

Report of the Stakeholders' Workshop

'Bringing genomics to the wheat fields: Implementation of molecular marker technologies in public wheat breeding programs'

February 22, 2004, at Kansas City MO

Supported by USDA-CSREES Competitive Program Unit.

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Background

In response to a request from the National Wheat Improvement Committee (NWIC) to include wheat in the 2005 RFP for the USDA-NRI CAP projects on translational genomics, USDA Under-Secretary Joseph Jen suggested that the wheat research community should first organize a national planning effort focused on bringing together a community of plant breeders, genome scientists, end-users, growers, and other experts to identify research needs and discuss the priorities in wheat translational genomics.

Objectives

The overall objective of this national meeting was to generate a document describing the research needs and priorities of the wheat research community in the area of translational genomics.

The first specific objective of this meeting was to prioritize the wheat traits amenable to improvement by genomics approaches based on input from the wheat industry (growers, millers, and bakers), wheat researchers, and wheat breeders representing all wheat market classes.

The second specific objective was to determine the best structure for a national program for marker assisted selection in wheat integrating public breeding programs, University research laboratories, and the four new USDA-ARS regional molecular genotyping centers.

Participants

The complete list of the 63 workshop participants (including four that sent their input by E-mail) can be found at the end of this document. The participants included 26 public wheat breeders (2 sent input by Email) from 25 different states, six representatives for the regional genotyping laboratories, nine representatives from the milling and baking industry, and 19 wheat researchers and private wheat breeders.

The public breeders represented states growing 93% of the total US wheat production (based on production averages 2000-2002), indicating an outstanding representation of the public wheat breeding programs. The four regional USDA-ARS high-throughput genotyping centers were also represented. The National Association of Wheat Growers (NAWG) and the National Wheat Improvement Committee (NWIC) representatives provided input on the growers' perspective. Finally, the president of the American Institute of Baking, the vice president for the North American Milling Association, and

representatives of large milling and baking companies provided excellent input from the industry.

Presentations

The meeting started with three short presentations by Jorge Dubcovsky for the *MAS*wheat consortium, Guihai Bai for the USDA genotyping laboratories, and Dave Van Sanford for the NWIC, to provide the background information.

The main points of the presentations were:

1. The Wheat National Marker Assisted Selection Program (*MAS*wheat).
 - Wheat is one of the major crops in the US (≈ 2 billion bushels/year).
 - The public sector plays a critical role in wheat breeding in the US. More than 60% of the current US wheat varieties were developed by the public sector.
 - Molecular markers are available for more than 50 favorable alleles including genes for resistance to fungal pathogens, insects and viruses. In addition, numerous genes and markers are available to manipulate quality parameters. Most of these markers have been developed by US scientists participating in the *MAS*wheat project.
 - Additional markers are still required for complex traits and for durable resistance to pathogens.
 - During the last two years the *MAS*wheat consortium (12 laboratories, 11 states) has introduced valuable alleles using MAS into the best 100 lines from the different growing regions and all market classes (**Phase I**). These parental lines can now be used to deploy these valuable alleles into a wider section of the germplasm using a high-throughput *MAS* approach (**Phase II**).
 - The *MAS*wheat consortium demonstrated that the public wheat researchers can work together effectively.
 - The marker information is mainly public and therefore, competitiveness is not determined by access to the information but by the speed and efficiency of the implementation of the technology in the breeding programs.

2. Overview of the USDA-ARS high-throughput Genotyping laboratories.
 - The goals of the Genotyping laboratories in basic and applied research largely complement those of the *MAS*wheat program. A synergistic relationship currently exists between the *MAS*wheat program and the first funded genotyping laboratory at Manhattan KS. This productive interaction provides a model of collaboration that can be extended to the three other genotyping laboratories, once they complete their hiring phase.
 - The Kansas Genotyping laboratory is starting to ramp up its operations to reach the objective of 50,000 data points per year. The laboratory has modern high-throughput equipment.

- The Genotyping laboratories are looking forward to integrated projects with the wheat breeding programs.
3. The growers' perspective on breeding priorities (Dave Van Sanford, Chair NWIC and Patricia Buschette NAWG).
- NWIC has gone through a formal process to collect input on research priorities from the different wheat growing regions and discussed these priorities with NAWG to have appropriate growers' input in the process. Therefore, NWIC research priorities are the result of an organized discussion among the wheat research community.
 - The largest requests in the FY05 legislative agenda from NWIC/NAWG include support for the ARS Wheat Quality Laboratories, the ARS Genotyping laboratories, the National Stripe Rust initiative, and the *MAS*wheat consortium.
 - Most of the NWIC/NAWG supported projects included the use of molecular markers. Growers and millers support the development and deployment of this technology.
 - Competitive *MAS* programs are being implemented in Canada and Australia.

DISCUSSION GROUPS

GROUP 1. PRIORITIES IN TRAIT SELECTION FOR RESEARCH.

Millers and bakers indicated repeatedly that their main priority is to maintain a stable supply of sound wheat, and that breeders should continue their work on **yield and disease resistance**. They recognized that farmers must have grain yield potential in a wheat variety or they will not grow it. There was a unanimous consensus that improvements in quality should not be at the expense of the main agronomic characteristics. Virgil Smail (American Institute of Baking (AIB)) pointed out that if we do not focus on production efficiency, it won't be long before our domestic buyers start sourcing their milling wheat from outside the US. Mark Stearns (baker, Interstate Brands) indicated that high grain yields, good test weight and disease resistance are our best hedge against poor quality. Stephen Baenziger (NE breeder) emphasized that we need to maintain our focus in the big agronomic and disease resistance issues.

The most frequently used word during this discussion was “**consistency**”. Stephen Baenziger (NE breeder) pointed out that inconsistency is generally due to genotype by environment interactions, and that efforts to lessen environmental impacts by superior genetics are needed. He indicated that we need to be careful when we fix chromosome regions to be sure that we do not end up with wheat varieties that are more environmentally sensitive. Millers and bakers promoted the idea that we could best ensure consistency by focusing on disease resistance, and suggested that disease resistant wheat will be better buffered against seasonal variation and epidemics. The two main concerns in the area of disease resistance were Fusarium Head Blight and Stripe Rust. Millers Dave Green (miller, ADM) and Brian Walker (miller, Cargill) also emphasized

the importance of concentrating breeding efforts on disease resistance. There was no consensus among the participants from different growing regions on the use of Identity Preservation programs to improve consistency.

An additional trait that was of interest to most millers was **milling yield**. Jorge Dubcovsky (CA breeder) mentioned the existence of numerous studies in mapping populations from Australia but more limited research in the US wheats for this trait. Jay Romsa (miller, General Mills) indicated the need to study milling yield with more detail. He pointed out that an important component of high extraction rates is the level of first break flour. He indicated that some varieties like Klasic have unusually high levels of first break flour suggesting that there is a significant genetic component for this trait. Mark Sorrells (NY breeder) indicated that he has done some research in this area showing that total milling yield was moderately heritable, and that in the eastern soft wheats there was a moderate negative correlation between total flour yield and first break flour yield. Dave Green (miller, ADM) indicated that this correlation was not observed in the hard wheats. Two out of the three millers that sent their input by mail also listed milling yield as one of their research priorities.

Seed uniformity and appropriate **test weights** were also important traits in the eyes of the end users. The importance of these traits was emphasized by Jay Romsa (miller, General Mills) and in the Email from Jim Bair (North American Millers' Association). Millers Dave Green (ADM) and Brian Walker (Cargill) pointed out that kernel size is more uniform and consistent in the hard spring wheats from Canada relative to the US. Mark Stearns (baker, Interstate Brands) indicated that when test weight is down, millers and bakers both have problems. Rick Siemer (miller, Siemer Milling) commented that usually the cause of low test weights are diseases, rain during dry down, or stress (e.g. heat) during grain fill. Dave Green (miller, ADM) indicated that test weight is still a good overall predictor of grain quality.

Hardness and **particle size** were also listed as important traits for the bakers. Puroindoline A and B have been identified as the main genes determining hardness, and allelic variants at these genes are available to increase or decrease hardness. Herb Ohm (IN breeder) and Mark Sorrells (NY breeder) commented that they are investigating the possibility of making soft wheats even softer by including additional active puroindoline genes from *Triticum monococcum*. Opposite hardness characteristics are required for soft and hard wheats. Virgil Smail (AIB) pointed out that the bakers need more information on the effect of hardness and particle size variation on **water absorption**. He indicated that we need to understand better the overall effect of the different hardness genes on flour yield and water absorption, their relationship with particle size, and their overall effect on quality. Mark Stearns (baker, Interstate Brands) indicated that the current measure of total water absorption is not sufficient. This measure does not consider the need of fast hydration, adapted to the new faster processing processes. Brian Walker (miller, Cargill) commented that water absorption in many of the current varieties is not quick enough for the hydration schedules that are used in modern bakeries. The new bakeries have extrusion technologies that are very fast. He pointed out the need for more research to understand the interaction between gluten strength and the speed of water

absorption, and how that interaction affects specific end products. High water absorption is important because it is usually associated with increased shelf life. The genetic control of fast hydration was suggested as a new interesting area of research.

Gluten strength was also included by the bakers as a desirable trait for breadmaking hard wheat varieties. Virgil Smail (AIB) indicated that the bakers need information on the high-molecular weight glutenins (HMW), low molecular weight glutenins (LMW), and their impact on water absorption. Jorge Dubcovsky (CA breeder) pointed out that although we have good information on the effect of the HMW glutenins on breadmaking parameters, there is limited information on the specific effects of the different LMW glutenin alleles on gluten strength, or their interactions with the HMW glutenins. Mark Stearns (Interstate Brands, baker) mentioned that particular gluten characteristics are now required for faster processing with shorter hydration schedules. Gluten combinations that result in shorter mixing times but good stability might be useful for this purpose. It is still important to allow enough time for gluten to develop properly. For the soft wheats, Carl Griffey (VA breeder) pointed out the need to identify weak gluten and strong gluten types within the adapted germplasm. Rick Siemer (miller, Siemer Milling) confirmed that they are interested in SRW wheat varieties with strong gluten. He indicated that if he had to choose between SRW with weak or strong gluten, he would choose strong gluten because they can be used for a more diverse set of products.

Dave Green (miller, ADM) brought to the discussion the importance of **preharvest sprouting** in many of the wheat growing regions. Different public breeders commented that this problem is usually more severe in the white varieties. Since USDA is promoting the increase of the cultivated area with white wheat varieties through an incentive program, increased attention should be placed on this problem. Mark Sorrells (NY, breeder) pointed out that there are markers from one QTL for preharvest sprouting but there was agreement that additional sources of preharvest sprouting resistance were necessary and that molecular markers for the genes present in those sources would be useful tools to control this problem. Additional sources of resistance to preharvest sprouting have been identified in the Australian and Canadian varieties and in synthetic wheats. Rick Siemer (Siemer Milling) ranked preharvest sprouting as his second priority after Fusarium resistance.

Mark Stearns (baker, Interstate Brands) pointed out that white bread is still the most important product of the bakery and that we need to look at ways to **increase dietary fiber** in this product. The introduction of white wheat varieties can be a step in that direction. Another characteristic needed in the hard white class for the noodle market is the reduction of the **Polyphenol Oxidase (PPO)** levels that result in noodle discoloration. Jay Romsa (General Mills) indicated that this was an important trait in the western growing region for the Asian export market. Bill Berzonsky (ND breeder) suggested that **partial waxy** genotypes were also important for the noodle export market.

Mark Stearns said that the bakers still value high **protein content** in the hard wheats because it helps water absorption and is positively correlated with loaf volume. He indicated that for the bakers, protein content is more important than protein quality,

because if the flour has enough protein the baker can complement the dough with gluten and other additives to obtain the desired product. Protein quantity in the hard wheat regions is important also for the growers who are frequently paid a premium for high protein content. The importance of this trait in ND was emphasized by Bill Berzonsky (ND breeder).

Brian Walker (miller, Cargill) indicated that for durum quality **semolina color**, protein quality and extensibility were important traits. In an Email sent by Jim Bair (Vice President North American Millers' Association) compiling answers from several millers, the priorities listed for the durum wheats included semolina yield, color, and gluten strength. In his Email input to the meeting, Frank Manthey (ND, quality lab) listed gluten strength, large and uniform kernel size, color and sprout tolerance as the most important traits for the durum wheat in North Dakota. Jorge Dubcovsky (CA breeder) indicated that semolina yield, pasta color, and protein content were his priorities in the Desert Durum growing area (CA and AZ).

In the area of Fusarium Head Blight resistance, it was suggested that we need to pyramid additional resistance sources in addition to the chromosome 3BS QTL from Sumai 3 (e.g. the chromosome 5A QTL). Carl Griffey (VA breeder) voiced his concern with the current stripe rust situation and with the adequacy of our current sources of resistance. Gina Brown-Guedira (USDA, Manhattan, KS) favored the development of better markers for the slow rusting complexes *Lr34/Yr18* and *Lr46/Yr29* and the pyramiding of these markers with some of the race specific genes. Jorge Dubcovsky (CA public breeder) indicated that it is a priority for his program to pyramid these two slow rusting complexes with the race specific resistance genes *Yr15* and *Yr5* that are still effective against the current races of stripe rust. There was agreement that additional sources of resistance were urgently needed. Bill Berzonsky (ND breeder) mentioned that Orange Blossom Wheat Midge and Wheat Stem Sawfly are additional insect problems in his region. Brett Carver (OK breeder) indicated that a better molecular understanding of acid-soil tolerance of winter wheat would greatly contribute to improve consistency in his region (E-mail input).

Mark Sorrells (NY breeder) suggested including funding in new grants to perform QTL studies in different wheat growing regions and using mapping populations from different market classes. These mapping populations will be useful to find new markers for the genes controlling the traits identified by the wheat industry in this discussion. It was suggested that mapping could be accelerated by the development of a centralized facility to produce double haploid populations. This idea was supported by other breeders.

In summary:

1. Focus on the big ticket items: yield, production consistency, disease resistance.
2. Important quality traits were milling yield, preharvest sprouting, hardness and particle size, water absorption, gluten strength and protein content. Traits of secondary importance were PPO and dietary fiber levels.
3. More research is necessary to adjust water absorption to rapid hydration schedules, to identify genes affecting the different components of milling yield, to

- identify gluten combinations adequate for the modern processing technologies, to understand the interactions of the different hardness genes with particle size and overall quality, and to identify markers for new sources of preharvest sprouting and reduced PPO activity.
4. In the soft wheats there is a need for two classes –weak and strong gluten. This may be formalized in the future.
 5. In the durum wheats the main traits were semolina yield, pasta color, gluten strength and protein content.

GROUP 2. STRATEGIES TO INTEGRATE PUBLIC BREEDING PROGRAMS AND GENOTYPING LABORATORIES

The group focused on four questions:

1. How can genotyping be used to advance U.S. wheat breeding?

There was a general consensus that implementing marker-assisted selection in the public wheat breeding programs will have a positive impact on wheat improvement in the US.

It was pointed out that one of the benefits of MAS for wheat breeding is that a single technique can be used to select for multiple traits, particularly for those traits that are expensive to select for in the field, or difficult to select for in early stages of the breeding program. There is also a benefit for traits determined by several genes and for which combinations of those genes are beneficial (e.g. pyramiding of resistance genes). The need for building pyramids of effective major and minor genes for resistance to leaf and stripe rust as well as powdery mildew was mentioned by several breeders. Increasing the durability of resistance through deployment of resistance gene combinations has been an elusive goal for most U.S. breeding programs.

Quality traits were also mentioned as a category for which MAS can have a significant impact, by facilitating early selection.

In summary, MAS was viewed as a powerful means of addressing some of the most difficult problems facing wheat breeders.

2. What are the needs of the breeding community for a genotyping database, software, and marker profiles of U.S. varieties?

There was interest in expanding the genotyping database to include information about the molecular markers currently used in the different breeding programs. This information can help breeders to improve the selection of parental lines for their crossing blocks. The participants suggested that the genotyping database should also include pedigree information, polymorphism information content (PIC), map positions, common alleles, and a picture of a representative gel for the commonly used markers. It was suggested that these data can be compiled from different laboratories, as long as a common check such as Chinese Spring is included.

Having marker profiles for key breeding lines and/or new releases was viewed as a useful tool. One suggestion was that breeders within each region could nominate commonly used parents and other key germplasm for evaluation with a set of markers. There was interest in developing a cultivar database for known molecular marker alleles (e.g. *Rht1*, *Rht2*, *Rht8*, *Hardness*, *Vrn-1*, *Waxy*, HMW glutenins) as well as alleles for markers linked to important traits.

Gina Brown-Guedira pointed out that having alleles that are identical in state does not always mean that they are identical by descent. Therefore, a database of allele sizes for linked markers (haplotypes) would be most useful for determining whether there are polymorphic chromosome segments between parents of a cross. She pointed out that haplotyping with several closely linked markers will be needed to infer the presence of the target gene in unrelated germplasm.

Marker profiles could be determined for key breeding lines, new releases, or a representative set of genotypes, such as the regional nurseries, so that the frequency of marker alleles can be determined. There was not much enthusiasm for the idea of fingerprinting ancestral lines. The group noted that marker density would probably have to be large in order to trace chromosome segments through the complicated pedigrees typical of small grain breeding programs. Heterogeneity, within certain regions in some cultivars could further complicate the development of marker profiles.

In spite of the interest on the genotyping database, the group recommended that the regional genotyping laboratories concentrate first on the implementation of MAS in the public breeding programs. The development of marker profiles of the US varieties was considered useful, but a secondary priority.

3. What are the priority areas for collaborative research programs between the wheat breeders and the genotyping laboratories?

Some practical difficulties experienced by the Kansas genotyping laboratory were discussed. For example, populations have been sent in without their parents or new, untried markers have been requested. A suggestion was made to define better the service mission of the genotyping laboratories: offer services only for markers that have been validated, request detailed information for mapping populations, and include the original parents with each submitted population. The methods for allocation of resources to the different programs, sample submission, and data reporting need to be clear and transparent.

It was decided that the regional genotyping laboratories should work with their stakeholder working groups to establish priorities within each region. The breeders participating in the discussion indicated that an important role of the genotyping laboratories is to maximize the utilization of currently available markers. The refinement of high throughput genotyping methods was a recommended area of collaborative research.

The consensus was that implementing MAS in the public breeding programs and improving the throughput capacity of genotyping laboratories were the highest priorities.

Some discussion was devoted to the idea of choosing crosses within regions, developing recombinant inbred populations, and genotyping them. Breeders in the region could phenotype the population for several traits of interest while the genotyping laboratories develop the molecular maps for those crosses. A similar idea was proposed by Mark Sorrells (NY, breeder) at the end of the discussion for Group 1, reflecting a common interest of the participants of the workshop in the development of new mapping populations. The use of double haploids was proposed as an alternative to recombinant inbred populations to accelerate the development of mapping populations.

It was recommended that breeders and genotyping laboratories work together to develop collaborative proposals to secure additional funding for specific mapping projects or marker development (e.g. NRI competitive grants or CAP grants). Alternative sources of funding were also recommended for projects aimed to accelerate the incorporation of genes by whole genome selection. This type of activity requires a relatively large investment, which needs to be funded by collaborative grant proposals rather than by the operational funding of the genotyping laboratories.

4. What should be the role of the genotyping laboratories in the training of the breeding programs in MAS?

The training component is important in order to bring marker assisted selection tools into more breeding programs. With some training, part of the marker assisted selection work could be performed in the breeder laboratory, which would free resources from the genotyping laboratories for new research projects. As an example, personnel in the breeding programs could be trained to perform high-throughput DNA extractions to improve the throughput of the genotyping laboratory.

Jorge Dubcovsky (CA, breeder) indicated that the members of the *MAS*wheat consortium have accumulated valuable experience during the last three years, and that this experience could benefit additional breeding programs. The implementation of a system of internships in the *MAS*wheat laboratories and the genotyping centers was proposed for future grant proposals.

GENERAL DISCUSSION

Breeders, growers, and end users were well educated about the potential benefits of current marker technologies and were very supportive of this initiative. Rapid implementation of marker technologies into the public breeding programs was a priority for the wheat research community. Many participants indicated that there is a strong need to generate new cultivars and improved parental lines using marker assisted selection. The *MAS*wheat consortium has provided proof of concept of the immediate benefits obtained by dedicating a significant proportion of resources to the implementation of available markers.

The *MAS*wheat project has completed the incorporation of valuable alleles in 53 lines that are currently under field testing for potential variety releases (Phase I). Participants of the *MAS*wheat consortium indicated that this project needs to be continued and expanded for maximum impact. They suggested that the current *MAS* backcrossing strategies should be

complemented with forward breeding strategies to deploy the selected genes across a larger segment of the breeding programs. It was suggested that the adapted parental lines developed in Phase I can be used to deliver the selected genes to a large number of lines using high-throughput technologies (Phase II). The new USDA-ARS genotyping centers have the potential and the interest to make this objective possible. A synergistic collaboration between the genotyping laboratories, the *MAS*wheat consortium, and additional public wheat breeders was considered essential to develop a successful innovation system for the use of genomic tools in wheat breeding.

There was general consensus on the benefits of expanding the current *MAS*wheat consortium to additional public breeding programs. Rick Ward (MI breeder) asked for transparent rules to define the participants on any new national MAS initiative and for clear criteria to define progress. He also pointed out the need for permanent input from an advisory committee. Bill Berzonsky (ND breeder) suggested including export representatives in the advisory board for a future MAS initiative. Ed Souza (ID breeder) suggested the idea of implementing a consulting mechanism through the WEB sites of the state wheat commissions or NAWG.

The broad participation in this workshop demonstrated the interest of the wheat research community in a rapid implementation of translational genomics projects. It also showed that the basic organizations (e.g. the *MAS*wheat consortium and the USDA-ARS genotyping laboratories), the required materials (markers and adapted lines), and sound strategies, are in place to develop a successful program. A national MAS wheat program will be an efficient way to showcase the potential benefits of biotechnology to the general public. The US wheat researchers have developed a large proportion of the available molecular markers and have worked with the public breeders to implement a coordinated national effort to use these tools. The wheat research community is now ready to expand this effort to all the US wheat producing regions and to implement a new high-throughput translational genomic project.

Document prepared by J. Dubcovsky (CA), D. Van Sanford (KY), G. Brown-Guedira (KS), & K. Campbell (WA), with feedback from J. Anderson (MN), S. Baenziger (NE), B. Bowden (KS), B. Carver (OK), C. Griffey (VA), S. Haley (CO), Mohamed Mergoum (ND), H. Ohm (IN), D. Skinner (WA), M. Sorrells (NY), and E. Souza (ID). The final document was circulated among all the participants in the meeting.

ACKNOWLEDGEMENT

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List of participants on the workshop ‘Bringing genomics to the wheat fields:
Implementation of molecular marker technologies in public wheat breeding programs’

Name	State	Affiliation	Comment
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Bacon, Robert	AR	Univ. of Arkansas	Breeder
Berzonsky, Bill	ND	North Dakota State Univ.	Breeder
Baenziger, Stephen	NE	University of Nebraska	Breeder
Bai, Guihua	KS	USDA-ARS, Manhattan	Genotyping Center
Bair, Jim	DC	North Am. Millers’ Assoc.	Miller (Email input)
Barnett, Ron	FL	Univ. of Florida	Breeder
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Brown-Guedira, Gina	KS	USDA-ARS, Manhattan	Genotyping Center
Buschette, Pat	DC	NAWG	Growers representative
Byrne, Pat	CO	Colorado State University	Marker support
Campbell, Kim	WA	Washington State Univ.	Breeder
Carver, Brett	OK	Oklahoma State Univ.	Breeder, (Email input)
Chao, Shiaoman	ND	USDA-ARS, Fargo	Genotyping Center
Chung, Okky	KS	USDA-ARS	Quality Lab
Clark, Dale	MT	WestBred	Private Breeder
Clayton, Seaman	KS	Kansas State University-ARCH	Breeding support
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Costa, Jose	MD	Univ. of Maryland	Breeder
Dubcovsky, Jorge	CA	University of California	Breeder
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Gill, Kulvinder	WA	Washington State Univ.	Marker support
Glover, Karl D.	SD	South Dakota State University	Breeder
Green, Dave	MN	ADM	Miller
Griffey, Carl	VA	Virginia Tech	Breeder
Haley, Scott	CO	Colorado State University	Breeder
Kaleikau, Ed	DC	USDA-CSREES	National Program Leader CSREES
Kolb, Frederic	IL	University of Illinois	Breeder

List of participants. Continued.

Name	State	Affiliation	Comment
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Mergun, Mahomed	ND	North Dakota State University	Breeder (Email input)
Manthey, Frank	ND	North Dakota State University	Durum quality (Email input)
Marshall, David	NC	USDA-ARS	Genotyping Centers
Matthews, Dave	NY	USDA-ARS	GrainGenes
Menz, Monica	TX	TAMU	Marker support
Milus, Gene	AR	University of Arkansas	Assoc. Prof. Plant Pathology
Morris, Craig	WA	USDA-ARS	Quality laboratory
Murphy, Paul	NC	North Carolina State University	Breeder
Ohm, Herb	IN	Purdue University	Breeder
Peterson, Jim	OR	Oregon State University	Breeder
Riera-Lizarazu, Oscar	OR	Oregon State University	Marker support
Romsa, Jay	MN	General Mills	Miller
Rudd, Jackie	TX	Texas A&M Univ.	Breeder
Seyran, Esra	AR	University of Arkansas	Plant Pathology
Siemer, Rick	IL	Siemer Milling	Miller
Skinner, Daniel Z.	WA	USDA-ARS, Pullman	Research leader
Smail, Virgil	KS	The Am. Inst. of Baking	Baker
Sneller, Clay	OH	The Ohio State Univ.	Breeder
Sorrells, Mark	NY	Cornell Univ.	Breeder
Souza, Ed	ID	Univ. of Idaho	Breeder
Stearns, Mark	KS	Baker. Interstate Brands	Baker
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Talbert, Luther	MT	Montana State Univ.	Breeder
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van Ginkel, Maarten	Mex.	CIMMYT	Breeder
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Ward, Rick	MI	Michigan State	Breeder
Walker, Brian	KS	Cargill	Miller
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