of marker/phenotype relationships. Biparental cross populations sometimes involve poorly adapted parents, exhibit maximum linkage disequilibrium, and are limited to two alleles per locus. Association mapping can be conducted directly on the breeding material greatly facilitating the practical use of information in a crop improvement program. Because there is more genetic variation in a breeding program than in a biparental cross, phenotypic variation and marker polymorphism are much higher. Genotypic data can be combined with phenotypic data from routine screening and variety trial evaluations to facilitate selection for low heritability traits. Probably the most important advantage for a breeding program is that novel alleles can be identified and the relative allelic value can be assessed as often as necessary. To minimize statistical error, correction for population structure is critical in a collection of genotypes, especially in a breeding program where relationships are highly variable. Simulations suggest potential problems associated with unknown marker/QTL relationships and can be used to forecast the response to marker-assisted selection.

The Wheat–CAP Project: Wheat applied genomics.

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The Wheat Coordinated Agricultural Project (WheatCAP) is a consortium funded by USDA–CSREES National Research Initiative that includes public breeders from 25 states and four USDA–ARS genotyping centers, and integrated with GrainGenes. Because public wheat cultivars account for 78% of the wheat production in the United States, this project has a significant economic impact. The competitiveness of US public wheat breeding is being increased by the incorporation of marker-assisted selection (MAS). With input from regional stakeholders, each breeder has determined the most important traits to select through MAS and has access to 5,000 analyses per year. During the first two years of the project, the high-throughput, USDA–ARS genotyping centers have generated more than 190,000 datapoints. The traits selected include disease and pest resistance genes (65%), quality traits (17%), tolerance to abiotic stresses (12%), and agronomic or special purpose traits (9%). Molecular markers for new traits are being identified using QTL analysis in 18 segregating populations created by the breeding programs using parental lines adapted to the different U.S. wheat-growing regions. As part of our outreach efforts, we are informing growers and end-users of the economic advantage of lines developed by MAS through field days and demonstration plots. We are training over 90 students at all levels in agricultural sciences and breeding as part of our educational objectives. Through September 2007, the WheatCAP participants have published 25 papers in peer-reviewed journals, presented 71 lectures and posters, and organized three experiential trips and 51 workshops and field days. For further information see http://maswheat.ucdavis.edu.

Wheat SNP markers: Discovery and utilization.

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For the purposes of marker-assisted selection, association mapping, genetic mapping, and positional cloning, the availability of a large number of molecular markers is critical. In the foreseeable future, single nucleotide polymorphisms (SNPs) will become the marker of choice for all the above-listed applications. Polyploidy, large genome size, and low level of polymorphism make the development of wheat SNP markers very challenging. However, recent advances in high-throughput sequencing and genotyping led to the development of technological platforms that could easily overcome all the limitations of the wheat system. New sequencing platforms could be used to discover the required number of SNPs over larger regions of the wheat genome; new genotyping platforms could overcome the limitations caused by polyploidy and allow genotyping a large number of plants at large number of SNP loci. New technologies, combined with new methods of statistical analysis, are extremely powerful tools for studying wheat at the whole-genome level and dissecting the genetic basis of complex traits. An overview of recently developed wheat SNP resources and their application to the analysis of wheat genome will be presented.