

Barley Coordinated Agricultural Project Work Plan FY07 (4/1/07 – 3/31/08)
Peter Bradbury

1) Describe the research, education, and outreach activities you are planning for the next year (4/1/07 – 3/29/08)

- Haplotype block analysis – An analysis of haplotype blocks will start with the development of a suitable working definition for haplotype blocks. We will then look for the existence and extent of haplotype blocks in the project germplasm. Haplotype blocks will be interesting from two perspectives. First, they may give us information useful for identifying haplotype block “tag” SNPs in order to develop a more efficient set of markers. Second, they can provide information about population structure in the germplasm since certain haplotypes may be diagnostic for important subpopulations. Because SNPs within haplotype blocks will be in strong linkage disequilibrium (LD) this analysis relates closely to the second item, evaluation of LD structure.
- Evaluate LD structure of core germplasm and first year lines as barley OPA genotyping data becomes available – Evaluating the rate at which LD decays between linked loci will shed light on how well our marker set is providing coverage of the whole genome. Evaluating LD between unlinked markers will indicate to what extent population structure and relatedness among lines will confound trait-marker associations.
- Simulate Marker Assisted Selection (MAS) – Simulating QTL at various map positions will provide a way to compare the effectiveness of QTL detection methods. One method of simulating QTL would be simply to convert known markers to QTL by assigning an effect to each marker state and adding random error. It will be important to model different numbers and sizes of QTL effects. The simulation work will focus on evaluating alternative methods of calculating the kinship coefficient matrix used in a mixed model approach like the one implemented by QTL Miner. Alternatives include using pedigree information alone, using marker information alone, or combining both types of information.
- Hire a post-doc
- Evaluate potential for implementing a GDPC (Genomic Diversity and Phenotype Connection) service for THT (The Hordeum Toolbox). GDPC is data retrieval middleware designed to provide data access to a variety of applications including a generic GDPC browser and the TASSEL genetic analysis software.

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.

- Post-doc hired
- With Jean-Luc Jannink develop a plan for analysis and publication of haplotype block and LD analysis studies

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.

- If Jean-Luc and I agree it is worthwhile, publication of a manuscript using haplotype blocks rather than single SNP to perform association analyses on Year1 data
- Platform (software) built for simulating QTL analysis based on genotype data collected by the BarleyCAP project.
- In consultation with Julie Dickerson and others, decision made on whether to implement a GDPC service for THT.

Barley Coordinated Agricultural Project Biannual Progress Report
FY06 (4/1/06 – 3/31/07)
Peter Bradbury, USDA-ARS, Cornell University

1. Describe the research, education, and outreach activities you completed in Year 1

Research

I discussed plans for haplotype analysis with Dr. Jean-Luc Jannink, who will also be working on research on that topic.

Education

Outreach

Presented information about Barley CAP on a poster that was part of a USDA booth at the NY Empire Farm Days in August 2006.

2. List specific outcomes and deliverables accomplished in Year 1.

I have no specific outcomes and deliverables to report for year 1.