

Leveraging Opportunities for “Bringing Barley to the Table”

This project will generate resources – germplasm, genotype data, and phenotype data – that offer many opportunities for leveraging value from the AFRI investment. At the core of these opportunities is that fact that the seed is doubled haploid and therefore an “immortal” resource for (i) re-analysis of existing data/seed, (ii) spin-off locations projects during the life of the project, (iii) spin-off planting dates, and (iv) future analyses.

Following are examples of these opportunities:

- (i) Seed archive: We will maintain archived samples of seed from all steps of the project – including the original doubled haploids that go into head rows and grain samples from each location of assessment of the training and validation populations. At any time, these seed samples can be used for analysis of quality traits not assessed in the AFRI project and/or advance to field trials of doubled haploids with alleles/phenotypes for non-target traits.
- (ii) Locations: When apprised of this project, colleagues may elect to participate outside the funding structure of the AFRI grant. An example is Dr. Steve Jones (MT. Vernon, WA). Food barley nutritional quality is an important breeding objective for Dr. Jones and he had his own resources to grow the field trials and is optimistic that he can find external funding to conduct the quality analyses. This increases the power of our project and benefits stakeholders in western Washington.
- (iii) Planting dates: A major advantage of facultative growth habit is that germplasm can be planted at any time. Growth habit can be predicted from genotype data based on the deletion of *VRN-H2*. Within the funding framework of this project, however, we have only one opportunity to empirically assess growth habit and that is during one cycle of head row assessment of doubled haploids that will be selected for the training population. Each of the four participating breeding programs will assess the training and validation populations under spring-sown conditions, using local resources. Flowering time will be measured in all trials and the data made available to all cooperators. Other traits, and germplasm advance, will be at the discretion of cooperators.
- (iv) Archived phenotype and genotype data: These provide a long-term resource for evaluation of new analysis tools and protocols. By way of example, the Oregon Wolfe Barley population – developed and distributed nearly 20 years ago - remains a standard for assessment of new genotyping assays (e.g. Chutimanitsakun et al., 2011; Cistue et al., 2011; Poland et al., 2012). Likewise, the Barley and TCAP data sets are a resource for allele discovery and comparison of analysis procedures (e.g. Gutierrez et al. 2011).