

NRI-CGP. Applied Plant Genomics – Coordinated Agricultural Project (CAP)
"WHEAT APPLIED GENOMICS"

INTRODUCTION

Wheat (*Triticum* spp.) is grown in all regions of the United States, and is directly consumed by humans more than any other grain. Wheat also holds a unique place in the economy of rural America. In the semi-arid regions of our plains it is the dominant crop, sustaining farms where no other crop would survive. In high-rainfall and irrigated agriculture it is an essential rotation crop for other high-value crops. Ten types of wheat are grown in the U.S., including soft red winter (SRW), soft white (winter SWW and spring SWS), club (winter and spring), hard red winter (HRW), hard red spring (HRS), hard white winter (HWW), hard white spring (HWS) wheat (*T. aestivum* L.), and durum wheat (*T. durum* L.). The end-use properties of each class of wheat are different, which has led to targeted breeding efforts for each class.

Private investment in wheat breeding is limited by the self-pollinating nature of wheat and the small yield gains of hybrid wheat relative to homozygous lines, which facilitate the utilization of saved seeds and limit returns on private investment. The insufficient private investment, coupled with the need for continuous wheat improvement to sustain the U.S. rural economy, provide the rationale for developing strong public breeding efforts. The presence of a large, productive, and vibrant public sector involvement in variety development is a unique hallmark of wheat compared with other agronomic crops. According to the last available survey¹, 60% of the wheat breeders were in the public sector, whereas only 7% of the corn breeders and 35% of the soybean breeders worked in the public sector. In addition, **public wheat cultivars accounted for 78% of the wheat production in the U.S. from 2001-to 2003** (<http://maswheat.ucdavis.edu/cap2005/PublicVarieties.htm>), which represents an average of 38 million metric tons per year valued at more than \$ 5 billion. In contrast, a very small proportion of the U.S. maize or soybean production is obtained from public varieties.

The goal of wheat breeding is to combine desirable genes from different lines into new varieties. However, it is often difficult to monitor for the presence of multiple desirable genes during the selection process. Genomics has revolutionized plant breeding by providing tools for high-throughput marker evaluations, which can be used in **Marker-Assisted Selection (MAS)** strategies for variety improvement. Significant progress in this area was achieved by the *MAS*wheat consortium during the last four years. This group, which included researchers from 12 public breeding programs, has used marker-assisted backcrossing to incorporate 27 different disease and pest resistance genes and 20 alleles with beneficial effects on breadmaking and pasta quality into approximately 180 lines adapted to the primary U.S. production regions (300 lines will be completed by the end of 2006).

Funding for public wheat breeding programs is typically provided by wheat growers associations. However, low wheat prices and disease epidemics have reduced the resources available to U.S. wheat growers. Restricted investment in the implementation of new technologies for genetic improvement also has contributed to a significant reduction in the level of U.S. participation in the world wheat export market. Average U.S. wheat exports decreased by nearly 30% during 2000-2004 compared with 1980-1985. In contrast, Australian exports increased by approximately 100% during the same period. Marker technologies have been utilized by our international competitors to improve the consistency and performance of their wheat crop, making the need for rapid improvement of U.S. wheat even more imperative.

The most efficient way to couple the growers' investment in public wheat breeding with the value of new genomic technologies is to fund public sector translational genomics research².

This strategy is well known to our competitors. A National Wheat Molecular Marker Program was initiated in 1996 in Australia (\$15 million) and a similar, more recent program was established in Canada to support high-throughput MAS programs. Ironically, even though our competitors rely heavily on U.S. investments in basic research, they have reaped the benefits of this basic knowledge faster than the U.S. has by directing a large part of their investment to application-based projects. The Australian grain funding board recently recommended dedicating 75% of the MAS investment to implementation projects.

Public wheat breeding programs can improve the competitiveness of the U.S. wheat by using funds from this CAP grant to integrate the improved germplasm developed by the MASwheat consortium, with the new genomic tools and the high-throughput capacity of the recently created USDA-ARS Regional Small Grains Genotyping Laboratories (genotyping laboratories hereafter)³. Four Regional Genotyping Laboratories (Fig. 1) have been equipped with high-throughput equipment to provide genotyping services to the breeding programs. This project will implement a high-throughput forward-breeding MAS strategy in all wheat market classes to accelerate the deployment of valuable traits in public wheat breeding programs. The improved germplasm will be freely exchanged among public and private wheat breeders (see collaboration letters in pages 397-399) multiplying the benefits of the CAP grant and transferring the value of genomic research directly to the wheat growers and the wheat industry. Enhanced quality, including improved nutritional value (e.g. higher levels of antioxidants in pasta wheat), will directly benefit consumers.

Although markers are available for several genes (<http://maswheat.ucdavis.edu/protocols/>), additional markers are needed for the complex traits prioritized by the wheat industry at a recent national workshop (<http://maswheat.ucdavis.edu/PDF/MeetingFeb22.pdf>). Mapping populations generated from adapted parents for each of the various wheat market classes are required to genetically characterize and identify markers for many of these high value traits including grain yield, flour yield, grain protein, and pre-harvest sprouting (PHS) tolerance. The CAP grant provides a unique opportunity for developing the mapping populations required for discovering markers linked to the targeted traits, and for implementing MAS strategies to rapidly deploy valuable alleles across market classes and production regions.

Finally, integrating new genomic techniques into existing public wheat breeding programs provides an opportunity to train the next generation of breeders in translational genomics, to enhance end-users' awareness of opportunities generated by new genomic techniques, and to transfer the benefits of these new tools directly to the wheat fields. The four regional breeding networks proposed here will educate the future breeders in multi-location teams similar to those employed by the private industry (<http://www.hrt.msu.edu/pbsymp/>).

GENERAL OBJECTIVE

The overall goal of this proposal is to transfer new developments in genomics to wheat improvement by combining the expertise of genomics researchers, wheat breeders, and end-users. We envision a multi-state, multi-institutional, and multi-disciplinary network of public wheat breeding programs and high-throughput genotyping laboratories working together to discover new valuable QTLs and genes, and rapidly deploying them into adapted varieties throughout the country using forward MAS strategies.

SPECIFIC OBJECTIVES

Objective 1. Enhance market demand for major U.S. wheat classes through production and end-use quality improvements

- 1.1. Improve bread, pastry, noodle and pasta quality through the utilization of available markers for gluten strength, grain texture, protein content, starch properties, flour and semolina color, and pre-harvest sprouting.
- 1.2. Reduce pesticide use in wheat production through improved host plant resistance using available markers to rapidly deploy resistance genes for fungi, viruses and insects into improved varieties.
- 1.3. Integrate available markers into high-throughput forward breeding strategies.

Objective 2. Create long-term public genetic resources to map complex traits in wheat

- 2.1. Develop mapping populations from superior parental lines for each of the market classes grown in each of the primary production areas in the U.S.
- 2.2. Generate genetic maps covering all 21 chromosomes for each of these populations.
- 2.3. Evaluate populations in multiple environments for the agronomic and quality traits prioritized by the wheat industry, and determine the location of genes affecting these traits through QTL analysis.
- 2.4. Validate and deploy QTLs into germplasm from public wheat breeding programs.
- 2.5. Generate a core collection of genotyped U.S. wheat germplasm for future use in association mapping studies.

Objective 3. Guarantee the competitiveness of U.S. wheat by continuous incorporation of high-value traits into improved varieties using the most efficient technologies.

- 3.1. Analyze mapping population parents with 1800 SNP markers and map polymorphic ones. Compare polymorphism levels and implementation cost of microsatellite and SNPs.
- 3.2. Explore novel strategies for efficiently screening SNPs in polyploid wheat
- 3.3. Foster scientific interactions among wheat genomics researchers and wheat breeders.

Objective 4 (Outreach). Enhance public awareness of the potential of genomics for providing a stable and safe food supply.

- 4.1. Develop hands-on wheat molecular markers courses for public and private breeders, growers, wheat commissioners, millers, bakers and end-users.
- 4.2. Use wheat varieties improved through MAS to showcase the benefits of the genomics revolution to growers, end-users, and the general public.
- 4.3. Incorporate new mapping and genotyping information into Gramene, GrainGenes and the MASwheat web site, and make the information user-friendly for the wheat breeders.

Objective 5 (Education). Enhance student awareness of research and job opportunities in agriculture.

- 5.1. Train graduate students and postdocs in the practical application and integration of genomics-based tools with efficient traditional breeding strategies through regional collaborative networks.
- 5.2. Attract new undergraduate and graduate students to agriculture through their participation in MAS projects and symposia, summer internships and field and industry tours.

RATIONALE AND SIGNIFICANCE

Wheat is unique among major crop plants in that public sector researchers not only conduct the basic experiments that underpin applied genetics, but also are largely responsible for supplying new varieties to U.S. farmers. The link between modern genomics research and variety

development is inherently strong in wheat. A historic challenge in developing a formal interaction between wheat breeders and associated researchers has been the diversity among wheat market classes. However, the genomics revolution is rapidly changing this dynamic. We all work with the same basic genome, and even though different classes of wheat may require specific alleles at certain loci, the tools for analysis are readily transferable across classes. This realization prompted the creation of a successful effort by a group of twelve wheat breeders and researchers from diverse areas of the country (<http://maswheat.ucdavis.edu>) to implement MAS into variety enhancement strategies. One of the goals of the present proposal is to expand this synergistic effort to wheat breeders and geneticists representing the vast majority of wheat acreage in the U.S. This team will work to map, characterize and deploy the complex traits prioritized by the U.S. wheat industry. The inclusive nature of this proposal, and our successful track-record in implementing collaborative programs, place the wheat research community in an excellent position to transfer the benefits of genomic technologies to the wheat farmers.

Although variety development is the most visible aspect of the public plant breeding efforts, germplasm development in the public sector also has major impacts on private wheat breeding efforts (see pages 397-399). Broad based economic development in wheat has largely originated from innovations in the public sector. For instance, of the ten inter-specific translocations involving the introgression of novel genes into cultivated germplasm that significantly impacted U.S. wheat production, nine were developed in public plant breeding programs. These public breeding efforts result in 40 to 60% returns on public research investment⁴, providing convincing evidence of the broad impact of public wheat breeding efforts.

Recent progress in genomics has been cited as the beginning of a new "Green Revolution". However, these discoveries must be deployed into new varieties to realize that potential. The MAS strategy can quickly capitalize on available markers and incorporate valuable traits into elite lines, effectively demonstrating the power of these technologies to the public. Public wheat breeding programs provide an excellent infrastructure for implementing this strategy. Several U.S. universities have hired a new generation of wheat breeders well trained in molecular genetics. The integration of the public breeding programs with the high-throughput genotyping laboratories will create new efficiencies that will directly benefit growers and consumers.

The incorporation of a new generation of molecular markers based on the detection of single nucleotide polymorphisms (SNP) can further increase the throughput of the genotyping laboratories. SNP assays are amenable to high throughput and high levels of multiplexing, which can significantly select multiple traits at low cost. Despite the polyploid nature of wheat, SNPs are being rapidly generated for this species by the NSF wheat-SNP project (J. Dvorak, <http://wheat.pw.usda.gov/SNP/>).

During the last four years (9/01-8/05), the *MAS*wheat consortium has developed protocols for more than 40 molecular markers (<http://maswheat.ucdavis.edu/protocols/>) for resistance genes and quality traits. Marker-assisted backcrossing was used to transfer targeted traits into 180 varieties and breeding lines from ten different market classes. The successful completion of the parental line development phase resulted in the transfer of valuable genes to the best germplasm from each region and market class. These lines can now be used to deploy the targeted genes across the breeding programs using forward breeding MAS technologies. The high-throughput capacity of the genotyping laboratories will provide breeders with the thousands of data-points required for using this approach. Forward MAS strategies are superior to MAS backcrossing because targeted genes are introgressed at the same time that superior gene combinations are created.

Most of the genomic information for wheat is publicly available; therefore, international competitiveness of the U.S. wheat is determined by the speed of implementation of these technologies. This represents both a challenge and a fantastic opportunity for U.S. wheat breeding programs that have the expertise required to successfully utilize these technological advances. As part of the previous *MAS*wheat consortium (ending in September 2005), a large group of graduate students, postdocs, and technicians have been trained in MAS and wheat genetics. With the support of this wheat CAP project these well trained human resources have the potential to capitalize on recent accomplishments by rapidly adopting new high-throughput MAS technologies.

Rationale for Objective 1. Enhance market demand for major U.S. wheat classes through production and end-use quality improvements: Milling and baking quality are major factors in determining the global market share of the U.S. wheat crop. Market competition continues to increase as exporting countries target specific customer end-use quality needs and increase their wheat exports. Grain marketing systems are placing greater emphasis on end-use quality and functionality in determining value. In response, specific aspects of end-use quality must be improved for each of the wheat classes produced in the U.S.

Fortunately, recent advances in our understanding of the genetic basis of various quality parameters will facilitate the manipulation of these complex traits through MAS⁵. We now have “perfect markers” (markers based on the DNA mutations directly responsible for the phenotype) for many of the critical determinants of bread, pasta and cookie quality, including gluten strength^{6,7}, grain texture⁸, protein content⁹, and starch composition^{10,11}. Closely linked molecular markers also are available for several other quality traits (<http://maswheat.ucdavis.edu/protocols/>).

In addition to improving quality, wheat must be grown efficiently to maintain profitability and to provide a reliable supply to local and export customers. The numerous pathogens of wheat significantly increase costs and threaten a reliable supply of high quality wheat. Genetic resistance has been repeatedly proven to be an effective and environmentally sound method for controlling serious yield-reducing pathogens. The use of disease resistant varieties reduces pesticide use and thus contributes to a reduction in environmental contamination¹². Industry and grower representatives have ranked several disease resistance genes as high priority (<http://maswheat.ucdavis.edu/PDF/MeetingFeb22.pdf>).

Accumulating multiple genes for resistance within a plant, which is referred to as "gene pyramiding", and combining seedling resistance (race-specific) and adult-plant resistance (broad spectrum) genes into a single genotype are effective strategies for creating durable resistance¹³. However, gene pyramiding can be difficult without MAS. Once an effective resistance gene is present in a breeding line, it is difficult to select for additional resistance genes due to epistatic interactions. Fortunately, molecular markers can be used to pyramid different resistance genes into elite lines while maintaining preexisting, effective resistance genes. The development of markers and mapping populations for Fusarium Head Blight were excluded from this grant because separate research efforts are funded through grants to the U.S. wheat and barley scab initiative (<http://www.scabusa.org/>).

The recent appearance of new stem rust races in Africa that are virulent on current stem rust resistance genes represents a new threat to the U.S. wheat crop. The development of markers for resistance genes against these new races is a priority for our group. Introduction of these virulent, new races in the absence of resistant germplasm could mirror levels of devastation predicted for Asian soy rust, which was first detected in the U.S. in late 2004. However,

stopping the devastating stripe rust epidemic that is currently generating multimillion dollar losses to wheat crops across the U.S. (\$400 million loss, <http://www.cdl.umn.edu/loss/loss.html>), is much more urgent than preventing either of these potential threats. Our group will focus on the immediate deployment and pyramiding of adult plant rust resistance genes complexes (e.g. *Lr34/Yr18*, *Lr46/Yr29*, *Lr37/Yr17/Sr38*, and *Yr36*), which have a broad spectrum of resistance to various races and have been more durable than single seedling resistance genes. The introduction of multiple and diverse sources of resistance can mitigate unpredictable future pest problems generated by the evolution of the natural pathogens or by the introduction of new pathogens.

Rationale for Objective 2. Create long-term public genetic resources to map complex traits in wheat: Over the last 20 years molecular markers have been developed for several major wheat genes affecting quality, height, flowering time, and disease resistance. However, few markers are available for the complex agronomic and quality traits prioritized by the U.S. wheat industry (<http://maswheat.ucdavis.edu/PDF/MeetingFeb22.pdf>). Since these traits are affected by genetic background and environmental factors, mapping them requires multi-location testing using parental lines from specific market classes. The main wheat mapping population used in the U.S., the “ITMI population”, is a cross between a normal and a synthetic-wheat, resulting in relatively high levels of polymorphism. This population is very useful for mapping large numbers of markers, but it is not appropriate for mapping genes affecting complex traits.

The mapping populations developed for this project will be deposited in the Small Grain Collection to serve as long-term resources for mapping complex traits in the different U.S. wheat market classes. In addition, all of the parental lines will be extensively genotyped (1500 microsatellites and 1800 SNPs) forming the core of a genotyped germplasm collection that will be expanded each year of the CAP grant by 48 genotypes. This will be a useful resource for validating results from future association mapping studies.

Rationale for Objective 3. Guarantee the competitiveness of U.S. wheat by continuous incorporation of high-value traits into improved varieties using the most efficient technologies: Land and labor costs are higher in the U.S. than in most other wheat producing countries and therefore, the competitiveness of U.S. wheat relies heavily upon the rapid implementation of new and more efficient technologies. A new generation of markers, such as SNPs, promises to increase efficiencies. SNPs are facilitating the execution of large-scale genetic association studies in humans, and therefore a large number of SNP detection and multiplexing technologies are being developed for rapid and inexpensive detection. We intend to apply these improved technologies to wheat.

Current costs per data point make SNPs appealing for wheat breeders. However, the polyploid nature of wheat imposes complexities that require dedicated research efforts for SNP implementation. The investment in developing and implementing SNP detection techniques in polyploid wheat also will benefit other polyploid crops facing similar challenges. Finally, this grant will provide a framework to enhance and expand the interactions between basic researchers involved in SNP development and wheat breeders representing most of the U.S. wheat.

Rationale for Objective 4. Enhance public awareness of the potential of genomics for providing a stable and safe food supply: Public awareness of agricultural biotechnology is often limited to the GMO debate. This project will showcase alternative biotechnological tools (MAS) that are being used to support a stable and safe food supply. Development of new varieties and germplasm with improved quality and nutritional parameters, as well as with reduced pesticide application requirements will benefit directly end users, stakeholders, and consumers, providing

tangible evidence for the advantages of the new tools. These varieties will be showcased by extension specialists and breeders at field days across the U.S.

Technology and science are moving so quickly that even trained individuals can be left behind without an adequate program of continuous education. Updated information about new developments and tools in genomics is also a prerequisite for identifying new commercial opportunities and new possible products for the wheat industry. Public wheat breeding programs can play a pivotal role in the education of the wheat industry including small private wheat breeding programs, growers, and end users. Hands-on courses on MAS will help educate the wheat industry about biotechnology and provide a framework for interactions between research laboratories and the private sector.

Rationale for Objective 5. Enhance student awareness of research and job opportunities in agriculture: Within U.S. academic institutions, research and teaching of biological sciences are increasingly focused on molecular or cellular systems that explain form and function across taxonomic kingdoms. The emphasis on model systems, such as yeast or *Arabidopsis*, is understandable, but also erodes *mission-oriented science* at land grant universities. Turning from mission-oriented science towards context-free science has produced students with inadequate understanding of the context and opportunities of agricultural research.

The PDs involved in this proposal are a unique group of instructors and researchers that bridge multiple levels of biological organization. Most PDs lead public breeding programs, and are active in publishing basic and applied research (see attached CVs). Wheat breeders work at the interface between research and implementation and can provide a unique insight to students: how to integrate genomics into the most fundamental unit of economic production, the American farm. The PDs involved in the previous IFAFS grant have trained more than 80 students (<http://maswheat.ucdavis.edu/cap2005/EducationalImpact.htm>).

Many academic departments training plant scientists have reduced the number of faculty with field-based teaching and research appointments, limiting the resources available to train students in the field context of plant sciences. By integrating researchers with diverse expertise into regional educational projects, this proposal seeks to combine resources to train students interested in field-based sciences with sufficient breadth to lead the next generation of crop improvement. This regional approach has the additional advantage of training students as members of a team, which is an essential component of any modern private breeding enterprise, where the majority of the future breeders will work.

PRELIMINARY RESULTS (Support Online information at <http://maswheat.ucdavis.edu/cap2005/>)

Survey of Industry priorities: The wheat research community was the first to prepare the preliminary information required by the CAP projects. At the beginning of 2004 a National Stakeholders Workshop was organized in Kansas City, MO (February 22 2004) to request input from the wheat industry (growers, millers, and bakers), wheat researchers, and wheat breeders about the traits that should be prioritized for future genomics research efforts. The 63 participants of this workshop included 26 public wheat breeders from 25 different states, six representatives for the regional genotyping laboratories, nine representatives from the milling and baking industry, and 19 other wheat researchers and private wheat breeders. The public breeders represented states that produce 93% of the total U.S. wheat crop. The four regional Genotyping Laboratories were represented. Representatives from the National Association of Wheat Growers (NAWG) and the National Wheat Improvement Committee (NWIC) provided input from 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 concerning industry needs. A formal document was prepared to detail the research priorities for each of the different market classes ([http://maswheat.ucdavis.edu/PDF/ MeetingFeb22.pdf](http://maswheat.ucdavis.edu/PDF/MeetingFeb22.pdf)). These priorities served as the basis for the research objectives of this proposal.

Planning grant meeting: A second meeting was held in Denver, CO (August 16-17, 2004) to discuss the best research strategies for implementing the research priorities determined in the previous National Stakeholders Workshop. The meeting was preceded by intense discussions that were summarized in questionnaires distributed by email to all participants before the meeting and that are included at the end of the meeting' report. Participants included 23 public wheat breeders/researchers representing all of the major wheat growing states in the U.S., five scientists from the Genotyping Laboratories, 12 wheat researchers, and the leaders of the Australian and Canadian wheat MAS programs. After two days of discussion a research plan was elaborated and summarized in a detailed report, which constituted the basis of this grant application (http://maswheat.ucdavis.edu/PDF/Denver04_Report.pdf). This document was made available to the Barley, Soybean, and Cotton research communities to assist them in preparing for their own planning meetings which occurred months later.

Mapping populations: 17 populations were selected at the Denver meeting for mapping traits prioritized by the end users (Table 1). Seeds from parental lines were sent to UCD and high quality genomic DNAs were extracted from leaves and distributed to the four genotyping laboratories in May 2005. Seeds were recovered from the same plant used for DNA extraction.

Polymorphism screening: A detailed characterization of the selected common wheat parental lines from Table 1 was completed with perfect markers for major genes for gluten strength (*Glu-1*), grain texture (*Pina* and *Pinb*), starch composition (*Wx*), protein content (*Gpc-B1*), dwarfing genes (*Rht1* and *Rht2*), vernalization genes (*Vrn-1*), Al tolerance (*Al*), and with linked markers for disease resistance genes *H9*, *Lr21*, and *Lr37/Yr17/Sr38*, and *High temperature Adult Plant* (HTAP) stripe rust resistance, and others (<http://maswheat.ucdavis.edu/cap2005/Alleles.htm>).

DNAs are being extracted for 24 resistant and 2 susceptible lines to the new African isolate of stem rust at UCD, the University of Minnesota, and the Genotyping Laboratories at Raleigh and Manhattan. These DNAs will be included in the 1500 microsatellite polymorphism screening that will be conducted during the second year of the CAP grant.

Finally, DNAs for the parental lines (Table 1) have been transferred to the NSF-SNP project to initiate the SNP screening. The PD and two co-PDs from the CAP project are co-PDs of the NSF-SNP project providing a direct link between the two projects (see collaboration letter pg. 365). A total of 4,500 conserved primers, 792 genome specific validated primers, and 428 SNPs are currently available from the NSF-SNP project (based on June 2005).

MANAGEMENT PLAN

J. Dubcovsky (CA), was the PD in the previous USDA-IFAS project including 12 of the participants in this new project; and will be the PD for this new CAP project. He will supervise a project manager and an educational specialist supported by the grant, will be responsible for the overall administration of the budget, and for reporting to USDA. Four Regional Coordinators will facilitate activities at the regional level (Fig. 1). The four coordinators are: L. Talbert (MT), A. Fritz (KS), J. Anderson (MN), and C. Griffey (VA) for the West, Central, North Central and East regions, respectively.

Since the East region, covers a broad geographical area comprised of 16 breeding programs, it was further divided in four sub-regions coordinated by M. Sorrells (Northeast, NY

& MI), J. Johnson (Deep South, GA, AR, LA, SC, & FL), C. Griffey (Mid-Atlantic, VA, NC, MD, KY), and H. Ohm (Corn Belt IN, IL, OH, MO, TN) (Fig.1). Each sub-region received additional funding for quality testing and phenotyping activities to accommodate the needs of multiple breeding programs within each sub-region. The Genotyping Laboratories co-PDs are G. Brown-Guedira (Raleigh, NC), S. Chao (Fargo, ND), G. Bai (Manhattan, KS), and K. Campbell (Pullman, WA).

Responsibilities of the Genotyping Laboratory: The technician assigned to each Genotyping Laboratory will be responsible for providing 20,000 data-points in year one and 25,000 data-points each of the three following years. This will result in approximately 4000-5000 data-points for MAS per year for each of the breeding programs. In addition, the Genotyping Laboratories will collaborate, using their own resources, with the mapping efforts. The ND Genotyping Laboratory is currently screening all 34 parental lines for polymorphisms with 1500 microsatellite markers. This data will be completed prior to the start date of this grant. Genotyping Laboratories also will work with the project coordinator to develop and test new SNP technologies in wheat.

Responsibilities of the mapping laboratories: Each breeding program is expected to deliver 15,000 mapping data points per year (150 markers for 100 lines or 75 markers for 200 lines); phenotypes for all lines from 4-6 environments; 3,000-4,000 MAS samples for the genotyping lab laboratory, and semiannual reports on MAS progress. Each of the breeding programs is expected to provide regular exchanges of ideas and data; actively collaborate with the educational and outreach activities, and assure that students and postdocs are receiving an integrated training.

Responsibilities of the regional coordinators: The regional coordinators have already coordinated the selection of the mapping populations. They will organize one regional meeting each year in coordination with the Wheat Workers regional meetings and will maintain fluid communication among researchers from within each region. The regional coordinators will compile progress reports on mapping and MAS activities within the region every 6 months. They will be responsible for the integration of breeding and educational activities on a regional scale, and for promoting a team approach to solve the problems faced by local breeding programs.

Responsibilities of the project coordinator: The project coordinator (PC) will monitor the advancement of the project every six months and organize one general meeting coordinated with Plant & Animal Genome in San Diego, CA. The PC also will produce yearly reports for the complete project and send it to all participants. The PC will have a research component focused on testing new SNP detection techniques in wheat and will collaborate with the WA genotyping Laboratory in the SNPs in two populations.

Responsibilities of the educational coordinator: The Educational Coordinator (EC) will serve all regions. The EC will travel at least once a year to each region, organize MAS symposiums, conferences, group meetings, coordinate activities for graduate students, organize summer seminars, and help organize the educational activities for students in all regions.

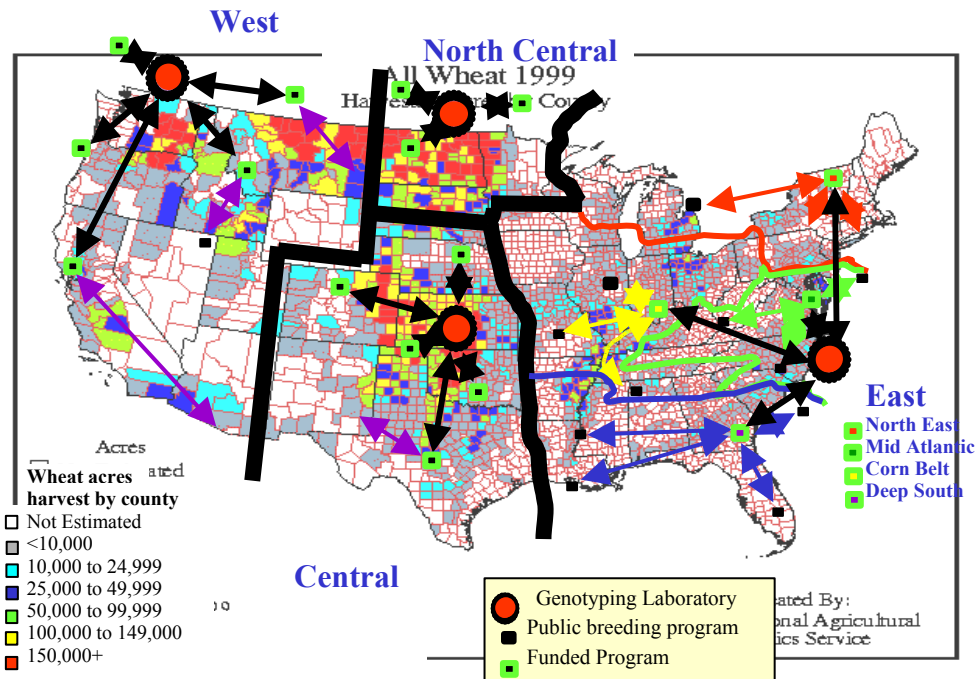


Figure 1. Regional organization of the project. Thick black lines delimit the four regions. Colored lines delimit the four-sub-regions in the East. **Wheat breeders included in this project develop varieties for more than 95% of the U.S. wheat production area.**

Funds will be allocated on an annual basis according to the proposed budgets. Allocation of each year's funding will be dependent on progress towards the consortium's goals. This will be reviewed collectively with input from the Advisory Committee. The AC will include a member of the National Association of the Wheat Growers (NAWG) to represent the wheat growers' interest, and two scientists (D. Somers, Canada MAS program and P. Cregan, Soybean Genomics and Improvement Lab, Beltsville) to provide a scientific evaluation of the progress (see commitment letters pages 378-379). The AC will provide written input and strategic directions to ensure relevance of the results of this project to the U.S. agriculture.

EXPERIMENTAL APPROACH

Experimental approach for Objective 1. MAS will be implemented in the breeding programs using a forward-breeding approach¹⁴. Utilization of markers will vary based on the origin to the target gene donor (adapted or not adapted germplasm) and on the type of cross or breeding strategy used (top crosses, F_2 , SSD, etc.). For example, for a top cross, maximum benefit is obtained by selecting heterozygous BC_1 plants carrying the target gene. This step increases the frequency of the desired allele(s) by 50%, and can be followed by additional cycles of MAS at BC_1F_{2-3} . If a non-adapted parent is used as donor of the targeted gene it is more efficient to delay MAS to field selected headrows. A schematic representation of some of the points where MAS would be used is presented in Fig. 2.

The backcross strategy used during the previous *MAS*wheat consortium was effective for developing improved parental lines within different wheat market classes and to test the agronomic effects of the newly introduced genes in isogenic backgrounds. These lines can be now used for gene deployment in more ambitious forward breeding MAS strategies (Fig. 2). The high-throughput genotyping laboratories will facilitate the implementation of these strategies.

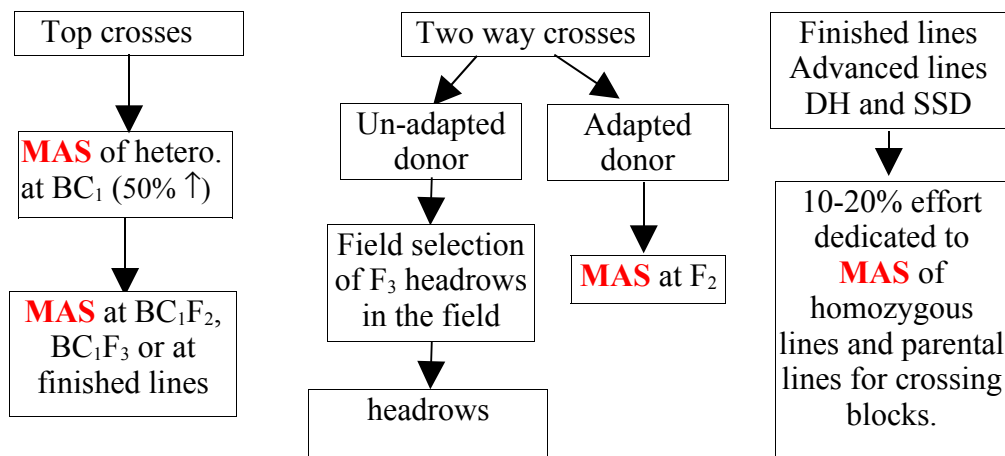


Figure 2. Strategies to integrate MAS into wheat breeding programs.

A detailed plan for the first round of MAS selection in each of the breeding programs is available in a supporting web Table (<http://maswheat.ucdavis.edu/cap2005/MasFirstPoints.htm>). This Table includes detailed information about parents of the segregating populations, number of lines, targeted traits, and markers that will be used in the first **66,000 data points** planned for the first year of MAS. Graduate students and postdocs will work with researchers associated with the local breeding programs. They will participate in the MAS, will collect and submit lyophilized tissue samples to the regional Genotyping Laboratories, and will be involved in field evaluations. They will be also responsible for analyzing the results and discussing them with the breeders.

Experimental approach for Objective 2.

Mapping populations: Mapping populations of approximately 200 individuals genotyped with 200-300 markers will be used to detect QTLs for targeted traits (Table 1). Parental lines have been already screened for several genes (<http://maswheat.ucdavis.edu/cap2005/Alleles.htm>). Double haploids or RILs populations with six or more generations of self-pollination, will be used for the QTL mapping. Parental lines of mapping populations will be screened for stem rust and leaf rust in the Cereal Disease Laboratory (Yue Jin and Jim Kolmer) and for stripe rust in WA (Xianming Chen). See collaboration letters in pages 375-377.

Populations will be evaluated in at least two locations for two years and using two replications within each location to explore G x E interactions. Augmented designs and incomplete block field plot designs will be used to handle the evaluation of the large populations in the field. A significant portion of the time of personnel assigned to the mapping laboratories will be used for detailed phenotyping. Agreements have been made with several national and state wheat quality laboratories for quality evaluations. See collaboration letters in pages 366-374.

QTL analysis will be performed using the public software QTL Cartographer version 2.5 (<http://statgen.ncsu.edu/qtlcart/WQTLCart.htm>). QTL Cartographer has the capability of performing interval mapping, composite interval mapping (CIM), and Multiple Interval Composite Mapping (MIM) and can accommodate the multi-location testing that will be used in this project. Mixed Model SAS programs will be used to incorporate replications within environments and the experimental designs used in each location.

The CAP project also will collaborate with Dr. Yue Jin at the Cereal Disease Lab in the development of mapping populations for resistance genes to the virulent stem rust isolates from Africa (see collaboration letter page 375). The NC Genotyping Laboratory will provide screening and mapping for *Sr22*, *25*, *26*, *27*, *29*, *32*, *35*, *37*, *38*, *39*, and *44* whereas the ND Genotyping Laboratory will provide screening with 1500 microsatellite markers for 13 spring parental lines carrying unknown genes. DNAs of these lines have been extracted at UCD. Polymorphic markers will be used to screen selected bulks of 20 homozygous susceptible and 20 homozygous resistant $F_{2,3}$ lines selected by Dr. Jin. Linked markers will be obtained by Bulk Segregant analysis¹⁵. Breeders will start crosses with donors of *Sr24*¹⁶ and then incorporate additional sources of resistance as new markers become available.

Quality controls: Seeds from the same plant of each parental line used for DNA extraction are being increased at UCD and will be distributed to all the Genotyping Laboratories. Seeds from the parental lines and the mapping RILs or DH will be deposited at the USDA-ARS Small Grain Collection, with backups at the originating laboratories and at the wheat Genetics Resource Center, Kansas State University (KS).

Each of the submitted lines will be characterized with a set of eight polymorphic microsatellite markers. The same markers will be used to confirm the correct identity of the lines evaluated in the field to rule out planting and/or harvesting errors. In addition, the breeder that developed the mapping population will characterize the lines for morphological markers to facilitate line identification during subsequent field trials.

QTL validation and implementation strategies: QTL validation and implementation will start as soon as reliable QTLs are identified. Based on heritability, preliminary results, and economic value, each breeder will prioritize one or two traits that will be included in the validation and implementation strategies. One of the following strategies will be used depending on QTL characteristics and objectives.

The main objective of the first validation strategy is to generate populations for future fine mapping of the selected QTLs and simultaneously develop materials and preliminary data for future positional cloning projects. This strategy is appropriate for QTLs with large phenotypic effects and high economic value. To have genetic materials ready by the time the QTLs are discovered the following materials will be produced as soon as the grant is funded. An F_1 similar to those used to produce the mapping populations will be backcrossed twice to each of the parents. DNAs will be extracted from 40 BC_1 and 40 BC_2 plants. BC_1F_2 and BC_2F_2 seed will be saved. Once the desired QTLs are identified, BC_2 lines heterozygous for both flanking markers will be selected ($P > 0.99$). The corresponding BC_2F_2 will be the starting point for the high-density mapping population. Additional BC_2F_3 seed will be produced from selected BC_2F_2 heterozygous plants. Five hundred $BC_2F_{2,3}$ lines will be tested for recombination within the QTL region. Selected plants will be self-pollinated and homozygous recombinant and non-recombinant near isogenic $BC_2F_{3,4}$ lines will be selected and used for dissection of the QTL. The increased genetic homogeneity of the BC_2F_3 near isogenic lines (94% homozygous) will facilitate a precise mapping of the QTL, generating the necessary preliminary results for future positional cloning efforts. We have used a similar strategy before to precisely map a QTL for high-grain protein content within a 0.3-cM interval^{17,18}. We have also demonstrated that positional cloning in wheat is possible^{19,20}. UCD will offer a 3-day course on positional cloning in wheat for participant interested in this strategy.

The second strategy is aimed at the immediate deployment of QTLs in breeding programs by determining the usefulness of the detected QTLs in different genetic backgrounds. Parental lines will be crossed with the best breeding lines. The progenies from these crosses will be

advanced to F₄. Once the flanking markers for a QTL are established, they will be used to search for F₄ lines heterozygous for the targeted region. These lines will be self-pollinated to generate segregating populations of near isogenic lines. The effect of the QTL region will be then evaluated in these different genetic backgrounds. This procedure directly incorporates the selected QTLs into the breeding activities, provides a robust test of QTL effects in relevant germplasm, and accelerates the release of improved varieties.

Depending on the traits and the growth habit of the population, the phenotypic evaluation of the new recombinant lines may extend beyond the end of this grant. The main objective of the validation activities is to generate the lines for the fine mapping of the QTLs and/or for the incorporation of the QTLs in different breeding lines. These lines are important for the breeding programs, and breeders will continue their phenotypic evaluation beyond the end of this grant.

As part of the implementation strategies, each breeding program will characterize haplotypes of at least 20 cultivars or advanced breeding lines for the region of the selected QTLs, using available SNP and microsatellite markers. Because of the large linkage blocks present in elite wheat germplasm the use of 5-6 markers within 10-cM regions generally provides useful estimations of QTL alleles present in a particular breeding line (D. Somers personal communication). This haplotype characterization will be used to select germplasm more likely to benefit from the incorporation of the QTL. In addition, the haplotype analysis will identify putative new alleles that will be compared with the ones in the mapping population.

Experimental approach for Objective 3

We currently use microsatellite markers because they are abundant (>2000), polymorphic, have been mapped in wheat, and are relatively simple and inexpensive to use. However, we are aware that new SNP technologies have the potential to become cheaper and to achieve higher multiplexing levels than microsatellites. Therefore, we propose to explore the application of different SNP technologies to incorporate these markers into the wheat maps (Table 1, marked by *). We have established a collaboration with the NSF-Wheat SNP project led by Dr. Jan Dvorak and budgeted the screening of 24 parental lines with 1800 SNP markers using the SNaPshot technique (ABI SNaPshot ddNTP primer extension kit, manual).

To solve the problem imposed by polyploidy, the SNaPshot technique in wheat involves two steps. First, genome specific primers are generated and then, the SNaPshot analysis is performed in an aliquot of the first PCR. Most SNP multiplexing strategies in wheat will likely have to include this two-step procedure, and can be optimized at each of the steps. The four genotyping laboratories and the project coordinator will be responsible for evaluating SNP detection techniques and for the incorporation of at least 50 polymorphic SNP markers in three mapping populations per region (Table 2). The project coordinator will collaborate with the NSF-SNP project and WA genotyping center in the exploration of SNaPshot multiplexing strategies combining different dyes and primers lengths.

Table 2. Laboratories responsible for SNP mapping, and SNP technology.

	CA&WA	ND	KS	NC
Populations	CA, ID, WA	ND, ND/SD, MN	CO, NE, KS	IN, NY, VA
Technique	SNaPshot multiplexing	Fluorescent polarization	SNaPshot multiplexing	SNaPshot multiplexing

Outreach Plan for Objective 4.

The *MAS*wheat consortium has a proven track record of outreach activities including approximately 100 field days and presentations to wheat growers and end-users and 38 peer reviewed scientific publications (<http://maswheat.ucdavis.edu/Production.htm>). One of the most powerful outreach tools of the *MAS*wheat consortium has been the presentation of *MAS* improved lines (<http://maswheat.ucdavis.edu/Germplasm/index.html>) to growers and end-users during field days across the U.S. Growers have been particularly impressed by the side by side presentation of susceptible and resistant near-isogenic lines developed through *MAS*. In addition, we have included *MAS* improved lines in collaborative quality testing programs with industry that convinced millers and bakers of the advantages of precisely engineering quality traits. If the CAP project is funded, we will expand these two successful outreach activities to all of the U.S. public wheat breeding programs. The educational coordinator will prepare a brochure on *MAS* that will be distributed during field days across the U.S. to improve the outreach efforts. Individual programs within the CAP project will produce a single page addition to the brochure including local information on the benefits of *MAS*. This outreach model will continue as an integral part of the CAPS program with each co-PD making at least two field days and stakeholder presentations every year.

Hands-on, one-day courses on wheat molecular markers have been an effective tool for educating growers and end-users in new genomic technologies. Wheat commissioners, millers, bakers and end-users with no previous training in biology, perform DNA extractions from local wheat varieties, do PCR reactions for markers relevant to the region, and select lines carrying the beneficial gene using gel electrophoresis. Participants typically are surprised by the simplicity of the procedures and enjoy the experience (e.g. <http://maswheat.ucdavis.edu/achievements/images/CAGrowersWorkshop.htm>, http://www.agls.uidaho.edu/cerealsci/grower_workshop.htm). These courses favor the exchange of ideas between breeders and growers and forge excellent personal relationships. Finally, we will continue with the development and enhancement of the *MAS*wheat web site, which is an outreach portal, widely used by public and private wheat breeders all over the world (see support survey at <http://maswheat.ucdavis.edu/cap2005/Survey.htm>).

The mapping and genotyping information generated by the project will be incorporated in GrainGenes and Gramene. Funding has been allocated for the development of a web submission service that will be directly integrated with the ‘Grainotypes’ database (see Data Management). S. Chao, a previous member of GrainGenes and current member of our CAP grant will be responsible for the interactions between our project and GrainGenes (see attached collaboration letter page364). The incorporation of U.S. wheat genotyping information from all market classes will improve *MAS*wheat and GrainGenes’ value to wheat breeders worldwide.

Educational Plan for Objective 5.

Consumers in the U.S. are increasingly disconnected from their food supply due to urbanization. This disconnect causes a lack of appreciation and awareness, which in turn results in lack of public concern and funding and in a reduced number of students interested in

agriculture. The goal of our educational program is to bridge this gap and attract a new generation of students to agricultural research. Students will participate in the following activities 1) regional field and industry tours; 2) short exchange projects for graduate students among regional universities; and 3) short work-study projects for undergraduates of underrepresented groups or students outside traditional crop production related fields.

Regional field and industry tours: Each year we will provide the opportunity for 10-20 college students in each region to connect with each step in food production, using wheat and wheat products as a model system. We also will invite high-school teachers and future educators to participate in these tours, so that this acquired appreciation will be shared. Every year over the lifetime of the grant one group within each region will organize a field trip that encompasses all levels of production including: 1) Research and development – Field day presentations at Experiment Stations detailing applied agricultural research; 2) Production - At least one farm where growers can demonstrate production strategies; 3) Transportation – Grain elevator or some other part of the transportation grid; 4) End use – a mill and a bakery or noodle company; 5) Government – The students will meet with a commodity group or legislative body to gain an understanding how the government affects grain production. The educational coordinator will help organize these tours and will seek additional financial support from the participating companies and organizations to increase the frequency of these tours. A budget has been assigned to each regional coordinator to cover local expenses. This program is based on an educational program successfully implemented at Montana State University (http://maswheat.ucdavis.edu/achievements/images/MT_outreach2.htm).

Exchange projects: The educational coordinator will work with the universities within each region to coordinate training programs in plant breeding and to develop collaborative activities and student exchange visiting programs.

Work-study projects for undergraduates of underrepresented groups: The educational coordinator will organize activities to train and attract minority students. Summer internships will be implemented in each laboratory if possible in collaboration with locally funded genomics grants from USDA and NSF. Examples of activities from our group within this area are the summer internships for Community College students (http://maswheat.ucdavis.edu/achievements/images/UCD_intern.htm) and the hands-on laboratory visits organized for Native American students (http://maswheat.ucdavis.edu/achievements/images/MT_outreach.htm). The genotyping and phenotyping activities related to the mapping populations provide a unique opportunity to give students experience in both lab and field settings.

Graduate students and postdocs training: Postdocs and graduate students from all programs will go to North Carolina State University for a 4 day course on QTL analysis, (http://statgen.ncsu.edu/brcwebsite/summer_institute_ral.php#10) offered by the ‘QTL Cartographer’ developer Dr. Z.-B. Zeng. An additional short course on positional cloning in wheat will be offered by the PD at the beginning of year 3. Laboratories with previous experience in MAS will share their experience in a 2-3 day hands-on workshop for postdocs and graduate students from other regional breeding programs. Postdocs and graduate students will be trained in high-throughput technologies by the Genotyping Laboratories; and also in traditional breeding techniques to increase their future job opportunities.

Symposia and meeting organization in Marker Assisted Selection: The project coordinator will propose MAS symposia for the CSSA meeting in 2006, the AAAS Symposium in 2007, and the Cereal Chemistry Symposium in 2008.

DATA MANAGEMENT PLAN

This project will provide an unprecedented data set regarding the genetic basis of variation for important traits in wheat. A natural connection among the experiments outlined here is the use of the same set of DNA markers and collection of a core agronomic data set across genotypes. Maximum use of this information will be coordinated by the incorporation of all the germplasm, mapping and allelic information into the 'Grainotypes' database, GrainGenes, and from there into Gramene. GrainGenes is currently collaborating with Gramene on the development of a new Gramene database module for genotyping and phenotyping data from wheat, rice, maize and other grass species, using the 'Genomic Diversity and Phenotype Data Model' (GDPDM, <http://www.maizegenetics.net/gdpdm/>).

Personnel from laboratories participating in the CAP grant will be trained to submit the mapping information to the Fargo (ND) Genotyping Laboratory in a format ready to be deposited in GrainGenes and Gramene. Mapping laboratories will submit their mapping information every six months. The database for the project will be coordinated with the database for the Genotyping Laboratories. A web data service with a similar structure as the one created for the NSF wheat EST project (<http://wheat.pw.usda.gov/NSF/>) will be created to upload the samples for the Genotyping Laboratory and download the results (Fig. 3).

Each breeder will upload the information for each sample to a password protected web site using an Excel file with a predetermined format. Samples will be submitted in 96-well format. The file will include 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 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 laboratory 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.

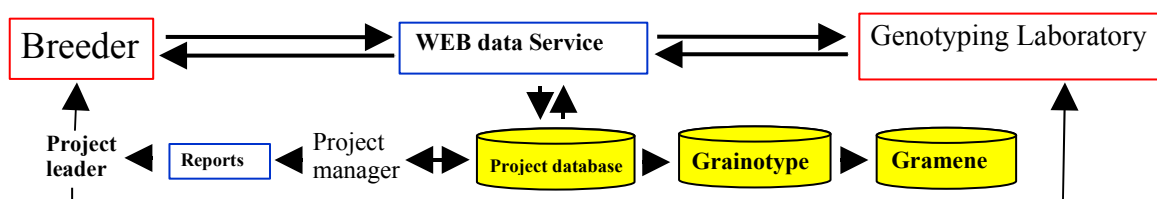


Figure 3. Web data server and information flow

Project members 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 (see collaboration letter page 364).

INTELLECTUAL POLICY AND PUBLICATION POLICY

Germplasm: Each university will retain rights to the varieties that they develop through MAS and can protect them via Plant Variety Protection (PVP). Germplasm will be made freely available for crossing under the Wheat Workers' Code of Ethics

(<http://wheat.pw.usda.gov/ggpages/awn/44/Textfiles/WWCOE.html>). Released lines will be sent to the USDA-National Small Grain Collection for distribution.

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, the QTL data will be made publicly available through GrainGenes and scientific journal articles.

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 Laboratory that performed the parental screening or that contributed to the mapping effort will be a coauthor of that publication. If other breeding programs, quality laboratories or disease resistance laboratories contribute phenotypic data, they also will be included in the publication.

MAS developed varieties of germplasm. If a member of a Genotyping Laboratory 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 included in authorship.

EXPECTED OUTCOMES

- An integrated multi-state breeding collaboration.
- Superior wheat germplasm adapted to all U.S. production regions and in all market classes.
- Improved molecular markers and SNPs for marker-assisted breeding.
- An integrated National Program of Marker Assisted Selection in wheat.
- Increased public awareness of the benefits of genomics.
- The next generation of plant breeders.
- A MAS web site integrated with GrainGenes and Gramene.
- Enhanced understanding of the genetic basis of complex traits in wheat.

The high relevance of this project to the U.S. wheat industry is documented by support letters from national associations of growers, exporters, bakers, and millers; breeding and food companies; and state organization from 24 wheat growing states (pages 381-399).

TIME TABLE

	Year One	Year Two	Year Three	Year Four
Marker implementation	-----			
SNP screening	-----			
SNP Mapping		-----		
Map development	-----			
Trait evaluation		-----		
QTL analysis		-----		
QTL validation			-----	
Education and outreach	-----			

Table

1

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.	2 CA (2 years each).
OR	OR9900553	SWW	Stephens	SWW	165	F5:6	Extra soft texture, HTAP stripe rust, and yield.	2 OR, 2 WA, 2 ID
ID*	Rio Blanco	HWS	IDO444	HWS	300	F7:8	HTAP stripe rust, Hessian fly, baking and milling quality, starch, and yield.	ID, UT
WA*	Louise	SWS	Penawawa	SWS	200	F2:F6	Stripe rust, quality, and yield.	2 WA, CA
MT*	McNeal	HRS	Thatcher	HRS	125	F6:8	Stripe rust, milling and backing, yield.	MT, ID, WA
CO*	Plate	HWW	CO940610	HWW	250	DH	Milling, baking, Asian noodle quality.	CO, KS, OK, TX
TX	Weebill	HRS	Jupeteco	HRS	200	F6	Leaf rust resistance.	Mexico, TX
OK	2174	HRW	Jagger	HRW	275	F ₅ derived	Germination, FHB, rust, BYDV, WSMV, Al tol., lodging, shattering, Pm, dough strength, absorption, milling, test wt.	3 OK, 2KS , CO, TX
KS*	Heyne	HWW	KS01HW163-4	HWW	250	DH	PHS, FHB, Septoria leaf blotch, tan spot, WSMV, WSSMV, tolerance to drought, winter hardiness and end use quality	2KS, CO, OK, NE
NE*	Tam105	HRW	Jagger	HRW	250	DH	Drought, strip rust, WSMV, WSSMV, Septoria, tan spot, quality, vernalization, hardiness, shattering, & acid soil tol.	2 NE, 3 OK, 2 KS, CO, TX
ND/SD	Steele-ND	HRS	ND735	HRS	212	F2:8	Tan spot, FHB, shattering, and lodging	SD, 2ND
ND*	Maire	Durum	Rugby	Durum	190	DH	Gluten strength, pasta quality.	2NS
MN*	Grandin* 5/ND614	HWS	NY/Clark's Cream RIL40-1	SWW	101	BC1F8	Pre-harvest sprouting.	2 MN, SD
NY*	NY Cayuga	SWW	Caledonia	SWW	220	DH	Milling and baking, PHS, yield, height.	1NY 1 MI
IN*	P91193	SRW	P92201	SRW	200	F8:11	Septoria, rust, powdery mildew.	IN, NC, OH, VA, IL, MO.
VA*	USG3209	SRW	Jaypee	SRW	290	F8:9	Powdery mildew adult plant resistance.	VA, NC, MD, KY
GA	SS 550	SRW	26R46	SRW	150	F5:8	Stripe rust, WSSMV, milling and baking traits.	GA, AR, LA

* 12 populations included in the SNP polymorphism analysis.

Detail information about the common wheat parental lines is available at <http://maswheat.ucdavis.edu/cap2005/Alleles.htm>

LOX: lipoxygenase activity; HTAP: high temperature adult plant resistance; FHB: fusarium head blight; BYDV: Barley yellow dwarf virus, WSMV: Wheat Streak Mosaic virus; WSSMV: Wheat Spindle Streak Mosaic Bymovirus; Al tol.: Aluminum tolerance; Pm: Powdery mildew; PHS: Pre harvest sprouting.

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