

Barley CP Spring Planning Meeting Report

“Developing a Two Year Coordinated Project for Barley FHB Research”

April 12, 2011, Rm 105 Cargill Building St. Paul Campus of the University of Minnesota

In Attendance: Kevin Smith, Lynn Dahleen (by phone), Gary Muehlbauer, Rich Horsley, Robert Bruggeman, Frances Trail, Wynse Brooks (by phone), Andy Kleinhofs (by phone), Ruth Dill-Macky, Marvin Zutz, Mike Davis and Art Brandli

Purpose / Description

The barley research community will submit a two-year coordinated project (CP) in the fall of 2011. In this meeting, we evaluated progress in the current funded grant and developed plans for the next two-year funding cycle.

The meeting was conducted with two primary objectives:

I. Review Research Progress and Barley CP Milestones

II. Discussion of Draft Letters of Intent

Prior to the meeting each PI submitted a one page draft letter of intent for each project they are planning to submit as part of the Barley CP. These were compiled and distributed to the group prior to the meeting.

Much of the meeting concentrated on reviewing current research. During this review, there was discussion about future directions and plans for the next two-year funding cycle. At the end of the review the group summarized the most important considerations for developing the next two-year plan that would strengthen the overall mission of the CP as described in the attached flow chart.

Summary of Discussion Points

1. Transformation Pipeline - There are two transgenic lines that have been evaluated in the field for the past four years that show a 40% reduction in DON. Others are in the pipeline. There were several suggestions about how the transformation pipeline could be improved. One suggestion is that the number of insertion events should be determined in transgenic lines as early as possible to facilitate marker assisted backcrossing into elite backgrounds. Robert Bruggeman had some suggestions and offered to work with Lynn Dahleen to develop and implement a scheme. Gary Muehlbauer suggested that a commercial method was available to epitope tag transgenes. This is a much easier way to monitor protein production from a transgene than the current method of making specific antibodies for each transgene. The group also discussed how to accelerate backcrossing of transgenes into elite cultivars or breeding lines. It should be possible to use new genotyping platforms to do background selection in a cost effective manner and produce elite lines carrying transgenes more quickly. Lynn will work with Kevin Smith and Rich Horsley to develop an accelerated backcrossing scheme.

2. Field Capacity for Transgenics - Currently, two field nurseries are used to evaluate transgenic material in Minnesota and North Dakota. Ruth Dill-Macky indicated there is substantial cost in setting up each of these sites, however, that cost does not increase

appreciably by adding more lines to the nursery. This suggests that there is additional capacity at the current field testing sites at virtually no or very little additional cost that could be exploited. Those working to develop transgenic lines are asked to consider whether earlier testing of material would be useful given the availability of this resource.

3. Screening Midwest winter barley for FHB resistance - The University of Minnesota has recently started a winter barley breeding program that will soon be producing lines for preliminary and advanced yield testing. While lines with improved FHB resistance from the spring program have been used as parents, there has been no field testing of winter breeding lines for resistance. This winter program is focusing on facultative winter types, thus they can be spring-planted and evaluated with the spring program. The suggestion was made that it is now time to expand current FHB screening efforts to include this winter program as FHB resistance will be an important trait for winter barley in the Midwest.

4. Chr 2H mapping focus on recombinants - Andy Kleinhof's project has made good progress toward assembling BACs across the region of the chromosome 2H that harbors the Vrs1 gene and FHB resistance from CI4196 and analyzing this sequence information. Andy suggested that given cheap genotyping that a 1X genome sequence of CI4196 be obtained to complement the BAC sequence already obtained for Morex. Andy also indicated that his group would probably not take the lead in doing this work. After some discussion, the suggestion was made that additional sequencing should wait. The immediate focus for this project is to accurately assess the phenotypes of the recombinants in this region to make the case that resistance is independent from spike morphology, heading date, and plant height. Kevin Smith and Rich Horsley will include recombinants in field FHB nurseries this year and will insure that plants are tied up to avoid problems with lodging. Second, the focus should be on developing and characterizing addition backcross derived recombinants to facilitate both the genetics work and breeding.

5. SNP platform for Virginia mapping effort - The Virginia Tech group is developing several mapping populations for FHB in winter barley. Various suggestions were made about using the barley SNP platforms developed through the Barley CAP as an alternative to SSR markers to both facilitate speed in mapping and translation of mapping results into marker assisted selection. Kevin Smith will work with this group to plan SNP genotyping.

6. DON forecasting monitor accuracy - The current DON forecasting model is 80 -86% accurate and will go live to the public this year through the NDSU website. Jeff Stein feels that further research to refine the model is not necessary and did not submit a draft LOI. The group felt that it is still important to track the accuracy of the model with future field data sets that will be generated through breeding trials and regional nurseries. Jeff is encouraged to submit a modest proposal to fund "maintenance" of the DON model.

7. Exploit regional nursery data for association mapping - The barley regional scab nursery, called the NABSEN, has been in existence for over 10 years. This nursery has included 30-50 entries from at least five breeding programs and a common set of checks over this period of time. Each year the nursery is planted in about eight locations providing a deep data set of FHB severity and DON. The lines in the NABSEN comprise the most important sources of

resistance and therefore the NABSEN data represent a valuable resource for genetic mapping. We propose genotyping the NABSEN entries with a custom designed Illumina SNP assay and using the historical NABSEN data to conduct association mapping.

Process Going Forward

The group decided that when the call for letters of intent is sent out by the NFO, that a PI could submit a LOI for each project that they planned to submit, rather than just one LOI per PI. When LOIs are received by the CP committee, they will be sent out with a survey to the PIs and a stakeholder group to be evaluated and prioritized. The CP committee will use this information to make decisions about inclusion in the CP and funding allocation.

