

**Barley Coordinated Agricultural Project Work Plan Year 4 (4/1/2009 – 3/31/2010)**  
**Shiaoman Chao, USDA-ARS, Fargo, ND**

1) Describe the research, education, and outreach activities you are planning for year 4 (4/1/2009 – 3/31/2010)

Research : We expect to receive leaf materials for year 3 breeding lines collected in fall 2008 at the beginning of 2009, and to start extracting DNA from these samples possibly in March or April, 2009. Genotyping of BarleyOPA1 and 2 will be carried out for year 3 materials subsequently after DNA is extracted. All genotyping data when become available will be uploaded to Chao's website for release. Year 4 materials are expected to be grown out in the fall of 2009 in Minnesota. DNA will be extracted from year 4 samples in early 2010. Genotyping of BarleyOPA1 and 2 is expected to carry out and finish before the summer of 2010.

Education : We will provide the training on the use of the Illumina system to students, postdocs or scientists who intend to use the system and the OPAs generated in the barley CAP for their own research.

Outreach : This will be done through the program set up by the project members at NDSU.

2) List specific outcomes and deliverables that will be accomplished in the first 6 months (4/1 – 9/30). These will be used as benchmarks for your bi-annual progress report.

- Continue DNA extraction for 2008 CAP breeding lines (the third set of 960 samples).
- Carry out SNP genotyping on 2008 CAP breeding lines (the third set) using BarleyOPA1 and 2.
- Upload final data to Chao's website, and release data to breeders and to Iowa State University.

3) List specific outcomes and deliverables that will be accomplished in the second 6 months (10/1 – 3/31). These will be used as benchmarks for the bi-annual progress report.

- Continue SNP genotyping on 2008 CAP breeding lines (the third set) using BarleyOPA1 and BarleyOPA2, in case there is a delay on reagent delivery from Illumina.
- Upload SNP data to Chao's website, and release data to breeders and to Iowa State University.
- Start DNA extraction for 2009 CAP breeding lines (the fourth and final set of 960 samples).
- Carry out SNP genotyping on 2009 samples using BarleyOPA1 and 2

**Barley Coordinated Agricultural Project**  
**Six-Month Progress Report**  
**(4/1/08 – 9/30/08)**

**Shiaoman Chao, USDA-ARS, Fargo, ND**

**1) Describe the research, education, and outreach activities you completed (4/1/08 to 9/30/08)**

Research. The Fargo lab started genotyping 960 of year 2 samples collected in 2007 with Barley OPA1 in late March, 2008. This work was finished by late April, 2008. The data were

subsequently analyzed and released to Chao's SharePoint site for breeders access in early May, 2008.

Barley OPA2 was synthesized and shipped to Fargo in July 29, 2008. Around that time, the second scheduled shipment of GoldenGate genotyping reagents from Illumina was delivered to Fargo. During the period of August and early September, 2007, 960 breeding lines collected in 2007 (year 2 samples) were genotyped with Barley OPA2. The genotyping data calls were sent to Tim Close's lab for call validation. Final data will be released by September 30, 2008 to breeders from Chao's SharePoint site.

The Fargo lab continued Barley OPA2 genotyping on 960 of 2006 samples (year 1) starting in mid September, 2008. It is scheduled to finish by late October, 2008. Expected date for data delivery is in early November, 2008.

The raw data, and validated OPA1 data for 2007 (year 2) samples were sent to Iowa State University to be integrated in The Hordeum Toolbox in June, 2008. The OPA2 data for year 2 samples will be mailed to Iowa by September 30, 2008.

The Fargo lab also genotyped 96 pooled BAC clones from Tim Close's lab with Barley OPA2 for deconvoluting the relationships between the SNP markers and the BAC clones containing the SNP markers.

Education. We trained a graduate student from Rich Horsely's lab at North Dakota State University on the use of Illumina genotyping system for mapping agronomic traits of interest.

Outreach. Participated in the barley CAP association genetics and marker assisted selection workshop in June 2008, and discussed the platforms used for high throughput SSRs and SNPs genotyping, and the functionality of the ARS genotyping labs. The participants, including breeders, scientists and students, are project members of barley, wheat and rice CAP programs.

## **2) List specific outcomes and deliverables accomplished (4/1/08 to 9/30/08)**

- Carry out SNP genotyping on 960 breeding lines collected in 2007 (year 2 samples) using BarleyOPA1.
- Release OPA1 SNP data for 2007 (year 2) samples to breeders.
- Send final and verified year 2 OPA1 data set to Iowa State University.
- Carry out SNP genotyping of breeding lines collected in both 2006 (year 1) and 2007 (year 2) using Barley OPA2
- Send OPA2 data to Tim Close's lab for data validation in mid September, 2008.
- Release OPA2 data for the year 2 (2007) samples to breeders in late September, 2008.
- Carry out SNP genotyping on 96 pooled BAC clones as a part of BAC deconvolution studies.