



Triticeae CAP
Coordinated Agricultural Project

Tcap Transmission

Winter Issue

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Director's notes – Gary Muehlbauer and Jorge Dubcovsky



The TCAP is an ambitious project that seeks to identify and exploit novel **genes** for wheat and barley improvement to mitigate the impact of climate change. The TCAP is a diverse group of researchers focused on developing wheat and barley that exhibit high levels of nitrogen and water use efficiency, and disease resistance. As the TCAP proceeds we seek to take advantage of the



germplasm collections and breeding populations coupled with **genomics** and the T3 database to develop more efficient wheat and barley breeding. At the beginning of the second year overall progress has been excellent. The Plant Breeding Training Network is developed, which promises to reinvent and reinvigorate plant breeding graduate education on a nation-wide scale. The Triticeae Toolbox (T3) is developed and is being adopted as the hub for all wheat and barley breeding activities. **Genotyping** of the wheat and barley National Small Grain Core Collections with ~9K **SNP markers** resulted in over 40 million data points. These datasets will be instrumental in the exploitation of novel variation for barley and wheat improvement. More advanced **genotyping** technologies are also in development, including **gene capture assays** and **genotyping by sequencing** for both barley and wheat. These technologies promise to revolutionize our ability to genotype **germplasm** at an unprecedented density and scale. Molecular breeding approaches to increase the breeding efficiency are being adopted in both wheat and barley. We have also completed our initial set of trials for nitrogen and water use efficiency, including the first set of analyses to detect marker-trait associations. The identification and exploitation of disease resistant **germplasm** is another objective of the project, which has begun with evaluation of wheat and barley **germplasm** and detection of marker-trait associations in wheat for stem, stripe and leaf rust. The first year has been tremendously successful with regards to data generation. During the second year, we expect initial outputs from the project as we analyze the data and begin to implement novel approaches to wheat and barley breeding.

Definitions to all red words can be found in the "Jargon Free Zone" on page 2

24X Morex Barley Shotgun Assembly Now Available for BLAST

By: Tim Close

A partial **genome sequence** assembly generated using the software SOAPdenovo (soap.genomics.org.cn/soapdenovo.html) from 24X coverage of the Morex barley genome is now available for BLAST through www.harvest-blast.org and sequence retrieval through www.harvest-web.org/utimenu.wc including an option to receive the entire assembly. This assembly is the outcome of a USDA-NIFA project entitled

"Advancing the Barley Genome" and is but one of many rapidly developing advances from the International Barley Sequencing Consortium (www.barley-genome.org). For additional information on the 24X Morex barley assemble, please refer to Barley Genetics Newsletter (2011) 41:10-11 (<http://wheat.pw.usda.gov/ggpages/bgn/41/Alpert.htm>)"

To CAP it off—Year One

- National small grain collection genetically characterized with 40 million data points that will be used to identify unique **genes** for wheat and barley improvement
- New markers are under development that will provide even higher resolution for genetic characterization with improved efficiency
- First year field trials completed and will serve as a basis for trait/marker associations.
- New populations (eg. **Nested association mapping populations**) are under development that will be characterized with markers and in the field to make and/or confirm trait/marker association
- Triticeae Toolbox under development and adoption to empower breeders
- Plant Breeding Network developed and actively attracting and training students

Jargon Free Zone –

All areas of expertise have a specific vocabulary. Practitioners of a specialty become so familiar with that vocabulary they often forget it has no meaning for most people. It is our goal in the jargon free zone to explain some of the vocabulary particular to the TCAP. In TCAP articles look for red words that will be explained on this page. If there is TCAP jargon you would like to be explained in the future send a request to jsheman@montana.edu.

Germplasm is a collection of genetic resources, which in wheat and barley is usually a collection of seed. An important resource for the TCAP, the **National Small Grain Core Collection**, maintains, evaluates and distributes 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.

Deoxyribonucleic acid (DNA) is the genetic material for most organisms. An organism's complete set of DNA is called its **genome**. **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. A specific instruction is analogous to a specific gene. 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.

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. An important part of the TCAP project is to make **marker/trait associations**. In other words, identify good bookmarks for the instructions that are important. Once marker/trait are made markers can be used to make selection in both **marker assisted selection** and **genomic selection**. The TCAP is employing several methods to make marker/trait association including Quantitative trait analysis in bi-parental populations and Association mapping. These two techniques vary in the types of populations used and the statistical methods. **Nested Association Mapping** is a hybrid technique that uses attributes of both.

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 determin-

ing the phenotype is like testing the product created after following the instructions. A new phenotyping tool the TCAP is exploring is called **Canopy Spectral Reflectance (CSR)**. 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.

DNA is composed of building blocks (**nucleotides**) that you can think of as the letters making up the instruction book. The instruction book for wheat is composed of 16 billion letters or nucleotides(= **16GB**). **A single nucleotide polymorphisms (SNPs)** is a difference of one letter. An advantage of **SNPs** is more potential differences and so more markers at a higher resolution, making it easier to make marker/trait associations.



It is the order of the building blocks that store the genetic information. Reading that order is called **sequencing**. 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**.

TCAP Annual Meeting

By: Gary Muehlbauer

The TCAP held its annual meeting in San Diego, CA on January 15. TCAP co-PIs, students, stakeholders, the scientific advisory board and USDA administrators attended the meeting. There were two primary goals of this meeting including: (1) reporting our progress to our stakeholders, scientific advisory board and to the USDA-NIFA administrators; and (2) to organize the activities for the coming year. The morning was devoted to reporting progress and the afternoon was devoted to planning future activities.

The meeting began with Jamie Sherman (Montana State University) providing an overview of the education effort. The overall goal of the education team is to attract and train a new generation of plant breeders while supporting continued development of plant breeding professionals through development and implementation of Plant Breeding Training Network. Specific activities to recruit new students into plant breeding include: collaboration with Minority Serving Institutions, mentoring undergraduates, creating educational materials with plant breeding examples, and producing educational materials and recruitment films. Specific activities to train graduate students include: immersing students in plant breeding programs, creating an online collaborative space, providing online courses and workshops, and supporting scientific meeting attendance. Some examples of these activities are on pages 7-11 of this newsletter. Currently, the TCAP is funding 24 Ph.D. students 22 of them attended the meeting. Jamie described the development and implementation of the Plant Breeding Training Network. She also showed a recruitment film about plant breeding featuring TCAP co-PIs that students from Montana State University developed.

Shaioman Chao (USDA-ARS, Fargo, ND), Gina Brown-Guerdira (USDA-ARS, Raleigh, NC) and Eduard Akhunov (Kansas State University) updated the group on the **genotyping** efforts. Shaioman described **genotyping** the National Small Grain Core (NSGC) Collections for 4,416 wheat and 2,417 barley accessions with 9 K **SNPs**. For barley, 6,915 **SNPs** were polymorphic resulting in over 16 million data points! For wheat, 5,634 **SNPs** were polymorphic resulting in almost 25 million data points!! These data have been used to select parents for the **nested association mapping populations** and will be used for further genetic exploration of the core collections. Gina discussed the marker assisted selection and genomic selection work being conducted to improve barley and wheat **germplasm**. Genomic selection is being conducted for low temperature tolerance in barley. Marker assisted selection is being conducted in both wheat and barley. In wheat, 2000 lines have been assessed with 48 **SNPs**. In barley, 4,000 lines have been assessed with 48 **SNPs**. These efforts will accelerate over the next year as more samples begin to arrive at the **genotyping** centers. Finally, Eduard discussed the development of wheat and barley **gene capture assays** that Roche/Nimblegen is developing and our **genotyping by sequencing (GBS)** efforts. The gene capture development is a large international collaboration of wheat and barley

geneticists. The wheat assay has the capacity to capture ~110Mb of gene space and the barley assay has the capacity to capture ~90 Mb of gene space. The initial design was tested by Roche/Nimblegen and performed at a high level. The TCAP will begin to test the capture assays in the near future. We plan to use this technology to further understand the genetic diversity in wheat and barley **germplasm** collections. Eduard also described **GBS** technology and its use in mapping biparental populations and **genotyping germplasm** collections. **GBS** is an exciting technology and has the potential to vastly increase our capacity to genotype. (Page 3)

There were short updates on the phenotyping efforts on water use efficiency by Luther Talbert (Montana State University) and Pat Hayes (Oregon State University), on nitrogen use efficiency by Kevin Smith (University of Minnesota), and Clay Sneller (The Ohio State University), and on diseases by Brian Steffenson (University of Minnesota) and Mike Pumphrey (Washington State University). One highlight was the markers identified associated with resistance to wheat stem, stripe and leaf rust. These markers will be validated and then moved into marker-assisted selection programs with the intent to increase the level of resistance in wheat to these diseases. Jianli Chen (University of Idaho) updated the group on the evaluation of the wheat NSGC core for water and nitrogen use efficiency. She also presented a preliminary analysis showing marker-trait associations for several agronomic traits including yield. In addition to the phenotyping update, Kevin and Luther also presented the progress of developing **nested association mapping populations** in barley and wheat, respectively. These populations will be important for identifying and exploiting genetic diversity from the NSGC Collections.

The use of canopy spectral reflectance to measure water and nitrogen use efficiency was also a topic of the meeting. Tyson Howell (UC, Davis, graduate student in the Dubcovsky lab) gave a summary of his characterization of drought resistance derived from the wheat 1RS:1BL translocation. His work showed that drought tolerance was conferred by the rye 1S chromosome and that canopy spectral reflectance was useful for identifying drought tolerant plants. There was discussion about the best instrument for measuring canopy spectral reflectance, with some groups deciding to purchase a new more user friendly instrument.

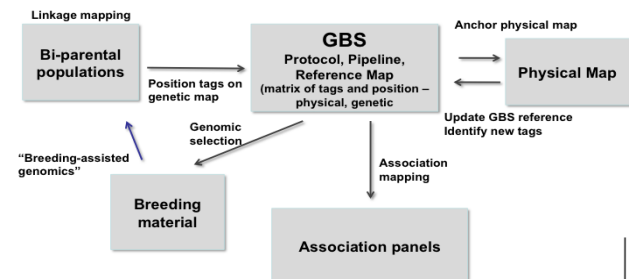
The afternoon portion of the meeting was spent planning for the coming year. Three breakout groups composed of the wheat breeders, barley breeders and the **genotyping** team met. The T3 database team members were split between the groups. The meeting ended with comments and suggestions from the scientific advisory board that were overall positive.



A New Genotyping approach for Wheat

By: Jesse Poland

The wheat genome is extremely large and complex at 16 **gigabases (GB)** (in comparison the Rice Genome = 0.46 GB and the Human genome = 3 GB), which has limited the pace of developing molecular markers for use in wheat genetics and marker assisted breeding. A new approach for **genotyping** using “next-generation sequencing” has recently emerged and



Integration of new GBS approach with genetic mapping and breeding objectives for wheat germplasm improvement.

is now being applied to wheat **genotyping** in the lab of Dr. Jesse Poland. This new approach termed “**Genotyping-by-Sequencing**” or **GBS** utilizes the capacity of new sequencing machines such as the Illumina HiSeq2000, which can generate sequence data for hundreds of millions of short pieces of DNA in a single run. By combining this sequencing capacity with “DNA barcodes”, many samples can be sequenced at the same time, greatly increasing the throughput and decreasing the per-sample cost. The first results from wheat indicated that **GBS** is a very useful approach even in this large complex genome. Dr. Poland has been able to identify tens of thousands of useful molecular markers from the wheat data. This method for wheat **genotyping** along with the discovered markers can now be put to use in wheat breeding programs for marker-assisted selection of superior wheat breeding lines.

Poland, J.A., Brown, P.J., Sorrells, M.E. & Jannink, J.-L. Development of High-Density Genetic Maps for Barley and Wheat Using a Novel Two-Enzyme **Genotyping-by-Sequencing** Approach. *PLoS one* 7, e32253 (2012).

Triticeae CAP publications

Multiple publications are being written describing the work based on the TCAP or tools developed by the TCAP. A complete list of all publications can be found at the TCAP website (<http://www.triticeaecap.org/>). Below is a list of some recent publications:

Li, P., J. Chen, and Pute Wu. 2011. Evaluation of Grain Yield and Three Physiological Traits in 30 Spring Wheat Genotypes across Three Irrigation Regimes. *Crop Sci.* 52:1-12.

Pradhan G.P., P.V.V. Prasad, A.K. Fritz, M.B. Kirkham, and B.S. Gill. 2011. Response of Aegilops species to drought stress during reproductive stages of development. *Functional Plant Biology*, 2012. 39:51-59. <http://dx.doi.org/10.1071/FP11171>

Edwards, J.T., R.M. Hunger, E.L. Smith, G.W. Horn, M.S. Chen, L. Yan, G. Bai, R.L. Bowden, A.R. Klatt, P. Rayas-Duarte, R.A. Osburn, J.A. Kolmer, Y. Jin, D.R. Porter, K.L. Giles, B.W. Seabourn, M.B. Bayles, and B.F. Carver. 2012. ‘Duster’ wheat: A durable, dual-purpose cultivar adapted to the southern Great Plains of the USA. *J. Plant Reg.* 6:1-12.

Morrell, P., L. Buckler, Edward S. and R.-I. Jeffrey. 2011. Crop genomics: Advances and applications. *Nature Reviews Genetics*, advance online publication. doi:10.1038/nrg3097.

Baenziger P.S., I. Salah, R. S. Little, D. K. Santra, T. Regassa, and M. Y. Wang. 2011. Structuring an efficient organic wheat breeding program. *Sustainability*. 3(8):1190-1206.

Baenziger P.S., R. A. Graybosch, T. Regassa, L.A. Nelson, R. N. Klein, D. K. Santra, D.D. Baltensperger, L. Xu, S. N. Wegulo, Y. Jin, J. Kolmer, M.S. Chen, and G. Bai. 2012. Registration of ‘NE01481’ hard red winter wheat. *Journal of Plant Registrations*, 6:1:49-53, doi:10.3198/jpr2011.02.0101crc

Baenziger P.S., R. A. Graybosch, T. Regassa, L.A. Nelson, R. N. Klein, D. K. Santra, D.D. Baltensperger, J. M. Krall, S. N. Wegulo, Y. Jin, J. Kolmer, M.S. Chen, and G. Bai. 2012. Registration of ‘N104421’ hard red winter wheat. *Journal of Plant Registrations*. 6:1:54-59, doi:10.3198/jpr2011.02.0102crc

Gauch, Jr., H.G, P.C. Rodrigues, J.D. Munkvold, E.L. Heffner, and M.E. Sorrells. 2011. Two new strategies for detecting and understanding QTL by environment Interactions. *Crop Sci.* 51: 96-113. (2005- 05130)

Heffner, E.L., J.L. Jannink, and M. E. Sorrells. 2011. Genomic selection accuracy using multi-family prediction models in a wheat breeding program. *The Plant Genome*. 4:65-75. (2005-05130)

Heffner, E.L., J.L. Jannink, H. Iwata, E. Souza, and M.E. Sorrells. 2011. Genomic selection accuracy for grain quality traits in biparental wheat populations. *Crop Sci.* 51:2597-2606. (2005- 05130)

Somyong, S., J.D. Munkvold, J. Tanaka, D. Benschler, and M.E. Sorrells. 2011. Comparative genetic analysis of a wheat seed dormancy QTL with rice and Brachypodium identifies candidate genes for ABA perception and calcium signaling. *Funct Integr Genomics* 11:479–490. (2005-05130)

Sorrells, M.E., J.P. Gustafson, D. Somers, S. Chao, D. Benschler, G. Guedira-Brown, E. Huttner, A. Kilian, P.E. McGuire, K. Ross, J. Tanaka, P. Wenzl, K. Williams, and C.O. Qualset. 2011. Reconstruction of the synthetic W9784 x Opatá M85 wheat reference population. *Genome* 54:875-882. (2005- 05130)

Yu, L-X, A. Lorenz, J. Rutkoski, R.P. Singh, S. Bhavani, J. Huerta-Espino, and M.E. Sorrells. 2011. Association mapping and gene-gene interaction for stem rust resistance in CIMMYT spring wheat germplasm. *Theor. Appl. Genet.* 123:1257-1268. (2005- 05130)

Heslot, N., H-P. Yang, M.E. Sorrells, and J-L. Jannink. 2012. Genomic selection in plant breeding : A comparison of models. *Crop Sci.* 52:146-160. (2005- 05130,2011-68002-30029)

Yu, L-X, A. Morgounov, R. Wanyera, M. Keser, S. Kumar Singh, and M.E. Sorrells. 2012. Identification of Ug99 Stem Rust Resistance loci in Winter Wheat Germplasm Using Genome-Wide Association Analysis. *Theor. Appl. Genet.* Accepted. (2005- 05130,2011-68002-30029)

Leng, Y. and Zhong, S. 2012. Sfp-type 4'-phosphopantetheinyl transferase is required for lysine synthesis, tolerance to oxidative stress and virulence in the plant pathogenic fungus *Cochliobolus sativus*. *Molecular Plant Pathology*. doi:10.1111/j.1364-3703.2011.00756.x

Successful Adoption of Spring Wheat Cultivars with Moderate Resistance to FHB by Growers in the North Central Region

By Jim Anderson

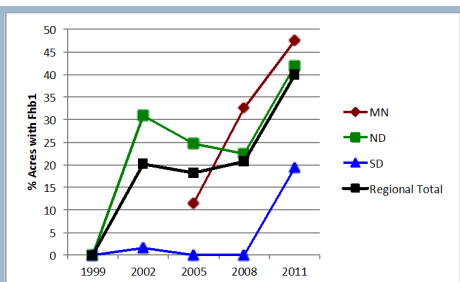
More than \$1 billion in direct economic losses in the spring wheat region were attributed to Fusarium head blight (FHB) from 1993-2000. Growers continue to incur losses when susceptible cultivars are grown and environmental conditions are conducive to disease. Sustained breeding efforts for resistance to FHB date to the late 1980's when the Chinese cultivar 'Sumai 3' was first introduced. Since the epidemics of the 1990's, breeding for FHB has been a top priority for the North Central Region. In addition to Sumai 3, many sources have been used by breeders to diversify the

resistance to FHB.

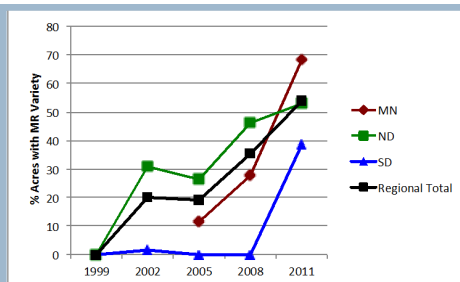
Our group mapped *Fhb1*, a major Fusarium head blight (FHB) resistance gene that reduces disease symptoms by 25-30%. DNA markers associated with *Fhb1* have been widely used in wheat breeding programs worldwide. Facilitated by the IFAFS (2001-2005) and WheatCAP (2006-2010) projects, marker-assisted selection for *Fhb1* and other FHB resistance genes has been critical to our program. Since 2005, more than 23,000 pre-yield trial lines were screened for the presence of *Fhb1* and up to nine other important

genes using DNA markers. Most of these marker assays were processed by the USDA-ARS Genotyping Lab in Fargo, ND.

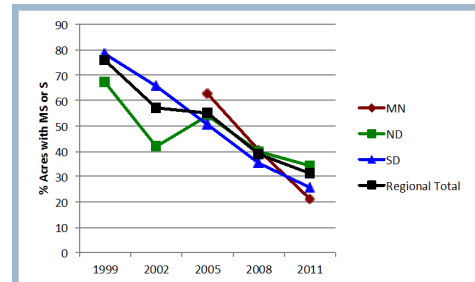
To quantify the impact of our FHB breeding efforts, we obtained cultivar acreage data from the Minnesota Association of Wheat Growers, and the USDA-National Agricultural Statistics Service. Data summarized in graphs below indicate that competitive yielding cultivars with good grain quality and improved FHB resistance are popular with the regions' growers. Employing resistance genes using markers is a successful breeding strategy.



The presence of *Fhb1* was assessed based on a closely linked DNA marker. No cultivars containing *Fhb1* were grown on a significant acreage prior to 2000.



Moderately resistant cultivars were grown on 54% of the region's spring wheat acreage in 2011, compared with 0, 20, 19, and 36% in 1999, 2002, 2005, and 2008, respectively.



The proportion of the region's acreage occupied by moderately susceptible or worse cultivars dropped from 76% in 1999 to 31% in 2011. Employing resistance genes using markers is a successful breeding strategy.

Acknowledgements

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TCAP Project Synopsis

By: Liana Nice—Graduate Student—University of Minnesota

During the process of crop domestication and improvement, genetic bottlenecks occur which limit the genetic diversity available for crop improvement. If the lack of variation is severe, crop improvement can stagnate. But, because of the complex nature of malting quality in barley, the process of expanding the genetic diversity of a breeding program can be difficult. Over the course of breeding, many advantageous traits have accumulated in elite breeding material, and many deleterious traits remain in unimproved barleys. Therefore, we must find ways to identify and deploy those genes which confer resistance to troublesome pathogens or aid in tolerance to environmental stressors such as limited water or nitrogen availability, without introducing those deleterious genes which confer low yield, poor malting quality, or traits unadapted to modern agriculture such as seed dispersal. To accomplish this, we have identified a set of 25 wild barley accessions which encom-

pass a large proportion of the genetic diversity present in wild barley. These accessions were obtained from a variety of ecosystems in barley's native range across the Middle East and have been shown to confer resistance to several barley diseases. Each of these accessions has been crossed to a single elite Minnesota barley line *Rasmusson*, and backcrossed twice to that same line to produce a population of individuals with small introgressions of exotic genes surrounded by a predominately *Rasmusson* genome. Over the course of the next few years, these lines will be genotyped and analyzed in the field for many traits, including yield, nitrogen use efficiency, water use efficiency, and malting quality characteristics. By analyzing the wild introgressions in a cultivated background, we will be able to more quickly and accurately deploy beneficial genes for the continued improvement and sustainability of barley breeding in the face of future climatic and disease pressures.



Winter Barley goes facultative and heads east—the long march.

Patrick Hayes, Alfonso Cuesta-Marcos, Scott Fisk, and Kevin Smith

Hayes, Cuesta-Marcos and Fisk are at Oregon State University; Smith is at the University of Minnesota. All are proud members of the T-CAP.

Overview: Climate change does not mean Minnesota will become a leading sugarcane producer in the next 100 years. It does mean that production of fall-sown barley may be possible in areas, such as Minnesota, that were once “off the map”. Why even consider the prospect? Fall-sown barley, if it can survive the winter, will yield more than spring-sown barley and it will make better use of water resources. In other words, it will be more water use efficient. To be successful, fall sown barley requires low temperature tolerance (LTT) that gives a plant the capacity to survive a harsh winter.

Fall-sown barley is a relatively new crop. Current varieties lack sufficient LTT for extensive production in cold environments. Fall planted varieties are generally winter types meaning they require cold treatments before they can flower while spring types can flower without cold treatment. Most varieties in the region have been spring types. Facultative types can be planted in spring or winter. Therefore, a winter hardy facultative type would provide flexibility for growers. Selecting for improved LTT in a crop that has undergone intensive selection for the past ~10,000 years as a spring type is a challenge.

Key findings: Measuring LTT is a challenge. We tested the populations under field conditions in Colorado, Minnesota, Montana, Nebraska, and

Oregon. We also tested the populations in growth chamber freeze tests at the Martonvasar Research Institute in Hungary. Everything lived in Oregon and everything died in Montana. There was differential survival in the other tests. By far the most informative phenotype data came from the field trial in Minnesota. These data allowed us to map important QTL’s for LTT. Understanding the genetic basis of a complex phenotype is a pre-requisite for effective use of molecular breeding tools.

Practical implications of this research:

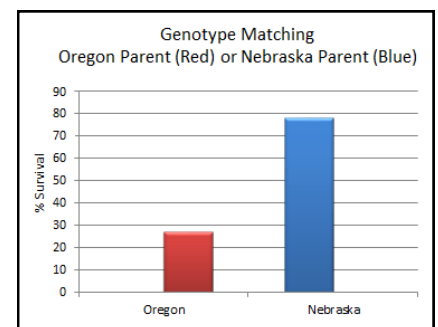
Fall-sown barley offers numerous advantages in many production environments. Likewise, within the fall-sown class, facultative types offer advantages to both breeders and producers. A pre-requisite to realizing these advantages is sufficient LTT as well as agronomic performance (i.e. yield and resistance to biotic stresses) and grain that can command a premium in the marketplace. We have shown, with this research, that gene discovery and breeding can be coupled, via bi-parental QTL mapping, to generate new knowledge and useful facultative **germplasm**. Selected lines have been incorporated into the OSU and UMN breeding programs and both malting quality and food quality analyses are in progress based on assessment of these lines in multiple environments.

What’s next? Winter and facultative

barley varieties are on the march, eastward. The facultative variety Maja is in commercial malting and brewing trials. The winter varieties Alba and Streaker are proposed for release in 2012. These varieties have excellent track records of agronomic performance in the Pacific Northwest (see <http://barleyworld.org/breeding-genetics/data> for reports) and they look great in the field at Corvallis this year. But how are they faring on the long march east? When they survive in Minnesota, they do well. It remains to be seen how they fared over the winter of 2011-2012. The 2011 Maja crop from Vermont is on its way into local beer and spirits, raising hopes for future successes as winter and facultative barley head east. It should be noted that great barley moves in all directions - there is also a westward movement of excellent winter barley varieties from Europe.

Acknowledgements:

Special thanks to Stephen Baenziger (University of Nebraska) for his generous sharing of **germplasm**. This work was based on an international team that included, in addition to the authors of this short report, Luis Cistué (Spain), Joanne Russell and Robbie Waugh (Scotland), Zoltán Bedo and Ildikó Karsai (Hungary), and Stephen Baenziger (Nebraska). Ann Corey and Tanaya Filichkin were key contributors at Oregon State University.



TCAP plots during winter at Corvallis, OR (left) and Saint Paul, MN (right). Selection for winter survival at Corvallis, based on plot appearance, would be futile, because all lines survive. In MN, selection based on appearance

would be effective at the stage shown. But if low temperatures persist, or if they get lower, all plots may die. Selection is as futile if everything dies as if everything lives. Genetic information, however, is a constant in this variable

picture. As shown at the far right, lines with a specific portion of chromosome 1H tracing to the Nebraska parent have a greater likelihood of survival than those with the chromosome region tracing to the Oregon parent.



Triticeae CAP
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Education News

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Annual Graduate Student Meeting

On Jan 13, 2012 19 graduate students, 6 faculty and one industry representative met. Two of the faculty represent minority serving institutions.

After gathering with refreshments, we became acquainted and shared our favorite basic science question. In order to begin working on industry's request that we improve all plant breeding human capital, we brainstormed the following list of skills needed by professionals:

- Organizational skills
- Team work – interdependent and interdisciplinary
- Developing teams – industries are matrix organizations rather than hierarchical. A potential problem with this system is losing track of the process/progress.



- Flexibility – open minded to

different ways of doing things

- Resource management – people, budgets
- Leadership
- Ability to prioritize
- Decision-making
- Grant writing
- Networking
- Collaboration within a company
- Know when to change focus
- Creative thinking
- Work-life balance
- Ability to communicate with producers, communication styles to meet needs of audience – including speaking and listening
- Breadth of knowledge
- Inter-cultural awareness and competency
- Tolerance – positivity at work
- How to recruit – identify good people and recruit them
- Motivation
- Ability to make use of opportunities
- Self-development (professional)



Next students suggested ways that these skills could be improved including:

- Mock job search activity, learn how to decipher position announcements
- Have students organize meetings at TCAP
- Networking events at TCAP
- Authentic exercises
- Working with data generated by TCAP
- Have groups present on their research topics: traits, methods, challenges
- Invite representatives from small industries to interact with students
- Students organize TCAP seminar series

Next we broke into small research groups and discussed our research topics. Finally, we enjoyed a Happy Hour with other members of TCAP

Collaborative Projects

Faculty serving at minority serving institutions and TCAP faculty are participating in collaborative research projects. Recently, faculty were introduced to the PBTN as a communication tool. Faculty will continue to meet to plan a NSF – Research Experience for Undergraduates grant proposal.

During the spring semester, Jamie Sherman will visit four collaborating institution, presenting an educational film, providing information about plant breeding and TCAP graduate programs. Sherman visited University of Arkansas Pine Bluff February 29th and Rusk College March 1st, and will visit (see story page ??), Chicago State University March 26th, and Lehman College May 7th.

Spring Undergraduate Schedule

January – TCAP project goals and get acquainted

Invited speaker: Jamie Sherman – Project overview

Undergrads: research project and progress. Identifying your strengths and weaknesses.

February – Plant science careers in industry

Don Cummings

Undergrads: In what ways is your experience preparing you for industry? How can it be better?

March – Applying to grad schools

Undergrad discussion: how are you preparing? How can TCAP experience help you? What additional help could you use?

April – Presenting results

Undergrad discussion: How will you present the results of your research?

May – Reflection

Undergraduate discussion: Self evaluation of strengths and weaknesses.

Undergraduate Instructional Materials

At the University of Nebraska instructional materials are being developed for undergraduate students. Two deliverables were developed for year one. They include an interactive wheat breeding lesson (current draft under review can be viewed at http://passel.unl.edu/animation/Wheat_Breeding2/Wheat%20Breeding%20Activity%202.swf) and a text based lesson discussing the principles of segregation (current draft under review can be viewed at <http://passel.unl.edu/communities/index.php?idinformationmodule=1130447158&idcollectionmodule=1130274157>). The text based lesson is also supported with two videos created with the help of Dr. Steve Baenziger and the New Media Center at UNL. A nitrogen use efficiency lesson is well under way for year two, and an interactive learning environment is being created to deliver content regarding quantitative traits. Mini activities encouraging ap-

Introduction to Plant Breeding Learning Activity: Wheat

Click on Step 1 to begin. Follow the steps in order to complete the breeding process. Use the links in the side bar on the right to learn about other important concepts in plant breeding. At each step make sure to answer the notebook question found in the lower left corner of the page.

Step 1: The Plant Breeder's Goal

Step 2: Selecting Parents and Making Crosses

Step 3: Growing Offspring of parental Crosses (F1)

Step 4: Growing the Second Generation and Making Selections.

Step 5: Continuing Evaluation and Selection

Step 6: Further Evaluation

Step 7: Release a Line

Information for Teachers
This activity discusses the basic process used in a traditional breeding program. Crossing, genetic variation, selection and elements of DNA technology are discussed within this activity. The material is aimed towards high school or introductory life science

Why is Traditional Plant Breeding Still Important?
Summary of Plant Breeding Process
Practice Plant Breeding

plication of plant breeding concepts to topics addressed in TCAP research are also being developed to support these lessons. We are constantly looking for new examples to use in our materials. If you have topics related to your research that you think would be well suited for undergraduate education materials please e-mail Amy Kohmetscher (akohmetscher2@unl.edu) and Don Lee (dlee1@unl.edu).

TCAP Seminar Series

- On Thursday February 23rd Stephen Baenzinger presented our first TCAP Seminar Series with *Understanding Grain Yield: It's a journey, not a destination*. 47 people attended the seminar. If you were unable to attend you can view it on line at <https://connect.unl.edu/p8kqrxydmk/>
- March 15 at 3:00 central Deana Namuth-Covert will present: *Cyberspace: New Frontiers in Learning and Networking*
- Thursday March 29 at 3:00 central Eduard Akhunov will present on *Usage of genome-wide genotyping approaches to understand the genetics of agronomically important traits in wheat*.
- April 12 at 3:00 central Jean-Luc Jannink, Vic Blake, Clay Birkett and Dave Matthews will be presenting *Introduction to T3*
- Thursday April 26 at 3:00 central Jorge Dubcovsky will present on *Regulation of development in wheat*.
- May 3 at 3:00 central Martin Matute will present *Plant Parasitic Nematodes-the Farmer's Hidden Enemy*
- If you are interested in presenting a topic on the TCAP seminar Series please e-mail deanna.crow@montana.edu to get set up.
- All meetings will be held at <https://connect.unl.edu/pbtn/>. Enter as a guest. System works best if you have a headset with microphone and a hardwire internet connection.



Join the PBTN at <http://passel.unl.edu/communities/>

Recruitment Trip

By Jamie Sherman

At the end of February I had a wonderful opportunity to visit two of our TCAP collaborating institutions—University of Arkansas Pine Bluff and Rust college in Mississippi, both of which are historically black colleges. At Pine Bluff undergraduate students working with Dr. Matute introduced me to nematodes collected from Washington State University soil samples. I learned how to count, isolate, and differentiate the parasitic nematodes from the free feeders. Next Dr. Onyilagha and his student introduced me to their work on identifying new phenotypic measures of drought tolerance. They are testing some spring wheat lines from Montana. Dr. Okiro introduced me to his cow pea breeding project, and is interested in future collaboration. At Rust College I met all of the science

and math faculty at lunch hosted by the department chair Dr. Yeh. Several of the faculty expressed interest in collaborating with us. Dr. Zhu introduced me to her students bioinformatics search for drought tolerance.

At both institutions I showed the film "Plant Breeding: The future in the palm of your hand," gave a seminar to over 100 students, and handed out TCAP brochures. Most students felt their awareness and understanding of plant breeding increased and several students expressed an interest in graduate school. Thanks to everyone involved for their lovely, warm hospitality. I was hosted to meals and met with department heads from both schools. The faculty were generous in showing their projects and introducing me to potential graduate students. Students have contacted me for more information about graduate school or internships. Faculty looking for students should contact Jamie Sherman at jsherman@montana.edu



Dr. Zhu with two undergraduates working on the project with another faculty member



Dr. Matute's students at Pine Bluff

TCAP Supports Workshops

TCAP is supporting student attendance at summer workshops. Each TCAP graduate student can request travel support to attend one of these summer workshops. Students should submit workshop attendance plans to DeAnna Crow at deanna.crow@montana.edu by May 31st. Students will submit receipts for travel up to \$500 to deanna.crow@montana.edu within a 2 week post travel deadline.

Summer Workshops



Colorado State University is offering a 2-week summer course on plant breeding for drought tolerance (June 11-22), which includes a 2-day symposium on June 21-22. The symposium is also available for stand-alone registration. Both events are described at <http://www.droughtadaptation.org/>. To encourage attendance by TCAP grad students, we are offering scholarships of \$500 for the short course. This can be combined with a \$500 scholarship from TCAP central funding for a total reduction of \$1,000. Registration fee for the symposium will be waived for TCAP students. To take advantage of either of these opportunities, please communicate with Annie.Heiliger@colostate.edu.

TCAP sponsored workshops:

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



Plant Breeding for Drought Tolerance 2 day symposium

When: June 21-22

Contact information see above

Registration fee waved for TCAP students

Rust Research Methodology

When: July 8-July 10, 2012

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

Cost: \$150

Topics to be covered include:

- 1) rust surveys
- 2) rust collection methods,
- 3) rust storage methods,
- 4) race identification and nomenclature;
- 5) field methodology for inducing epidemics;
- 6) rust phenotyping, and
- 7) Rust resistance genetics.

For more information contact Brian Steffenson and Pablo D. Olivera (PhD).

University of Minnesota. Department of Plant Pathology

Phone: (612) 625-9776

E-mail: oliv0132@umn.edu



Tentative schedule:

July 8 (Sun) travel day to St. Paul, reception and mixer

July 9 (morning) instruction on cereal rust methodology and (afternoon) lectures on specific topics related to cereal rust research

In the evening, we will have a BBQ or something similar.

July 10 (morning) field tour. In the afternoon, people can head home.

Meet MSI Faculty—DR. JOSEPH ONYILAGHA: TCAP PROJECT

Project:

Wheat competes with other crops, such as rice, corn, cotton, and soybean as a good source of revenue for Arkansas farmers. About 80% of wheat produced in Arkansas is winter wheat. There is the notion that spring/summer wheat may not be profitable due to Arkansas' hot-humid summer conditions. We are interested in conducting studies to identify and select wheat varieties that may tolerate and succeed in Arkansas summer conditions. We are collaborating with Dr. Luther Talbert (Montana State University) in this research. We will evaluate about 41 wheat lines from Dr. Talbert's collections under water-stressed conditions accompanied by high temperature/humidity.



Dr. Joseph Onyilagha

Interest In TCAP Project:

This project gives us the opportunity to participate in an important national research project. It also affords us the opportunity to interact and share our research findings with colleagues in other institutions. We will expose undergraduate HBCU students to field research and help them to favorably consider Plant Breeding as a higher degree option.

Work In Progress:

We have received 41 wheat cultivars from Dr. Talbert. We are currently conducting a germination test of the lines. Greenhouse trial has commenced. We have planted out these cultivars in the greenhouse. Water stress experiments on seedlings have commenced. A student is conducting these experiments.



der water-stressed conditions accompanied by high temperature/humidity.



TCAP Course for Spring

TCAP course - Basic Quantitative Genetics in Plant Breeding will be offered March 23rd and running through the week of April 27th in the PBTN

The course will consist of archived lectures prepared by Dr. Clay Sneller, The Ohio State University, Department of Horticulture and Crop Science; practical examples from OWBM population by Dr. Patrick Hayes, Oregon State University; and practical experience in mapping and QTL

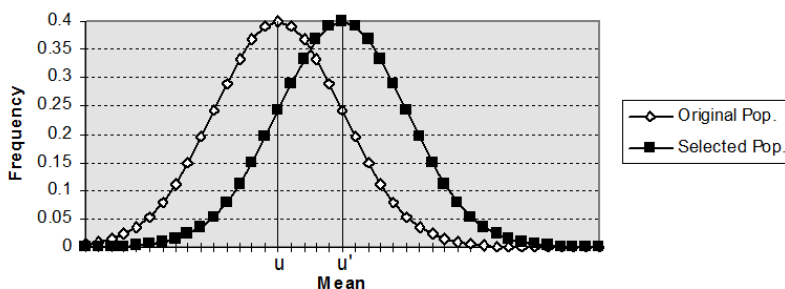
analysis by Dr. Jamie Sherman, Montana State University. *Topics will include – Allele and genotype frequencies, Genetic effects, Heritability, Variance, and Gain From Selection, Genetic mapping and QTL analysis.*

The structure of the course will include asynchronous work with archived lectures including related questions and problems. As well as synchronous working group meetings for data analysis. The class will be broken

into working groups according to students schedules. Working groups will complete a genetic map and qtl analysis. 80% of assignments must be completed to achieve a certificate of completion.

The class should require five hours of work per week for the average student. If interested contact Jamie Sherman at jsherman@montana.edu or join class at <http://passel.unl.edu/communities/pbtn?idsubcollectionmodule=1130274184&idindependentpage=192>

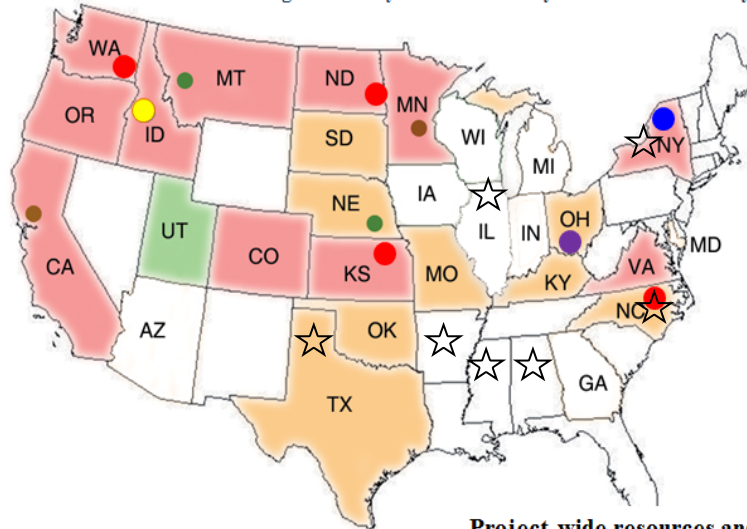
Comparison of the Original Population and the Population Derived From Randomly Mating Selected Individuals of the Original Population



TCAP Participants

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

PIs Jorge Dubcovsky UC Davis and Gary Muehlbauer University of Minnesota



The T-CAP includes:

- 56 funded participants
 - 28 institutions
 - 21 states.
- Most have previous experience in the BarleyCAP and WheatCAP projects

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

Project-wide resources and activities

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

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