



Triticeae CAP
Coordinated Agricultural Project

TCap Transmission

Spring Issue 2012

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Directors Notes

By: Gary Muehlbauer and Jorge Dubcovsky



We are in the middle of year 2 of the TCAP and we are beginning to accelerate our progress on both the education and research objectives of the grant.

The TCAP education team is developing and delivering state-of-the-art online education experiences for graduate and undergraduate students. For example, in the spring, the TCAP education team initiated an online seminar series for those within and outside the project. Six seminars were presented on a range of topics including: high-throughput **genotyping**, the T3 database, online learning, canopy spectral reflectance, plant parasitic nematodes and breeding for grain yield. The education team also conducted online courses in the spring on "Entering Mentoring" and quantitative genetics for the graduate students. Fifty-nine graduate students (of which 33 are fully or partially funded by the TCAP) have participated in one or more of these activities and twenty undergraduate students are being mentored by TCAP graduate students. These education and mentoring activities are bringing a new cohort of graduate and undergraduate students into the wider plant breeding community.

The research objectives of the TCAP are

also progressing well.

For example, see descriptions of new **genomics** tools for wheat breeding (page 2) and **association mapping** of insect and pathogen resistance in winter wheat (page 3). Noteworthy is the unique collaboration that Tom Blake (Montana State University) developed with barley breeders in Kazakhstan. Tom's idea was to share barley CAP **germplasm** with Kazakhstan barley breeders and have them evaluate the performance of those lines in their environment. Remarkably, some of the lines performed very well (have been used in crosses in their breeding programs) and the data are being used by Tom to conduct **association** genetics for agronomic traits, disease resistance and grain quality. This type of effort exemplifies the power of collaboration.

Two workshops that may be of interest to the TCAP community and others are the "Plant Breeding for Drought Tolerance Workshop" in Fort Collins, CO on June 11-22 led by Pat Byrne (see page 5) and the "Rust Research Methodology Workshop" in St. Paul, MN on July 8-10 led by Brian Steffenson and Pablo Olivera (see page 5 for details).

Participating Programs

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**

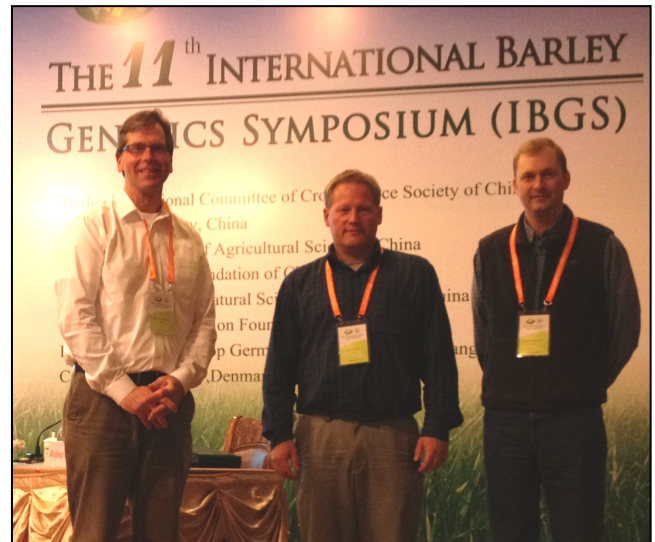
Collaborating Institutions with Student Projects

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

TCAP PIs attend the International Barley Genetics Symposium By: Gary Muehlbauer

The 11th International Barley Genetics Symposium was held in Hangzhou, China on April 15-19. The meeting was divided into nine sessions including: Barley development and the economy; utilization of **germ-plasm**, genetic resources, and genetic stocks; biotic and abiotic stresses; new and renewed breeding methodology; barley physiology, and end uses; breeding success stories, barley **genomics** and all other “omics”. Four PIs on the TCAP attended the symposium and presented results from the barley CAP and TCAP. Patrick Hayes (Oregon State University) presented a talk on his breeding program, the incorporation of **genomics** tools to characterize winter hardiness and the future outlook for increased incorporation of **genomics** tools in barley breeding. Kevin Smith (University of Minnesota) presented a talk on the use of barley CAP data to conduct **genomic selection** for Fusarium head blight resistance, presenting promising results for utilizing **genomic selection** in the development of new varieties. Brian Steffenson and Gary

Muehlbauer presented posters describing the work in the barley CAP to map spot blotch resistance, and an overview and recent results of the TCAP, respectively.



Brian Steffenson, Kevin Smith and Gary Muehlbauer at the International Barley Genetics Symposium

New **genomics** tools for wheat breeding

By: E. Akhunov, KSU

Genome-wide analysis of genetic variation is one of the important steps towards understanding the genetic basis of agronomic traits in wheat.



Until recently, **genotyping** was an expensive and labor-intensive procedure. With the advent of new **sequencing** and **genotyping** technologies the analysis of the wheat **genome** was raised to a new level where researchers can simultaneously analyze **single nucleotide polymorphisms (SNPs)** at hundreds of thousands of sites across the **genome** in a population of thousands of wheat plants. The TCAP team actively collaborates with the international wheat SNP consortium on the deployment of new **genotyping** platforms in breeding programs. Recently, the SNP consortium developed two custom Illumina SNP **genotyping** assays (also referred to as iSelect) including 9,000 and 92,000 **SNPs** (<http://wheatgenomics.plantpath.ksu.edu/snp>). Both **genotyping** assays are based on **SNPs** found in **genes** by **sequencing** wheat transcripts using next-generation **sequencing** tech-

nologies. The data for SNP discovery have been provided by the international wheat community including research groups from USA, Australia, UK, France, Italy and Germany. A diverse set of wheat accessions including worldwide collections of cultivars from national breeding programs, landraces, synthetic wheat lines, and durum wheat was used for generating sequence data to ensure adequate sampling of genetic variation in wheat and broad utility of developed assays.

These **genotyping** assays have been adopted by the TCAP and used for the **genotyping** of thousands of wheat lines including mapping populations and the diverse collections of cultivars and landraces. In total, the international wheat community in 2012 is **genotyping** more than 46,000 wheat lines using the 92,000 SNP wheat iSelect assay. This effort will generate more than 4.2 billion **genotyping** datapoints by fall of 2012 providing a rich resource to wheat breeders and geneticists for **gene** discovery and wheat improvement. TCAP actively collaborates with the SNP consortium on the development of tools for **genotyping**; data storage and analysis. More details about the wheat iSelect assays can be found at the wheat SNP development project website <http://wheatgenomics.plantpath.ksu.edu/snp>.

The Kazakhstan-US Barley Improvement Collaboration (KUBIC)

By: Tom Blake

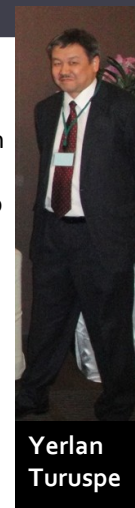
In 2002 and 2003, I enjoyed the opportunity to serve as Head of the **Germplasm** Program (the crop improvement group) at the International Center for Agricultural Research in Dry Areas (ICARDA). My team had projects throughout North Africa, West Asia and Central Asia. To my mind, the true genius of Dr. Norman Borlaug (the founder of the International Agricultural Research Centers) was his recognition that the best and least expensive way to globally improve our crop varieties is through extensive **germplasm** exchange coupled with expert local **germplasm** evaluation. Exchange of genotyped lines is especially useful because these permit identification of those **genes** that contribute to adaptation, both local and general. In an unpredictably changing environment, knowing how barley's **genes** and genotypes contribute to adaptation across the broadest possible array of environments could be critical to design and selection of future varieties.

A friend and colleague, Dr. Yerlan Turuspekov, returned to Kazakhstan in 2008 as Associate Director of the Kazakhstan Institute for Plant Biotechnology (KUBIC). He requested seed from the spring barley CAP entries, and with permission of breeders and institutions I sent seed from six of our eight contributing spring barley programs to Yerlan in the winter of 2008. He increased the seed and distributed the 674 entries (plus many check varieties) to eight

breeding stations in Kazakhstan. The breeders and pathologists at these eight stations were excited and enthusiastic collaborators and have now supplied two years of data (2010 and 2011) for several agronomic, grain quality and disease resistance traits. I've managed to successfully format about half of their data for TASSEL, and am in the process of analysis. I had the good fortune to attend a research conference about the Barley CAP lines and their performance put on by Yerlan and his breeder colleagues in Almaty in February, 2012. Some of our CAP lines perform remarkably well in the saline environments between the Caspian and Aral Seas, and many of our lines outperform check varieties at each of their stations. The breeders have all made crosses with our lines, and may ask the originators of high-performing lines about collaborative varietal releases.

If you were to move Montana 180° around the world, it would cover much of the Southern third of Kazakhstan. Our Northern Plains are similar in many ways to Kazakhstan's small grains production regions. While many of our crop production constraints are similar, much of the acreage in Western Kazakhstan is salinized, and salt tolerance is a premium trait between the Caspian and Aral Seas. KUBIC data will help us unravel the genetics underlying variation for salt tolerance in our **germplasm**, and for resis-

tance to local races of several pathogens. As the Northern-most of the 'Stans, Kazakhstan has neighbors to the South and East that are important to us (notably Afghanistan and China). Collaboration provides them with a broadened barley **germplasm** base, and us with high quality data. As climate changes, our locally-derived datasets will prove less informative, and expanding our data collection into new environments that might better-mimic our local environments of the future should help mitigate the classic breeders' problem: breeding for last years' disaster. I'd like to thank the breeders and institutions that enable me to distribute their barley **germplasm** through KUBIC and the breeders, agronomists and pathologists who have taken the data that I'll be analyzing this spring.



Yerlan Turuspe



Barley Field in Aktobe

Association analysis in a panel of eastern U.S. winter wheat lines

By: Keith Merrill

My name is Keith Merrill, and I am originally from Orem, UT. Together with my wife, Katie, I have a son, Charlie, who is 16 months old. I obtained my BS and MS degrees in Genetics and Biotechnology from Brigham Young University in Provo, UT, and I am currently working on my PhD in Plant Breeding and Genetics at North Carolina State University, under Dr. Gina Brown-Guedira. We are working on a multi-year study to discover new disease and insect resistance **genes** within a diverse panel of 449 eastern U.S. winter wheat lines. The panel is comprised of both landrace and elite cultivars of current or historic importance to eastern U.S. wheat breeding programs. Lines were submitted by eastern U.S. wheat breeders for inclusion in the panel. The diseases of primary focus are powdery mildew (*Blumeria graminis* f. *sp. tritici*), leaf rust (*Puccinia triticina*), and leaf and glume blotch



(*Stagonospora nodorum*). The insect of primary focus is Hessian fly (*Mayetiola destructor* (Say)). These diseases and insects can significantly decrease yields and quality of winter wheat in the eastern U.S. While resistance **genes** do currently exist for each of these diseases or insects, novel **genes** are needed to continue to incorporate into breeding programs as current resistance begins to break down. Phenotypic data coupled with SNP data from Illumina 9k chip will be used in **association analysis**. Population structure, seedling vigor, maturity at rating, and heading date will all be used as covariates in the analyses. We anticipate the use of my results in helping to characterize the genetics of resistance to these pests and pathogens and also in providing breeders with additional tools for **marker-assisted** selection.



Triticeae CAP
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Education News

Spring Courses

Entering Mentoring—

Five TCAP graduate students (from University of Minnesota, Colorado State and UC Davis) completed Entering Mentoring spring of 2012. Mentoring was supported through a process of action and reflection. Graduate students mentored undergraduates in research projects and reflected on that experience through online meetings guided by Jamie Sherman. “I learned a lot from these students sharing their experiences and appreciate their openness to the process” said Sherman. Several graduate students were surprised how much time mentoring required and gained a better appreciation of their own mentors. Most of the students found the experience to be positive and reported that their mentoring skills had improved. Two students felt the experience would have been more beneficial later in their academic careers. Another section of Entering mentoring will be offered in 2013. Students need to be actively mentoring an undergraduate to participate.

Quantitative Genetics

Clay Sneller deserves kudos for his contribution to Quantitative Genetics spring of 2012. He created lectures that cover the following topics: allele and genotype frequencies, diversity, genetic distance, genetic effects, breeding value, variances and covariance of relatives, heritability, gain from selection, and gain from indirect selection using **markers**. These lectures are part of the permanent archive at <http://passel.unl.edu/communities/pbtn>. Jamie Sherman created lectures guiding students through linkage and **QTL mapping** utilizing MapDisto and QTLcartographer software. Students used data from Oregon Wolfe Barley mapping

population to create their own maps and practice QTL analysis. Most student respondents indicated the course was useful. Students encouraged refinement of use of group discussion and group projects. Several made suggestions for changes to online environment. An important suggestion was to split the course in two and in the future provide a Quantitative genetics course and a **QTL mapping** course. A few student comments were “The course is nice and it basically improved my knowledge level in quantitative genetics.” “I wanted to learn how to use software for **QTL mapping**. This course, especially the project did fulfill my expectations.”

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Summer Workshops

Cereal Rust Phenotyping Workshop University of Minnesota July 9-10, 2012

Phenotyping wheat and barley **germplasm** to rust diseases is an important facet of the Triticeae Coordinated Agricultural Project (TCAP). This two day workshop will provide useful information on various aspects of the cereal rust research, including rust biology and epidemiology; rust collection, inoculation and storage techniques; race identification and nomenclature; rust resistance genetics; and rust phenotyping.

Instructors: Brian Steffenson and Pablo Olivera
University of Minnesota, Department of Plant Pathology
Phone : 612-625-4735
e-mail : bsteffen@umn.edu

When: July 8-10, 2012

Location: Room 136, Plant Growth Facility
St. Paul Campus, University of Minnesota



For Registration: http://tcap_cereal_rust_workshop_2012.eventbrite.com

Registration fee: \$150

For Details contact: Lynne Medgaarden for inquiries: 612-625-4742 or medga001@umn.edu

Deadline for registration: June 15, 2012

Schedule:

July 8 (Sunday): travel day to the Twin Cities. A welcome social will be held at 6:30pm in the Radisson Hotel

July 9 (Monday): 8:30am-12:00pm: presentations
1:30-5:00pm: demonstrations
6:30pm: BBQ on campus

July 10 (Tuesday): 8:30am-12:00pm: tour of Cereal Disease Lab & field plots
1:30-3:30 optional follow up visits with scientists

Accommodations:

A block of 20 rooms has been reserved at the Radisson Hotel in Roseville, Minnesota at the rate of \$89.00 per night. Reference the **TCAP Rust Phenotyping Workshop** to get the special room rate.

If you would like to save on accommodations and know someone else who will be attending the workshop, feel free to share a room.

The contact information for the hotel is:
2540 North Cleveland Ave, Roseville, Minnesota 55113
651-636-4567 hotel | 651- 367-3940 fax

Plant Breeding for Drought Tolerance - 2 week summer course

When: June 11-22

Who: Pat Byrne

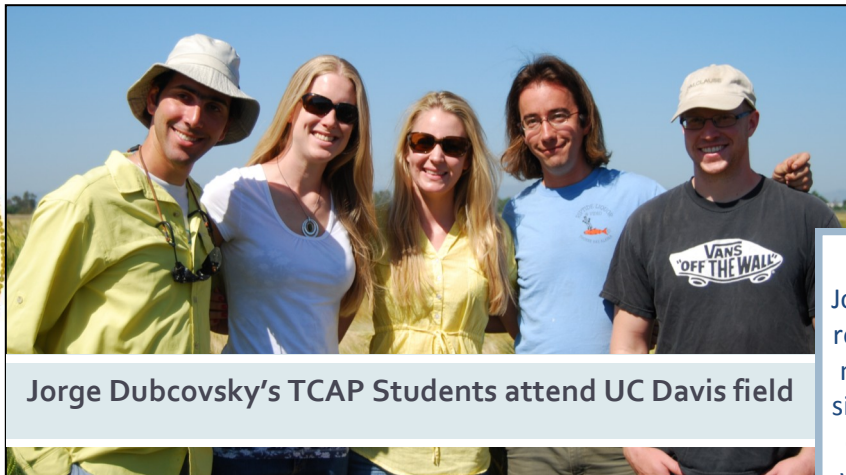
Where: Colorado State University, Ft Collins CO

For more information: <http://www.droughtadaptation.org/> or

Annie.Heiliger@colostate.edu

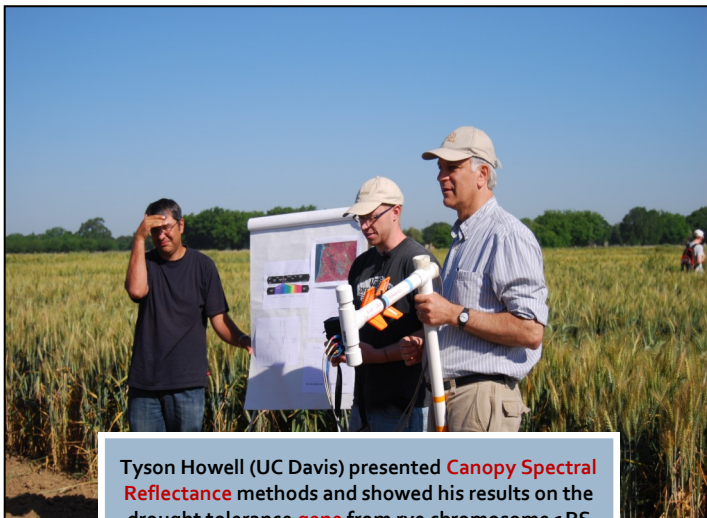
TCAP student scholarships \$500

TCAP Students make Presentations at field days



Jorge Dubcovsky's TCAP Students attend UC Davis field

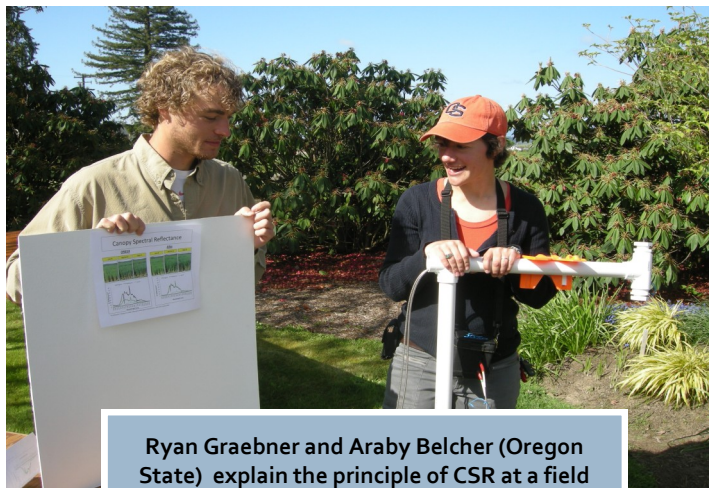
Josh Hegarty presented his results on the high-density mapping of stripe rust resistance genes *Yr48* and its deployment in California wheat breeding program.



Tyson Howell (UC Davis) presented **Canopy Spectral Reflectance** methods and showed his results on the drought tolerance gene from rye chromosome 1RS



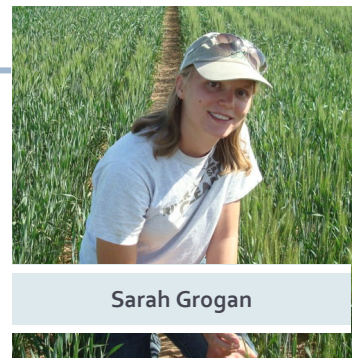
Brittany Hazard (UC Davis) presented her recent results on the increase of resistant starch in the wheat grain (Crop Science in Press)



Ryan Graebner and Araby Belcher (Oregon State) explain the principle of CSR at a field day held for "Leadership Corvallis"

Sarah's Success Story By Sarah Grogan

Throughout the spring semester, I worked with Kelsey Salvo, a junior at Colorado State University on a molecular biology project as part of the TCAP Entering Mentoring seminar. The scope of the project was meant to introduce Kelsey to different molecular techniques, as well as give her responsibility over her own project and teach her to formulate hypotheses and draw upon different types of results. Kelsey was working to genotype individual BC1F3 plants for glaucousness, the trait responsible for wax production that is thought to, among other things, reflect excess radiation and reduce the amount of water loss to transpiration. The families we were working with came from a cross between a non-glaucous synthetic line and the elite (glaucous) cultivar Hatcher and were segregating for the trait. I showed Kelsey how to start a literature review and identify **genes** that might be associated with glaucousness and wax production in our plants, and then use consensus maps on GrainGenes to identify flanking **markers**. Kelsey spent the next several months tending to her plants in the greenhouse, extracting **DNA**, running PCR, and interpreting polyacrylamide and agarose gels. This was Kelsey's first opportunity for comprehensive, ongoing molecular work, a subset of skills she expressed interest in exploring before thinking about graduate school. Additionally, our weekly mentoring sessions also covered topics like writing a good resume, searching

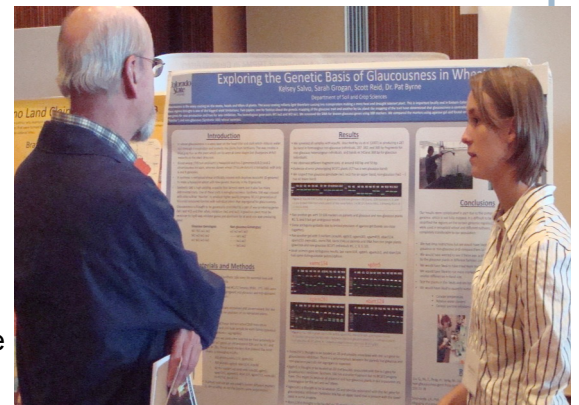


Sarah Grogan



TCAP provided Kelsey with her first ever substantial molecular research experience. In this picture she is running a gel with PCR product from several synthetic-derived backcrossed wheat families and SSR primers for markers thought to be located near **genes** for glaucousness and wax production.

for and applying to summer internships, and discussing post-graduate options and tips about finding a good graduate school for her interests. Kelsey's project culminated at the end of the semester, when she developed a poster to present at the CSU 2012 "Celebrate Undergraduate Research and Creativity" symposium.



CSU undergraduate Kelsey Salvo presenting her research poster at the CURC (Celebrate Undergraduate Research and Creativity) 2012 symposium on 04/17/12. Kelsey participated in a mentorship with graduate student Sarah Grogan as part of the TCAP Entering Mentoring seminar. Her project involved investigating the genetic basis of glaucousness in winter wheat

TCAP seminar series

To encourage communication about the TCAP project a seminar series was held online. Six seminars were presented by TCAP faculty, students and collaborating faculty from minority serving institutions. Participants view the seminar series as an important tool that will help ensure the success of the project. A particular advantage is that very

CYBERSPACE: NEW FRONTIERS IN LEARNING AND NET-WORKING

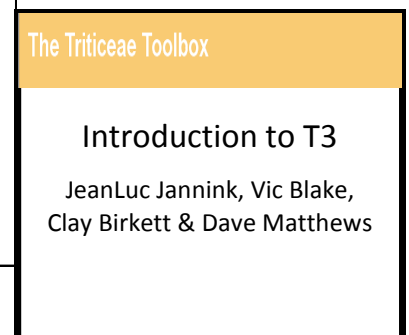
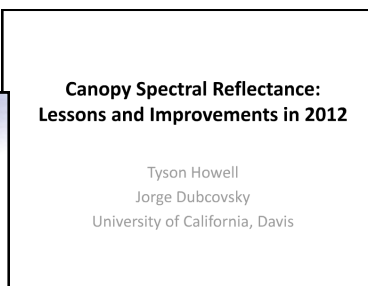
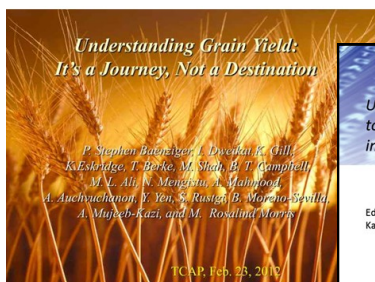
Deana Namuth-Covert, PhD
Univ of Nebraska
TCAP Education Team Member
March 16, 2012 TCAP Webinar Series

new information can be transmitted to the group to facilitate implementation of new tools e.g. T3 database or CSR.

All the seminars have been archived at

<http://passel.unl.edu/communities/pbtn>. Graduate students are design-

ing the TCAP seminar series for fall. On average 30 people attended each seminar.



Plant Interaction Project at Fayetteville State University

Wheat (*Triticum aestivum* L.) is the sixth largest crop in North Carolina. The Hessian fly [*Mayetiola destructor* (Say)] is a destructive pest of wheat plants and a newly emerging pest in North Carolina. We are interested in studying metabolisms of wheat plants in response to Hessian fly infestation in compatible and incompatible interactions under normal and stressed environments.

We have studied the differential changes of carbon/nitrogen metabolism, phytohormone metabolism, and lipid metabolism of wheat plants under Hessian fly attacks. We found that Hessian fly infestation induced a shift of carbon/nitrogen metabolism in wheat plants, possibly through glycolysis and related pathways (Zhu et al. 2008), we identified the characteristic

phytohormones in compatible and incompatible interactions, respectively (Zhu et al. 2010), and we revealed that the Hessian fly induced changes in phytohormone accumulations are more rapid in resistant wheat plants than in the nonhost rice plants (Zhu et al. 2011). Furthermore, we disclosed that Hessian fly infestation rapidly mobilized membrane lipids in wheat leaf-sheathes during incompatible interactions (Zhu et al. 2012). In the process, we trained eight high school students, three undergraduate students in research for different programs at Fayetteville State University, such as CPSER (Center for Promoting STEM Education and Research), ISAS (Integrated STEM Academic Success), and Coco-Cola Scholar Program etc.

Project related to TCAP

Wheat resistance **genes** to the Hessian fly can be temperature-sensitive. Under high temperature, resistance of wheat cultivars can be compromised. In a study partially supported by T-CAP, we investigated the changes of phytohormone and fatty acid accumulation in a resistant wheat cultivar “Molly” under high temperature stress. This research has been used to train eight graduate students in the Advanced Genetics class in designing experiments, applying treatments, analyzing data, and writing manuscripts. The results obtained from this research have been processed,



and currently we are working on a manuscript for submission to the Journal of Plant Interactions.

Work in Progress

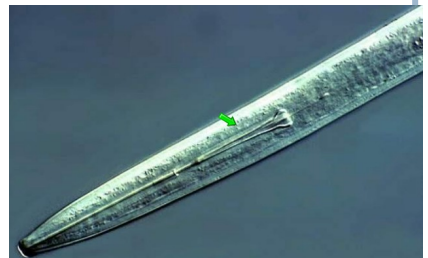
TCAP provides funds to give extra supports to our graduate students to keep them focused on research. With the support, we were able to arrange graduate student Ms. Yaleaka Currie to work in Dr. Ming-Shun Chen’s lab at Kansas State University over the summer. We anticipate that Yaleaka will complete two research projects: 1, Molecular responses of Hessian fly-resistant wheat plants to high temperature stress; 2, Impact of humidity on egg hatching of Hessian flies. Additionally, graduate student Mr. Joshua Underwood is working on the impact of externally applied salicylic acid on resistance of wheat plants to Hessian fly infestation.



Plant Parasitic Nematodes: The Farmer’s Hidden Enemy

Martin Matute, University of Arkansas Pine Bluff a Historically Black College, is collaborating with Arron Carter, the winter wheat breeder at WSU. Matute delivered a seminar during the TCAP seminar series this spring. He introduced us to nematodes and shared preliminary results of his TCAP collaborative research. Matute and his group of our undergraduate students have assayed soil from wheat fields in Washington for numbers and type of parasitic as well as useful nematodes.

The hope is to find lines not only resistant to parasitic nematodes, but also encourage development of useful nematodes. The same students from Pine Bluff are interning at WSU for 6 weeks this summer and two have expressed interest in graduate school.



Xiphinema: Ecto-parasitic Nema



Hoplolaimus: Semi-Endoparasitic Nema



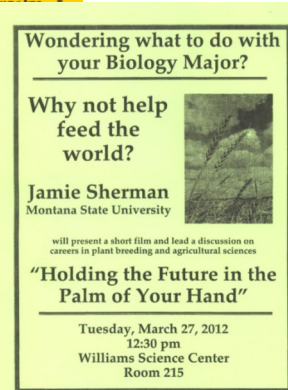
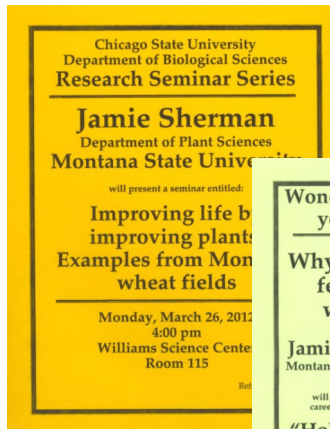
Pratylenchus: Endoparasitic Nema

Recruitment

MSU Film students (funded and advised by TCAP) created *Plant Breeding – Holding the future in the palm of your hand*. Jamie Sherman has shown the film to almost 200 students during recruitment visits. The film has had a positive impact on students, changing their view of plant sciences as a career. Film can be viewed at <http://passel.unl.edu/communities/pbtn>

All are encouraged to make use of the film in outreach or classes. An accompanying brochure is also available on the website.

Research projects and recruitment visits are attracting new students. After recruitment visits more than 10 student have inquired about internships and 2 students have applied to graduate school in TCAP programs



Meet MSI student and faculty – Dr. Shuyu Liu and Serina England



Project: One major problem decreasing wheat production in the U. S. High Plains is drought. The Texas Panhandle is the major wheat production areas of Texas and

has semi-arid climate which is similar to west Kansas, the panhandle of Oklahoma, and southeast Colorado. The annual precipitation ranges from 380 to 580 mm. In 2011 alone, drought stress resulted in the loss of more than 240 million bushels of winter wheat with a cost of about \$1.33 billion in the Southern Great Plains. A hard red winter wheat variety, TAM 111, is widely planted in these areas and shows some drought tolerance. Due to the dry conditions, insects including greenbug and Russian wheat aphid can be severe. Wheat streak mosaic virus (WSMV) transmitted by curl mites often causes damage during the whole wheat growing season. The **germplasm** line 'CO 960293-2' has the Wsm2 gene, resistant to WSMV. An F6 recombinant inbred line population was developed from the cross of CO 960293-2/TAM 111 by Texas AgriLife Research at Amarillo, TX. Serina Nelson is a senior undergraduate student majoring in Biotechnology at West Texas A&M University (WTAMU), Canyon, TX. She was supervised by Dr. Shuyu Liu, working with Texas A&M University. In collaboration with Dr. Jianli Chen (University of Idaho – Aberdeen Research and Extension Center), they are

trying to map QTL associated with drought tolerance in TAM 111 and fine map the **gene** Wsm2.

Interest in TCAP project:

With the unique drought condition in the Texas Panhandle, Texas AgriLife Researchers planted the winter wheat association panel lines (330) in Bushland (dryland) and Etter (Irrigated), TX to collect yield data and other important traits. In addition to Serina, the wheat genetic program has trained several other students from WT and Amarillo College.

Work in Progress: A set of 220 **recombinant inbred lines (RILs)** was planted in the field and irrigated with 67% field capacity. These double row lines were then infested with curl mites, which transmitted WSMV, in collaboration with the pathology group at the Amarillo Research Center. The results will be recorded for WSMV ratings if the infection is sufficient. Seed increase for this RIL population is conducted in Arizona and yield plot trials will be planted in several locations this fall.

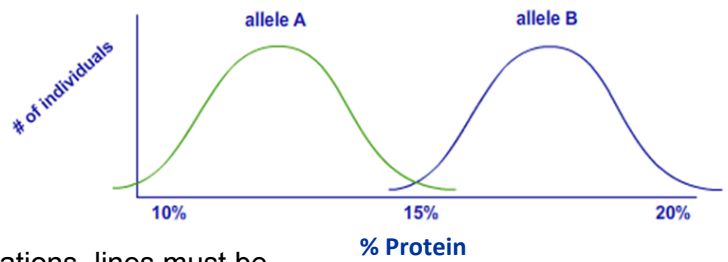


Jargon Free Zone—

Making Marker/Trait Associations: DNA

Markers can facilitate breeding by making selections more efficient. Before they can be used in breeding, markers that are good bookmarks for important **genes** must be identified. To make associations, lines must be

genotyped and phenotyped. An example of a good bookmark is in the figure above. All the individuals in the population were analyzed for a marker. In this example, there are two possibilities for this **marker** – **allele A** and **allele B**. The seed from each individual was also tested for percent protein and is graphed above (allele A individuals in green and allele B in blue). Most of the individuals with the **A marker type** have lower protein than most of the individuals with the **B marker type**, so that this marker would be a good marker to predict differences in seed protein concentration.



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.
- **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 analogy, determining the genotype would be like reading the 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.
- 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**, an important resource for TCAP, is an extensive collection of seeds representing material from around the world. TCAP participants are evaluating 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 **QTL mapping** and **association mapping**.
- **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.
- **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 identify marker/trait associations using a population from a cross between two lines (bi-parental) 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 a difference of one building block and so equivalent to a change in a single letter 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.