

# **Report of the planning conference for a 2005 Coordinated Agricultural Project (CAP) on wheat translational genomics**

August 16-17, 2004, at Denver CO

Supported by USDA-CSREES Competitive Program Unit.

Organized by J. Dubcovsky

## **1. Background**

Wheat is unique among the major crops in that the public sector is largely responsible for the development of commercial varieties (more than 60% of the current varieties). A competitive US wheat industry depends upon the capability of public wheat breeders to adapt new technologies to applied breeding efforts. To address this issue, wheat breeders and allied researchers from across the US will prepare a Coordinated Agricultural Project to implement new marker technologies in wheat improvement.

In 2003, USDA Under-Secretary Joseph Jen suggested that the wheat research community should 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.

The first step in this direction was the organization of a National Workshop at Kansas City, MO, February 2004. This meeting was well attended by industry representatives, breeders and associated researchers (63 participants). During this meeting industry representatives and breeders prioritized the traits to be improved and discussed the role of the new USDA genotyping centers in wheat improvement. The complete Kansas report is available at <http://maswheat.ucdavis.edu/PDF/MeetingFeb22.pdf>.

To implement the industry recommendations at the Kansas workshop we planned a conference in Denver (August 16-17, 2004) and presented a proposal to USDA to support this planning effort (<http://maswheat.ucdavis.edu/PDF/CRISReport.pdf>). The proposal received excellent reviews and \$12,000 was awarded for the planning effort (<http://maswheat.ucdavis.edu/PDF/ReviewsPlanningGrant.pdf>).

## **2. Objectives**

The general objective of this planning meeting was to develop a research plan addressing the priorities established by the wheat industry, and a sound management plan integrating training, education, and extension activities.

An additional objective of this meeting was to determine the best structure for a national marker-assisted-selection (MAS) program in wheat encompassing public wheat breeding programs, University research laboratories, and the four new USDA-ARS regional molecular genotyping centers.

### **3. Participants**

The complete list of the 45 conference participants is included at the end of this document (Table 1). The participants included 23 public wheat breeders/researchers, 5 scientists from the genotyping centers, 12 wheat researchers, 2 international speakers and 1 representative from USDA.

The attending wheat breeders and researchers represented 25 different states that together grow 93% of the total US wheat (based on 2000-2003 production averages). The participation of such a large proportion of wheat breeders, during harvest time, documents their interest in incorporating marker technologies into their programs.

The leaders of the Canadian and Australian efforts on wheat MAS, Drs. Daryl Somers and Peter Langridge made detailed presentations summarizing the history and current efforts in MAS in their countries.

### **4. E-mail questionnaires before the meeting**

To initiate the discussion for the Denver meeting, and to use the meeting time productively, we organized two E-mail surveys that were actively circulated among the public breeders, wheat researchers and genotyping centers the month before the planning conference. We also initiated discussion groups about association mapping, breeding strategies, genotyping laboratories, and management plan, among others. The summary of the two questionnaires and the tabulated answers from 33 participants are included in Appendix 1 at the end of the report. The original summary tables circulated within the group included the complete comments from each participant as inserts within the relevant cells from the Excel file (complete Tables can be requested from [jdubcovsky@ucdavis.edu](mailto:jdubcovsky@ucdavis.edu)).

Based on the E-mail discussion we were able to reach agreement on the proportion of resources allocated to research and breeding activities, the general theme of the research effort, the participants, and the regional organization and preliminary management plan. The main results from these surveys are included in the presentation below.

### **5. Presentations**

#### **5.1. D. Van Sanford “Summary of the Kansas City, MO workshop and the E-mail survey”**

Dr. Van Sanford (KY) presented a summary of the Kansas City, MO Workshop and the traits prioritized by the wheat industry. The objective of this presentation was to keep the participants focused on the mandate from the wheat end users.

The main conclusions from the Kansas City, MO meeting were:

- Focus on the big-ticket items: yield, production consistency, and disease resistance (prioritize resistance to Fusarium Head Blight and stripe rust).

- Quality traits: prioritize milling yield, preharvest sprouting, hardness and particle size, water absorption, gluten strength, and protein content. If possible also include in the list levels of dietary fiber and of Polyphenol Oxidase (PPO). In the durum wheats focus on pasta and semolina color, semolina yield, gluten strength and protein content.
- Regarding the USDA-ARS regional molecular genotyping laboratories the recommendation was to focus on MAS implementation in public wheat breeding programs using a high-throughput forward MAS strategy. A second priority was the development of a marker database for the US wheat cultivars.

Dr. Van Sanford also summarized the results from the two Email surveys (Appendix 1). The main agreements from the E-mail discussions were:

- Allocate approximately 55% of the resources and efforts to research on the traits requested by industry for which we currently do not have enough information. Allocate the other 45% of the effort to implementation of forward MAS strategies in the public wheat breeding programs.
- Use a QTL mapping approach to generate markers and information for the complex traits requested by industry. Use adapted US germplasm as parental lines for the mapping populations.
- Favor an inclusive approach that incorporates most of the US wheat public breeding programs. Use a fixed list of participants rather than an annual grant structure.
- Divide the country in four regions including a genotyping laboratory and managed by a regional coordinator.

### **5.2. J. Dubcovsky “Current and future status of the MASwheat consortium**

J. Dubcovsky presented an overview of the current progress of the 12-laboratory MASwheat consortium. The objectives of this 4-year program were to develop molecular markers to major disease resistance and quality traits and to introgress those traits into adapted parental lines within the different market classes (Phase I: “Parental line development”).

By the end of the project in September 2005 there will be 178 adapted lines in the different market classes ready to deliver numerous resistance and quality genes. This number will increase to approximately 300 by 2006 (see Table 2 at the end of the document). In summary the adapted lines carrying the desired alleles will be available for the CAP grant (Phase II: “Forward MAS”). In addition molecular markers are available for approximately 50 traits.

Although good markers are available for several diseases and quality traits, a dedicated research effort is necessary to address the complex traits requested by the wheat end users at the Kansas City, MO meeting.

To generate molecular markers for these complex traits it would be necessary to develop new mapping populations using adapted US germplasm and evaluate them in multiple environments to develop robust QTL maps. Validation of those QTLs should be also an integrated part of the research proposal.

### **5.3. G. Brown-Guedira & S. Chao “Current & future status of the Genotyping Centers”**

The goals of the Genotyping laboratories in basic and applied research largely complement those of the MASwheat program. A synergistic relationship currently exists between the MASwheat breeding programs 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 the hiring phase.

Dr. Brown-Guedira (KS) and Dr. Shiaoman Chao (ND) presented the current funding and capabilities of the four genotyping centers and the expected capabilities by September 2005. They also discussed their expected throughput increase by the incorporation of a half time technician supported by the CAP grant.

#### **5.3.1. Kansas Laboratory.** Leader: Guihua Bai. Current funding: \$530,000

- Current equipment: 2 Li-cor and 1 ABI 3100, 2 384-wells and 5 96-well thermocyclers, and liquid handling robots.
- Personnel: 1 Category 1 scientist, 1 Category 3 scientist, 1 technician, 1 post-doc, 1 student.
- Expected lab capacity in September 2005: extraction of 500 DNA samples a day, 1000 SSR data-points daily. Based on current funding the operating capacity will be 50,000 research data-points, 50,000 service data-points.
- Increased capacity from CAP grant 0.5 technician: 20,000-40,000 data-points

#### **5.3.2. North Carolina Laboratory.** Leader Gina Brown-Guedira. Funding: \$530,000

- Current equipment: ABI 3100 DNA analyzers, 6 thermocyclers, and liquid handling robots.
- Personnel: 1 Category 1 scientist, hiring other positions.
- Expected lab capacity in September 2005: 50,000 research data-points, 50,000 service data-points based on current budget.
- Increased capacity from CAP grant 0.5 technician: 20,000-40,000 data-points

#### **5.3.3 Washington Laboratory.** Leader: Kim Campbell. Current funding: \$160,000

- Current equipment: 2 Li-Cor DNA analyzers and 3 thermocyclers.
- Personnel: 1 postdoc and 0.5 time technician.
- Expected lab capacity in September 2005: 10,000 research data-points, 10,000 service data-points.
- Increased capacity from CAP grant 0.5 technician: 20,000 data-points

#### **5.3.4 North Dakota Laboratory.** Leader Shiaoman Chao. Current funding: \$790,000

- Current equipment: two ABI 3100 DNA analyzers, 2 384-wll thermocyclers, and liquid handling robots.
- Personnel: 1 Category 1 scientist, hiring 1 category 4 and 1 technician.

- Expected lab capacity in September 2005: 100,000 research data-points, 100,000 service data-points based on current budget.
- Increased capacity from CAP grant 0.5 technician: 20,000-40,000 data-points

All four genotyping laboratories will provide high-throughput MAS for the public breeding programs in their regions. In addition, the ND laboratory will be responsible for the screening of 36 parental lines of the 18 mapping populations with a collection of 1,500 microsatellites during the first six months of the grant. Primers are available and have been tested in three pairs of parental lines.

The two major needs for the CAP project regarding the genotyping centers will be to increase the funding level of the WA Genotyping Center (similar to other genotyping laboratories), and to establish an informatics position at ND that can establish a WEB interface to upload and download information from the breeding programs (See 11. Data Management).

#### **5. 4. D. Somers. *Wheat MAS in Canada***

Dr. Daryl Somers presented an overview of the Canadian MAS program. Canada has funded a large initiative in wheat genomics in the order of \$40 million Canadian dollars to incorporate molecular technologies to their wheat programs. Their long term vision is that these technologies have significant potential to accelerate variety development.

As an initial step they developed several mapping populations based mainly on adapted Canadian germplasm and constructed high-density maps using all available microsatellite markers. A consensus map from these populations is in press in *Theoretical and Applied Genetics*, and the data will be deposited in GrainGenes. They have also developed a database including graphical display software for maps and SSR polymorphisms, which will be also shared with GrainGenes.

Mapping populations are being evaluated in different environments for agronomic traits and several milling and baking quality parameters, starch characteristics, pre-harvest sprouting (PHS), and other traits important to farmers and others in the wheat industry.

Doubled haploids (DH) have been used to accelerate the development of these populations. DH central facilities are available to Canadian researchers and breeders and are being extensively used.

Dr. Somers presented their high-throughput strategy to incorporate Fusarium Head Blight (FHB) resistance into elite Canadian germplasm. Briefly, four high-throughput streams were generated to incorporate different Quantitative Trait Loci (QTL) using two backcrosses and recurrent parent background selection (100 individuals and approximately 80 microsatellites). DHs were used to accelerate the combination of the four streams in the final steps of the project.

### **5. 5. P. Langridge. *The Australian National Program on Marker Assisted selection.***

Peter Langridge presented first a chronological review of the Australian National Program on MAS. The program has two phases, one from 1996-2002 and the other one 2002-2005. Approximately 15 million AU\$ have been invested in this program.

During the first phase, five DH populations based on Australian adapted parental lines were mapped and evaluated in multiple environments. Several agronomic and disease resistance traits were evaluated. Quality traits were evaluated for bread-making, and for white salted noodle and yellow alkaline noodle production.

The central mapping populations continued to be used beyond the end of the project, documenting the high value of these genetic resources. The results from the QTL analysis of the first five populations were published in 2001 in the Australian Journal of Agricultural Research. Mapping populations for specific purposes have been continuously added and now more than 60 mapping populations are available in Australia.

Among the problems noted in the first phase of their program Peter Langridge emphasized the insufficient resources for coordination and the lack of resources for phenotyping, which resulted in some programs having patchy assessments. He also pointed out problems with the end use quality data: lack of clear definition of the quality parameters, inconsistency among quality laboratories, high variability, multiple correlated parameters, etc. An uneven level of training among programs was also a problem. In addition, some of the programs wasted a lot of resources in RAPD markers development.

The things that worked well in the Australian program were: working with defined populations, the involvement of all the breeding programs and marker groups, the use of phenotyping expertise in different programs, a higher rigor in the quality analysis, and extensive phenotyping by the breeders.

The new phase of the Australian program includes validation and implementation of the QTLs found in the first phase of the program, development of new markers for slow rusting and drought tolerance, and haplotype characterization of the Australian germplasm using microsatellites. Characterization of several varieties and breeding lines with 200-400 markers have already shown that large linkage blocks are conserved within the Australian breeding programs.

In summary, the presentations from the two international speakers showed the existence of large and sophisticated efforts in MAS in the wheat programs from other countries. These two programs made extensive use of mapping populations developed from locally adapted germplasm, and are now focused on developing strategies to integrate marker technologies in their breeding programs and in the haplotype characterization of their germplasm. Both programs offered valuable models for the planning discussion.

## 6. Traits and mapping populations selected for the four regions

The first day of the Denver meeting each coordinator presented a list of tentative mapping populations and traits that they would like to address during the CAP project. These lists were previously developed through E-mail discussions and conference calls among the participants from each region.

Fusarium Head Blight resistance was a high priority for the millers at the Kansas City, MO meeting. However, this trait is not included in this proposal because the U.S. Wheat and Barley Scab Initiative (USWBSI) is already providing funding for mapping and breeding work on FHB.

The second day of the Denver meeting, after a more detailed discussion of the responsibilities involved in the mapping effort (see 10.2 Management), each regional group met for two hours (plus a working lunch) to further prioritize their mapping populations and trait selection. A summary of the current status of the populations and traits is included in Table 3 at the end of the report.

## 7. Strategies to incorporate MAS into the breeding programs

Since MAS technologies are relatively new, there are no standard strategies to incorporate them efficiently into the traditional breeding programs. Therefore, it was important to discuss possible strategies in detail.

There was a long and intense discussion led by E. Souza (ID) and P. S. Baenziger (NE). The international speakers also provided valuable input. The interest of the participants in this discussion was demonstrated by the permanence of the 45 participants until 10:00 pm, well beyond the end of the planned agenda.

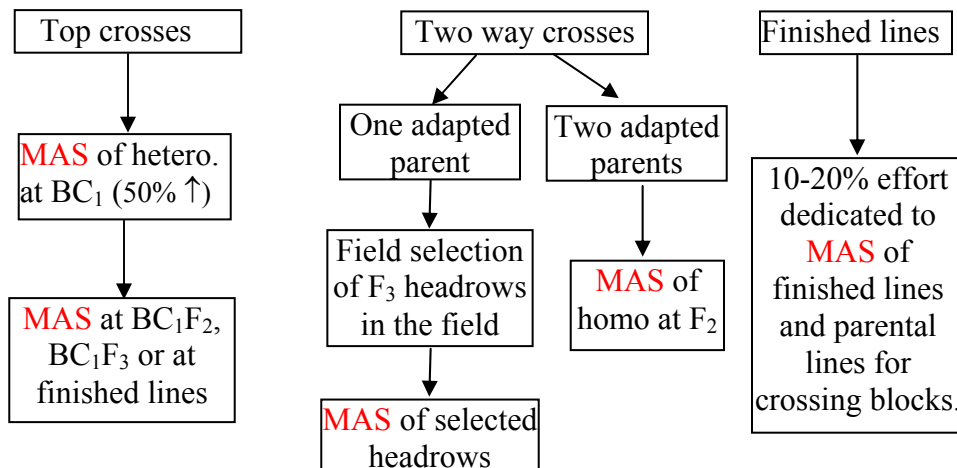


Figure 1. Strategies to integrate MAS into the current wheat breeding

Figure 1 presents a summary of the different points where MAS was suggested to maximize the cost/benefit relation. In top crosses, the maximum benefit is obtained by selecting heterozygous  $BC_1$  plants carrying the target gene. This step increases the

frequency of the desired alleles by 50%, and can be followed by additional cycles of selection at BC<sub>1</sub>F<sub>2</sub> or BC<sub>1</sub>F<sub>3</sub>.

In the case of two-way crosses, the optimum strategy depends on the number of expected un-adapted progeny. If one of the parental lines is not adapted to the region of a particular breeding program, a large proportion of the progeny will most likely be discarded early in the selection process, wasting a large proportion of the MAS resources used in earlier generations. In this case, it is more efficient to select among F<sub>3</sub> headrows in the field and use MAS only on the adapted lines.

If the two parents are well-adapted lines that are not segregating for any of the major quality or adaptation genes it would be efficient to apply MAS during the F<sub>2</sub>. Finally, it was decided that a limited proportion of the effort (10-20%) should be used to characterize finished lines for the presence of the favorable alleles and for validation of parental lines in crossing blocks.

The backcross strategy used during the previous MASwheat was effective to develop improved parental lines within the different market classes and to test the agronomic effects of the newly introduced genes. Now that these lines are available it is possible to move into more ambitious forward breeding MAS strategies such as the ones outlined in Figure 1. The high-throughput genotyping laboratories will facilitate the implementation of these strategies.

## **8. Mapping populations**

It was recommended that the mapping populations should be composed of at least 200 individuals, and that the resulting map should include approximately 200 microsatellite markers. This population number and marker density was suggested to have the power to detect small QTL effects that explain 10% or less of the phenotypic variation. In the case of RILs, it was agreed that they should have at least five generations of self-pollination and if possible six before increasing the seeds for the phenotypic evaluation of the mapping populations. It was recommended to evaluate the populations in six year/location combinations to test the robustness of the QTLs and to explore the G x E interactions. The minimum number of environments was established at two locations, two years and two replications in each location. Augmented designs incomplete block field plot designs were discussed as possible ways to handle the evaluation of the large populations in the field.

It was suggested that populations need to avoid the segregation for major genes with large epistatic effects (e.g. vernalization requirement, dwarfing genes, and major hardness and high molecular weight glutenin genes) in order to maximize the discovery of new alleles with smaller effects.

There was a general agreement that with increasing genotyping resources, phenotyping would be the limiting factor. It was agreed that a significant portion of the time of the personnel assigned to the mapping laboratories should be used for phenotyping. L. Talbert (MT) suggested including standardized evaluation of yield components as part of the phenotyping activities in all the programs.

Quality controls for the parental lines and the mapping populations were also discussed. We agreed to grow seeds from a single spike from the parental lines and extract DNA from a single plant. DNA aliquots will be distributed to the genotyping laboratories. Seeds from the plant used in the DNA extraction will be increased and deposited in the USDA-ARS Small Grain Collection.

Breeders acknowledged that mistakes are sometimes made during planting and harvesting and that appropriate quality controls should be used. It will be responsibility of each mapping laboratory to characterize all the submitted lines with eight polymorphic microsatellite markers. After the second year of field trials, all the lines grown in the field will be characterized again with the same microsatellites to rule out planting and harvesting errors. In addition, the breeder that developed the mapping population will characterize the lines for morphological markers during the first year to facilitate line identification during the subsequent field trials.

Seeds from the mapping populations will be maintained at the University of Missouri – Columbia (MO) with backups at the laboratory that developed the population and at the Wheat Genetics Resource Center, Kansas State University (KS).

## **9. QTL validation strategies**

It was agreed by all participants that QTL validation should be part of the CAP proposal (last two years) and that it was responsibility of each mapping laboratory.

Two different strategies were proposed for QTL validation. The main objective of the first validation strategy was to generate a fine map of selected QTL regions and to develop the preliminary data for future positional cloning efforts. This strategy would be appropriate for QTLs with large phenotypic effects. Briefly, a population of 1000 F<sub>2</sub> lines will be grown from the same cross used in the QTL mapping population. DNAs will be extracted from all lines and stored. The microsatellite markers flanking the selected QTLs will be used to screen the 1000 DNAs and to select the lines with recombination events between the markers flanking the QTL. Homozygous F<sub>3</sub> lines for the recombinant chromosomes will be selected, and seeds increased for phenotype evaluation. This strategy can generate the preliminary results necessary for a positional cloning of the genes responsible for the major QTLs. Forrest Chumley (KS) indicated that the positional cloning of genes important to wheat improvement will have a long term value.

A second strategy was proposed by J. Anderson (MN) that is more focused in the immediate use of the QTLs in a breeding program. The main objective of this strategy is to determine the usefulness of the detected QTLs in different genetic backgrounds and to generate near isogenic lines segregating for the QTL. Briefly, the parental lines are crossed with the best breeding lines of the program. The progenies from these crosses are advanced to F<sub>4</sub>. Once the flanking markers for a QTL are established, they are used to search for F<sub>4</sub> lines heterozygous for that region. These lines are self-pollinated to generate segregating populations of near isogenic lines. The effect of the QTLs region is then evaluated in different genetic backgrounds. The advantage of this procedure is that the validation of the QTL is directly incorporated into the breeding activities, thus

accelerating the release of improved varieties. In addition, high-density mapping populations based on near-isogenic lines can be generated to refine the QTL mapping.

It was also suggested that the characterization of the different haplotypes in the QTL region, in a collection of regional germplasm, would be a valuable activity for each mapping laboratory. Daryl Somers indicated that in his experience, the use of 5-6 microsatellites within a 10 cM region was a good predictor of the QTL allele present in a breeding line. This haplotype characterization is useful to predict which germplasm can benefit from the incorporation of the QTL and which germplasm might provide new alleles that will be worthwhile to compare with the best allele identified in the QTL mapping.

## 10. Management Plan

Based on the answers to the pre-meeting Email surveys (Appendix 1), and on regional conference-call discussions the following organization was agreed for the CAP project. J. Dubcovsky (CA) will be the project leader and will supervise a project manager supported by the grant. Four Regional Coordinators will facilitate the coordination of activities at the regional level. The four coordinators are: L. Talbert (MT) for the West region, A. Fritz (KS) for the Central region, J. Anderson (MN) for the North Central region, and C. Griffey (VA) for the East region. The East region was further divided in four sub-regions coordinated by M. Sorrells (NY, Northeast sub-region), J. Johnson (GA, Deep South sub-region), C. Griffey (VA, Mid-Atlantic sub-region), and H. Ohm (IN, Corn Belt sub-region). The genotyping center PIs will be G. Brown-Guedira (NC), S. Chao (ND), G. Bai (KS), and K. Campbell (WA).

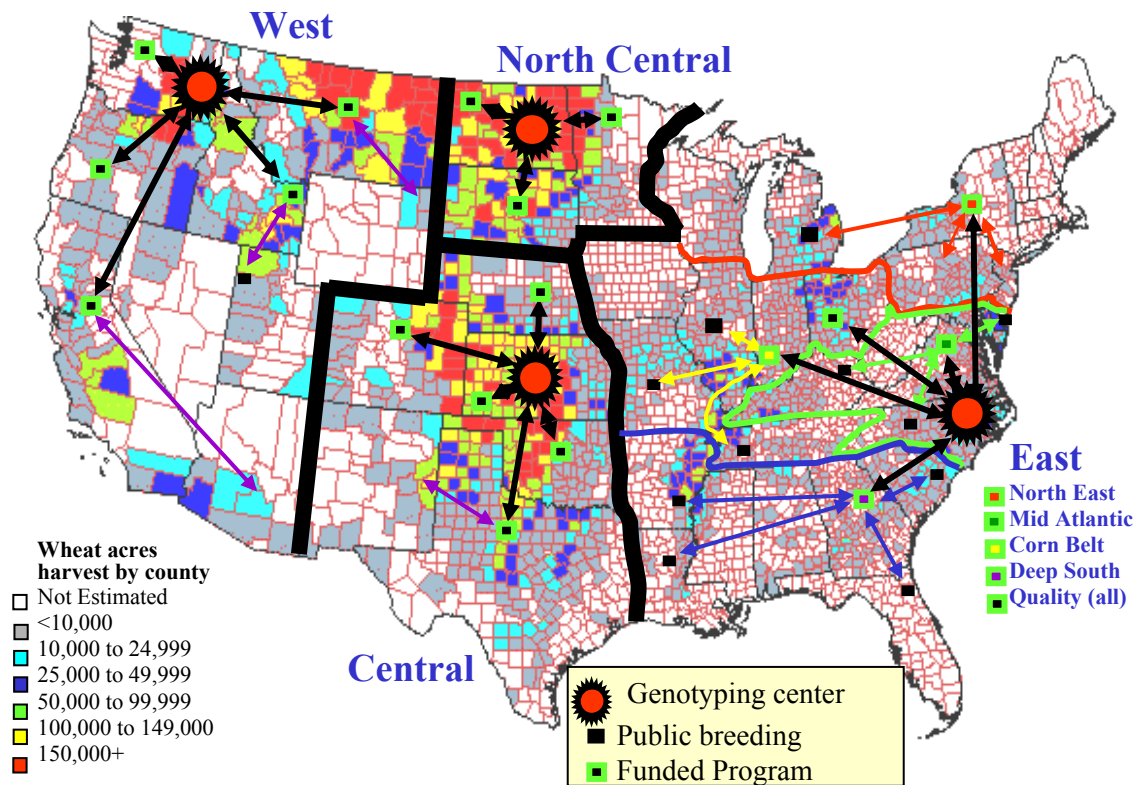
Eighteen wheat breeding programs divided in four regions (Figure 2) will be funded to integrate MAS strategies and to develop 18 mapping populations (Table 3):

- West Region: five positions tentatively assigned to CA, OR, ID, WA, and MT.
- North Central Region: three positions tentatively assigned to ND, SD-ND collaboration, MN.
- Central Region: five positions tentatively assigned to KS, NE, CO, OK, and TX.
- East Region: five positions total. One position tentatively assigned to each of the sub regions: Northeast (NY, MI), Corn-belt (IN, IL, OH, MO, TN), Mid-Atlantic (VA, NC, MD, KY), Deep South (GA, AR, LA, SC, FL). The underlined state indicates the coordinating program that will be responsible for the administration of the funding.

The fifth position in the East regions was assigned to the quality laboratory (OH) to address quality traits common to the soft wheat region.

A total of \$32,000 per year will be allocated to each of the 18 programs responsible for one of the mapping populations. The funded programs will provide the matching resources and funding required to achieve the proposed objectives. A similar level of support will be provided to each of the genotyping centers. The half-time technician from the genotyping center will be responsible to provide 2000-5000 data-points for MAS a year to each of the participating programs. This distribution of

resources reflects the decision made by the participants to serve the maximum number of public wheat breeding programs with limited and equal support to all participants.



**Figure 2.** Regional organization of the project. Thick black lines delimit the four regions. Colored lines delimit the four-sub-regions in the East.

### 10.1. Responsibilities of the genotyping center

The technician assigned to each genotyping center will be responsible for providing 20,000-40,000 data-points (depending on the high throughput capacity of the genotyping center). This will result in 2000-5000 data-points for MAS per year for each of the participating breeding programs. In addition the genotyping centers will collaborate with the developments of some of the regional populations using their own resources.

### 10.2. Responsibilities of the mapping laboratories

Each of the programs with a position funded by the CAP grant would be expected to deliver 15,000 mapping data points per year (100 lines= 150 markers or 200 lines 75 markers). In addition, the program receiving a postdoc is required to submit DNA samples for 2,000-5,000 data points a year to the genotyping lab (depending on genotyping lab capacity).

A semiannual report indicating the how the allocated markers were used will be submitted to the regional coordinator by each breeding-program. It is also the

responsibility of each mapping laboratory to evaluate the population in at least two environments in years 1-3 or 2-4, and to report the traits evaluated to the regional coordinator once a year. Mapping laboratories can establish individual collaborations with their regional genotyping lab in order to accelerate the mapping process.

### **10.3. Responsibilities of the regional coordinator**

The regional coordinator will organize one regional meeting each year in coordination with the Wheat Workers regional meetings.

He/she will coordinate the selection of mapping populations and maintain a fluid communication among the breeding programs and researchers from each region.

The regional coordinator will also compile a six month progress report on mapping and MAS and send a regional report to J. Dubcovsky.

### **10.4. Responsibilities of the project coordinator**

The project coordinator will monitor the advancement of the project every six months and organize one general meeting coordinated with the annual Crop Science Society of America meeting. He will produce a yearly report for the complete project and send it to all participants.

If the performance of a participant falls below the minimum requirements established for mapping and MAS selection, the project coordinator will send a letter to the PI with copy to the regional coordinator. The group will be offered help to solve their problems and will be given one year to correct their problem. If one year after the reception of the letter the participant fails to meet the minimum requirements, he/she will be separated from the project. The funding will be reassigned within the same Region, which will decide how to replace the terminated program or how to better redistribute those resources among the other participants to address the regional objectives.

The project coordinator will be also responsible for the overall budget and for all the reports to the granting agency.

### **10.5 Advisory board**

An advisory board was proposed as part of the Management Plan. The proposed members of the board include

- 1 representative from the National Association of Wheat Growers
- 1 representative from the North American Milling Association
- 1 representative from the American Institute of Baking
- High throughput experience: **Daryl Somers**, Canada: Agreed  
(Peter Langridge, Australia: *Ad hoc.*)
- 1 representative from the US Wheat. Biotech committee NAWG.

Dave Van Sanford (KY, NWIC) offered to help with the organization of the Advisory Board.

## 11. Data management.

D. Matthews (NY) made a presentation of the current status of the ‘Grainotypes’ database that will be able to accommodate germplasm and allelic information for molecular markers. He indicated that GrainGenes is ready to receive the mapping data from this project. We agreed that personnel from the laboratories participating in the CAP grant will be trained to submit the mapping information to the ND Genotyping Center in a format that is ready to be deposited in GrainGenes. Mapping laboratories will submit their mapping information every six months.

For data tracking it was suggested to coordinate the database for the project with the database for the genotyping centers. It was also agreed to create a Web data service (similar structure as the one created for the NSF wheat EST project, <http://wheat.pw.usda.gov/NSF/>) to upload the samples for the genotyping center and download the results (Figure 3).

A breeder will upload the information for each sample to a password protected Web site using an Excel file with previously determined format. Samples will be submitted in 96-well format. The file will include information for the breeder's name, genotyping laboratory where the sample is submitted, if it is a sample for mapping or breeding, trait, plate number, well number, sample name, and marker. Samples from varieties or finished lines with associated phenotypic data will be identified with a germplasm accession name that already exists in the database or with a new name and its passport information will be provided.

This information will be deposited in the CAP/Genotype database and will generate an automatic Email to the corresponding genotyping laboratory. The genotyping lab will perform the analysis and upload the information in their Web interface including date and allele size for each well. The allelic information will be appended to the plate information in the database.

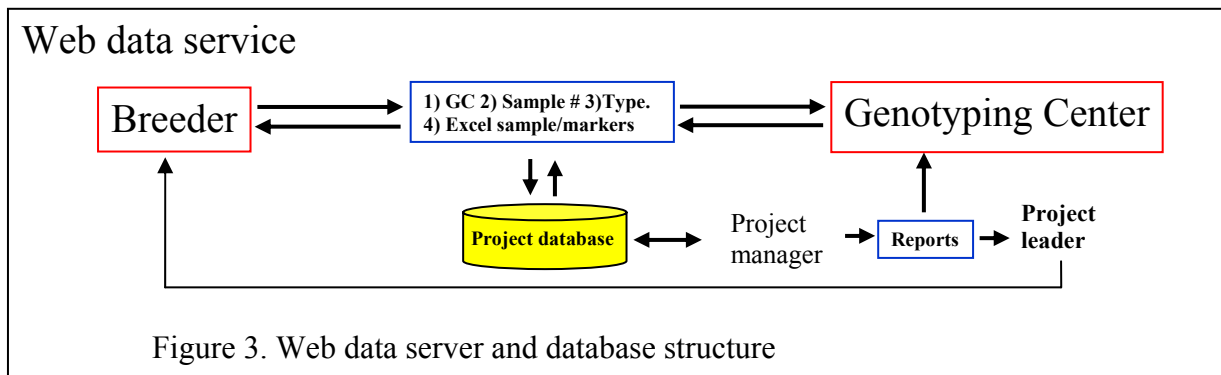


Figure 3. Web data server and database structure

The project manager, the project leader and the genotyping laboratory coordinators will have access to query the database. They will be able to monitor the amount of work submitted by each program, the data points generated by each genotyping laboratory, and the time between submission and data production. This database will be used by the CAP grant coordinator to monitor progress and to prepare reports to USDA.

The database will be hosted on the GrainGenes server at Albany CA, which will minimize the costs of server security. Approximately \$15,000 will be needed to program the Web data server. S. Chao (ND) indicated the possibility to hire a computer person for the ND Genotyping Center to coordinate this activity. G. Brown-Guedira (NC) offered to help.

## **12. Education and outreach.**

Different ideas were proposed for education and outreach:

### **12.1. *Growers outreach***

Bob Zemetra (ID) suggested producing a brochure explaining the basic concept of MAS and the scope of the CAP project and the benefits of MAS in cultivar development. The brochure would be produced in a two-page format that would be easily downloaded and printed by participants in the CAP program for distribution at grower meetings and field days. Individual programs within the CAP project could produce a single page addition to the brochure giving more specific information on how MAS is being used to benefit producers in that particular region. The brochure would be made available by June 2006 to be available for presentations the first year of the wheat CAP project.

. The extensive contact between breeders and members of the wheat industry means that this brochure will reach a large number of people each year. This brochure will be also placed on line in the Educational section of MASwheat and will be offered to the wheat commissions and grower associations for inclusion in their Web sites.

We will present the MAS improved lines during field days and grower meetings as an educational activity on the potential benefits of biotechnology. We will clarify that these lines are not considered Genetically Modified Organisms (GMO). We will also implement hands-on visits of the growers and wheat industry representatives to the molecular marker laboratories.

### **12.2. *Crop Technology lessons***

A website developed by D. Lee at the University of Nebraska to explain crop technology is an excellent education resource that has recently won the Educators award and the ASA award. We will incorporate examples of successful MAS stories in the MAS modules. P. S. Baenziger (NE) is committed to write a wheat breeding unit for the technology web site.

### **12.3. *Symposia and meeting organization in Marker Assisted Selection***

Suggested meetings where we can try to propose MAS talks or symposia include:

- July 2005 APS meetings: on MAS. B. Bowden (KS) offered to coordinate this effort.
- AAAS Symposium 2007 on MAS. P. S. Baenziger (NE) offered to coordinate this effort.
- Symposium on MAS at CSSA. J. P. Gustafson (MO) is coordinating C7 and offered to coordinate this effort.

- Cereal Chemistry MAS in quality 2008

#### **12.4. Training for new CAP participants and small breeding programs**

Within each region, one of the laboratories with previous experience in MAS from the IFAFS grant will share their experience in MAS techniques in a 2-3 day hands-on workshop, by inviting other public and private breeding and research programs to participate.

For all the participating postdocs the wheat CAP program will focus on early career development. The postdocs will be trained not only in molecular genetic techniques, but also in breeding techniques in order to increase their future opportunities in the job market. Exposure to high-throughput technologies and visits to the genotyping centers will also enrich their training experience.

#### **12.5 Graduate and undergraduate training**

A survey of the participants in the meeting indicated that approximately 30% of the positions will impact graduate education. As in the case of the postdocs we will integrate training in molecular genetics with training in breeding and high-throughput technologies. The wheat CAP program will establish networks of graduate students within each region.

At the undergraduate level, K. Campbell (WA) offered to explore the possibility of USDA training for undergraduates with emphasis on minorities and women. The target will be an internship program at the USDA genotyping labs.

The wheat CAP program will also continue with summer internships in MAS for undergraduates and local high school students.

Peter Langridge (Australia) offered access to the education and school programs developed as part of the Australian MAS program. He mentioned an interesting program for grower's education called "Science in the Pub", in which scientists from the project organized meetings with the growers in rural pubs to talk about crop improvement and new technological developments.

### **13. Intellectual Policy**

#### **13.1 Germplasm**

Each University will retain the rights to all the varieties that they develop through the incorporation of MAS and can protect them via Plant Variety Protection (PVP).

Germplasm will be made freely available for crossing under the Wheat Breeders Code of Ethics. Released lines will be sent to the USDA-National Small Grain Collection for distribution.

#### **13.2 Information**

Mapping data and genotyping data of parental lines will be deposited every six months in GrainGenes.

Phenotypic and QTL data will be made available to members of the group in the annual regional and general meetings. After validation of the QTLs for at least two years the data will be made publicly available through GrainGenes or scientific journal publications.

## 14. Publication policy

**14.1 Mapping papers.** Each laboratory that constructs a molecular map and integrates the QTL information will be responsible for the publication of that population and will have the first and last author positions. The leader of the genotyping center that performed the parental screening or that contributed to the mapping effort will be a coauthor in that publication. If other breeding programs, quality laboratories or disease resistance laboratories contribute phenotypic data, they will be also included in the publication

**14.2 MAS developed varieties of germplasm.** If a member of a genotyping center contributes to the development of a variety or germplasm he/she will be coauthor on the Crop Science Registration. Other ARS scientists who contribute data relevant to the development of the variety will be also included in authorship.

## 15. Budget

The \$12,000 provided for the meeting were mainly used to support lodging for all participants and meeting rooms and audiovisual equipment.

Rooms:	\$ 8577.05
Rooms/ Audiovisuals/	\$ 2,278.51
Daryl Somers travel	<u>\$ 1,150.00</u> Estimated
Total	\$12,005.56

The expenses for Peter Langridge will be covered from funds for the workshop in Kansas City, MO and with travel funds from the IFAFS grant.

## 16. Concluding remarks

This planning grant has provided a unique opportunity to bring the wheat research and breeding community together. Almost all public wheat breeders and several wheat researchers were present in this meeting (Table 1) providing a unique forum for scientific discussion. This meeting was essential to interchange ideas and plan the future of public wheat breeding in the US. These interactions would not have been possible without the USDA support of the planning meeting and the existence of the CAP program.

**Table 1.** List of participants

	<b>State</b>	<b>Email</b>
<b>International speakers</b>		
Somers, Daryl	Canada	somersd@agr.gc.ca
Langridge, Peter	Australia	plangridge@waite.adelaide.edu.au
<b>Genotyping laboratories</b>		
Bai, Guihua	KS	gbai@bear.agron.ksu.edu
Bowden, Robert	KS	rbowden@ksu.edu
Brown-Guedira, Gina	NC	gbg@ksu.edu
Campbell, Kim	WA	kgcamp@wsu.edu
Chao, Shiaoman	ND	chaos@fargo.ars.usda.gov
Total 6	4	
<b>USDA</b>		
Kaleikau, Ed		
<b>Wheat Breeders/Researchers</b>		
Anderson, Jim	MN	ander319@umn.edu
Bacon, Robert	AR	rbacon@uark.edu
Baenziger, P. Stephen	NE	agro104@unlnotes.unl.edu
Campbell, Kim	WA	kgcamp@wsu.edu
Carver, Bret	OK	bfc@mail.pss.okstate.edu
Costa, Jose	MD	jc274@umail.umd.edu
Dubcovsky, Jorge	CA	jdubcovsky@ucdavis.edu
Fritz, Allan	KS	akf@ksu.edu
Glover, Karl	SD	Karl_Glover@sdstate.edu
Griffey, Carl	VA	cgriffey@vt.edu
Haley, Scott	CO	shaley@lamar.colostate.edu
Johnson, Jerry	GA	jjohnso@griffin.uga.edu
Kidwell, Kim	WA	kidwell@mail.wsu.edu
Kolb, Fred	IL	f-kolb@uiuc.edu
Murphy, Paul	NC	njpm@unity.ncsu.edu
Ohm, Herb	IN	hohm@purdue.edu
Rudd, Jackie	TX	j-rudd@tamu.edu
Sneller, Clay	OH	sneller.5@osu.edu
Sorrells, Mark	NY	mes12@cornell.edu
Souza, Ed	ID	esouza@uidaho.edu
Talbert, Luther	MT	usslt@montana.edu
Van Sanford, David	KY	dvs@uky.edu
Bob Zemetra	ID	rzemetra@uidaho.edu
Total breeders: 23	21 States	

**Table 1.** Continuation.

<b>Wheat Researchers</b>		
Bikram, Gill	KS	bsg@ksu.edu
Byrne, Patrick F.	CO	pbyrne@lamar.colostate.edu
Chumley, Forrest	KS	fchumley@oznet.ksu.edu
Gill, Kulvinder	WA	ksgill@wsu.edu
Gustafson, Perry	MO	pgus@missouri.edu
Kianian, Shahryar	ND	s.kianian@ndsu.nodak.edu
Lapitan, Nora	CO	nlapitan@lamar.colostate.edu
Menz, Monica	TX	mmenz@tamu.edu
Marshall, David	NC	david_marshall@ncsu.edu
Matthews, Dave	NY	matthews@greengenes.cit.cornell.edu
Riera-Lizarazu, Oscar	OR	Oscar.riera@oregonstate.edu
Roche, Dominique	UT	droche@mendel.usu.edu
Soria, Marcelo	CA	masoria@ucdavis.edu
Total researchers: 13	12 States	

**Table 2.** New lines developed using adapted recurrent parents and molecular markers for more than 40 disease resistance and quality traits.

<b>Market Class</b>	<b>Complete 9/05</b>	<b>Complete 9/06</b>
<b>Durum</b>	23	29
<b>HRS</b>	80	90
<b>HRW</b>	20	62
<b>HWS</b>	22	35
<b>HWW</b>	12	19
<b>SRW</b>	15	28
<b>SWS</b>	6	11
<b>SWW</b>	0	23
<b>Sum</b>	<b>178</b>	<b>297</b>

**Table 3.** Preliminary mapping populations selected by the participating programs.

State	Parent 1	Class	Parent 2	Class	No.	Gen.	Traits	Testing locations
CA	UC1113	Durum	Kofa	Durum	96	F8	Gluten strength, pasta color, LOX activity, stripe rust, yield	Sacramento Valley (CA), Imperial Valley (CA).
OR	OR9900553	SWW	Stephens	SWW	165	F5:6	Extra soft texture, HTAP stripe rust	Corvallis (OR), Pendleton (OR), Pullman (WA), Moscow (ID), Aberdeen (ID)
ID	Rio Blanco	HWS	ID444	HWS	300	F7:8	HTAP stripe rust resistance, Hessian fly, baking and milling quality, starch, yield.	Aberdeen (ID), Utah
ID	Coda	SWWc	Brundage	SWWc	300	F5:6	Stripe rust, foot rot	Aberdeen (ID), Moscow, Corvallis, Mt. Vernon, Pullman (WA)
WA	Louise	SWS	Penawawa	SWS	200	F2:6	Stripe rust, quality , yield	Mt Vernon (WA), Pullman (WA), Davis, (CA).
MT	McNeal	HRS	Thatcher	HRS	125	F6:8	Yield components, stripe rust, milling and backing quality	Bozeman, Aberdeen (ID), Pullman (WA)
CO	Plate	HWW	CO940610	HWW	250	DH	Milling, baking and Asian noodle quality traits	Fort Collins (CO), Hugoton (KS), Goodwell (OK), Bushland (TX)
TX	Weebill	HRS	Jupeteco	HRS	200	F6	Leaf rust resistance.	Obregon (Mexico), Castroville (TX)
OK	2174	HRW	Jagger	HRW	275	F <sub>5</sub> derived	Heat-sensitive germination, FHS, Lr, Yr, Sr, BYD, WSMV, Al tolerance, straw strength, shattering, Pm, dough strength, absorption, milling components, test wt.	Enid (OK), Stillwater (OK), Lahoma (OK), Hutchinson (KS), Manhattan (KS), Fort Collins (CO), Bushland (TX)
KS	Amadina	HWS	Avocet	HWS	170	F6	Leaf rust resistance.	Obregon (Mexico), Castroville (TX)
NE	Tam105	HRW	Jagger	HRW	250	DH	Drought tolerance, strip rust, WSMBV, WSSMV, Septoria tritici, tan spot, quality, vernalization requirement, shattering, winter-hardiness, and acid soil tolerance	Lincoln (NE), Sidney (NE), Enid (OK), Stillwater (OK), Lahoma (OK), Hutchinson (KS), Manhattan (KS), Fort Collins (CO), Bushland (TX)
SD/ ND	ND735	HRS	Steele-ND	HRS	212	F7	Grain shattering, Septoria, FHB, tan spot, quality.	Brooking (SD), Prosper (ND), Langdon (ND).
ND	Maire	Durum	Rugby	Durum	190	DH	Gluten strength, pasta quality	Casselton and Prosper
MN	Grandin* 5/ND614	HWS	NY/Clark's CreamRIL#40-1	SWW	101	BC1F8	Pre-harvest sprouting	St. Paul, Morris, Crookston MN

**Table 3.** Continuation

<b>State</b>	<b>Parent 1</b>	<b>Class</b>	<b>Parent 2</b>	<b>Class</b>	<b>No.</b>	<b>Gen.</b>	<b>Traits</b>	<b>Testing locations</b>
NY	NY Cayuga	SWW	Caledonia	SWW	220	DH	Milling and baking, seed dormancy, yield, height	New York, Michigan
OH	Pioneer 25R26	SRW	Foster	SRW	192	F5:6	Gluten strength, water absorbtion, flour yield, texture, cookie diameter	Wooster (OH); Warsaw (VA), West Lafayette (IN), Lexington (KY), Griffin (GA)
IN	P91193	SRW	P92201	SRW	200	F8:11	S. nodorum, Lr37-Yr17-Sr38, Lr, PM, S. tritici	IN, NY, NC, OH, AR, VA, IL, MO.
VA	USG3209	SRW	Jaypee	SRW	290	F8:9	Powdery mildew APR	Warsaw (VA), Kinston (NC), Wye (MD), Lexington (KY)
GA	SS 550	SRW	PIO26R61	SRW	150	F5:8	Stripe rust, SBMV, seed weight	Griffin and Plains, Keiser (AR), Baton Rouge (LA)

## **APPENDIX 1. E-mail Questionnaires and tabulated answers**

### **Questionnaire 1**

#### **1. Overall research proposal**

Please indicate your preference between

- 1.1.** 100% research with no MAS implementation
- 1.2.** 75% research, 25% MAS implementation
- 1.3.** 50% research, 50% MAS implementation
- 1.4.** 25% research, 75% MAS implementation

Please indicate your preference between the following research approaches.

- 1.5.** QTL mapping using adapted US parents and including yield, diseases and quality evaluations. If you select this option please answer 1.5.2.
- 1.5.2.:** Do you agree with imposing the requirement to produce a complete map and 2 years of phenotyping for those programs receiving funds from this grant?
- 1.6.** Cloning of important agronomic traits using a candidate gene approach.
- 1.7.** Positional cloning of important agronomic traits.
- 1.8.** Association mapping.
- 1.9.** Development of reverse genetic resources in wheat.
- 1.10.** Focus on the sequencing of the wheat genome, contributing to the sequencing of target region with important agronomic value.
- 1.11.** Develop perfect markers for available genes (Luther Talbert's suggestion).
- 1.12.** SNP development in collaboration with Jan Dvorak NSF project.
- 1.13.** Any other research proposal that you would like to suggest.

#### **2. Budget**

- 2.1.** "Grant allocation system" in which researchers will submit proposals every year and a scientific panel will decide which proposals will be funded.
- 2.2.** "Fixed allocation system". The funded participants are decided at the beginning of this grant and those that made adequate progress remain in the grant.

Under the "Grant allocation system" (2.1):

- 2.3.** Do you prefer a larger number of projects with small support, or a small number of projects with large support?
- 2.4.** If there is \$1 million per year, which should be the maximum support per grant?

Under the "Fixed allocation system" (2.2):

- 2.5.** 12 breeding programs plus 4 genotyping centers (Salary: 30K Supplies:14K)

- 2.6.** 15 breeding programs plus 4 genotyping centers (Salary: 28K Supplies:10K)
- 2.7.** 18 breeding programs plus 4 genotyping centers (Salary: 25K Supplies: 7K)
- 2.8.** Do you agree with the idea to provide some type of extra support for the breeding programs that do not receive direct financial support from this grant?
- 2.9.** Do you think that is a good idea to request matching funds from the local funding organizations? The amount can be discussed later and will depend on the number of programs and the available support per program.
- 2.10.** Do you think that a letter indicating the compromise of matching funds in case of USDA funding should be a pre-requisite for a program to be selected for funding from this grant?

## Questionnaire 2

- 1.** Do you agree that the allocation of a postdoc should take into account the wheat production (we will discuss “how” later) served by the breeding programs?
- 2.** Do you agree that the allocation of a postdoc should take into account the demonstrated capacity of the program to generate the promised molecular map and to evaluate the required phenotypes?
- 3.** Do you agree that the allocation of a postdoc should take into account the availability of a mapping population before planting time 2005 (to have 2 years of field data)?
- 4.** Suggest other criteria
- 5.** Do you agree to divide the participants in four regions each including a genotyping center and a group of breeding programs with certain capacity of decision?
- 6.** Do you agree to have a regional coordinator, rotated every year in each of the regions?
- 7.** Do you agree with the subdivision below?

**West:** Genotyping: Pullman. Breeding: AZ, CA, ID, MT, NM, NV, OR, UT, WA, WY

**North Central:** Genotyping: Fargo. Breeding: IA, MN, ND, SD, WI.

**Central:** Genotyping: Manhattan. Breeding: CO, KS, NE, OK, TX.

**East:** Genotyping Raleigh. Breeding: AL, AR, DE, FL, GA, IL, IN, KY, LA, MD, MI, MO, MS, NJ, NC, NY, OH, PA, SC, TN, VA, WV.

- 8.** Would you agree with the following assignment of the 18 postdocs and mapping populations? If you disagree please propose alternative scenarios.

**West:** 5

**North Central:** 4

**Central:** 4

**East:** 5

## Tabulated answers questionnaire 1

Question	1.1	1.2	1.3	1.4	1.5	1.5.2	1.6	1.7	1.8	1.9	1.10	1.11	1.1	1.13	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	2.1	
1=Yes 0=No	100% R	75%R 25%MAS	50%R 50%MAS	25%R 75%MAS	GTL maps	Map requirem.	Candidate gene	Position cloning	Assoc. map.	Reverse genetics	Genome sequen.	Perfect markers	SNP	Others	Grant	Fixed	Small: 0 Large:1	\$ Grants	12 breed 4 genot	15 breed 4 genot	18 breed 4 genot	not funded	Match fund	Requir matching	
State	1.1	1.2	1.3	1.4	1.5	1.5.2	1.6	1.7	1.8	1.9	1.10	1.11	1.12	1.13	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	2.10	
MN	Anderson, Jim	0	1	0	0	1	1	0	0	0	0	0	0	0	0	1			0	0	1	1	1	1	
AR	Bacon, Robert	0	0	1	0	1	1	0	0	0	0	0	0	0	1	0	1	50000					1	1	0
KS	Bai, Guihua	0	0	1	0	1	1	0	0	1	0	0	0.5	0	0	1	1	60000		0	0	1	1	0.5	0.5
NE	Baenziger, P. Stephen	0	0	1	0	1	0.5	0	0	0	0	0	0	0	0	1	1			0	0	1	0.5	1	0
KS	Brown-Guedira, Gina	0	0	1	0	1	0.5	0	0	0.5	0	0	0	0	0	1				0	0	1	1	1	1
CO	Byrne, Patrick	0	0	1	0	1	1	0	0	0.5	0	0	0	0	0	1	1	60,000			1		1	0	0
OK	Carver, Bret	0	1	0	0	1	1	0	0	0	0	0	0	0	0	1	1			0	0	1	1	1	1
WA	Campbell, Kim			1		1	0.5			0.5						1						1	1	1	
MD	Costa, Jose	0	0	1	0	1	0.5	0	0	0	0	0	0	0	0	1	1	60,000		0	0	1	0.5	1	1
CA	Dubcovsky, Jorge	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	1	60,000		0	0	1	1	1	1
ND	Elias, Elias	0	0	0	1	1	1	0	0	0	0	0	0	0	0	1				0	1	0	0	0	1
KS	Fritz, Allan	0	0	1	0	1	0.5	0	0	0	0	0	0	0	0	1				0	0	1	1	1	1
WA	Gill, Kuvinder	0	1	1	0	0.5	1	1	0	0.5	0	0	0	1	0	1				1	0	1	0	1	1
SD	Glover, Karl	0	0	1	0	1	1	0	0	0	0	0	0	0	0	1	1	55,500		0	0	1	1	1	1
VA	Griffey, Carl	0	0	0	1	1		0	0	0	0	0	0.5	0		0.5	1	60000		0	0	1	1	1	1
MD	Gustafson, Perry	0	1	1	0	1	1	0	0	0.5	0	0	0	0	0	1				0	0	1	1	1	1
CO	Haley, Scott	0	0	1	0	1	1	0	0	1	0	0	0	0	0	1				0	0	1	0.5	0	0
GA	Johnson, Jerry	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	1			0	0	1	1	1	0
ND	Kianian, Shahryar	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	70,000		0	1	0	0	1	1
WA	Kidwell, Kim	0	0	1	0	1	1	0	0	1	0	0	0	0	0	1		40,000		0	1	0	0	1	1
IL	Kolb, Fred	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1			0	0	1	0	1	0
CO	Lapitan, Nora	0	0	1	0	1	1	0	1	0	0	0	0	0	0	1	0			0.5	0.5	0		1	0
TX	Menz, Monica	0	0	1	0	1	1	0	0	0	0	0	0.5	0	0	0	1	1			0	0	1		0
ND	Mergoun, Mahomed	0	0	0	1	1	1	0	0	0	0	0	0	0	0	1				0	1	0	0	0	1
IN	Ohm, Herb	0	0.5	1	0	1	1	0	0	0	0	0	0	0	0	1	1			0	0	1	0	1	0
OR	Riera-Lizarazu, Oscar	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0			0	0	1	1	1	1
OR	Peterson, Jim	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0			0	0	1	1	1	1
TX	Rudd, Jackie	0	0	1	0	1	1		0	0	0	0	0	0	0	1				0	0	1	0	1	1
OR	Sneller, Clay	0	1	0	0	1	1	0	0	0.5	0	0	1	1	0.5	0.5	0								1
NY	Sorrells, Mark	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	1			0	0	1	0	1	1
ID	Souza, Ed	0	0	1	0	1	0	0	0	0	1	0	0	0	0	1	0			0	1	0	1	0	0
MT	Talbert, Luther	0	0	1	0	1	1	0	0	0	0	0	0	0	0	1	0	50,000		0	0	1	0	1	1
KY	Van Sanford, David	0	1	0	0	1	1	0	0	0	0	0	0	0	0	1	1			0	0	1	1	1	0
	Total	0.0	11.5	26.0	3.0	31.5	26.5	1.0	1.0	7.0	1.0	0.0	2.5	1.0	1.0	1.5	31.0	15.0	565500	15	6.5	24.0	18.5	27.5	19.5
	Average	0.00	0.36	0.79	0.09	0.95	0.83	0.03	0.03	0.21	0.03	0.00	0.08	0.03	0.03	0.05	0.94	0.68	56550	0.05	0.22	0.80	0.62	0.83	0.63

## Tabulated answers questionnaire 2

	Questions	1	2	3	4	5	6	7	8
State	1=yes 0=No	State production	Molec. Expertize	Mapping Pop	Others	Division 4 regio	Regional Coordin.	States to Regions	Postdocs to regions
MN	Anderson, Jim	0.5	1	1		1	1	0.5	1
KS	Bai, Guihua	0.2	0.3	0.5	0	1	1	1	1
NE	Baenziger, P. Stephen	1	1	1		1	1	MO to E, NE	1
KS	Brown-Guedira, Gina	1	1	0.5		1	0.5	0.5	1
ND	Berzonsky, Bill	1	1	1	0	1	1	1	1
CO	Byrne, Pat	0.5	0.5	1		1	1	1	0.5
OK	Carver, Bret	1	1	1		1	1	1	1
WA	Campbell, Kim	1	1	0.5		1	0.5		1
MD	Costa, Jose	0.5	0.5	0.5		1	1	0.5	1
CA	Dubcovsky, Jorge	1	1	1	0	1	1	1	1
ND	Elias, Elias	1	1	1	0	1	1	1	0
KS	Fritz, Allan	1	1	0		1	1	1	1
WA	Gill, Kulvinder	0	1	1	Priority traits	1	1	1	1
SD	Glover, Karl	1	0	0		1	1	1	1
VA	Griffey, Carl		1	1		1	1	1	1
MO	Gustafson, Perry	1	1	1	0	1	1	1	1
CO	Haley, Scott	1	1	0		1	1	1	1
GA	Johnson, Jerry		1	1		1	1	1	1
WA	Jones, Stephen	1	1	1	0	1	1	1	1
ND	Kianian, Shahryar	1	1	0	0	1	1	1	0.5
WA	Kidwell, Kim	0	1	0		1	0	1	1
IL	Kolb, Fred	?	?	?		1	1	1	1
CO	Lapitan, Nora	1	1	0.5	Uniqueness and val	1	1	1	1
TX	Menz, Monica	1	1			1	1		
ND	Mergoum, Mohamed	1	1	1	Need to consider th	1	1	1	0: I suggest 4:5:4
IN	Ohm, Herb	0	1	1		1		1	1
OR	Riera-Lizarazu, Oscar	1	1	1	0	1	1	1	1
TX	Rudd, Jackie	1	1	0.5		1	1	1	1
OR	Sneller, Clay	1	1	1		0	0.5	0	0
NY	Sorrells, Mark	1	1	1		1	1	1	
ID	Souza, Ed	0	1	1		1	1	1	0.5
MT	Talbert, Luther	1	1	1		1	1	1	1
KY	Van Sanford, David	0	1	1		1	1	1	1
	Total 33								
	<b>Average</b>	0.76	0.92	0.74		0.97	0.92	0.92	0.88

**Note:** The original questionnaires contained the comments by the participants within each of the cells