

### Gary's Update



The barley CAP is about to complete the first year of the project. Significant progress has been made in all areas. We held our annual meeting in San Diego, CA, on January 12, 2007. CAP participants, stakeholder and scientific advisory board members, growers, industry representatives, and barley geneticists from around the world were in attendance. In total, almost 80 people attended the meeting, including over 30 that are not directly associated with the project, indicating the interest the barley community has in the project.

Progress on all aspects of the project was reported (see this page, right). In a written review of the project, the scientific and stakeholder advisory boards were suitably impressed by the progress and cooperation of the barley CAP participants.

Over the past few months, the first phase of the SNP genotyping platform was completed. The first phase, referred to as barley OPA1, results in the capacity to genotype 1,536 SNPs in a single assay. To receive the best pricing for the SNP genotyping, an international group of barley geneticists have placed a combined order for 21,000 samples. The barley CAP will use 3,840 samples, with the remaining samples going to other U.S. and international projects. This coordinated international order exemplifies the cooperative spirit among barley geneticists worldwide.

Within this newsletter you will see a description of the activities in various aspects of the barley CAP and barley genomics. Tom Blake's group at Montana State University (page 4), Shiaoman Chao's genotyping center at Fargo, ND (page 5), and grower outreach activities with Marv Zutz and David Ruark (page 6) are highlighted. In addition, the development and structure of the International Barley Genome Sequencing Initiative is also described (page 7).

The second year continuation proposal was submitted on February 9, 2007. The continuation proposal can be viewed on the website ([www.barleycap.org](http://www.barleycap.org)). Due to budget issues in the federal government, the second year funding will likely be delayed. Make sure to plan for the delayed funding. First year progress reports are due on April 1, 2007. Please send your progress reports to Lynne Medgaarden ([medga001@umn.edu](mailto:medga001@umn.edu)).

### Barley CAP Annual Meeting

by Gary Muehlbauer

January 12, 2007, Hacienda Hotel, San Diego, CA, Barley CAP participants present: Byunk-Kee Baik, Rex Bernardo, Tom Blake, Peter Bradbury, Victoria Carollo, Shiaoman Chao, Timothy Close, Blake Cooper, Julie Dickerson, Carl Griffey, Patrick Hayes, Rich Horsley, David Hole, Lee Jackson, Jean-Luc Jannink, Jennifer Kling, Peggy Lemaux, Stefano Lenardo, Gary Muehlbauer, Stephen Neate, Don Obert, Mark Schmitt, Paul Schwarz, Kevin Smith, Brian Steffenson, Mitch Wise, and Roger Wise.

Scientific advisory board members present: Mike Davis, Sally Leong, David Marshall, Diane Mather, Brian Rossnagel, Howie Smith, 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. In addition to the PIs and advisory board participants, approximately 10 graduate students and post docs that work on the project, and approximately 30 scientists not directly associated with the project attended the meeting. The meeting consisted of a series of short presentations and discussion.

### Overview of project

An overview of the barley CAP was provided by Gary Muehlbauer. In his presentation he discussed the development of an authorship policy. A formal authorship policy will be developed soon. He also discussed the development of a framework to avoid duplication of work. A list of barley CAP participants and their research area will be placed on the website.

### Outreach and education

Brian Steffenson (Univ of Minnesota) and Peggy Lemaux (Univ of California, Berkeley) outlined the outreach and education component of the project. Peggy presented the materials that she and Barbara Alonso have developed including: the barley CAP logo, a business card, powerpoint slides, technical and nontechnical posters, and a brochure. The slides and

*Barley CAP Annual Meeting Continued from Page 1*

posters have been placed on the barley CAP website for download and use. These materials have been used for numerous stakeholder and scientific meetings.

Brian presented a logic model for the extension/education activities (Figure 1). This model will help set the short, medium and long-term priorities of the extension/education effort of the barley CAP. An important point made in this description of the logic model is that we need to ensure we integrate the outreach and education efforts in all aspects of the project.

To enhance our efforts, the barley CAP has teamed with the Institute of Barley Malt Sciences (IBMS) on the outreach/education component. The barley CAP is partially funding the salary of a communication specialist (Karen Hertsgaard) located in Fargo, ND at the IBMS. The IBMS and barley CAP have conducted a survey of producers and users to determine their needs in optimizing barley production, end-use, utilization, etc. and the best means of disseminating information to these stakeholders. Data from the survey have been obtained and the results will be made available soon.

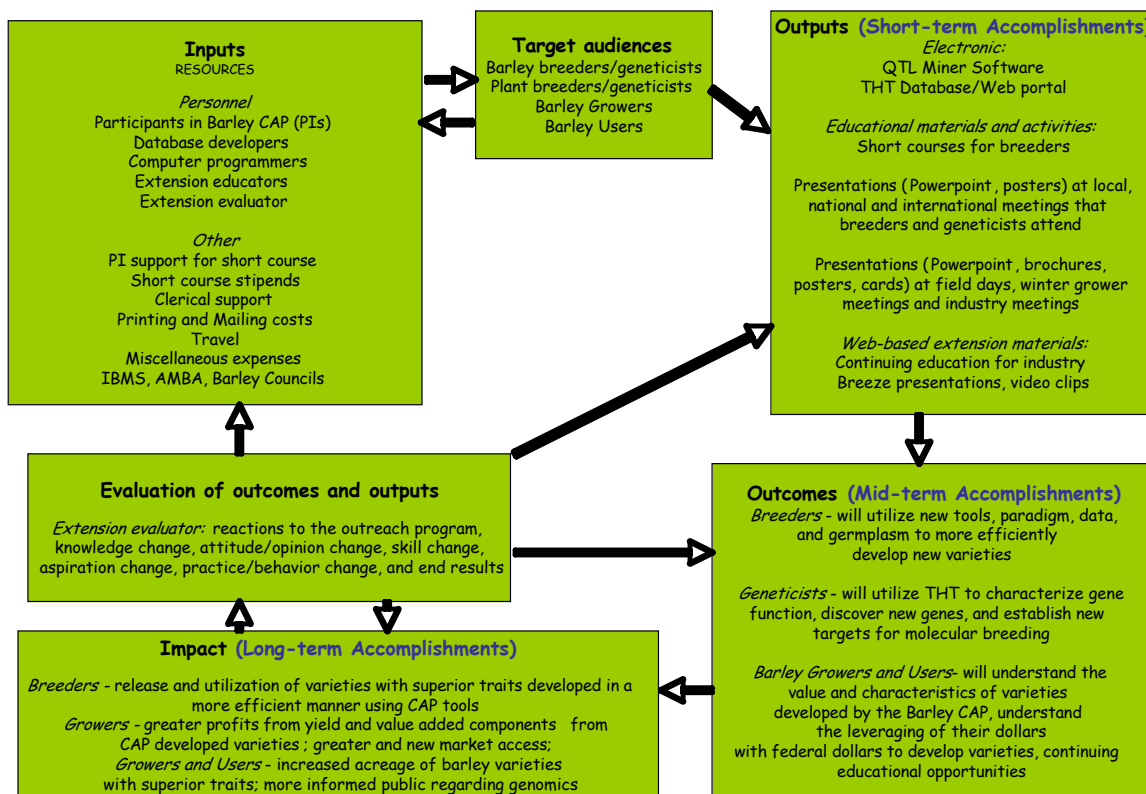
Brian also described another approach the barley CAP is using to enhance our outreach efforts. We are enlisting extension educators who will disseminate Barley CAP information in each state. We have identified at least one extension educator in all of the participating Barley CAP

states (with significant acreage of barley production) to assist in outreach and extension activities. These educators will make presentations about the Barley CAP and deliver printed material to barley growers. In Minnesota, we are working with Hans Kandel (extension educator) and Marv Zutz (Minnesota Barley Council). We have provided brochures, cards and a nontechnical poster. These materials have been presented at grower meetings in Minnesota in Fall 2006 and Winter 2007. The success and constraints of the Minnesota effort will help direct future efforts of this kind in other states.

One goal is to educate the next generation of scientists. Nine graduate students, three post-doctoral research associates, two technicians, and seven undergraduates were hired on the Barley CAP. These individuals will be involved in research, and outreach and extension activities.

Another important outreach goal is to enhance the linkages with barley growers and end users on the applied outcomes of the project. To this end, Marv Zutz (Minnesota Barley) and David Ruark (Washington State barley grower), presented short talks on the outreach efforts that grower groups would like to see. For a complete description of all outreach and education activities of the barley CAP, please see the year 2 continuation grant on the barley CAP website.

**Figure 1. Barley CAP outreach/education logic model**



### *Barley CAP Annual Meeting Continued from Page 2*

#### **SNP mapping and genotyping**

Tim Close (University of California, Riverside) described the Illumina SNP technology and 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 mapped SNPs will be used to design two OPAs (3,072 SNPs) for genotyping. In addition, we plan to integrate the BAC-based physical map with the mapped SNPs.

The design was completed for the first of two project pilot OPAs. The name PilotOPA1 refers to a pilot OPA that was developed prior to BarleyCAP in an NSF-funded project of Close and Lonardi. Using PilotOPA1, data were obtained from 96 samples from each of the three mapping populations (Morex x Barke, Oregon Wolfe Barley, Steptoe x Morex) provided by Nils Rostoks (SCRI) and a set of 96 European germplasm selections from Nils Stein (IPK). Subsequent to this effort, the barley CAP funded genotyping of the barley CAP core (96 genotypes that represent U.S. diversity) with PilotOPA1.

PilotOPA2 was a product of the barley CAP. PilotOPA2 was ordered, synthesized, received and used at the University of California, Los Angeles genotyping lab to generate data from 480 DNA samples. These included 96 samples for each of three mapping populations, the barley CAP core, and the 96 European germplasm selections. Pat Hayes (Oregon State University) developed a SNP-based map of the Oregon Wolfe Barley population. Taken together, PilotOPA1 and PilotOPA2 resulted in 1,810 high quality mapped SNP markers to an evolving SNP-based barley genetic linkage map.

The first permanent OPA, BarleyOPA1, was designed using only highly successful SNPs from PilotOPA1 and PilotOPA2. The content includes only loci that have a minor allele frequency of at least 8%; of these 1536 loci, 1314 have been genetically mapped and 222 have not been genetically mapped.

The barley CAP will be using the USDA-ARS genotyping lab (S. Chao) for genotyping breeding lines. The Illumina Bead Station was purchased and shipped in late August and installed October 24. The training was completed November 27 to December 1, 2006. Ten people attended the training, three from the USDA-ARS Fargo

genotyping lab, three students from Rich Horsley's lab, one student from Shahryar Kianian/Elias Elias's lab, one post-doc from Brian Steffenson's lab and two post-docs from Tim Close's lab. Chao subsequently obtained high quality pilotOPA1 data from the barley CAP core.

#### **Bioinformatics**

Bioinformatics are key enabling technologies in the barley CAP. Two major areas of work are in the development of The Hordeum Toolbox (THT) database and the QTL miner software program. Julie Dickerson (Iowa State University) described the progress on the development of THT. THT will house all genotype and phenotype data collected from the 10 barley breeding programs. This database will enable barley breeders to more efficiently breed superior varieties.

Rex Bernardo (University of Minnesota) provided an update on the development of QTL Miner. QTL miner will provide the ability to identify marker-trait associations in breeding lines. THT and QTL miner are both expected to be ready for beta testing by the end of the first quarter of 2007.

#### **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 (University of Minnesota) provided an update on the seed collection, dispersal and phenotyping. To facilitate consistent data collection and seed dispersal, an updated participants guide has been developed by Kevin and is now on the website. The phenotype data are being collected for most of the 40 traits and should be available in the near future. Developing pedigrees for each of the breeding lines is another important task for downstream mapping applications. Jennifer Kling (Oregon State University) described her efforts to obtain pedigrees from each breeding program and to place them in a standard format. Scientific Stakeholder Advisory Board Reports

#### **Advisory Board Activities**

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.

## Montana State University Barley Crew

by Victoria Carollo and Tom Blake

The barley improvement program at Montana State University focuses on combining the best available genetics technologies with classic pedigree-based breeding to develop barley varieties that fit our markets and our predominately dryland production environments. Our primary objective is to improve the livelihoods of Montana barley growers, and to develop techniques and germplasm to enable the advancement of barley improvement programs worldwide.

Our primary contribution to the 2006 barley CAP was providing one of the two seed production environments for the spring barley multi-program nursery. In 2007, we will use seed produced in our 2006 nursery to plant a replicated dryland and a replicated irrigated nursery. We will estimate relative dryland and irrigated performance from these 876 lines, hopefully providing the phenotypic data needed to do an association analysis of adaptation. Photos of the Bozeman CAP nursery are available at <http://hordeum.oscs.montana.edu/capnursery/>

MSU's barley improvement program is unique in its long collaboration with MSU's rumen nutrition program, headed by Dr. Jan Bowman. We train undergraduate scholars to work in the field, in the laboratory and *in rumen*.

Jeremy Jewell, our CAP-supported MS student, is completing his MS degree this spring and will likely join Washington State University's plant molecular biology group this summer to begin his Ph.D. studies. Stan Bates runs our field breeding program and began his graduate program in the winter of 2007. Victoria Carollo, a GrainGenes curator, joined the Blake lab in April 2006.

While we graduated many PhD and MS scientists over the past two decades, we have refocused our efforts on the development and advancement of undergraduate scholars. We believe we can have even greater impact on future American plant breeding by infusing Montana undergraduates with enthusiasm for barley breeding and applied genetics. These students directly participate in our CAP-focused research efforts, and will become the graduate students and educators of future generations.



Victoria Carollo and Tom Blake



Barley CAP personnel include our four undergraduates, Kyle and Jessica Patrick, Duke Pauli and Chris Shafer.



This photo shows Kyle Patrick, one of our CAP-supported undergraduates, working with Buelah, one of our bovine barley digestibility bioassay technicians.



Jessica Patrick doing a DNA extraction.

## High Throughput SNP Genotyping with the Illumina's Beadstation 500GX

by Shiaoman Chao, USDA-ARS, Fargo, ND

One of the main components of the barley CAP program is to genotype 3,072 barley SNP markers on 960 barley breeding lines contributed from 10 breeding programs in the country each year for four years. The large amount of SNP data will be the basis for the association genetics studies in the barley CAP program. The high throughput SNP genotyping assays will be performed in the USDA-ARS small grains genotyping center at Fargo, ND. The SNP genotyping platform we will use is the BeadArray system developed at Illumina. By using the GoldenGate assay, 1,536 SNP markers can be genotyped on 96 samples in parallel on the BeadArray. The BeadStation 500GX (Fig. 1) was purchased and shipped to Fargo on August 24, 2006 and installed on October 24, 2006. The training, including performing the GoldenGate assay, scanning the array on the BeadStation, and analyzing data using the BeadStudio v.2 software, was conducted between November 27 and December 1, 2006. Ten people attended the training, three from the USDA-ARS Fargo genotyping lab, three students from Rich Horsley's lab, one student from Shahryar Kianian/Elias Elias's lab, one post-doc from Brian Steffenson's lab and two post-docs from Tim Close's lab.

To compare the DNA purification methods and to optimize the genotyping techniques, a pilot study was subsequently initiated after the training. The barley PilotOPA1 developed and used by Tim Close previously was re-synthesized. To facilitate the optimization, 96 US barley core germplasm provided by Patrick Hayes and Tim Close were used, four of which were previously genotyped with the original batch of PilotOPA1. The leaf samples at seedling stage were collected from a single plant and freeze dried. Genomic DNA was individually extracted using the SDS-based method in order to cross-check and compare genotyping data generated using the Qiagen kit as the DNA purification method in Tim Close's lab. The results should allow us to determine if both DNA extraction methods are equally adequate to generate high quality of genotyping data.

I visited Tim Close's lab in January 2007 to compare the new pilot data with Tim's previous data for all 1,536 SNPs in the PilotOPA1. Our conclusions were that the new data from all samples are of excellent quality, thus, the SDS purification method is fine, and the new synthesis of PilotOPA1 gave the same genotype calls as the original batch.



Figure 1. The BeadStation 500GX with an array matrix being loaded for scanning.

The work plan for 2007 is that I will first finish the pilot study with samples sent from various labs. When barley OPA1 becomes available, the focus will be to genotype 960 breeding samples collected in 2006 and 2007. The leaf samples will be collected and freeze dried by Kevin Smith and shipped to us. Because a single assay will take a minimum of three days to process, and all the assays will be manually performed, I will be able to assay two 96-well plates per week for a total of 40 plates per year. The samples from the barley CAP program will be given the highest priority. Therefore, collaborators with samples from projects outside the barley CAP should consider the UCLA genotyping lab as an alternate genotyping service provider to obtain results in a timely manner.



## Minnesota Barley CAP Extension and Outreach

by Marvin Zutz

Marvin Zutz, Minnesota Barley Council, and Hans Kandel, Minnesota Extension Regional educator, have been attending grower education meetings and trade shows for the past several months speaking to growers about the Barley CAP project funded by the USDA CSREES.

The investment in the Barley CAP by CSREES has expedited the communication between barley breeders, pathologists, computer scientists, geneticists, and food and malt scientists across all barley regions. Breeders will use marker assisted selection in their programs to accelerate the introduction of new, improved varieties. Breeding programs, in general, generate large volumes of data. The Barley CAP will allow breeders to share germplasm and conduct marker-assisted selection to enhance barley breeding traits. The Barley CAP extension outreach program has been delivered to thousands of producers in Minnesota and North Dakota. Successes of the Barley CAP will be presented to the growers in Phase 2 and 3 of the project.



*Marvin Zutz, presenting Barley CAP and Wheat CAP Posters at North Dakota Ag Expo, Fargo*



*Representative Colin Peterson, D-MN, Chair, House Ag. Comm in front of Wheat CAP poster.*

## Barley CAP Outreach in Washington

by David Ruark

While research is the real key to the success of the Barley CAP, educational outreach to growers and industry is an important component. I am located in southeast Washington State and am one of two barley growers - the other in Minnesota - who serve on the CAP stakeholder advisory board. I will discuss some of the education and outreach programs being conducted in Washington.

We are blessed with the Washington Barley Commission (WBC) and Washington State University (WSU), located in the major barley growing area of the state. I have concentrated on enlisting their support and cooperation to help carry this important message to the growers and industry.

Winter and the early spring are the times for grower meetings in the barley production area. These meetings provide an excellent chance to present the details of this program to larger groups. Spokane, WA, is the home of an Ag Expo each January or February which draws a large number of growers and industry people from mainly Washington State, but also Idaho, Montana and Oregon. The WBC presents several mini-workshops during the three-day event, where attending growers are awarded pesticide credits. Expo is our biggest opportunity for education and information dissemination on the Barley CAP. The WBC and John Burns, extension agronomist, presented Barley CAP information at these workshops.

I gave presentations and passed out brochures and information cards to the WBC at their December 13 meeting with 7 key growers and 2 industry reps, and at the Clearwater Direct Seeders Meeting, January 16 with 25 growers from Washington and Idaho using Direct Seeding. I have made arrangements with the WBC to present information and disseminate brochures and information cards at grower meetings on February 21, 23, 26, and 28.

John Burns will present information and materials at the growers' meetings he attends. Steve Ullrich, WSU, will discuss CAP benefits at meetings throughout the year.

Another opportunity for outreach is via the local fertilizer/chemical dealers and local grain elevators. We are able to provide CAP information at these locations.

Additionally there are several area agricultural trade publications with circulation in our four state area that we hope will carry the Barley CAP story in due time. Washington State Wheat Growers (wheat growers are also barley growers), has a monthly publication, which will carry the story as will the WBC which has a quarterly publication, distributed to state barley growers.

These are some of the avenues and organizations that I have utilized to get the CAP story out. I am always looking for more ways to make barley growers and the barley industry aware of how this CSREES program will benefit them in the very near future.

## The International Barley Genome Sequencing Consortium (IBSC)

During the International Triticeae Mapping Initiative (ITMI, <http://wheat.pw.usda.gov/ITMI/>) meeting, August 27- 31, 2006 in Adelaide, Australia, representatives of the leading barley research groups in Australia, Europe, Japan and USA assessed the status of barley genomics. They decided to undertake a major, worldwide initiative to sequence the barley genome using state of the art sequencing technologies. This initiative will include: (i) shared use of existing resources, (ii) the continued coordination of ongoing research activities and (iii) a coordinated strategy to raise funding on the national and international level.

To reach the goal of a genomic sequence of barley they formed the International Barley Genome Sequencing Consortium (IBSC) (<http://barleygenome.org/>). The consortium was charged to:

- summarize the present status of research and resources development
- prepare a strategic research agenda (white paper)
- outline an agreed-upon sequencing strategy
- further enhance the existing research network
- coordinate activities to bundle projects into a generally agreed research program
- provide an interface for the interaction with other sequencing consortia
- garner political support
- facilitate funding on the national and international level

The consortium met at the Plant and Animal Genome Meetings in San Diego in January 2007. Andreas Graner and Nils Stein were selected as co-chairs of the consortium.

To implement the program of the consortium, a steering committee was nominated consisting of eight internationally renowned scientists representing leading research groups:

- Peter Langridge, Director, Australian Centre for Plant Functional Genomics (ACPF), Australia
- Roger Wise, Research Geneticist, USDA-Agricultural Research Service (USDA-ARS) at Iowa State University (ISU), USA
- Andreas Graner, Head of Department, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany
- Takashi Matsumoto, Head of plant genome research lab, RGP, National Institute of Agrobiological Sciences (NIAS), Japan

- Kazuhiro Sato, Associate Professor, Okayama University (OU), Japan
- Robbie Waugh, Program Leader Genetics, Scottish Crop Research Institute (SCRI), Scotland
- Timothy Close, Professor of Genetics, University of California Riverside (UCR), USA
- Alan Schulman, Professor at MTT/BI Plant Genomics Laboratory, University of Helsinki, Finland

Membership in the consortium will be open to any institution from the public and the private sector willing to provide an active, specific contribution.

The **objective of the IBSC** is to physically map and sequence the barley gene space, with the near-term need being the identification of the ~50,000 barley genes, including the 5' and 3' regulatory regions, and the longer-term goal an ordered physical map linked to the genetic map to accelerate crop improvement.

The initial steps to sequencing barley are described here. Germany will provide a whole-genome physical map integrated with the current NSF-funded map (PI Close). Australia will provide new BAC libraries for physical mapping in addition to targeted sequencing efforts on 7H (to be linked with wheat group 7). An SCRI-led effort will provide BAC-end sequences anchored to the genetic map. The Japanese group will provide additional gene discovery and targeted BAC sequencing. The efforts of this group have jump-started barley genome sequencing.



## Cooperative Research Focus of Barley Improvement Conference

by Karen Hertsgaard

The cooperative nature of barley research and improvement efforts was evident at the 36th Barley Improvement Conference in San Diego, CA, January 10-11, 2007.

Nearly 80 barley researchers, scientists, industry officials and outreach personnel from the U.S., Canada, Scotland, Australia and the Czech Republic attended. Researchers from the USDA-CSREES-funded Barley CAP also attended and held their annual meeting on January 12.

Ten educational sessions and breakout meetings were held to discuss malting barley research, agricultural policy and quality evaluation issues. Session topics included international barley disease control, malting quality standards, biofuel production, barley winter hardiness, health benefits of food barley, and genomics and technology methods to enhance barley breeding.

The capstone of the conference was a speech by Richard Groven, Northwood, ND, farmer and vice president, National Barley Growers Association, titled “Barley – the Outlook and the Look-Outs.”

Changes in barley production have been dramatic in recent years. According to Groven, production has decreased from 118,800,000 bushels in 2003 to 48,755,000 bushels in 2006. Barley acreage decreased from 1,980,000 acres in 2003 to 995,000 acres in 2006.

Recent events give cause for increased optimism for barley producers. Prices increased since July and the feed barley market has revived due in part to increased need for corn for ethanol production. Dry conditions have forced increased consumption of carryover stocks. New variety research looks promising. Groven stated that “sound varieties and improved prices allow for an optimistic outlook for barley in 2007.”

### Calendar

**March 23 - 27, 2007**

[2nd International Conference on Plant Molecular Breeding](#)

Sanya, Hainan, China

**April 2 - 4, 2007**

[North American Cereal Rust Workshop](#)

University of Minnesota, St. Paul

**April 1, 2007**

Year 1 progress reports due to Gary Muehlbauer

**April 16-20, 2007**

Aaronsohn-ITMI Workshop, Gai Beach Hotel, Tiberias on the Sea of Galilee, Israel. Wild emmer wheat, *Triticum turgidum* ssp. *dicoccoides* (genome BBAA), the progenitor of domesticated wheat, was discovered in 1906 by A. Aaronsohn in Northern Israel. Aaronsohn had the pioneering vision that the progenitor of wheat would become a source of genes for wheat improvement. To celebrate the 100th anniversary of the discovery of wild wheat by Aaronsohn, the Israeli Gramineae Consortium will host the next [ITMI Meeting \(April 16-20, 2007\)](#) on the shore of the Sea of Galilee, where wild emmer wheat was discovered.

**May 6 - 10, 2007**

[EWAC -- The European Cereals Genetics Co-operative](#)

Istanbul, Turkey

**October 26–28, 2007**

120th Anniversary Convention of the Master Brewers Association of the Americas in Music City USA—Nashville, Tennessee

**Jan. 12-16, 2008**

International Plant and Animal Genome Conference, Plant & Animal Genome XVI, San Diego, CA

### 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.

