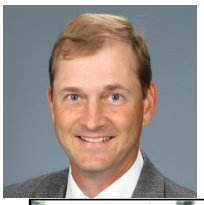
Triticeae CAP
Coordinated Agricultural Project

TCap Transmission

February 2014

Funded by the USDA National Institute of Food and Agriculture

Directors notes: Gary Muehlbauer and Jorge Dubcovsky



TCAP Annual Meeting

The TCAP annual meeting was held on January 12, 2014 in San Diego, CA at the Town and Country Convention Center. Approximately 100 people attended the meeting including TCAP participants (PIs and students), stakeholders and the scientific advisory board (Peter Langridge, Robbie Waugh, Nick Tinker, Mike Davis and Ed Buckler). The meeting was split into four parts including: (1) a reporting session for the stakeholders; (2) a reporting session for the scientific advisory board; (3) a breakout session to coordinate the year 4 activities and; (4) a student poster session. Gary Muehlbauer (University of Minnesota) reported to the stakeholders some of the highlights of the project. This was followed by a discussion with the stakeholders about traits and the future of the TCAP effort. To start the scientific reporting session, Jorge Dubcovsky (UC, Davis) presented an update of the overall progress of the project. During his talk it was obvious that in all aspects of the project the group has exceeded the original objectives of the grant. Jamie Sherman (Montana State University) and Mary Brakke (University of Minnesota) reported on the efforts of the education team. Over 100 graduates students have been participating in TCAP activities (42 gradute students are at least partially funded by TCAP), indicating the large impact the project is having on training plant breeders. As part of the education session, Steven Baenziger (University of Nebraska) discussed the skills needed to become an effective breeder. Reports were also provided on the status of T3 (Jean-Luc Jannink, USDA-ARS, Ithaca, NY), and genotyping (Gina Brown-Guedira USDA-ARS, Raleigh, NC; Shiaoman Chao, USDA-ARS, Fargo, ND). The progress on the wheat phenotyping for nitrogen use efficiency (NUE) and water use efficiency (WUE) was presented by Luther Talbert, (Montana State University) with specific projects and results highlighted by three graduate students: Katherine Frels (University of Nebraska), Kyle Shroyer (Kansas State University), and Shiferaw Gizaw (Washington State University). Kevin Smith (University of Minnesota) and Alfonso Cuesta-Marcos (Oregon State University) presented the progress on barley phenotyping for NUE, WUE and low temperature tolerance. Brian Steffenson (University of Minnesota) and Mike Pumphrey (Washington State University) reported the disease phenotyping efforts and results. Two short sessions were devoted to elevator speeches given by the students that focused on introducing themselves and providing a short synopsis of their projects. The scientific reporting session was followed by breakout groups focused on discussing future efforts related to T3, barley phenotyping and breeding, wheat phenotyping and breeding, genotyping, and data analysis. Ed Buckler (USDA-ARS, Ithaca, NY), a member of the scientific advisory board, ended the reporting session with a very positive assessment of the progress of the project and suggestions for improving the project outcomes. The meeting ended with a reception and student poster session. The breadth and depth of the project was highlighted in the poster session as the students presented results from all aspects of the project.

Definitions to all red words can be found in "TCAP Terminology" on page 11

United States Department of Agriculture
National Institute of Food and Agriculture

INSIDE RESEARCH:

Kernel of Truth

Look for this symbol to get highlights of TCAP stories

Identification of Genes for Drought Tolerance in Wheat Landraces

By: Luther Talbert

Participants: USDA Small Grains Collection, Nancy Blake, Jamie Sherman, Eduard Akhunov, Shiaoman Chao, Karl Glover, Luther Talbert, Jorge Dubcovsky, Mike Pumphrey

Jamie Sherman takes time out from her educational duties to thresh head-rows on a beautiful summer day in Bozeman

The USDA Small Grains Collection in Aberdeen Idaho houses wheat varieties that were selected and grown by ancient farmers throughout the world. In comparison to modern wheat varieties, these landraces are typically extremely tall and low-yielding with poor milling and baking quality. Any given landrace is typically susceptible to the insects and diseases that plague wheat production in most areas of the world. However, amongst all of the negative genes, the landraces also harbor desirable genes. Beneficial genes for disease and insect resistance have been identified and introduced by breeders into modern varieties that are grown throughout the world. These genes confer phenotypes, such as lack of disease, that are easy to see. There is little doubt that the landraces also harbor good genes for traits that are more difficult to identify based on phenotype of an individual. The T-CAP group is especially interested in improving drought tolerance in our modern wheat cultivars. How can we find the good genes for this trait in landraces, when the landrace itself has poor performance due to a preponderance of negative genes?

- Landraces are ancient varieties that may harbor useful genes
- Lines from 32 crosses between landraces and an early semidwarf variety will be tested in 2014 for drought resistance

The approach the T-CAP group has taken to this problem is referred to as nested association mapping. This has involved selection of a set of landraces representing worldwide genetic diversity, and crossing these to a common modern wheat variety. The common variety is the CIMMYT-developed 'Berkut', which is a semidwarf variety with relatively early heading time. We have developed recombinant inbred line populations for 32 Berkut/landrace crosses. The recombinant inbred lines from these crosses were selected for semidwarf growth habit and acceptable maturity characteristics. Our first opportunity to view these lines in the field in 2013 suggested that the lines were of an acceptable height and maturity, and thus we have completed the first step of introducing the genes from the landraces into lines that can be evaluated in our standard field trials.

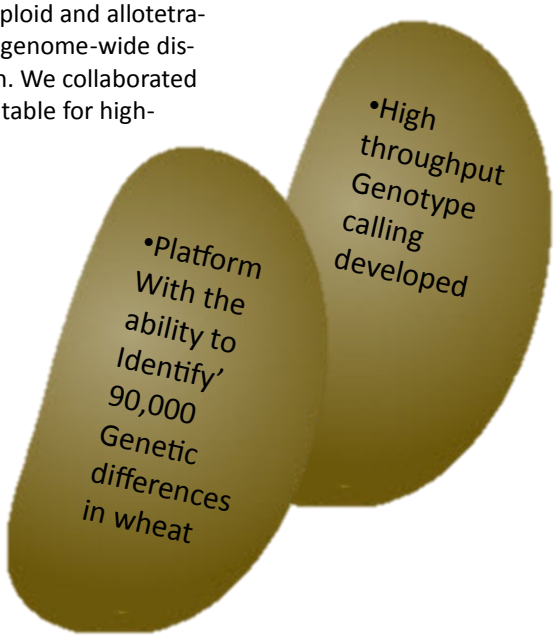
Seed harvested from the recombinant inbred line populations is currently being packaged for planting field trials in 2014. We have a total of 32 crosses with 75 lines per cross to be evaluated. DNA has been extracted from all of the lines, and large scale genotyping is currently in progress. The coupling of the genotype information with the field evaluation of our genetic populations will allow us to evaluate genes from the landraces as opposed to the poorly adapted landraces themselves. We will begin the process of matching genotype information with phenotype after completion of field trials in 2014 and 2015. The nested association approach has allowed us to isolate the landrace genes from the landraces and place them into a genetic background that will allow field evaluation. The next step is to match genotype and phenotype to identify the genes for use in our current wheat breeding programs.

- DNA from these lines will be analyzed to identify the drought resistant genes from the landraces
- Promising genes will be transferred to lines that can be used as parents inbreeding programs

SNP

By: Eduard Akhunov

"High-density single nucleotide polymorphism (SNP) genotyping arrays are a powerful tool for studying genomic patterns of diversity, inferring ancestral relationships among individuals in populations and studying marker-trait associations in mapping experiments. TCAP team collaborated with international partners to develop a genotyping array including about 90,000 gene-associated SNPs and used it to characterize genetic variation in allohexaploid and allotetraploid wheat populations. The array included a significant fraction of common genome-wide distributed SNPs that are represented in populations of diverse geographic origin. We collaborated with Illumina, Inc. to develop a density-based spatial clustering algorithms suitable for high-throughput genotype calling in complex datasets obtained for polyploid wheat. We showed that these model-free clustering algorithms provide accurate genotype calling in the presence of multiple clusters including clusters with low signal intensity resulting from significant sequence divergence at the target SNP site or gene deletions. We found that assays detecting low-intensity clusters can provide insight into the distribution of presence-absence variation (PAV) in the wheat populations. A total of 46,977 SNPs from the wheat 90K array were genetically mapped using a combination of eight mapping populations. The developed array and cluster identification algorithms provide an opportunity to infer detailed haplotype structure in polyploid wheat and will serve as an invaluable resource for diversity studies and investigating the genetic basis of trait variation in wheat."



Additional information about array can be found at
http://wheatgenomics.plantpath.ksu.edu

Reference: S. Wang, D. Wong, K. Forrest, A. Allen, S. Chao, E. Huang, M. Maccaferri, S. Salvi, S. Milner, L. Cattivelli, A. M. Mastrangelo, A. Whan, S. Stephen, G. Barker, R. Wieseke, J. Plieske, IWGSC, M. Lillemo, D. Mather, R. Appels, R. Dolferus, G. Brown-Guedira, A. Korol, A. R. Akhunova, C. Feuillet, J. Salse, M. Morgante, C. Pozniak, M. Luo, J. Dvorak, M. Morell, J. Dubcovsky, M. Ganal, R. Tuberosa, C. Lawley, I. Mikoulitch, C. Cavanagh, K. J. Edwards, M. Hayden, E. Akhunov (2014). Characterization of polyploid wheat genomic diversity using a high-density 90,000 SNP array. Plant Biotechnology Journal (in communication).

What's new in the Triticeae ToolBox (T3)

By: Victoria Blake

What's New in The Triticeae ToolBox (T3).
October 2013 - January 2014.
- Victoria Blake, T3 Curator

New Genotyping Results in T3

Barley Trials	Collaborator	Description
OWB_GBS_2012	Poland et al, (2013) PLoS One e32253	34,396 markers on the Oregon Wolfe Barley population. Poland, et al. (2011) PLoS One e32253
WildBarleyIntrogression_9K_Parents	Gary Muehlbauer	7,308 markers on 26 lines.
VC_MNWC4_2013_384	Kevin Smith	VeraCode 384 chip on cycle 4 of the Minnesota genomic selection for LTT program
TCFW6_LTT_9K	Patrick Hayes	6,892 markers on 768 facultative winter 6rows

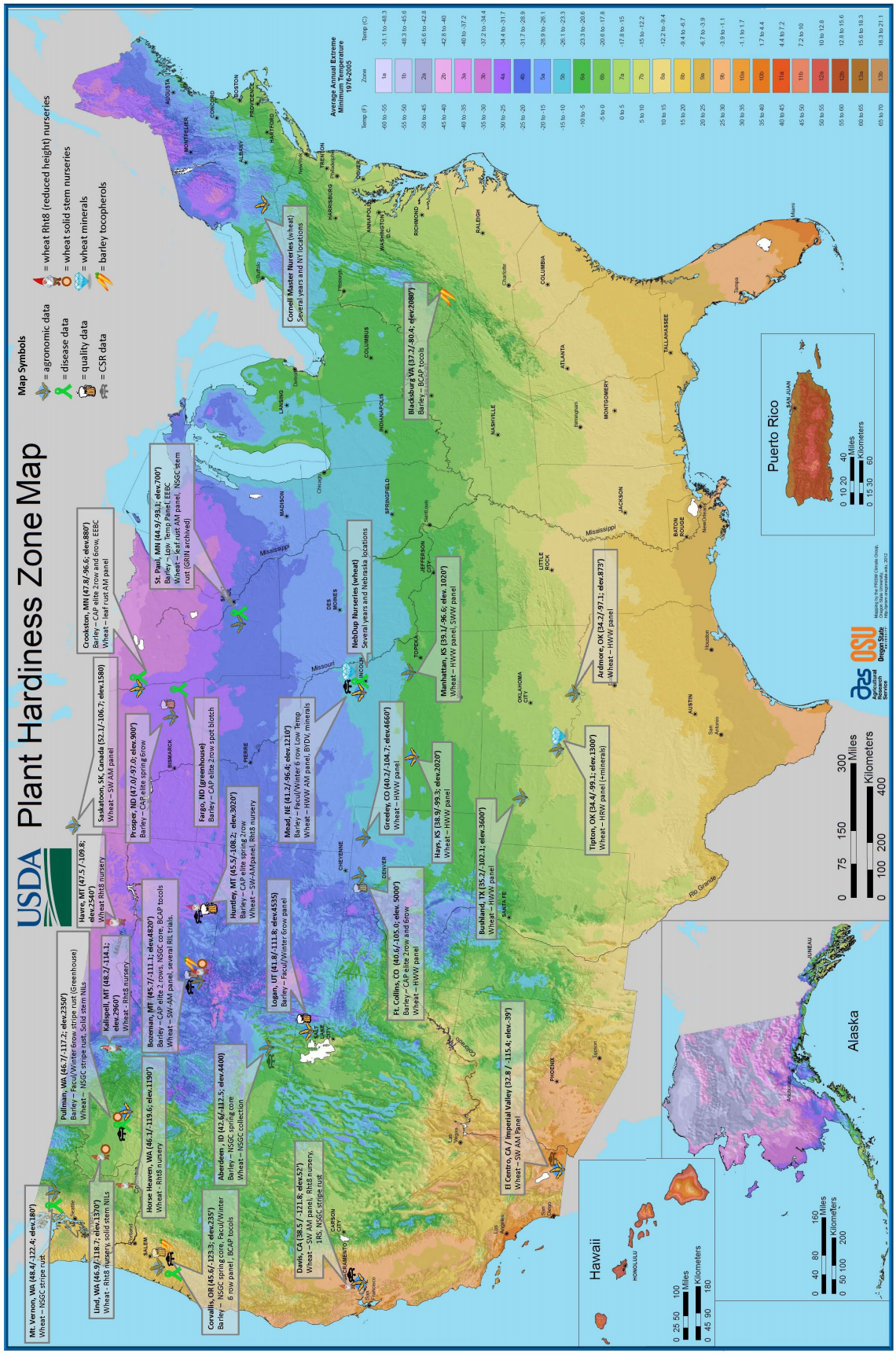
Wheat Trials	Contributor	Description
SynOP_GBS_2012BinMap	Poland et al, (2013) PLoS One e32253	19720 bin-mapped GBS markers on 165 DH Synthetic x Opata lines
SynOP_GBS_2012AntMap	Poland et al, (2013) PLoS One e32253	1485 markers on 165 DH lines that created the Synthetic x Opata de novo AntMap

See page 4 for the TCAP Research Sites Map

To view the above map with greater resolution please visit http://tcap.pw.usda.gov/zonemap/TCAP_ZoneMap.pdf

TCAP Research Sites in North America

Updated 1/29/2014



TCAP Research Sites in North America

The TCAP project was designed to capture growing conditions and challenges for several market classes and specific research populations of barley and wheat. The map shows the experimental sites with data represented in T3 as of January 29, 2014 overlaid on the USDA Plant Hardiness Zone Map.

The TCAP map was created and is maintained by Victoria Carollo Blake, Ph.D. Curator, The Triticeae Toolbox (T3)
USDA-ARS-WRRC, Albany, CA victoria.blake@ars.usda.gov

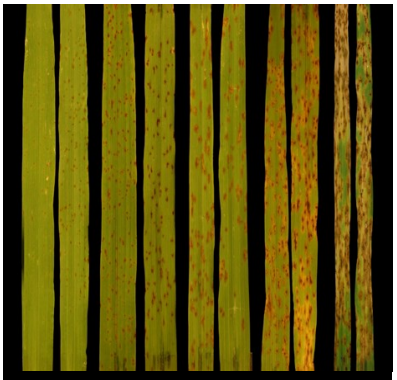
Acknowledgement

The Triticeae Toolbox is part of the Triticeae CAP project, supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68002-30029 from the USDA National Institute of Food and Agriculture.

Barley Disease Phenotyping:

TCAP Newsletter Update: January 2014

The Barley Disease Phenotyping group includes Shaobin Zhong (North Dakota State University [NDSU]), who is evaluating germplasm to the spot blotch pathogen (*Cochliobolus sativus*); Robert Brueggeman (NDSU) and Tim Friesen (USDA-ARS Fargo, ND), who are evaluating germplasm to both the spot form net blotch (*Pyrenophora teres* f. *maculata*) and net form net blotch (*Pyrenophora teres* f. *teres*) pathogens; Patrick Hayes (Oregon State University), who is evaluating germplasm to the stripe rust pathogen (*Puccinia striiformis* f. sp. *hordei*); and Brian Steffenson (University of Minnesota), who is evaluating germplasm for resistance to domestic and African races of the stem rust pathogen (*Puccinia graminis* f. sp. *tritici*). All of the projects were successful in identifying resistant accessions and detecting significant marker-trait associations. Two percent of the barley core collection was found resistant to the virulent *C. sativus* isolate ND4008, and a significant marker-trait association was detected on chromosome 6H. The barley core collection was evaluated to four isolates of *Pyrenophora teres* f. *maculata* from North Dakota, Denmark, New Zealand, and Australia. The number of highly resistant accessions found at the seedling stage ranged from 12 to 66 to the four isolates. Genome-wide association studies (GWAS) identified 30 different quantitative trait loci (QTL) for resistance to the spot form net blotch isolates. QTL were detected on each of the seven chromosomes, and some were effective to more than one isolate of the pathogen. Additional evaluations to the net form net blotch pathogen are in progress. With respect to stripe rust, a number of highly resistant accessions were identified in the spring core collection, the winter core collection, and the low temperature tolerant collection. GWAS identified a number of QTL for stripe rust resistance at genomic positions where resistance loci were previously reported, but also some at unique locations. A set of near-isogenic reference lines carrying quantitative and qualitative stripe rust resistance alleles has been developed and will be utilized for determining the identity of resistance loci from the core collections. The barley core collection was evaluated to the African stem rust race TTKSK at the adult plant stage in Njoro, Kenya and also at the seedling stage within the Biosafety level-3 containment facility in St. Paul, MN. A number of resistant accessions were identified at both the seedling and adult plant stages. GWAS identified resistance QTL on chromosomes 2H, 3H, and 5H. Additional bi-parental crosses have been made in each of the projects to validate the identified resistance loci and incorporate them into advanced breeding lines.



Different reaction types found in barley response to the spot form net blotch

Stripe rust of barley

Stem rust of barley

- TCAP barley scientists in ND, MN and OR are searching barley germplasm collections for resistance to spot blotch, net blotch, stripe rust and stem rust
- All have found lines with some resistance to at least one disease, and have identified DNA markers to track the resistance genes in crosses
- Crosses have been made in each project to confirm that resistance genes can be transferred to breeding lines and will provide effective disease resistance in the target environments

Education News

Triticeae CAP
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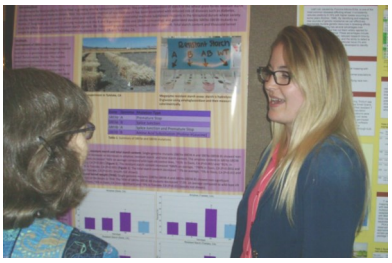
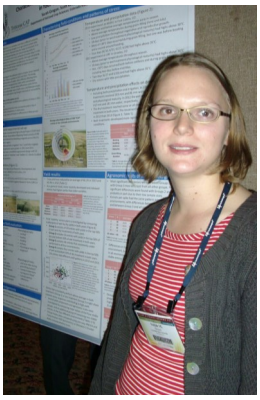
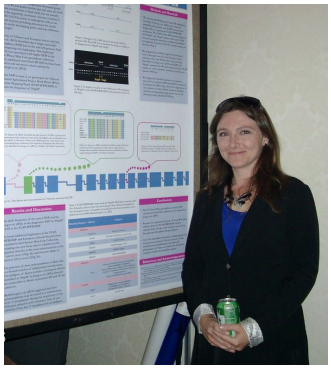
INSIDE EDUCATION

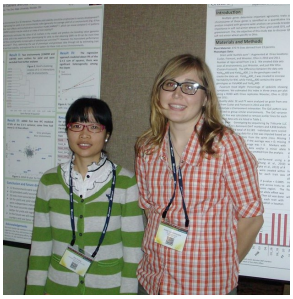
2014 TCAP Poster Session

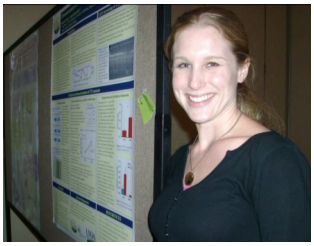


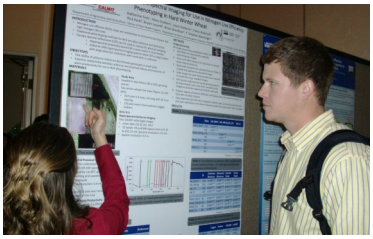
36 TCAP Graduate Student posters were presented

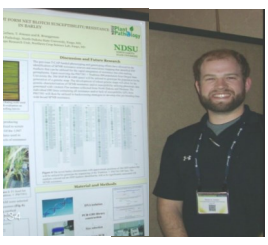


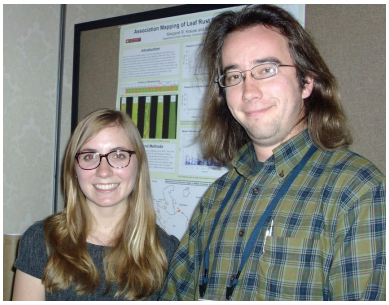












TCAP Graduate Student Workshop

On January 10, 2014 TCAP Education team, Mary Brakke, Deana Namuth-Covert and Jamie Sherman, provided a workshop for graduate students "You have your degree, now what? The workshop began with an opportunity for students to get to know each other. A discussion then ensued of a recent study describing the skills needed by the plant breeding industry (Miller et. Al., JNRLSE, 2011). The students formed small groups to develop questions for a panel of plant breeding employers in order to clarify experiences and skills they value. Panel members included Donn Cummings, Fred Bliss, Allen Van Deynze, Ed Souza, Sally Clayshulte, Stephen Baenzinger, and Bob Dietrich. Each panel member was interviewed by a single student group for 30 minutes and then switched to a new group. Each student group was able to visit with 3 panel members. The students then shared the insight they had gained as well as the questions they still had. Panel members were able to continue to contribute. We ended with a brainstorming session of potential actions we could take to better prepare students for future jobs

Both the students and the professional panel have indicated the success of this workshop. Fifty nine percent of students indicated an improvement of both their awareness of skills valued by plant breeding employers and knowledge of tools and strategies useful in obtaining those. Forty seven percent of students were interested in developing and improving skills valued by employers of plant breeders. Student comments included:

- I was surprised at how consistent the answers were across panel members.
- It was very nice and very helpful to be able to talk with experienced representatives in small groups and hear about their personal experiences
- Writing your questions on the cards. In an interview you can't write down the questions you are too afraid to ask openly. This is a safe environment to practice interview skills with people who genuinely want to help you improve! All of the panel that I talked to encouraged each student to ask questions other than those on the cards, and each student responded.
- I was surprised at the diversity of experiences between the reps - some had experience in academia, USDA and industry.
- I was surprised that several of the "industry reps" had had positions in the public and private sectors. It was helpful to hear their accounts of differences in their different work places.
- It was great that the industry reps were willing to spend so much time with us.
  The reps were quite candid about their experiences and really opened up in response to our questions. Many shared challenging experiences and described the good and bad aspects of their different positions.
- I definitely intend to look into more leadership training, quantitative genetics, statistics, seed industry issues, and crop and plant physiology.
- I knew the strengths and weakness of my program already due to strong contact with industry. The program helped me think of ways to deal with it.
- I really appreciated the effort of contacting students with academic and industry people. However, everyone in the panel worked pretty much in plant breeding at the end of the work flow, thus we didn't get any perspective in other areas of plant improvement (e.g.molecular genetics, gene discovery, comparative genomics,etc). I am pretty sure the expectations for a PhD going to a breeding position is very different from one going into the more genetic/ computational positions.
- Need more female breeders on the panel- many of the TCAP students are female, and we need to be exposed to good role models. An hour shorter would be better. The debriefing is important to coalesce ideas, but everyone was worn out by the end and not that responsive.
- It would be great to have a bit more time with each rep, and be able to talk with all of them. If there is a way to extend the time we have with them.

TCAP Undergraduate Research Academy - 2014

The goal of the Academy is to provide undergraduate students involved in TCAP research with experiences that help prepare them for graduate studies.

Program Benefits

Involvement in small group conversations with graduate students and faculty conducting research in plant genetics and plant breeding
A chance to informally present posters or talks and receive feedback that enhances the presentation
Travel funds to present research at scientific meetings
Opportunity to apply for funds to assist with travel to TCAP institutions to conduct summer research
Opportunities to talk with graduate faculty to learn about graduate programs in plant breeding and plant science around the country
Opportunities to talk with graduate students about grad school!
Guidance in the graduate school application process
Opportunities to talk with representatives from private enterprise about internships and co-ops

Eligibility Criteria

Must have a class standing as sophomore, junior or senior
Must currently be working as research intern in a lab participating in the TCAP
Must have a desire to pursue a M.S. or Ph.D. in a related field at some point after graduating
Must have a minimum overall GPA of 3.0

If you missed the application deadline for this semester, watch for another opportunity for fall 2014

New Online Courses Being Offered Spring 2014 in PBTN

Collaborative Course on Computational Methods – March 31 – May 4

Ashu Guru, a professor of the Raikes school at UNL and Deana Namuth-Covert, professor in Agronomy and Horticulture at UNL have joined together for this project. This cross disciplinary course is intended for plant breeding and computer science students/professionals. In the initial offering of the course, March 31- May 4, we anticipate mostly TCAP members. Through the 5 week course, participants will gain experience in working on a project with collaborators from other disciplines. There are 3 self-paced learning modules that participants will complete over the 5 week timeframe which demonstrate examples of using R to analyze samples of actual TCAP data collected by graduate students. Each week there will be a live synchronous session in Adobe Connect with Ashu Guru where "questions of the week" will be discussed. The course was delayed a few weeks so that it will start after TCAP students return from CIMMYT.

Following this initial offering, the modules will be available for self-paced learning. In the Fall 2014 session, there will once again be synchronous components with computer science and management students from the UNL Raikes school participating.

Sign Up: http://passel.unl.edu/communities/ computational

Contact: Deana Namuth-Covert at dcovert2@unl.edu

TCAP Undergraduate Research Experience

There are currently about 50 undergraduate students conducting research with the TCAP. Each year we survey students to get feedback that helps us understand their experiences. To give you an idea of what students want out of the experience, what they like and suggestions they have for improving their experiences, responses from 2012 and 2013 to several questions are summarized below.

What do you hope to gain from your research experience? (quotes)

- Understanding and knowledge in a topic, along with experience in research techniques, experimental design, and quantitative analysis.
- As much as I possibly can. I want more knowledge on my career path.
- The mentoring process has helped me become more confident in my abilities.
- I hope to gain teamwork and leadership skills on top of the experience.

What do you like most about your research experience? (quotes)

- It's hands on and very real, as opposed to lab experience that I've had in class.
- Independence and the excitement of doing something novel.
- I've had the opportunity to learn a lot of different lab techniques.
- I love the people I am working with.

What could make your research experience better? (quotes)

- A more complete understanding of what I'm doing and why I'm doing it.
- My mentor spending more time in the lab. A lot of the time I feel I have to teach myself.
- I did not get an independent project in my lab, and the project I am working on is quite well defined. I don't get the experience of planning or influencing its direction.
- I wish I were doing more lab work and data analysis.
- It could have included more required presentations. I feel like I was less prepared for those than I thought there should be.

How long have you been working on a TCAP research project? (n = 29)

Duration	% of respondents
Greater than one year	28
7 – 12 mo.	34
6 mo. or less	38

64% of respondents said that "Gathering, analyzing and managing data" and "reporting results" were "very valuable" to their education. (n = 33)

What do you like most about your mentoring experience? (quotes)

- [My] mentor is always available to answer questions and provide guidance.
- I have guidance when analyzing data and using statistical programs. I also like the insight into graduate student life that I get from my mentor.
- My mentor is willing and happy to advise me whenever I need it, but allows me autonomy when I am confident I know what I am doing.
- I like the fact that it is easy to communicate with my mentor. Since it is easy to communicate with my mentor I feel secure asking questions when I do not know how to do something, have ideas about the research, or even need clarity on the research. Every question is viewed as a learning experience to my mentor. This creates a great learning environment.

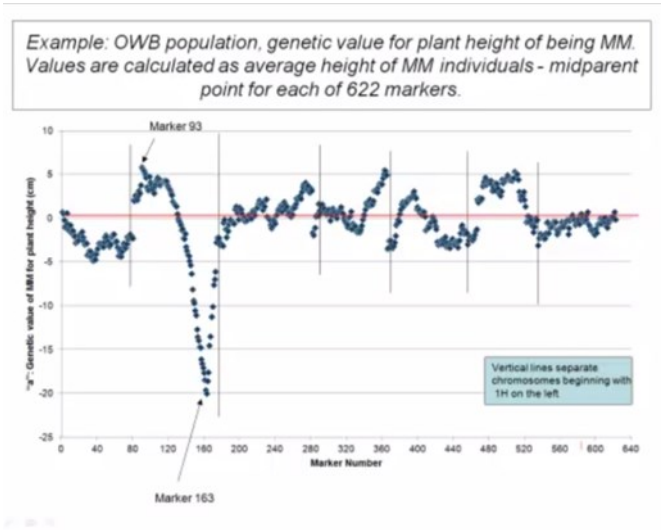
What could make your mentoring experience better? (quotes)

- Scheduling a regular meeting to discuss any questions I have about my project or my work.
- I am unsure of how to initiate my own research, because my primary area of interest strays from that of my graduate student mentor's.
- I think having his expectations explained would really help me understand what he wants.
- My mentoring experience might be better if my mentor could suggest some papers I might read to better understand the concepts she is trying to teach me.

Self-Paced Course on Quantitative Genetics – Opens March 17

Sign Up: http://passel.unl.edu/communities/tcapquant
Contact: Deana Namuth-Covert at dcovert2@unl.edu

In response to many requests to offer the Quantitative Genetics course again, we have repackaged the materials to make it available as a self-paced learning course. We have broken the video lectures into smaller segments and added quizzing for guiding participants through the material. In this course participants are presented with basic elements of quantitative genetics in order to fully understand implications to plant breeding, as well as provide practical experience in linkage and QTL mapping. Clay Sneller, from The Ohio State Univ, created recorded lectures on basic quantitative genetics as those topics apply to plant breeding. Through other recordings, Jamie Sherman, from Montana State Univ, introduces participants to Linkage and QTL mapping using the free software Mapdisto (http://mapdisto.free.fr/) and QTLcartographer (http://statgen.ncsu.edu/qtlcart/). Participants will go to websites and download software. Data to be analyzed can be downloaded from this site. Working groups can form for collaborative data analysis.



TCAP Participating Programs (see http:www.triticeaecap.org for more information)

Universities

Soil and Crop Sciences, **Colorado State University**
Plant Breeding, **Cornell University**
Plant Pathology or Agronomy, **Kansas State University**
Plant Sciences and Plant Pathology, **Montana State University**
Department of Crop Science, **North Carolina State University**
Plant Pathology, Plant Sciences, **North Dakota State University**
Environmental Natural Resources, or Horticulture & Crop Sciences, **Ohio State University**
Plant and Soil Sciences, **Oklahoma State University**
Crop and Soil Science, **Oregon State University**
Plant Sciences, **South Dakota State University**
Soil and Crop Science, **Texas A&M University**
Plant Sciences, **University of California, Davis**
Botany and Plant Sciences, **University of California, Riverside**
Aberdeen Research & Extension Center, **University of Idaho**
Plant and Soil Sciences, **University of Kentucky**
Plant Sciences and Landscape Arch., **University of Maryland**
Agronomy & Genetics, Plant Pathology, **University of Minnesota**
Division of Plant Sciences, **University of Missouri**
Agronomy and Horticulture, **University of Nebraska Lincoln**
Plant, Soils and Climate, **Utah State University**
Crop and Soil Environmental Sciences, **Virginia Tech**
Crop and Soil Science, **Washington State University**

USDA-ARS

GMPRC, Manhattan, KS
WRRC, Albany, CA
Aberdeen, ID
Raleigh, NC
BRL Fargo, ND
NCSL, Fargo, ND
Ithaca, NY
St. Paul, MN
Pullman, WA

Collaborating Institutions with Student Projects

Chicago State University
Tuskegee
West Texas A&M
University of Arkansas, Pine Bluff
Lehman College
Rust College
Favetteville State University

TCAP Terminology

- **Association mapping** is a technique used to identify marker-trait associations in lines that are not derived from a single cross.
- **Bacterial Artificial Chromosomes (BAC)** are pieces of DNA that can be used as vectors for a variety of purposes. For example, genomic DNA from barley is cut into smaller pieces and inserted into BACs, creating a complete library of the Barley DNA. BACs can be amplified creating a source for DNA sequencing. Since BAC libraries are created with random pieces of the Barley DNA, there will be overlap between BACs, thus providing a complete sequence that has a physical relationship and can be anchored.
- **Canopy Spectral Reflectance (CSR)** is a new phenotyping tool TCAP is exploring. It is based on the observation that plants under stress reflect different colors of light. Measuring the light reflected might be a way to predict plant performance.
- **Canopy Temperature Depression (CTD)** plants need $C0_2$ for photosynthesis and acquireit through window-like structures in leaves simultaneously releasing o_2 and H_20. When a plant is water stressed, the windows in the leaves through which this gas exchange occurs must close, reducing photosynthesis and thereby reducing yield. When the windows are open not only can photosunthesis occur, but also as H_20 is released the temperature around the plant decreases due to evaporation. CTD can act as a proxy for measuring the plants ability to continue to photosynthesize under drought stress.
- **Copy Number Variation (CNV)** are differences in DNA between individuals that occurs when a large number of building blocks called nucleotides are either duplicated or deleted. CNVs generally range in size from thousands of base pairs to millions of base pairs. In contrast, SNPs are another DNA difference that only involves single base changes. The number of CNVs reported here in Barley of 15% is in a similar range as what has been reported in humans.
- **Deoxyribonucleic acid (DNA)** is the genetic material for most organisms. An organism's complete set of DNA is called its **genome**.
- A **gene** is the instructions for a specific structure in the organism. For an organism to survive certain instructions (genes) are required. However, the details or order of the instructions may vary from organism to organism and it is these differences that we are looking for to improve wheat and barley.
- **Genomics** is the study of the **genome**. The genome is a complete set of instructions for the organism. You can think about it like an instruction manual for that organism.
- **Genomic selection** is when markers spread throughout the genome are used to predict the performance of individuals to facilitate breeding.
- **Genotyping** is when the genetic makeup of an organism is characterized. The genotype controls the way an organism looks, which is called the **phenotype**. In our instruction manual analogy, determining the genotype would be like reading the instruction manual, while determining the **phenotype** is like testing the product created after following the instructions.
- **Germplasm** is a collection of genetic resources, which in wheat and barley is usually a collection of seed.
- **KASP™ Markers** are a cost efficient method of SNP genotyping developed by KBioscience. KASP stands for Kompetitive Allele Specific PCR. Advantages of KASP over other systems: may be less expense, greater flexibility, and higher conversion rate
- A **marker** is a difference in the DNA that acts like a bookmark indicating the position of a certain set of instructions. It can be a difference in the instructions **(gene)** itself but it can also be a difference in a neighboring part of the DNA.
- Making **Marker/trait associations** is identifying good bookmarks for the instructions that are important. Once marker/trait associations are made, markers can be used to make selections.
- **Marker Assisted Selection** is a technique that uses DNA markers to identify individuals carrying certain genes to facilitate breeding.
- **National Small Grain Core Collection**, NSGC collection is an important germplasm resource for the TCAP. TCAP participants will be evaluating and distributing an extensive collection of seeds representing material from around the world. TCAP is searching this material for unique **genes** that will be used to improve wheat and barley.
- **Nested Association Mapping** is a hybrid technique that uses attributes of both bi-parental mapping and association mapping.
- **Nitrogen use efficiency (NUE),** Nitrogen is required by plants for growth and enters plants from soil through roots. Farmers replenish nitrogen using fertilizers and have found maximizing nitrogen can increase yields; however, nitrogen can be costly not only for farmers but also to the environment. An important goal of the TCAP is to improve the NUE of wheat and barley, both saving money and the environment.
- **Nucleotides** are the building blocks of DNA and can be thought of as the letters making up the instruction book. The instruction book for wheat is composed of 16 billion letters or nucleotides (= **16GB**). It is the order of the building blocks that store the genetic information.
- **Principle Coordinate Analysis (PCoA)** is a method to explore and visualize dissimilarities in data. For example, on page 3 each accession is plotted by how different the genotyping data is from every other accession, creating scatter plots with more similar accessions closer together. The scatter plots are two dimensional, while the data can have multiple dimensions. To better view the information the plots can be rotated to obtain multidimensional views.
- **Quantitative Trait** is a trait that can be measured and is controlled by many different locations in the genome. The different locations controlling a specific quantitative trait are called QTL (Quantitative Trait Loci). In our analogy of the instruction manual, several different instructions (QTLs) together control a trait. Most traits important to stakeholders are quantitative (e.g. yield and quality).
- **QTL Mapping** is a technique used to make marker/trait associations using a **bi-parental mapping** population from a cross between two lines that are different for a trait of interest.
- **Sequencing** is reading the order of the **nucleotides.** Some of the new technology we are exploring are methods that look for differences by determining the sequence, for example **gene capture** and **genotyping by sequencing**.
- **Single nucleotide polymorphism (SNPs)** is the difference in one building block (nucleotide) in the DNA sequence. In our analogy it is like changing "TAG" to "GAG" in our instruction manual. An advantage of **SNPs** is more potential differences and so more markers at a higher resolution, making it easier to make marker/trait associations.
- **Water Use Efficiency (WUE),** Water is the limiting resource in much of the world today and is likely to continue to be in the future due to climate change and loss of arable land. An important goal of the TCAP is to improve WUE of wheat and barley, providing resistance to drought and new varieties for low moisture areas.