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Abstract

Malted barley is a key component of beer. Most research on the genetics of malting quality in barley has focused on carbohydrate and protein synthesis and degradation, as these factors determine the performance of malt during brewing. We are using the 2062 spring habit accessions in the USDA National Small Grains Germplasm Collection World Core set as the starting point for a genome-wide study of the determinants of beer flavor. Very little research has been conducted to assess genetic variation in barley related to positive flavors in beer. If results from this subset are promising, a larger sample of accessions, sufficient for Genome Wide Association Scanning (GWAS), will be characterized for beer flavor.

Results and Discussion

A principal component analysis of the Single Nucleotide Polymorphism (SNP) data for these accessions shows similar patterns in the full set (n=2062) and in the lines with sufficient yield for sensory analysis (n=501) (Figure 2). This gives us confidence that we should be able to retain a reasonable representation of the original genetic diversity in the final 100 lines that will be used for sensory analysis. Presumably, genetically distinct groups that are underrepresented in our subset were less adapted to conditions and diseases found in Corvallis, OR.

Malt analyses may only be relevant when grain proteins fall between 8.5% and 12.5%. As shown in Figure 1, 231 of the 264 accessions fall within this range. Because so were removed due to low or high protein, we will have more flexibility in making our final selections, which should allow us to retain a high level of genetic diversity

Acknowledgements

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The Process

- 2062** → **Accessions in Barley World Core:** The collection was characterized in Corvallis, OR in 2011-2012 for resistance to biotic stresses under the auspices of the USDA-NIFA Triticeae CAP Project. Three checks (Full Pint, Baronesse, and Robust) were replicated throughout the experiment.
- 709** → **Accessions Harvested:** We harvested 709 accessions with resistance to prevailing diseases in Oregon's Willamette Valley.
- 501** → **Accessions with Sufficient Yield:** A minimum of 250g are required for sensory analysis. As shown in Figure 3, 501 accessions met this requirement.
- ~100** → **Accessions for Sensory Evaluation:** Due to the high cost of sensory assessment, we will only be able to perform sensory analyses on ~100 samples. We will use a combination of grain properties (kernel plumpness, test weight, grain protein, and color) and genetic data to choose this subset. Fermented and unfermented congress wort produced from these accessions will be assessed via sensory and analytic methodologies by Sierra Nevada Brewing Co. and New Glarus Brewing Co.
- 6915** → **Polymorphic SNP loci in the collection:** Each of the 2064 original accessions was characterized with the 9k Illumina Infinium iSELECT chip.

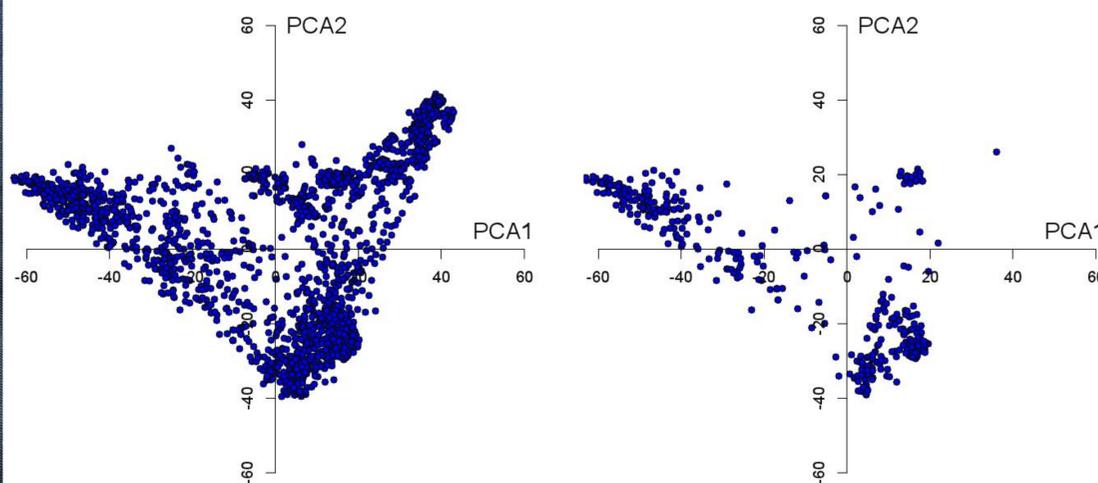


Figure 2 Principal component analyses showing the genetic diversity in 2062 accessions (left) and the genetic diversity in the 501 lines with sufficient grain for sensory evaluation (right).

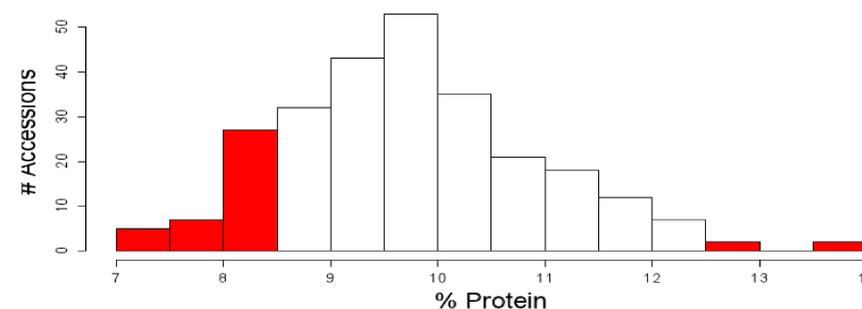


Figure 1 Grain Protein. Area in red designates accessions with protein levels that are either too high or too low for sensory evaluation.

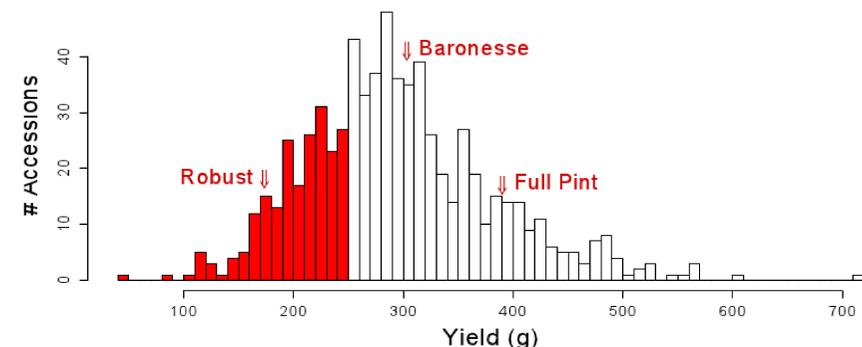


Figure 3 Grain yield from harvested accessions. Area in red designates accessions that yielded less than the 250g required for sensory evaluation.