



Triticeae CAP
Coordinated Agricultural Project

Tcap Transmission

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INSIDE TCAP:

Improving germplasm for changing environments 2

TCAP genotyping: moving beyond SNP arrays 3

TCAP Entering Mentoring Online 3

Barley six-row NAM population goes live this summer 4

2014 CIMMYT Highlights 5

CIMMYT Pictures 6

Celebrating Dr. Norman Borlaug's 100th Birthday 7

TCAP Undergrad Research academy 8

Online Computation Methods and Quantitative Genetics Course 9

Directors notes Gary Muehlbauer and Jorge Dubcovsky

The TCAP has made great strides in establishing a nation-wide collaborative community focused on developing improved wheat and barley varieties. As mentioned in this column before, numerous germplasm collections, mapping populations and breeding materials have been genotyped and phenotyped, enabling marker-assisted selection and genomic selection strategies to be implemented. In addition, The Triticeae Toolbox (T3) database continues to be the core of the project. T3 has been rapidly expanding with additional data and tools that support all aspects of the project. Recent progress is described throughout the newsletter. On page 3, Gina Brown-Guedira describes how the project has moved from fixed SNP assays to genotyping-by-sequencing based approaches, which has enabled increased flexibility and efficiency. Development of the barley nested **association mapping** population populations are highlighted on page 4. In the future, the barley NAM populations will be an excellent resource for mining beneficial alleles. The TCAP education group has developed numerous opportunities for undergraduates and graduate students to develop a better understanding of breeding and genetics and to develop the appropriate professional skills for a successful career. For example, 19 TCAP students traveled to CIMMYT in March to observe all aspects of the breeding programs (see story on page 5). To foster the development of research skills that will prepare undergraduates for a successful graduate school experience, Mary Brakke established the Undergraduate Research Academy. Three students (Nathan Wyatt, North Dakota State University; Nikayla Strauss, Colorado State University; and Ge Cheng, Fayetteville State University) are participating in the Academy (see page 8). Two online courses in Computation



Methods, and Quantitative Genetics were offered (see page 9). The computation methods course was offered by Ashu Guru (University of Nebraska) and Deana Namuth-Covert (University of Nebraska), and the Quantitative Genetics course had 21 students and was offered by Jamie Sherman (Montana State University) and Clay Sneller (The Ohio State University). Both courses received excellent reviews from the students. Taken together, the TCAP has established itself as an outstanding education and training platform for the next generation of plant breeders.

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

Kernel of Truth

Look for this symbol to get highlights of TCAP stories

Improving Barley and Wheat Germplasm for Changing Environments

Gary Muehlbauer

Award Amount: \$25M total (5 yrs., \$5M/yr.) continuation grant funded by the AFRI Climate Change Challenge Area. Update Summary: TCAP is now in its 4th year of funding. Excellent progress was made during the third year on all of the objectives of the grant and in several cases exceeded the original milestones. The original objectives of the grant were:

- Discover and deploy beneficial alleles from diverse wheat and barley germplasm
- Accelerate breeding through marker-assisted selection and genomic selection
- Implement sequence-based genotyping methodologies to discover new allelic diversity in wheat and barley
- Implement web-based tools to integrate marker-assisted selection and genomic selection strategies into breeding programs
- Develop and implement a Plant Breeding Training Network.

Highlights of 2013:

- Phenotyped and genotyped large collections of wheat and barley germplasm and **association mapping** panels and the first associations between alleles and phenotypes are being established.
- Implemented nation-wide Marker Assisted Selection (MAS) approaches for wheat and barley improvement.
- Initiated Genomic Selection (GS) projects.
- Implemented Genotype By Sequencing (GBS) and gene capture technologies for assessing and using genetic variation in wheat and barley.
- Enhanced and expanded “The Triticeae Toolbox” (T3) database, integrating phenotypic and genotypic data .
- Established the Plant Breeding Training Network (PBTN) as a central hub for education activities. The educational activities are not only training graduate and undergraduate students, but are also attracting new students into plant breeding.
- Mapping and **association mapping** activities yielded the first favorable alleles (and cloned genes) for NUE, WUE, and disease resistance. This information is being used to develop new varieties that can ameliorate the negative impacts of climate change.
- High-throughput marker-based breeding approaches are being implemented nation-wide and commercial varieties and improved germplasm using marker-assisted selection are being released.
- The precise genotypic and phenotypic characterization of the large U.S. core collections of wheat and barley, and the organization of this information in a breeding database (T3) will serve current and future generations of barley and wheat breeders.

Deliverables 2013:

One of the most important deliverables in 2013 has been the expanded phenotype and genotype data uploaded to T3 and specifically, including contributions by breeding programs for the first time are now contributing to T3 that had not contributed before. Data submission to a public database represents a significant new step in the research cycle for a number of TCAP co-PDs.

TCAP participants generated a total of 51 new peer reviewed publications in 2013 which includes several articles in high impact journals: Nature, Science, PNAS, Genome Biology, Genetics, and two in PLoS Genetics. More than 360 people (undergraduates, graduate students, postdocs, visiting scientists and PIs) have participated in training through the TCAP. A total of 117 graduate students have participated in the plant breeding training network. Eighty-seven undergraduates have participated in the TCAP with forty-nine being mentored by TCAP faculty and graduate students, and 36 by MSI faculty. Fourteen MSI students have spent time at TCAP institutions over the life of this grant so far. TCAP has trained a total of 20 Post-Doc’s and 25 visiting scientists.

Summary:

A large cohort of plant breeders are being trained in traditional and modern breeding strategies and a new, and more diverse generation is being attracted to plant breeding. These actions will provide the continuity required for sustainable cereal breeding activities in the United States.

A major new outcome of the TCAP activities is the renewed interest in the wheat and barley core germplasm collections. The detailed genotyping and phenotyping for WUE, NUE and disease resistance has increased the value of the US wheat and barley National Small Grains Core (NSGC) germplasm collections. This added value is attracting breeders to utilize this germplasm in their breeding programs.

And finally, since the last report, TCAP has released an additional 20 new cultivars, 16 new germplasm and 13 new mapping populations.

TCAP genotyping: moving beyond SNP arrays

Gina Brown Guedira

TCAP researchers have made significant contributions to the development and application of high-density SNP arrays for wheat and barley. The project has developed a database of SNP genotypes for thousands of accessions that, combined with the wealth of phenotypic data generated, has led to increased understanding of the genetic architecture of important traits in both species. However, the cost per sample of the high-density SNP arrays is beyond the reach of breeders wanting to apply genome-wide marker data for genomic selection (GS). Since recent advances in DNA sequencing technologies have resulted in increased outputs and reduced costs, the genotyping technology for many of the TCAP projects has shifted to sequence based approaches, including sequencing of multiplexed amplicons and genotyping by sequencing (GBS).

TCAP collaborators are using GS to improve low temperature tolerance (LTT) in barley and nitrogen use efficiency (NUE) and yield in winter wheat. Efforts are underway to move away from the 384 VeraCode SNP array for genotyping the barley LTT population that is in the fifth cycle of genomic selection. To do this, GBS libraries were prepared from 960 progeny from crosses among plants selected in the previous cycle using the 384-SNP array. Libraries were also prepared from DNA of 96 selected plants from cycle 4, including parents of the cycle 5 plants. The libraries were pooled at the 192-plex level for sequencing on the Illumina HiSeq 2000. The TASSEL-GBS pipeline will be used for SNP calling.

In winter wheat, the elite panels evaluated for NUE and yield that were genotyped using the iSelect wheat array having 90,000 SNP are also being evaluated with GBS of libraries produced using the *PstI-MseI* enzyme combination. This will result in a database of SNP genotypes and GBS tags for approximately 1,200 lines of hard and soft winter wheat. The genotypic data, combined with phenotypic data on these lines, will be used for association mapping and validation studies and also to train genomic selection models. Genome wide marker profiles are being developed using GBS for an additional 2500 winter wheat lines over the next two years as part of the allele-based breeding approach involving multiple hard and soft winter wheat breeding programs. At a cost of approximately \$20 per sample, GBS is currently the most cost-effective method of genotyping for GS.

TCAP Entering Mentoring Online Course: Fall 2014: Report

The Entering Mentoring course lasted for 8 weeks from February 11 to April 8, 2014. Participants were graduate students from the University of California, Davis and University of Nebraska, Lincoln/Bayer Crop Science. Participants were prompt and fully participated and the discussions went back and forth between academia and industry settings. Common themes were clear and discussions on unique or peculiar environments generated lots of interest and attention because students recognized the long term applicability.

The quality of the online synchronous discussions was supported by the fact that participants were assigned readings on specific mentoring topics in advance. Each week students completed writing assignment that encouraged them to think more deeply about some aspect of mentoring. Assignments were anonymously shared as discussion posts. Discussions often revolved around common themes in written assignments as well as revelations arrived at by participants due to their current or past mentoring experiences.

At the end the students/participants were very satisfied and admitted that their notion of a mentor had not only changed but that they considered themselves better equipped now to be mentors in academia and /or industry. It was a mutually beneficial experience for the students and the facilitator. Because they found the course and sessions very valuable, participants thought that there was need to have many more students participate in this online course. They suggest more aggressive and early publicity and a consensus on meeting times by all registered participants that will take into consideration all the time zones of the USA.

Participants did a short midcourse evaluation and a survey monkey at the end of the 8 weeks. Certificates of completion were awarded to the participants because they met and exceeded the required attendance and participation rate.

Martin Matute: Facilitator

Deanna Leingang: Technical Assistance

Barley six-row NAM population goes live this summer.

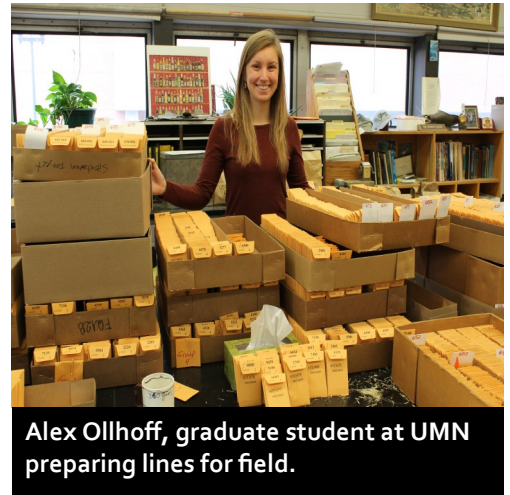
Kevin Smith

The TCAP is funding the construction of two large nested **association mapping** (NAM) populations in barley. One of the populations (NAM6) was initiated in the fall of 2011 with crosses between a diverse set of six-row accessions from the USDA National Small Grains Collection (NSGC) core and the six-row variety Rasmusson. A total of 91 NSGC core accessions were crossed to Rasmusson.

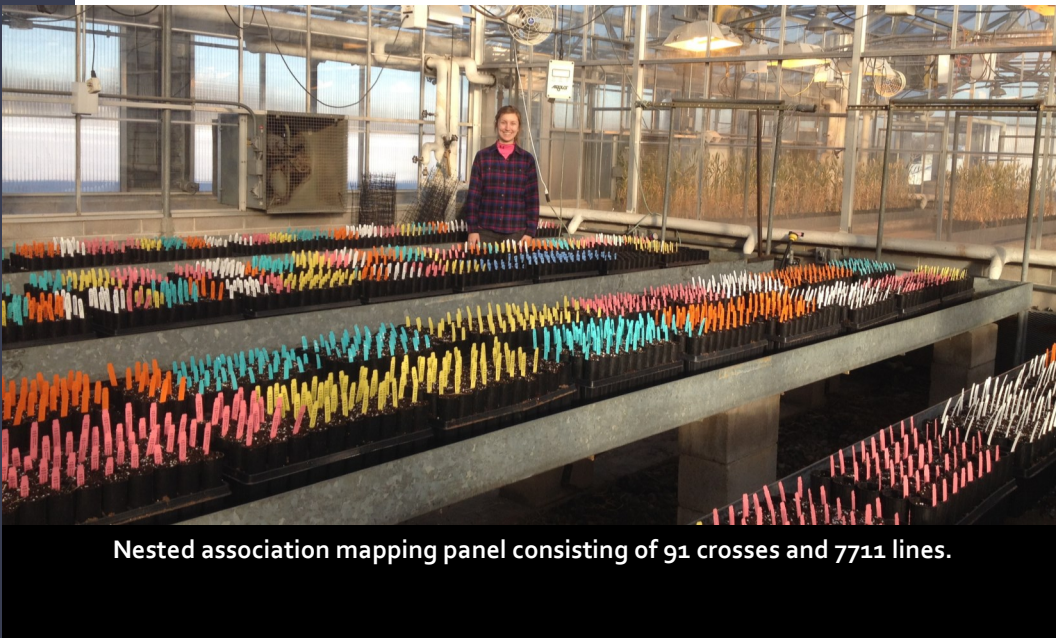
These 91 populations were advanced by single seed decent to produce a set of 7711 inbred plants which were grown in the greenhouse in St. Paul this winter.

Tissue samples from each of these plants were harvested and sent to Gina

Brown-Guedira at the USDA Genotyping Center in Raleigh. DNA extraction is under way and these samples will be genotyped using genotyping by sequencing (GBS). Graduate student Alex Ollhoff at the University of Minnesota is harvesting the seed from each of these plants and will plant a single row plot from each plant in the field in Crookston, MN this summer. The main purpose of this trial will be a seed increase for future experiments, however she will also be collecting data on heading date, height, and grain protein concentration. Alex also plans to collect hyperspectral data using an unmanned aerial vehicle which will fly over the plots three times during the summer. We will compare this remote reflectance data to ground-based **canopy spectral reflectance** data collected on a subset of plots. The data from the seed increase this summer will inform us as to the kinds of data and data collection procedures that will be used next year when NAM6 is grown out in two locations in Minnesota and North Dakota. Ultimately, these NAM populations will be used to map a wide range of traits in barley and provide a starting point for breeders to introgress novel alleles from the NSGC to new barley varieties.



Alex Ollhoff, graduate student at UMN preparing lines for field.



Nested association mapping panel consisting of 91 crosses and 7711 lines.

USDA's Nat'l. Small Grains Collection harbors many genes that may be useful to breeders and stakeholders. To access these genes, Univ. of MN barley researchers crossed 91 lines to an adapted variety, Rasmusson. This summer, data will be collected (including reflectance data collected by unmanned aerial vehicles) on the crosses to begin the complex process of finding and transferring the useful genes to breeding programs.

2014 CIMMYT Trip Highlights

18 TCAP students from 8 different universities traveled to the CIMMYT conference in Obregon Mexico for 9 days.

TCAP Students who visited CIMMYT commented on the following:

Breeding

- The yield workshop: optimal physiological traits, such as improved photosynthetic efficiency, are being moved into the breeding program in an effort to improve yield.
- Field days: Featured CIMMYT varieties, from the very first green revolution variety to the newest CIMMYT variety, to be released as Borlaug100.
- Technology: Smart phone apps to benefit small holder farmers; advances in computational speed to predict management decisions for particular regions or sites.
- Genetic progress: Historic pre-Green Revolution varieties in the field growing alongside popular, modern varieties.

Phenotyping

- Drought resistance: Drought trials including drip irrigation.
- High throughput phenotyping: the octocopter and the blimp they use for CSR measurements.

Rust

- New developments in gene discovery, mapping, and deployment
- Importance of sustained rust resistance breeding efforts

Networking - TCAP students were able to meet and interact with:

- CIMMYT scientists
- Scholars from around the world
- CGIAR scientists from the international centers
- Groups who described new partnerships, collaborations, and initiatives

Global – TCAP students were made to feel part of a global village and noted in particular:

- a humbling experience to observe the hard work and dedication these scientists put into research work.
 - the meeting was a reminder that many people in the world today still suffer from hunger
 - Policy will play a pivotal role in meeting the food production goals for 2050.
 - Sustainability is key: research into low-input system and input use efficiency is the future.
- This largely aligns with the goals of TCAP.

Bonus – students also loved the:

- asadas (BBQs)
- poster competition
- warm weather
- inspiration provided by Dr. Borlaug's life, achievements and well-deserved recognition from all over the world





Celebrating Dr. Norman Borlaug's 100th B-Day in Ciudad Obregon, Sonora, Mexico

By: David Chappell

I had the privilege to travel to the Centro Internacional para Mejoramiento de Maíz y Trigo (CIMMYT), known in English as the International Center for Maize and Wheat Improvement in Ciudad Obregon, Sonora, Mexico to celebrate the legacy of Dr. Norman Borlaug on what would have been his 100th birthday. Dr. Borlaug was the founding father of the Green Revolution of the 1950s, 60s, and 70s in which tremendous yields in wheat and rice were attained around the world through the discovery of major stem rust resistance genes, reduced height (*Rht*) genes, photoperiod insensitivity genes, and improvements in crop management practices. Dr. Borlaug's contributions to agricultural science saved millions of people from starvation, earning him the Nobel Peace Prize in 1970, the Presidential Medal of Freedom in 1977, and the Congressional Gold Medal in 2007, just to name a few of his many recognitions.

Despite these awards and recognitions he received from many different governments and organizations around the world, Dr. Borlaug remained a humble man and preferred to be out in the field training the next generation of agricultural scientists. He insisted that much work remained to ensure continued food security for the world's growing population, which is projected to reach 9 billion people by the year 2050. In order to feed the burgeoning population, scientists estimate that crop yields must increase by 70% from current levels. When compounded with projected climate change scenarios, decreasing availability of irrigation water, and increasing urbanization of agricultural lands, agricultural scientists do indeed have their work cut out for them.

As much as this meeting was a celebration of Dr. Borlaug's life and legacy, it was also a gathering of scientists from around the world to address the many challenges facing global agriculture. While in Ciudad Obregon, I attended the Borlaug Global Rust Initiative (BGRI) meeting, which focused on work being done around the world to mitigate the effects of rust fungi, a major pathogen of wheat responsible for dramatically reducing yields in many portions of the world. Dr. Borlaug's discovery of major stem rust resistance genes have been durable in most regions of the world since the 1950s, but in 1999, a new strain of stem rust was discovered in Uganda that was able to overcome these resistance genes. The new stem rust strain has spread throughout most of East Africa and is now moving into the Middle East and South Asia. Fortunately, strides have been made against the new stem rust strain, which has since been named *Ug-99*. The Ethiopian delegation of scientists was recognized at the meeting for their contribution to *Ug-99* stem rust resistance and several wheat varieties containing *Ug-99* resistance are in the CIMMYT pipeline for release to farmers in East Africa and South Asia.

The BGRI culminated with a field day at CIMMYT, in which agricultural scientists working at the research station presented their latest advances in crop improvement techniques. We learned about conservation agriculture practices being undertaken to ensure continued agricultural sustainability, including permanent crop beds and crop residue retention to minimize irrigation water loss, increased organic matter content, and reduced monetary and labor inputs. We also witnessed CIMMYT's abiotic stress tolerance studies on heat and drought stress and learned about the latest techniques to improve these traits. The physiology group conducted a demonstration utilizing blimps, drones, and ground equipment to measure key physiological traits such as canopy temperature and chlorophyll content, which are indicative of crop performance under heat and drought stress. We were also able to observe CIMMYT's legacy varieties going all the way back to Dr. Borlaug's first stem rust resistant variety, Yaqui 50, which was released in the Sonoran wheat growing region in 1950. Staple cultivars of the Green Revolution, including Siete Cerros, Sonalika, Pavon 76, and Seri 82 were represented in this legacy nursery. CIMMYT's most advanced germplasm nursery was immediately adjacent to the legacy nursery and included wheat cultivars possessing such traits as heat tolerance, drought tolerance, *Ug-99* resistance, and zinc biofortification. The field day concluded with a mariachi band fiesta complete with barbecued beef, freshly made flour tortillas, pico de gallo, and plenty of cervesa.

I think Dr. Borlaug would be proud of the ongoing work being done by scientists around the world to advance the cause of sustained food security for a growing population. However, as he always said, there are no miracles in agricultural production and there is always more work to be done. Agricultural scientists must not falter in the quest to obtain a 70% yield improvement to ensure an adequate food supply for the future of humanity. As Dr. Borlaug said, "if you desire peace, cultivate justice, but at the same time, cultivate the fields to produce more bread; otherwise there will be no peace. Almost certainly, the first essential component of social justice is adequate food for all mankind."

TCAP Undergraduate Research Academy - 2014

Mary Brakke

The purpose of the Academy is to provide undergraduate students with experiences that help prepare them for graduate studies. Students discuss research in online meetings, receive funding to present their research at a national meeting, and learn about graduate programs in plant breeding. Three undergraduate students are currently participating in the program. Their project descriptions are given below.



Nathan Wyatt, North Dakota State University

Nathan is conducting research on spot form of net blotch in barley in Dr. Richard Brueggeman's lab and is being mentored by graduate student, Steven Carlsen. Nathan is helping to develop and characterize pathogen populations using *Pyrenophora teres* f. *maculata* isolates that differ for virulence on local and international lines. Nathan will be involved in single-sporing progeny isolates to develop a segregating pathogen population. Individual progeny from this *P. teres* f. *maculata* population will be genotyped using a genotyping-by-sequencing approach to identify SNP markers. Marker data will be used to generate maps for the identification of genomic regions conferring virulence on local and international barley lines. Nathan will be involved in the phenotyping of each of these progeny isolates on a set of barley lines showing disease reaction differences between the pathogen parents used in developing this population. Genotypic data, in conjunction with phenotypic data, will be used to identify genomic regions conferring virulence.



Nikayla Strauss, Colorado State University

Nikayla has been working in Dr. Scott Haley's lab assisting with emasculations in the greenhouse and providing support for wheat-maize doubled haploid production. The majority of her time is spent supporting the TILLING (Targeted Induced Local Lesions in Genomes) project. The project works to identify novel traits such as human health related traits, pest/pathogen resistance, herbicide resistance and various wheat quality traits. Nikayla's main role in the TILLING project has been the genome-specific amplification of candidate genes for mutant identification. In addition to greenhouse and lab experience, Nikayla assists with field work.



Ge Cheng, Fayetteville State University, NC

Ge Cheng is assisting Dr. Lieceng Zhu with research on the impact of 12-oxo-phytodienoic acid (OPDA, a jasmonic acid precursor) and salicylic acid (SA) on the resistance of wheat plants to Hessian fly infestation. This is a TCAP collaborative research project with Drs Ming-Chun Chen and Guihua Bai, USDA-ARS. Ge's work includes researching the impact of OPDA and SA on the resistance of wheat plants under normal conditions and under high temperature stress and investigating the molecular mechanism of SA and OPDA application. This summer Ge is working with Drs. Chen and Bai at the USDA-ARS Grain Marketing Production Research Center in Manhattan, KS.

Online Computation Methods and Quantitative Genetics Course

Deana Namuth-Covert

At the time of writing this article we have had 67 people sign up to participate in the Computation Methods online course which uses TCAP grad student data to teach key tools in R, 21 people have completed most of the work provided. Worldwide participants in plant breeding and computer science disciplines come from TCAP and beyond. For 5 weeks participants were able to interact with each other and course instructors, Ashu Guru and Deana Namuth-Covert. The course is still open for participants to continue at their own pace and when they are needing to learn more about R. Early feedback has been that the video modules are very easy to follow and meet the needs of both those brand new to R and those individuals who have used R some in the past. Plans are to offer a synchronous session again in the fall, joining with computer science students. You can find the course at: <http://passel.unl.edu/communities/computational>

The screenshot shows the homepage of the 'Collaborative Course on Computational Methods'. The header includes the course title, a search bar, and navigation icons. Below the header is a banner image with three panels: a green field, a DNA double helix, and golden wheat. A navigation bar contains 'Lessons', 'Animations', 'Glossary', and 'Join Now'. The main content area features a central text block: 'This new course designed for people in plant breeding professions, as well as those in computational/computer programming will run March 31 - May 6. You will work through some analysis examples of large plant breeding and genetics data sets, in particular using R.' To the right of this text is a vertical graphic with the words 'Computational Thinking', 'correlation', 'CSR', and 'Canopy Spectral Reflectance'. Below the main text are instructions on how to find discussion boards and use Adobe Connect. A sidebar on the left lists 'Course Participants', 'Course Instructors', and 'Courses', with a link to the 'Collaborative Computational Course'. The footer shows the URL 'edu/forms/index.php'.

The self-paced quantitative genetics course is also now running, with 38 participants signed up so far. This course utilizes presentations developed by Jamie Sherman and Clay Sneller, packaged in a manner that creates an interactive learning experience by participants. Upon successfully completing quizzes, participants earn an electronic badge. The course can be found at: <http://passel.unl.edu/communities/tcapquant>

The screenshot shows the homepage of the 'Self-paced TCAP Quantitative Genetics' course. The header includes the course title, a search bar, and navigation icons. Below the header is a banner image with three panels: a green field, a DNA double helix, and golden wheat. A navigation bar contains 'Lessons', 'Animations', 'Glossary', and 'Un-register'. The main content area features a central text block: 'This self-paced course will present basic elements of quantitative genetics emphasizing implications to plant breeding, as well as providing practical experience in linkage and QTL mapping. Dr. Clay Sneller from The Ohio State University provides presentations on basic quantitative genetics concepts. Dr. Jamie Sherman from Montana State University provides presentations that introduce Linkage and QTL mapping topics using the free software Mapdisto (http://mapdisto.free.fr) and QTLcartographer (http://statgen.ncsu.edu/qtlcart/). In this course you will go to websites and download software. You are also welcome to do exercises using other software and compare results. Data to practice analyzing is available within the course. After successfully completing course materials in each unit, including review quizzes, course participants will be sent electronic badges of completion for documenting their professional development. To begin the full course, click on the link to the left.' At the bottom center is the 'Triticeae CAP' logo, which includes a stylized wheat stalk and the text 'Triticeae CAP Coordinated Agricultural Project'. The footer shows the day 'Wedne'.



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
 WRRRC, 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
 Fayetteville 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 CO₂ for photosynthesis and acquire it through window-like structures in leaves simultaneously releasing O₂ and H₂O. 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 photosynthesis occur, but also as H₂O is released the temperature around the plant decreases due to evaporation. CTD can act as a proxy for measuring the plant's 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 expensive, 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.