Triticeae CAP
Coordinated Agricultural Project

TCap Transmission

October 2014

Funded by the USDA National Institute of Food and Agriculture

USDA
United States Department of Agriculture
National Institute of Food and Agriculture

INSIDE RESEARCH:

Kernel of Truth

Look for this symbol to get highlights of TCAP stories

Directors notes: Gary Muehlbauer and Jorge Dubcovsky

The TCAP is rapidly coming to the end of year four and is ready to tackle the research and education goals for year five. Graduate student projects are maturing with amazing impact via tool and germplasm development for wheat and barley improvement. Two terrific examples of graduate student projects are highlighted on pages 7 and 8. The Triticeae Toolbox team continues to increase the utility of T3 with new analysis and query tools, and BIG data are being added (see pages 4-6 for details). These tools and data will provide the platform for breeding and genetics programs for years to come. The TCAP education team has laid the foundation for the legacy of the TCAP: student education and training. The team has launched the highly successful fall webinar series, the schedule for the series can be found on page 2. The education team has also begun its undergraduate online meetings, which aims to enhance the undergraduate experience in both content-based learning as well as soft skills. Please encourage your undergraduate students to attend the online meetings. The education team is also facilitating research experiences for students from minority serving institutions (see page 12). Noteworthy, was the significant presence of TCAP graduate students at the recent National Association of Plant Breeders meeting in Minnesota (see page 9). Taken together, the TCAP has excelled at enhancing the ability of wheat and barley breeders to develop new varieties for changing environments and to provide cutting-edge student education. Make sure to mark your calendars for January 11, 2015 for the annual TCAP meeting in San Diego (see page 2-3 for details). One important activity for the meeting will be to begin to plan TCAPII, please bring your best ideas to share at the meeting. We look forward to seeing you in San Diego!

Definitions to all red words can be found in "TCAP Terminology" on page 14

TCAP annual meeting at PAG January 9th – 11th.

All TCAP undergraduate and graduate students are welcome to attend and present a poster.

Activities will begin with a graduate/undergraduate student meeting at The Handlery Hotel San Diego from 4 to 8 pm Jan 9th.
4:00 to 6:00 pm, select graduate students will present research seminars. Interested students submit abstract to DeAnna Crow as described below.
6:00 to 8:00 pm, students will be involved in a visioning process for the next grant.
Supper will be provided and potential employers will be invited to the talks.

HANDLERY HOTEL SAN DIEGO

On Jan 11th the regular TCAP meeting will begin at 8:00am at the Town and Country Convention Center (Windsor Room).
The focus of the meeting will be 1) reporting on grant progress and 2) visioning for the future.
Eight graduate students will be invited to share research seminars that are indicative of the research and education success of TCAP. **All** TCAP students will present elevator speeches and posters to share research results.

Stakeholders will share challenges a future grant could address. Students will be asked to share the results of their visioning process held on Friday with the whole group. Small groups discussions about future grant will occur.

To be considered as a speaker for either meeting Jan 9th or 11th, Graduate students must submit a 250 word abstract to DeAnna Crow by **October 15th** Students need to **RSVP** for the Friday student meeting and dinner, submit title for poster session and request travel support by e-mailing DeAnna Crow (deanna.crow@montana.edu) by **October 15th**.

Triticeae CAP Annual Meeting Agenda (Tentative)

January 11, 2015
Town and Country Convention Center (Windsor Room)

8:00 – 10:00 am	**Stakeholder session**
8:00 – 8:30 am	Overview of project Jorge Dubcovsky (UC, Davis) Gary Muehlbauer (University of Minnesota)
8:30 – 9:20 am	Panel discussion - stakeholders focused on challenges Mike Davis, AMBA Eric Jackson, General Mills Glen Weaver, Ardent Mills Gary Hanning, Anheuser Busch Marz Zutz, Minnesota barley Paul Kramer from Rahr Malting
9:20 – 9:40 am	Industry – University partnerships Ed Souza, Bayer/Crop Science
9:40 – 10:00 am	Open Discussion
10:00 – 10:30 am	Break
10:30 am – 5:00 pm	**Scientific reporting session**
10:30 – 11:30 am	Four student talks (15 minutes each) *Jorge and Gary will coordinate and identify speakers that represent all aspects of the project*
11:30 am – noon	Elevator speeches Graduate students
noon – 1:00 pm	Lunch on your own
1:00 pm – 2:00 pm	Four student talks (15 minutes each) *Jorge and Gary will coordinate and identify speakers that represent all aspects of the project*
2:00 – 2:30 pm	Elevator speeches Graduate students
2:30 – 3:00 pm	Future Robbie Waugh, James Hutton Institute, Scotland TCAP students
3:00 – 4:00 pm	Break/Breakout groups discuss future activities *The groups will be given questions before the meeting and before the breakout session to help guide their discussion*
4:00 – 4:30 pm	Team leader feedback from breakout session
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)** (Food and cash bar)

Big Data comes to T3

Victoria Blake, Ph.D.

The T3 team has been busy ramping up the 'horsepower' of The Triticeae Toolbox (T3) to handle large genotype datasets. We have also made it simple for users to observe existing trials (Fig 1), select germplasm lines included in genotype trials (Fig 2) The ability to chose between consensus allele scores for markers used in more than one genotyping trial or individual allele scores from a single trait has also been added. (Fig 3). T3 What now has data for array-based SNPs, GBS SNPs and DArTs (Table 1) and T3 Barley has data for array-based SNPs and GBS SNPs (Table 2) .

Figure 1. The left menu on T3 now has a quick link to genotype trials

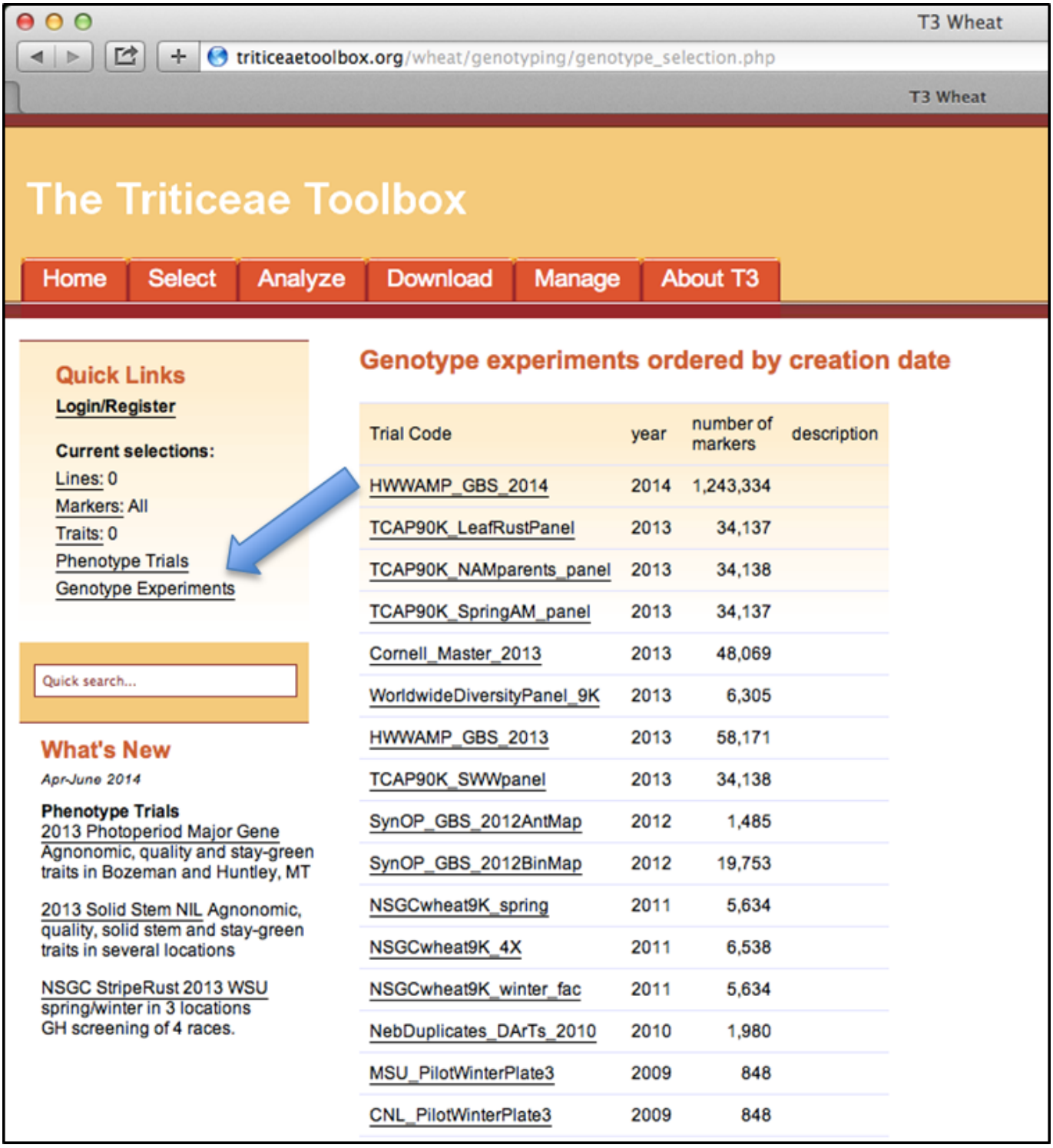


Figure 2. Germplasm can now be selected by genotype trials

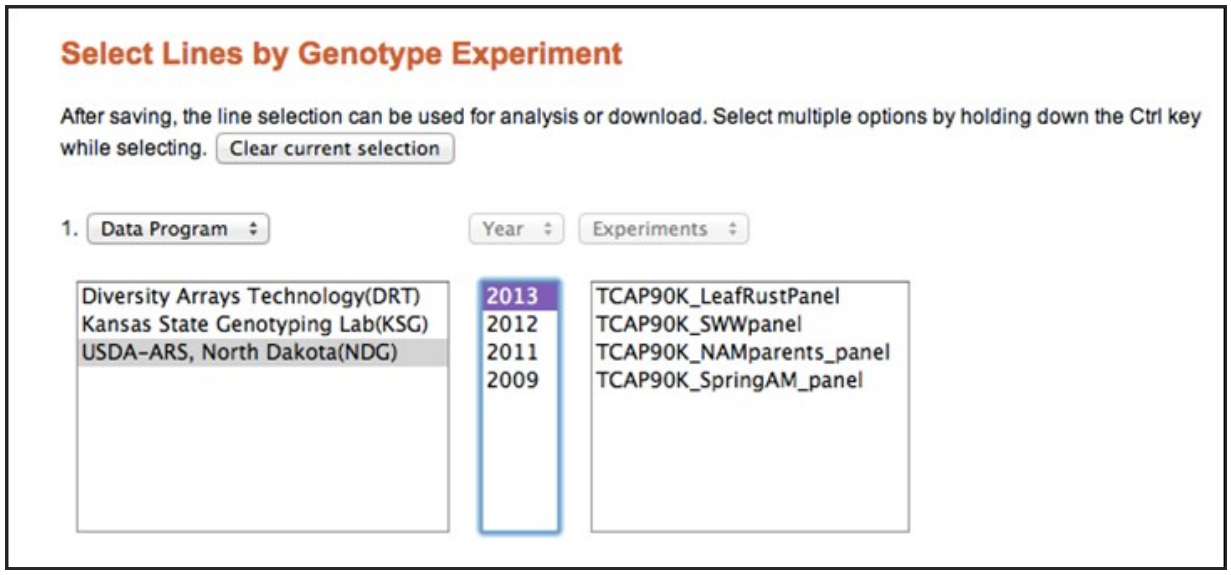


Figure 3. When building datasets for GWAS, users can now select a consensus allele score, or scores for individual trials

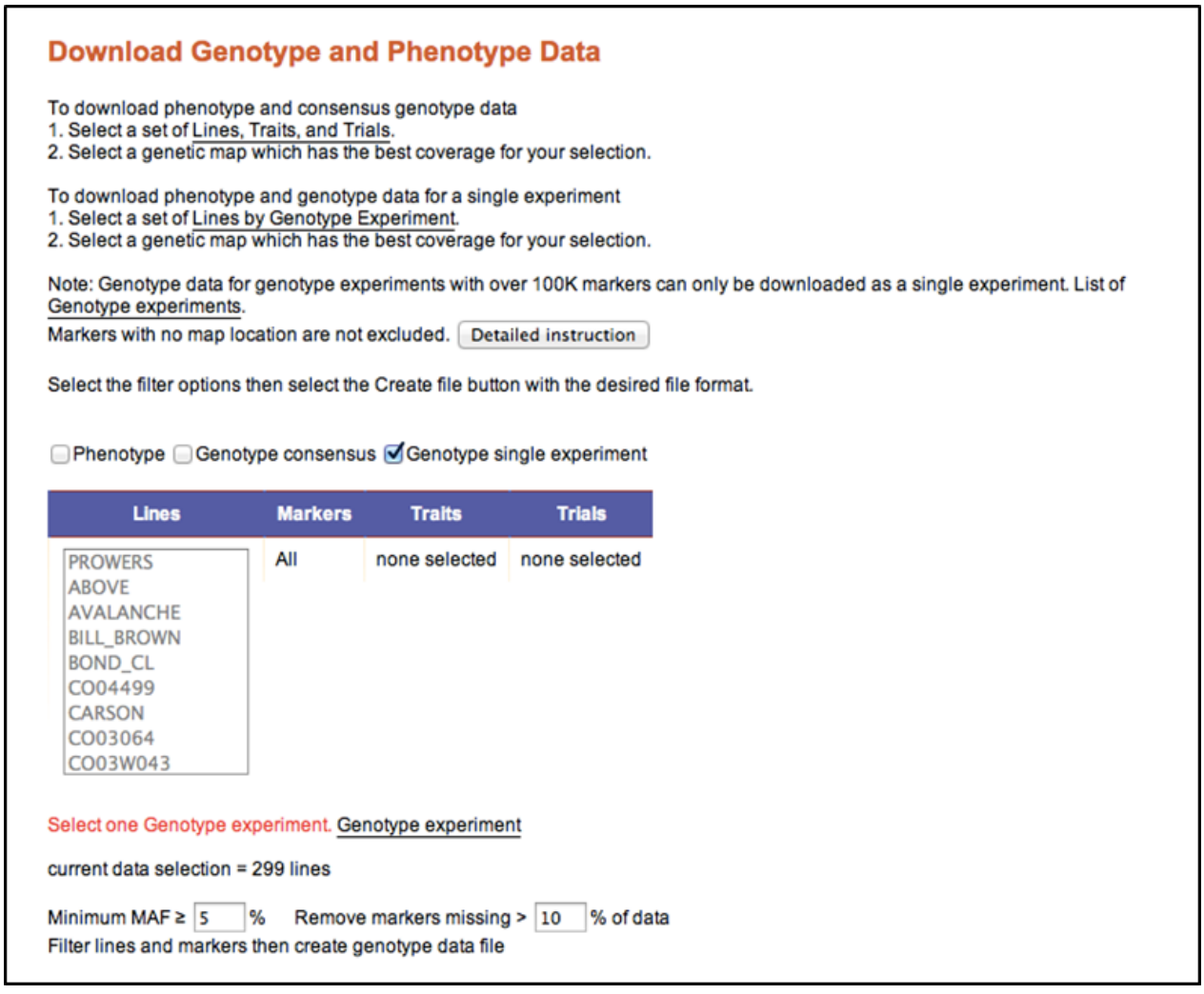


Table 1. Genotype Data in T3 Wheat

Trial Name	Year	Markers/ Platform	Population	Lab	Details
NNN_Pilot Winter/Spring Plate	2009	848 WOPA Array SNPs GoldenGate	Breeding Programs, various #	USDA-ARS Fargo, ND	28 separate small genotype experiments in 2009
NebDuplicates_2010	2010	1980 DArTs	278 Nebraska breeding lines	Diversity Arrays Technology	From S. Baenziger's Lab
NSGCwheat9K_winter_fac	2011	5,634 Illumina Infinium 9K	1674 NSGC wheat core lines	USDA-ARS Fargo, ND	Winter and facultative lines from the National Small Grains Collection
NSGCwheat9K_spring	2011	5,534 Illumina Infinium 9K	2196 NSGC wheat core lines	USDA-ARS Fargo, ND	Spring lines from the National Small Grains Collection
SynOP_GBS_2012BinMap	2012	19,753 gbs markers	162 Synthetic x Opata pop.	USDA-ARS/KSU Manhattan, KS	From Poland et al (2012) PLoS one. e32252.
SynOP_GBS_2012AntMap	2012	1,485 gbs markers	164 Synthetic x Opata pop + parents.	USDA-ARS/KSU Manhattan, KS	From Poland et al (2013) PLoS one. e32252.
TCAP90K_SWWpanel	2013	24,138 Illumina HD Ultra	317 AM panel lines	USDA-ARS Fargo, ND	Soft winter wheat TCAP association mapping panel
TCAP90K_SpringAM_panel	2013	34,137 Illumina HD Ultra	249 AM panel lines	USDA-ARS Fargo, ND	Spring wheat TCAP association mapping panel
TCAP90K_NAMparents_panel	2013	34,138 Illumina HD Ultra	61 AM panel lines	USDA-ARS Fargo, ND	Nested association mapping parental lines
TCAP90K_LeafRustPanel	2013	34,1387 Illumina HD Ultra	339 AM panel lines	USDA-ARS Fargo, ND	Leaf rust TCAP association mapping panel
WorldwideDiversityPanel_9K	2013	6,305 Illumina Infinium 9K	2,259 diverse lines	Univ. Calif. Davis	From Cavanaugh et al (2013) PNAS 110:8057
HWWAMP_GBS_2013	2013	58,171 gbs markers	289 AM panel lines	USDA-ARS/KSU Manhattan, KS	From Poland et al (2013) PLoS One e32253
Cornell_Master_2013	2013	48,069 gbs markers	1128 Cornell breeding lines	USDA-ARS/KSU Manhattan, KS	From M.Sorrells lab
HWWAMP_GBS_2014	2014	1,243,334 gbs markers	311 AM panel lines	USDA-ARS/KSU Manhattan, KS	

Table 2. Genotype Data in T3 Barley (not including THT BOPA work)

Trial Name	Year	Markers/ Platform	Population	Lab	Details
2010BOPA1_MN_GS_PARENTS	2010	1,536 BOPA Array SNPs GoldenGate	161 spring lines	USDA-ARS Fargo, ND	Genomic selection parents in the MN breeding program
2011BOPA1_MN_WC0	2011	1,536 BOPA Array SNPs GoldenGate	45 winter lines	USDA-ARS Fargo, ND	Genomic selection parents in the MN winter breeding program
CAPV2011_MN_9K	2011	6,684 Illumina Infinium 9K	95 breeding lines	USDA-ARS Fargo, ND	MN breeding program, continuing from BCAP
2011_9K_NB_allplates	2011	6,913 Illumina Infinium 9K	2419 NSGC core lines	USDA-ARS Fargo, ND	National Small Grains Collection lines
MorexBarke_GBS_2012	2012	21,385 gbs markers	91 DH lines	USDA-ARS/KSU Manhattan, KS	From Poland et al (2013) PLoS One e32253
OWB_GBS_2012	2012	34,396 gbs markers	82 DH lines	USDA-ARS/KSU Manhattan, KS	From Poland et al (2013) PLoS One e32253
WildBarleyIntrogression_9K_Parents	2012	7,308 Illumina Infinium 9K	26 lines	USDA-ARS Fargo, ND	Parental lines from wild barley introgression trials
Ethiopia_Eritrea_9K	2013	6,702 Illumina Infinium 9K	298 lines	USDA-ARS Fargo, ND	Cultivars collected in Ethiopia and Eritrea
TCFW6_LTT_9K	2013	7,203 Illumina Infinium 9K	768 winter lines	USDA-ARS Fargo, ND	Low temperature tolerance study

Drought tolerance verses cereal quality: Can we have it all?

By: Tyson Howell

During my time at UC Davis, I have been working to map a locus affecting yield and drought tolerance. The short arm of chromosome 1 from rye has been bred into wheat and replaces the wheat short arm of chromosome 1B. The rye segment provides wheat with drought tolerance and yield stability, but is reported to make low quality bread. My project was initially to correct bread quality while maintaining yield and drought tolerance. A line was developed that carried less of the rye chromosome because it had two interstitial pieces of wheat that were thought to improve bread quality. Unfortunately, when we created sister lines (near isogenic lines, or NILs), where one sister carried the complete rye segment while the other sister carried the rye segment with the wheat insertions (Fig 1A and 1B), the later NILs (rye and with wheat insertions) had a much lower yield (reduction of 25 to 40%) than the NILs with the complete rye segment. Using canopy spectral reflectance (CSR), I also was able to show that lines with the smaller 1RS chromosome arm consistently had worse canopy water status (NWI-3) and green biomass (NDVI). Interestingly, the original 1RS lines maintained their advantage under both normal and deficit irrigation regimes, though the advantage was larger under deficit irrigation.

We genotyped the NILs for both of the cultivars and after confirming that they were highly isogenic, I then made crosses between the NILs to separate the two interstitial wheat segments (Figures 1C and 1D). Seed limitations precluded planting yield plots, but I was able to use CSR and found that the distal wheat segment in the recombinant 1RS chromosome arm was responsible for the field performance effects, a finding confirmed in further field studies. This indicates that the gene for yield stability and drought tolerance are in one of the rye segments that had been replaced with a wheat segment.

Goal: create wheat lines with improved drought tolerance without negative impact on quality.

Our next step was to determine which of the two replaced segments were involved in yield and drought tolerance. To ensure that the difference involved the rye segment and not some other genetic difference, we investigated the physiological basis for the difference in field performance and found that the NILs with the original 1RS translocation had higher carbon isotope discrimination (CID). CID is determined by both stomatal conductance and photosynthetic rate, so we measured both of these traits to determine which was causing the difference. We found significant differences in stomatal conductance of the NILs, but no significant differences in photosynthetic rate. This result, combined with the canopy water status measurements, suggests that the original 1RS lines have access to more water in the soil throughout the season.

We are moving the recombinant 1RS.1BL chromosome containing only the proximal interstitial wheat segment into our breeding program, along with another gene that we hope will mitigate the bread making quality defects associated with the 1RS.1BL translocation. Moving forward I hope to be able to clone the gene(s) responsible, allowing us an entry point into the pathways which control plant water status.

Tyson Howell on the combine harvesting for a Davis trial

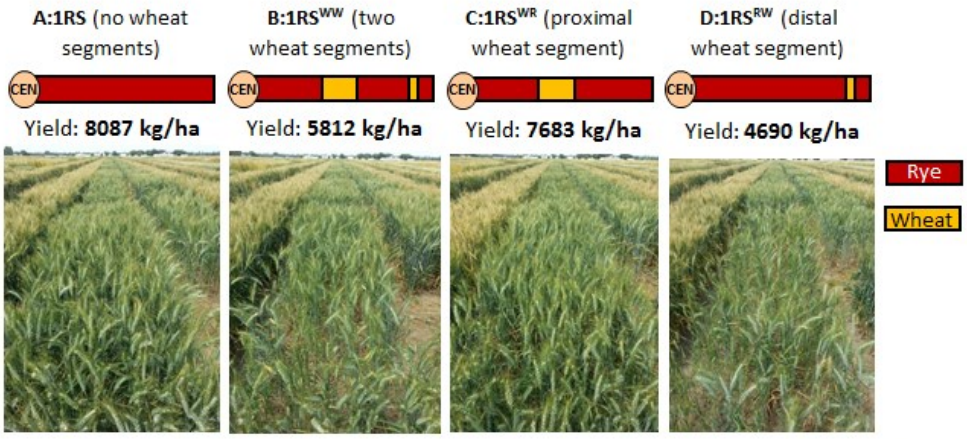


Figure 1: Diagram of the short arm of chromosome 1B for each of the lines pictured in the field plot below. Yield measurements for field plots are indicated above pictures. In chromosome diagrams circles indicate the centromeres, red bars rye segments and yellow basr wheat segments. A: Complete rye segment, B: Rye segment with two wheat insertions, C: Rye segment with proximal (closer to centromere) wheat insertion, D: Rye segment with distal (farther from the centromere) wheat insertion. Note that highest yielding lines (A and C) have the distal rye (red) segment.

The boss and an undergraduate student using the jaz for CSR on 1RS NILs

Lab to Farm to Fork: Development of a Nutritional Trait in Durum Wheat

Brittany Hazard

Resistant starch, a component of dietary fiber, has become the focus of recent dietary trends as awareness of its associated health benefits has increased. Resistant starch differs from ordinary starch in that it is able to escape digestion where starch is normally broken down into sugars that subsequently enter the blood stream. Brittany Hazard, a Ph.D. candidate in the Dubcovsky laboratory at UC Davis has used induced mutations in durum wheat genes to increase resistant starch content in the grain by over 750%.

Wheat food products are an important source of resistant starch since wheat provides almost 20% of the calories consumed worldwide. To accelerate the deployment of the high resistant starch trait in wheat, the germplasm carrying the mutations were recently registered in the Journal of Plant Registrations and have been made available as a resource for wheat breeders.

To determine other potential effects of the mutations, Brittany is currently evaluating agronomic and quality characteristics of the high resistant starch line to determine if there are any changes in yield or end product quality. She conducted three yield trials across California and spent this past summer at the California Wheat Commission evaluating the grain, semolina and pasta quality of material harvested from these sites.

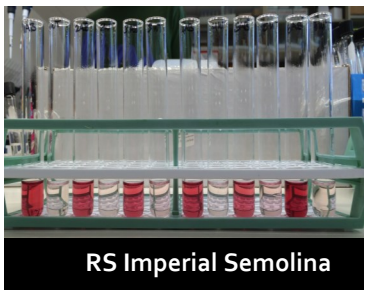
Brittany is also interested in the nutritional and health effects of resistant starch and is conducting a rat feeding study with her material this fall to measure indices indicative of bowel health. Instead of breaking down into glucose, resistant starch is able to pass through to the large intestine where it can be fermented by gut microbes, which can help maintain a healthy colon and digestive system. Foods with increased resistant starch contents also have lower glycemic indices and are considered good food choices for the prevention and management of diseases like type 2 diabetes and obesity. The development of this trait in wheat will make food products with increased resistant starch available to consumers as a healthy alternative and source of dietary fiber.

Pasta Extrusion

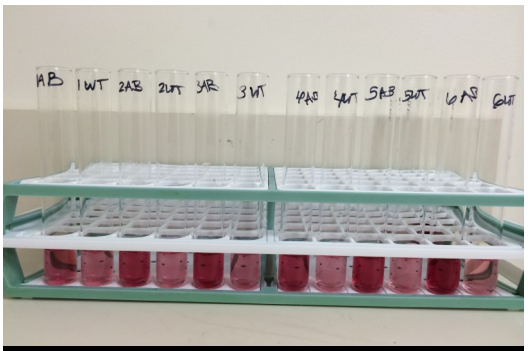
Five points harvest

Pasta

Breeding wheat with reduced glycemic index for improved health



RS Imperial Semolina



RS Imperial Pasta

Education News

Triticeae CAP
Coordinated Agricultural Project

INSIDE EDUCATION

TCAP members attend the National Association of Plant Breeders Meeting

by Katherine Frells

The 2014 joint annual meeting of the National Association of Plant Breeders and the Plant Breeding Coordinating Committee was held August 5-8 in Minneapolis, MN. The meeting was hosted by Syngenta with a theme of Breeding for Tolerance to Water Stress. TCAP was a sponsor of the meeting contributing financial support of all attending students.

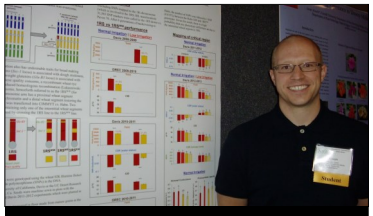
TCAP was well represented at the meeting with approximately 20 students and faculty attending. Thirteen TCAP graduate students presented posters that were displayed throughout the meeting. Poster presenters were asked to give a one minute introduction of their poster during the general meeting sessions to encourage all meeting attendees to visit and discuss the research.

Several TCAP members were invited to give research presentations during the meetings. Sarah Grogan, Ph.D. student from Colorado State, was selected as one of three graduate student presenters. Sarah presented "Multi-environment analyses of winter wheat heading date across the US Great Plains: Can we better optimize genotypes for specific environments?" which discussed her work analyzing heading date variation in the Hard Winter Wheat Association Mapping Panel in multiple years and environments. Dr. Pat Byrne, also from Colorado State, presented "Improving drought tolerance of hard winter wheat through the Triticeae Coordinated Agricultural Project". Mark Sorrells, Cornell University, presented an invited talk called "Genomic Selection: Training Populations and GXE".

Araby Belcher, Pat Hayes' student from Oregon State

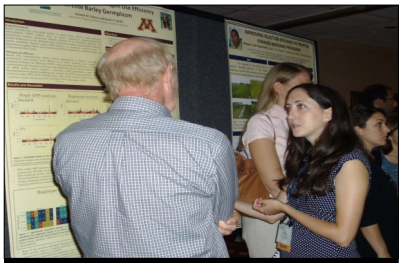
Sarah Grogan gave an invited presentation

Other TCAP members hosted workshops and organized sessions Duke Pauli, a recent PhD graduate from Montana State, was involved in organizing a mixer and the workshop "Private Breeding Perspectives". Celeste Falcon and Araby Belcher hosted two sessions. Jamie Sherman became chair of the Plant Breeding Coordinating Committee and chaired a strategic planning meeting for NAPB.



Tyson Howell a student of Jorge Dubcovsky's from UC Davis

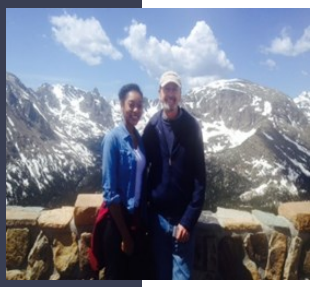
As well as attending research and informational sessions, meeting attendees participated in two half day tours. Syngenta hosted the first tour at the Stanton, MN research station and displayed new technologies in corn, soybean, and sweet corn research. University of Minnesota faculty and graduate students from the Department of Agronomy and Plant Genetics and the Department of Horticulture Science displayed a wide variety of research from turf grass and ornamental breeding to wheat, barley, and other row crop breeding. Members of TCAP from University of Minnesota, including Kevin Smith presented at field days.



Celeste Falcon, Kevin Smith's student from the University of Minnesota, discusses her work with Mark Sorrels.

Undergraduate students introduced to wheat breeding

Jessica Bess



My summer 2014 TCAP experience at Colorado State University was excellent. I learned a lot about Wheat Breeding and enjoyed my work relationship with Dr. Pat Byrne, Sarah Grogan and the rest of the research team. Currently, I am a senior majoring in Biology (minor Chemistry) and will graduate from Prairie View A&M University in May 2015.

Field Work

My research at CSU involved many different projects while working at two field locations. I worked in the field daily analyzing and collecting phenotypic data on wheat. Additionally, I analyzed data from the field that was used for specific experiments involving drought tolerance. I gained an appreciation and a wealth of knowledge for the various types of wheat grown this summer. My favorite wheat variety is "*Prairie Red"* because of it color, although it only had a moderate yield. Yield can be described as a measurement of the amount of a crop (grain, seed) that was harvested per unit of land area. Our objective in the field centered on determining the highest yielding wheat variety under drought conditions. However, this summer was not ideal conditions due to many nights of rain and hail. I learned that soil and weather conditions have a major impact on wheat growth and development. I also learned how weeds are harmful to the wheat and why it is important to remove them from the field. The pictures below depict the wheat at maturity and before harvest.

Maturity

Harvest

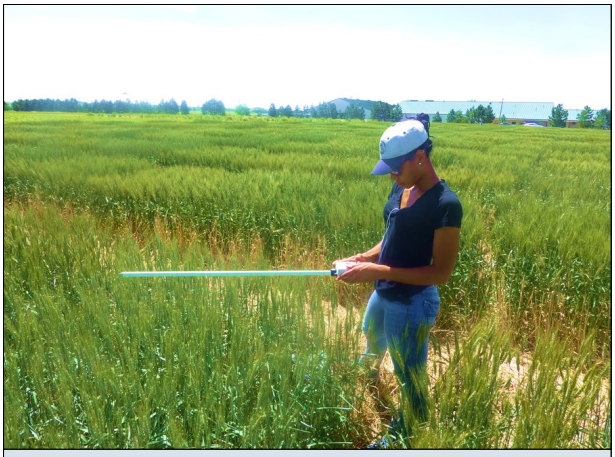
Lab Work

My TCAP experience included analyzing data collected in the field such as: leaf area index (LAI), relative water content, biomass weight, yield etc. I inserted data measurements into a spreadsheet for further research. Additionally, I compared the different varieties of wheat performance in the field. I also performed manual calculations to find LAI and other data points. During these various processes, I learned how valuable it is to ensure that all data points are accurate by taking multiple samples and double-checking the work.

Overall this was an excellent learning experience for me. I gained an interest in agriculture and possibly will explore future graduate degree opportunities. I want to thank the TCAP program for giving me this experience. Also special thanks to the following people for providing me guidance and support: Dr. Byrne, Sarah G., Angie, Scott, Brian, Amy and Hayley.

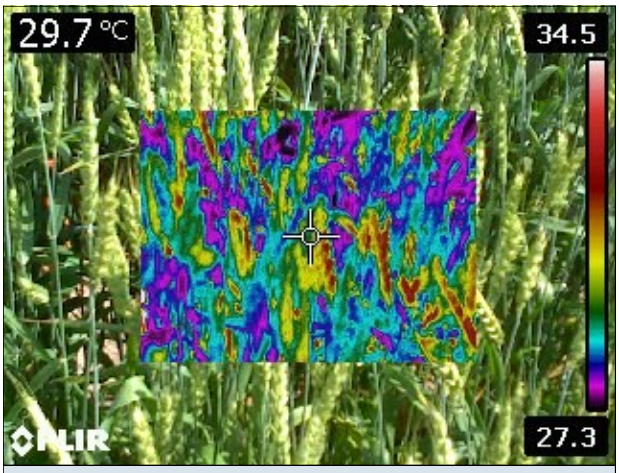
TCAP Students gain a variety of experiences in 2014

Roshan Acharya shares the goal of his field experiment to identify new drought tolerant genes with growers in Sydney, Montana.

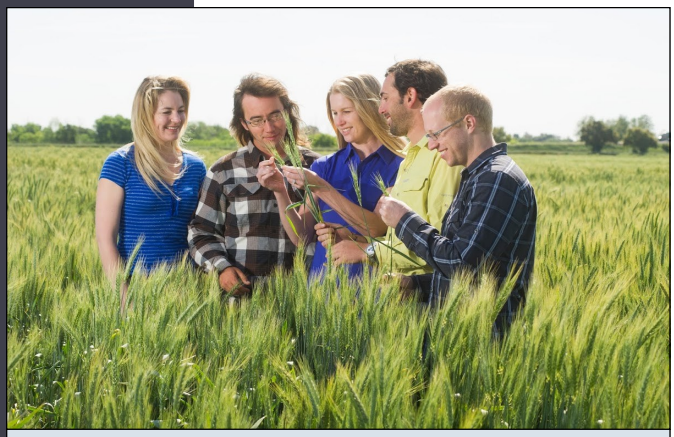


Jessica Bess—Handheld lightbar, measuring photosynthetically active radiation (PAR) transmitted through the canopy.

Roshan Acharya harvests his field experiment in Bozeman, Montana.



David Chappel is learning what wheat looks like through the lens of a thermographic camera. Hoping to see if the results can be used for heat stress research



UC Davis Students—Brittany Hazard, Josh Hegarty, Rebecca Nitcher, Nicolas Cobo, Tyson Howell enjoy a photo shoot

Graduate student Steve Carlsen (left) helping undergraduate Nathan Wyatt (right) score barley seedlings for SFNB infection

Fall 2014 TCAP Undergrad Online Meeting Schedule

TCAP undergrad online meetings help students to

- Get connected to the broader TCAP research community
- Build communication skills as a scientist
- Learn about graduate school and opportunities in industry

Conversations take place on the undergraduate community website at http://passel.unl.edu/communities/tcapundergrads
Feel free to access the site at any time. Help using the site will be available 20 prior to each meeting. Plan to use a headset—it's just better. Each lab should purchase a headset (about $20) and make it available to interns. Materials related to discussions will be posted on the Plant Breeder Training Network - Undergrad Community website.

Date/Time **	Topic	Discussion lead
15 Sep, 3 – 4:00	Internship opportunities with DuPont Pioneer	Dr. Tabare Abadie, DuPont Pioneer
29 Sep, 12 – 1:00	A day in the life of a Syngenta intern	Michael White, APS undergraduate, University of Minnesota
6 Oct, 12 – 1:00	How to make your internship work for you!	Dr. Mary Brakke University of Minnesota
13 Oct, 12 – 1:00	Genetic basis of wheat cell wall biosynthesis	Dr. Christopher Botanga Chicago State University
23 Oct, 3 – 4:00	Hessian fly resistance in wheat	Dr. Lieceng Zhu Fayetteville State University
27 Oct, 12 – 1:00	Mechanisms of cadmium transport in wheat	Dr. Renuka Sankaran Lehman College, CUNY
3 Nov, 12 – 1:00	Barley resistance to SPNB	Nathan Wyatt, NDSU TCAP Research Academy Recipient
13 Nov, 12 – 1:00	Wheat breeding with CAPS markers	Nikayla Strauss, Colorado State U. TCAP Research Academy Recipient
19 Nov, 3 – 4:00	Biochemistry of wheat seeds	Dr. Joseph Onyilagha University of Arkansas
Dec 1, 12 – 1:00	Presenting your TCAP Research	Dr. Mary Brakke University of Minnesota

***NOTE: All times are CENTRAL time zone.**

Increasing Student Diversity through Research

Candice Watts, Marsha Jordan, Aremu Azeez and Brianna Mackey; working in the Botanga

Chris Botanga of Chicago State University mentored four students over the summer on a research project in collaboration with Jamie Sherman of Montana State University. The students were evaluating hollow- and solid-stem genotypes of wheat in an effort to see if there are any polymorphisms in cell wall biosynthetic genes. Bioinformatics approaches were used to design primers for genes involved in cell wall biosynthesis. The primers are being used to amplify and sequence wheat genes. The expression of these genes will also be evaluated. In order to begin addressing these objectives, the specific activities undertaken by the students involved DNA isolation and quantitation, primer dilution, PCR, agarose gel electrophoresis, and scoring for the presence or absence of amplicons.

Aremu Azeez, Brianna Mackey, and Candice Watts; presenting end-of-program presentation

Marsha Jordan, Candice Watts, Aremu Azeez and Brianna Mackey; working in the Botanga Lab at CSU

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

Universities

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

USDA-ARS

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

Collaborating Institutions with Student Projects

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

TCAP Terminology

- **Association mapping** is a technique used to identify marker-trait associations in lines that are not derived from a single cross.
- **Canopy Spectral Reflectance (CSR)** is a new phenotyping tool TCAP is exploring. It is based on the observation that plants under stress reflect different colors of light. Measuring the light reflected might be a way to predict plant performance.
- **Canopy Temperature Depression (CTD)** plants need $C0_2$ for photosynthesis and acquireit through window-like structures in leaves simultaneously releasing o_2 and H_20. When a plant is water stressed, the windows in the leaves through which this gas exchange occurs must close, reducing photosynthesis and thereby reducing yield. When the windows are open not only can photosunthesis occur, but also as H_20 is released the temperature around the plant decreases due to evaporation. CTD can act as a proxy for measuring the plants ability to continue to photosynthesize under drought stress.
- **Copy Number Variation (CNV)** are differences in DNA between individuals that occurs when a large number of building blocks called nucleotides are either duplicated or deleted. CNVs generally range in size from thousands of base pairs to millions of base pairs. In contrast, SNPs are another DNA difference that only involves single base changes. The number of CNVs reported here in Barley of 15% is in a similar range as what has been reported in humans.
- **Deoxyribonucleic acid (DNA)** is the genetic material for most organisms. An organism's complete set of DNA is called its **genome**.
- A **gene** is the instructions for a specific structure in the organism. For an organism to survive certain instructions (genes) are required. However, the details or order of the instructions may vary from organism to organism and it is these differences that we are looking for to improve wheat and barley.
- **Genomics** is the study of the **genome**. The genome is a complete set of instructions for the organism. You can think about it like an instruction manual for that organism.
- **Genomic selection** is when markers spread throughout the genome are used to predict the performance of individuals to facilitate breeding.
- **Genotyping** is when the genetic makeup of an organism is characterized. The genotype controls the way an organism looks, which is called the **phenotype**. In our instruction manual analogy, determining the genotype would be like reading the instruction manual, while determining the **phenotype** is like testing the product created after following the instructions.
- **Germplasm** is a collection of genetic resources, which in wheat and barley is usually a collection of seed.
- **KASP™ Markers** are a cost efficient method of SNP genotyping developed by KBioscience. KASP stands for Kompetitive Allele Specific PCR. Advantages of KASP over other systems: may be less expense, greater flexibility, and higher conversion rate
- A **marker** is a difference in the DNA that acts like a bookmark indicating the position of a certain set of instructions. It can be a difference in the instructions **(gene)** itself but it can also be a difference in a neighboring part of the DNA.
- Making **Marker/trait associations** is identifying good bookmarks for the instructions that are important. Once marker/trait associations are made, markers can be used to make selections.
- **Marker Assisted Selection** is a technique that uses DNA markers to identify individuals carrying certain genes to facilitate breeding.
- **National Small Grain Core Collection**, NSGC collection is an important germplasm resource for the TCAP. TCAP participants will be evaluating and distributing an extensive collection of seeds representing material from around the world. TCAP is searching this material for unique **genes** that will be used to improve wheat and barley.
- **Near Isogenic lines (NILs)** are lines that are essentially identical except for one location of interest in the genome. Markers can be used to create sister lines that are "+" or "-" for the location. NILs are a powerful tool for careful testing of the effect of the location on the way the line performs. It is like having an on/off switch.
- **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.