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Summary:

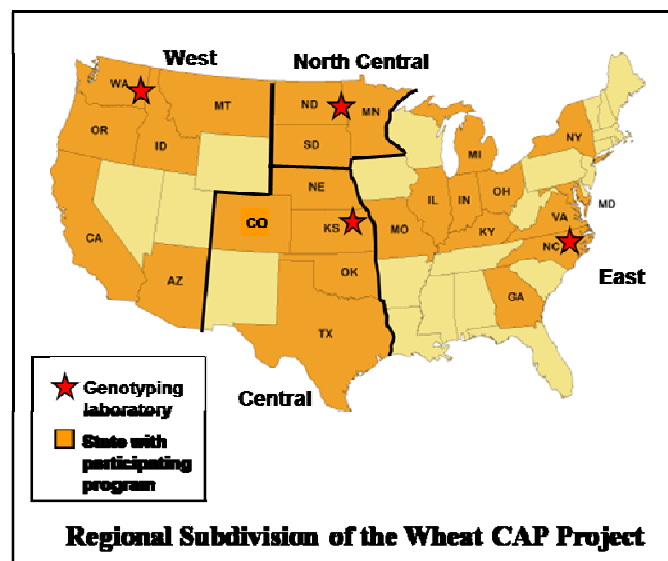
Wheat cultivar development is dependent on a continued supply of genetic variability. Thus, our project is focused on the use of molecular marker-facilitated introduction of factors that control cereal yellow dwarf virus (CYDV) and *Cephalosporium* stripe resistance, grain protein, iron, and zinc content (*Gpc-B1*), and adult plant resistance genes against stripe rust (*Yr18*, *Yr29*, *Yr30*, *Yr36*, and *htap-1*) into wheat adapted to our region. So far, we have produced wheat germplasm based on Stephens, OR943576, Weatherford, and Winsome that now carry the grain protein gene *Gpc-B1* and the stripe rust resistance gene *Yr36*. This finished material is being evaluated and characterized under field conditions. We have also developed molecular markers for the strawbreaker foot rot (eyespot) resistance gene *Pch1*. Marker assays for the *Pch1* marker are now available to wheat breeders through the USDA-ARS regional genotyping center in Pullman, WA. End use quality in wheat is primarily determined by grain hardness or texture. The ‘super-soft’ grain characteristic has been found to positively affect flour yield and end-use quality with the potential to widen export markets. Consequently, there is now an interest in understanding the genetic basis of this trait and to identify markers for its manipulation. To this end, we are using map-based methods to better understand the ‘super-soft’ characteristic and to develop markers. Another component of our research effort addresses celiac disease, an allergic reaction to some seed storage proteins in wheat flour. Seed storage proteins, known as gliadins, have been identified as the principal allergy-eliciting agents and removal of gliadins from flour or dough yield food that are tolerated by celiac disease patients. Thus, we have a project to use transgenic technology to engineer gliadin-free wheat that would be a much needed food alternative to manage this important human ailment.

This Month’s Article: The following article is an update on marker assisted wheat breeding and the Coordinated Agricultural Project (CAP) project for wheat (Wheat CAP, <http://maswheat.ucdavis.edu/>), a multi-institutional project that integrates genomics and wheat improvement activities across the U.S. My research group is part of Wheat CAP and activities in this project are complimentary to our work on the identification and manipulation of genes of agronomic interest using DNA-based marker technologies.

Marker assisted wheat breeding in the U.S.

Most U.S. wheat breeding programs are in the public sector and public wheat varieties account for ~75% of the wheat production in the U.S. This represented 1.5 billion bushels of production valued at ~\$US 7.5 billion in 2007. Funding for public wheat breeding programs is typically provided by the State and wheat grower's associations since very few private enterprises are involved in wheat cultivar development. Thus, limited investment by the private sector and the need for continued wheat production and improvement to sustain rural economies, have provided the impetus to develop and maintain strong public breeding efforts. With the advent of DNA-based and other genomics technologies, opportunities to improve the efficiency of some aspects of wheat breeding now exist. This represents both a challenge because resources for new technology adoption are limited and an opportunity because U.S. wheat breeding programs are poised to employ these new advances. Because most of the new genomic information for wheat is publicly available, competitiveness is determined by the speed of implementation of newer technologies. There is, therefore, a need to quickly integrate the use of new tools in wheat improvement in order to maintain a competitive advantage.

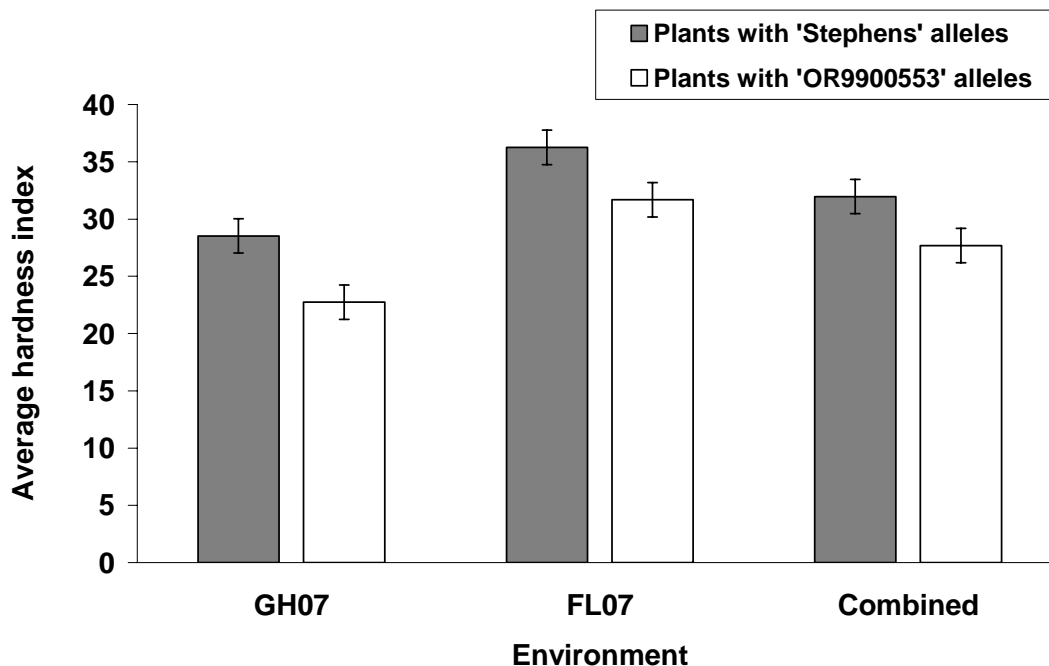
In 2005, the wheat breeding and genetics community [with funding from the U.S. Department of Agriculture (USDA) Cooperative State Research, Education, and Extension Service (CSREES) National Research Initiative Competitive Grants Program (http://www.csrees.usda.gov/funding/nri/nri_about.html)] initiated a coordinated multi-institutional public-sector project with the goal to translate and integrate genome discoveries into new tools for wheat improvement. Thus, a network of public wheat breeding programs in collaboration with four newly established federal regional high-throughput DNA fingerprinting (genotyping) laboratories has been established to accelerate the incorporation of valuable genes into adapted wheat varieties. Our group at Oregon State University is one of 17 groups representing 25 States that are participating in this Coordinated Agricultural Project titled "Applied Wheat Genomics" (<http://maswheat.ucdavis.edu/>) (Figure 1 shows the regional subdivision of Wheat CAP). This multi-state, multi-institutional, and multi-disciplinary network works together to discover new genes of agronomic relevance and to rapidly deploy these into adapted varieties using forward marker-assisted selection (MAS) strategies.



The central technology being utilized by the Wheat CAP project is called marker-assisted selection (MAS). Marker-assisted selection is based on the association of certain DNA variations with genes that underlie or control a trait of agronomic importance. Thus, selection for a specific DNA marker results in the indirect selection of a chromosome segment harboring a factor that regulates the trait of interest. Because a DNA-based marker assay can be performed at any time and with plants at any stage of development, markers add flexibility to the selection process. For example, marker-assisted selection can be used for traits that have low heritability, traits that are difficult or expensive to measure, traits that cannot be measured until the end of a growing cycle or at later generations, and traits that require the combination of various factors of small effects.

The use of MAS, in general, can increase the speed, efficiency, and precision of selection for certain trait combinations. Thus, wheat researchers have invested time and effort in the development of protocols for more than fifty molecular markers for disease resistance genes, quality, and abiotic stress tolerance traits (Table 1). In collaboration with the USDA-ARS regional genotyping laboratories in Washington, North Dakota, Kansas, and North Carolina, assays for these markers are now available to breeding programs across the country. Although the use of DNA marker technology for forward breeding is relatively new in wheat, markers have been used to incorporate valuable genes in a wide array of breeding lines and cultivars from various programs (Table 2). Nevertheless, there are a number of traits of interest that have not been studied and for which no molecular marker has been identified. Thus, the research component of the Wheat CAP project is focused on mapping, validating, and implementing new markers for traits that have been prioritized by the wheat industry, for each of the different wheat market classes grown in the U.S. (Table 3). Our contribution to the CAP project involves a study of the ‘super-soft’ grain characteristic that positively affects flour yield and end-use quality. In order to understand the genetic basis of this trait, we have constructed a genetic map (*I*) using a population derived from a cross between ‘Stephens’ (hardness index ~37) and ‘OR9900553’ (hardness index ~20), a breeding line with the ‘super-soft’ grain characteristic. In a preliminary analysis, we have determined that this trait is controlled by various factors but a factor on chromosome 4D is the most important. We have also identified a DNA-based marker that is significantly associated with this characteristic. Figure 2 shows the average grain hardness index of lines that carry ‘Stephens’ or ‘OR9900553’ alleles of this marker. An individual and combined analysis of seeds from plants grown in the greenhouse (GH07) and the field (FL07) showed that plants with the molecular marker type from ‘OR9900553’ have significantly softer seeds than plants that carry the marker donated by ‘Stephens’. This association suggests that we have identified one useful marker for the ‘super-soft’ trait. Nonetheless, we know other factors are involved. Thus, a more thorough assessment is ongoing to identify additional players.

Association between a molecular marker and grain softness



As new markers become available, assays for these markers will be provided to breeders by the USDA-ARS genotyping laboratories. These laboratories already provide DNA fingerprinting services to wheat breeding programs, of their region, in a way that is similar to the wheat quality and disease testing services that are now provided by the pertinent federal laboratory. As an example, my research group has recently identified three molecular markers (*Xorw1*, *Xorw5*, and *Xorw6*) that are linked to the strawbreaker footrot (eyespot) resistance gene, *Pch1* (2). We have transferred this information to the USDA-ARS regional genotyping center in Pullman, WA and breeding programs, of our region, can now obtain assays to test for the presence of *Pch1* in breeding materials using these markers.

The concept of a network of public wheat breeding programs in collaboration with four federal regional high-throughput DNA fingerprinting laboratories used by the Wheat CAP project (<http://maswheat.ucdavis.edu/>) seems to be working. New marker-trait associations are being discovered and U.S. wheat breeders are using genotyping laboratories for marker assisted selection (MAS) to improve quality and disease resistance. An important highlight, this year, is the molecular marker screening of U.S. germplasm for a resistance gene (*Sr36*) that is effective against the new virulent race of stem rust UG99 from Africa (3) and the release of breeding lines with resistance (Table 2). It is hoped that this synergism will continue to yield more success stories in the future.

References

1. G. Wang, J. M. Leonard, A. S. Ross, J. Peterson, O. Riera-Lizarazu, in *Plant & Animal Genome XVI*. (San Diego, CA., 2008) pp. P280.

2. J. M. Leonard *et al.*, *Theor Appl Genet* **116**, 261 (Jan, 2008).
3. T. J. Tsilo, Y. Jin, J. A. Anderson, *Crop Sci* **48**, 253 (January 16, 2008, 2008).

Table 1. An example of traits with marker assays that are available for marker-assisted selection (MAS) in wheat^a.

Trait	Gene	Trait	Gene	Trait	Gene
Rusts	<i>Lr19, Sr25</i>	<i>Septoria tritici</i> blotch	<i>Stb2</i>	High grain protein content	<i>Gpc-B1</i>
Rusts	<i>Lr21</i>	<i>Septoria tritici</i> blotch	<i>Stb3</i>	Pre-harvest sprouting	<i>QTL</i>
Rusts	<i>Lr29, Lr25</i>	<i>Septoria tritici</i> blotch	<i>Stb5</i>	Waxy	<i>Wx- A1</i>
Rusts	<i>Lr34, Yr18</i>	<i>Septoria tritici</i> blotch	<i>Stb7</i>	Waxy	<i>Wx- B1</i>
Rusts	<i>Lr35, Sr39</i>	<i>Septoria tritici</i> blotch	<i>Stb8</i>	Waxy	<i>Wx-D1</i>
Rusts	<i>Lr37, Yr17, Sr38</i>	Tan spot	<i>Tsn1</i>	Grain texture	<i>Pina</i>
Rusts	<i>Lr39</i>	Wheat streak mosaic virus	<i>Wsm1</i>	Grain texture	<i>Pinb</i>
Rusts	<i>Lr46, Yr29</i>	Barley yellow dwarf virus	<i>Bdv2</i>	Gluten strength	<i>Glu-A1</i>
Rusts	<i>Lr47</i>	Barley yellow dwarf virus	<i>Bdv3</i>	Gluten strength	<i>Glu-B1</i>
Rusts	<i>Lr50</i>	Wheat spindle streak mosaic bymovirus	<i>QTL</i>	Gluten strength	<i>Glu-D1</i>
Rusts	<i>Lr51</i>	Hessian fly	<i>H9</i>	Gluten strength	<i>GluA3</i>
Rusts	<i>Yr5</i>	Hessian fly	<i>H13</i>	Semolina color	<i>QTL</i>
Rusts	<i>Yr15</i>	Hessian fly	<i>H25</i>	Semolina color	<i>Y</i>
Rusts	<i>Yr36</i>	Hessian fly	<i>H31</i>	Aluminum tolerance	<i>AltBH</i>
Rusts	<i>Pm34</i>	Hessian fly	<i>Hdicocum</i>	Drought and root biomass	<i>IBL.IRS</i>
Rusts	<i>Sr36</i>	Russian wheat aphid	<i>Dn2</i>	Drought and root biomass	<i>IAL.IRS</i>
Rusts	<i>Pm35</i>	Russian wheat aphid	<i>Dn4</i>	Dwarfing	<i>Rht-B1</i>
Eyespot	<i>Pch1</i>	Wheat stem sawfly	<i>Qss.msab-3BL</i>	Dwarfing	<i>Rht-D1</i>
Eyespot	<i>Pch2</i>	Greenbug	<i>Gb3</i>	Dwarfing	<i>Rht8</i>

^a Source of data: Wheat CAP (<http://maswheat.ucdavis.edu/>)

Table 2. Released germplasm^a developed through marker-assisted selection (MAS) with improved quality, disease, and stress resistance.

Germplasm name or ID	Incorporated genes	Traits
'Lassik' (CA-HRS)	<i>Lr37/Yr17, Yr36/Gpc-B1, Glu-D1/A1</i>	Gluten strength, protein, & rust resistance
'Patwin' (CA-HWS)	<i>Lr37/Yr17/Sr38</i>	Rust resistance
UC1113-Lr19-Sr25 (CA durum)	<i>Lr19, Sr25</i>	Leaf rust and stem rust resistance (UG99)
'Expresso' (CA and Westbred)	<i>Yr15, Lr37/Yr17/Sr38</i>	Rust resistance
Recombinant 45 (CA and Argentina)	Short segment of <i>T. monococcum</i> chromosome	Extra softness
PI 632710 (ID)	<i>Glu-D1a</i>	Gluten strength
PI 642363 'UI Pettit'	<i>Glu-D1a</i>	Gluten strength
PI 642364 (ID)	<i>Wx-A1, wx-D1, wx-B1</i>	Waxy wheat (starch)
PI 642365 (ID)	<i>Wx-A1, wx-D1, wx-B1</i>	Waxy wheat (starch)
PI 632713 (ID)	<i>H25</i>	Hessian Fly resistance
PI 634567 (ID)	<i>Als1</i>	Herbicide resistance
PI 642361 'UI Cataldo'	Alturas SWS NIL with <i>H25</i>	Hessian Fly resistance
PI 642378 'UI Alta Blanca'	<i>Glu-D1d</i>	Gluten strength
PI 642379 (ID)	Lolo HWS NIL with <i>Lr47</i>	Leaf rust resistance
PI 642380 (ID)	Lolo HWS NIL with <i>Lr47</i>	Leaf rust resistance
PI 642381 (ID)	IDO673 sister with <i>Lr47</i>	Leaf rust resistance
PI 642382 (ID)	IDO673 sister with <i>Lr47</i>	Leaf rust resistance
PI 642383 (ID)	Jubilee SWS NIL with <i>Lr47</i>	Leaf rust resistance
PI 642384 (ID)	IDO676 sib with <i>Lr47</i>	Leaf rust resistance
PI 642385 (ID)	Jubilee SWS NIL with <i>Lr47</i>	Leaf rust resistance
VA02W-713 (VA)	FHB QTL	Fusarium head blight resistance
USG 3555 (VA)	<i>Sr36</i> , 2 powdery mildew res. QTL	Stem and powdery mildew resistance
WA7975 (WA-HRW)	<i>Yr36/Gpc-B1</i>	Protein content and stripe rust resistance
'Hallam' (NE)	<i>Rht1</i>	Plant height
'Infinity' (NE)	<i>Rht1</i>	Plant height
NE01643 (NE)	<i>Rht1</i>	Plant height
'Vida' Wheat (MT)	<i>Xgwm340</i>	Solid steam and stem sawfly resistance
PI 63400-PI 643419 (MT 20 lines)	<i>Pina / Pinb</i>	Grain hardness
PI 651502-PI 651517 (MT 16 lines)	<i>Yr36/Gpc-B1</i>	Protein content and stripe rust resistance
PI 642415 'OK Bullet'	<i>ALMT1</i> , 2 QTL	Aluminum tolerance
AGS2026 (GA)	<i>Lr37/Yr17/Sr38, H13</i>	Rust and Hessian fly resistance
USG3295 (GA)	<i>Sr36, 1BS.1RL</i>	Stem rust resistance (UG99)
AGS2031 (GA)	<i>Sr36, 1BS.1RL</i>	Stem rust resistance (UG99)
SS8641 (GA)	<i>Lr37/Yr17/Sr38, Pm1</i>	Rust and powdery mildew resistance

^a Source of data: Wheat CAP (<http://maswheat.ucdavis.edu/>)

Table 3. Targeted traits by the Wheat CAP participants (State)^a.

State	Targeted traits
CA	Gluten strength, pasta color, lipoxygenase activity, stripe rust resistance
CO	Milling, baking, Asian noodle quality
GA	Stripe rust resistance, WSSMV resistance, milling and baking traits
ID	Stripe rust resistance, Hessian fly, baking and milling quality, starch, and yield
IN	Septoria resistance, rust resistance, powdery mildew resistance.
KS	Minor AP resistance genes to leaf and stripe rusts
MN	Preharvest sprouting
MT	Stripe rust, milling and backing quality, yield.
MT	Stem sawfly attraction and quality
ND	Gluten strength and pasta quality
ND/SD	Tan spot resistance, FHB resistance, shattering, and lodging.
NE	Stripe rust, WSMV, WSSMV, Septoria tritici, and tan spot resistance. Drought tolerance, vernalization, hardiness, shattering, quality, and acid soil tolerance
NY	Milling and baking, Pre-harvest sprouting, yield, height
OK	Resistance to FHB, rust, Pm, BYDV, WSMV. Tolerance to aluminum, lodging, and shattering. Germination, dough strength, absorption, milling, test weight.
OR	Extra-soft grain texture.
TX	Leaf rust resistance
VA	Powdery mildew adult plant resistance.
WA	Stripe rust, quality and yield

^a Source of data: Wheat CAP (<http://maswheat.ucdavis.edu/>)