



**Triticeae CAP**  
Coordinated Agricultural Project

# TCap Transmission

May 2013

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United States Department of Agriculture  
National Institute of Food and Agriculture

## INSIDE RESEARCH:

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### Directors notes: Gary Muehlbauer and Jorge Dubcovsky



In this issue of the TCAP newsletter you will find successful examples of TCAP research, collaboration with Minority Serving Institutions (MSIs), and graduate student training. Eduard Akhunov (Kansas State University) and colleagues published a paper in the Proceedings of the National Academy of Sciences in which they genotyped over 3,000 wheat accessions with approximately 9,000 SNPs. They used the data to identify regions of the genome that are under human selection and regions of the genome that contribute to differentiation between varieties grown in different regions of the world. These results will be important for future wheat improvement. Scott Haley (Colorado State University) described the success of the Hard White Winter (HWW) Wheat variety Snowmass and his effort to continue to develop novel HWW germplasm and varieties for Colorado and surrounding regions. Also highlighted in the newsletter are collaborations with TCAP faculty and faculty and students at MSIs. Two of Professor Martin Matute's students (Delois Moss and Paige Walker) at the University of Arkansas-Pine Bluff have been involved in examining the community structure of nematodes in Washington State wheat fields. This research resulted in an initial understanding of the nematode community structure (nematodes that are beneficial and those that are deleterious to wheat) in wheat fields and signifies the additional research that is needed to determine the appropriate management strategies for optimal nematode communities. This summer five and two undergraduate students from MSIs will work as interns at the University of Minnesota and Washington State University, respectively. The research projects that two TCAP graduate students (Katherine Frells, University of Nebraska and Sruthi Narayanan, Kansas State University) are conducting are also highlighted. Katherine described her work focused on examining the genetic control of nitrogen use efficiency program while Sruthi described her work to dissect the genetic control of root architecture. Understanding the genetic control of nitrogen use efficiency and root architecture are key to the success of developing wheat for changing climates. Finally, a big congratulations to Jorge Dubcovsky for his election to the National Academy of Sciences, well deserved!

Definitions to all red words can be found in "TCAP Terminology" on page 12

## Congratulation Jorge Dubcovsky!

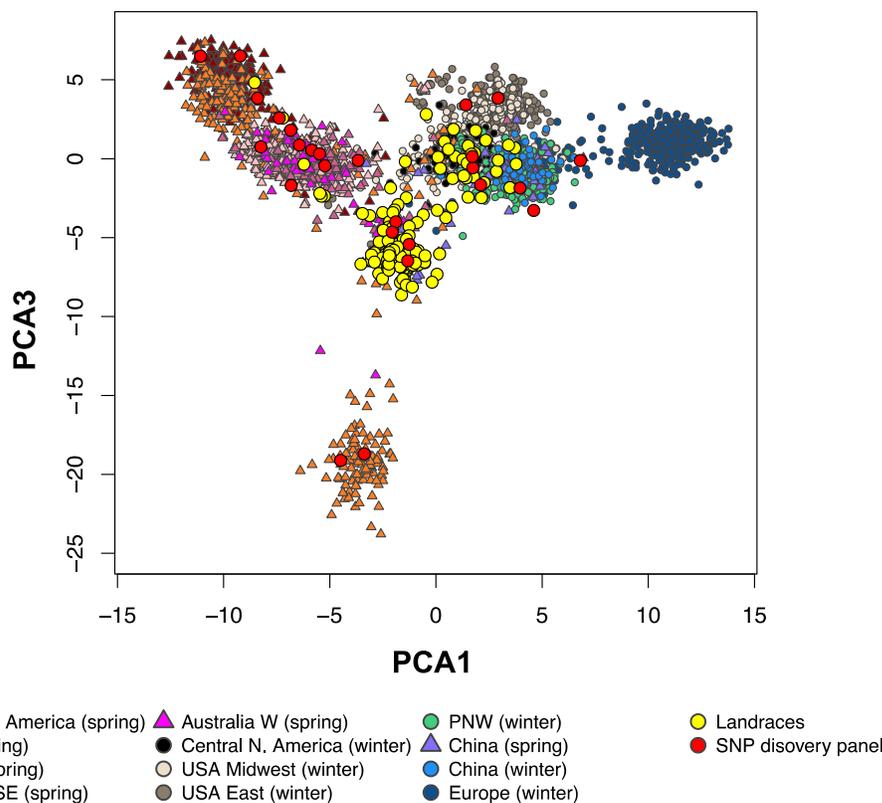


At the 150<sup>th</sup> annual meeting of the National Academy of Sciences, TCAP project director Jorge Dubcovsky was elected as a member of the National Academy of Sciences in the section of Plant, Soil, and Microbial Sciences in recognition for his significant contributions to wheat genetics and wheat improvement.

# National Academy of Science Study By: Eduard Akhunov

In the study published in the Proceedings of the National Academy of Sciences, Eduard Akhunov and the Triticeae CAP team in collaboration with an international consortium including wheat geneticists from Australia, UK, Germany, France, India, and Mexico investigated the impact of human-mediated improvement on the wheat genome. This was the largest diversity analysis project so far performed in wheat that includes nearly 3,000 wheat varieties collected across the world. In this study we have investigated the genomic impact of breeding aimed at creating new varieties adapted to grow in diverse agro-climatic conditions across the world.

For this purpose we have developed the wheat 9,000 SNP iSelect genotyping assay and genotyped a worldwide collection of landraces and modern wheat varieties. The analysis of genetic variation revealed strong genetic differentiation among wheat lines originating from different geographic areas (Fig. 1).



The comparison of genetic variation between landraces and modern varieties helped us to detect the variants of genes that were selected by breeders to make wheat cultivars adapted to grow in diverse environments, from Argentina to Norway and Russia. Selective sweeps were found around genes involved in the regulation of flowering time and phenology. An introgression of a wild relative-derived gene conferring resistance to a fungal pathogen was detected by haplotype-based analysis. The majority of the selected alleles were present at low frequency in local populations suggesting either weak selection pressure or temporal variation in the targets of directional selection during breeding probably associated with changing agricultural practices or environmental conditions.

Our study provides the first insights into the role of humans in

shaping the genetic diversity of wheat. By understanding better the changes made to the wheat genome we can develop better approaches to improve this staple crop. The developed SNP chip and map of genetic variation provide a resource for advancing wheat breeding and supporting future population genomic and genome-wide association studies in wheat.

Link to PNAS: <http://www.pnas.org/content/110/20/8057.abstract>

## New Gene Study Published

A study published online last week in Crop Science, by V. Williamson and TCAP project director Dr. J Dubcovsky describes a new gene that produces resistant to root-knot nematodes in wheat. Although root-knot nematodes do not cause much damage to wheat, they are very detrimental to other high-value crops including tomatoes, carrots and cucurbitaceous species. The nematode resistant wheat can be used in rotations as a trap crop to “trick” the nematodes into starting their life cycle but then prevent them from reproducing. This reduces the population of nematodes in the soil, benefiting the next crop. Three varieties developed by the TCAP project (Lassik, Patwin and Patwin 515) carry the resistance gene and are commercially available to growers. A press release of this article can be found at <https://www.crops.org/news-media/releases/2013/0514/586/> and the Open Source Crop Science article is available at <https://www.crops.org/publications/cs/articles/0/0/cropsci2012.12.0681>.



# Snowmass Hard White Winter Wheat

By: Scott Haley

While hard white wheat (HWW) has been under development since the 1970s, very little acreage is currently planted to HWW in the Great Plains. Over the last 20 years, the promise of HWW led many to believe that it could replace a significant portion of the acreage in the hard red winter (HRW) region. Unfortunately, as breeding programs developed improved HWW varieties that were competitive with the best HRW varieties, various production and marketing problems hindered adoption by farmers. The most important of these were the appearance of stripe rust as an endemic problem in 2001 and wet conditions at harvest particularly in 2003 that favor sprouting in the head (pre-harvest sprouting, PHS). Both of these problems can be addressed through breeding and in fact Kansas State University released the HWW variety 'Danby' in 2005 that was a big step forward for both stripe rust resistance and sprouting tolerance.

A primary driver for HWW development has been the promise of enhanced export market opportunities for wheat producers. Over the last 10 years, however, domestic demand for HWW has increased dramatically, fueled largely by increased interest in whole grain products. Whole wheat flour from white grain makes a product similar in color to white flour, but retaining health benefits of whole wheat. In order to capture value of HWW in whole grain applications, some companies have chosen to manage HWW production and marketing on a contract basis with the intention of more successfully managing supply and quality. For such a program to be successful for HWW, the intrinsic quality of the HWW varieties is of paramount importance.

In fall 2009, Colorado State University (CSU) released the HWW variety 'Snowmass'. Snowmass, which takes its name from one of Colorado's 53 mountains above 14,000 ft. elevation, carries a unique combination of **genes** that give it very strong dough mixing properties and increased water absorption in the baking process. Snowmass is marketed by the Colorado Wheat Research Foundation (CWRF) in a unique partnership with ConAgra Mills called the "CWRF ConAgra Mills Ultragrain® Premium Program". Under this program, producers contract their production of Snowmass and in return are paid a 30-90 cent per bushel premium, depending on protein concentration of the grain. ConAgra Mills uses Snowmass and other select HWW varieties in whole-grain flours known as "Ultragrain" (<http://ultragrain.com>). Additionally, a novel whole-grain

flour product made solely from Snowmass by ConAgra Mills is marketed under the name "Ultragrain High Performance™ (HP)". In

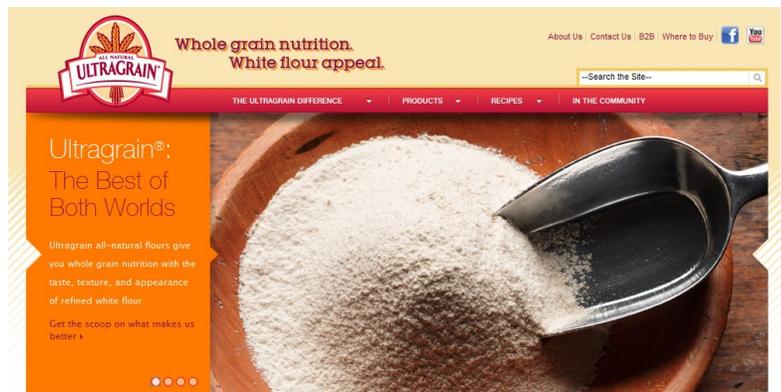
2013, approximately 5% of Colorado's 2.2 million wheat acres are planted to Snowmass, making it the fourth most widely grown variety in Colorado.

At the time it was released in 2009, Snowmass carried very good stripe rust resistance, although new stripe rust races virulent to Snowmass and several other varieties were identified in the central and southern Great Plains in 2012. Pre-harvest sprouting tolerance of Snowmass is equivalent to adapted hard red winter wheat (HRW) varieties in the High Plains region, an area which is generally less prone to wet conditions at harvest that favor sprouting. In addition to its agronomic and quality characteristics, Snowmass carries a unique **gene** (Wsm2) for near-immunity to Wheat streak mosaic virus (WSMV). Through collaboration with CSU led by Texas A&M AgriLife Researchers, excellent **markers** associated with Wsm2 have been identified. These **markers** are in routine use in **marker-assisted selection** to develop improved Snowmass replacements, along with **markers** for herbicide tolerance, disease and insect resistance, and various quality-related characteristics.

Additional technologies being implemented at CSU to develop the next generation of Snowmass varieties include doubled haploid breeding methods, **genomic selection**, and novel trait development via TILLING. The breeding program at CSU is optimistic that these technologies will foster more rapid development of HWW varieties with enhanced productivity and positive consumer traits.



Scott Haley with two PhD students in Yuma AZ



# What's new in The Triticeae Toolbox (T3)

Below is the data newly uploaded to T3

## Wheat

Population	Location	Traits
Hard Winter Wheat Association Mapping Panel	Greeley, CO	WUE, NUE, agronomic,
Hard Winter Wheat Association Mapping Panel	Tipton, OK	Agronomic, minerals
Nebraska Duplicate Nursery (non TCAP)	10 Nebraska sites	Agronomic

## Barley

Population	Location	Traits
T-CAP Facultative Winter 6row	Logan, UT	WUE, NUE, agronomic, winter hardiness
U.Minn. Cycle 1,2,3 LTT selection	n/a	VeraCode 384 Genotypes
Morex x Barley	n/a	GBS
Oregon Wolfe Barley	n/a	GBS

# Interns Head to UMN and WSU

The TCAP is working to increase the diversity of plant scientists and plant breeders by funding collaborative research with minority serving institutions and sponsoring summer research internships for minority students.

This summer five students will travel to TCAP institutions to participate in TCAP-related research. The University of Minnesota will host three students from 10 June through 2 August. Andra Smith from University of Arkansas, Pine Bluff will be working in Brian Steffenson's lab. Arianh Smith, also from UAPB will work with graduate students Kathryn Turner and Prabin Bajgain in Jim Anderson's lab. Margie Stringfield from Fayetteville State University, North Carolina will work in Peter Morrell's and Gary Muehlbauer's labs. Washington State University will host two students from University of Arkansas, Pine Bluff. This is the second year that Arron Carter has provided internships for students from UAPB. Students traveling to UMN and WSU this summer have been working on TCAP collaborative research projects at their home institutions during the past year.

TCAP summer research internships provide students from diverse backgrounds with knowledge of wheat and barley breeding and opportunities to broaden their skills as plant researchers. The internship program aims to enhance student interest in, and preparation for, graduate studies in plant sciences.



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# Education News

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## TCAP Education

A goal of TCAP education is to improve the recruitment and education of plant breeders. An important step in the process is thorough evaluation. TCAP evaluators Eric Moore, Francis Lawrenz, Mao Thao and Abdi-Rizak Mohamed recently completed an extensive evaluation report of the TCAP educational activities. The report summarizes surveys and interviews of TCAP participants completed during 2012 and also compares with data gathered in 2011. Please see the complete report at <http://www.triticeaecap.org/> for analysis and recommendations.

Through the evaluation process TCAP education continues to adapt programming to best meet the needs of participants, such as providing a seminar series and having the graduate students more directly involved in planning and delivering educational sessions. In 2013, TCAP education will enlarge upon the effectiveness of minority serving institution (MSI) collaborations in attracting more diverse students by providing additional funds for research and travel support. Through these funds, we will encourage more face to face interactions between people from MSIs and TCAP institutions. We have also created a travel fund for both undergraduate and graduate students to attend meetings and will prioritize students active in all facets of the TCAP to incentivize participation. ( Look for upcoming announcements on the application process.) TCAP educational offerings have impacted students beyond those funded by the program. In celebration of the extension “beyond TCAP” evaluators are tracking participation and determining a TCAP dosage which will provide important information about the broader impacts of TCAP.



## Visiting UAPB

By: Martin Matute University of Arkansas Pine Bluff (UAPB)

Dr. Carter visited University of Arkansas, Pine Bluff from April 2-4, 2013. He first met with UAPB administrators, including the Biology Chair, the Dean of Arts and Sciences, and the Vice Chancellor for Academic Affairs. They were all very impressed at the way in which he explained and sold the TCAP Project and the need for UAPB to consider it a participative partnership. The Vice Chancellor was so impressed that she requested Arron be interviewed by the UAPB TV as a good example of partnership (see link <https://www.youtube.com/watch?v=a-5Pv2g1sbU&list=UUT1VAXhvr9S9-UsqhH6WYQ&index=4>).



Dr. Carter also gave a great presentation. Arron also visited with Dr. Onyilagha and his students in their lab. He was hosted in our Nematology lab where the students demonstrated how we extract and identify nematodes. We also discussed some modifications/difficulties of our collaborative research. Arron visited our University Museum and was also a guest at our senior students seminar presentations.

## Biochemistry of Water Stressed Wheat

By: Michelle Poe, Joseph Onyilagha, and Luther Talbert

Wheat (*Triticum aestivum*) is one of the most important cereal crops in the world. However, drought is a serious factor facing wheat farmers worldwide and causing substantial yield loss. Therefore, the aim of this study is to identify particular compounds produced during times of water stress that enable the plant to cope. The vacuolar compounds in the stems, leaves, and flower spikes of water-stressed and unstressed McNeal and Thatcher varieties were analyzed using HPLC and compared for differences and/or similarities. The stems, leaves, and flower spikes of both varieties showed mainly phenolic compounds including phenyl propanoids and flavonoids. Of the phenyl propanoids, chlorogenic acid was prevalent, and, of the flavonoids, luteolin glycosides were dominant. Apigenin was also present in the flavonoids. However, further analyses indicated that the concentrations of luteolin and apigenin were frequently higher in the water stressed varieties compared to the unstressed varieties. In contrast, chlorogenic acid concentrations were frequently higher in the unstressed varieties. This fluctuation in concentration of luteolin, apigenin, and chlorogenic acid could be a coping mechanism used by the plant to deal with water stress.

Michelle Poe presented this research at the 97th annual meeting of the Arkansas Academy of Science in Little Rock, AR April 5-6 hosted by Arkansas Tech.



## Pine Bluff students research nematode community structure



Bacterivorous nematode

Martin Matute, nematologist from the University of Arkansas Pine Bluff mentors undergraduate students as a TCAP collaborator. Two of Martin Matute's students, Delois Moss and Paige Walker, presented their research on Nematodes to the undergraduate community in March. Both surveyed soil samples from wheat plots in association with Washington State University. The goal of the collaboration between WSU and UAPB is to understand both potential positive and negative impacts of nematodes on crop production.

Bacterial feeding nematodes (Ba) are known to release nitrogen in the soil in excess of their metabolic demands.

Ms. Moss investigated the numbers and types of bacterial feeding nematodes at pre planting, mid season, and post harvest. She documented two colonizer-persister(cp) classes Ba<sub>1</sub> and Ba<sub>2</sub>. Nematodes of the Ba<sub>1</sub> populations were dominated by the genus *Panagrolaimus* and the Ba<sub>2</sub> populations were dominated by the genus *Acrobeloides*. Both populations had higher numbers at mid season with 172.6 to 321.6 individuals/100 ml of soil, resulting in a biomass of 2,055bu to 4,559bu of bacterial feeding nematodes. Ms. Moss' findings indicate mid season to be the optimal sampling time for the bacterivorous nematodes and emphasizes the important effect nematodes may have on nitrogen availability.

While nematodes can have a positive impact on crops, certain nematode species are crop parasites. In her presentation, Paige Walker, explained how sampling time impacted the nematodes recovered. She too surveyed samples of soil from WSU wheat fields pre planting, mid season, and post harvest, finding two main populations of parasitic nematodes, one dominated by *Tylenchus costatus* (PI<sub>2</sub> nematodes) and the other dominated by *Pratylenchus* (PI<sub>3</sub> nematodes). The PI<sub>2</sub> nematode populations climaxed in numbers in mid season while the PI<sub>3</sub> nematode populations climaxed at post harvest, suggesting peak population times for plant-parasitic nematodes is dependent on the cp class. Up to 276.5/100ml parasitic nematodes were recovered. Such high population numbers were attributed partly to the relatively high numbers at planting.

Ideally, nematode research by UAPB students could help identify ways to maximize nematodes that benefit crop production while minimizing crop parasites, but a more realistic goal maybe to understand nematode population dynamics in order to maintain a balanced population that could benefit crop production.



Plant-parasitic nematode



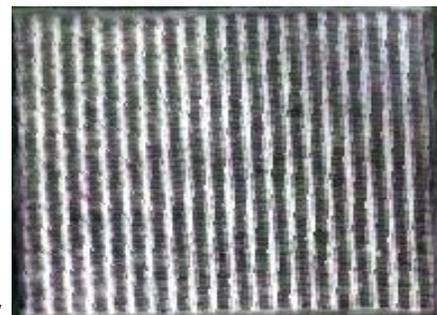
# Student Success

By: Katherine Frells

I joined Dr. P. Stephen Baenziger's University of Nebraska wheat breeding program in July 2011 after graduating with a BS degree in Agronomy from Iowa State University. I am currently in my second year of a PhD program in Agronomy, Plant Breeding and Genetics. My project involves improving high-throughput phenotyping methods such as **canopy spectral reflectance** (CSR) for use in selecting **nitrogen use efficient (NUE)**.

During the 2012 growing season I worked with University of Nebraska's Center for Advanced Land Management Information Technologies' (CALMIT) to use their two spectrometer ground based system to measure **CSR**. The two spectrometer system measures both upwelling and downwelling light simultaneously making the system usable in less than ideal conditions. The system is remotely controlled by a laptop computer, and data is automatically transferred and saved on the laptop after each scan. Measurements were made in 660 plots (one replication) of the Hard Winter Wheat **Association Mapping** Panel of which 330 plots were in a low nitrogen treatment and the rest in a moderate nitrogen treatment. We successfully gathered **CSR** data from May 1 to June 6<sup>th</sup>, 2012 and have calculated a number of vegetation indices. We are currently determining the proper indices and the most appropriate implementation of those indices in selection of NUE. Ultimately, the indices will be used to select for genes associated with **NUE** in the hard winter wheat **association mapping** panel (HWWAMP).

In another collaboration with CALMIT, the same HWWAMP trial was measured for **CSR** by flyover with CALMIT's AISA Eagle Imaging System. The AISA system uses a similar two spectrometer system, but is able to capture **CSR** over a large area in a short time span. **CSR** data from the AISA system is output into images that include measurements from visible to near infrared wavelengths. During the past semester, my colleague Mary Guttieri and I have been developing methods to extract data from the AISA images and calculate vegetation indices for use in **association mapping** and prediction of plant physiological characteristics. We have found moderate correlations with the ground based data and are excited to improve both the airborne data collection and data extraction methods. The future looks bright for high throughput phenotyping for **NUE**!



Hyperspectral aerial image of HWWAMP trial grown in Ithaca, NE produced by CALMIT AISA Eagle Imaging

## **PLANT BREEDING FOR DROUGHT TOLERANCE Online course - Fall 2013**

Colorado State University will offer a one-credit, graduate-level online course in Plant Breeding for Drought Tolerance from August 26 to December 13, 2013. This distance course is targeted to graduate students in the plant sciences, as well as to professionals in the public and private sectors interested in increasing their knowledge in this area. The primary instructor is Dr. Patrick Byrne, Department of Soil and Crop Sciences, with TCAP grad student Sarah Grogan as Teaching Assistant.

**The tuition and course fee will be waived for up to four TCAP graduate students.**

Additional information on the course content, format, and cost is available at <http://droughtadaptation.org/>. For questions, please contact the Program Assistant, Kierra Jewell ([Kierra.Jewell@ColoState.edu](mailto:Kierra.Jewell@ColoState.edu)). Applications will be accepted through August 1, 2013 or until the class is full (20 students).

# Student Success Story

## - Sruthi Narayanan

I started my PhD program under Dr. P.V. Vara Prasad at Kansas State University in Fall 2011. I decided to work with him for my PhD program because I wanted to work on stress physiology and he is an expert in this field. My PhD dissertation is on heat stress in wheat, but I was also interested in doing some additional research projects that would be highly relevant to stress tolerance and crop improvement. Dr. Prasad encouraged this and gave me some ideas for a project on characterizing wheat **germplasm** collections for root traits. So I went underground, so to speak. The more I read on this topic, the more interested I became. The productivity of wheat under dry land conditions is often limited by drought stress, and root traits are an important factor in the plant's ability to tolerate drought conditions. Root traits are critical for the plants in soil exploration, nutrient and water uptake, lodging resistance, and tolerance to mineral toxicity. In short, extensive root growth is vital for increased shoot growth and yield when wheat is grown under marginal environments with insufficient supply of water or nutrients. Most wheat improvement programs have concentrated on the above-ground components, such as plant height and harvest index, rather than root traits.

While I was searching the literature for research on root traits, I realized that very few studies have explored drought-adaptive root traits in wheat. This is not too surprising. The quantification of root system structure and development is highly challenging, in part because separating roots from soil without breakage or loss is extremely difficult. Furthermore, the complexity of root traits, effect of soil environments on these traits, and lack of rapid and cost-effective screening methods have limited the progress of research on roots. All of this only increased my interest in evaluating the genetic variability in wheat for root traits, knowing improving roots could increase wheat productivity under drought conditions. Therefore I conducted a study to quantify the genetic variability of root traits in Triticeae CAP **Association Mapping** Panel of 256 spring wheat genotypes.

We observed significant genetic variability for root and growth traits. The range for major root traits was 67 - 165 cm (rooting depth), 1700 - 5816 cm (total root length), and 0.12 - 3.55 g (root weight). Genotypes IDO686, Treasure, IDO377s, SD4243, and UC1602 ranked high for rooting depth, total root length, surface area and volume. Among the root traits, rooting depth had the maximum heritability (0.52). Interestingly, plant height did not show correlation with any of the root traits.

The results from this study indicate that considerable genetic variability exists in Triticeae CAP wheat **Association Mapping** Panel for root traits. My hope is that this variability can be exploited to improve drought tolerance and/or resource capture in wheat. The contrasting genotypes identified in this study for root traits offer critical plant materials for breeding programs for drought tolerance in wheat. Another PhD student in our lab (Kyle Shroyer) is screening the same **germplasm** for yield under field conditions. Thus, our future research will evaluate the correlations between yield and root traits under irrigated and dry land conditions. We are also planning to utilize the contrasting genotypes to test for **water use efficiency** in a controlled environment and under field conditions. This exciting research maybe crucial for future crop improvement programs in times of climate change. I take this opportunity to thank Triticeae CAP for funding this research.



## Entering Mentoring Spring 2013

Another session of **Entering Mentoring** was offered in Spring of 2013 to support the full development of plant breeder human capital. As loss of public plant breeding programs continues, supporting excellent mentoring is critical to attract and train new plant breeders. **Entering Mentoring** supports new mentors as they develop a mentoring philosophy and mentoring skills. Graduate students practice mentoring and then reflect on that process through discussions online. When surveyed all mentors viewed the experience positively and would recommend to other graduate students. One student summed up the experience as follows: "This experience has taught me how to reflect, how to one goes about effectively mentoring, and how to build a successful mentor/mentee relationship." Students report that the group discussions facilitate their development as a mentor by helping to clarify individual experiences, as well as providing an opportunity to learn from the experiences of others. The students met weekly for eight weeks with Entering Mentoring facilitator Jamie Sherman. Congratulations to David Chappell, Ana Gonzales, Andres Salcedo and Lynn Veenstra for completing this program. **If you would like to improve your mentoring skills join us for another session of Entering Mentoring in Fall of 2013.** The sessions are tentatively scheduled to begin September 30<sup>th</sup> and to run for eight weeks.

Free webinars  
Wednesdays  
at 3 pm CST



SPRING 2013 WEBINAR SERIES  
AHEAD OF THE CURVE: Technologies for  
next-gen plant breeding

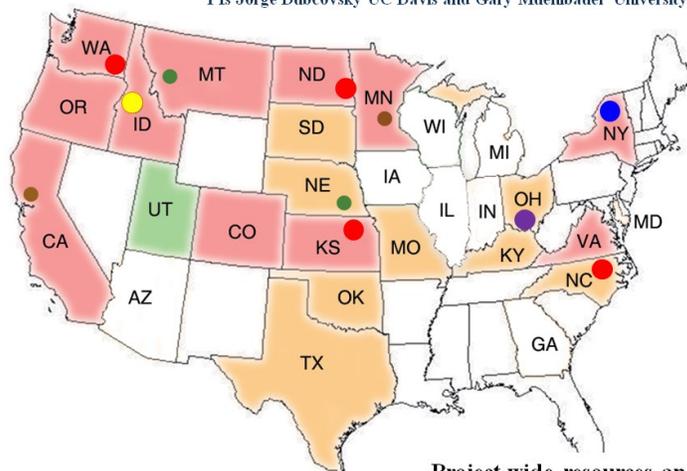
Graduate Students Jayfred Godroy and Sarah Grogan organized the TCAP spring webinar series that included a variety of topics. First Gina Brown-Guedira introduced **KASP**, a breeder friendly way to genotype **SNPs** for molecular breeding. Kevin Murphy discussed breeding quiona in Washington state. Paul Gepts

reported that bean genetic diversity was well maintained by farmers.

Sanford Eigenbrode introduced us to a USDA funded grant researching cropping systems for climate change, known as REACCH and invited TCAP collaboration. Jiaming Yu emphasized the importance of allelic frequency in breeding and genetic studies, citing examples from sorghum, corn and human genetics. Jesse Polland discussed field-based high-throughput phenotyping for plant breeding and genetics. Two additional seminars were presented to meet the request of TCAP PIs and students for support in experimental design by Araby Belcher, Alfonso Cuesta-Marcos, Celeste Falcon and Ken Kephart. Both presentations gave practical suggestions in design and analysis of different types of augmented experiments, even sharing necessary code. If you missed a seminar and would like to view it please visit <http://passel.unl.edu/communities/pbtn> and click on archived webinars. Students interested in planning Fall 2013 series should volunteer by e-mailing [jsherman@montana.edu](mailto:jsherman@montana.edu)

## **Triticeae -CAP: improving barley & wheat germplasm for changing environments**

PIs Jorge Dubcovsky UC Davis and Gary Muehlbauer University of Minnesota



The T-CAP includes:

- 56 funded participants
- 28 institutions
- 21 states.

Most have previous experience in the BarleyCAP and WheatCAP projects

- States with former BarleyCAP and WheatCAP programs
- States with WheatCAP programs
- States with BarleyCAP programs

### **Project-wide resources and activities**

- Genotyping labs, SNP development, KS also GBS
- National Small Grain Collection
- Database, web resources & tools
- Project direction
- Education coordination
- Industry liaison coordination

## **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 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**.
- 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.