T-CAP quarterly report year 1 (2/1/2011-8/22/2011)

Executive summary

Genotyping

Genotyping platforms including 9000 molecular markers have been developed and used successfully in both barley and wheat. Genotyping of the NSGC barley core collection was completed (2,446 accessions) and the wheat core collection is in progress and will be finished by September 2011 (4,416 accessions). In addition, we completed the genotyping of a set of 5,520 wheat breeding lines and mapping populations with a separate 9000-SNP wheat assay. More than 3,000 polymorphic SNPs are being integrated into a wheat consensus genetic map. This extensive SNP information provided a detailed description of the genetic composition of the US wheat and barley germplasm. This data will be used to identify associations between SNP markers and the agronomic and disease resistance traits evaluated during the first year of the T-CAP project.

A successful pilot study for exon capture in wheat was completed with a 3.5 Mb capture array. The results are in press in Genome Biology. Larger capture designs (~60Mb) have been developed in barley and wheat as part of two international consortia in collaboration with Roche-Nimblegen. We are in the final iteration of the design before the initial tests.

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 Crop Science.

The T3 database was established and the SNP and phenotypic data generated during the first year of the project are being entered into T3. A user group has been formed and has defined templates and pipelines to upload data to T3. This database is becoming a central hub for the US barley and wheat breeding programs.

Phenotyping

To standardize the water and N use efficiency phenotyping 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 and isogenic lines. Near-isogenic lines for potential drought tolerance QTL have been investigated in rainfed and irrigated environments. 540 wheat accessions from the core NSGC have been planted in 3 environments in Aberdeen and have been evaluated for water and N use efficiency using CSR. Experiments have been harvested.

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.

One thousand lines of the wheat NSGC core collections were evaluated for stripe rust in CA and WA and for leaf rust and stem rust in MN. 1050 barley lines were also evaluated for resistance to spot blotch. The data is being incorporated to T3 database and the resistance lines into the breeding programs crossing blocks. Screening of 1050 barley lines for the spot form of net blotch was completed and data is being analyzed.

The research activities resulted in 21 manuscripts accepted for publication in peer reviewed journals, numerous presentations in scientific meetings and the release of 13 new germplasm.

Education

Seventeen PhD students have initiated their training programs (five above original target). 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 received 12 proposals that were evaluated and 8 were awarded (total awards $80,000). MSI and TCAP faculty are beginning to build collaborative relationships.

The education team organized a successful launching meeting in San Diego, an online meeting with advisory panel, a Canopy Spectral Reflectance training in Denver, developed educational and evaluation tools and published the first issue of the educational newsletter. The education team also hosted a talk for breeding for climate change at the National Association for Plant Breeders and supported attendance of over 70 students from around the country.

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 (2,446 acc.) and wheat (4,331 acc.) NSGC core collections and AM panels***

The SNP iSelect Illumina platform for wheat was developed by Eduard Akhunov (KSU) and the barley one by a collaboration including Martin Ganal (IPK, Gaterslaben, Germany) and Robbie Waugh (James Hutton Institute, Dundee, Scotland). DNAs were extracted from the 6900 accessions from the core barley and wheat NSGC collections in Aberdeen. Shiaoman Chao (USDA-ARS, Fargo, ND) used the SNP iSelect Illumina platform to genotype the barley and wheat core collections.

Barley results: The planned genotyping work for the barley NSGC was **completed**. Of the SNPs on the chip, 6,915 SNPs performed well, and were found polymorphic among all samples assayed (16.9 million datapoints). The genotype data for 2,446 accessions, along with other relevant information were submitted to the T3 database in August, 2011. A copy of all the data files were also deposited and archived in a password protected SharePoint site developed for TCAP by the Fargo genotyping lab and maintained by USDA-ARS. The SNP genotyping data is being used to select the 200 parents that capture the greatest amount of genetic diversity in the NSGC barley core. These 200 accessions will be used to develop the barley NAM populations. Crossing to develop the barley NAM populations will begin in the fall of 2011.

Wheat results: The wheat 9K iSelect assay developed by a USDA-AFRI funded wheat SNP project (PI: Eduard Akhunov) was used to genotype 5,520 wheat breeding lines and mapping populations submitted from labs throughout the US, Mexico, Canada and Germany. After cross-validating genotype calls with colleagues in Australia (Matt Hayden and Colin Cavanagh), approx. 5,234 SNPs produced scorable data and were polymorphic among all samples assayed (26 million datapoints). Genotype data were released to all labs in June, 2011. The Synthetic x Opata DH map currently includes ~2700 SNPs and is being integrated with SNPs mapped on four other populations in the project (Louise x Penawawa RIL, Klein Chaja x Klein Proteo RIL, Coda x Brundage, and Finch x Eltan populations).

The winter wheat AM mapping panel used by TCAP for mapping drought, disease resistance and nitrogen use efficiency traits has been genotyped with 9,000 SNPs, providing a powerful trait mapping tool to U.S. wheat breeders. In addition, this panel was genotyped by sequencing using *Pst*I-*Msp*I restriction enzymes. A total of six 48-plex libraries were prepared and each sequenced on a single lane of HiSeq2000. The data are currently being analyzed.

We are now using this wheat 9K SNP design to genotype a set of 4,416 NSGC wheat core collection, including 546 tetraploid wheat (*Triticum turgidum* subsp. *durum*) and 3,870 hexaploid wheat (*Triticum aestivum* L.) accessions. The genotyping assays will be completed by September 2011. Genotype data and other relevant information will be submitted to the T3 database in September, 2011, as well as to the SharePoint site for archival.

In summary, we have completed this year one objective for barley and we are on track to complete it for wheat.

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

Barley: barley materials and SNP information were provided by Kevin Smith and Pat Hayes. 55 SNP assays for barley were developed for key winter hardiness, disease resistance, and malting quality targets throughout the genome. SNPs were tested by the genotyping laboratory at WA for use on the Sequenom platforms using validation sets provided by Pat Hayes. SNPs are assayed in two separate reactions with 20 to 30 SNP each. An email inquiry was sent by Pat Hayes to barley breeders in May 2011 for submitting samples for MAS to the genotyping lab in WA. Thus far, 768 barley samples have been evaluated with panels of 55 markers and data reported to T-CAP barley breeders.

In the KS genotyping laboratory, a test of transferring barley SNP to Sequenom assays was done with 48 SNP targeted to disease resistance loci. The first conversion round showed a 92% concurrence with Golden Gate data. Almost all SNP worked after some optimization suggesting that the transfer between the two platforms will not result in a large proportion of lost markers. Up to thirty-four SNP were successfully assayed in a single Sequenom reaction.

In the NC genotyping laboratory, the possibility to use DNA extracted from ½ seeds was evaluated using 48 SNP on the BeadExpress platform. In the parental homozygous lines, DNA from seed and tissue showed 100% correspondence. In reciprocal F_1 progenies we observed good agreement among platforms but shifting of the alleles from the maternal parent were observed. In the 3-way and backcross F_1s, the shifting of the heterozygous clusters was very pronounced, resulting in less than 80% identical allele calls. Based on these results, it was decided that leaf tissue will be used as a source of DNA from plants undergoing genomic selection.

Vera Code assays for the 384 SNP chips for genomic selection were ordered and the genotyping is expected to be completed by Sept 23.

Wheat: In collaboration with all the genotyping labs and the breeding programs, mapping populations from 15 crosses between US wheat lines were genotyped, including populations that were developed and evaluated as part of the Wheat CAP project. More than 4,120 polymorphic SNP are being placed on the linkage maps in these populations. Additional wheat mapping populations are being genotyped during Fall 2011. These data are providing SNP markers linked to genes/QTL in wheat that can be used for MAS in the breeding programs. The association mapping panels developed by T-CAP are scheduled for genotyping in 2012 as originally planned.

The WA genotyping laboratory identified a set of 80 wheat SNP with high PIC values and converted them to Sequenom. These markers are being complemented by additional Sequenom SNPs developed from sequences from wheat genes and markers linked to important traits (e.g. *Fhb1*) in KS genotyping laboratory. For several markers the ability to call heterozygous individuals in the Sequenom was lower than in the original STS markers, and the assays required optimization.

A different approach was followed at the Raleigh Genotyping center. LD analyses were performed between data from the 9000 SNP chips and SSR and STS markers linked to or diagnostic for the presence of previously mapped valuable QTL, translocations, and genes in 253 winter wheat lines. SNP with high LD (r^2 between 0.80 and 1.0) with these SSR and STS markers have been identified. In some cases, 2-3 SNP are needed to predict the presence of a gene. Results so far suggest that we have predictive SNP for: 1RS.1AL, 1RS.1BL, *Sr36/Pm6*, *Bvd2/3*, *Glu-D1*, *WSBMV*, *FHB QTL on 5A* and 1B. Sequences for these SNP markers are being sent to WA and KS to design Sequenom assays for validation in previously genotyped material.

A VeraCode OPA having 96 test SNP is being designed that will include SNP reported in the literature. SNP linked to genes/QTL in the new maps and SNP in high LD with current markers. This will be ordered prior to August 31. Validation of the VeraCode OPA will be done using 1,440 advanced wheat breeding lines from all market classes for which genotypic and/or phenotypic data are available for the traits/genes (expected completion by Oct. 2011). These data will be the basis of development of working sets of SNP markers (48) specific to the different wheat growing regions, market classes and/or breeding programs.

Progress by technological deliverables

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

Gene capture

Barley gene capture: An international consortium of barley geneticists including Nils Stein (IPK, Gaterslaben, Germany), Robbie Waugh (James Hutton Institute, Dundee, Scotland), Andy Flavell (University of Dundee, Scotland) and the TCAP has been formed to work with Roche/Nimblegen on a Gene Capture design for the barley genome. The current design will provide the opportunity to capture all or most of the genes in the genome. The design will be delivered to Roche/Nimblegen by the end of August and all members of the consortium will have a chance to

ensure that all known genes are included in the design. After the design is completed it will be provided to the TCAP for databasing in T3. Each member of the consortium will receive 200 capture assays. The Roche/Nimblegen capture technology allows for pooling up to four genotypes in a single capture assay, indicating that we will be able to capture up to 800 genotypes. The current plan is to capture and sequence the 200 parents in the barley NAM population, and to work with our international collaborators to assess the genetic diversity in a large collection of cultivated, landraces and wild barleys.

Wheat gene capture: An international consortium of wheat geneticists including T-CAP developed and signed an agreement with Roche-Nimblegen to create liquid Gene Capture technology. The design of a 50 Mb wheat capture assay is being completed in collaboration with UK group (K. Edwards, University of Bristol; A. Hall, University of Liverpool). The sequence capture assay is targeting coding sequences of the wheat genome (genes orthologous to Brachypodium and low copy genes unique to wheat lineage). The current design is currently being compared with transcriptome sequence data stored in NCBI database supplemented by RNA-seq data generated E. Akhunov and J. Dubcovsky.

A pilot study was completed and the results published in Genome Biology (Saintenac et al., 2011). This study discusses the bioinformatics and statistical approaches for variation discovery in sequence data generated by Gene Capture technology for tetraploid and hexaploid wheat genomes and nucleotide sequence and gene copy number variation in the tetraploid wheat genomes (Saintenac et al., 2011).

Genotyping by sequencing (GBS)

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 have been genotyped by sequencing in wheat (ITMI mapping population) and barley (Oregon Wolfe Barley mapping population).

Sequencing libraries were developed using different combinations of restriction enzymes. We have generated and sequenced 48-plex *Pst*I-*Msp*I libraries from double haploid (DH) mapping populations in both barley and wheat. In barley we made two libraries from 82 lines from the Oregon Wolfe Barley population (OWB). In wheat, we made four libraries from 190 lines of the Synthetic M6 x Opata (SynOpDH) population. These libraries were sequenced on one lane of Illumina GAII or HiSeq2000. In the barley OWB population we identified over 56,000 SNP markers on the genetic map and 289,000 GBS tags were mapped as dominant markers. In the wheat SynOpDH population we mapped over 20,000 SNP markers and 150,000 tags as dominant markers. We have designed a 384-plex set of barcoded adapters for *PstI* and validated a 96-plex and 192-plex subset of these adapters. We have generated a 144-plex library from the barley Steptoe x Morex DH population which is currently being sequenced. We have generated 96-plex libraries for SynOpDH mapping population using the *Pst*I-*Mlu*I and *Pst*I-*Mse*I restriction enzymes. Each library was sequenced on one lane of HiSeq2000 instrument. The data is currently being analyzed and compared with previously generated GBS data for SynOpDH.

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

Sixty-four crosses were made using forty-seven facultative parents tracing to Oregon, Nebraska, Idaho and Minnesota breeding programs inFall of 2010. The resulting F_1 and F_2 were grown in the 2011greenhouse and in the field in St. Paul, MN, respectively. 768 (48 crosses x 16 lines per cross) F_3 plants for genotypingare being planted in August, 2011. Phenotypes to train the GS model include freezing tests and winter survival in St. Paul, MN and are available on a total of 209 lines from the Barley CAP. GEBV will be used to select parents for the nextround of crossing.

To select SNPs providing optimal genome coverage for these progeny, all parents were genotyped with the 1536 SNP BOPA1 assay. Of these SNP, 1326 had map locations and had low missing and heterozygous counts. A function was derived that quantifies the amount of segregation information captured by a set of markers over the genome and averaged over all crosses. We developed a method to identify marker subsets that maximize this function, used it to pick a 375 marker set, and then added nine markers known to be associated with low temperature tolerance for a 384 SNP assay.

VeraCode assays for 768 samples will be delivered in September for the first cycle of GS. The remaining 768 assays of the same 384 SNP VeraCode OPA will be shipped during December to perform the second cycle of selection. GoldenGate assays were re-designed for fourteen of the 384 submitted SNP to suit the VeraCode platform. The breeding programs will submit tissue samples of F_3 plants for genotyping at the end of August. Prior to Sept. 23, DNA isolation, assay performance and genotyping calls are expected to be completed and data provided to T3 and the breeding programs for analysis

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.

One simulation paper based on barley CAP SNPs comparing different models for genomic selection was recently published (Iwata and Jannink, 2011). A second manuscript on the same topic but using empirical datasets from barley, wheat, maize, and *Arabidopsis*, was accepted with minor revisions in Crop Science (Heslot et al., in revision).

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

The portal site for T3 is live at http://triticeaetoolbox.org/. The T3 portal links to The Hordeum Toolbox (THT) for barley and a functionally identical database tailored to wheat. Both are powered by THT code initially developed by the Barley CAP and that we are continually enhancing. Thus, the basic structure of T3 is in place. The underlying computing infrastructure is being provided and maintained by GrainGenes. The first wheat datasets have been uploaded. In particular, we are currently incorporating the new SNP data from the first 9000-SNP genotyping experiment in wheat. Early disease ratings are also being entered (e.g. stripe rust scores for 1000 NSGC lines from CA and WA). A complete list of wheat traits and their measurement protocols is being established. All traits are being assigned trait ontology numbers to improve leveraging of comparisons across species.

The large amount of data to be entered requires a smooth upload and curation processes. We have established a protocol to improve our informatics integration with the genotyping centers to limit manual interventions. We have devised a curation strategy that will allow new data to be

uploaded first to a T3 mirror making available previous T3 data to improve outlier detection in both phenotypes and marker scores. We have begun working on queries and formatting to report on the content of T3.

Though we are now focused on the database structure and interface, we have also begun work on new analysis functions to help breeders identify useful lines and improve decisions. A haplotype search function has been implemented enabling the user to specify markers and select lines on the basis of alleles present at those markers. This will be a useful tool for the breeders to select lines with particular allele combinations. T3 can also cluster lines based on their genome-wide genotype. The user can then select one of the clusters for further analysis. We are also improving how data associated with those lines can be downloaded, in particular formatting for different platforms (TASSEL, the iPlant environment, and JMP Genomics), and with what associated data (phenotype selection).

To facilitate the generation of reports and tracking of tasks we have developed a web site that lists all the different tasks, the responsible person within the T3 team, the priority of the task and the status of the project. The project directors and the executive committee have access to this website which is available on demand to project evaluators (e.g. SAB, NIFA, etc.). We are also developing an automated approach that can deliver information on the number of lines submitted to T3, the genotypic information generated and the total number of submitted datapoints, the number of submitted trials and total phenotypic datapoints. For all of these information categories, the results will be broken down by species.

- ***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 that represents all TCAP objectives and has heavy breeder representation. We have teleconferenced 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. The T3 User Group members also have access to a beta version of T3. There they may test new functions as they come out and provide feedback. They also prioritize ideas for new T3 functions.

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

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***.

Victoria Carollo-Blake (previous GrainGenes curator) was hired to cover the curator position. We initiated the uploading of the wheat SNP data and we are debugging data upload procedures. The database also began the incorporation of the phenotypic data generated during the first year of the T-CAP grant.

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. The 5 checks included drought tolerant and susceptible genotypes identified from previous studies (replicated 12 times in each treatment. These lines have been evaluated for yield, water and nitrogen use efficiency. We used normalized water and nitrogen indices (NWI and NNI) determined with a canopy spectral radiometer (CSR) at two different growth stages. We also assessed CT (canopy temperature), and leaf water content in the 60 check lines. Samples were collected for CID (carbon isotope discrimination) and leaf nitrogen content. In addition, the 540 lines and 5 checks have been 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 CSR data and agronomic measurements from the field evaluation. Phenotypic and genotypic data will be used for association mapping after harvesting. A preliminary study shows large genetic variation for all traits evaluated A Ph.D. student was recruited for this work and has participated on the work described above.

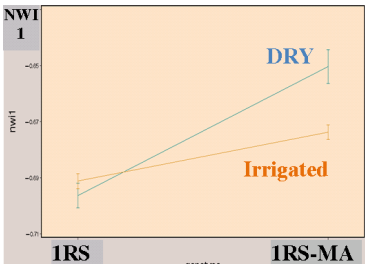
The University of Idaho (UI) team also assessed two additional sets of materials with CSR: a winter wheat mapping population and a set of 30 spring wheat cultivars at flowering, which were assessed for yield, phenology, CT, CCI, and CID in the past two years. For the UI breeding program they evaluated 1000 F3 lines pyramiding YR and HF resistances and high protein content from the CA variety Lassik (*Gpc-B1, Lr34/Yr18* and *Yr17*) and initiated the development of four spring wheat bi-parental mapping populations.

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) containing 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 that are absent in the engineered 1RS-MA chromosome include the gene for drought tolerance. This experiment showed that the selected CSR equipment is adequate to detect differences in drought tolerance. Significant differences between the 1RS and 1RS-MA lines were detected for grain yield (1520kg/ha in the Hahn background) and thousand kernel weigh (significant in drought but not watered conditions) in the same field experiment. Carbon isotope discrimination measures are in progress. Hydroponic experiments using the Hahn isogenic lines

showed significant differences in root length. These results will be replicated with other isogenic lines.



To determine which of the wheat segments is responsible for the reduced drought tolerance, we crossed Hahn-1RS x Hahn-MA and selected lines homozygous for each of the two wheat segments separately (from the cross Hahn-1RS x Hahn-MA). Three molecular markers have been developed to facilitate this selection.

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 and lower grain yield than wild type isolines, indicating that *Rht8* 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. Trials will be harvested before the end of the first year of the grant.

Experiment 4: NILs for a QTL conferring extended green leaf duration, which has been shown to cause increased seed size in dry environments, were planted in replicated trials in two Montana locations. A manuscript describing this QTL has been accepted for publication.

Experiment 5: 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 240 RIL (1/2 hexaploid and ½ tetraploid) from a hexaploid spring wheat by tetraploid durum wheat cross. 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.

Experiment 6. Heat tolerance. Two controlled environment experiments using chromosome substitution lines involving wild relatives of wheat were established in KSU to identify high temperature tolerant genotypes and understand the mechanism of high temperature tolerance in wheat.

6a. Twenty six chromosome substitution lines (Table 1) received from Wheat Genetic and Genomic Resources Center are being tested under controlled environmental conditions (16 h light, PAR 450 µmol m^{-2} s^{-1}, and 85% humidity). The genotypes are replicated six times in three growth chambers and half of the plants are transferred 10 d after anthesis to high temperature stress conditions (34/26°C day/night time temperature) for 10 d. Time series physiological data will be collected during stress period, and grain yield data will be measured at harvest.

6b. High temperature tolerance of 167 spring wheat lines are being evaluated under controlled environmental conditions. The 161 lines are of Asian origin and have been genotyped by the USDA Genotyping Lab in Manhattan, Kansas. Three high temperature tolerant and three high temperature susceptible lines were also included as checks. Plants of each line are grown in the non-stress conditions. At the post-anthesis stage, half of the plants from each line will be exposed to high temperature treatments. Data collection on chlorophyll, grain yield per plant, single seed weight, etc, is currently in progress. Association mapping methodology will be employed to map

QTLs underlying the high temperature tolerance. High temperature tolerant lines selected from this project will be useful for breeding program.
Experiment 7: WinRhizo software (Regent Instruments, Inc.) was tested in CO for digital analysis of root systems grown in 1-m long tubes. After initial trial and error to determine the best settings and parameters, we have now begun analysis of the root systems of 120 lines grown in a greenhouse study in spring, 2011.

Spring Wheat Drought AM panel: the lines for the spring wheat drought Association Mapping panel have been planted for seed increase and preliminary characterization. CSR readings were taken on the AM panel during early grain filling period. Genotyping of this association mapping panel with the 9000-SNP Infinium will be performed in year 2 as planned.

Winter Wheat Drought AM panel: Seed of the HWW Association Mapping Panel was increased in Yuma, AZ and returned to the University of Nebraska, where Stephen Baenziger is coordinating the determination of the final entry list and seed distribution. In fall 2011, field trials will be planted in Greeley, CO (two soil moisture environments), Manhattan, KS (Vara Prasad), and Amarillo, TX (Shuyu Yu, not a TCAP collaborator, but willing to grow the trial). This association mapping panel was fully genotyped with the 9000-SNP Infinium platform.

- ***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 irrigated and non-irrigated environments (Tom Blake).

Three barley 2-rowed populations, two (low and high N under irrigation) at Bozeman and one (terminal drought) at Huntley were planted. The Huntley will be harvested by the end of August and the one in Bozeman's about a month later. Plant height and heading date have been gathered for all plots. No significant disease pressure occurred on barley at either location. CSR measurements were taken on the trials at Bozeman (the equipment arrived late for Huntley).

Facultative 6-row AM panel: Seed increases are complete 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: We have developed a wild barley introgression population consisting of 25 wild barleys that represent 90% of the diversity in the 318 individuals of the wild barley diversity collection. These 25 wild barleys have been backcrossed twice to the elite six-row malting barley Rasmusson. At least thirty BC_2 individuals have been derived from each of the 25 wild barleys. Four generations of single seed descent have been conducted to derive inbred lines. We grew the population in St. Paul, MN in the summer of 2011 and obtained height, heading date, lodging and spike morphology data. We plan to genotype the lines in the fall of 2011 with a custom 384 SNP chip. The population will be grown in the field in 2012 and screened for agronomic traits. We are on track to screen the population as part of the TCAP WUE and NUE trials in the summer of 2013.

- ***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 was 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 10 elite lines from CA, MT, CIMMYT and Australia, have been crossed to the CIMMYT variety "Berkut" in order to establish a nested association mapping panel for analysis in years 3-5. F_2 seed are available for the 8 elite lines and F_3 heads are currently maturing in the greenhouse for the crosses between Berkut and the 38 landraces. 800 F2 seed were planted for most the land-race crosses, the final goal is 100 F4 plants per cross that are photoperiod insensitive and semi-dwarf. The goal is to have over 2500 lines selected for uniform maturity and height for analysis.

For the barley NAM populations we are currently analyzing the 9000 SNP data to select parental lines that maximize diversity. Crosse will start in September. 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 a 6-row NUE trial in Minnesota and the 2-row WUE trial in MT (mentioned above) this year. We also planted a seed increase of the 2-row panel in Minnesota. We do not anticipate that this delay will affect any other parts of the project. The 6-row NUE trial was planted as an augmented block with five repeated checks in low and high nitrogen environments. Data was collected on heading date, plant height, maturity, yield, and number of spikes per meter row. In addition, spike samples and grain samples were collected to generate data on spike length, kernels per spike, kernel size, spike internode length, percent plump kernels, and grain protein concentration. These experiments will provide preliminary data that will help us to characterize and genetically map NUE as well as provide a seed increase for the full suite of field trials in 2012. MN and MT received Jaz spectrometers and collected preliminary data this summer that should be useful to suggest protocols for use in the 2012 trials.

Wheat: The composition of the elite panels is nearly finalized. Experimental designs have been finalized for the soft wheat panel and entries assigned to plots. Seed is being treated and packaged for distribution to all cooperators.

Hard winter panel: the hard wheat breeders sent 322 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. Sufficient seed for the association mapping panel for both the Great Plains NUE and WUE studies was obtained. The hard wheat community will pair this list of lines to 300 lines for our NUE and WUE trials. Spatial designs for each location will be developed and seed distributed for planting in September and October of 2011.

Soft winter panel: This panel consists of 280 current elite breeding lines. Spatial designs have been developed centrally for each location and these will require 330 plots per rep. Seed is being treated and packaged centrally and will be distributed to all cooperators. Cooperators will receive seed in labeled envelopes ready to plant. 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).

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 received the Jaz spectrometers. Scientists in NE, OH, and VA have started to use the Jaz units in 2010-2012 Nitrogen rate studies to gain experience prior to using them on TCAP plots in the spring of 2012. A SAS program for working with the Jaz data files has been developed at Ohio State and will be distributed to all TCAP groups.

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 (Amber Hoffstetter) and NE (Kethrine Frells) have hired the proposed graduate students.

Accomplishments anticipated in the next three months (September-November 2011):

1. Composition of the elite panels will be finalized, seeding rates and experimental designs will be finalized, seed will be packaged for distribution, and planting should be finalized at all locations.

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. Crossing could begin in late November.

4. CSR data collected in the spring of 2011 will be analyzed.

<u>Phenotyping for disease resistance</u>

Barley spot blotch phenotyping *(Shaobin Zhong, North Dakota State University)*: The National Small Grains Collection (NSGC) core lines (1,050 in total) were received in January 2011, and seedling greenhouse evaluations to the widely virulent *Cochliobolus sativus* pathotype ND4008 have been completed. These NSGC lines, along with the five checks (Bowman, ND5883, NDB112, ND23329 and ND23345), were evaluated as seedlings in the greenhouse. One

accession was identified as resistant and 30 as moderately resistant. Data are being collated for uploading to the T3 website by October according to the recommended template.

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.

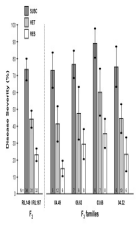
Barley spot form net blotch phenotyping *(Robert Brueggeman and Timothy Friesen, ND State Univ. & USDA-ARS, respectively)*: After a very late spring in the Midwest, 1050 NSGC core lines were sown in three nurseries located at Langdon, Osnabrock, and Fargo, North Dakota for spot form net blotch evaluations. Inoculations of the nurseries were completed in June, and disease scoring was completed in early August. Data will be collated for uploading to the T3 database by October 2011. 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)*: 1,050 NSGC core lines were sent to Greytown, South Africa for adult plant evaluation of resistance to African stem rust races. These lines were sown in early June to achieve the best disease development. The first inoculations were performed in mid August, and disease scoring will be completed by early November. Data will be collated for uploading to the T3 database by January 2012.

Wheat stripe rust phenotyping**:** 1000 lines from the wheat NSGC core collection were evaluated in CA Davis and in WA stripe rust nurseries at Pullman and Mt. Vernon. In Washington, disease ratings were taken twice at Mt. Vernon (at stem elongation and heading to flowering growth stages) and three times at Pullman (once at stem elongation and twice at heading to flowering stage) under heavy natural infection. Stripe rust severity for the susceptible borders and check ranged from 90 to 100%. At Pullman, 25% of the germplasm was resistant, 59% moderately resistant-moderately susceptible, and 16% susceptible. At Mt. Vernon, 20% of the germplasm was resistant, 44% moderately resistant-moderately susceptible, and 36% susceptible. In addition to the stripe rust scoring, data was collected on heading date, spike type (awnless, awned, apically awnletted, or awnletted), plant height, glume (hairy or non-hairy), and peduncle length. In Davis CA, 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, 25% moderately resistant and intermediate. Differences among locations in a few lines are likely cause by different race composition at the different locations. Association mapping will be completed using this combined data set and 9000 SNP genotype data by the end of 2011.

High density mapping of wheat stripe rust resistance QTL**:** 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). 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 F_2 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 F_2 results.



For *Yr48* 500 additional F_2 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 F_2 plants analyzed, three 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 marker completely linked to *Yr48* was identified and used to screen the BAC library. The selected BACs will be sequenced.

A line from the previous population including both major QTL was crossed to 10 CA elite lines and breeding populations were 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 was phenotyped at Rossville in 2011 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 and has been a strong and consistent source of stripe rust resistance. The Louise/Penawawa RIL population was genotyped with 9000 SNP markers and we identified 4 SNP's tightly linked to this stripe rust resistance QTL (covering a 4 cM interval) that collectively appear very useful for marker-assisted selection in broad germplasm. A BC_1F_1 population segregating for the 2BS QTL has been produced in an Avocet S background, and BC_1F_1 plants heterozygous for the QTL region were identified and self pollinated. The BC_1-derived population (1150 progeny) will be genotyped and advanced to F_4 before evaluating in 2012 screening nurseries. The tightly linked SNP markers we have identified will be used to identify recombinant progeny in the fine-mapping population and cloning initiated. These markers are also being included in a 48 SNP MAS strategy.

2) *Spring Wheat HTAP Nursery:* single plants from 510 entries were increased and DNA isolated in August 2011. Short rows of each entry will be planted (April 2012) in the field in Pullman for stripe rust and other disease 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 cross segregating for different D genome sources)**:** Infection types (IT) data for 272 F_2 seedling plants were completed in the greenhouse. F_3 plants will be evaluated in the greenhouse in 2011 with race PST-100. Genotyping will be completed in 2011. The two parents are being screened for polymorphism with 382 D-genome markers and 9000 SNP genotyping of both parents has been completed.

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 F_3 plants are currently being advanced in the greenhouse. The population will be advanced to F_5 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 advanced in the greenhouse for seed increase and purification. DNA was isolated for all entries and genotyping of this panel began in July 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 evaluated 1000 spring wheat entries from the NSGC core at two locations this spring for leaf rust and stem rust. The plots in St. Paul MN were successfully evaluated for leaf and stem rust resistance. Weather conditions in Crookston MN were not conducive for development of leaf and stem rust and were not evaluated. In the fall of 2011 the 1000 wheat lines will be tested as seedling plants with a mixture of leaf rust races used in the field tests and a leaf rust race that is highly avirulent to most leaf rust resistance genes. Similarly, the wheat lines will be tested as seedlings with a mixture of virulent stem rust races and with an avirulent stem rust race.

From the 2011 results, 30 NSGC accessions with resistance to leaf rust and 30 with resistance to stem rust resistant lines were selected for crossing to initiate new mapping populations. Seedling resistance screenings will be used to select populations with promising new sources of resistance. Two completed RIL populations were selected in MN for Ug99 stem rust resistance and for leaf rust resistance that were assigned to the graduate students.

The leaf rust spring wheat panel of 209 lines was planted at two locations and data collected at the St. Paul location. Multiple RIL populations were also planted for further leaf rust adult plant resistance screening.

The Winter Wheat Association Mapping panel was evaluated at Ashland Bottoms KS (3 reps each) for leaf rust infection type and severity. The panel will be expanded to 307 lines and will be planted again 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 received 12 proposals. After evaluation 8

proposals were funded at the requested level ($80,000). Funded MSI faculty members are from Chicago State University, Tuskegee University, Texas A&M (Amarillo), University of Arkansas (Pine Bluff, two proposals), Lehman College (New York), Zhu - Rust College, and Fayetteville State University. Successful MSI faculty members were paired with T-CAP faculty members and collaborative relationships are being built.

3.- Forty researchers and students, representing seventeen TCAP institutions met in Denver CO, April 8th 2011 for training in canopy spectral reflectance (CSR). A follow-up online meeting including 40 participants was also held over the PBTN and archived.

4.- The first issue of the educational newsletter was released.

5.- 17 PhD students started their PhD training programs in T-CAP, exceeding the original target of 11 for year 1. The additional PhD positions were funded by transforming one postdoc position to two PhD student positions and by savings from fellowships obtained by the students.

6.- PIs are creating lectures that will be archived on site by September. Those lectures will not only be used in the fall, but will continue to be freely available.

7. A Breeding for Climate Change talk was supported at the National Association of Plant Breeders meeting and cost of attendance of over 70 students from around the country was defrayed.

8. Evaluation Tools have been developed and implemented.

- TCAP and MSI faculty were surveyed to determine need for educational tools
- TCAP faculty and students were surveyed to determine baseline that will be used to assess change over the life of grant.
- A student evaluator will participate in online meetings using a rubric created to assess effectiveness.
- An interview tool was developed to assess faculty and student perceptions of educational activities.

Education proposed deliverables for year 1 and Actions taken

Goal	Deliverable	Action taken
Integrate Education and Research	Planning conference at PAG	Successful meeting 1/2011 Attendance: 60+
	Newsletter	Newsletter created and disseminated Spring 2011
	Logo	Graphic design student at Montana State University created logo
Recruitment	4 Short Films	Hired 2 film student Filmed CSR training Filmed in CO, NE, NY, WA, MN, ND and MT gathering 20 hours of footage and interviewing more than 25 researchers, students and stakeholders Footage being transcribed and students editing
	Invite interested MSI faculty to a planning conference (FEB)	8 faculty + education team met in Chicago focus group (see report) created RFP
	Visit interested MSIs	Exchanges between TCAP and MSI faculty being planned
	Publicize MSI grant opportunity (early spring)	RFP publicized

	Review MSI grant applications and grant $70,000 Encourage faculty and MSI students to participate in PBTN Encourage MSI students to participate in a TCAP meetings Review MSI student and faculty reports (late Dec) Encourage MSI students to present results at an appropriate venue 1 teaching resource customized for MSI student perspectives	43 HBCUs 20 Tribal colleges 18 Hispanic serving Created selection rubric 8 proposals funded at 80,000 (exceeding original objective) MSI faculty surveyed for content support
	Information for student fellowships placed on appropriate websites.	Admin assistant hired
	Information for student fellowships placed within institutions	Creating flier
Faculty support	Show and discuss recruitment film at appropriate venues e.g. Undergraduate research symposia, MSI national meetings PBL workshop planned and announced 2 PBL modules created and shared with MSI faculty	Recruitment film being created (see above) Surveyed for content suggestions Instructional Designer building
Online environment	The framework for the Plant Breeding Training Network has been refined with a customizable URL: http://passel.unl.edu/communities/pbtn .	Features/materials completed: • Customizeable left-hand menu buttons. • Discussion forum was refined and currently being tested. • Instructions for obtaining PBTN login account and accessing the Adobe Connect room were developed in word/pdf and placed online in the PBTN. • A testing/staging server is in place. In this environment, coding changes can be tested before going live on the main site; thereby reducing the number of broken links that result from coding updates. • Extra security certificates have been obtained, making it possible to share PBTN login information with a google apps space. Beta-testing of this is underway - a single login for users to utilize google collaborative apps such as google docs, chat, video chat, etc. within the PBTN. • Tracking of users and impact of PBTN has been discussed with programmers. Google analytics is now implemented and adjusted to also include data on animation views. • PBTN announcements are simultaneously posted to the site and emailed to member accounts. • An eLibrary facebook page was created in which PBTN announcements will also be available. http://www.facebook.com/PASSeLibrary • An eLibrary Twitter account was also created in which PBTN announcements will be posted for those who follow Twitter. http://twitter.com/#!/eLibrarypro
	Testing	Graduate students participated in 4 online meetings to give feedback and beta test
	Implementation	Students meeting online - 4 students presented research talks online over summer. All talks are archived at http://passel.unl.edu/communities/index.php?

		idcollectionmodule=1130274157. Liana Nice from Univ of Minnesota discussed her research on *Utilization of Wild Barley Germplasm through Multiparent Population Development with 9 participants.* Rebecca Nitcher of UC Davis presented her research on *Vernalization and Photoperiod Effect on Cereal Flowering* with 12 participants. Resistant Starch Brittany Hazzard and Drought tolerance Tyson Howell on Aug 9th with 12 participants
Undergraduate	Training plan	Researchers have funding to support one undergraduate research intern in their lab during this year. Interns will be mentored by T-CAP graduate student researchers and will also participate in an online plant breeding training network for undergraduates. The network will provide an opportunity for students to hear from members of the plant breeding industry, to learn about graduate studies in plant breeding, to socialize with other students conducting internships, and to receive additional training and guidance in research and career planning. Guidelines on implementing undergraduate research internships have been compiled and sent to coPIs
	Industry participation	Dr. Tabare Abadie will speak with undergraduate students about Pioneer research internships during summer 2012.
	11 undergraduates recruited and paired with graduate students	During fall 2011
Graduate	11 graduate students recruited and training initiated	17 students have been hired and are starting their PhD programs.
	Development of online curriculum	With PIs we identified 15 content areas. PIs agreed to create 15 short course modules Syllabus for Plant Breeding strategies for fall 2011 designed (see attached) 5 year plan for content delivery in development (see attached). TCAP members have agreed to develop several exciting courses and educational materials. For example, Pat Hayes is developing materials that will help students understand and practice genetic principals utilizing the OWMB mapping population. This material can be implemented online and will be available for undergraduate and graduated instruction.
	Create content standards for PBTN	
	Learning modules to meet content standards in on line meetings	
	PBL learning modules developed	Beginning to develop PBL implementation
	Mentoring Workshop	Syllabus designed
	All content developed housed online and freely shared	Student presentations archived
Workshops	High-throughput phenotyping for climate change workshop (CSR)	CSR training April 8th 2011 42 attendees
	Follow-up online CSR research presentation by Jorge Ducovsky and Tyson Howell	40 participants
	Plant Breeding for climate change symposium in coordination with NAPB	Money supplied, speakers invited See thank you attached Symposium May 23rd 2011 3 TCAP students attended, defrayed costs for over 70 graduate students outside TCAP (NAPB thank you letter available upon request)
Evaluation	Assessment tools prepared for Bridge activities, PBL materials, training materials, undergraduate training	Pre assessment tools created, pre-assessment summer of 2011 (results being procesed)
	Graduate students interviewed for	2 graduate student evaluators hired

	feedback to improve program Success of various recruitment efforts assessed	
Advisory	Members	Dr. Philipp Simon, Professor (USDA), Department of Horticulture, University of Wisconsin-Madison Dr. Allen Van Denzyne, Senior Scientist, Seed Biotechnology Center, University of California, Davis Dr. Valerie Williams, Program Evaluator, Global Learning and Observations to Benefit the Environment Dr. Robin Wright, Assoc. Dean, College of Biological Sciences, Professor Dept., Genetics and Cell Biology, University of Minnesota Members added August 2011: Dr. Tabare Abadie, Senior Research Manager Dr. Janet Poley, President, American Distance Education Consortium Dr. Abdelmajid Kassem, Professor and Chair, Dept. of Natural Sciences, Fayetteville State University, NC (invited) Dr. Sid Perry, Branch Manager, Westbred LLC (invited)
	Meeting	The advisory panel teleconferenced July 5th 2011 (minutes archived on line and summarized below).

Miscellaneous:
Our learning objects created, during the wheat CAP are being used as educational tools by other groups (e.g. http://www.teachersdomain.org/asset/ate10_int_wheat/).

As part of the educational efforts of our TCAP grant, a student of Jorge Dubcovsky's, Nestor Kippes, will supervise one of UC Davis Young Scholars Program. The student will participate in the high density molecular mapping of a gene for wheat flowering.

T-CAP Education Advisory Board meeting on July 5th 2011

The advisory board requested information of the demand for breeding jobs. We provided evidence of a large demand from listing in seedquest.com (site for seed professionals) and at the NAPB website plantbreeding.org. We also provided information of employment of students from our previous CAP projects.

The EAB also asked about access to our online courses and content. We communicated our intention to make them freely available. There was a suggestion by the EAB to publicize materials that are developed and made them available online. They suggested having a communications person who will distribute information on activities of the project to media sources. We agreed to implement these ideas.

The EAB asked about teaching experiences for the graduate students and their participation on the selection of undergraduate students working with them. We described the mandatory mentorship course and the mentorship experience of undergraduate students. The graduate students will actively participate in the preparation and advertisement of the undergraduate positions and will participate in the selection interviews. The participation as Teaching Assistant in formal courses will vary among institutions, with some requesting 1-2 quarters of teaching during the PhD program.

The EAB asked if industry was interested in providing internships and why we only listed Pioneer and Monsanto. We answered that those were the companies that have formally offered support for the project/interns but that others have indicated in personal contacts that they were also interested in providing plant breeding internships.

The EAB asked how we will investigate the factors that hinder or limit minority students from pursuing degrees in the plant sciences. We shared our positive experience with interviews to MSI faculty and students conducted as part of the evaluation.

The EAB ask about the input requested on what learning objects planned to teach genetics principles. We surveyed instructors at T-CAP institutions and will make the education objectives explicit to students.

The EAB asked about other social networking applications. We communicated our students' preference to avoid using Facebook for school applications.

Conclusions:

Continue meetings every 6 months,

Use emails with specific and important requests to get more immediate attention.

Asking specific questions

Web/phone conferencing was adequate to review and provide feedback to questions, but brainstorming requires face-to-face interaction. It was agreed to meet face-to-face within 6 months, probably in MN. Meanwhile, slides, prep material, and minutes will be posted to a site on PBTN where they can be reviewed easily.

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 (20)

Included in previous reports (May 2011)

1.- 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.

2.- 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 (DOI 10.1007/s11032-011-9590-x).

3.- 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. *In press*.

4.- 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.

5.- 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.

6.- 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.

7.- 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 54: 460-470.

8.- 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. DOI: 10.1007/s00122-011-1646-0

New publications for this report

9.- Saintenac, C., D. Jiang, **E. Akhunov**. Targeted analysis of nucleotide and copy number variation by exon capture in allotetraploid wheat genome. Genome Biology, In press.

10.- Cantu, D., M. Govindarajulu, A. Kozik, M. Wang, X. Chen, K. Kojima, J. Jurka, R.W. Michelmore, and **J. Dubcovsky**. 2011. Next generation sequencing provides rapid access to the genome of *Puccinia striiformis* f. sp. *tritici*, the causal agent of wheat stripe rust. PlosOne. *In press*.

11.- Kalous, J. R.**,** J. M. Martin, **J. D. Sherman**, **N. K. Blake**, S. P. Lanning and **L. E. Talbert**. 2011. Phenotypic variation and patterns of linkage disequilibrium associated with introduced genes in spring wheat. Crop Sci. *In press*.

12.- Blake, N.K., S.P. Lanning, J. E. Berg, P. L. Bruckner, **J. D. Sherman** and **L.E. Talbert**. 2011. Registration of spring and winter habit wheat lines derived from elite cultivars of the alternate growth habit. J. Plant Reg. 5:418-421.

13.- Li, P., **J. Chen**, P. Wu, J. Zhang, Ch. Chu, **D. See**, **G. Brown-Guedira**, R. Zemetra, and E. Souza. 2011. QTL analysis for the effect of *RhtB1* dwarfing gene on coleoptiles length, seedling root length and numbers of bread wheat (*Triticum aestivum* L.). Crop Sci. *In Press*.

14.- A.j. Noriel, X-C Sun, W. Bockus and **G-H Bai**. 2011. Resistance to tan spot and insensitivity to Ptr ToxA in wheat. Crop Sci. 51:1059-1067

15.- 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. Theor. Appl. Genet. *In press*.

16.- Prasad PVV, Pisipati SR, Momcilovic I and Ristic Z. 2011. Independent and combined effects of high temperature and drought stress during grain filling and plant yield and

chloroplast EF-Tu expression in spring wheat. Journal of Agronomy and Crop Science (Published Online doi:10.1111/j.1439-037X.2011.00477.x).

17. Pradhan G.P., **P.V.V. Prasad**, A.K. Fritz, M.B. Kirkham, and **B.S. Gill**. 2011. High temperature tolerance in Aegilops species and its potential transfer to wheat. Crop Science *In press*.

18. Heslot, N., H.-P. Yang, **M.E. Sorrells**, and **J-L. Jannink**. 2011. Genomic selection in plant breeding: A comparison of models. Crop Science. Accepted with minor revisions.

19.- Naruoka, Y., **J. D. Sherman**, S. P. Lanning, **N. K. Blake**, J. M. Martin, and **L. E. Talbert**. 2012. Genetic analysis of long green leaf duration in spring wheat. Crop Sci. Accepted with minor revisions.

20.- Hao, Y., Z.Chen, Y.Wang, D. Bland, J. Buck, **G. Brown-Guedira** and J. Johnson. 2011. Characterization of a novel major QTL for adult plant resistance to stripe rust in US soft red winter wheat. Theor. Appl. Genet. *In press.*

21. Iwata, H. and **J.-L. Jannink**, 2011. Accuracy of genomic selection in barley breeding programs: a simulation study based on the real SNP data. Crop Sci. 51:1915-1927.

Under review in peer review journals (2)

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 (revised version in review).

Hao, Y., Y.Wang, Z.Chen, D. Bland, **G. Brown-Guedira** and J. Johnson. 2011. Conserved locus conditioning *Soil-borne wheat mosaic virus* resistance on chromosome 5DL in common wheat. Submitted to Crop Sci

Articles in Proceedings

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.

TCAP presentations

Ali, S., Zhong, S., and Puri, K. D. 2011. Virulence variability and genetic diversity among *Cochliobolus sativus* isolates recovered from barley and wheat in North Dakota. APS Annual Meeting, Honolulu, HI, August 6-10. Phytopathology 101:S5. (Poster).

Horsley, R. 2011. Breeding Success Workshop. American Society of Brewing Chemists Meeting

Friesen, T. 2011. Identification of a proteinaceous necrotrophic effector and its corresponding sensitivity locus on barley chromosome 6H. 4th International Workshop on Barley Leaf Blights, Dundee Scotland.

Friesen, T. 2011. Progress in Pyrenophora teres: genome sequencing and beyond. North American Barley Researcher's Workshop, Corvallis OR, Biotic and Abiotic Stress Section.

Hole, D. 2011 Improving barley and wheat germplasm for changing environments. International Conference on Efficient Water Use for Arid Agriculture, Yangling China.

Muehlbauer, G.J. 2011. Genomics approaches to Triticeae improvement. Oregon State University, Corvallis, OR

Muehlbauer, G.J. 2011. Genome-wide association studies in barley: gene discovery and applications. University of Missouri, Columbia, MO

Muehlbauer, G.J. 2011. Genome-wide association studies in barley: gene discovery and applications. University of Georgia, Athens, GA.

Anderson, J. "2011 Spring Wheat Variety Selection" presented at 11 MN locations (1/17-21/11) ~600 attendees

Steven Baenziger, 7/28/2011. Presentation to Ag Builders on the importance of resource efficiency in agriculture was made on July 28, 2011. Approximately 20 agricultural leaders/supporters in NE attended the presentation.

Sneller, C. 3/9/2011, Wooster, Ohio. Presentation to USDA Soft Wheat Quality Review outlining the TCAP grant. Attendance was approximately 120 breeders, millers, bakers, and others associated with the soft wheat industry.

Sneller, C. 4/12/2011, Custar, Ohio. Presentation to a NE Ohio wheat growers clinic on need to improve yield, stress tolerance, and role of genomic selection and TCAP in obtaining these goals. Attendance was approximately 25 wheat growers.

Pumphrey, M.O. 2011. Development of SNP markers for rust resistance. Western Wheat Workers Annual Conference, Aberdeen, ID.

Sneller, C. 4/12/2011, Chicago Illinois. Presentation to NAWG Wheat Summit outlining the TCAP grant. Attendance was approximately 70 leaders of the US wheat industry.

Sneller, C. 4/18/2011, Dallas, Texas. Presentation to Eastern Wheat Workers and Southern Small Grains Workers outlining the TCAP grant. Attendance was approximately 35 breeders and wheat scientists.

Sneller, C. 5/6/2011, Columbus, Ohio. Presentation to the OSU department of Horticulture and Crop Science on the OSU wheat breeding programs and the need to improve yield, stress tolerance, and role of genomic selection and TCAP in obtaining these goals. Attendance was approximately 35 faculty, students and staff.

Chen, J. 2011. Evaluation of Drought Tolerance in Wheat. 2011 Western Wheat Workers Meeting.

Chen, J. 2011. Introduction of T-CAP projects. 2011 growers field days

Chen, J. 2011. Breeding for drought tolerance. 2011 spring graduate seminar class

Chen, J. 2011. Evaluation of drought tolerance and N use efficiency in wheat. Ethiopian Ag industry representatives

Germplasm releases (13)

Germplasm releases included in previous report

Two adapted hard red spring wheat donor lines carrying three new stripe rust resistance QTLs (Lowe et al. 2011, TAG. 123:143–157).

- **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.

New Germplasm releases

Six isogenic lines of hexaploid wheat for vernalization alleles to provide access for wheat breeding programs to genes from elite cultivars possessing the alternate growth habit (Blake et al. 2011, JPR 5: 418-421).

Backcrossing introgression of the *vrn-A1*allele for winter growth habit into spring varieties

- **PI 660648** (winter line NB474-23): 'NuSky'/6*'McNeal'.
- **PI 660649** (winter line NB475-12): 'Paul'/6*McNeal.

Backcrossing introgression of the *Vrn-A1*allele for spring growth habit into winter varieties

- **PI 660650** (spring line NB481-23-1): 'Choteau'/6*'Yellowstone'.
- **PI 660651** (spring line NB489-54-1): 'Reeder'/6*NuSky.
- **PI 660652** (NB085WS03686): Choteau/6*Paul.
- **PI 660647** (NB085WS03690): Choteau/6*Paul.

MN98550–5/MN99394–1 hexaploid wheat recombinant inbred mapping population. This population comprises 139 F6:8 recombinant inbred lines (RILs) adapted to the Upper Midwest region of the USA.

- **PI 660540** MAP (MN98550–5) x **PI 660541** MAP (and MN99394–1).

Pending releases

Soft and hard winter wheat cultivars from ID with good yield performance under water limited conditions, to be released in 2011.

IDO599 (SWS)

IDO671(SWS)

IDO694 (HWS)