# Poster# BREWING SUMMIT Omics Analysis of Malt from Heirloom Barley: The Potential for New Traits and G 0 2018 Flavors from an Old World



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## Introduction

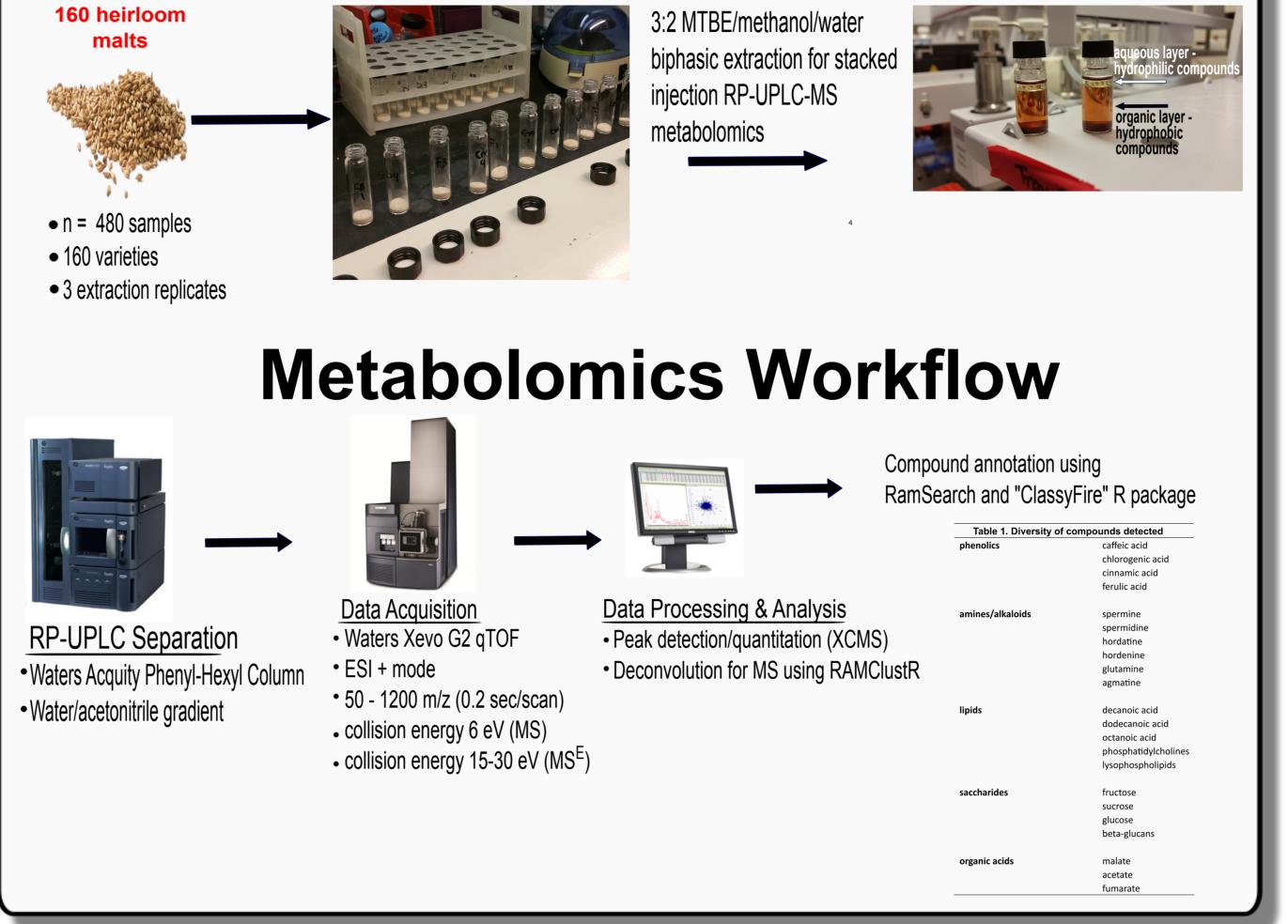
#### **Background**:

 Identifying superior ingredients that provide distinct flavors (e.g. taste, aroma) is an important area of research. Brewers seek to identify raw ingredients to improve the stability of flavors during storage.

There is a potential role for heirloom barley varieties to

## **Experimental Design**

An experiment was designed to profile metabolites for 160 heirloom varieties of malt, cultivated at Montana State University (MSU). Malts were analyzed for malting quality at MSU.





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- RP-UPLC-MS analysis detected 2,669 metabolites, 848 were annotated and assigned to a super and sub-class based on chemical ontology.
- ANOVA for genotype (with FDR adjusted p < 0.05) on the 848 metabolites revealed that 411 varied among the 160 lines. The metabolites that varied are indicated by the numerator in parethesis.

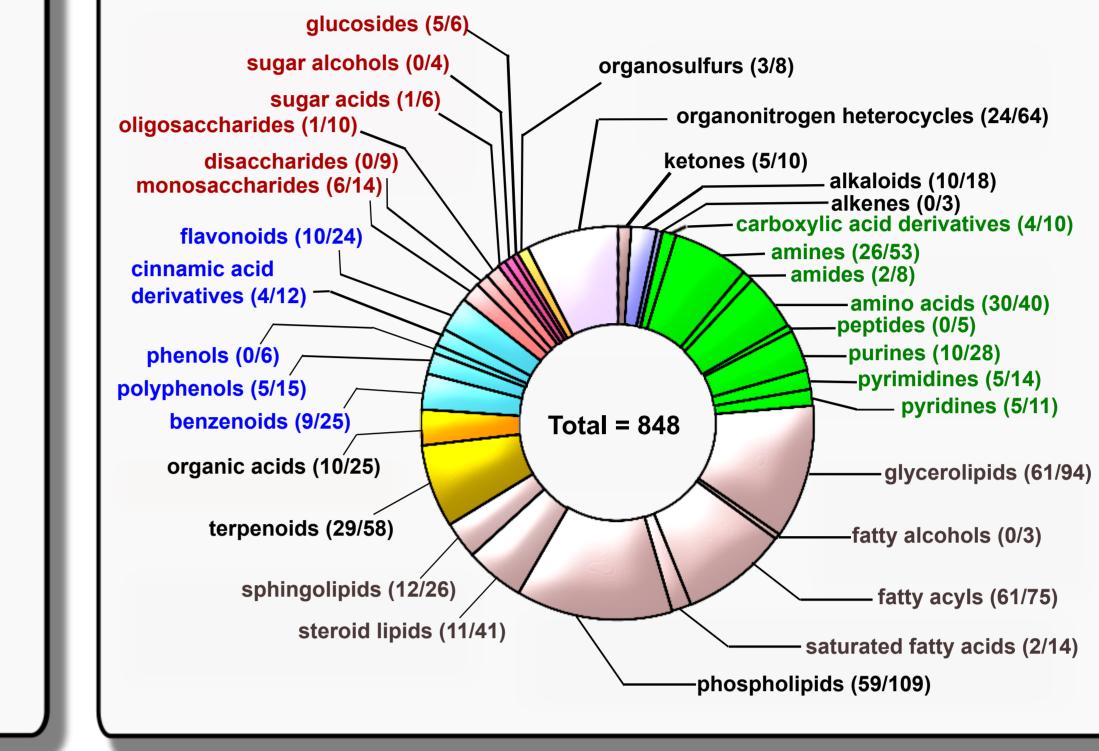


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- provide distinct attributes to the brewing process.
- Current research demonstrates a link between barley genetics and barley grain and malt chemistry.

#### **Rationale and Hypothesis:**

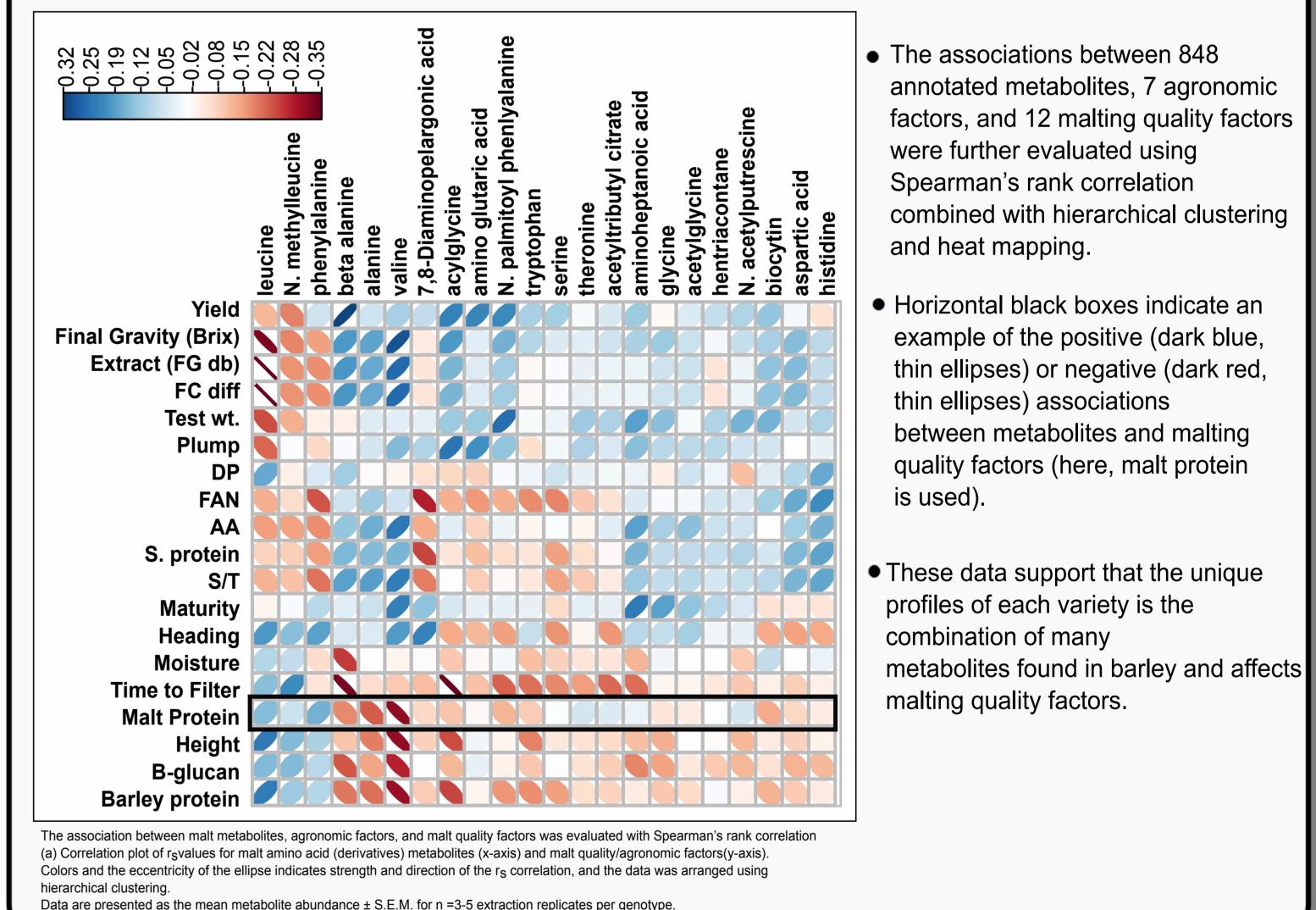
- Current barley lines contain relatively narrow genetic diversity. Recent efforts between the Montana **State University** (MSU) breeding program and the **Rocky** Mountain Malting Barley Cooperative are introgressing germplasm from heirloom barley to expand the existing genetic and chemical diversity.
- We therefore **hypothesize** that these new barley lines will contain unique chemical diversity, and this will impact malt flavor/aroma, fermentation quality, beer flavor, and beer flavor stability.



### Non-volatile Metabolites Contribute to 14 Variation in Heirloom Malt Varieties

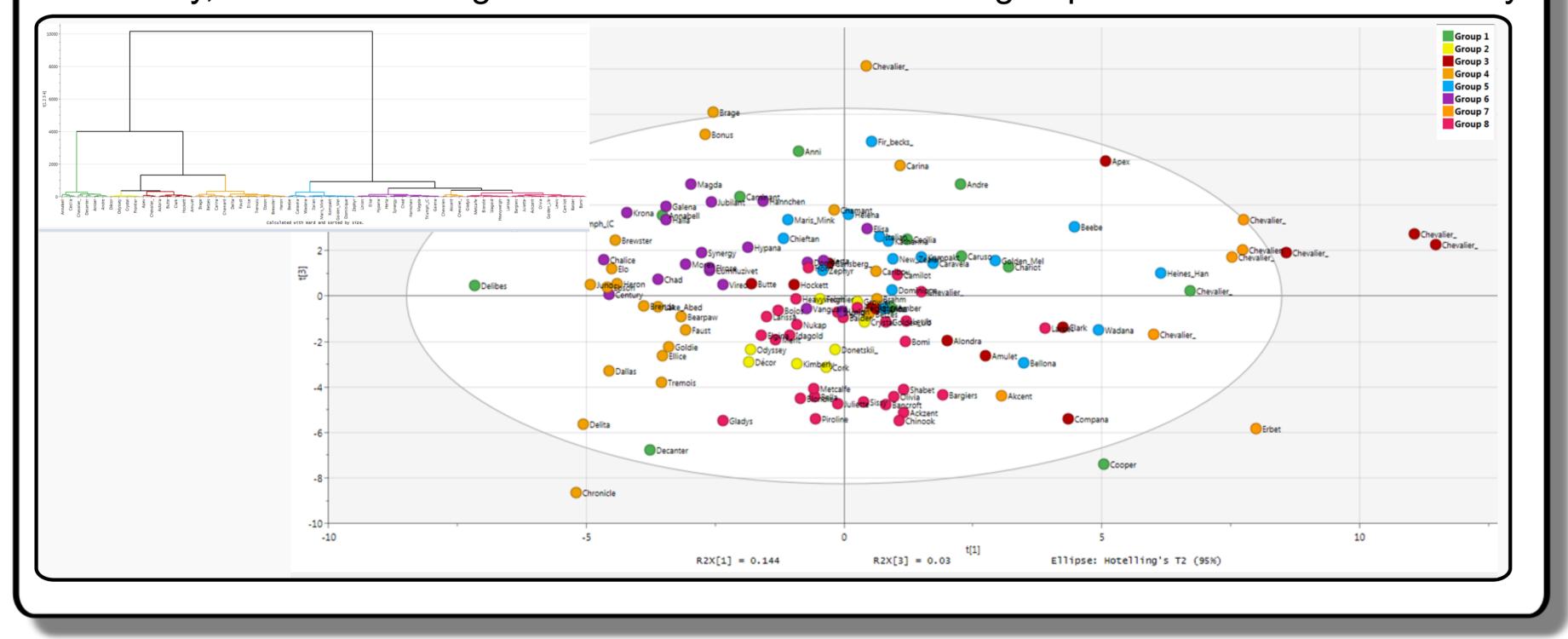
 Principal Component Analysis (PCA) was performed on 848 annotated malt metabolites to evaluate variation among the 130 2-row heirloom varieties. PCA can be used to characterize population structure based on chemical similarities and differences. PC scores plot for PC1 and PC3 explained 17.4% of chemical variation in malt.

## **Association of Malt Metabolites** with Malting Quality Factors

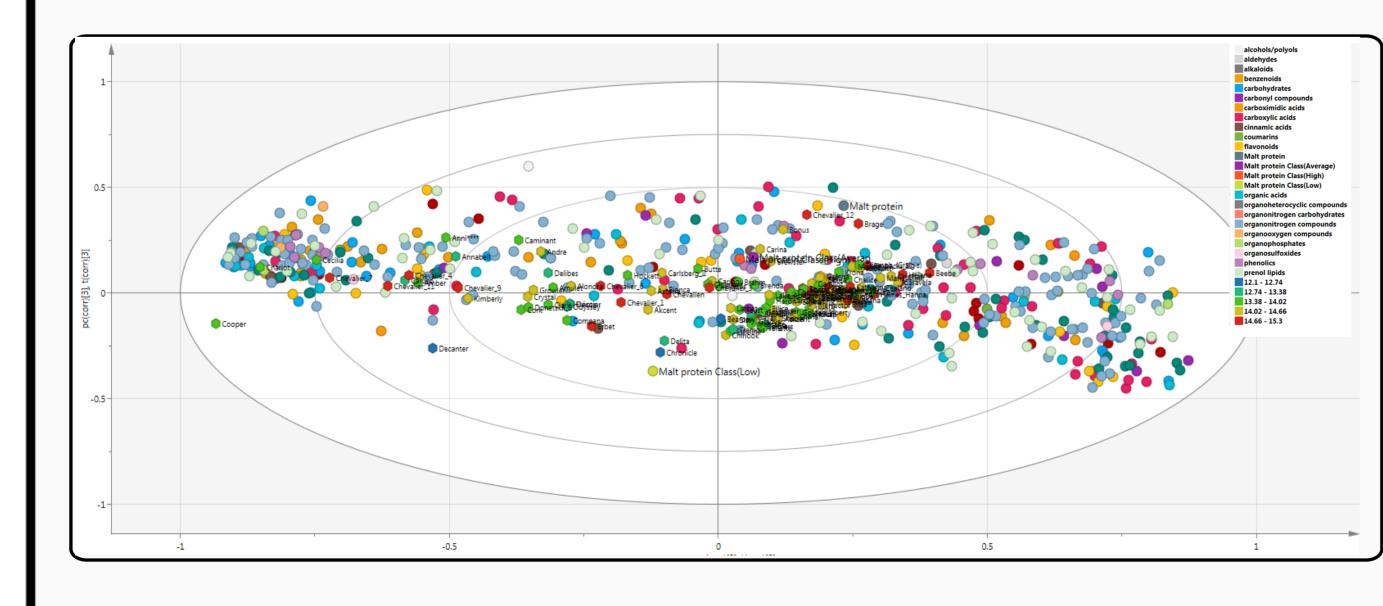




• Hierarchical Cluster Analysis (HCA) was used to assign classes to varieties based on similarity, wherein the length of the branches that link two groups is related to this similarity.



6 O2PLS Association of Malt Metabolites with Malting Quality

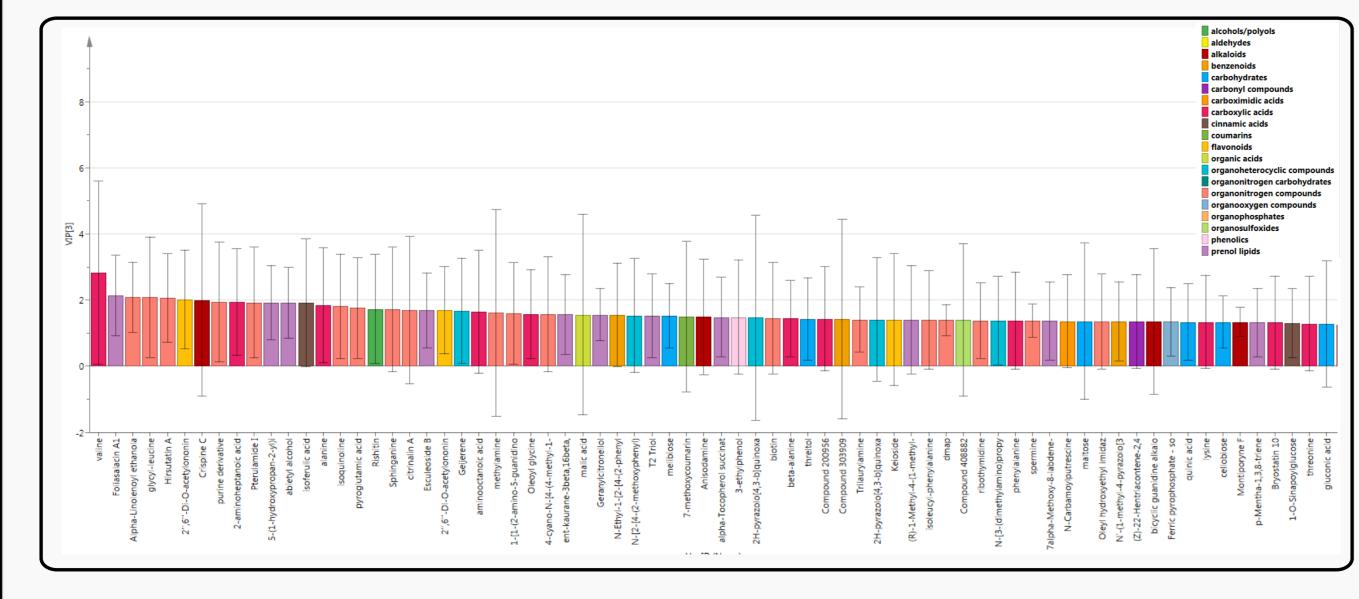


 Two-way Orthogonal Partial Least Squares (O2PLS) analysis was performed on the 848 metabolites and 11 malting quality factors

## Conclusions

Malt chemistry was characterized through metabolomics.

• Variation in the malt chemistry, as well as associations between metabolite chemistry and



(malt protein, malt moisture, fine extract, turbidity, color, FAN, beta-glucan, alpha-amylase, S/T protein, and diastatic power (DP)).

• Biplot (top) displays the co-varying relationships, regarding protein, among variety (colored by protein level), metabolites (colored by chemical class, and malting quality factors (malt protein class). However, not all metabolites are associated with malting quality and may be associated with factors such as flavor.

• Variable Importance Projection plot (VIP) (bottom) displays the highest contributing (most important) metabolites which correlate to the malting quality/agronomic factors in this model.

malting quality/agronomic factors were observed.

• Heirloom barley genetics can provide new chemical diversity in malt.

• This malt chemical diversity is expected to impact flavor.

## **Future Directions**

- To determine which differences in malt chemistry are reflected in the chemistry of the beer.
- To determine if the differences in the beer chemistry impact sensory attributes of beer, through flavor and flavor stability.
- To determine if there are barley and/or malt metabolites that can be markers for beer flavor and/or flavor stability for future breeding into lines adapted to dryland farming to the brewing process.

## Acknowledgements

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