



Triticeae CAP
Coordinated Agricultural Project

TCap Transmission

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Funded by the USDA National Institute of Food and Agriculture

Directors notes: Gary Muehlbauer and Jorge Dubcovsky



United States Department of Agriculture
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We are entering the fifth year of the wildly successful TCAP. During the past four years the wheat and barley breeding and genetics communities have made great strides at developing breeding platforms (e.g., populations, identified QTL, marker-assisted selection and genomic selection strategies, T3 database, high-throughput genotyping, etc.) that are enabling the efficient development of new cultivars. These cultivars are beginning to be grown in farmer's fields and having an impact on rural communities. In addition, the fundamental science that the TCAP is producing will provide a foundation for the wheat and barley breeding communities for years to come. In parallel, the TCAP has trained a large cohort of graduate students in the art and science of plant breeding. These students are beginning to graduate and we wish them well as they move into the next phase of their careers. In addition, we are also working hard to engage undergraduate students (see pages 5, 6 and 12) and students from Minority Serving Institutions in research projects (see pages 11 and 12). To date, 118 Undergraduates have been mentored in research by TCAP's PIs or MSI PI's our goal of encouraging undergrads to go to graduate school is being realized. All of these activities were on display at the TCAP annual meeting held in San Diego during the Plant and Animal Genome Meeting (see page 2). The meeting captured the strength of the TCAP research and education activities. In this newsletter, we are also highlighting the identification of stripe rust resistant wheat accessions from around the world (page 3), and a study of the genetic control of tillering in barley (page 7). Finally, a sign that we have developed a world-class collaborative research project is our award for the NIFA Partnership for Program Improvement Through Global Engagement (see page 2). Everyone should be proud of the accomplishments of the TCAP, we have all done a terrific job.



TCAP Annual Meeting

The TCAP annual meeting was held on January 11, 2015 in San Diego, CA at the Town and Country Convention Center. Approximately 100 people attended the meeting including TCAP participants (PIs and students), stakeholders, the scientific advisory board (Peter Langridge, Robbie Waugh, Nick Tinker, Mike Davis and Julie Ho) and representatives from USDA-NIFA. There were three main goals for the meeting including: reporting on previous work, understanding the future needs of stakeholders and industry-university partnerships, and planning for future grants and coordinated activities. Jorge Dubcovsky (UC, Davis), Gary Muehlbauer (University of Minnesota) and Jamie Sherman (Montana State University) kicked off the meeting with presentations that highlighted the tremendous progress of the project. It was clear from these presentations that the TCAP has exceeded all original objectives. These presentations were followed by a panel discussion of industry stakeholders composed of Mike Davis (American Malting Barley Association), Glen Weaver (Arden Mills), Gary Hanning (Anheuser Busch) and Paul Kramer (Rahr Malting), and a presentation by Frank Curtis (Limagrain) on the future of industry – university partnerships. The stakeholder panel and industry-university partnership discussions provided critical feedback of stakeholder and industry needs as the TCAP begins to plan for future grants and coordinated activities. To highlight both the progress of the project and the quality of the TCAP students, eight students gave short presentations on the project. This was the highlight of the meeting as all eight students gave polished professional talks that demonstrated the high quality and impact of the TCAP research. One of the goals of the meeting was to discuss and plan future grant proposals and coordinated activities. To initiate this discussion Robbie Waugh (James Hutton Institute), Peter Langridge (University of Adelaide) and a small group of TCAP students presented their vision for research and breeding activities that the TCAP might tackle in the future. Breakout groups continued this discussion and focused on future efforts related to T3, barley phenotyping and breeding, wheat phenotyping and breeding, and genotyping. A member of each breakout group reported to entire group the major areas they saw that the group should focus on in the future. The discussion of future plans helped to solidify the directions the TCAP will pursue. Following the discussion of future activities, Nick Tinker (Agriculture and Agri-Food Canada) presented some brief comments on the scientific advisory board's assessment of the progress of the TCAP. Overall, the scientific advisory board was impressed by the research progress, the integration of genomics into breeding programs, the development and utilization of T3, and the undergraduate and graduate student training environment that the TCAP had fostered. A poster session and reception followed the formal meeting. The breadth and depth of the project was highlighted in the poster session as the students presented results from all aspects of the project.

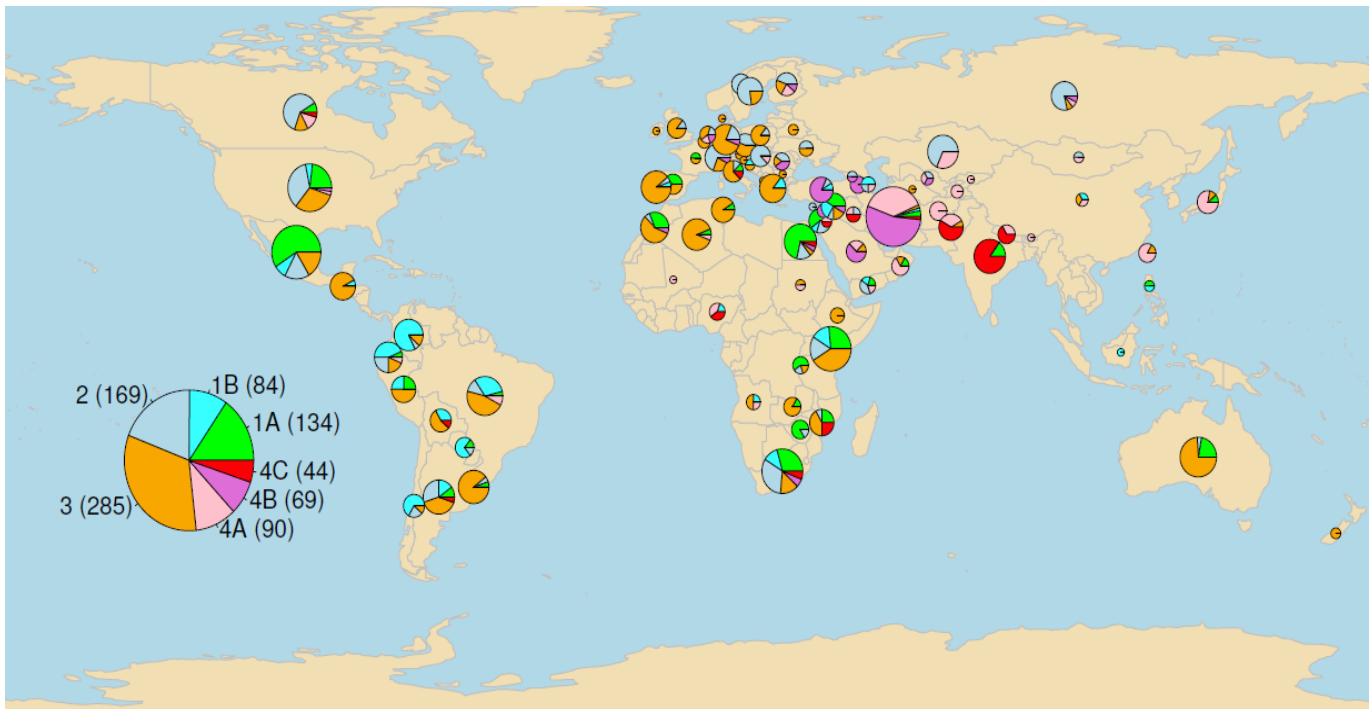
Jorge Dubcovsky receives the NIFA Partnership Award for Program Improvement through Global Engagement for TCAP October 2014.



Jorge Dubcovsky receives the TCAP award
Left: Dr. Cathie Woteki, Under Secretary for Research, Education & Economics
Right: Sonny Ramaswamy, Director NIFA

The TCAP global study on stripe rust resistance in wheat is now in press , Jorge Dubcovsky

New races of *Puccinia striiformis* f. sp. *tritici*, the causal pathogen of wheat stripe rust, are responsible for large yield losses in the USA and the rest of the world. These new races, which appeared in the USA in the year 2000, showed high virulence to previously deployed resistance genes. A group of USA wheat researchers funded by the USDA National Institute of Food and Agriculture (Triticeae-CAP, Grant 2011-68002-30029) completed a genome-wide association study using a worldwide collection of spring wheat accessions to identify new sources of resistance. This team discovered a high level of stripe rust resistance in accessions from Southern Asia, which is the likely center of origin of this pathogen. The researchers identified new resistance genes that will be useful to diversify the current resistance genes deployed by wheat breeding programs to control this devastating disease. This study provides an integrated view of global stripe rust resistance resources in spring wheat (published online in *Genes, Genomes and Genetics*: <http://g3journal.org/content/early/2015/01/20/g3.114.014563.abstract>).



The accessions originated from 87 countries on six continents and are representative of the diverse wheat growing areas in the world. The characterization of these 875 accessions using a set of non-redundant genome-wide tagSNPs



R Course offered online spring 2015

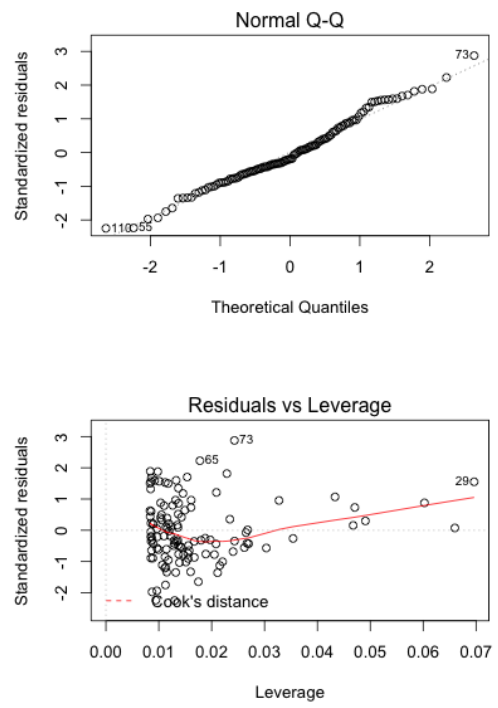
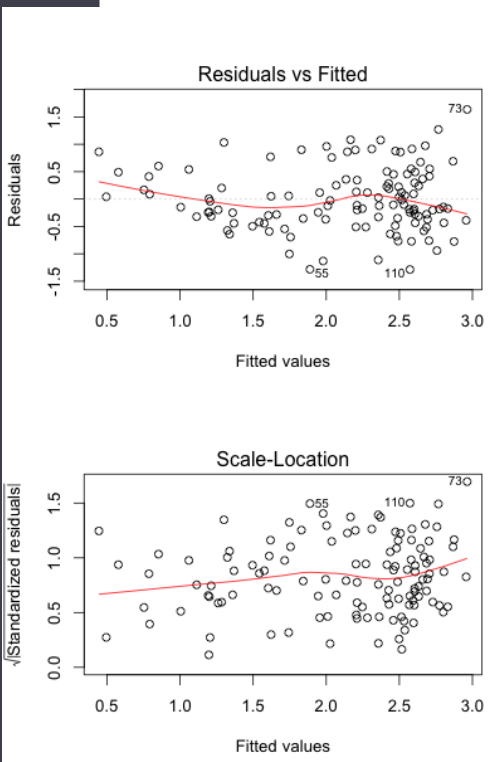
A hands-on course on a widely available software package "R" will run March 30 through April 27. You may also complete the course at your own pace. R is a computing environment that provides a wide variety of statistical and graphical programming techniques. R is highly extensible and is extensively used in academics, research and industry.

This course is designed for people in plant breeding professions, as well as those in computational/computer programming. You will work through examples of analysis of large plant breeding and genetics data sets. Our goal is to assist you in increasing use and fluency in utilizing modeling techniques and statistical environments such as R to help you in making conclusions from your large data sets.

In addition to video lectures, exercises and quizzes you will get a chance to interact with the instructors on a weekly schedule through live meetings conducted via Adobe Connect. No prior knowledge or experience with R is needed.

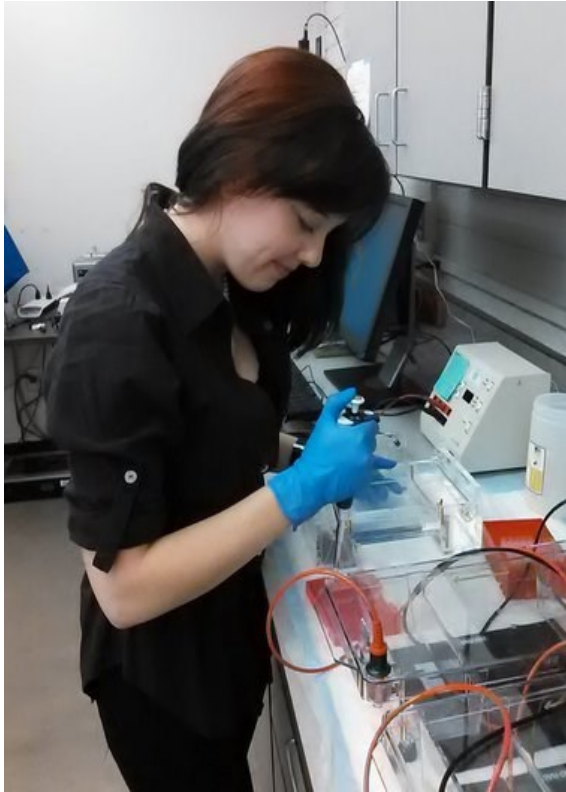
This year we will be charging a registration fee in order to allow these types of courses and the Plant Breeding Training Network to be self-sustained beyond the life of the TCAP grant. There are scholarships available in 2015.

Registration links and other information will be available from the Plant Breeding Training Network at: <http://passel.unl.edu/communities/pbtn?idsubcollectionmodule=1130274157&idindependentpage=418>



You may also contact the instructors directly with questions: Ashu Guru at agu-ru2@unl.edu or Deana Namuth-Covert at namuth-covert.1@osu.edu

TCAP Undergraduate Research Academy - Update



Undergraduate students Nikayla Strauss, Nathan Wyatt and Ge Cheng, TCAP Research Academy participants for 2014 – 2015, have been hard at work conducting research in wheat and barley and sharing their results.

Nikayla Strauss began working on water stress in wheat using KASP genotyping in Dr. Scott Haley's lab, Colorado State University. She spoke about her experiences during the fall meetings of the TCAP undergrad research community (<https://vimeo.com/112833488>). She is now focusing on a gene involved in wheat response to stem sawfly.

"I have recently started working on KASP assay development for the CHAT gene in the A and D genomes of winter wheat. I am currently working on optimizing the PCR reaction for the genome specific primers that I designed. Once the reactions are optimized, I will sequence both wild type and mutant DNA to confirm the specificity of the primers. I am also spending this time researching the CHAT gene."



Characterization of Virulence Factors in Spot Form Net Blotch

Nathan Wyatt, North Dakota State University, has been working in Dr. Tim Friesen's lab on Spot form net blotch in barley.

Spot form net blotch (SFNB) is a significant foliar disease of barley (*Hordeum vulgare L.*) A goal is to better understand the virulence of the causative fungal pathogen. Two isolates demonstrating differential levels of virulence were crossed creating a mapping population. The 118 fungal progeny were phenotyped using popular local barley varieties grown across the Upper Great Plains along with resistant and susceptible checks. Fungal genotyping was conducted utilizing genotype-by-sequencing (GBS).

The resulting map will provide information about the genetic control of SFNB virulence. Ge Cheng, has been working in Dr. Lieceng Zhu's lab, Fayetteville State University, NC., on Hessian fly resistance. Ge will give a talk to the TCAP undergraduate research community at 4 pm on Thursday, 5 March (<http://passel.unl.edu/communities/tcapundergrads>).

Nathan presented a poster at the 2015 Plant and Animal Genome conference. You can hear Nathan's online presentation to the TCAP undergrad research community at <https://vimeo.com/113955776>

TCAP Undergraduate Research Academy - 2015

The Academy provides experiences that help prepare students for graduate studies.

Program Benefits

Gain experience presenting a poster or talk in a casual setting

Receive travel funds to present research at a 2015 scientific meeting (includes conference registration, transportation, hotel and meals)

Speak with industry representatives about internships

Apply for a travel scholarship to conduct summer research at a different TCAP institution

Learn about graduate programs in plant breeding and plant science

Get guidance on the graduate school application process

Eligibility Criteria

Must have a class standing as sophomore, junior or senior

Must currently be working as research intern in a lab participating in the TCAP

Must have a desire to pursue a M.S. or Ph.D. in plant sciences

Must have a minimum overall GPA of 3.0

To Apply

TCAP faculty members should submit a one-page nomination with the following,

Name of the undergraduate nominee

Name of nominating faculty member and other faculty members involved in the students' work

Brief description of research with which the undergraduate is currently involved

Description of accomplishments that reflect the students' abilities and potential to succeed in graduate school (e.g., research problems that have been addressed, independent efforts, special recognition, poster or papers presented, etc)

Other information you believe should be considered

TCAP undergrad students should submit a one-page statement describing,

Research and career interests

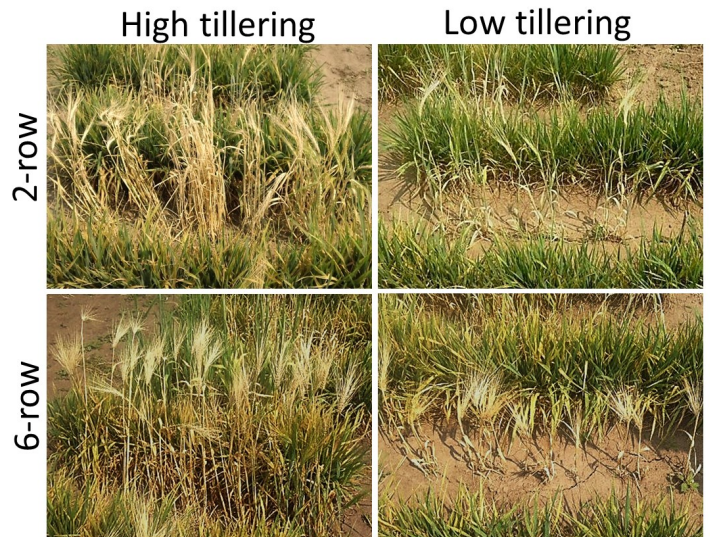
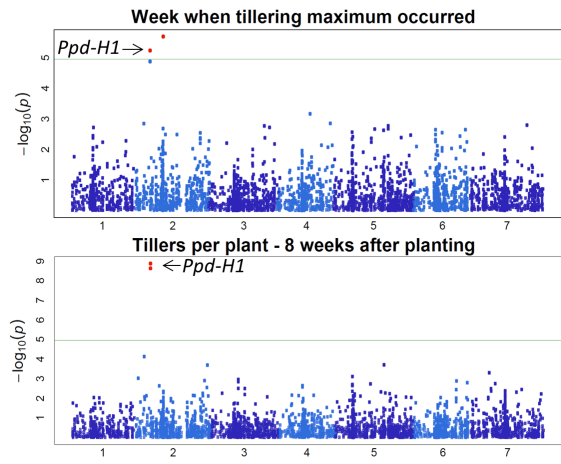
Knowledge and experience you would like to obtain by participating in the Research Academy

Submit nominations by Monday, 16 March, 2015 to brakk001@umn.edu. Students and nominating faculty will be notified by 30 March, 2015.

Allison Haaning—University of Minnesota

Association mapping of QTL for tillering traits in barley

The majority of grain yield in barley comes from tillers. Despite this fundamental relationship between tillering and yield, the underlying genetics are not well understood. In my work the global genetic diversity of barley represented in the National Small Grains Core Collection (NSGCC) was exploited to maximize detection of QTL associated with tillering. A subset of the most genetically diverse 2-row and 6-row spring barley lines was grown in a common garden in Saint Paul, Minnesota in the summer of 2014. Tillering traits including average tillers per plant, were measured for each line, weekly from two weeks until eight weeks past emergence. Additional traits, like plant height and heading date, were also measured. Flowering time was positively correlated with average tiller number and the week that tillering ceased. Furthermore, genome-wide association mapping of average tiller number and the week that tillering ceased consistently detected a QTL overlapping the *Ppd-H1* locus, which controls flowering time. These results indicate that both tillering capacity and duration are strongly influenced by flowering time in barley.



Summary of focus group results with graduate students

During the 2014 Plant and Animal Genome (PAG) meeting, Mao Thao, evaluation graduate student University of Minnesota, faculty told three focus groups with a total of 10 graduate students. Graduate students were asked about their perceptions of online education and the Plant Breeding Training Network (PBTN), experiences with the T3 database, and experiences in the TCAP. The following are key findings:

Perceptions of online education & the PBTN

1. Students felt the PBTN had good resources that are specifically focused on plant breeding. While other resources (eg. eXtension) were more general.
2. Of the PBTN resources the recorded webinars were most valued.

Student #1: *"The thing that I like about the PBTN – is how the webinars are archived."*

Student #2: *"Yeah, that's really nice."*

Student #1: *"Because sometimes you can't always make it to attend the webinar, but you can go back and watch it on your own time."*

3. The majority of the students have used the online meeting room, independent of attending a course or webinar, primarily for meetings with faculty members, collaborators, and/or other students.

Suggested additions to PBTN:

- video tutorials on data management, data analysis, and R coding
- list of upcoming publications resulting from the TCAP to help inform their work
- organization of the recorded webinars by section
- points system for completing courses or webinars to encourage greater collaboration
- feature to ask an expert questions
- peer-to-peer messaging.

Experiences with the T3 database

The T3 database serves as a repository for students to upload their data and download their collaborator's data. Students reported infrequent use of the data analysis tools available.

Suggested Improvements for T3:

Students had many suggestions for improving T3, including having video tutorials on how to upload and download data, improving the online data analysis tools to do more advanced analyses, having a cheat sheet of similar terms for SNP markers, and having updated user guides when T3 features were changed or updated.

Experience in the TCAP

Students overwhelmingly felt the CIMMYT trip was the most formative experience for them.

"I really enjoyed the experience of going to the Borlaug 100 Summit in, uh, Mexico this past March. It was excellent to gather all of the TCAP students and they decided to pay for students to go down there and have that remarkable experience – remarkable cultural experience. And then, seeing some of the research that is going on in the premiere wheat research facility in the world and maybe be able to take some ideas from there interacting with scientists from around the world – be able to bring some of that into our own research."

Students felt it was worthwhile to be part of the TCAP, primarily because they have broadened their network of faculty members and students in plant breeding. Two students reported that they specifically chose their university to be part of the TCAP.

"There's a lot of grad students I know [at my institution] who have great projects and things like that, but they don't get exposure to other folks around the country, around the world, doing the same things that they're doing. And every year, we come here to TCAP and there's 50-something PIs and a couple dozen graduate students all kind of going after the same goal."

Suggested additions to TCAP

- internship opportunities,
- opportunities to visit collaborating labs
- greater focus on applied plant breeding (e.g. writing skills, basic agriculture).

TCAP graduate students meet to share research results and plan future activities

Friday afternoon on January 9th in San Diego about forty graduate students and professors participating in the TCAP met **11** students gave short talks describing the TCAP research . The talks detailed research involving from virus induced silencing to high throughput phenotyping. Marker trait associations were reported involving WUF NUE and disease resistance. The students then participated in a grant planning session. Jamie Sherman led a discussion on utilizing logic models for grant planning . The students broke into groups to develop ideas for outputs for the next generation of CAP grants. A group of students synthesized the ideas and are reported below.

TCAP Grad Student Meeting Summary

1. Implement web based system to integrate genotype and phenotype
 - T3 has many tools, but users aren't comfortable navigating the site and utilizing them. Better, updated, and accessible tutorials could be hosted in PBTN. Many of the existing tutorials and instructions are outdated.
2. Develop and implement PBTN
 - Develop community where students can collaborate and work through research problems, data handling or analysis. Preserve these discussions and webinars for students to refer back to. Good examples: Association Mapping course
 - Encourage students to travel and work at other locations and see other environments and programs. Funds were available, but students didn't know about this opportunity.
 - Set up funds for graduate student off season exchanges to other research programs, including genotyping and quality labs
3. Implement sequence based genotyping
 - Lots of work has been done, but we need a pipeline to work with this data that is available to all skill levels
 - pipelines can be shared via objective 2
4. ID new valuable alleles in diverse wheat and barley
 - This goal was successful but it became obvious that for some traits such as NUE more investigation is needed to find more than major genes.
 - NAMs can be used to dissect traits. For traits such as disease resistance, we can move the focus to #5
5. Accelerate breeding using markers
 - TCAP produced many populations that have been well characterized with markers, but focus was on genotyping. Strong focus on high throughput phenotyping is needed to realize value of markers.
 - Populations (NAMs) were developed and will be integral for transitioning from associations to confirmed QTL. QTL can be evaluated in isogenic backgrounds to find actual allele effects
6. High throughput phenotyping (HTP)
 - Packaging CSR tools so that they can be used efficiently and collaboratively
 - Methods need to be standardized
 - Create HTP hubs that can serve multiple participants rather than each university struggling with its own equipment.

One of the best things about this grant was the heavy student involvement in planning, decision making, and follow up. Students were treated as full participants in the grant rather than just the research labor. This was **GREAT** experience for us. Thank you! As the next grant is developed please continue to empower students to be part of the grant writing process, education component, and research objectives. Areas that could include larger student roles: developing teaching materials, developing standard operating procedures for research goals, and writing sections for annual reports.

An Undergraduate-to-Graduate Student Transition Beyond 1,200 Miles

Jeff Neyhart

During one of the first meetings I had with my undergraduate advisor at Cornell University, he asked if I intended to go to graduate school. Not wanting to seem without direction, and figuring I could change my plan as I sorted out my intentions, I gave an uneasy “yes.” Graduate school was just not a relatable goal for me; neither of my parents received a graduate degree, and I knew very few others who had attended. Nevertheless, as of this writing, I am in my first year as a Ph.D. student at the University of Minnesota, no less a freshman to my environment now than when I actually held the title. While I have found a comfortable niche in graduate school and certainly have made the right choice, I have yet to fully complete the transition. Throughout it, however, I have taken note of the changes and the similarities, and I hope to provide some perspective to those considering this next step.

At Cornell, I worked on an individual research project as a part of the TCAP undergraduate program. Even though there were setbacks and the outcome was not as hoped, I thoroughly enjoyed the experience because I had ownership in the direction and objectives of the project, a motivational responsibility for me. When first starting in Minnesota, I was lucky enough to spend some time rotating through several lab groups. One of the deciding factors for me joining the barley breeding group was that I would still have that level of ownership in my research. The transition has been much smoother in this regard because I identified both an aspect of research that motivated me and an advisor that provided a comfortable level of interaction and mentoring. I tried to be proactive and ensure a more enjoyable change to graduate school, however some aspects of this were not under my control.

Over the summer between Cornell and Minnesota, I ran into an old high school teacher, who, after learning of my plans to attend graduate school, remarked that it was a great way to delay getting a “real job.” I find this comment has stuck with me, mainly because I disagree with its definition and have come to consider graduate school a real job in itself. There are still expectations and demands, and like any other job there focus expands to include the facets of life largely ignored in college. One now must balance the requirements of a full-time research job with classes, while also becoming more financially responsible and meeting other obligations, perhaps even for a family or with community. Being a graduate student requires intense self-motivation; one is not monitored pervasively, a reality that places the accountability for completing tasks squarely on oneself. For me, it is not difficult justifying calling graduate school a “real job” when nearly every other aspect of life gains the distinction.

While the responsibilities of graduate school have made the transition more “real,” so too has getting to know my cohorts. In college, the people I associated with regularly were very similar; they might have had different majors or hometowns, but we were all at the same relatable stage in our lives. Now, though, I appreciate how heterogeneous one’s colleagues become. Some people leave the comforts of their home, home state, or even home country in making the transition, while others are less than an hour from where they grew up. Some bring a significant other, or a marriage, or even children of their own. Some are older with life or work experience under their belts. The similarities are now mostly defined by a passion for research in the program subject, as well as personal interests, while as a group, the other life dimensions are much more sundry. It is incredible for me to interact with such a diverse group of people whose different ideas and viewpoints can be counted on to provide a new way to frame, or a different angle to, my own work.

It is fitting that I write this during my program’s new student recruitment season, as it reminds me of when I interviewed here. One point of emphasis that applies in any year and at any school is the importance of asking graduate students for perspective. From my time interviewing then to meeting prospective students now, I have learned that graduate students are nearly always willing to talk, and I encourage those considering graduate school to spend time with students already there. It is difficult to get appreciable advice about the transition from undergraduate to graduate education from any other source.



MSI at PAG by Silvano Occheyá—Texas A&M

Genetic Mapping of Resistance Gene to Wheat Streak Mosaic Virus and tolerance to drought

For the last couple of years we have been working to finely tag Wsm2 gene, which confers resistance to Wheat Streak Mosaic Virus (WSMV), one of the biotic stresses in the U.S. Southern Great Plains. The primary objective is to improve yield and genetic gain through development of markers for rapid assaying of genotypes for resistance to WSMV. A biparental mapping population of 217 RILs was developed from a cross between CO960293-2 and TAM 111. TAM 111 was developed by Texas A&M AgriLife Research and CO960293-2 was developed by Colorado Agricultural Experiment Station. A total of 90 K SNP markers were used for genotyping using Illumina's Infinium genotyping assay. The genotyping was conducted at the USDS-ARS genotyping lab in Fargo, ND. The population together with checks were screened for WSMV in 2013 and replicated in 2014 in the growth chamber at Kansas State University Agricultural Research center in Hays, KS with disease severity rating taken at 21 and 28 days post infection. The Wsm2 gene was mapped on chromosome 3BS with nine flanking markers within 2 cM. Validation studies were done using the KASP platform. Six array SNP markers were converted to KASP markers and used for validation to verify the persistence of Wsm2 in an independent population of known resistant and susceptible lines. In all the cases, the markers grouped the genotypes into two distinct groups corresponding to resistant and susceptible genotypes. A journal paper covering the WSMV work has been prepared and will be published soon.

Our second study focuses primarily on drought tolerance with the ultimate objective of improving yield through introgression of drought tolerance QTL into stem rust resistant lines from Kenya. The donor parent for DT allele is TAM 111, a known drought tolerant and widely planted variety in the Southern Great Plains of U.S. Phenotyping was conducted under both drought and well-watered environments to obtain data for mapping as well as select drought tolerant wheat lines that have no yield penalty when environmental conditions are favorable. Data were collected from seven environments during 2013 and 2014. We have mapped several QTL for grain yield, yield components and biomass on chromosome 1A and 2B. Validation of the tagged QTL is ongoing with new sets of phenotypic data expected this year. Crosses between TAM 111 and three spring wheat cultivars from Kenya possessing Ug99 resistance have also been made. The crosses between spring wheat from Kenya and winter wheat from the U.S. is important for potential improvement in yield as well as genetic diversity. A backcross population to respective parents are being tested at CIMMYT/Kenya Agricultural and Livestock Organization, Njoro, Kenya and in the U.S. under both stress and non-stress environments.

This project was started with the funding from T-CAP Education Network. The proposal was prepared by Dr. Shuyu Liu from Texas A&M AgriLife Research and Dr. Jianli Chen from University of Idaho. It was conducted by a minority undergraduate student, Ms. Serina Nelson, from West Texas A&M University. After she graduated, a Ph. D. candidate, Mr. Silvano Occheyá continued the project. The Texas wheat team developed a proposal and it was funded by Monsanto Beachell-Borlaug International Scholarship. Dr. Liu and Dr. Amir Ibrahim are co-chairs and Dr. Jackie Rudd and Dr. Qingwu Xue are the advising committee members for Mr. Occheyá's research.

In addition to the MBBIS, Silvano was also selected as the Borlaug Next Generation Delegate in 2014. He won the graduate student Research award from Texas Plant Protection Association in 2014. In collaboration with CIMMYT-Kenya, Dr. Liu and Mr. Occheyá were awarded the Borlaug Leadership enhancement in Agricultural programs in 2014 from USAID. Mr. Occheyá was invited to The Agriculture Biotechnology International Conference in 2014 held at Saskatoon, Canada and to present his research in the Plant Breeding Symposium held on February 19, 2015 in College Station, Texas.

The T-CAP Plant Breeding and Education Network really help students to learn and know from whom to learn. It bridges the gaps within the U.S. and across countries. The next step for Mr.

Occheyá's work is to validate what he found from a biparental mapping population using the T-CAP winter wheat association panel lines tested in the Great Plains including Texas.



Silvano was recording in the field.



The wheat genetic group finished the field sample collection



The wheat genetic group was cutting field samples.



MSI Experience at PAGXXIII

Leticia Meza

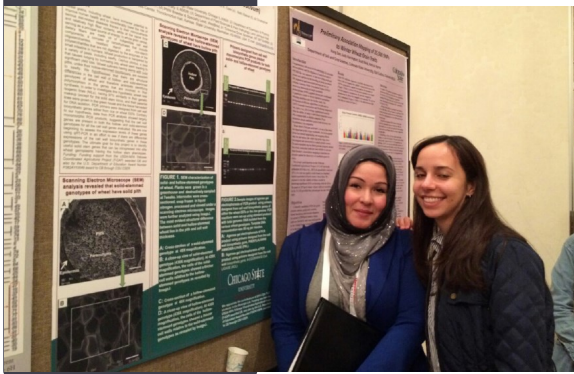
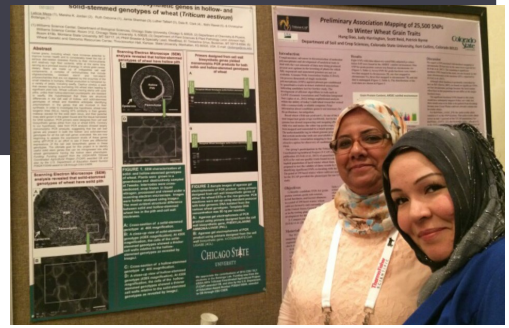
As an undergraduate student, I immerse myself into my studies and research. Although it is well intentioned, routines can sometimes lend themselves to tunnel vision. Recently, that was remedied by attending my first professional conference, The Plant and Animal Genome (PAG) XXIII Conference and the Triticeae CAP (TCAP) annual meeting. It was a great experience to attend and present my poster at PAGXXIII as well as the TCAP annual meeting. It was an extremely valuable and motivating experience as it expanded my forward looking lens and excited me to continue working diligently towards my goals.

I have been involved in wheat research at Chicago State University, under direction of Dr. Christopher Botanga, for over a year and a half. Working with Dr. Botanga on different wheat projects has been such a wonderful and impactful addition to my academic life. He has exposed me to viable pathways in agro-research and plant breeding/genetics, taught me the potential global impact, and the benefits of pursuing research. As an aspiring plant scientist, participating in PAGXXIII and the TCAP meeting was an important milestone, putting me on a path to my career goals. Seeing all the research that is being conducted in genetics and plant breeding on massive scale reminds me of the arduous challenges our world faces and how science can resolve some of these challenges. It was positively overwhelming to be among such great thinkers, designers, and problem solvers in an arena as massive as the PAG.

So much was offered to me at the PAGXXIII: I was exposed to cutting edge genome projects, new biotech tools, and international research projects. I met many people from around the world, including Germany, Australia, Pakistan, and Canada, some of which I intend on building relationships with and who are involved in wheat research. During the poster session, I was pleased to find many people were curious about my research project titled, "Evaluation of cell wall biosynthetic genes in hollow- and solid-stemmed genotypes of wheat (*Triticum aestivum*)" including a research investigator who focuses on plant breeding and crop production issues in cocoa and wheat at a very well known snack company in the Midwest. Similarly, participating in the annual TCAP meeting was a positive experience. It was impressive and thought provoking to see an immense collective effort to improve wheat and barely production. It was wonderful to hear a progress report on all that TCAP has accomplished from the leaders of TCAP initiatives and the USDA. Exposure to aims, funding, and future plans are not normally part of an undergraduate experience, but I found it gave me a well-rounded appreciation for research initiatives. I also gained so much insight into the current and future needs of wheat and barley research from both the public and private sectors. More notably, I gained an appreciation on the importance of cultivating these partnerships. Participating in the annual TCAP meeting also allowed me to interact with others within the TCAP community. It was great to have pleasant encounters with Dr. Sherman and Dr. Talbert; they are collaborators on

the project I am working on, but I have never had the chance to meet them in person prior to this meeting. I held engaging conversions with graduate students from Montana State University and Colorado State University with whom I hope to build collaborative relationships.

I am fortunate to have such wonderful educational and mentor experiences that empower and motivate me to pursue my research and career goals in the plant sciences. I look forward in participating in the PAG XXIV and the next annual TCAP meeting, as this year's participation has truly enhanced my research experience and gave me a new found appreciation for the work we are doing.



Student research presentations on PBTN

Graduate Students will be presenting their TCAP work, below is the schedule, please show your support to the graduate students and attend their presentations when you can!

All presentations are 3-4pm central time at <https://carmenconnect.osu.edu/pbtn>

March 25 – Sruthi Narayanan

April 1 – Nicolas Cobo

April 8 – David Chappel

April 15 – Tyson Howell

April 22 – Andrea Varella

April 29 – Allison Haaning

May 6 – Ana Poets

May 13 – Austin Case

May 20 – Rui Wang

May 27 – Sarah Grogan

June 3 – Matthew Haas

June 10 – Andres Salcedo

June 17 – Roshan Acharya

June 24 – Steven Carlsen

Spring Course—Entering Mentoring

Entering Mentoring is a eight week module that will be offered beginning April

6. The **Entering Mentoring Seminar** will accelerate the process of learning to be a mentor by providing an intellectual framework, an opportunity to experiment with different mentoring techniques, a forum to discuss mentoring dilemmas, and second-hand exposure to more students and situations through group sharing. Attendees must be actively involved in mentoring to participate. Required Group discussions of reading materials and experiences will be held on Mondays from 1- 2pm central online beginning April 6th. Interested parties should become a member of PBTN

<http://passel.unl.edu/communities/pbtn> and enroll in Entering Mentoring <http://ati.osu.edu/node/1607>

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.
- **Canopy Spectral Reflectance (CSR)** is a new phenotyping tool TCAP is exploring. It is based on the observation that plants under stress reflect different colors of light. Measuring the light reflected might be a way to predict plant performance.
- **Canopy Temperature Depression (CTD)** plants need CO₂ for photosynthesis and acquire it through window-like structures in leaves simultaneously releasing O₂ and H₂O. When a plant is water stressed, the windows in the leaves through which this gas exchange occurs must close, reducing photosynthesis and thereby reducing yield. When the windows are open not only can photosynthesis occur, but also as H₂O is released the temperature around the plant decreases due to evaporation. CTD can act as a proxy for measuring the 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.
- **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.