



**Triticeae CAP**  
Coordinated Agricultural Project

# TCap Transmission

October 2013

Funded by the USDA National Institute of Food and Agriculture



United States Department of Agriculture  
National Institute of Food and Agriculture

## INSIDE RESEARCH:

Directors Notes

TCAP Annual Report

T3 2

Ug99 breakthrough 3

Impact of Barley, wheat and TCAP 3

Andra Bates 4

Publication of the first catalog of CNV in 5

## Directors notes: Gary Muehlbauer and Jorge Dubcovsky



As we come to the end of the third year of the TCAP, the progress we have made from the beginning of the project has been outstanding. High-throughput **genotyping** approaches have been employed and coupled with large-scale field based **phenotyping** on large **germplasm** collections are resulting in detection of numerous QTL. The Triticeae Toolbox has been expanding rapidly with heaps of phenotype and genotype data, and new visualization and analysis tools. Beneficial alleles are making their way into breeding programs through either **genomic selection** or **marker-assisted selection**. The speed of QTL discovery and incorporation into breeding programs has been one of the highlights of the project. Another highlight and the true legacy of the TCAP are the students trained. To date, 117 graduate students and 87 undergraduates have participated in the Plant Breeding Training Network. In addition, six students from Minority Serving Institutions spent six weeks at a TCAP institutions (see page 4 for an example of one of the MSI student experiences, and page 8 for additional details on the MSI student experiences). TCAP undergraduate online meetings are underway and the lineup of speakers is excellent and promises to provide an avenue for undergraduates to enhance their education in breeding and genetics and to refine their professional skills (see page 10). Please encourage your undergraduates to attend the online sessions. The Fall Webinar series has also started and we have an impressive lineup of speakers (see page 11). The TCAP is also sponsoring a graduate student trip to CIMMYT so if you are interested please contact Jamie Sherman (see page 12). Please mark your calendars for the annual TCAP meeting to be held on January 12, 2014 at the Town and Country Convention Center in San Diego (see page 7).

**See you in San Diego!**

Definitions to all red words can be found in "TCAP Terminology" on page 13

## TCAP Annual Report

To obtain funding each year, the TCAP project must submit a report to USDA-NIFA that describes our progress from the previous year. This year the report was due in September. A tremendous amount of progress has been made in the first three years of the project in all major objectives. Here, we highlight a few of the major accomplishments from the last year that were described in the annual report. As part of the **genotyping** effort a 92K iSelect wheat chip was developed and used to genotype association mapping and **nested association mapping** panels. **Exon capture arrays** for both wheat and barley were developed and used to assess the genetic variation in a subset of the wheat and barley accessions used in the **nested association mapping** population development. The Triticeae Toolbox (T3) has been greatly expanded with data (15,000 lines with 540,000 phenotypic data points, and 22,000 lines with 111 million genotypic data points) and new tools for data visualization and analysis. Phenotypic data for nitrogen use efficiency, **water use efficiency** and several fungal pathogens have been collected on the **National Small Grain Core Collections** and **association mapping** panels for wheat and barley. The best drought and pathogen resistant lines have been incorporated into breeding programs. Noteworthy, is the legacy of students trained through TCAP. One hundred and seventeen graduate students have participated in the Plant Breeding Training Network, of which 81 are directly mentored by TCAP PIs. In addition, 87 undergraduates have participated in the TCAP, of which 49 are mentored by TCAP PIs, 36 by faculty in Minority Serving Institutions (MSI), and two not affiliated with the TCAP. Six MSI students spent time at TCAP institutions in 2013. Finally, 51 peer-reviewed papers have been published, and 20 cultivars, 16 **germplasm** and 13 new mapping populations have been released.

## What's New in T3?

### Wheat

Population	Details	Contributor(s)
Worldwide Diversity Panel	9K WPOPA on 2259 lines	Ed Akhunov
NSGC spring and winters	Stripe Rust Resistance in WA	Mike Pumphrey / Peter Bulli
SWW and HWW Panels	Agronomic traits in Manhattan, KS	Kyle Shroyer / Vara Prasad
Near-Isogenic Lines	Evaluation of Ppd-D1 and Ppd-B1	Luther Talbert /
Leaf Rust AM Panel	Adult and Seedling	James Kolmer / Amy Fox
wSNP 2013 Consensus Map		Cavanagh <i>et al</i> , 2013

### Barley

Population	Details	Contributor(s)
CAP 2-row	Agronomic data for 2012 and CSR in 2013 in Bozeman, MT	Tom Blake / Duke Pauli
Ethiopian Eritrean Barley Collection	Minnesota and Ethiopia, agronomic, nutrient and pathogen traits and 9K genotyping data.	Brian Steffanson / Bullo Mamo
CAP 2row Spot Blotch	NDSU seedling screening	Shaobin Zhong
TCAP Facultative-Winter 6row	Greenhouse race-specific resistance and field trials, CSR data	Pat Hays / Xianming Chen / Araby Belcher

The Triticeae Toolbox Tutorial (T4) Outline. A suite of online tutorials is in production and will be available on Vimeo in Fall 2013. Below is a planned outline of 5-10 minute tutorials.

#### Unit 1 - Sleuthing

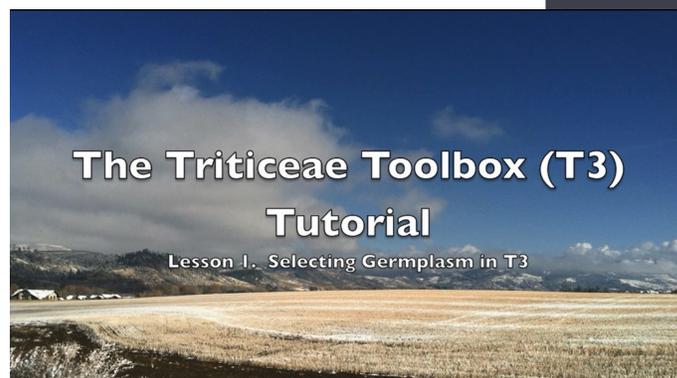
- Lesson 1. Lines
- Lesson 2. Traits and phenotypes
- Lesson 3. Maps and Markers

#### Unit 2 - *In situ* data analysis using tools in T3

- Lesson 4. Cluster Lines by Genotype
- Lesson 5. **Canopy Spectral Reflectance (CSR)**
- Lesson 6. Genomic Association
- Lesson 7. Genomic Prediction
- Lesson 8. T3 to TASSEL
- Lesson 9 and 10. T3 to R

#### Supplemental - Care and Feeding of T3

- Lesson 10. How to submit lines
- Lesson 11. How to submit phenotype data (including **CSR**)
- Lesson 12. How to submit genotype data



TCAP researchers Eduard Akhunov and Jorge Dubcovsky identified a **gene** that enables resistance to the Ug99 of wheat stem rust, a disease that is producing large wheat yield losses throughout Africa and Asia and threatening global food security. This study identified a **gene** called Sr35 that confers near-immunity to this new race. Using natural variation, mutants and transgenic plants, the researchers confirmed that this **gene** was both necessary and sufficient to confer resistance. When SR35 is transferred into a common wheat variety that is susceptible to the disease, by recombination or transgenics, the plant becomes resistant to Ug99. This discovery opens the door for biotechnological approaches to fight this devastating disease and provides an entry point to understand better the wheat-rust pathosystem. The study was published in the journal Science.

## Impact of barley, wheat and Triticeae CAPs

The TCAP was also asked to provide the economic impact of the barley, wheat and Triticeae CAPs with regards to both varieties that farmers are growing and student training. A portion of our response was:

### *Economic impact of public wheat and barley varieties: \$12-billion/year*

We completed a survey that includes information for 33 states for wheat and 10 states for barley and that cover 97% of the US wheat acreage and 84% of the barley acreage. Production of small grains in the US in 2012 resulted in a \$17.8 billion value for wheat and \$1.4 billion value for barley (based on USDA-NASS 2012 statistics). Based on our survey, public varieties account for 68% of the wheat (\$11.5 billion) and 34% of the barley (\$413 million) total production. These numbers indicate that public breeding programs are still making a significant contribution to the production of these two crops in the US. The \$12-billion production value of public wheat and barley varieties is amplified multiple times through the milling, baking, malting, and brewing industries that contribute additional jobs and value to the economy. Private companies routinely use public varieties in their crossing blocks, transferring part of this value to the private sector and further multiplying the economic benefits of the public breeding activities.

### *Impact of CAP projects on production values of wheat and barley varieties*

Based on our survey, we estimated that wheat and barley varieties developed with total or partial support of the CAP projects (WheatCAP, BarleyCAP and TCAP) represent roughly 20% of the wheat and 4% of the barley harvested acreage, with a production value of \$3.5 billion for wheat and \$62 million for barley.

To estimate how much of this value was specifically added by the CAP projects (BarleyCAP, wheatCAP and TCAP), we made the following conservative assumptions:

- 1) If a variety is grown commercially there must be a perceived increased value compared to other available varieties. Thus, we assumed that the currently grown varieties developed by these projects have at least a 5% advantage in production values to justify the grower's decision to buy seed for a new variety. Therefore, we calculated first the 5% of the production value for wheat (\$170.8 million) and barley (\$3.1 million).

- 2) Varieties differ in the proportion of funds received from CAP projects and local breeding programs for their development. Some were completely developed using funds from CAP projects (e.g. MAS backcrossing programs such as Patwin 515 in CA) and others received funds from CAP projects for part of the variety development costs (e.g. selection of parental lines used in the initial crosses or selection of favorable alleles with markers). To be conservative we estimated that, on average, 10% of the variety development was contributed by the CAP projects.

We then calculated this 10% over the 5% additional production value of the CAP barley and wheat varieties (0.5% of their total value). The resulting estimate was \$17.2 million per year of added value to current barley and wheat varieties by CAP projects. This is more than three times the value of current TCAP investment per year including education and overhead costs. The return value of breeding activities only materializes 5-10 years later when the resulting varieties are released, so return from the current investments are expected to extend into the future and expand as high-throughput **marker** technologies permeate more and more breeding activities.

### *Economic impact of the information and technological tools generated by CAP projects*

In addition to the value captured by the public sector, part of the value of this investment is also transferred to the private sector. The maps, **marker** information, and **marker** technological developments (ISelect 9K and 92K chips, exome capture platforms, maps, etc.) are actively used by the wheat and barley private sector in the US. Many private companies use markers developed by the public sector, and even use the USDA **marker** labs.

### *Economic impact of the training provided by the CAP grants*

We performed a survey to identify the current positions of people trained during the barleyCAP, wheatCAP and TCAP projects. We identified 57 individuals that currently hold positions in breeding and seed companies located in the US. Forty are currently working in academic institutions in the US and 18 are working in other countries (public or private). These data confirm that the CAP projects have contributed significantly to the training of the personnel currently working in the private sector and academia.

## Andra Bates Research Experience Summary

In June, 2013, I travelled to St. Paul, Minnesota to study stem rust and its variants in Dr. Brian Steffenson's lab. The goal of the project I worked with was to identify a barley line that is resistant to stem rust race Ug99 (also known as TTKSK). Ug99 is considered to be a major threat to world food security due to its virulence in over 97% of barley cultivars worldwide (Steffenson et al. 2012), including barley lines that have the *Rpg1* gene (Steffenson and Jin 2006). The only locus known to confer resistance to Ug99 is the *rpg4/Rpg5* resistance locus that was characterized from the Steptoe x Q21861 cross (Brueggeman et al. 2008)

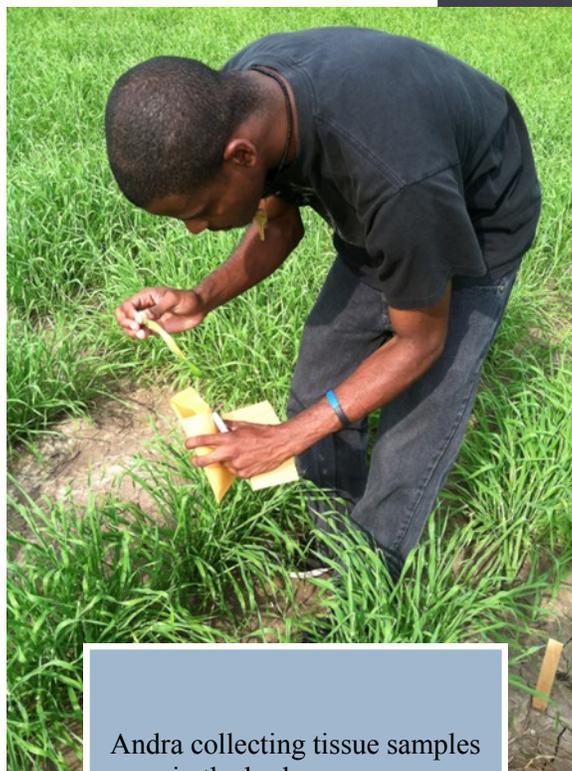
I worked with PhD student, Austin Case. The goals of Austin's project were to locate barley lines in the nursery resistant to stem rust race QCC, locate the gene(s) that conferred resistance to stem rust, and transfer the gene(s) to future barley plants to strengthen diversity as well as resistance to current and future stem rust epidemics. My role was to assist him with the project.

As the race TTKSK poses a significant threat to U.S. agriculture, it must be contained in the Biosafety Level 3 (BSL3) facility. To conduct field screening we used a domestic surrogate of race TTKSK named race QCC. We have two different domestic races of stem rust in separate nurseries: QCC and MCC. QCC was isolated from MCC in order to prevent contamination because QCC was discovered to be virulent on *Rpg1* plants in North Dakota (Roelfs et al. 1991). It is crucial to segregate the two races in order to obtain optimum results and decrease error.

Barley line Q21861 has a high resistance to QCC as well as race TTKSK and it contains both *Rpg1* and *rpg4/Rpg5*. Since QCC is a surrogate of TTKSK, it was important to use Q21861 as a standard to identify other barley plants in the nursery that showed high resistance to QCC. An approach Austin and I used for comparative analysis included resistant and susceptible plant standard checks in the nursery. I also learned how to conduct PCR and gel electrophoresis as a confirmation method of pinpointing specific barley lines that contain the *rpg4/Rpg5* genetic complex.

There was one barley line in particular that conferred resistance to stem rust that I identified in the nursery based on observational analysis throughout its growth stages. The line is called IV/32. IV/32 was found to actually have a higher resistant rating than the Q21861 standard that was used in the nursery. Observing its resistance poses the question: Could this line be propagated and sent to Africa to combat Ug99?

As I conclude this, I must say that my experience in St. Paul, Minnesota, as well as Minneapolis, has been worthwhile and my confidence in research, in all honesty, has increased exponentially. I am also grateful that I was able to work in a prestigious department of plant pathology with scientists who continue Dr. Norman Borlaug's work to increase crop yield and end world hunger.



Andra collecting tissue samples in the barley nursery.

# Publication of the first catalog of CNV in the barley genome

By: Maria Munoz-Amatriain

Finding new sources of genetic diversity that results in phenotypic diversity is one of the main goals of the TCAP project. Although single nucleotide changes (SNPs) are the most frequently examined type of genetic variation, there is evidence that that Copy Number Variation (CNV) affects more nucleotides per genome than SNP variation. CNVs include deletions and duplications ranging from a few to several thousand base pairs in size. These alterations can change gene dosage or interrupt coding sequences, which can have important phenotypic consequences.

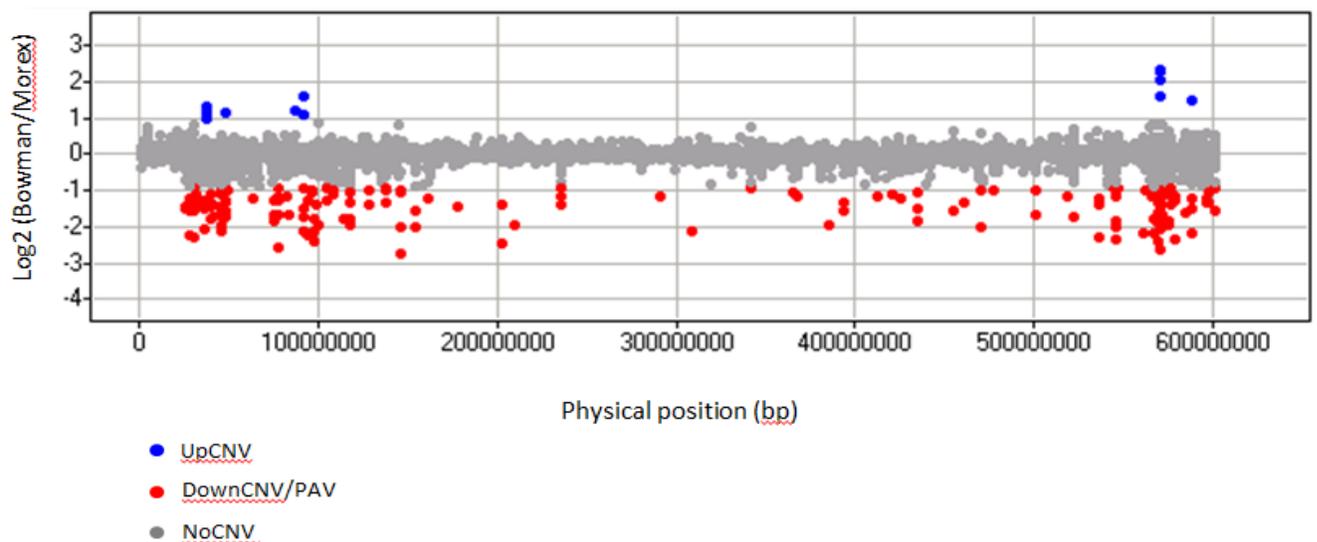
In collaboration with IPK-Gatersleben (Germany) and other University of Minnesota researchers, we explored the extent of CNV in the genome of cultivated and wild barley. Array Comparative Genomic Hybridization (CGH) technology was used for this purpose and involved the development of a custom microarray containing 2.1 million DNA probes representing almost 50 Mbp of non-repetitive barley sequence (from the reference genotype cv. Morex). In an attempt to capture most of the barley genetic diversity, a total of 14 genotypes including 8 cultivars and 6 wild barleys were analyzed in comparison with reference genotype Morex. For each genotype tested, the analysis revealed chromosomal regions of copy number increase, copy number decrease or sequence absence, and genomic regions that completely lack CNV relative to the reference genotype Morex (See example Fig. 1).

The study detected high levels of CNVs in the barley genome, with almost 15% of the sequences surveyed by the array showing CNV in at least one genotype. Variants were more frequent in regions of high recombination, such as near the ends of the chromosomes. Chromosome 4H was an exception, showing a different distribution pattern and containing significantly lower levels of CNV. The reduced recombination rate on chromosome 4H and on centromeric and peri-centromeric regions of all barley chromosomes were likely the cause of the reduced frequency of variants that we found in these genomic regions. Cultivated barleys had reduced levels of CNV diversity compared to the wild accessions, indicating that the loss of genetic diversity was a consequence of barley domestication and breeding.

CNV has the potential to contribute to phenotypic variation in barley, as 9.5% of the coding sequences represented on the array contained CNVs. Those variants were enriched for disease-resistance and stress response genes. This study constitutes the largest CNV analysis in a *Triticeae* species and provides a resource for identifying CNV affecting genes of agronomic importance.

Link to Genome Biology: <http://genomebiology.com/2013/14/6/R58>.

## Chromosome 7H



The x axis indicates the physical position on the 7H chromosome. The y axis indicates the variety bowman and the reference morex. Note that for most 7H sequences Bowman has as reduced copy number as compared to morex. Also note more variation occurs distally.



Triticeae CAP  
Coordinated Agricultural Project

# Education News

## INSIDE EDUCATION

TCAP Students at PAG	
TCAP Meeting agenda	7
MSI Summer travels	8
NAPB	9
Undergrad meeting schedule	10
R course	11
Webinar schedule	11
Borlaage information	12

## TCAP Students to attend PAG

TCAP meeting at PAG provides important opportunities that support the development of TCAP students.

### Schedule of events

#### Friday Jan 10<sup>th</sup> 1-5 (Handlery Hotel)

*I have my degree, now what?*

Students are invited to meet with plant breeders working in private and public sectors. Through small group discussions, find out what they are looking for in an employee. Are you on target to get the job you want? Before attending, get a better idea of what industry wants by reading the paper at this link: <https://www.agronomy.org/publications/nse/articles/40/1/82>

#### Saturday

Attend PAG scientific meeting.

#### Sunday

8-5 TCAP annual meeting

5-7 TCAP poster session

All graduate students are asked to present a poster. The poster session gives an important overview of all the research being accomplished by TCAP, and provides an opportunity for continued networking. This year Turkish plant breeders collaborating with the USDA have been invited to present posters as well. Posters size should be vertical and 2 feet 10 inches wide by 3 feet 10 inches high. (1.17 meters x 1.17 meters).

Students register for events by filling in the survey at <https://www.surveymonkey.com/s/PAG2014>



HANDLERY HOTEL  
SAN DIEGO

# Triticeae CAP Annual Meeting Agenda

January 12, 2014

Town and Country Convention Center (Windsor Room)



**8:00 – 9:15 am**

## Reporting session for stakeholders

8:00 – 8:45 am

Topics to discuss:

- Brief update on project
- Graduate student pipeline
- University – Industry partnerships
- TCAP – International collaborations
- Jorge Dubcovsky, Gary Muehlbauer, Jamie Sherman

8:45 – 9:15 am

Discussion with Stakeholders

9:15 – 9:30 am

Break

**9:30 am – 3:00 pm**

## Reporting session for Scientific Advisory Board and USDA

9:30 – 10:00

- Overview of project
- Jorge Dubcovsky (UC, Davis)
- Gary Muehlbauer (University of Minnesota)

10:00 am – 11:00

- Education
- Jamie Sherman (Montana State University)

11:00 am – 11:20 am

- Developments in T3
- Jean-Luc Jannink (USDA-ARS, Ithaca, NY)

11:20 am – 11:50 am

Student elevator speeches (15)

11:50 – 1:10 pm

Lunch on your own

1:10-1:30 pm

- Genotyping**
- Gina Brown-Guedira (USDA-ARS, Raleigh, NC)
- Eduard Akhunov (Kansas State University)

1:30 – 1:50pm

- Wheat **phenotyping**
- Clay Sneller (The Ohio State University)
- Luther Talbert (Montana State University)

1:50 – 2:10 pm

- Barley **phenotyping**
- Kevin Smith (University of Minnesota)
- Pat Hayes (North Dakota State University)

2:10 pm – 2:30 pm

- Disease **phenotyping**
- Barley - Brian Steffenson (University of Minnesota)
- Wheat – Mike Pumphrey (Washington State University)

2:30 pm – 3:00 pm

Student elevator speeches (15)

3:00 pm – 3:30 pm

Break

3:30 pm – 4:30 pm

- Breakout groups
- T3, **Genotyping**, Barley, Wheat

4:30 pm – 5:00 pm

Feedback from Scientific Advisory Board and Discussion

5:00 pm – 7:00 pm

Reception and poster session (Hampton Room)

# MSI Summer Travels



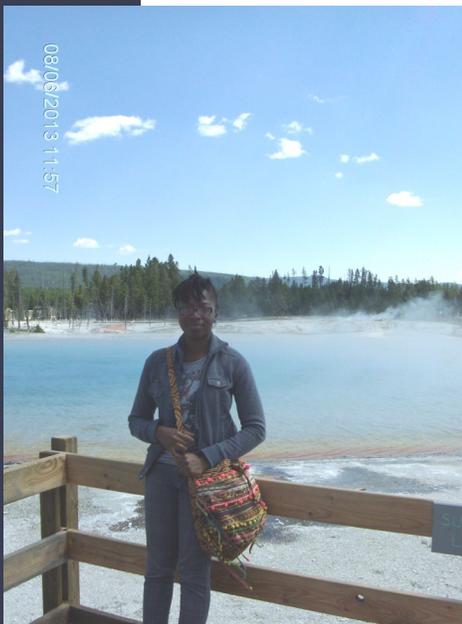
From June 10 – August 3, Margie Stringfield (Fayetteville State University, NC), Andra Bates (University of Arkansas, Pine Bluff) and Arianh Smith (UAPB) worked on projects in wheat and barley breeding and genetics in the labs of Peter Morrell and Gary Muehlbauer (Stringfield), Brian Steffenson (Bates) and Jim Anderson (Smith).

## Ruth Osborne visits Montana

Ruth Osborne a graduate student of Chris Botanga from Chicago State University is collaborating with Jamie Sherman and Luther Talbert from Montana State University. She is completing an anatomical study of solid stem development using scanning electron microscope. She is also working to identify important genes related to stem development. In August Ruth visited Montana and wrote the following about her experience



Ruth presenting at Bozeman field days.



Ruth in front of a thermal formation at Yellowstone park

“I have gained invaluable experience in wheat research by taking a trip to Bozeman, Montana. Prior to the trip, I was only familiar with researching wheat on a small-scale and within the confines of a greenhouse. While in Montana, I was exposed to the large-scale experimentations being done with wheat within the field. I also had the opportunity to discuss my research with different professors at Montana State University. The insight that I gained from these professors and from the trip as a whole helped to improve my project and motivated me to continue my research”.

# National Association of Plant Breeders



Vic Blake Presenting T3

The National Association of Plant Breeders (NAPB) and the Plant Breeding Coordinating Committee (PBCC) held their joint 2013 Meeting June 2-5 in Tampa, Florida. Titled "*Positioning Plant Breeding for the Future*", the meeting focused attention on how plant



Duke Pauli presenting his award winning poster

breeders, institutions, agencies and companies can optimize the future by recognizing breeding-relevant challenges, opportunities and trends. **Genomics**, high-throughput **phenotyping**, global positioning systems, biotechnologies, other "-omics", and "big data" are among the high-impact opportunities for enhancing plant breeding. Challenges include the need to regain resources and programs to sustain public plant breeding, breeding research and plant breeding education, so that we can provision our nation adequately and sustainably. A major need is to increase societal understanding and thus appreciation for the contributions of plant breeding and agriculture to food security and environmental sustainability on national and international scales.



Rebecca Nitcher invited to give oral presentation

Members of the Triticeae CAP participated in a variety of ways. TCAP supported student attendance and TCAP students Sarah Grogan (CSU—Pat Byrne) and Duke Pauli (MSU Tom Blake) presented posters. Rebecca Nitcher (UC - Davis - Jorge Dubcovsky), gave an invited talk, while Vic Blake was invited to talk about T3. Dr. Patrick Byrne of Colorado State University assumed a new leadership role as Chair of PBCC as did PBCC Vice-Chair Dr. Jamie Sherman of Montana State University.



Sarah Grogan introducing her poster

A workshop addressing Life Skills for professional plant breeders was sponsored by TCAP and led by Kim Kidwell and Jamie Sherman. The **2014** annual meeting will be held in Minneapolis, August 5-8.



Sarah Grogan presenting an elevator talk

## Barley News Blog

Articles regarding barley are posted <http://blogs.extension.org/barleynews/> here to keep growers up-to-date on the latest issues.

Barley in the news

Latest news for barley growers



## TCAP Undergrad Online Meeting Schedule Fall 2013

This series of online conversations will give undergrad students an understanding of the Triticeae Coordinated Agriculture Project (TCAP) and help them see how they are connected to a broad community of scientists. Students will be introduced to elements of plant breeding research and become familiar with methods and tools. Students will share experiences and thoughts on getting the most from their internships and learn about internships with plant breeding companies. Using a series of case studies, we'll take a "behind the scenes" look at TCAP research on key traits in wheat and barley. We'll discuss tips on communicating in science and practice writing an abstract for a scientific conference. Students will learn about preparing for, and applying to, graduate school and how to succeed as a graduate student.

Conversations take place on the undergraduate community website (<http://passel.unl.edu/communities/tcapundergrads>)

Please encourage your student(s) to participate. Each lab should purchase at least one headset (about \$20) and make it available to their intern so that they are able to participate in conversations. Materials related to discussions will be posted on the undergraduate community website (go to <http://passel.unl.edu/communities/tcapundergrads> and click on "Courses." You must register for access). For questions, contact Mary Brakke (brakk001@umn.edu).

Date and Time (CENTRAL TIME)	Topic	Discussion Lead
Sept 9, 2 – 3:00	What's a "TCAP"?	Gary Muehlbauer, University of Minnesota (UM)
Sept 16, 2 – 3:00	Getting the most from internships	Mary Brakke, UM
Sept 23, 2 – 3:00 (tentative)	Beyond TCAP: Internships in industry	Tabare Abadie, Dupont Pioneer
Sept 26, 3 – 4:00	An overview of plant breeding research methods	Jamie Sherman, Montana State University
3 Oct, 2 – 3:00	A research case study: <b>NUE</b> in barley	Celeste Falcon, UM
Oct 7, 2 – 3:00	A research case study: <b>WUE</b> in wheat	Sarah Grogan, University of Nebraska
Oct 10, 3 – 4:00	A research case study: Low temperature tolerance in barley	Margaret Krause, UM
Oct 28, 3 – 4:00	A research case study: Rust resistance in wheat	Austin Case, UM
Nov 14, 3 – 4:00	Talking science – Presentations	Mary Brakke, UM
Nov 18, 2 – 3:00	Writing science – Abstracts and posters	Mary Brakke, UM
Nov 26, 3 – 4:00	Getting ready for grad school	Brian Steffenson, UM
Dec 3, 3 – 4:00	Succeeding in grad school	Tyson Howell, University of California, Davis



Ashu Guru, a professor of the Raikes school at UNL, is creating a cross disciplinary course for plant breeding and computer science students. The cross disciplinary and collaborative nature is highly supported by industry. To begin Dr. Guru is working closely with TCAP students, to determine what common analysis we are doing in R. He is then creating learning modules for his computer science student using these real life examples. TCAP students participating thus far are from CSU, KSU, WSU, MSU and UNL.

**Objectives of R collaborative course**

- 1) Bring real world data (especially large datasets) from research into classroom to be used during the instruction of various modeling and statistical analysis techniques.
- 2) Increase use and fluency in using modeling techniques and statistical environments such as R among Raikes students and Plant Breeding graduate students.
- 3) Creating a collaboration roadmap between Raikes students and Plant Breeding students so both groups enhance their communication and collaboration skills while working in cross-functional teams.

Free webinars  
Wednesdays  
at 3 pm CST



## FALL 2013 WEBINAR SERIES

### ALL SYSTEMS GO: Integrating resources, tools, and technologies for plant breeding and genetics

September 25th	<b>Dr. Shuyu Liu</b> Texas A&M	<i>Detection of epistasis and QTL by environment interaction using QTLNetwork</i>
October 23rd	<b>Dr. Rex Bernardo</b> University of Minnesota	<i>Strategies for the routine use of genomewide selection in an inbred development program</i>
November 6th	<b>Dr. Craig Morris</b> USDA-WWQL: Pullman, WA	<i>Wheat grain composition: what it is, how we measure it and why</i>
November 20th	<b>Dr. Michael Gore</b> Cornell University	<i>Connecting genotype to phenotype: Progress with a next-generation platform in maize and cotton</i>
December 4th	<b>Student Presentations</b>	<i>Two 20 minute presentations by TCAP graduate students</i>

**We are seeking TCAP graduate students to give 15-minute presentations during the fall webinar series. Please email Sarah at [sarah.grogan@colostate.edu](mailto:sarah.grogan@colostate.edu) for more information!**

## TCAP students are invited to apply for travel funds for 2013/2014.

TCAP education will support student travel that broadens student experience by exposing students to plant breeding institutions outside the US or outside of academia. TCAP education will ensure support is distributed as evenly as possible across programs, favoring students closer to graduation. There will be other opportunities for travel support in 2015.

Applications are due by Oct 30<sup>th</sup> 5:00pm CST, submit via <https://www.surveymonkey.com/s/CIMMYT2014>  
Applications will include TCAP student and PI name, TCAP student's expected graduation date, description of the travel and expected benefits, Support requested and indicate if you have other sources of support.

One opportunity that we encourage TCAP students to attend is a visit to CIMMYT, which will include a tour of breeding and research projects and attendance at the Borlaug Global Rust Initiative meeting.

### CIMMYT Trip Tentative Schedule

March 20, 2014 Arrive at Obregon

March 21, 2014 Tour CIMMYT research projects at Obregon

March 22- 24<sup>th</sup> Attend BGRI meeting

Students may also stay for the Borlaug Celebration and the Summit on World Food Security March 25-28.

### Costs:

Air travel to Obregon from most major airports = \$1000

Registration for BGRI \$200

Hotel about 70US\$ per night \$250-\$350

Food (Breakfast covered by hotel) 20US\$per diem= 100



## 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  
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 CO<sub>2</sub> for photosynthesis and acquire it through window-like structures in leaves simultaneously releasing O<sub>2</sub> and H<sub>2</sub>O. 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 H<sub>2</sub>O 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**.
  - **Exon Capture** - Selectively sequences the gene coding portions of the genome to identify polymorphisms greatly reducing the amount of sequencing and targeting more significant regions
  - 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.