We are coming to the end of our second year and have gained tremendous momentum on all original objectives of the project. The research portion of the project has made great strides in all aspects of the project. For example, Brittany Hazard, a graduate student in Jorge Dubcovsky’s lab developed wheat lines with increased amylose and resistant starch (page 3). Another example is that the T3 database is being recognized internationally as an important tool for barley and wheat breeding and the T3 database team has been asked to help coordinate international database efforts. To address the database coordination need, Jean-Luc Jannink is organizing a workshop titled “Managing Crop Phenotype Data” at the Plant and Animal Genome meetings on Saturday morning, 12 January 2013, at 10:20 AM. The education portion of the project continues to attract undergraduates to plant breeding and prepare the next generation of plant breeders. The Plant Breeding Training Network (PBTN) has 125 members from across the world. In the fall, PBTN hosted a course on the theory and application of association analysis including genomic selection taught by Clay Sneller, Mark Sorrells, Jean-Luc Jannink and Jeffrey Endelman (page 7). Over 100 participants enrolled in the online course and on average 33 participants attended each session. In addition, three graduate students (Sarah Grogan, Celeste Falcon and Katherine Frels) developed the popular Fall 2012 TCAP seminar series. PBTN plans to host another seminar series starting in March 2013. The TCAP annual meeting (see page 5 for agenda) will be held in San Diego at the Town and Country Convention Center in the Windsor Room on January 13 from 8 am – 7 pm. There are three components to the meeting: from 8-10 am will be the stakeholder session, from 10 am – 5 pm will be the research reporting, and from 5 pm – 7 pm will be a reception and student poster session. In addition, on Friday January 11th there is a graduate student workshop (see page 6) and a meeting for the phenotyping working group (page 2). We hope to see you at the meeting!
Members of the TCAP are organizing a workshop titled “Managing Crop Phenotype Data” at the Plant and Animal Genome meetings on Saturday morning, 12 January 2013, at 10:20 AM. The workshop will concentrate on the topic of specifying phenotypes for efficient query in databases. A phenotype exists at the intersection of an individual (a breeding line for crop scientists), a trait, and a trial. There are challenges in specifying all three axes of this intersection. With genotyping costs down, we now live in a phenotype-limited research environment making it sensible to focus on storage and access to this precious resource. Furthermore, phenotypes are now linked to each other through their connection to genotypes and we gain inferential strength by cumulating them. We invite groups to present how they specify phenotypes and their related trial, trait, and plant or seed identities.

Invitees:

<table>
<thead>
<tr>
<th>Name</th>
<th>Title</th>
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<tbody>
<tr>
<td>Jeffrey White</td>
<td>“Managing phenotypic data for use in crop simulation: lessons from the ICASA standards”</td>
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<tr>
<td>Dave Matthews</td>
<td>“Traits, Trials and Tribulation in the Triticeae Toolbox”</td>
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<tr>
<td>David Marshall</td>
<td>“Phenotype Data— the Final frontier?”</td>
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<tr>
<td>Graham McLaren</td>
<td>“Managing Phenotyping Data in the Integrated Breeding Platform (IBP)”</td>
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<tr>
<td>Yaniv Sernel</td>
<td>“Phenom Networks’ view of crop improvement”</td>
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<tr>
<td>Lukas Mueller</td>
<td>“solgenomics.net: A comprehensive system for managing phenotyping projects.”</td>
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<tr>
<td>Sook Jung</td>
<td>“Integrating phenotypic data with genomic, genetic and genotypic data using Chado”</td>
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The working group using canopy spectral reflectance (CSR) and canopy temperature depression (CTD) as proxies for drought tolerance and nitrogen use efficiency will meet to discuss successes, challenges and brainstorm solutions on the Friday before PAG.

Time: 5-7 pm Friday Jan. 11
Place: Best Western Seven Sees PG Room

Objectives:
1) Summarize experiences and data from 2012 season.
   a) Technical Issues with the machines
   b) Scientific findings
2) Develop strategies for 2013 season.

Preparation for the Meeting
Data summaries from 2012 from all interested participants should be uploaded onto the CSR forum. This preparation will help to insure that our 2 hour meeting in San Diego is as fruitful as possible.
Spring webinar on development and use of KASP markers in wheat and barley

Utilizing the abundance of SNP data from the Illumina barley OPA and the 9,000 SNP Wheat Infinium Assay, T-CAP researchers have identified markers associated with important genes in bi-parental and association mapping populations. In order for individual breeding programs to do routine selection with markers coming from these highly multiplexed Illumina platforms, new assays that can be assessed using breeder’s existing laboratory equipment must be developed. In addition, high-throughput genotyping assays specific for alleles of cloned genes affecting plant development, end-use quality and disease resistance in wheat and barley are needed by public and private breeding programs. The KASP technology (K-Biosciences, UK) is one approach to low-plex, high-throughput genotyping being implemented by the T-CAP project. This technology can be utilized to select for small numbers of genes in many individuals, and may also be combined with genome-wide selection approaches.

KASP genotyping utilizes a competitive PCR reaction with allele-specific forward primers, each having unique tail sequences. Each tail is homologous to a sequence labeled with either FAM or HEX dyes so that through PCR the product specific to an allele is labeled with one of the dyes. Allele discrimination is done by taking end-point readings with either an RT-PCR machine or a fluorescent plate reader. One advantage is that assays are “closed-tubed”, meaning that no post-PCR handling of samples is required. Also, KASP provides flexibility in assay design, making it well-suited for use in polyploid wheat, and is low-cost relative to other closed-tube genotyping methods. Reported sequence variation (SNPs and indels) in wheat for reduced height, vernalization and photoperiod response genes have been targeted for development. In addition, allele specific assays have been developed for cloned disease resistance and end-use quality genes in wheat. Assays for barley have been developed using sequences corresponding to SNP markers selected from the Barely OPA.

Given widespread interest in use of the KASP genotyping system by T-CAP breeding programs, a webinar on KASP marker development and utilization will be presented by Dr. Brown-Guedira, USDA-ARS, Raleigh, NC during Spring 2013.

http://www.lgcgenomics.com/how-does-kasp-work
When searching for labs for my graduate education, I found that Jorge Dubcovsky’s wheat genetics lab at UC Davis was a perfect fit for me because I was interested in studying genetics in a high-impact crop, as well as, improving traits related to nutritional value. Jorge and I discussed my interests and potential projects, one of which involved using starch branching enzyme II (SBEII) mutants to increase the amount of amylose and resistant starch in the wheat grain. Resistant starch is considered a component of dietary fiber and studies have shown that it can provide protection from several diseases such as colon cancer, diabetes, obesity, and cardiovascular diseases. I was immediately attracted to this project because of its potential to have a large impact on the health of the population. By increasing the resistant starch content in the wheat grain it may be possible for consumers to obtain many of the same health benefits associated with the dietary fiber of whole grains while still eating the refined grain products they prefer.

Before I began working on this project the lab had already screened TILLING (Targeted Induced Local Lesions in Genomes) populations of durum and bread wheat to identify mutations in SBEII genes (SBEIIa and SBEIIb). TILLING mutants are not considered genetically modified organisms (GMOs) and breeding programs can introgress useful mutations into elite varieties using marker assisted selection (MAS).

My ultimate goal for this project is to develop the germplasm needed for breeders to produce high-amylose varieties and thus provide healthier refined grain products to consumers. So far, my project has been successful and my initial results are promising. During my first year in the lab, I worked on combining SBEII mutations in both genomes of the durum wheat variety Kronos. When evaluating these mutants I found that double-genome SBEIIa mutants had up to a 22% increase in amylose content and 115% increase in resistant starch content. These results were published in the July-August issue of Crop Science and the seeds were made available to the public. Since then we have been receiving seed requests from breeders around the world.

Funding for my research has been provided by the USDA-NIFA Triticeae Coordinated Agricultural Project, UC Discovery Grant, Colorado Wheat Research Foundation, ConAgra Mills, UC Davis Department of Plant Sciences, and the Henry A. Jastro Graduate Research Scholarship.
Triticeae CAP Annual Meeting Agenda

January 13, 2013
Town and Country Convention Center (Windsor Room)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8:00 – 10:00 am</td>
<td>Reporting session for stakeholders</td>
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<tr>
<td>8:00 – 9:00 am</td>
<td>Research and Education overviews</td>
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<tr>
<td></td>
<td>Jorge Dubcovsky, Gary Muehlbauer, Jamie Sherman</td>
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<tr>
<td>9:00 – 9:30 am</td>
<td>Discussion with Stakeholders</td>
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<tr>
<td>9:30 – 10:00 am</td>
<td>Break</td>
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<tr>
<td>10:00 am – 2:40 pm</td>
<td>Reporting session for Scientific Advisory Board and USDA</td>
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<tr>
<td>10:00 – 10:30</td>
<td>Overview of project</td>
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<td></td>
<td>Jorge Dubcovsky (UC, Davis)</td>
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<td></td>
<td>Gary Muehlbauer (University of Minnesota)</td>
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<tr>
<td>10:30 am – 11:20</td>
<td>Education</td>
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<td></td>
<td>Introductions -Jamie Sherman (Montana State University)</td>
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<td></td>
<td><strong>Graduate Student/Undergraduate mentoring</strong></td>
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<td></td>
<td>Sarah Grogan (Colorado State University)</td>
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<td></td>
<td><strong>TCAP – MSI interaction success story</strong></td>
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<td>Arron Carter (Washington State University)</td>
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<td></td>
<td><strong>Successful Online Class Offering</strong></td>
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<td>Jeffrey Endelman (USDA-ARS, Ithaca, NY)</td>
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<tr>
<td>11:20 am – 11:40 am</td>
<td>Developments in T3</td>
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<td></td>
<td>Jean-Luc Jannink (USDA-ARS, Ithaca, NY)</td>
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<tr>
<td>11:40 am – 1:00 pm</td>
<td>Lunch on your own</td>
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<tr>
<td>1:00 pm – 1:40 pm</td>
<td>What have we learned from the <em>genotyping</em> efforts?</td>
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<td>Eduard Akhunov (Kansas State University)</td>
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<td>Maria Muñoz-Amatriain (University of Minnesota)</td>
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<tr>
<td>1:40 pm – 2:00 pm</td>
<td><strong>Genomic selection in barley</strong></td>
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<td>Kevin Smith (University of Minnesota)</td>
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<tr>
<td>2:00 pm – 2:20 pm</td>
<td><strong>Association mapping</strong> of disease resistance in wheat</td>
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<td>Mike Pumphrey (Washington State University)</td>
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<tr>
<td>2:20 pm – 2:40 pm</td>
<td>Low temperature tolerance in barley</td>
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<td></td>
<td>Pat Hayes (Oregon State University)</td>
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<tr>
<td>2:40 – 3:40 pm</td>
<td>Breakout groups</td>
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<tr>
<td></td>
<td><strong>T3, Genotyping, Barley, Wheat</strong></td>
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<tr>
<td>3:40 – 4:00 pm</td>
<td>Break</td>
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<tr>
<td>4:00 – 5:00 pm</td>
<td>Feedback from Scientific Advisory Board and Discussion</td>
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<tr>
<td>5:00 – 7:00 pm</td>
<td>Reception and poster session (Hampton Room)</td>
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Graduate Student Workshop

All graduate students are invited to come and network at the afternoon workshop on Friday January 11th from 1:00-5:00 at the Best Western Seven Seas. The workshop: Life Skill Enhancement: The Gateway to Becoming an Extraordinary Plant Breeder will be led by Kim Kidwell and Mary Kay Patton. Industry representatives (potential future employers) will be present to share ideas on what makes a great plant breeder.

Poster Session

TCAP graduate students will be giving posters at a reception following the TCAP meeting Sunday January 13th from 5:00-7:00. All posters must be hung in the Hampton Room at the Town and Country prior to 8:00am. This is a great opportunity for students to share their work with TCAP colleagues as well as our stakeholders, informing us of the breadth and reach of the project. Representatives from USDA, industry, as well as researchers from other projects will be present, providing students with an opportunity to network.

TCAP Success Story by Ryan Graebner

Last May, I had the good fortune of being hired into the barley lab at Oregon State University as the TCAP undergrad. Coming into the lab, I had no prior experience in plant breeding. However, the faculty and lab members tolerated my short-comings and have included me in several projects. Not long after I started, I was brought into a beer flavor project, where we will use genome wide association scanning to search for Quantitative Trait Loci (QTL) that relate to positive flavors in beer. Early last month, we sent a very diverse subset of 114 accessions from the USDA World Core Collection for barley to be malted by Rahr in Minnesota. The malted barley will then be sent to Sierra Nevada where it will be used to make wort (the first liquid stage in the beer-making process). This wort will be tested for chemical and taste characteristics using a combination of machines and human taste panels. Promising accessions will be re-grown next spring at three locations.

In addition to the research, the TCAP has connected me with researchers from around the country. In early August, the project allowed me to present my research at the National Association of Plant Breeders (NAPB) annual meeting in Indianapolis. While there, I met graduate students that were part of the TCAP and from other research projects. I also attended very interesting presentations on both the scientific and bureaucratic sides of plant breeding, which gave me a much better understanding of the state of the field around the world. More recently, I’ve taken part in the online seminars and undergraduate meetings organized by the TCAP. This experience has presented an excellent opportunity to connect with others in barley and wheat breeding.

My time as a TCAP undergraduate is coming to an end, but this January, I’ll be starting graduate school as a part of Oregon State’s Barley Project. Overall, this experience has been a great way to transition into the world of plant breeding, and I expect that it will continue to serve me well throughout my studies.
Ahead of the Curve: Technologies for next-gen plant breeding, the Fall 2012 TCAP Seminar Series was organized by three TCAP students: Sarah Grogan, CSU; Celeste Falcon, UMN; and Katherine Frels, UNL. The series was organized during the summer and began October 3rd with a statistics presentation by Dr. Kent Eskridge from University of Nebraska-Lincoln and ended on December 12 with a genomic selection presentation from Dr. Gustavo de los Campos from University of Alabama-Birmingham.

The seminars, hosted online at the Plant Breeding Training Network, were well attended with 15-45 people participating in each. Most of the seminars have been structured like a typical on campus seminar; however, the committee is trying to utilize the online format in different ways. The October 31st seminar with representatives of Bayer CropScience (Dr. Sally Clayshulte, Dr. Janet Lewis, and Kayse Onweller) developed into a panel discussion about transitioning from graduate school to industry work where seminar participants could ask questions through the Adobe Connect system.

The committee would like to thank all of the fall series presenters for their time and knowledge. Presenters include Dr. Kent Eskridge, Dr. Sally Clayshulte, Dr. Janet Lewis, and Kayse Onweller, Dr. Jianli Chen, Dr. Pat Hayes, and Dr. Gustavo de los Campos. We would also like to thank Dr. Jamie Sherman, Dr. Deana Namuth-Covert, Deanna Leingang, Amy Kohmetscher, and DeAnna Crow for their assistance.

The Spring 2013 seminar series will begin in March 2013. Speaker recommendations and nominations for student committee members are gladly accepted! The seminar series committee needs your help to plan this next set of seminars. For more information or to submit recommendations, please contact Sarah Grogan at sarahgrogan@gmail.com.

Pilot Evaluation of TCAP

Educational Materials - Carol Speth

A pilot study was designed to measure effectiveness of the TCAP supported materials for teaching. A larger study is planned for the spring semester. Three instructors encouraged their students to use and evaluate materials designed in part through the TCAP e.g. Holding the future in the palm of your hand and the Wheat Breeding Activity. The first 104 responses have been analyzed. The educational materials were all housed on-line. Four were primarily print based, while three were video based. The educational materials were all part of the regular course assignments, but evaluating them allowed the students to receive extra credit. Students answered questions in Blackboard to demonstrate actual use of the lessons, while preserving confidentiality of survey. Included below are some highlights from the survey.

Most students used 4 to 5 of the seven total offered resources
More students used the video based resources than the print based (96 vs 51%)
The students that used the most resources indicated their reason as “I am always striving to

compete and be successful in all my courses,” or “I am interested in this subject and want to learn as much as I can about it.”

Many students indicated that the resources taught concepts essential to their career goals
Most students indicated that the materials were helpful in teaching concepts in the course they were taking.

Content questions were used to determined if utilizing more resources improved learning. Two-tailed Pearson correlations indicated that students did significantly better with increasing number of resources used.

TCAP resources changed students perceptions

76% reported change in awareness of Plant Breeding as a career
88% reported change in knowledge about what Plant Breeders do
50% reported change in willingness to put time and effort into learning from these resources
56% reported change in knowledge of how segregation is used in Plant Breeding
More than 50 undergraduate students at 25 different institutions across the U.S. are currently participating in TCAP-funded research projects. Typically, students are mentored by TCAP-funded graduate students. Students frequently begin by assisting graduate students with tasks in the field or lab and are encouraged to develop and implement an independent study as they become familiar with the project. By providing students with first-hand experience, internships help students gain confidence as researchers. The program aims to increase student interest in graduate studies in plant science and to equip them with skills that will help them succeed in graduate school. In addition to a stipend, the TCAP provides research interns with travel funds to a conference at which they present results of their research.

Monthly online meetings with TCAP research interns are held through the Plant Breeding Training Network and facilitated by Mary Brakke. The meetings are informal and aim to broaden student understanding of research through interaction with other research interns as well as experienced plant scientists. In September a meeting was held to acquaint students with the TCAP, other research interns and online meeting features of the Plant Breeder Training Network. On 11 October, Dr. Jim Anderson met with interns and provided suggestions on how they can use their internships to prepare for graduate school.

Online meetings with TCAP research interns give students opportunities to talk about their own research and develop skills in communicating science. In November, two MS students presented results of research they conducted as part of the TCAP-MSI collaborative research effort. On 19 November, Yaleaka Currie, MS student at Fayetteville State University, NC, discussed her research on molecular responses of Hessian-fly resistant wheat plants to high temperature stress (https://connect.unl.edu/p5py3qywn8a/). On 29 November, Michael Tavarez, MS student at CUNY Lehman College, NY, discussed differences in cadmium uptake and transport in isogenic lines of wheat.

Online meetings with TCAP research interns provide students with opportunities to learn from both novice and expert researchers and share their own knowledge. Here are a few recommendations made by students this fall:

- Don’t be afraid to ask questions
- Write down everything you do during your research
- Keep an open mind. Your research may not go as you expect (remember, it’s research) but you can still learn from it
- Always accept help
  (Y. Currie)
- Make sure the project is doable (it should have an end point)
- Learn as much as possible, especially different techniques. You will be able to apply these to other questions
- When you get discouraged with your research, talk to people who can help you figure out what is going wrong.
  (M. Tavarez)

**PBTN Success**
The Plant Breeding Training Network [http://passel.unl.edu/communities/pbtn](http://passel.unl.edu/communities/pbtn) now has 125 members from across the globe. In November 2012 alone, the PBTN registered 353 views from 41 countries. A TCAP course offered fall of 2012 on the Theory and Application of Association Analysis had 107 registrants. The course was a mixture of recorded and live lecture, as well as analysis demonstrations. On average 33 attended each session and more than 20 received the certificate of completion. Clay Sneller created more than three hours of lecture introducing students to quantitative genetics. Mark Sorrells gave two lectures discussing the implementation of association mapping and genomic selection in a breeding program. Jeffrey Endelman introduced students to association mapping using the R package he created (rrBLUP), providing scripts so that participants can run their own analysis. Jean-Luc Jannink used the same R package to demonstrate genomic selection, providing scripts as well. Students were encouraged to analyze data from the T3 database or their own data, with Jeffrey and Jean-Luc providing support. Of thirty participants responding to a survey, 97% indicated the course was useful.
Visiting University of Arkansas at Pine Bluff

Luther Talbert had the opportunity to visit collaborators Dr. Joseph Onyilagha and Dr. Martin Matute at the University of Arkansas-Pine Bluff on October 29th. Undergraduate students Michelle Poe, Kerian Trice and Jessica Bailey presented their work with Dr. Onyilagha to characterize biochemical response of wheat to drought stress. They were using HPLC to analyze plant material grown under varying levels of stress supplied by Dr. Talbert. Dr. Matute’s students Delois Moss, Paige Walker and Quinton Williams demonstrated techniques for analysis of nematodes in Arkansas soils. Dr. Matute has a joint project with Dr. Arron Carter from WSU. Dr. Talbert presented a seminar entitled ‘Past, Present and Future of Plant Improvement’ to approximately 80 students in the Biology program. Students surveyed after his presentation indicated a significant change in awareness of plant breeding, an change in knowledge as to what plant breeders do. Eighteen students indicated a change in interest in plant breeding as a career.

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
Plant Biology, 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
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 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.