Implementing marker-assisted selection in wheat variety development.

Jamie Sherman and Luther Talbert. Department of Plant Sciences, Montana State University, Leon Johnson Hall, Bozeman, MT 59717, USA.

Marker-assisted selection (MAS) has become a routine part of wheat breeding, enabling efficient backcross breeding, pyramiding of genes, and creation of isolines that allow for the genetic dissection of traits. The wheat genetics group at Montana State University has developed markers and implemented MAS for traits of importance to our state. One successful example of marker development and implementation is with markers for white seed. Resources for breeding programs in much of the Great Plains largely have been directed to hard red wheat development and, as a result, agronomic performance of hard white wheat varieties has tended to be inferior. Based on demands from the Montana wheat industry, we developed markers for white kernel color and used these to convert our best hard red wheat varieties into hard white. Development of markers for white seed required analysis of three mapping populations, each segregating for one of the three controlling loci. Once identified, the markers linked to white seed color pose several challenges in application to variety development. Because white is recessive and controlled by three genes, red-seeded plants have unknown genotypes, so that the breeder does not know how many genes need to be converted. Also, a certain sized band is not diagnostic of all white-seeded lines. Despite these caveats, we were able to use the markers in a backcrossing program to covert the best hard red wheat varieties into hard white isolines. These hard white wheat lines are currently being tested in breeding trials, with the expectation that agronomic performance will equal that of the hard red varieties. In addition, the ability to develop isolines with red versus white kernel color provides the opportunity for experiments that are otherwise difficult to conduct. Our experience with the markers for white kernel color, and with markers for other traits, has provided insights that have helped us refine marker implementation in variety development.

Breeding wheat somewhere between the poverty level and the 99% confidence level.

Brett Carver and Liuling Yan. Department of Plant and Soil Sciences, Oklahoma State University, Stillwater, OK 74078, USA.

The Oklahoma State University (OSU) wheat breeding program has operated continually for the past 60 years but not without significant shifts in financial base support and breeding strategy in only the last decade. The next shift, already in motion, will invoke gene-targeted selection among inbred lines as a means to reduce costs and/or maximize selection gains for adaptation traits relevant to the southern Great Plains. The USDA–CSREES–CAP population, 'Jagger/2174', provided OSU's cornerstone for QTL discovery and mapping of critical traits for reproductive development patterns (stem elongation, heading, and physiological maturity) and disease reaction (leaf rust, stripe rust, and powdery mildew). As a result of their alignment with phenotypic-based selection in our program, most informative among these markers are *VRNA1*, *PPD-D1*, *VRN-D3*, *Lr34*, *Pm3*, and a novel gene on chromosome 2A that confers adult-plant resistance to stripe rust. Little variation was found among elite lines in the OSU wheat breeding program at *VRNA1*, a major locus that regulates the timing of stem elongation, apparently is consequential to intense selection pressure in prior generations against precocious winter dormancy release. All of the gene markers enable selection pressure for traits that may not be consistently measurable from year to year or traits that have very low heritability due to human error. Their high diagnostic capability provides a healthy balance between costs and confidence.