

Poster 2. Association analysis of soft wheat quality traits in eastern U.S. soft winter wheat.

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Soft wheat quality is highly heritable, controlled by multiple loci, and has been mapped in a number of bi-parental crosses. We expanded the mapping information determining soft wheat quality by using association analysis between genetic markers and quality phenotyping in 187 soft winter wheat cultivars from the eastern U.S. Quality samples were obtained from 2007 production environments in Ohio, Indiana, New York, and Virginia. Samples were milled at the USDA-ARS Soft Wheat Quality Laboratory, and flour was evaluated using the solvent retention capacity test (AACC Method 56-11) and the sugar snap cookie method (AACC Method 10-52). Results from the genetic marker analysis identify a region of chromosome 2B associated with a complex set of milling traits, likely controlled at multiple, linked loci. These traits are best marked by the microsatellite primers, BARC98, GWM429, and BARC010. Genetic markers specific to the high-molecular-weight glutenin locus, *Glu1D*, identified the Dx5 allele associated with coarser flour texture. Association analysis for quality traits in this population should prove useful for identifying new markers for agronomically important traits.

Poster 3. Genome-wide identification of the quantitative trait loci associated with end-use quality of bread wheat grown under drought conditions.

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Improving the end-use quality of bread wheat is a major target for many breeding programs. The process can be accelerated by using molecular markers tightly linked to the genes controlling the end-use quality. This study was conducted to identify qualitative trait loci (QTL) related to grain quality (grain hardness, kernel weight, and kernel diameter), flour quality (flour protein content, flour yield, and flour paste viscosity), mixing quality (mixing peak time and height, mixing tolerance, and mixing absorption), and baking quality (SDS-sedimentation (SED)). A population of 180 recombinant inbred lines was generated from a cross between Rio Blanco, a hard white winter cultivar, and IDO444, a hard red winter wheat line. The two parents have same glutenin subunits on chromosomes 1A (2*) and 1D (5+10) but have different subunits on 1B (7+8 and 13+16), and a different GBSS locus on 4A. The end-use quality of each line was evaluated separately from seed samples harvested from two dryland locations, Rockland and Arbon in southern Idaho in 2006–07. A total of 438 marker loci were mapped on the 20 linkage groups, except chromosome 1D, with the total map length spanning 3,051 cM. Overall, 53 QTL (LOD > 2.5) with various significances were detected on 15 chromosomes, and 20 manifested in both locations. The most significant QTL associated with flour viscosity was identified and located on chromosome 4A and explained over 60% of phenotypic variation. Our results confirmed that end-use quality is a complex trait that was affected by various loci on multiple chromosomes. The novel QTL and tightly linked markers identified in this study provided very useful information for improving the end-use quality of bread wheat.