

T-CAP Quarterly report May 23, 2011

One page executive summary

Genotyping

Genotyping platforms including 9000 molecular markers have been developed and tested successfully for both barley and wheat. Genotyping of the core collections for both crops (~7000 accessions) is on track to be completed by the end of year one. This will provide a detailed description of the genetic composition of the US wheat and barley germplasm.

Genotyping of a winter wheat association mapping panel and of a collection of 5000 wheat breeding lines with the 9000 SNP chips has been completed. These markers are being used to identify associations with important agronomic traits.

An international consortium of barley and wheat geneticists developed an agreement with Roche-Nimblegen to create Gene Capture technology for both wheat and barley. A successful pilot study was completed and a paper has been submitted.

We have trained several different genomic selection models in barley for agronomic, disease, and grain quality traits. A manuscript comparing different GS models was submitted to Genetics.

The T3 database was established to accommodate the initial data. A user group has been formed and has defined templates and pipelines to upload data to T3. This database will be a central hub for the US barley and wheat breeding programs.

Phenotyping

540 wheat accessions from the core NSGC have been planted in 3 environments in Aberdeen and are being evaluated for water and N use efficiency using Canopy Spectral Reflectance (CSR).

A CSR workshop was completed (40 participants). The first drought experiments confirmed the usefulness of CSR to detect differences in drought tolerance among wheat cultivars.

New genes for resistance to stripe rust have been identified and published. A high-density map of the *Yr48* resistance gene was completed and the positional cloning of this gene was initiated.

1000 lines of the barley and wheat core collections are being evaluated for stripe, leaf and stem rust. The barley lines are also being evaluated for spot blotch and for the spot form of net blotch.

Education

The Plant Breeding Training Network has been launched and is being used. About a dozen graduate students have been meeting regularly to help test the PBTN, and in the process have begun to build community and share ideas.

The Education team and evaluators had a successful meeting with representatives from Minority Serving Institutions (MSI) to establish collaborations. MSI recommendations made through a focus group were implemented in the creation of a request for proposals (RFP). The RFP was distributed to about 80 MSIs and we have received 12 proposals that are being evaluated.

The education team organized a successful launching meeting in San Diego, a CSR training in Denver and published the first issue of the educational newsletter.

Nine manuscripts have been accepted for publication and 6 germplasm have been released.

Detailed progress report

Progress is described by objectives and by deliverables proposed for the first year of the project. Publications and released germplasm are listed at the end of the report

Progress by genotyping deliverables

- ***Deliverable: Genotyping with 9000 SNP chip barley (2,571 acc.) and wheat (4,331 acc.) NSGC core collections and AM panels***

DNAs have been extracted from the 6900 accessions from the core barley and wheat NSGC collections and are ready for genotyping. Barley NSGC samples have been shipped to Fargo ND (25.5 plates of samples) to start genotyping by May 30, 2011. Genotyping for wheat is expected to start in June 2011.

Two 9000- SNP chips have been developed for wheat and barley. Initial testing of these SNP platforms showed excellent results. Large-scale orders have been placed to complete the NSGC core collections for wheat and barley.

More than 5000 wheat breeding and mapping lines were genotyped with the 9000 SNP chip in collaboration between the T-CAP wheat breeding programs and USDA-AFRI wheat SNP project (PI: Akhunov). A manuscript describing the 9,000 SNP assay development has been submitted.

The genotyping of the winter wheat Association Mapping panel with 9000 SNPs has been completed providing a powerful tool to map drought (CO), disease (KSU) and NUE (NE). Several programs have sent parental lines of their mapping populations for the 9K SNP screening, including some of the CAP populations.

- ***Deliverable: Marker assisted selection (MAS) with smaller SNP chips***

Barley: barley materials and SNP information was provided by Kevin Smith and chips will be tested by the end of May 2011. Additional optimization will be done during the summer.

The WA and KS genotyping laboratories are testing SNP panels for the Sequenom platforms to characterize Midwest six-row barley and materials from OR. The genotyping labs are also testing out seed DNA isolations from barley in preparation for GS this fall.

For the 384 SNP chips, eight 96-well plates of barley breeding lines are scheduled for the fall and eight for the winter.

Wheat: 25 SNP linked to important agronomic and quality traits are being tested (2nd round) using hard winter wheat materials from regional nurseries.

The design of additional 48 and 384 chips is waiting for the analysis of the 9000 SNP data. Until these data become available SNP-based markers are being selected based on reports from the literature. A list of useful SNP in agronomically important gene has been compiled for wheat.

A graduate student at Raleigh NC is looking at LD in a set of lines included in a panel tested with SNP, SSR and STS markers linked to previously mapped valuable QTLs and translocations. SNP with high LD with the useful SSR markers will be selected.

Progress by technological deliverables

- ***Deliverable: gene capture and genotyping by sequencing (GBS) technologies evaluated in barley and wheat.***

An international consortium of barley and wheat geneticists developed and signed an agreement with Roche-Nimblegen to create liquid Gene Capture technology for both wheat and barley. The Gene Capture technology will provide the opportunity to assess the variation at most of the genes in the wheat and barley genomes for hundreds of lines in the germplasm collections. This technology will be developed and tested over the period of fall 2011 – winter 2012.

The bioinformatical and statistical approaches for variation discovery in sequence data generated by Gene Capture technology was developed and experimentally validated for tetraploid and hexaploid wheat genomes. The manuscript describing nucleotide sequence and gene copy number variation discovery in tetraploid wheat genomes is submitted (Saintenac et al., 2011).

The approach for genotyping wheat and barley lines using next-generation sequencing technology has been tested and now is being expanded to genotype diverse sets of lines and mapping populations in wheat and barley. Two mapping populations are being genotyped by sequencing in wheat (ITMI mapping population) and barley (Oregon Wolfe Barley mapping population) with the expected delivery of data in summer 2011. These maps and diversity data will include hundreds of thousands of genotyping data points allowing for high-resolution dissection of marker-trait associations in the TCAP.

- ***Deliverable: Start barley genomic selection (GS).***

Approximately 60 crosses were made last fall to construct the cycle 1 population for the winter barley GS breeding project. The F₁'s were grown in the greenhouse and the F₂'s were planted this spring in the field in St. Paul, MN. The parental lines are being genotyped with 1,536 SNPs. Results from this screening will be used to design the 384 SNP in June 2011. The first cycle of GS on F₃'s using the 384 SNP will begin this fall.

We have trained different genomic selection models on agronomic, disease, and grain quality traits obtained from the Barley CAP. In cross-validation tests, correlation between the predicted and observed phenotypes ranged between 0.5 (for yield) and 0.7 (for plant height) using training populations of 300 individuals.

A manuscript was submitted to Genetics comparing different models for genomic selection in plant breeding

- ***Deliverable: a user group that will propose, describe, and prioritize data access, analysis, and visualization tools, test new applications and identify educational needs.***

A user group has been formed and has met several times. We have defined how data will be uploaded to T3. The templates and pipelines we have developed can be used for data from TCAP-funded experiments *and* for individual breeding program data. In the next 2-3 months we will have hired a database programmer and will initiate processes for the user group to propose new functionality to be implemented.

- ***Deliverable: an adapted Triticeae Toolbox (T3) database system***

The entry web site for T3 was developed at <http://triticeaetoolbox.org/>. It links to The Hordeum Toolbox for barley and to the future wheat data for wheat. . The Hordeum Toolbox is the

database used in the Barley CAP. Thus, the basic structure of T3 is already in place. The underlying computing infrastructure is being provided and maintained by GrainGenes. The first wheat dataset will be uploaded within a month.

T3 User Group members also have access to a beta version of T3 at <http://feline.pw.usda.gov/t3/wheat/>. In the next 2-3 months, we will begin implementing analyses of genotypic data. Such analyses will include:

1. Line selection based on clustering genotypic data
2. Haplotype searches
3. Dendrogram construction
4. Identification of subpopulation structure
5. Missing marker imputation
6. Identification of genotyping errors

Finally, we have begun implementing a download interface to send data to TASSEL, the iPlant environment, and JMP Genomics

- ***Deliverable: A database website to upload and download data, run basic data quality checks, and incorporate data that passes those checks to the database.***

Data upload is partially available at <http://triticeaetoolbox.org/wheat/>. Recent deliverables of the T-CAP database are the development of data input sheets for the wheat and barley phenotype data to be collected in the TCAP and curation protocols to handle the data.

- ***Deliverable: Tools to accommodate next-generation sequencing data.***

We will have hired a database programmer in the next month, at which point we hope to make progress on these tools. We are in communication with other groups who are working on this same issue and hope to leverage their solutions.

- ***Deliverable: A project curator that monitors data quality.***

We are currently making progress toward hiring an experienced curator and hope that will be accomplished by the end of June. Hiring of new USDA personnel is a complex process that required several steps.

In the next 2-3 months, we will have debugged data upload procedures. Spreadsheet templates will be in place, each with instructions. A detailed description of the overall upload sequence from importing information on new lines, genotypic data, trial annotations, trait definitions, and experimental phenotypes will be available. In the next three months, the database will begin to receive data from the TCAP. In addition to the data that is obtained from the TCAP, T3 will also be expanded to handle individual breeding program data.

Progress by phenotyping deliverables

This section describes first the efforts to phenotype the barley and wheat core collections at the NSGC, and then the progress in the three major phenotyping areas: 1) water use efficiency, 2) nitrogen use efficiency, and 3) disease resistance.

- **Deliverable: NSGC spring wheat core collection evaluated for yield, NUE and WUE under three different treatments.**

540 spring wheat accessions from the NSGC core collection and five widely grown checks were planted in an augmented complete block design in a drip irrigation nursery at Aberdeen, ID. The design was replicated under three different water/nitrogen treatments: normal water and normal nitrogen, terminal drought and normal nitrogen, terminal drought and low nitrogen. These lines are being evaluated for yield, water and nitrogen use efficiency using normalized water and nitrogen indices (NWI and NNI) determined with a multiple spectral radiometer.

The 540 lines and 5 checks are currently being assessed for coleoptile length (CL) and seedling root length (RL) and root numbers (RN) in a lab germination test. Data of CL, RL, and RN will be correlated with the CSD data from the field evaluation. Phenotypic and genotypic data will be used for association mapping after harvesting. A Ph.D. student was recruited for this work.

Phenotyping for water use efficiency

- **Deliverable: dedicated spring wheat populations evaluated for CSR and WUE.**

Experiment 1: Two varieties of wheat (Attila and Hahn) containing the 1RS.1BL translocation were compared with near isogenic lines (NIL) contain a 1RS arm engineered with two interstitial 1BS chromosome translocations in the *Sec1* and *Gli-B1* loci (henceforth, 1RS-MA). Previous results showed that the complete 1RS lines had higher yield under water stress than the 1RS-MA isogenic lines. Two independent experiments were performed in CA in 2011 comparing irrigated and terminal drought environments (RCBD with 6 blocks). Lines were evaluated using Canopy Spectral Reflectance (CSR) with the new JAZ spectrophotometers. Water indexes NWI-1 (see figure) and NWI-3 were calculated from the infrared part of the spectrum. Lines with the



complete 1RS segment showed significantly better water indexes than the lines with the engineered 1RS-MA ($P < 0.0001$).

Differences were significantly larger in the dry environment than in the irrigated environment ($P < 0.0001$). These results indicate that the 1RS chromosome segments replaced in the 1RS-MA engineered chromosome include the gene for drought tolerance. This experiment showed that the selected CSR equipment is adequate to detect differences in drought tolerance.

Experiment 2: NILs for three semi-dwarf genes, including *Rht8* which has been suggested as a source of early vigor and drought tolerance, were planted in replicated experiments in environments with diverse water status at four locations in Montana, two locations in Washington, and two locations in California. Lines with the *Rht8* gene showed increased lodging indicating that it might not be a good source of drought tolerance in the tested locations.

Experiment 3: NILs for solid versus hollow stems were planted at two Montana locations. The solid stem trait is hypothesized to confer drought and heat tolerance due to storage and remobilization of water soluble carbohydrates.

Experiment 4: NIL for a QTL conferring extended green leaf duration were planted in replicated trials in two Montana locations.

Experiment 5: Controlled environment experiments using chromosome substitution lines involving wild relatives of wheat were established in Kansas. A subset of the lines has also been planted in Montana.

Experiment 6: Recombinant inbred line populations derived from a cross between drought-tolerant durum wheat (tetraploid) and drought-tolerant spring wheat (hexaploid) have been planted in an augmented design in Montana. The trial includes approximately 100 hexaploid and 100 tetraploid RIL. The goal is to identify favorable alleles for transfer between ploidy levels. Seed produced this year will be sent to cooperators in 2012 for additional replicated trials.

- ***Deliverable: seed increased for the barley populations to be evaluated for CSR and WUE***

Spring 2-row and 6-row panels: Due to herbicide damage in the Yuma seed increase, extensive phenotyping of the spring 2-row and 6-row panels will be deferred until 2012. The available seed was sufficient for a limited phenotyping in 2011 of the 2-row AM panel in MT in non-irrigated environments (Tom Blake). The same lines will be evaluated under low and high nitrogen.

Facultative 6-row AM panel: Seed increases are underway for 2011 fall planting as planned.

Barley low temperature tolerance (LTT) experiments: The Barley World Core will be planted as planned in fall 2011 in Oregon and Minnesota (NSGRC will supply seed).

LTT Panel: Germplasm was solicited from around the world. ~ 500 accessions were recommended by prospective cooperators and 384 accessions selected. The SCRI has agreed to provide seed of 344 accessions. This germplasm has not been phenotyped for LTT before.

Wild barley introgression population. 700 BC₂F₄ lines, derived from crosses of 25 wild barley accessions with the six-row spring barley Rasmusson, are being grown this summer in St. Paul for seed increase and to sample single plants for DNA isolation. Genotyping of these lines with a custom 384 SNP chip will be in the fall.

CSR training: Approximately 13 individuals representing the barley and wheat WUE group attended the CSR training in Denver in April. One machine is in operation (Dubcovsky, see results above), and results have been used to refine the configuration of machines which have been ordered by the rest of the WUE group.

- ***Deliverable: Seed increases for the wheat AM drought and elite panels.***

A spring wheat elite AM panel containing 250 experimental lines was established in an augmented design in Montana. Seed from this trial will be the source for 2012 trials. This trial contains lines from major spring wheat programs in Canada, the US, and Mexico. In addition to seed increases this trial will be used to provide preliminary agronomic, canopy spectral reflectance and canopy temperature depression data.

The winter wheat association mapping panel is being increased in Yuma AZ,

- ***Deliverable: Completed crosses and first SSD generation for the spring NAM populations and crosses for the winter NAM population***

A total of 50 lines, including 38 landrace accessions and several elite lines, have been crossed to the CIMMYT variety Berkut in order to establish a nested association mapping panel for analysis in years 3-5. F₂ seed has been planted in the greenhouse for the landrace crosses at this writing to begin the single seed descent process. The goal is to have over 2500 lines selected for uniform maturity and height for analysis.

Barley and winter wheat groups are waiting for the information generated from the 9000 SNP chips to select the most diverse parents from the NSGC core collections for crossing to the selected central parent of the NAM populations.

Phenotyping for Nitrogen Use Efficiency (NUE)

Dr. Kent Eskridge (NE) has become part of the group to review field plot experimental designs. He has provided valuable advice on augmented designs with replicated checks.

Barley: Due to herbicide damage at Yuma Arizona winter increase we have used limited available seed to plant two NUE trials in Montana and Minnesota this year. These will provide preliminary data on NUE and canopy spectral reflectance as well as provide a seed increase for the full suite of field trials in 2012. We do not anticipate that this delay will affect any other parts of the project.

Wheat: Sufficient seed quantities have been obtained for the hard and soft winter wheat panels, which are ready for fall planting in all the proposed locations.

Hard winter panel: the hard wheat breeders sent 331 historic to modern hard winter wheat lines representing the historic to modern diversity in the Great Plains to Yuma, AZ for seed increase. Each line was from a single head selection. Most of the lines were grown in two row plots to provide sufficient seed for the association mapping panel for both the Great Plains NUE and WUE studies. It is expected that the hard wheat community will pair this list of lines to 250 lines for our NUE and WUE trials.

Soft winter panel: about 330 soft winter wheat accessions are available and the final 285 entries for the soft winter elite panel will be selected based on seed amounts available following the June 2011 harvest. The panel includes lines from several 2010-11 and 2011-2012 uniform trials and then elite lines from the main participating breeding programs (MO, KY, OH, VA, MD). Seed is being increased this season (2010-11).

OH and NE have sown a spring crop of oats and forage sorghum-Sudan-grass hybrid, respectively, to draw down the N prior to our fall 2011 NUE experiment.

Both the hard and soft winter wheat breeders have ordered the Jaz spectrometers. Researchers for both wheat classes should be able to obtain valuable experience on current N-rate studies this season prior to the start of the actual TCAP work in the spring of 2012.

Personnel from many of the participating programs attended the Ocean Optics Jaz training session in Denver CO on April 8th. We have finalized the specification for seven Jaz spectrometers and orders have been placed. Several of projects (OH, VA, NE, and OK) will use available non-TCAP N-rate trials to gain experience in the use of the spectrometers prior to collecting data for the TCAP experiments.

OH and NE have both hired the proposed graduate students.

Accomplishments anticipated in the next three months (June-August 2011):

1. Composition of the elite panels will be finalized, seeding rates and experimental designs will be established and seed will be packaged and distributed.
2. Plant tissue will be collected from all entries of each elite panel. DNA isolation will begin.
3. Parents will be selected and planted in the greenhouse to start the crossing to initiate the hard and soft winter wheat NAM populations.

Phenotyping for disease resistance

Barley spot blotch phenotyping (*Shaobin Zhong, North Dakota State University*): The National Small Grains Collection (NSGC) core lines (1050 in total) were received in January 2011, and seedling greenhouse evaluations to the widely virulent *Cochliobolus sativus* pathotype ND4008 are nearly complete. These NSGC lines, along with the five checks (Bowman, ND5883, NDB112, ND23329 and ND23345), were evaluated as seedlings in the greenhouse. The second and third inoculation experiments will be completed in late May. Preliminary results revealed that most accessions are susceptible to isolate ND4008; however, a few accessions were resistant and will be tested for their reaction at the adult plant stage.

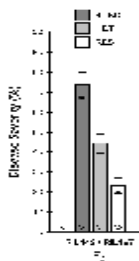
Barley stripe rust phenotyping (*Patrick Hayes, Oregon State University*): NSGC core lines (1050 in total) for stripe rust assessment will be planted in a single experiment in fall 2011. Fall planting allows for timely planting and optimum epidemic development the following spring. Five hundred additional barley lines from the NSGC (that are not part of the core collection) were planted in California and were evaluated for stripe rust.

Barley spot form net blotch phenotyping (*Robert Brueggeman and Timothy Friesen, ND State Univ. & USDA-ARS, respectively*): After a very late spring in the Midwest, 1050 NSGC core lines were sown in three nurseries located at Langdon, Osnabrock, and Fargo, North Dakota for spot form net blotch evaluations. Inoculations of the nurseries will start in June, and disease scoring will be completed by early August. Recombinant inbred line populations are being developed with North Dakota lines (2ND26333, ND25160 and ND23898) that have shown good adult plant resistance against populations of the pathogen under field conditions.

Barley stem rust phenotyping (*Brian Steffenson*): 1050 NSGC core lines were sent to Greytown, South Africa for adult plant evaluation of resistance to African stem rust races. These lines will be sown in early June to achieve the best disease development. Inoculations will commence in September, and disease scoring will be completed by early November.

Wheat stripe rust phenotyping: 1000 lines from the wheat NSGC core collection were planted in CA Davis and in WA stripe rust nurseries at Whitlow and Mt. Vernon. Reactions to stripe rust at the adult-stage will be evaluated in WA in July. In Davis CA, the evaluation for stripe rust resistance has been completed. The nurseries were scored 4 times (twice by two different people) under very heavy natural infection (all susceptible borders reached 100% severity). Approximately 63% of the accessions were susceptible to highly susceptible; the frequency of resistant materials was encouraging, with 12% highly resistant, 8.6 % moderately resistant, and 16.5% intermediate. This data set will be combined with screening results in Pullman, WA and used for association mapping in 2011.

The mapping of resistance genes to stripe rust in the UC1110 x PI61075 population was completed and the results published in Theoretical and Applied Genetics (see publications at the end of the report). This growing season significant progress was made on the dissection of the two major QTLs from this population on chromosome arms 3BS and 5AL(*Yr48*). For the 3BS QTL(UC1110, 1000 F₂ plants segregating only for this gene were grown in the field in CA. Leaf samples were genotyped at the WA-Genotyping lab with flanking markers. Recombinant plants were identified and seed is being harvested for progeny tests to validate the F₂ results.



For *Yr48* 500 additional F₂ plants segregating only for *Yr48* were planted in the field in CA and analyzed with flanking markers in WA-Genotyping lab. Phenotypic analysis of the genotyped individuals showed that *Yr48* exhibits clear additive gene action (see figure on the left). These results support the quantitative nature of the *Yr48* resistance. Among the 1,004 F₂ plants analyzed, 3 critical recombination events were identified that reduced the *Yr48* region to **0.11 cM**, a distance amenable to chromosome walking using available wheat BAC libraries.

A line from the previous population including both major QTL was crossed to 10 CA elite lines and breeding populations are being advanced to validate the QTLs in different genetic backgrounds and to diversify the sources of resistance in the CA breeding program.

In KS, the Winter Wheat Association Mapping panel (226 hard winter wheat lines already genotyped with 9000 SNP markers) was phenotyped with stripe rust race PST-100 in the field (3 reps) and in the greenhouse (3 subsamples). The same AM panel is being phenotyped at Rossville with a new race of stripe rust that is virulent on *Yr17*. Twenty crosses were made by the KS coPIs to develop additional mapping populations for stripe rust resistance genes.

CoPIs at WSU (WA) are characterizing three populations for QTL for high temperature adult plant resistance (HTAP) to stripe rust

- 1) *Louise QTL on the short arm of chromosome arm 2BS*. This QTL was originally identified in the cross Louise/Penawawa. A BC₁F₁ population segregating for the 2BS QTL has been produced in an Avocet S background. BC₁F₁ plants will be genotyped to produce a large BC₁-derived population.
- 2) *Spring Wheat HTAP Nursery*: single plants from 510 entries are being grown in the greenhouse at WSU for seed increase and purification. The plants will be harvested in April 2011, and short rows of each entry will be planted (April-May 2011) in the field in Pullman for stripe rust and other diseases evaluation. Lines will be genotyped with emerging DNA markers linked to stripe rust resistance loci and sent for SNP genotyping.
- 3) *TA3418 x TA3416 F₂ Mapping Population* (synthetic crosses segregating for different D genome sources): Infection types (IT) data for 272 F₂ seedling plants were completed in the greenhouse. F₃ plants will be evaluated in the greenhouse in 2011 with race PST-100. Genotyping will be completed in 2011.

Three additional populations for stripe rust resistance mapping are being advanced by the WA coPIs:

- 1) *TA3416 x TA3417* is being advanced by SSD. A total of 274 F₃ plants are currently being advanced in the greenhouse. The population will be advanced to F₅ and adult plants will be evaluated for reaction to stripe rust in the field in 2012.

2) 'Avocet S' was crossed to 70 spring wheat and 136 winter wheats with HTAP resistance to stripe rust to generate backcross and bi-parental populations segregating for new sources of stripe rust resistance.

3) *Winter Wheat HTAP Nursery*: Individual plants of 486 entries with HTAP resistance genes were transplanted in the greenhouse for seed increase and purification. DNA was isolated for all entries and genotyping of this panel will begin in June 2011. The entries will be planted in the field in fall 2011 and 2012 for stripe rust evaluation and association mapping.

Leaf and stem rust: In MN, Jim Kolmer and Jim Anderson planted 1000 spring wheat entries from the NSGC core at two locations this spring for leaf rust and stem rust screening.

The leaf rust spring wheat panel of around 300 lines (Tc lines; sources of leaf rust resistance; common cvs from US, Canada) was planted at two locations. Multiple RIL populations were also planted for further leaf rust adult plant resistance screening.

Several new populations are now being advanced in MN for leaf rust genetic mapping.

The Winter Wheat Association Mapping panel is currently in the ground at Hutchinson and Ashland Bottoms KS (3 reps each) to evaluate it for leaf rust. Notes will be completed in June 2011. The original panel of 226 lines was expanded to 307 and will be planted in the fall at two locations in Kansas and in Castroville.

Progress by Education deliverables

Most significant education accomplishments:

- 1.- The Plant Breeding Training Network has been launched and is being used (<http://passel.unl.edu/pagespbtn/>). About a dozen graduate students have been meeting regularly to help test the PBTN, and in the process have begun to build community and share ideas.
- 2.- The Education team and evaluators had a successful meeting with representatives from Minority Serving Institutions (MSI) to establish collaborations. MSI recommendations made through a focus group were implemented in the creation of a request for proposals (RFP). The RFP was distributed to about 80 MSIs and we have received 12 proposals that are being evaluated.
- 3.- Forty researchers and students, representing seventeen TCAP institutions met in Denver CO, April 8th 2011 for training in canopy spectral reflectance (CSR).
- 4.- The first issue of the educational newsletter was released (attached)

Milestones expected in the next three months

MSI proposal will be reviewed and funding decisions made by June.

PBTN will continue to be built and used. 15 PIs are creating lectures that will be archived on site this summer. Those lectures will not only be used in the fall, but will continue to be freely available.

Education proposed deliverables for year 1 and Actions taken

Goal	Deliverable	Action taken
2011		
Integrate Education and Research	Planning conference at PAG	Successful meeting 1/2011
	Newsletter	Attendance: 60+ Newsletter created Spring 2011
Recruitment	4 Short Films	Hired 2 film student Filmed CSR training Scheduled filming around country in 2011
	Invite interested MSI faculty to a planning conference (FEB)	8 faculty + education team met in Chicago
	Visit interested MSIs	focus group (see report) created RFP
	Publicize MSI grant opportunity (early spring)	RFP publicized
	Review MSI grant applications and grant \$70,000	43 HBCUs
	Encourage faculty and MSI students to participate in PBTN	20 Tribal colleges
	Encourage MSI students to participate in a TCAP meetings	18 Hispanic serving
	Review MSI student and faculty reports (late Dec)	Created selection rubric
	Encourage MSI students to present results at an appropriate venue	Reviewing proposals. Decisions by June
	1 teaching resources customized for MSI student perspectives	MSI faculty surveyed for content support
Faculty support	Information for student fellowships placed on appropriate websites.	Admin assistant hired
	Information for student fellowships placed within institutions	Creating flier
	Show and discuss recruitment film at appropriate venues e.g. Undergraduate research symposia, MSI national meetings	
	PBL workshop planned and announced	
Student Training	2 PBL modules created and shared with MSI faculty	Discussing needed content
	Creation and testing of online learning environment	PBTN being built Graduate students participated in 4 online meetings to give feedback and beta test Graduate students will meet in collaborative environment soon to build relationships
	11 graduate students recruited and training initiated	11 students have been identified. Several started, and all will be in place by fall 2011
	11 undergraduates recruited and paired with graduate students	
	Create content standards for PBTN	
	Development of online curriculum	With PIs we identified 15 content areas. PIs agreed to create 15 course modules
	Learning modules to meet content standards in on line meetings	
	PBL learning modules developed	Beginning to develop PBL implementation
	Mentoring Workshop	
	All content developed housed online and freely shared	
Evaluation	High-throughput phenotyping for climate change workshop (CSR)	CSR training April 8 th 2011 42 attendees
	Plant Breeding for climate change symposium in coordination with NAPB	Money supplied, speakers invited Symposium May 23 rd 2011
	Assessment tools prepared for Bridge activities, PBL materials, training materials, undergraduate training	Pre assessment tools created, pre-assessment summer of 2011
	Graduate students interviewed for feedback to improve program	2 graduate student evaluators hired
	Success of various recruitment efforts assessed	

Publications acknowledging T-CAP support

Most of these initial papers report efforts started within the BarleyCAP and WheatCAP and were completed with T-CAP support. T-CAP coPIs are indicated in bold.

Accepted and in press in peer reviewed journals (9)

- Lowe, I., D. L. Jankuloski, **S. Chao**, **X. Chen**, **D. See** and **J. Dubcovsky**. 2011. Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat. *Theor Appl Genet.* 123:143–157.
- Chen, J.**, Ch. Chu, **E.J. Souza**, **M.J. Guttieri**, **X. Chen**, S. Xu, **D. Hole**, and R. Zemetra. 2011. Whole genome-wide mapping for high-temperature adult-plant resistance to stripe rust (*Puccinia striiformis* f. sp. *tritici*) in a hard red winter wheat germplasm IDO444. *Molecular Breeding* (In press).
- Zhang, D., **G. Bai**, R. M. Hunger, W. W. Bockus, J. Yu, **B. F. Carver**, and **G. Brown-Guedira**. 2011. Association study of resistance to *Soilborne Wheat Mosaic Virus* (SBWMV) in U.S. winter wheat. *Phytopathology* (Accepted)
- Bernardo A. N., H. Ma, D. Zhang, and **G. Bai**. 2011. Single Nucleotide Polymorphism in Wheat Chromosome Region Harboring *Fhb1* for Fusarium Head Blight Resistance. *Mol Breed.* DOI 10.1007/s11032-011-9565-y
- Li, T. **G. Bai**, S. Wu and S. Gu. 2011. Quantitative Trait Loci for Resistance to Fusarium Head Blight in a Chinese Wheat Landrace Haiyanzhong. *Theor Appl Genet.* DOI 10.1007/s00122-011-1549-0.
- Tsilo, T., G.A. Hareland, **S. Chao**, and **J.A. Anderson**. 2011. Genetic mapping and QTL analysis of flour color and milling yield related traits using recombinant inbred lines in hard red spring wheat. *Crop Sci.* 51:237-246.
- Tsilo, T.J., G.L. Linkert, G.A. Hareland, and **J.A. Anderson**. 2011. Registration of the MN98550–5/MN99394–1 wheat recombinant inbred mapping population. *J. Plant Registrations* 5:257–260.
- Tsilo, T.J., S. Simsek, J.-B. Ohm, G.A. Hareland, **S. Chao**, and **J.A. Anderson**. 2011. Quantitative trait loci influencing endosperm texture, dough-mixing strength, and bread-making properties of the hard red spring wheat breeding lines. *Genome*. In press.
- Naruoka, Y., **L. E. Talbert**, S. P. Lanning, **N. K. Blake**, J. M. Martin and **J. D. Sherman**. 2011. Genetics of productive tiller number and its relationship to economic traits in spring wheat. *Theor. Appl. Genet.* In press.

Under review in peer review journals (7)

- Wang, H., **K.P. Smith**, E. Combs, **T. Blake**, **R. Horsley**, and **G.J. Muehlbauer**. 2011. Effect of population size and unbalanced data sets on QTL detection using genome-wide association mapping in barley breeding germplasm. Submitted to *Theor. Appl. Genet.*

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- Li, P., **J. Chen**, and Pute Wu. 2011. Evaluation of Grain Yield and Three Physiological Traits in 30 Spring Wheat Genotypes across Three Irrigation Regimes. Crop Sci (Accepted with a major revision).
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- C. Saintenac, D. Jiang, **E. Akhunov**. Targeted analysis of nucleotide and copy number variation by exon capture in allotetraploid wheat genome. Genome Biology, submitted.
- Heslot, N., H-P Yang, **M.E. Sorrells**, and **J-L. Jannink**. 2011. Genomic selection in plant breeding: A comparison of models. Genetics. submitted.
- Naruoka, Y., **J. D. Sherman**, S. P. Lanning, **N. K. Blake**, J. M. Martin, and **L. E. Talbert**. 2011. Genetic analysis of long green leaf duration in spring wheat. Crop Sci., submitted.

Workshops

- E. Akhunov**, **S. Chao**, V. Catana, **D. See**, **G. Brown-Guedira**, **M. Sorrells**, A. Akhunova, **J. Dubcovsky**, C. Cavanagh and M. Hayden. New tools for wheat genetics and breeding: genome-wide analysis of SNP variation. Proceedings of BGRI Technical Workshop, June 13-16, 2011, St. Paul, Minnesota, U.S.A.

Germplasm releases

Two adapted spring donor lines carrying all three stripe rust resistance QTL

- GSTR 13606 (RIL148 UC1110 x PI610750) = *QYr.ucw-3BS*, *Yr48* (5AL), & *QYr.ucw-2BS*.
- GSTR 13634 (RIL191 UC1110 x PI610750) = adapted spring donor line carrying stripe rust resistance QTL *QYr.ucw-3BS*, *Yr48* (5AL), and *QYr.ucw-2BS*.

Two adapted spring donor lines carrying only the *QYr.ucw-3BS* stripe rust resistance QTL (i.e. they are susceptible for 5AL and 2BS).

- GSTR 13600 (RIL140) = *QYr.ucw-3BS* alone.
- GSTR 13664 (RIL233) = *QYr.ucw-3BS* alone.

Two adapted spring donor lines carrying only the stripe rust resistance locus *Yr48* (i.e. they are susceptible for 3BS and 2BS).

- GSTR 13504 (RIL4) = *Yr48* alone.
- GSTR 13618 (RIL167) = *Yr48* alone.

Mapping populations deposited in the NSGC: GSTR numbers 13501-13687= 186 recombinant inbred lines from the cross UC1110 x PI610750.