

Barley Coordinated Agricultural Project Work Plan for Year 4 (4/1/2009 – 3/31/2010)
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1. Describe the research, education, and outreach activities you are planning for Year 4 (4/1/2009-3/30-2010)

Research

Population Structure Analysis

A recognized method for assessing population structure, a prerequisite to doing association mapping, is through the use of the program Structure by Pritchard et al. Structure, however, is not a simple software to use, particularly with large datasets as the Barley CAP germplasm dataset. I will be running Structure to determine justifiable numbers of subpopulations and subpopulation compositions.

Haplotype block analysis

Haplotype blocks are sets of consecutive markers in high LD. Barley CAP data allow such blocks to be identified within CAP germplasm. We will compare blocks across different subpopulations in the germplasm as part of a discussion of its structure and its use in association studies.

Marker Imputation Analysis.

We have submitted a manuscript showing that multilocus haplotype imputation methods work well on Barley CAP germplasm. The next step is to assess how these methods might best feed in to gene discovery and breeding value prediction. We will develop simulations to address these questions.

Cross validation

In collaboration with Kevin Smith, use data from the Minnesota program to cross-validate predictions from genomic selection.

Education

Short Course

The short course organized primarily by Kevin Smith in 2008 was a success (at least judging by the number of participants) and I will be part of a team teaching the next iteration in 2009. The topic of the short course remains association mapping applied to marker assisted selection.

Outreach

We have nothing planned in outreach

2. List specific outcomes and deliverables that will be accomplished in the first 6 months. These will be used as benchmarks for your bi-annual progress report.

Population Structure Analysis.

My group will contribute to a manuscript on population structure in the Barley CAP germplasm.

Marker Imputation Analysis.

We will submit a manuscript on imputation in the Barley CAP germplasm and its potential in gene discovery.

MAS

We are still working on a manuscript predicting the efficiency of genomic selection in barley given marker densities made available through the CAP.

3. List specific outcomes and deliverables will be accomplished in the second 6 months. These will be used as benchmarks for the bi-annual progress report.

MAS

A second manuscript comparing different statistical methods of genomic selection on the basis of Barley CAP data will be submitted.

Gene Discovery

I will work with Peter Bradbury on a manuscript assessing the power and false discovery rates for gene discovery using Barley CAP germplasm.

Short Course

- Will prepare syllabus and team-teach short course on association mapping applied to marker-assisted selection

Barley Coordinated Agricultural Project Six-Month Progress Report

(4/1/08 – 9/30/08)

Jean-Luc Jannink, USDA-ARS, Ithaca, NY

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

Research

Marker Imputation Analysis.

Methods developed in human genetics allow missing marker data to be imputed from surrounding multi-locus haplotype data. We have tested these methods on Barley CAP core data to complete datasets with missing markers and as a method of using tagging SNP. We found that the method worked well and we believe that it will become an important component of association analysis. We have submitted one publication on barley CAP core data and are preparing a second one on barley CAP breeding line data.

Structure, LD, and haplotype block analysis

In human, blocks in relatively high LD are broken by short segments where high levels of historic recombination have taken place. We have determined that Barley CAP breeding line data allow us to identify haplotype blocks and believe these to be almost entirely due to drift processes. We are preparing a publication on these findings that will also include discussion of levels of LD in barley CAP breeding line data, and population structure in those data.

MAS

Genomic selection

We are in the final throws of preparing a manuscript on the accuracy of breeding values predicted by genomic selection using barley CAP core data with simulated phenotypes.

Education

Short Courses

With Kevin Smith, Shiaoman Chiao, and Rex Bernardo, I was be part of a team teaching a short course on association mapping applied to marker assisted selection 16-18 June 2008.

Instructor at the Summer Institute in Statistical Genetics, June 29-July 2, 2008, Co-taught the Plant and Animal Association Mapping Module with Michel Georges. Some examples and insight were derived from the Barley CAP.

Outreach

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

Marker Imputation Analysis.

- A manuscript describing the use of marker imputation to increase the available density for association studies in crops, applied in particular to barley has been submitted to The Plant Genome.

Short Course

- Prepared syllabus and team-taught short course on association mapping applied to marker-assisted selection