

Barley Contributions to Beer Flavor

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Rationale:

The goal of this project is to assess, in a preliminary fashion, if there are positive beer flavor attributes that have been lost during the recent history of intensive barley breeding for specific beer styles.

We hypothesized that if there are positive flavor attributes, a good starting point would be in a very diverse collection of barley genetic resources, rather than in contemporary breeding material.

Procedures:

Under the auspices of the USDA-NIFA Triticeae Coordinated Agricultural Project (T-CAP) the Oregon State University Barley Project grew the USDA World Core Collection of barley (n = 2062 accessions) at Corvallis, Oregon for the purposes of mapping genes determining resistance to diseases. The entire collection has been genotyped with 9,000 Single Nucleotide Polymorphisms (SNPs). The phenotype and genotype data are integrated through a procedure known as Genome Wide Association Scanning (GWAS) to locate genes of interest. In this project, we are leveraging the genetic resources and genotype data to assess beer flavor.

We selected 709 accessions (not including repeated check varieties) based on disease resistance. These selections were harvested, threshed, weighted, and grain protein has been measured on a subset of 9 accessions.

Results:

Principal Coordinate Analysis of the genotype data reveals abundant genetic diversity in the entire collection (Figure 1A) and in the selected subset (Figure 1B).

The seed weights of the selected accessions range from 43g to 711g, with 503 having over 250 grams (the minimum Sierra Nevada indicated would be required for sensory assessment) (Figure 2).

Grain protein content measured to date ranges from 8.4 – 12.2%. A minimum of 310 g are required for grain protein measurement using available NIR equipment. 271 accessions meet this minimum requirement.

Conclusions:

1. Selected accessions are representative of the genetic diversity in the full collection.
2. There is sufficient seed for sensory assessment of at least 503 (or 310, if grain protein data is a prerequisite).
3. Grain protein values are within the range where malt data should be reasonable.

Next steps:

1. Sierra Nevada and New Glarus are both supporting the project:
 - a. Will they two breweries perform sensory tests on the same or different accessions?
 - b. Due to seed limitations, it may not be possible to do sensory evaluations on the same accessions at both breweries, but we do have repeated samples of a check variety – Full Pint. Both breweries could use Full Pint as the common check.
2. How many accessions will each brewery test?
3. What criteria will be used to select accessions?
 - a. Possibilities include: genetic data, geographic origin, spike type (2 or 6), grain type (hulled, hull-less), grain color (white vs. other), grain protein, ???
4. Do we continue to pursue involvement with other brewers?

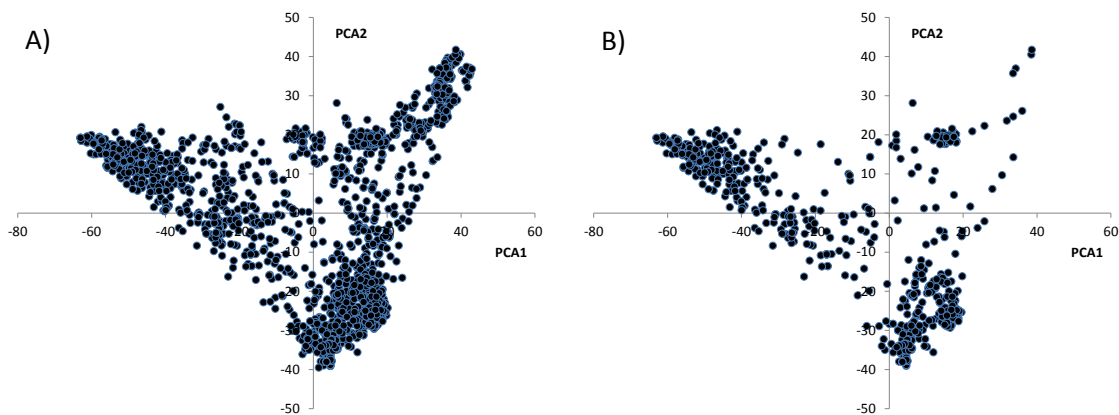


Figure 1. Principal Component Analysis of A) the complete barley world core collection and B) the subset of accessions harvested in 2012 for the Barley Contributions to Beer Flavor project. Principal components were calculated using genotypic information from 9,000 SNPs

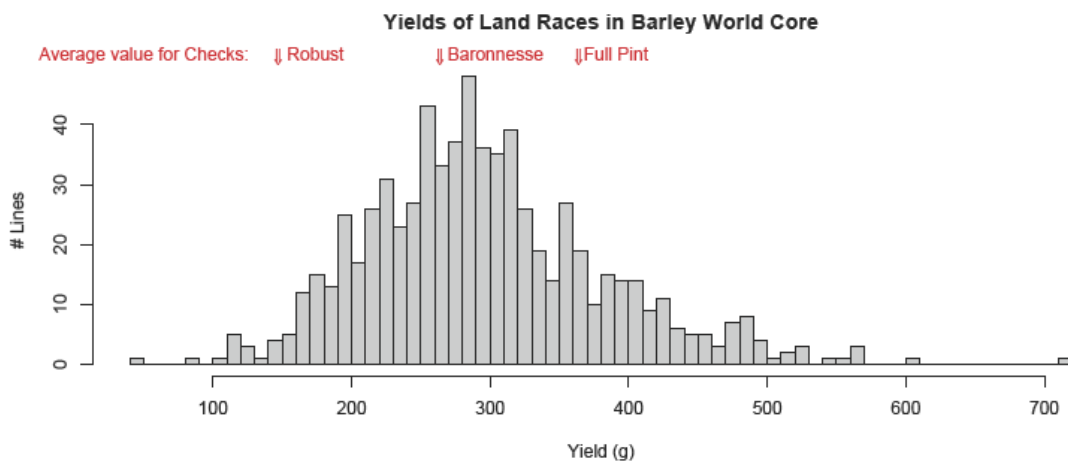


Figure 2. Grain yields (g) of individual single rows of barley world core accessions harvested at Corvallis, Oregon in 2012 for the Barley Contributions to Beer Flavor project. The check varieties are Robust (6-row, malt), Baronesse (2-row feed), and Full Pint (2-row malt).