

Gary's Update



The six-month progress reports have been submitted and are now on the website (www.barleycap.org). They show that the project is progressing nicely towards its goals. Rex Bernardo (University of Minnesota) has initiated the development of QTL Miner, a software program to identify regions of the genome controlling quantitative traits (see article on page 4). Timothy Close (University of California, Riverside), Patrick Hayes (Oregon State University) and international collaborators in Scotland (Robbie Waugh, Scottish Crop Research Institute) and Germany (Nils Stein, Institute of Plant Genetics and Crop Plant Research) have added 800 SNP markers to the barley genome, bringing the number of SNP markers mapped in barley to approximately 1,800. The design of pilot OPA3 is about complete and if you are interested in contributing known SNPs to the design please send them to T. Close (UC, Riverside) soon (see article on page 8). The breeding programs have begun to submit phenotypic data and pedigrees to Jennifer Kling (Oregon State University). Seed from each of the 960 breeding lines has been sent to CAP participants for examining malting quality, disease resistance and food quality traits. Shiaoman Chao (USDA-ARS, Fargo, ND) has received the Illumina Beadstation equipment and has recently had a training session on the SNP genotyping technology. Peggy Lemaux and Barbara Alonso have developed a brochure targeted to growers and industry representatives (see article on page 2). Please ask Lynne Medgaarden if you would like copies. Paul Schwarz (North Dakota State University) has hired a communication specialist, Karen Hertsgaard, who will help with the extension and outreach efforts. Within this newsletter you will see students and postdoctoral research associates that are working on the barley CAP.

The barley CAP will hold a meeting in San Diego on January 12, 2007 to discuss the recent progress and future work. The Barley Improvement Conference will precede the barley CAP meeting on January 11, 2007. Both meetings are important venues for barley researchers to discuss recent work on barley and all are encouraged to attend. See inside this newsletter for the location and agenda for the meetings. Finally, in the next few weeks I will be contacting each of the barley CAP participants to obtain information for the continuing grant that is due at USDA-CSREES on February 10, 2007.

Barley Meetings Planned for January

by Mike Davis

The 36th Barley Improvement Conference will be held at the Best Western Hacienda Hotel in historic Old Town, San Diego, California, on January 10 and 11, 2007. The Barley Improvement Conference, which was first held in 1946, provides barley researchers, barley producers, and malting, brewing, and grain trade personnel the opportunity to hear reports on the status of barley research programs and to meet and exchange information and ideas. The sponsors of the 2007 Barley Improvement Conference are: American Malting Barley Association, Inc.; Idaho Barley Commission; Minnesota Barley Research & Promotion Council; Montana Wheat & Barley Committee; National Barley Growers Association; North Dakota Barley Council; Washington Barley Commission.

Everyone who is interested in barley research is invited to attend the Barley Improvement Conference. The registration fee, which includes lunch, an evening banquet, and receptions, is \$180. Registration forms for the Conference are available from AMBA (414-272-4640) or joann.amba@sbcglobal.net or can be downloaded at <http://www.ambainc.org/ni/BIC.pdf>. Please submit registration forms to AMBA on or before December 27, 2006.

The Technical Program Will Include The Following Presentations

- Integrated Approaches to Addressing Fusarium Head Blight (Scab) of Barley – Stephen Neate, North Dakota State University
- USDA-CSREES Barley Coordinated Agricultural Project (CAP) – Gary Muehlbauer, University of Minnesota.
- Putting Fiber in your Fuel Tank: Converting Cereal Crop Residues to Ethanol - Michael A. Cotta, USDA-ARS, National Center for Agricultural Utilization Research, Peoria, IL.
- Have a Cold One: Update on Genetics of Winter Hardiness – Pat Hayes, Oregon State University

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Barley Conference Technical Program continued from page 1.

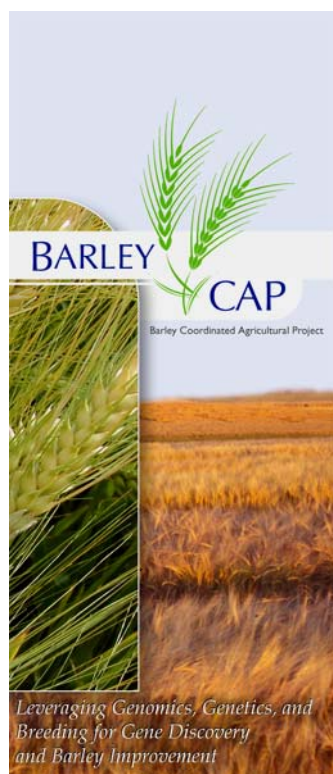
- Barley for Rural Development – Juliet Windes, University of Idaho
- Reactions of US Barley to the New African Stem Rust Race TTKS (or Ug99) – Yue Jin, USDA-ARS Cereal Disease Laboratory, St. Paul, MN
- Net Blotch of Barley: Host Resistance & Pathogen Virulence – Tim Friesen, USDA-ARS, Red River Valley Agricultural Research Center, Fargo, ND
- Malting Quality for Brewing – Gary Hanning, Anheuser-Busch, Inc.
- Quality Needs for Specialty Beers: Panel Discussion – Dave Kuske, Briess Malt & Ingredients Co. & John Mallett, Bells' Brewery, Inc.
- Seed proteomics of Harrington, *H. v. spontaneum* and their recombinant lines – Dominique Roche, Utah State University
- Barley Research Discussion Session

**Barley CAP Brochure Now Available**

by Barbara Alonso

A colorful tri-fold brochure was created to introduce the main objectives of the Barley CAP to growers, producers, breeders and the general public. The center panel highlights three of the categories of target traits being focused on by Barley CAP researchers - agronomic performance, disease resistance, and food and malt quality. The description of Barley CAP's goals is written in lay language to help readers easily understand the project's objectives. The brochure can be distributed separately or used in conjunction with either the

technical or non-technical posters. The text was prepared by Peggy G. Lemaux (UC Berkeley), Gary Muehlbauer, Kevin Smith and Brian Steffenson (University of Minnesota), and distills the Barley CAP's goals in a clear and concise way. The design was created by Barbara Alonso (UC Berkeley). The brochure can be viewed at the barley CAP website (www.barleycap.org). Copies of the brochures can be obtained from Gary Muehlbauer/Lynne Medgaarden.



How Will Barley CAP Help Improve Barley?

Harness the power of 10 barley breeding programs, database technologies and genomics to identify important genes for barley improvement.

Barley CAP will examine barley varieties from 10 breeding programs, focusing on over **40 TARGETS** for

- Agronomic Performance**
- Disease Resistance**
- Food & Malt Quality**

to improve barley for farmers, industry & consumers

How Do You Create 1 Breeding Program from 10?

- Barley CAP will combine data from ten breeding programs to aid germplasm exchange and coordinate breeding efforts.
- The **Hordeum Toolbox** is a centralized database containing analytical software and essential information (SNPs, breeding data).
- SNPs will be associated with traits in a process called **trait mapping**.
- USDA Genotyping Centers give breeders genetic information on thousands of breeding lines.
- Once traits are mapped with SNPs, marker assisted selection (MAS) will be performed.

What Are SNPs?

- SNPs, or Single Nucleotide Polymorphisms, are single letter changes in the genetic code or DNA - much like a single letter change in the text of a book.
- Genetic fingerprints of each breeding line will be generated using 3,000 SNPs to identify lines that carry the best combination of genes for a particular trait.
- Once traits are associated with specific SNPs, MAS will be used for crop improvement.

What is Marker Assisted Selection (MAS)?

- Breeders use markers as landmarks to indicate what specific genetic information is in a given plant, in a process called **Marker Assisted Selection (MAS)**.
- Breeding using MAS employs markers to introduce genes into commercial varieties by classical breeding.

How Will MAS Aid Breeding Efforts?

- Detailed "road maps" of SNP markers will be used to select for particular traits like yield, nutrition, malting quality and disease resistance.
- Having markers linked to particular traits makes breeding faster because large populations can be screened quickly, even when traits are not visible, like malting quality.
- When breeders use markers, it is like seeing a familiar landmark and knowing you are close to home.

People Hired on Barley CAP Projects

Byung-Kee Baik, Washington State University, hired Sindhu G. Nair. She joined the program in the Department of Crop & Soil Sciences in Fall 2006 for her Ph.D. degree in Crop Science. She received her M.S. degree in Botany from the University of Mumbai, in India. She will investigate the genetics and biochemistry of food use traits of barley. Dr. Steve Ullrich will be her co-adviser.

Rex Bernardo, University of Minnesota, hired a computer programmer, Mr. Srikanth Srinivasan, to write and develop QTL Miner software.

Thomas K. Blake, Montana State University, hired one graduate student, Jeremy Jewell, and four undergraduates worked on the project this summer.

Patrick Hayes, Oregon State University. A Ph.D. student, Juan Rey, started his thesis research on marker assisted selection (MAS) for winter hardiness and human nutrition traits. A Research Associate, Dr. Peter Szucs, is working with the allele sequence data and map construction.

David Hole, Utah State University. One graduate student and two undergraduate students are now working on the project. One MS student, Justin Clawson, is responsible for overall nursery management. Justin is also helping to supervise undergraduate researchers. All students are involved in carrying out field trials and collecting data.

Richard D. Horsley, North Dakota State University. Jennifer Bolivar will begin her PhD assistantship, funded through the CAP, in mid-January. Her dissertation research will include measuring the dormancy of the spring growth habit CAP lines and to use the data for association mapping.

Jean-Luc Jannink, Iowa State University. One graduate student, Cristina Andreescu, will start working on the project in May.

Stephen M. Neate North Dakota State University. Sanjaya Gyawali a PhD student, is working on common root rot disease. Gyawali is involved in design, planting, maintenance, agronomic and disease assessment of the common root rot field trials, and data tabulation.

Paul Schwarz, North Dakota State University, hired an information specialist for the Institute of Barley and Malt Sciences, Karen Hertsgaard. Her responsibilities include development of educational and promotional materials and a web page for the CAP. She has the M.S. in agronomy with strong background in extension and outreach. A post-doc, Dr. Yin Li, will determine beta-glucanase activity and thermal stability for CAP germplasm.

Kevin P. Smith, University of Minnesota. Two graduate students are now working on the project. One Ph.D. student, Carol Powers, is studying malting quality. MS student, Jon Massman, started in June and is working on Fusarium head blight. Both students are involved in carrying out field trials and collecting data. One

undergraduate student, Magan Friskop, is collecting morphological data originally proposed by Jerry Frankowiak who has left the Barley CAP.

Brian J. Steffenson, University of Minnesota, is searching for a Ph.D. student to work on association mapping of disease resistance in the Barley CAP germplasm. His current Ph.D. student, Ben Alsop, conducted spot blotch disease evaluations in 2006.

Mitchell L. Wise, USDA, ARS, Cereal Crops Research. An undergraduate student is being trained in the laboratory procedures to be conducted.

Barley CAP Meeting Agenda – January 12

The USDA-CSREES funded Barley CAP, will meet at the Best Western Hacienda Hotel in San Diego, California on Friday, January 12, 2007, to present the first year results and develop future plans.

Tentative Meeting Agenda

8:00-9:00 am	Continental breakfast
9:00-9:30 am	CAP overview, budgets, renewal proposal, authorship, etc <i>Gary Muehlbauer, University of Minnesota</i>
9:30-10:30 am	Extension and education <i>Peggy Lemaux, University of California, Berkeley/Brian Steffenson, University of Minnesota</i>
10:30-10:45 am	Break
10:45-11:30 am	SNP mapping and genotyping update <i>Tim Close, University of California, Riverside/Pat Hayes, Oregon State University</i>
11:30-11:45 am	Illumina bead station <i>Shiaoman Chao, USDA-ARS</i>
11:45-noon	Discussion
Noon-1:30 pm	Lunch
1:30-2 pm	The Hordeum Toolbox <i>Julie Dickerson, Iowa State University</i>
2:00-2:30 am	Pedigrees and data submission <i>Jennifer Kling, Oregon State University</i>
2:30-3:00 pm	Phenotypes and traits <i>Kevin Smith, University of Minnesota</i>
3:00-3:15 pm	Break
3:15-3:45 pm	QTL miner development <i>Rex Bernardo, University of Minnesota</i>
3:45-5:00 pm	Discussion
5:00 pm	Reception

Not Quite Your Darling Clementine: *QTL Miner* Under Construction

The development of *QTL Miner* software has been underway since September 2006 at the University of Minnesota. Dr. Rex Bernardo, professor and endowed chair in corn breeding and genetics, is leading this software-development effort and is supported by Mr. Srikanth Srinivasan, a computer programmer and M.S. student in electrical engineering at Minnesota.

QTL Miner is a software package for finding molecular markers associated with quantitative trait loci (QTL). The software will utilize a mixed-model, association mapping approach that will exploit pedigree, marker, and phenotypic data routinely generated in a breeding program. *QTL Miner* is designed to be a stand-alone program useful not only for barley but also for other self-pollinated species. "I believe this feature makes *QTL Miner* attractive," reiterated Dr. Bernardo, "as it can be used not only in the Barley CAP but in the Rice CAP and Wheat CAP as well."

Prior to beginning to write the C++ source code for *QTL Miner*, Mr. Srinivasan, whose background is in computer science, spent several weeks learning the genetic concepts behind mapping QTL. Dr. Bernardo emphasized that, "It was very important for Srikanth to understand the basic biology and statistics behind the mapping approach so that his programming won't be in a vacuum." To date, the source code for inputting and searching files and assembling the data in the appropriate matrices has been completed. *QTL Miner* will use input files created through the Barley CAP *THT* database being developed at Iowa State University but could accept data from any source as long as the data are in the needed format.

Dr. Bernardo is already thinking of ways to increase the flexibility of *QTL Miner*. "We started out with the concept that *QTL Miner* will perform only one type of analysis: that the SNP markers are assumed to have fixed effects and the primary output would be finding those SNP markers with the largest, significant effects. These significant SNP markers would then be used for QTL introgression," said Dr. Bernardo. However, current plans are for *QTL Miner* to also perform analyses without marker data, with the goal of identifying barley lines with the highest breeding values based on pedigree and phenotypic data. And when the analysis includes marker data, users will also have the option of specifying markers as having random effects rather than fixed effects. Having markers as random would be the preferred approach if the breeding objective is not to identify a few markers

for introgression, but instead to jointly use many markers as a selectable surrogate for the phenotype for a complex trait. These approaches will be discussed during the *QTL Miner* update at the Barley CAP annual meeting in San Diego in January 2007.

A fully working version of *QTL Miner* is projected to be available by May 2007. But Dr. Bernardo expects that further refinement of the program will continue beyond that date. "A nice thing about this whole project," said Dr. Bernardo, "is that we have the time and flexibility to work with barley breeders to see what their needs are in marker-assisted breeding. We want *QTL Miner* to be breeder-friendly, and this can only happen if we let breeders use the software over a period of time so that they can let us know how we can make the software best meet their needs."



Barley CAP Research in Photos

Photo from Carl A. Griffey



Bob Pitman, Superintendent, at the Eastern Virginia Agricultural Research and Extension Center, took this photo showing barley height measurement (from Carl Griffey, Virginia Tech).

Survey of 5,000 Barley Producers

by Karen Hertsgaard

Five thousand current and past barley producers in Idaho, Montana and North Dakota will be able to share their views on barley production by completing a survey assembled by major stakeholder groups. The survey is a cooperative effort of the Institute of Barley and Malt Sciences (IBMS), the Barley CAP, the Idaho Barley Commission, the North Dakota Barley Council and the Montana Wheat and Barley Committee. Members of the IBMS Board of Directors represent barley producer and malting and brewing industry groups. The independent nature of the survey should lend validity to the results.

Questions on the survey address the effectiveness of current producer support and available information, the factors influencing the decision to produce barley, and finally overall satisfaction levels with barley.

One anticipated outcome of the survey is that it will identify areas where producers need additional information or support. This could include aspects of barley production, varieties, malt quality specifications, as well as components of the farm program. In addition, the survey responses will help identify the most effective means for communicating newly developed information.

The information gathered will help inform processors of barley and policy makers on the concerns of barley producers. This is a very important component in addressing declining national production of barley.

Karen Hertsgaard, Barley Information Specialist for the IBMS is coordinating the survey effort. The USDA North Dakota Agricultural Statistics Service mailed forms in November, and will follow-up with telephone interviews in December. The survey should take about 15 to 30 minutes to complete and those who return it by December 15 will be entered into a drawing for gasoline gift certificates and other prizes. Prizes were donated by the American Malting Barley Association, Anheuser-Busch, Cargill Malt, International Malting Co, Molson-Coors Brewing, and Rahr Malting Co.

The IBMS Barley Information Specialist position is partially funded through the Barley CAP. The survey represents the first step in the development of outreach efforts by this program. Please contact Karen if you have any questions or ideas on the survey or future projects. Karen Hertsgaard, Department of Plant Sciences, NDSU, 701-231-8063, karen.hertsgaard@ndsu.edu.

North Dakota State University Barley CAP Group

by Karen Hertsgaard

North Dakota State University (NDSU) brings to the barley CAP a tradition of interdisciplinary research and education in the barley and malt sciences. Scientists from NDSU are Richard Horsley, Stephen Neate and Paul Schwarz. Dr. Schwarz is the director of the newly formed Institute of Barley and Malt Sciences (IBMS), centered at NDSU, which was created for the purpose of integrating barley and malt science research and education in one location.

Dr. Yin Li, a post-doc working with Dr. Schwarz, will be determining beta-glucanase activity and thermal stability for the CAP germplasm.

Dr. Horsley is a barley breeder who is screening 960 CAP breeding lines each year for dormancy, and screening the CAP breeding lines from the Midwest for FHB resistance in the Osnabrock nursery each summer. Horsley recruited a new PhD student, Jenny Bolivar, who will oversee the dormancy screening as part of her dissertation research.

Dr. Stephen Neate, plant pathologist, is supervising the screening of CAP germplasm for resistance to common root rot caused by *Cochliobolus sativus*, as well as collaborating with Dr Kevin Smith at University of Minnesota in screening for Fusarium Head Blight disease



Left to right: Richard Horsley, Stephen Neate, Karen Hertsgaard, Paul Schwarz

in two locations in ND. Dr. Neate's PhD student, Sanjaya Gyawali, is developing methods for efficient screening for common root rot resistance for his dissertation.

Karen Hertsgaard began work as Barley Information Specialist (BIS) for the IBMS on November 1. Karen has a M.S. in Agronomy and experience in Extension and agricultural education outreach. Her efforts will include developing educational programs and materials designed to reach all stakeholder (grower and industry) groups. The BIS position is partially funded through the Barley CAP.

Barley CAP Approach To Enhancing Marker-Assisted Selection In Barley

by Kevin Smith

This article is based on a presentation entitled “Detecting Marker-trait Associations in Barley Breeding Germplasm for MAS” presented in the Symposium--Marker-Assisted Selection Strategies in Crop Improvement at the ASA-CSSA-SSSA 2006 International Meeting in Indianapolis, IN on November 16, 2006.

A major focus of the Barley CAP is to bring the tools of genomics to breeding programs and expand the use of marker-assisted selection (MAS) in barley. MAS can be a very effective means to introduce novel genes into varieties and greatly enhance the efficiency and lower the cost of selection for many valuable traits such as yield, disease resistance, and quality. The barley research community has been actively involved in genetics studies to identify quantitative trait loci (QTL) for numerous important traits (Figure 1). Ironically, fewer than a third of the U.S. barley breeding programs use MAS in their breeding programs.

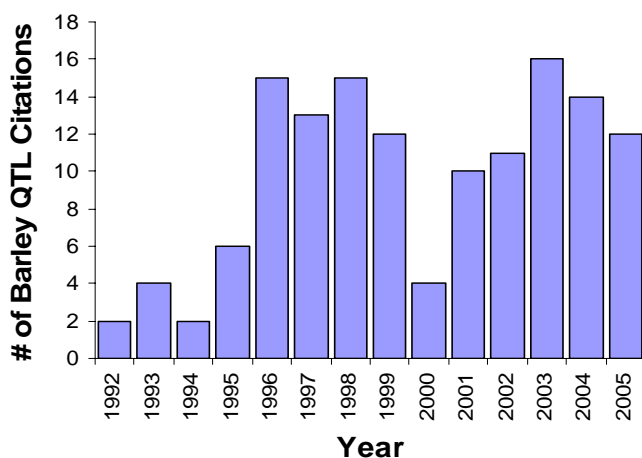


Figure 1. Number of published QTL mapping studies in barley from 1992 to 2005 based on Agricola search conducted November 3, 2006.

Barriers to MAS in Barley

Despite the wealth of QTL discovered in barley there are still significant barriers to effectively employing MAS breeding strategies.

- Cost of using markers has decreased dramatically, but is still a limiting factor for some programs.
- Often the parents used in QTL mapping studies are not relevant to breeding germplasm. An example is the case of malting quality QTL identified in the well-known Steptoe x Morex mapping population. The two major QTL regions identified in that mapping study have essentially been fixed for the Morex allele in the Univ of Minnesota breeding program making them of little use for MAS.
- Many of the traits studied in QTL mapping populations have relatively simple genetics and

can be selected effectively using traditional phenotypic selection.

- Because many QTL studies use unadapted parents the desirable gene can be tightly linked with undesirable genes often referred to as “linkage drag”. In this case additional fine-mapping studies are necessary to generate rare recombination events to free useful genes from their unadapted background.
- Often the effect of a gene in breeding germplasm is not the same as the effect that is predicted based on the QTL mapping studies. This can be due to the relatively small population sizes used in most mapping studies or the effect of the genetic background on the expression of the gene.

Traditional Mapping Approach: Marker-assisted selection for resistance to Fusarium head blight

Fusarium head blight (FHB) resistance is an excellent candidate for the use of MAS in breeding. This disease has devastated the Upper Midwest production areas, therefore resistance would be a very valuable trait for barley producers and the malting and brewing industries. Genetic studies have shown that resistance is controlled by numerous loci, scattered throughout the barley genome, each have relatively small effects (Figure 2). In addition, genetic resistance is not expressed consistently across environments.

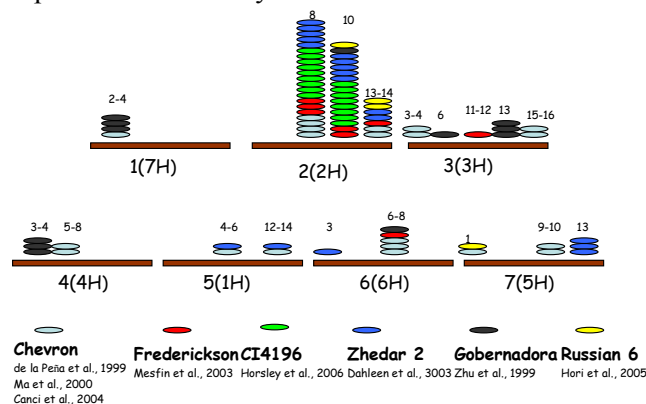


Figure 2. QTL for FHB identified in eight mapping studies using six different sources of resistance. Many loci have been identified, however several have been identified more consistently within and between different studies. Each colored oval indicates an environment in which a QTL for FHB severity was detected at that region of the genome. The numbers above the ovals indicate the Bin position on the chromosome.

Field screening for FHB resistance is also very expensive and labor intensive. This means that traditional breeding approaches will likely have a

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Enhancing marker-assisted selection continued from Page 6

difficult time consistently selecting for multiple genes with small effects that may not be expressed consistently in field screening nurseries. On the other hand, screening with markers linked to known resistant genes can be done cheaply and on large numbers of samples with nearly perfect reproducibility.

We have focused on two QTL regions associated with FHB resistance; one on chromosome 2(2H) bin 8 and the other on chromosome 6(6H). In each of these regions, we have encountered linkage drag. The chromosome 2(2H) QTL is associated with late heading which is not only undesirable but also interferes with accurate measurement of FHB severity. The region on chromosome 6(6H) is associated with high grain protein concentration which is undesirable in malting barley.

We have conducted genetics and breeding research on FHB in parallel (Figure 3). The initial mapping, validation, marker-assisted selection evaluation, and fine mapping studies for the chromosome 2(2H) region identified in the resistance source Chevron began in 1995. We have just now completed research that has fine-mapped the QTL for FHB and identified a recombinant that is both resistant and normal in heading date. We are using MAS with this line to utilize this resistance QTL in breeding for the first time.

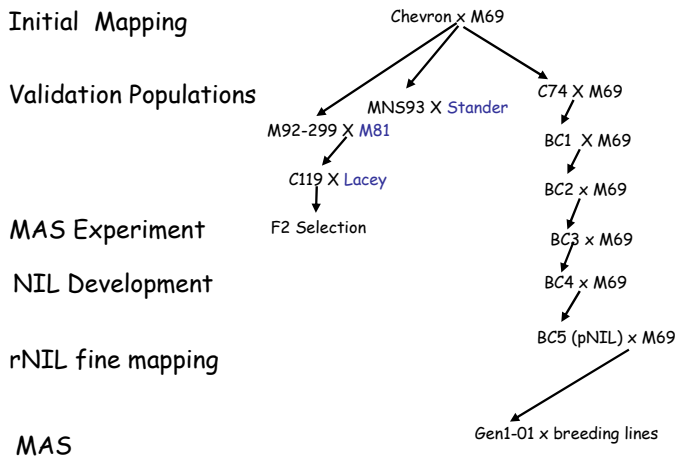


Figure 3. Time line for research on chromosome 2(2H) FHB QTL from initial mapping to utilization in MAS. After the initial mapping in the Chevron x M69 population, parallel efforts commenced to breed resistance and fine map the QTL through the development of near-isogenic lines.

Simultaneously, we have conducted traditional breeding for FHB resistance with over 10 other sources of resistance for which we have no genetic information. An example is shown in Figure 4, where over four breeding cycles we have developed a variety candidate with improved FHB resistance. Breeding for this line did not involve MAS and the line does not carry resistance alleles

at the known QTL for FHB. This line, M122, and many others like it represent a source of resistance genes that are free of linkage drag and proven to be effective in the relevant breeding germplasm. Barley CAP will map these and many other useful genes in breeding germplasm and provide a basis for manipulating them using MAS.

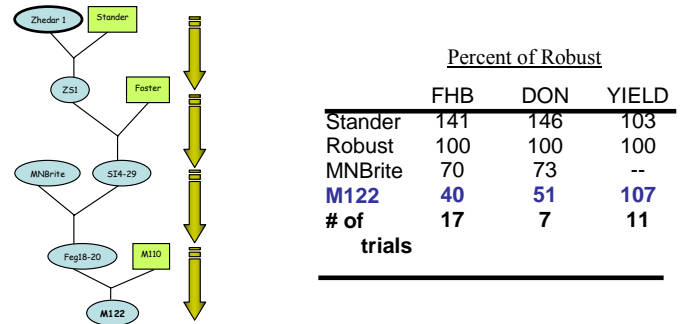


Figure 4. Performance of variety candidate M122. This line was developed over 4 cycles of breeding for improved FHB resistance, agronomic performance, and malting quality.

Barley CAP Approach to Mapping and Marker-Assisted Selection

The Barley CAP was designed to address the current barriers to widespread incorporation of MAS in barley. The technical issues related to the lack of useful high-throughput markers will be addressed by the construction of a 3,072 single nucleotide polymorphism (SNP) map. These markers will be used to conduct genome-wide association mapping for traits of interest. The partnership between the Barley CAP and USDA Genotyping Centers will insure that SNP markers that tag important traits will be quickly moved into a high-throughput format suitable for MAS. The Barley CAP will use very large population sizes (to increase statistical power) that consist of contemporary breeding germplasm (to insure that QTL discovered are relevant). This will be accomplished by asking each of 10 breeding programs to submit 96 breeding lines in each of four years to create a population size of 3,840. This large population of current breeding germplasm will be evaluated for over 40 traits. Much of this trait data will be collected as a part of the normal breeding program activities while other data will be collected by collaborating scientists within the Barley CAP. In addition all of the Barley CAP breeding lines will be genotyped with the 3,072 SNP markers and all the trait and genotype data will be housed in a newly developed database called The Hordeum Toolbox (THT). All the data in THT will be freely available to allow all researchers to conduct genetic mapping studies on a wide range of traits. Breeders will also be able to query the database to identify specific breeding lines that they will use in crosses and markers that can be used for MAS.

OPAs, Centerpiece of BarleyCAP Genotyping Activities

by Timothy Close

The centerpiece of BarleyCAP genotyping activities will be two Illumina oligonucleotide pool assays (OPAs), each designed to determine the genotype at 1536 points (single nucleotides) in the barley genome. These two OPAs, referred to as BarleyOPA1 and BarleyOPA2, are preceded by an initial testing phase headed by Timothy Close at the University of California, Riverside. This testing phase actually began prior to the start of BarleyCAP with the development of the first barley OPA, referred to as PilotOPA1. Close at UCR, supported by a grant from the National Science Foundation Plant Genome Research Program, with colleagues at the Scottish Crop Research Institute (SCRI) in Dundee, Scotland and the Leibniz Institute of Plant Genetics and Crop Plant Research in Gatersleben, Germany developed PilotOPA1 and have recently published a paper in Proceedings of the National Academy of Sciences describing the use of single nucleotide polymorphisms (SNPs) targeted by PilotOPA1 to clarify genetic relationships within cultivated barley germplasm.

PilotOPA1 provided 1237 high quality SNPs, 967 of which were mapped in at least one of three barley mapping populations: Morex x Barke, Oregon Wolfe Barley, Steptoe x Morex. In August 2006 the results from the first BarleyCAP OPA, PilotOPA2, were produced at the University of California, Los Angeles genotyping laboratory. Pilot OPA2 was designed in January 2006 by

Close and Luke Ramsay from SCRI, but it's purchase had to wait until July to allow time for each institution to set up accounts and transfer funds. PilotOPA2 yielded 1127 high quality SNPs, of which 843 were mapped in at least one of these same three mapping populations, taking the total number of mapped SNPs from the two pilot OPAs to just over 1800.

In December 2006 Close utilized the very best SNPs from PilotOPA1 and PilotOPA2 to design the first permanent OPA, BarleyOPA1, targeting only SNPs that proved to be highly successful on the two pilot OPAs. BarleyOPA1 targets SNPs at 1314 loci mapped in at least one of the three standard mapping populations and 222 unmapped SNPs. Each of the 1536 SNPs on BarleyOPA1 has a minor allele frequency of at least 8% in the germplasm that has been assayed so far. BarleyOPA1 will be implemented in the BarleyCAP project well ahead of the planned date of late 2007, perhaps as early as February 2007.

The BarleyCAP project is continuing this marker development effort with the design of PilotOPA3, which is due to be completed in the near future, so far having been designed mainly by Close and Nils Rostoks from SCRI. Once the results are available from PilotOPA3, then the second of two permanent OPAs, BarleyOPA2 will be designed.

Calendar

12/10-12/2006	2006 National Fusarium Head Blight (NFHB) Forum, Raleigh, North Carolina
1/5/2007	Year 2 work plans due to Gary Muehlbauer
1/11/2007	Barley Improvement Conference, Hacienda Hotel, San Diego, CA
1/12/2007	Barley CAP meeting, Hacienda Hotel, San Diego, CA
1/13-17/2007	Plant and Animal Genome XV Conference, San Diego, CA
2/10/2007	Barley CAP, USDA-CSREES continuation proposal due
4/2/2007	Year 1 progress reports due to Gary Muehlbauer

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.

