



Gary's Update



The barley CAP participants and advisory boards met in San Diego, CA, on January 10, 2008 to discuss progress and future plans. Over 55 people attended the annual meeting. Although lots of work remains, the stakeholder advisory boards were impressed by progress of the group.

A summary of the meeting can be found on page 1 of this newsletter.

The year 3 continuation proposal was submitted and a final draft of the proposal can be found at (www.barleycap.org), the Barley CAP website. If there are no problems each of the funded labs should receive their funding in the spring.

The development of the SNP genotyping platform is complete (see page 6). Timothy Close (UC, Riverside) worked tirelessly on the development of the SNP genotyping platform. The barley genetics community is grateful for all of Tim's hard work.

Evaluation of the extension, education and research efforts of the barley CAP is an important activity. On page 4 of this newsletter is an article that describes Jochum Wiersma's (U Minnesota) presentation to a grower group and the use of the Turning Point software to obtain immediate evaluation. The other article on page 5 describes some Sue White's extension evaluation activities.

The barley CAP association genetics and marker-assisted selection workshop will be held on June 16-18 in St. Paul, MN. This workshop will provide both theoretical and hands-on experience with association genetics and marker-assisted selection strategies. All CAP participants and students are encouraged to attend. For a look at the tentative agenda see page 7 of this newsletter. Use the registration form on the CAP website to register. Registration is free for CAP participants and a limited number of students will be provided a \$500 stipend to support their travel. Please register before May 15. I hope to see many of you at the workshop.

Report of 3rd Annual Barley CAP Meeting in San Diego, CA

by Gary Muehlbauer

The 3rd Annual Barley CAP meeting was held at the Hacienda Hotel in San Diego, CA, on January 10, 2008.

Barley CAP participants present: Byung-kee Baik, Rex Bernardo, Tom Blake, Peter Bradbury, Shiaoman Chao, Timothy Close, Blake Cooper, Julie Dickerson, Patrick Hayes, Cynthia Henson, Karen Hertsgaard, David Hole, Richard Horsley, Lee Jackson, Jean-Luc Jannink, Jennifer Kling, Peggy Lemaux, Sally Leong, David Matthews, Gary Muehlbauer, Stephen Neate, Mark Schmitt, Kevin Smith, Brian Steffenson, Peter Szucs, Susan White, Mitchell Wise, and Roger Wise.

Scientific advisory board members present: Mike Davis, Julie Ho, David Marshall, Diane Mather, and Robbie Waugh.

Stakeholder advisory board members present: Gary Hanning, Scott Heisel, David Ruark, and Marvin Zutz.

The barley CAP participants, and scientific and stakeholder advisory boards met to report on progress and discuss future plans. The meeting consisted of a series of short presentations in the morning, breakout sessions in the afternoon and a final reporting session.

Overview of project

An overview of the barley CAP was provided by Gary Muehlbauer (U Minnesota). In his presentation he described the formal authorship policy, and the policy for announcing and developing a manuscript. Both policies are on the website on the Project Management page.

Extension and education

Brian Steffenson (U Minnesota), Peggy Lemaux (U California, Berkeley), Karen Hertsgaard (Institute of Barley Malt Sciences, North Dakota State U) and Sue White (Extension evaluator, U Minnesota) presented the outreach and education component of the project.

Report of 3rd Annual Barley CAP Meeting in San Diego, CA - Continued

Brian Steffenson started by reiterating the logic model for the barley CAP and the importance of keeping the desired outcomes for the target audiences in mind as the extension/education effort progresses. The logic model can be found on the barley CAP website.

He also presented the results of the grower survey conducted by the Barley CAP and the Institute of Barley Malt Sciences (IBMS). Over 1,400 surveys were completed. The questions that are most pertinent to the barley CAP are: (1) what determines if you are going to plant barley; and (2) what sources do you use to obtain your information? Related to question 1, growers cited the price of the grain, production (e.g., varieties, pests, management practices), and the market as the leading factors. For the second question, the growers indicated they obtain their information from print media, extension educators, industry agronomists and contract meetings. The results of the survey highlight the need to educate growers on the general pace of cultivar development, characteristics of new varieties, and to maintain our current focus on print media delivered by extension educators and/or breeders. Brian also discussed a small-scale survey of industry representatives to determine what type of information is most important and where they receive their information. The results of this survey indicated that industry representatives obtain information

from print media, grower meetings and the web; and information on varieties and management practices (diseases, fertility, pesticides, and agronomy) was most important. Brian also described another approach the Barley CAP is using to enhance our outreach efforts. We have developed a small grant program for extension educators who will disseminate Barley CAP information in each state. We have awarded grants to Oregon State University, North Dakota State University and Washington State University. In addition, in Minnesota the Barley CAP is working with Marv Zutz (Minnesota Barley Council). The Barley CAP has provided Marv with brochures, cards and a nontechnical poster. These materials have been presented at grower meetings in Minnesota in the Fall 2007 and Winter 2008.

One important goal is to educate the next generation of scientists. Twenty-one graduate students, three postdoctoral research associates, five technical personnel, 13 undergraduates, one visiting professor and two high school students have, or are, currently actively working on the barley CAP. A list can be found on the Barley CAP website in the year 3 continuation proposal. To enhance our extension efforts, the barley CAP has teamed with the IBMS. Karen Hertsgaard discussed the activities of the



Report of 3rd Annual Barley CAP Meeting in San Diego, CA - Continued

IBMS. In collaboration with the Wheat CAP, the IBMS conducted a combine to kitchen tour. In addition, the IBMS has disseminated the IBMS newsletter to growers and industry representatives, and presented the Barley CAP and IBMS activities at grower and extension meetings. In collaboration with the American Malting Barley Association, the IBMS has established extension teams (composed of growers, extension agents and industry personnel) in Montana, North Dakota and Idaho. These extension teams will develop long-term extension programs that complement and enhance the current extension/education programs.

Peggy Lemaux discussed the development of three factsheets including: “Barley: It’s what’s for dinner,” “Barley, Malt and Beer,” “Plant Breeding: The path forward,” and “Marker-assisted selection.” Each factsheet is on the Barley CAP website and printed copies are available to CAP participants upon request.

Sue White is the Barley CAP’s extension evaluator and she discussed some of the evaluation activities that she has been conducting. One of her activities was to have growers, extension educators and industry personnel evaluate the Barley CAP brochure, website and factsheets. She explained that these groups have many suggested changes. These changes are being incorporated into these extension/education materials. For a complete description of all outreach and education activities of the barley CAP, please see the year 3 continuation grant on the barley CAP website.

SNP mapping and genotyping

Tim Close (U California, Riverside) described the progress on the development of the SNP genotyping platform. SNP development and mapping is an international effort of the Barley CAP, the Scottish Crop Research Institute (SCRI, Dundee, Scotland), and the Institute of Plant Genetics and Crop Plant Research (IPK, Gaterslaben, Germany). Tim described the plan to develop three pilot Illumina oligonucleotide pool assays (OPAs) each containing 1,536 single nucleotide polymorphisms. These three OPAs will be used to map three mapping populations and genotype germplasm sets from the US and Europe. From these three pilot OPAs, over 3,000 high quality SNPs will be used to design two OPAs (3,072 SNPs) for genotyping.

The design has been completed for the three pilot OPAs and used on the three populations and germplasm. PilotOPA1 and PilotOPA2 resulted in 1,810 high quality mapped SNP markers. The first permanent OPA,

BarleyOPA1 (BOPA1), was designed using only highly successful SNPs from PilotOPA1 and PilotOPA2. Shiaoman Chao (USDA-ARS, Fargo, ND) used BOPA1 to genotype the year 1 960 breeding lines. Excellent data was obtained from the lines. THT and each of the breeding programs have and are working with the genotyping data.

Bioinformatics

Julie Dickerson (Iowa State U) described the progress on the development of The Hordeum Toolbox (THT). THT will house all genotype and phenotype data collected from the 10 barley breeding programs. The database will enable barley breeders to more efficiently breed superior varieties. The database has been established and the Iowa State group is uploading data. Rex Bernardo (U Minnesota) provided an update on the development of QTL Miner and a QTL Miner simulation program. QTL miner will provide the ability to identify marker-trait associations in breeding lines. A beta version of QTL minor is available and being tested.

Phenotypes and traits

Phenotyping the breeding lines submitted to the barley CAP is a large and complicated task. Over 40 traits are being evaluated on 960 breeding lines each year of the project. Kevin Smith (U Minnesota) provided an update on the phenotyping, data curation and upload to THT. To track the progress of the data collection, curation and upload to THT, Jennifer Kling (Oregon State U) has developed an interactive spreadsheet that will be posted on the website.

Scientific Stakeholder Advisory Board Reports

The advisory boards were provided with summary progress reports from year 1 and summary work plans for year 2 (see barley CAP website for summary progress and work plans). In addition, the advisory boards attended the barley CAP meeting. The complete scientific and stakeholder advisory board reports along with the barley CAP responses can be found on the barley CAP website.

Barley Education Day Features Interactive Presentation on Barley CAP

by Karen Hertsgaard

Producers were able to learn about barley production and marketing, along with the work being done by barley Coordinated Agricultural Project (CAP) researchers, during a workshop held in Minot, North Dakota, on January 28. *Barley Production and Management for Profit* was organized and sponsored by the North Dakota State University Institute of Barley and Malt Sciences (IBMS) in cooperation with the USDA-CSREES-funded Barley (CAP), the North Dakota Barley Council, North Dakota Grain Growers Association, American Malting Barley Association, and the NDSU Extension Service. Ten presentations, a keynote luncheon address and a panel discussion of pertinent barley issues filled the day. Producers, industry representatives, crop consultants and researchers attended the workshop.

Presentations included information on local and world barley markets, best cropping practices including planting rates and fertilizer practices for dryland malting barley, the value of barley in crop rotations, whether barley will be competitive in 2008, availability and characteristics of barley varieties in North Dakota, crop insurance and key malt quality factors.



Jochum Wiersma, Extension specialist in the Department of Agronomy and Plant Genetics at the University of Minnesota, Crookston, explained the Barley CAP. Utilizing a new type of technology called "Turning Point," Wiersma received immediate feedback from the audience.

Turning Point utilizes the same technology seen on TV games shows such as *Who Wants to Be a Millionaire*. Asking preliminary questions such as "What is the Barley CAP?" and "What is DNA?" Wiersma then spent about 15 minutes explaining the goals and research of the barley CAP. He finished his presentation with an "Exit Poll" asking participants to rate whether they "needed the information presented today," "the instructor used language I understood," "I learned new things about the barley CAP," "I better understand how breeders use MAS to speed up breeding," and "I believe MAS will lead to new, improved barley varieties."



Producers answer Turning Point questions at Barley Production and Management for Profit program.



Producers answer Turning Point questions during Jochum Wiersma's Barley CAP Presentation

The results of this poll revealed that producers understand and appreciate the complex research being done by Barley CAP researchers. Wiersma's presentation and the Turning Point results are available for viewing on the Barley CAP website <http://www.barleycap.org/> under *Outreach*.

A panel of producer and industry representatives led the audience in a discussion at the end of the day. The panelists included Al Slater, Busch Agricultural Resources Inc.; Kelly Kotowicz, Alvarado Farmers Elevator; Jim Hettinger, Molson-Coors Brewing Co.; and producers Louis Arnold of Esmond and Doyle Lentz of Rolla.

Barley CAP Program at Virginia Tech

by Wynse Brooks

The barley breeding program at Virginia Tech University, with Carl Griffey and Wynse Brooks, focuses on combining the best available genetic tools with classical breeding to develop winter barley cultivars suitable for markets in the mid Atlantic region. Our primary objective is to develop high yielding and high quality winter barley cultivars designed for specific end uses and having desirable combinations of high value traits, such as hullless seed, waxy endosperm, lower fiber, reduced phytic acid content, higher protein, starch and energy, and high or low beta glucan content depending on end use. Our primary contribution to the 2007 barley CAP was evaluating 960 barley CAP lines for seedling reaction to two races of leaf rust and one isolate of powdery mildew in inoculated greenhouse tests.



Carl Griffey and Wynse Brooks with the Barley CAP at Virginia Tech.



Patrick O'Boyle evaluating barley seedlings inoculated with net blotch in growth chamber are attached.

Patrick O'Boyle is our PhD student, whose research project focuses on the inheritance of net blotch resistance in barley, and for which mapping work will be conducted during spring 2008. The goal of this project is genetic analysis of net blotch resistance in barley using a diallel cross. This study compares 'Nomini', a cultivar developed in the Virginia Tech Breeding Program, with several previously identified net blotch resistance sources. Seedling screening has been conducted to compare the resistance sources with each other as well as postulating gene number and mode of gene action. The initial phase of screening SSRs and SNPs to facilitate linkage mapping in a resistant x susceptible cross (Nomini x Hector) will begin this spring.

Evaluation of Barley CAP Extension and Education

by Sue White

Evaluation of Barley CAP extension and education efforts is underway and will be ongoing throughout the duration of the project. Extension Evaluator Sue White (U Minnesota) developed barley grower and user surveys to evaluate new Barley CAP written materials and to gather additional data about where growers and users prefer to look for information about barley as well as their internet access and frequency of use.

Initial evaluation efforts were designed to follow-up on the findings of the Institute of Barley and Malt Sciences (IBMS) survey indicating barley growers most preferred obtaining information from print media, agronomists, and state extension. State barley grower organizations helped identify growers who would be willing to participate in the survey. Barley CAP written materials, including fact sheets and an informational brochure, were mailed out to growers in ND, MN, MT, ID, OR, and WA. The American Malting Barley Association (AMBA) assisted evaluation efforts by identifying barley users employed in

the malting, brewing, and food barley industries to take part in the survey. The survey also included questions about the Barley CAP website. In addition to rating the written materials, grower and user survey respondents were asked to provide additional comments about specific ways the written materials and/or website could be improved.

Overall, the Barley CAP written materials were quite favorably reviewed by both growers and users, although there were many specific comments about ways they could be improved. The Barley CAP team has been very responsive to the survey results. For example, several of the new fact sheets have been revised based on feedback obtained from both barley growers and users. The updated fact sheets and brochure will be posted on the Barley CAP website as soon as they become available. Additionally, there were many suggestions about new linkages for the website, and it will be updated in the weeks ahead.

Progress with SNP platform development, an OPA-SNP-based genetic map and coupling of the physical and genetic maps

by Timothy Close

The data from PilotOPA3 (POPA3) were provided to the UC Riverside group (Timothy Close, Stefano Lonardi, post-doc Prasanna Bhat, Computer Sciences PhD students Yonghui Wu and Serdar Bozdog, Programmer Steve Wanamaker) by Joe DeYoung at the UCLA genotyping lab on January 11th. This included data from the same 480 DNA samples used for prior work in BarleyCAP and AGOUEB, including the Morex x Barke (MxB), Oregon Wolfe Barley (OWB) and Steptoe x Morex (SxM) doubled haploid mapping populations and US and European core germplasm samples. Special thanks to Robbie Waugh who heads our sister project AGOUEB, which covered all of the costs for POPA3 in a cost sharing agreement between BarleyCAP and AGOUEB. This partnership is a superb example of the spirit of cooperation and sharing that make the barley community a great one to be part of.

After several cycles of data analysis and map construction, the UCR team finished processing POPA3 data from the mapping populations in late February, resulting in some hundreds of new markers added to each of the three respective individual maps, along with a new consensus map. By making use of only very high quality marker calls, and using BOPA1 data generously made available by Dr. Kazuhiro Sato in Japan from a fourth DH

population, the consensus map now is composed of 2801 OPA-SNP markers distributed into 959 marker bins. A striking result is that there are no conflicts of marker order between any pair of individual maps or between the consensus map and any of four DH-derived individual maps.

The method used by the UCR team involved production of ordered bins of markers from each DH population, followed by production of a directed graph, followed by calculation of a non-conflicted linear map representing one possible solution of the directed graph. The MxB map contains 1552 SNPs in 432 bins, the OWB map contains 1468 SNPs in 498 bins and the SxM map contains 1183 markers in 386 bins.

It should be noted that Dr. Sato and Dr. Nils Stein in Germany deserve everyone's gratitude for generously making nearly 100,000 additional EST sequences available in early 2007, which made it possible to complete the design of PilotOPA3. Others who contributed specialized sequences for SNP selection and POPA3 content will discover upon analysis of the POPA3 data that most of their wishes for multiple haplotype discrimination were fulfilled. These individuals are Hattice Bilgic (Steffenson lab), Matthew Moscou (Wise lab), Peter Szucs (Hayes lab), Luke Ramsay

	KS	MB	OWB	SM	consensus
OPA1	353	509	553	421	1020
OPA2	379	555	465	374	945
OPA3	0	489	450	388	836
total	732	1553	1468	1183	2801

markers	KS	MB	OWB	SM	consensus
1H	93	199	153	133	317
2H	131	261	224	202	467
3H	123	228	233	219	447
4H	97	141	207	125	332
5H	108	282	263	213	511
6H	92	205	192	122	333
7H	88	236	196	169	394
sum	732	1552	1468	1183	2801

bins	KS	MB	OWB	SM	consensus
1H	46	59	62	45	120
2H	66	70	75	56	166
3H	58	75	90	61	150
4H	49	41	58	50	112
5H	58	74	87	79	175
6H	40	51	61	41	107
7H	47	62	65	54	129
sum	364	432	498	386	959

Progress with SNP platform development (continued from page 6)

(SCRI), and Peter Morrell (Clegg lab). The new consensus map contains 1020 markers from POPA1, 945 from POPA2 and 836 from POPA3. The number of markers per chromosome ranges from 317 for 1H to 511 for 5H, and the number of marker bins ranges from 107 for 6H to 175 for 5H. For all but a few of these markers, it is also clear which are on the short arm and which are on the long arm, based on BOPA1 results obtained with flow-sorted chromosomes in collaboration with Jaroslav Dolezel and members of his laboratory in Czech Republic, as part of the NSF project of Close and Lonardi which also involved former post-doc Jan Svensson.

Following the analysis of PilotOPA3 data, Close completed the design of the second production OPA for BarleyCAP and AGOUEB, referred to as BarleyOPA2 or BOPA2. The 1536 SNPs represented on BOPA2 include 1265 SNPs with known genetic map positions and 271 other SNPs with known polymorphisms, based on prior analyses of US and European germplasm using the Pilot OPAs. BOPA2 is expected to be available to the North Dakota laboratory and BarleyCAP by May 2008, accomplishing the objective of having two complete OPAs representing more than 3000 SNPs. The UCR team

also succeeded in the use of BOPA1 with combinatorial pools of Morex barley gene-rich BAC clones to assign more than 700 SNPs to BAC contigs. The number of SNPs assigned to BACs is expected to increase to more than 1000 once the same pools of BACs are applied to BOPA2. The vision of a well populated SNP map tied to the barley physical map is swiftly becoming a reality – special thanks to MingCheng Luo at UC Davis for excellent work on barley BAC physical mapping in partnership with Close and Lonardi in an NSF Plant Genome project. Recent and soon to be released enhancements of the HarvEST:Barley interface (<http://harvest.ucr.edu>) for Windows or online HarvEST (www.harvest-web.org) and its utilities provide interim access to the new consensus map and SNP-BAC data, along with the barley physical map viewer phymap.ucdavis.edu:8080/barley/, kindly provided by MingCheng Luo and Frank You (USDA, Albany). In the next several months it is anticipated that there will be wide dissemination of the new consensus map and SNP-BAC relationships to outlets including GrainGenes, Gramene, NCBI, the J Craig Venter Institute and of course foremost to THT and all BarleyCAP participants.

Barley CAP Association Genetics, Marker-Assisted Selection Workshop

Barley CAP has scheduled a workshop on Association Genetics, Marker-Assisted Selection for June 16-18, 2008, Cargill Building, University of Minnesota, St. Paul, MN. The workshop will be presented by Kevin Smith (U Minnesota), Rex Bernardo (U Minnesota), Jean-Luc Jannink (USDA-ARS, Ithaca, NY) and Shiaoman Chao (USDA-ARS, Fargo, ND).

Registration forms are on the barley CAP website at www.barleycap.org. Registration forms are due May 15, 2008. There is limited space so be sure to register early.

The workshop is free for Barley CAP participants and their students and postdocs; \$100 for non Barley CAP participants (payable by check or money order). The \$100 will cover three lunches, a reception and coffee breaks. A limited number of \$500 student stipends will be provided.

Rooms have been reserved at the Radisson University Hotel, 615 Washington Ave S.E., Minneapolis, MN 55414, Phone: 612-379-8888, Fax: 612-379-8682, www.radisson.com/hotels/universi Please reserve your room by May 15. Ask group: Barley CAP Workshop. Rate is \$107 plus tax

Please contact Lynne Medgaarden at (612) 625-4742, FAX: (612) 625-1268, medga001@umn.edu, University of Minnesota, Agronomy and Plant Genetics, 1991 Upper Buford Circle, 411 Borlaug Hall, St. Paul, MN 55108.

Participants are asked to bring laptop computers to load the new program and learn to use it during the workshop.

Tentative agenda for the workshop:

Session I

- A. QTL mapping
 - 1. Traditional approaches
 - i. Populations
 - ii. QTL detection methodologies
 - 2. Association mapping
 - i. Population structure
 - ii. Linkage disequilibrium
 - iii. Haplotype structure
 - iv. Markers, marker density, minor allele frequency
 - v. Hands on – QTL Miner Simulator, Haploview, THT/Germenate tools

Session II

- A. Genome-Wide Association Mapping
 - 1. Hands on – Tassel, QTL Miner
 - 2. Interpreting QTL mapping results
 - 3. Identifying targets for MAS

Session III

- A. Designing MAS Strategies
 - 1. Review phenotypic selection in barley breeding
 - 2. Overview MAS strategy-BC, allele enrichment, single locus, multiple loci, whole genome
 - 3. Marker Platforms: SSRs, Illumina Bead Station SNP, Florescent polarization
 - 4. High-throughput SNPs to markers that can be implemented in a breeding program

Calendar

- March 30-April 3, 2008.** Food Industry Environmental Conference - Sustainability in the Food Industry. Monterey, CA. Contact: Alan Carter, 2008 Conference Chair; +1.614.430.2706; E-mail: acarter@pirnie.com; or <http://affi.com/FIEC/events.asp>
- April 2-3, 2008** [Brewers and Vintners Scientific Symposium and Workshop](#), 2008, Davis, CA
- April 5-10, 2008** 10th International Barley Genetics Symposium, Alexandria, Egypt
- June 16-18, 2008** Barley CAP Association Genetics, Marker-Assisted Selection Workshop, Cargill Building, St. Paul Campus, University of Minnesota, St. Paul, MN
- June 22-25, 2008** American Society of Plant Biologists Annual Meeting, Merida, Mexico
- July 26-30, 2008** American Phytopathological Society Meeting, Minneapolis, MN
- August 2-6, 2008** [World Brewing Congress 2008](#), Honolulu, HI
- August 19-22, 2008** NCI/ASBC Barley Malt Quality Evaluation, Fargo, ND
- August 24-29, 2008** 9th International Congress of Plant Pathology, Torino, Italy. Italian Society for Plant Pathology (SIPaV), Italian Association for Plant Protection (AIPP) and International Society for Plant Pathology (ISPP).
- Aug. 30-Sept 2, 2008** 10th International Fusarium Workshop and Fusarium Genomics Workshop, Alghero, Sardinia (Italy)
- Sept. 7-10, 2008** The Worldwide Distilling Spirits Conference 2008, The Sheraton Grand Hotel and SPA Edinburgh
- October 5-9, 2008** ASA-CSSA-SSSA Annual Meeting, Houston, Texas



BarleyCAP

The Barley Coordinated Agricultural Project (CAP), funded by the National Research Initiative (NRI) of the USDA Cooperative State Research, Education and Extension Service (CSREES), involves government and public- and private-sector laboratories. The project links laboratory and field research with education and outreach. It uses modern tools of genomics to facilitate classical plant breeding efforts to develop superior barley varieties.

