

Barley Coordinated Agricultural Project Work Plan FY06 (3/1/06 – 2/28/07)
Timothy Close & Stefano Lonardi, University of California, Riverside

1) Describe the research, education, and outreach activities you are planning for the next year (3/1/06 – 2/28/07)

Research. We will design two Illumina pilot oligonucleotide pool assays (OPAs) to test the performance of 1536 SNPs each (a total of 3072), followed by two OPAs containing only successful SNPs. The 3072 SNPs for two final OPAs will be drawn from the 3072 tested in this project and 1524 SNPs that were tested previously in an NSF project of Close and Lonardi. We will lead the genotyping of doubled haploid mapping populations derived from crosses of Morex/Barke, Oregon Wolfe Barleys and Steptoe/Morex for at least the first of these two pilot OPAs, and possibly also the second, pending management decisions that will be made during the course of the work. We will ready the DNA, process the raw data, generate Illumina GenCall workspaces and summary tables in comma separated value (csv) format, create additional data tables in formats compatible with mapping programs including JoinMap 4.0, and provide the project with first-draft genetic linkage maps from each of the three populations and a combined map from all three populations. We will be engaged with Patrick Hayes to finalize the maps, and partnered continuously with collaborators at Scottish Crop Research Institute. We will receive 96 samples of US germplasm DNA from Pat Hayes, lead the collection of data from these samples, create GenCall workspaces and tables pertinent to the germplasm, and respond to requests from the barley CAP group for alternative data formats and clarifications on the nature of the data.

We will apply the Illumina OPAs to the deconvolution of BAC clone-locus relationships, particularly focusing on the two “final” OPAs described above. During the period of 3/1/06 to 2/28/07 the algorithms for deconvolution will be more fully developed. The locus-BAC relationships will be only partially solved by 2/28/07. New versions of HarvEST:Barley released by 2/28/07 may display the available information on locus-BAC relationships, but transfer of such data to other outlets will occur after 2/28/07, when the information will be more stable and complete.

Education. We have one PhD student who will be working on algorithms for locus-BAC deconvolution and data structures.

Outreach. Close will make presentations about the Barley CAP and the SNP methods that our project will employ. The first example was February 24, 2006 in Houston at the “Rice CAP PI Meeting”. Lonardi will be on call to explain the locus-BAC deconvolution algorithms to appropriate audiences. We will provide input and feedback to Peggy Lemaux in the design of brochures, posters, and powerpoint presentations in relation to the methodologies that we are leading on this project.

2) List specific outcomes and deliverables that will be accomplished in the first 6 months (3/1 – 8/31). These will be used as benchmarks for your bi-annual progress report.

- Design “pilot OPA2” and order it from Illumina
- Generate data from pilot OPA2 for three mapping populations and 96 US breeding genotypes
- Use results from pilot OPA2 to close the design of pilot OPA3
- Combine SNPs from pilot OPA1 (NSF project) and pilot OPA2 to design “final OPA4”

3) List specific outcomes and deliverables that will be accomplished in the second 6 months (9/1 – 2/29). These will be used as benchmarks for the bi-annual progress report.

- Generate data from pilot OPA3 for three mapping populations and 96 US breeding genotypes
- Transfer knowledge about Illumina data and SNPs to the marker lab in North Dakota
- Combine SNPs from all pilot OPAs to design “final OPA5”
- Modify the frequent itemset deconvolution algorithm to consider data from the OPAs

Barley Coordinated Agricultural Project Biannual Progress Report
FY06 (4/1/06 – 9/30/06)
Timothy Close and Stefano Lonardi, University of California, Riverside

1) Describe the research, education, and outreach activities you completed in the first half of the FY06 (4/1/06 – 9/30/06)

Research. We completed the design of the first of two project pilot oligonucleotide pool assays (OPAs), ordered and received it, and collected data from 480 DNA samples. These 480 samples included 96 for each of three mapping populations (Morex x Barke, Oregon Wolfe Barley, Steptoe x Morex), 96 European germplasm selections provided by Nils Rostoks at Scottish Crop Research Institute (SCRI, Dundee, Scotland) and Nils Stein at Institute of Plant Genetics and Crop Plant Research (Gatersleben, Germany), and 96 US germplasm selections provided by BarleyCAP partner Patrick Hayes (Oregon State University). We refer to this OPA and PilotOPA2. The name PilotOPA1 refers to another pilot OPA that was developed prior to BarleyCAP in an NSF-funded project of Close and Lonardi. GenCall workspaces were made for the data from PilotOPA2 and transmitted to Patrick Hayes. Data tables were exported from the GenCall workspaces and sent to Patrick Hayes and BarleyCAP partners Julie Dickerson and Roger Wise (Iowa State University). Close met in person with Dickerson and Wise in Washington DC to provide training on the GenCall workspace and explained the nature and structure of OPA data. Data from PilotOPA2 added more than 1000 SNP markers to an evolving SNP-based barley genetic linkage map, taking the total to about 2000.

The UCR team, with participation of Nils Rostoks (SCRI) who visited Close in California for two weeks, also made progress on PilotOPA3, designating approximately 900 SNPs that cover genes not addressed by PilotOPA1 and PilotOPA2. At the time of this report completion of PilotOPA3 design was still in progress, pending further consideration of data from PilotOPA1 and PilotOPA2 and high priority gene lists provided by several investigators. A current assessment of the results of PilotOPA1 and PilotOPA2 is that the two pilots were comparable, each providing about 1350 excellent SNPs. Thus, it appears that PilotOPA3 is very likely to elevate the total number of excellent SNPs above the goal of 3072 that are needed to create the two final, working OPAs for BarleyCAP.

The design of PilotOPA1 was conveyed to BarleyCAP partner Shiaoan Chao so that it can be used for the initial training at the N Dakota site which is scheduled for November.

Education. Two Computer Sciences students and two post-docs are working on the project. One PhD student, Serdar Bozdog, is improving the FPC assembly and minimal tiling path of gene-bearing BAC clones. The other PhD student, Yonghui Wu, began working on new combinatorial algorithms for the deconvolution of BAC-SNP relationships in September, shortly after passing his oral qualifying examination. One post-doc, Prasanna Bhat, has the lead role in genetic linkage maps from OPA data, which is part of an iterative workflow between genetic map production and manual supervision of the GenCall workspaces. Close, Bhat and the other post-doc, Jan Svensson have been jointly making the workspaces and working with Programmer Wanamaker to streamline the workflow between HarvEST, GenCall and JoinMap.

Outreach. Close made oral presentations on BarleyCAP at: 1) the RiceCAP meeting in Houston, Texas in February, 2) the USDA Western Regional Research Center in Albany, California in March, 3) a legume workshop in Asilomar, California in August (also a poster), and 4) the annual Society of Italian Agricultural Genetics Congress in Ischia, Italy in September. Close and Lonardi provided input and feedback to Peggy Lemaux and Barbara Alonso on preparation of BarleyCAP posters.

2) List specific outcomes and deliverables accomplished in the first half of FY06 (4/1 – 9/30)

- Designed PilotOPA2 by April and produced data by August
- Preliminary new genetic linkage map with >1000 new SNP markers by September
- Presentations in February, March, August, September