



Triticeae CAP
Coordinated Agricultural Project

TCap Transmission

FALL Issue

Funded by the USDA National Institute of Food and Agriculture



United States Department of Agriculture
National Institute of Food and Agriculture

TCAP – Significant Progress in Year 1

As TCAP approaches the end of the first year of funding, we are providing an update of the tremendous progress that has been made on all of the original objectives: (1) Discover and deploy beneficial alleles from diverse wheat and barley germplasm; (2) Accelerate breeding through marker-assisted selection and genomic selection; (3) Implement sequence-based genotyping methodologies to discover new allelic diversity; (4) Implement web-based tools to integrate marker-assisted selection and genomic selection strategies into breeding programs. (5) Develop and implement a Plant Breeding Training Network to train the next generation of plant breeders (see Education review page 7).

Research Update

The overall research goals of the project are to phenotype and genotype diverse barley and wheat germplasm pools to discover and deploy alleles that improve yield under biotic and abiotic stresses, and to use genetic markers to rapidly deploy favorable alleles and accelerate breeding cycles.

Phenotyping

Phenotypic characterization of the barley and wheat National Small Grain Core Collections (NSGC) to various pathogens is progressing nicely. One thousand lines of the wheat NSGC collection were evaluated for stripe rust, leaf rust and stem rust. 1050 lines of the barley NSGC collection were evaluated for resistance to spot blotch and spot form of net blotch. These data will be used to identify novel genes for resistance and as sources of resistance for breeding programs.



2 students evaluating NSGC in Idaho

One key aspect of the TCAP is to develop and utilize high-throughput phenotyping of climate-change related traits such as water use efficiency (WUE) and nitrogen use efficiency (NUE). To standardize WUE and NUE phenotyping we chose to use Canopy Spectral Reflectance (CSR) technology. 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 were investigated in rainfed and irrigated environments. 540 wheat accessions from the NSGC were evaluated for WUE and NUE. These data will be used to map genes conferring NUE and WUE.

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Genotyping

Significant progress has been made on genetically characterizing the barley and wheat NSGC collections

Research Update (continued)

(see page 4). Genotyping platforms have been developed for wheat and barley to enable examining 9,000 single nucleotide polymorphisms (SNP) in parallel. SNP assays provide a detailed description of the genetic composition of the NSGC collection. The barley data has been used to select parents for developing a nested association mapping (NAM) population, as well as confirming the diversity of the wheat NAM (see page 6). These data will be used in the near future to identify associations between SNP markers and agronomic and disease resistance traits.

To enhance our capacity to assess the genetic diversity in barley and wheat germplasm collections and to increase the efficiency of breeding, gene capture and genotyping by sequencing (GBS) technologies are in the process of being developed (see below). We are working with Roche/NimbleGen and an international consortium of wheat and barley geneticists to develop gene capture technologies for wheat and barley. The gene capture designs have been developed and the initial testing will be conducted in the near future. Currently, GBS is being used to develop genetic maps in wheat and barley mapping populations.

Molecular Selection

The TCAP has implemented strategies to accelerate breeding through marker-assisted selection and genomic selection, employing the USDA-ARS funded genotyping centers in collaboration with breeding programs. Marker-assisted selection is being conducted for disease resistance, agronomic and quality traits. In addition, the TCAP has trained several different genomic selection models in barley for agronomic, disease, and grain quality traits and genomic selection strategies are being pursued.

Database

To fully exploit the genotypic and phenotypic data produced through TCAP for plant breeding, a robust relational database is required. The Hordeum Toolbox (THT) database framework, created during the barley CAP, was used to establish The Triticeae Toolbox (T3) database. The SNP and phenotypic data generated during the first year of the project are being entered into T3 (see page 4). 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.



Wheat Gene Capture By: Eduard Akhunov

The complexity and large size of the wheat genome (6 times larger than human genome) are the major challenges for its detailed analysis. Reduction of the complexity of wheat genomic DNA by enriching it with valuable targets (genes, regulatory elements) will allow us to analyze a large number of samples at a relatively low cost. In this study, we successfully used a new enrichment method for targeted capture of genes in the wheat genome followed by their sequencing using a next-generation sequencing instrument. First, we evaluated the impact of polyploidy and intra-genomic gene duplications on the efficiency of genetic variation discovery in the wheat genome by empirically validating identified variable sites. Using the overall depth of sequence coverage across genes and the depth of coverage at variable sites, we were able to detect gene copy number variation resulting from gene deletions or duplications. Finally, we

used the identified cases of gene copy number variation, gene sequence divergence and polymorphism to estimate the extent of genetic differentiation in coding regions between cultivated and wild tetraploid wheat, assess the impact of discovered mutations on gene function and biological pathways and gain a better understanding of evolutionary forces that shaped patterns of divergence and variation across the wheat genome. The approach developed in this study will be utilized for the discovery of new allelic variants of useful agronomic genes in wheat.

Reference: Saintenac C, Jiang D, Akhunov ED. Targeted analysis of nucleotide and copy number variation by exon capture in allotetraploid wheat genome. *Genome Biol.* 2011 Sep 13;12(9):R88

Link: <http://genomebiology.com/2011/12/9/R88>

Taming plant breeding data in the genomics era:

The Triticeae Toolbox

By: Jean-Luc Jannink

A quick look at tables in the *Triticeae* CAP proposal that list datasets to be compiled by the project shows how ambitious it is: across wheat and barley, there are some 50 datasets, each multi-trait, multi-location, and multi-year, sometimes numbering into the thousands of entries and DNA markers. Beyond their massive scale, the raw data entering these sets will arrive asynchronously from many sources (e.g., different field-trial collaborators and genotyping centers). How will we ensure completeness and correct integration of the data? In short, how will we avoid utter chaos? But more importantly still, as a collaborative endeavor, how will TCAP ensure that each participant can access the most up-to-date, error-checked, and curated version of a dataset? How about asking each collaborator to email data they have collected to all other collaborators? Um... No. Instead, all data will be centrally located, curated, and accessible through a web interface in a database called The *Triticeae* Toolbox (T3).

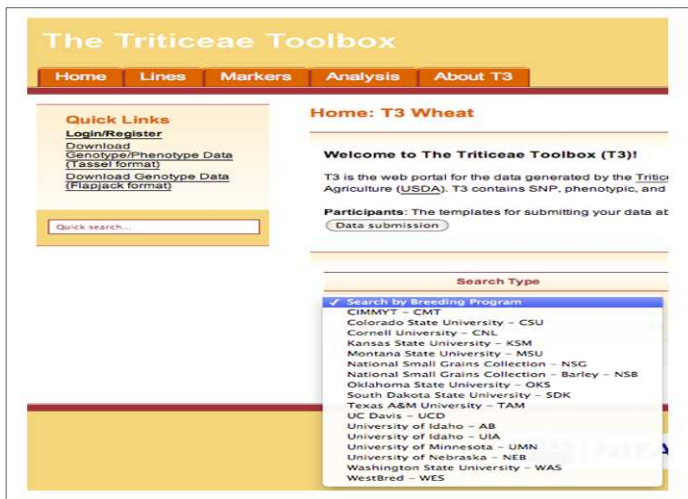


Figure 1. Screen shot of the wheat side of the T3 home page with **currently recognized wheat breeding programs listed.**

Accurate

The first T3 objective of ensuring complete and valid datasets is easier said than done. Any database requires more design and construction effort than simply entering values in a spreadsheet. To facilitate valid data integration, we have designed an upload process that unambiguously identifies and relates new data to existing data. Guaranteeing that germplasm names are unique, searchable, and link with other databases (e.g. the Germplasm Resource Information Network of the National Plant Germplasm System) has been a priority. Finally, because we have only a single curator, we have been working to make uploads simple, expecting the TCAP Objective Coordinators to become familiar with upload formats and procedures so that the files they deliver are ready to go.

Cluster Lines by Genotype

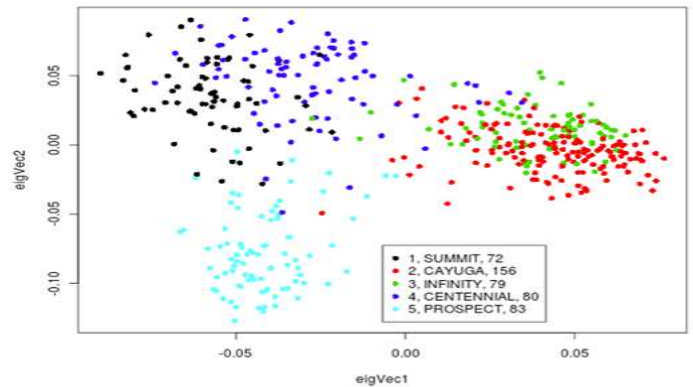


Figure 2. Screen shot of 470 wheat lines in T3/wheat plotted according to principal component analysis of their marker data and colored into five clusters. Representative lines, and the size of each cluster is listed.

Accessible

The second T3 objective is to make these data usefully accessible to participants. Our approach is to consult with a T3 User Group: a circle of both wheat and barley researchers who plan to analyze TCAP data and can accurately describe to us the ways in which they require the data to be accessed and formatted. The interface will allow users to specify germplasm, traits, and markers using several search and filter options. The corresponding data points will be assembled into two-way tables (germplasm ´ markers for genotypic data; germplasm ´ traits for phenotypes), allowing it to be imported to external analysis packages. We will also design and implement analyses to be run on the T3 servers themselves at the suggestion of the User Group.

Far reaching

Finally, our ambition is to make T3 useful to public-sector breeding programs beyond the specific TCAP datasets. Plant breeding is becoming a very data intensive activity. Without dedicated information technology support, breeders in the public sector have not been able to make the transition from spreadsheet-based data management to databases, but that transition is clearly needed. Even for public sector programs, the quantity of data available on each new breeding line is increasing tremendously and needs to be managed to streamline curation, integration, and validation of data prior to analysis. The TCAP goals of avoiding data chaos and improving accessibility are also valid within individual wheat and barley breeding and research programs. To this end, we strive to simplify the user interface, implement functions that the User Group find desirable, and develop tutorials.





Exploiting genetic diversity in wheat and barley using high density SNP genotyping technologies developed by Illumina

By: Shiaoman Chao, USDA-ARS, Fargo, ND

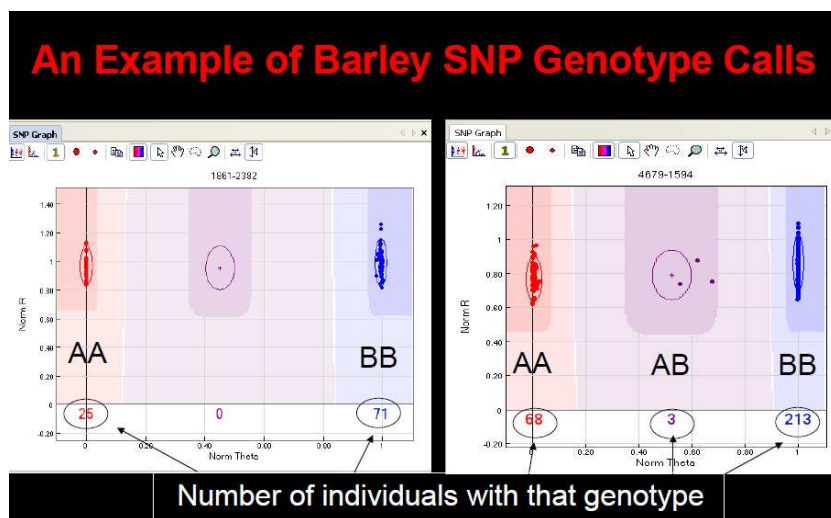
One of the TCAP objectives was to exploit genetic diversity present among wheat and barley National Small Grains Collections based on high density SNP marker data. SNP data will allow for the selection of diverse germplasm from the core collections to be used for genetic studies to discover favorable alleles and for breeding.

The recent advance of next generation sequencing technologies has accelerated large-scale SNP discovery. In wheat and barley, the Illumina iSelect BeadChip platform, containing 9,000 SNPs discovered in cDNA sequences, was developed prior to the start of TCAP. In wheat, the SNP discovery was carried out under the USDA-AFRI funded wheat SNP project (PI: Eduard Akhunov) in collaboration with International Wheat SNP Working Group (<http://wheatgenomics.plantpath.ksu.edu/IWSWG/home>). Using Illumina's Infinium genotyping assay, the genotyping performance for wheat 9,000 SNPs was evaluated using 5,500 samples, including both hexaploid and tetraploid genotypes. The assay success rate was close to 90%, with 60% and 70% polymorphism detected in hexaploid and tetraploid samples geno-

typed, respectively. In barley, the iSelect 9K platform was developed by scientists in Germany and UK. The SNPs in barley OPA1 and 2 previously developed under barley CAP were also included in the design. The genotyping performance was evaluated among European samples, and the information was generously made available to the Fargo lab before publications.

Both wheat and barley 9K SNP designs were subsequently used to genotype NSGC wheat and barley collections under TCAP. The 4,416 wheat collections assayed in-

cluded 3,870 common wheat and 546 durum wheat accessions. In barley, 2,448 cultivated barley accessions were used in the genotyping. All but four samples assayed produced genotype data. The high levels of polymorphism found among NSGC collections, 88% in barley, 65% in common wheat and 76% in durum, reflected the usefulness of evaluating these collections and the potential benefits of exploiting allele diversity for wheat and barley improvement.



Publications related to the TCAP

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

- 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.- 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.
- 3.- 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.
- 4.- 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.
- 5.- 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.
- 6.- 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
7. 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.

CAP Aids Fight Against Stripe Rust in California

By Lynne Medgaarden



One deadly plant disease found in wheat may have met its match. Yellow rust, also known as stripe rust, is one of three rust diseases found in wheat grown in cooler environments in northern latitudes. According to the USDA-ARS Cereal Disease Laboratory wheat stripe rust can cause losses of 40% with some wheat fields totally destroyed by the disease. It is a major disease of fall seeded wheat or spring wheat planted adjacent to infected fall seeded wheat. While stripe rust is lethal to wheat it does not produce toxins dangerous to human consumption like other fungi (e.g. Fusarium). It causes large yield losses and decreases the quality of wheat.

Fortunately, the development of large USDA Collaborative Agricultural Projects (CAP) in wheat and barley provided the support required to implement new breeding technologies and accelerate the development of resistant varieties. Dr. Jorge Dubcovsky, leader of the wheat breeding program at the University of California and of the Wheat-CAP (2005-2010) and Wheat-Barley CAP (2011-2016) and his team implemented these new technologies in California and were able to control the epidemic.

“Stripe rust is a devastating disease of wheat, and the appearance of more virulent races in the year 2000 resulted in large losses that reached 25% of the California wheat crop in 2003. These new races attacked the most productive wheat varieties from California so we had to look for new sources of resistance. The availability of more precise molecular methods of selection helped us to provide a fast answer to the stripe rust epidemics in the beginning of the 2000s so that today the epidemic in California is over and resistant varieties are available to the growers,” stated Dubcovsky.

Dubcovsky and his team of scientists and graduate students identified a gene with resistance to wheat stripe rust. “We use these genes to develop wheat varieties resistant to stripe rust that do not require the application of fungicides, which is beneficial to farmers, the environment, and the consumer. Today we have controlled the stripe rust epidemics and almost all the new varieties are resistant to these new races of stripe rust.” Dubcovsky has been working on stripe rust resistance projects for the last 15 years. This research was funded by the previous USDA’s National Institute of Food and Agriculture (NIFA) Coordinated Agricultural Project, WheatCAP, and the current Triticeae-CAP grants.

Dubcovsky’s team first worked in mapping the location of these genes on the chromosomes and then in developing molecular markers from these chromosome regions to help select varieties carrying multiple resistance genes. This technology, called marker assisted selection, accelerates the traditional breeding process. The resulting varieties are not considered genetically modified organisms, since they are obtained by normal crosses.

“Marker assisted selection makes the selection process faster and more precise. Another advantage of this technology is that we can pyramid multiple resistance genes to extend the durability of the resistance,” said Dubcovsky. Resistance genes are normal wheat genes and can be introduced in any wheat variety by simple

crosses. Then molecular markers are used to select the progeny of these crosses carrying the genes. Without this technology, once a breeder introduces one resistance gene, he doesn’t know when additional genes are being introgressed since the plants are all resistant. With the molecular markers scientists can follow the genes without the need to test for resistance.

In 2008 the first resistant wheat variety (Patwin) developed by marker assisted selection was released and today several resistant varieties developed by this technology are starting to be grown in California both from public breeding programs (e.g. Lassik, and Desert King-High Protein) and from collaboration between the UC-Davis program and private wheat breeding programs operating in California (e.g. Espresso, Blanca Grande 515, Summit 515, Westmore, New Dirkin, etc.). “We have also mapped new resistance genes and we are starting to introgress those in our varieties as a second line of defense, in case new races manage to overcome the first genes we put in,” Dubcovsky said.

Today the stripe rust epidemic is well controlled in California and the new varieties are resistant to the new virulent races of stripe rust eliminating the need of costly fungicide applications. “Fungicides may be effective in controlling stripe rust but they can be expensive, increasing the cost of production. Also the application of fungicides is not the best for the environment if they can be avoided,” Dubcovsky continued. “Resistant wheat and barley varieties have enabled growers to avoid costly fungicide applications, reduce yield losses caused by the pathogen and produce a higher quality crop.”



Nested association mapping project for spring wheat

By: Luther Talbert and Nancy Blake

An important goal of the T-CAP grant is to access genes from landrace accessions in the National Small Grains Collection to improve modern wheat varieties. The landrace accessions themselves are inferior to modern varieties for both agronomic and quality characteristics. However, there are many good genes hidden amongst the undesirable ones in these ancient varieties. The process of nested association mapping (NAM) was developed by the maize community to allow identification of favorable alleles from a diverse germplasm set (Yu et al., 2008). NAM combines the advantages of traditional linkage analysis with association mapping, providing higher resolution and power. Steps in NAM include 1) Creation of a set of inbred lines using diverse founders crossed with one common parent, 2) Dense genotyping of parental lines, 3) Less dense genotyping of progeny, 4) Phenotyping of progeny, and 5) Statistical analysis identifying marker-trait associations.

T-CAP is developing a spring wheat NAM population by crossing a genetically diverse set of 25 landraces to a common parent, named Berkut. Berkut was developed by CIMMYT for drought-stricken areas around the world. Extreme height and photoperiod sensitivity in the landraces make them difficult to phenotype in many of the target environments for the T-CAP. Among the genes that differentiate Berkut from the landraces are ones for semidwarf growth habit and photoperiod insensitivity. Thus, our strategy is to select, based on phenotype, a set of 100 F₄ plants from each cross that are photoperiod insensitive and have semidwarf growth habit. Recombinant inbred lines derived from these plants will be phenotyped by T-CAP participants throughout the spring wheat region of the United States. In addition, all lines will be genotyped by the USDA Genotyping Laboratories, and linkage analysis will be conducted to identify favorable alleles from the landraces that can be incorporated into our variety development programs.

At the present time, we are growing F₃ plants from over 30 crosses of landraces by Berkut, as well as about a dozen crosses involving local varieties and drought-tolerant lines from other sources. We began the inbreeding process with about 800 F₂ plants per cross, and are selecting in the F₂ and F₃ generations for lines we think are either homozygous or heterozygous for the gene conferring semidwarf habit. Our

goal is to test approximately 400 F₄ plants per cross under 12-hour days in growth chambers in spring 2012 to identify 100+ recombinant inbred lines that are both photoperiod insensitive and semidwarf. The Dubcovsky lab also has population development underway with lines that have shown potential in California, all crossed to the common parent Berkut. The number of final populations to be tested may be revised based on results from parental genotyping.

Our goal for the Berkut NAM populations is to have the genotyping completed for all lines by 2013 and to have sufficient seed available for phenotyping in the field in 2014 and 2015. In addition to the crosses with Berkut, we are also crossing each of the landraces with the variety Clear White. Clear White is a variety from California that has shown good performance in several places, including Montana. Following the procedure proposed by Pumphrey et al. (2007), and modified by Blake et al. (2011), we will use these populations to develop near-isogenic lines to confirm any important QTL identified in the Berkut populations.

The final stage of the project will be to cross the beneficial genes identified from the landraces into elite breeding material for incorporation into new varieties for spring wheat producers.

References

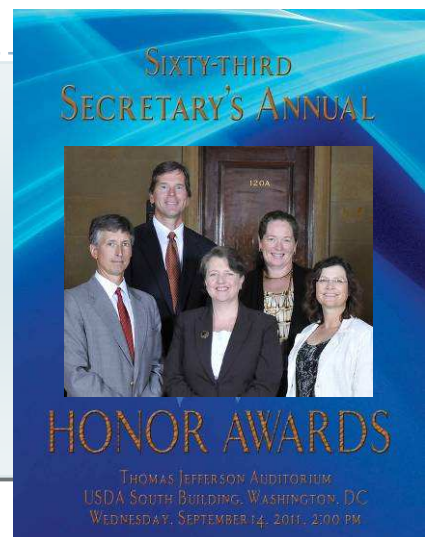
- Blake NK, Stougaard RN, Weaver DK, Sherman JD, Lanning SP, Naruoka Y, Xue Q, Martin JM, Talbert LE (2011) Identification of a quantitative trait locus for resistance to *Sitodiplosis mosellana* (*Gehin*), the orange wheat blossom midge in spring wheat. *Plant Breeding* 130:25-30
- Pumphrey MO, Bernardo R, Anderson JA (2007) Validating the *Fhb1* QTL for Fusarium Head Blight Resistance in Near-Isogenic Wheat Lines Developed from Breeding Populations. *Crop Sci.* 47: 200-206.
- Yu J, JB Holland, MD McMullen, Buckler, ES. 2008. Genetic design and statistical power of nested association mapping in maize. *Genetics* 178:539-551.

Barley and Wheat CAP Honored

The Barley, Wheat, Potato, and Tomato Coordinated Agricultural Projects funded by the National Institute of Food and Agriculture of USDA received awards from the Secretary of Agriculture September 14, 2011 in Washington DC in recognition of their scientific discoveries and their translation into beneficial agricultural products.



Brian Steffenson with honor award





Triticeae CAP
Coordinating Agricultural Project

Education News

PBTN – Plant Breeding Strategies - Course Overview - Fall

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During the first semester of PBTN, students are being challenged to understand the process of designing a plant breeding program and differentiating between approaches that may be used. In this introduction to Plant breeding strategies, a series of questions are guiding students in investigating TCAP breeding programs. As students work through the questions, they are becoming familiar with the planning process that underlies that research. Students are also being introduced to many of the research projects connected to T-CAP as they hear about the work of other

students. Because of the diversity of projects involved, students are being exposed to different schemes or approaches to designing breed-



ing programs. While a student may focus on a single scheme, more advanced students may come to realize that different traits are more amenable to different

schemes and will be able to differentiate between breeding approaches.

Student Learning Goals

- * Gain greater understanding of research objectives and approaches in their advisors' lab
- * Become acquainted with the diversity of research projects associated with T-CAP
- * Differentiate breeding approaches and identify factors that determine their use

Students are enrolled in one credit special problems at home university. Course will include 50 minute weekly discussion and 1 to 2 hours outside work per week.

PBTN - Online Environment

<http://passel.unl.edu/communities/pbtn>

Features/materials completed:

- Customizable 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>

Student Film By: Alain Douchinsky



Two Masters students from Montana State University Film School travelled the country this summer creating footage to be used in educational and recruitment films. Footage was shot at universities, experiment stations and genotyping centers in Colorado, Nebraska, New York, Washington, Minnesota, North Dakota and Montana. Students interviewed over 25 people including TCAP breeders, pathologists, molecular geneticists, students and growers. Twenty hours of footage is being transcribed which will be shared for development into multiple products. The students will create

at least two films this winter as part of their degree requirements. We enjoyed gathering footage over the summer, finding that most individuals seemed comfortable talking with us, almost forgetting the camera was there, which was surprising. I was really impressed by the depth of people's answers. We did not share our questions beforehand and yet the answers we got were very informative, passionate, and thoughtful. I have a knowledge of Biology, but not specifically of plant breeding and this trip taught me so much about what plant breeders do. It made me realize that even with my

background, I had no clue what kinds of plant research goes on and how it affects farmers and consumers, which made me that much more interested in educating the public about plant breeding. This trip gave me a greater appreciation for the land and the crops that we tend to take for granted. To be standing in a field of endlessly waving wheat as a golden sun sets, is a memory I will have forever."

*Request for
Proposals were
sent to*

- *43 Historically Black Colleges*
- *18 Hispanic Serving Institutions and*
- *20 Tribal Colleges*

MSI Proposals

Mary Brakke, Don Lee, Frances Lawrenz, Eric Moore and Jamie Sherman met with 8 representatives from minority serving institutions (MSI) in Chicago. Minority serving institutions that were represented included Arkansas State Pine Bluff, Alabama A&M, Chicago State, Delaware State, Elizabeth State, Fayetteville State and Fort Valley State. From interactions at this meeting, personal conversations with other

MSI faculty and the focus group report, the education committee with input from executive committee drafted a request for proposals (RFP). The RFP was sent to 43 Historically Black Colleges and Universities, 20 Tribal Colleges, and 18 Hispanic serving institutions. 11 Requests for Proposals were received, with 8 proposals receiving funding. Funded proposals all build relationship between MSI and

TCAP projects.

Funded MSI/TCAP partnerships include PIs from:

- Chicago State University/ UMN
- Tuskegee/MSU
- Texas A&M (Amarillo)/UI
- U Arkansas, Pine Bluff/ WSU
- U Arkansas, Pine Bluff/ MSU
- Lehman College (New York)/ UNL
- Rust College /CSU
- Fayetteville State University/KSU

New Faces on the Advisory Board

There are several new people on the Education advisory board. We appreciate the advise and direction that they provide.

Dr. Philipp Simon, Professor (USDA), Department of Horticulture, University of Wisconsin-Madison

Dr. Allen Van Denzyne, Senior Scientist, Seed Biotechnology Center, Univer-

sity 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 at Pioneer Hi-Bred Internationls Inc.

Dr. Janet Poley, President, American Distance Education Consortium

Dr, Sarwan Dhir, Fort Valley State University, Director of Center for Plant Biotechnology

Sid Perry, Ph.D., WestBred/Monsanto senior breeder for the Central Plains program



Graduate Students Online



More graduate students have been recruited and training has been initiated than the initial goal of 11 for the first year. During the summer a group of students attended a regular meeting online where 5 student's presented research talks

that are archived at <http://passel.unl.edu/communities/index.php?idcollectionmodule=1130274157>. Liana Nice from University 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. Brittany Hazard of UC Davis presented her research on

Development of Wheat with Increased Levels of Resistant Starch with 19 people participating. Tyson Howell also presented to the same group about his drought tolerance research. On August 30th, Josh Hegarty presented aspects of his wheat rust project. Student presentations provided an opportunity for students to be introduced as well as identifying bugs in the online environment.



CSR Survey Overview

What was the most important thing you learned from the training?

- The presentation from Ocean Optics was a good introduction to the instrument and how to use it. The most useful information came from Julian from

CIMMYT, who had good information from using the Jaz in the field.

- The fact that there are so many indirect methods of light based measurements
- Information about all of the different options available for configuring the Jaz device. This will be helpful in

ordering the device that is best for our purposes.

- The most important thing that I learned was about the file structure and data management issues that we will have to address as we initiate data collection.
- Technical aspects of theory

CSR participants came from all over

Institute	NDSU - 2
ARS USDA - 1	Ohio - 1
BUSCH - 2	Oregon - 1
CSU - 6	UC Davis - 3
Idaho - 2	UMN - 2
KSU - 4	UNL - 3
Maryland -1	Utah - 1
Missouri - 1	Virginia - 1
MSU - 7	WSU - 2



What best describes you?

Answer Options	Response Percent	Response Count
Graduate student	30.0%	6
Technician	30.0%	6
Post Doctorate	5.0%	1
Principle Investigator	35.0%	7
answered question		20

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.

High resolution TCAP logo now available for presentations and posters (contact jsherman@montana.edu)

Evaluation - Baseline Survey Results

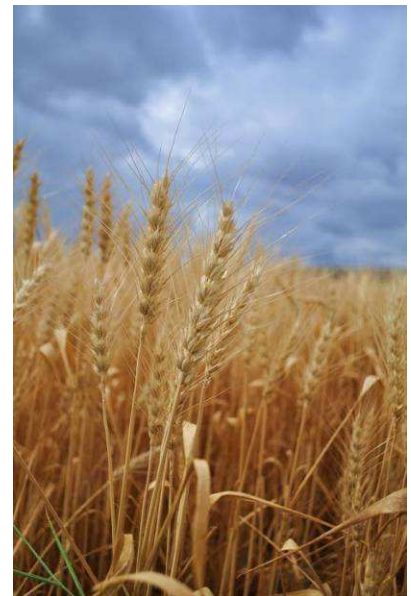
Graduate students

In early July 2011, a baseline survey was administered online to current students funded by the TCAP project. The survey assessed students' perceptions of plant breeding education, interest and motivation in the plant breeding field, perceptions of the TCAP educational programming, and collaborative networks with other students and researchers within and outside of the TCAP project.

All 12 students completed the survey, including six male students and five female students. All students were in their 20s. None of the students reported being of Hispanic or Latino origin and most students identified as White. Three-quarters of the students reported being U.S. citizens.

The following is a brief summary of key findings:

- Of the plant breeding knowledge areas, genetics received high ratings with almost half of all the students (42%) feeling that they are “very” confident in that area, while one-quarter of the students (25%) reported that they were “not at all” confident in teaching strategies.
- As for plant breeding skills, most students (83%) felt “very” confident in working collaboratively. According to the data, the skill most often used by students (42%) was observing and interpreting results. Half of those surveyed (50%) felt “not at all” confident in their skills to make genome wide selections. Choosing parents and making crosses (55%) and making genome wide selections (55%) were the least often used skills.
- About three-quarters of students (73%) expressed high interest in the plant breeding field and reported being highly motivated to pursue a plant breeding career.
- Conducting research was the most participated in activity, with 75 percent of the students reporting that they participate in conducting research “very often”. The most valued activity was problem solving (100%).
- Students reported interacting with their advisor “more than once a week” (80%), with half of these interactions identified as primarily social.



PIs

An online survey was administered to TCAP principal investigators (PIs) to assess their perceptions about the educational components of the TCAP project, including their perceptions of knowledge areas and skill sets in plant breeding, their collaborative networks and interactions with faculty from minority serving institutions (MSIs) and other research institutions, and their thoughts on plant breeding education.

Of 54 PIs, 42 PIs completed the survey in July 2011 for a response rate of 78%. Four PIs were excluded from the survey due to their close involvement in evaluation activities and the development of the survey. PIs ranged in age from 30 to 69 years old. Only a few PIs (11%) reported being of Hispanic or Latino origin. Most PIs identified themselves as White (76%), while others identified as Asian (16%), American Indian or Alaskan Native (5%), and mixed race (3%).

The following is a brief summary of key findings:

- Majority of the PIs reported research to be the most important component of TCAP (81%).
- When asked to identify the two most important things they see the TCAP education component achieving, the highest number of PIs suggested training students to be the most important factor (53%), while recruitment and attraction of students to plant breeding and technology and familiarity with genomic techniques emerged as the second most important thing.
- About one-third of the PIs identified the lack of interest and/or awareness of plant breeding (35%) as the top barrier to increasing the number of underrepresented minorities in plant breeding.
- When asked about their relationship with minority serving institutions (MSIs), the highest number of PIs (58%) reported their relationship was "not strong at all" while 5% reported having "very strong" relationship with the MSIs.
- Similarly, 76% of the PIs reported having no collaborations with MSI faculty and 2% (one PI) reported collaborating with MSI faculty a lot.
- Lack of mutual goals/fit was identified by about one-quarter of the PIs (23%) as the top barrier to collaborating with MSI faculty.
- Of the items listed as plant breeding knowledge areas, most all of the PIs (95%) reported experimental design to be the most valuable area.
- Three-quarters of the PIs (75%) thought laboratory experience and one-on-one mentoring to be the most important item of the educational components of TCAP, and exposure to students from different ethnic backgrounds as the least important (5%).
- When asked about their collaborative networking with others, 70% indicated never interacting with researchers from their own institutions or from industry while the most interactions were with their advisees (76% more than once a week). Most of their interactions with their advisees were about trouble shooting research (36%) or interpreting research results (25%).



Comparison of PI and students surveys

There are areas of agreement and disagreement between TCAP PIs and TCAP students with respect to knowledge areas and skill sets highly valued by the PIs and student confidence in those areas, as well as educational processes that both TCAP faculty and students considered to be extremely important and the nature of their collaborative networking with others. Data from the surveys indicated that most students seemed to have less confidence in most areas that PIs consider to be very valuable knowl-

edge areas or skill sets for graduating MS or PhD students in plant breeding. TCAP students and faculty were overall in agreement about what educational processes were most important. And while they agreed about who they interact with the most (advisor-advisee), the surveyed TCAP PIs and students differed in describing the nature of the interaction—with PIs indicating the interaction to be mostly about trouble shooting research or interpreting research data while the surveyed TCAP students re-

ported the interactions to be mostly social in nature. It is possible the differing views in describing the nature of interactions is mainly due to the PIs reporting broadly the type of interactions with their advisees and the surveyed TCAP students being in the early phase of their research labs, therefore lacking sufficient research experience that calls for the type of interactions the PIs reported.

Entering Mentoring

One of the skills many of us have learned through trial and error is mentoring. TCAP is employing “Entering Mentoring: A Seminar to train a new generation of scientists” that was developed through the Wisconsin program for scientific teaching to accelerate the development of mentors (Handelsman et al. 2005). We believe this is important since mentors of plant breeding students are needed now as much if not more than ever before. Graduate student mentors are paired with undergraduate mentees. This relationship provides undergraduates with a positive research experience and provides graduate students with the chance to mentor. Through the seminar, graduate students are developing a mentoring style. The seminar provides an opportunity for graduate students to mentor and then reflect on that experience to encourage improvement. Graduate students sharing their experiences so that each are exposed to more students and more situations.



Meet MSI Faculty - JiaQian Zhu

My name is JiaQian Zhu, PhD, Assistant Professor of Biology in the Division of Science and Mathematics at Rust College. Rust College is a HBCUs (Historically Black College and University) located in Holly Springs, MS. There are about 200 undergraduate students who are majoring in biology. 95% of our students are African Americans. Within the past ten years, no undergraduate students from Rust College have worked on any sort of plant breeding. After receiving the award for the MSI proposal, our college president, Dr. David Beckley, sent me a congratulation letter. The vice President of Academic Affairs, Dr. Paul Lampley, e-mailed all faculties about the news.

Project description

The project that will cooperate with a TCAP research institute - CSU to identify genes related to drought tolerance from wheat. The goal of the project is to train African American undergraduate students to identify important genes related to drought tolerant/resistant in common wheat (*Triticum aestivum* L) by using gene information from Arabidopsis.

Our objectives are: 1) To establish partnership between Rust College and CSU; 2) Recruit two students to participate in the TCAP wheat breeding project and learning

research skills; 3) Select three important drought tolerant genes from Arabidopsis using PGMapper program and obtain the DNA sequence; 4) Use BLAST program to identify potential orthologous genes controlling drought tolerance in a common wheat using gene information from Arabidopsis; 5) Create PCR markers to amplify and sequence wheat.

Reasons that make us interested in collaborating with the TCAP project.

1) This project opens a door for minority students encouraging interest in breeding and will improve student understanding in the principles of genetics.

2) The school leaders at Rust College always encourage faculty to write proposals for scientific and educational researches. After receiving an e-mail notice about a funding opportunity of TCAP, Dr. Paul Lampley, and Dr. Frank, Yeh (Chair of Division of Science and Mathematics), considered that it is a good project. They encouraged me to write a proposal and gave practical support in proposal writing. They think that this project will not only provide faculty research opportunities, but also provide students with hands on ex-

perience.

3) I am qualified to perform this project, having research experience in wheat genetics and breeding. My PhD project constructed a genetic map of common wheat, identifying genes related to wheat pre-harvest sprouting. In addition to teaching, I continue in active research simultaneously training minority students in research skills.

4) We welcome this type of partnership hoping it will increase student interest and competitiveness in applying to graduate study.



Triticeae CAP Annual Meeting



January 13, 2012

Courtyard Marriott
HOTEL CIRCLE
595 Hotel Circle South
San Diego, California 92108
T 619.291.5720

Graduate Student meeting

Schedule:
3:00—6:00 TCAP Graduated student presentations and discussion

6:00-7:00 **TCAP Mixer** for all participants with Hors d'oeuvre and cash bar (RSVP required to deanna.crow@montana.edu by December 7, 2011)

A block of rooms are being held at a reduced rate of \$129 per night. Please reserve your room by **December 7, 2011**. Individual attendees will make their guest room reservations directly with Hotel's Reservation Department at **888-236-2427**. Please request **TCAP Annual Meeting Room Block** rate in order to receive this special group rate. Standard check-in time is 3:00PM and check-out time is 12:00PM. Any individual cancellations or changes must be made at least 72 hours prior to the arrival date.

January 15, 2012

Town and Country Convention Center, Windsor Room part of Regency Ballroom

(see map below indicated with arrow)

- 8:30 am - noon **Reporting session**
- 8:30 – 9:00 Education Jamie Sherman
- 9:00 – 9:30 T3 database Jean-Luc Jannink
- 9:30 – 10:00 Genotyping (MAS and Genomic selection) Gina Brown- Guerdira
- 10:00 - 10:30 Genotyping (Gene capture, Genotyping by sequencing) Eduard Akhunov
- 10:30 – 10:50 Break
- 10:50 – 11:30 Phenotyping
Mike Pumphrey, Brian Steffenson, Pat Hayes, Luther Talbert, Kevin Smith, Clay Sneller,
- 11:30 – noon Canopy Spectral Reflectance
Jorge Dubcovsky, Luther Talbert,
- noon – 1:30 pm Lunch on your own
- 1:30 – 3:00 Breakout groups (T3 data base, Genotyping, Phenotyping)
- 3:00 – 3:20 Break
- 3:20 – 4:30 Breakout groups report on future plans
- 4:30 – 5:00 Advisory board response and discussion

