Exploring high throughput secondary trait phenomics to improve grapevine breeding

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Abstract (250 words)

Modern grapevine breeding programs have overcome many challenges using genomic selection, which has allowed breeders to make targeted selections at earlier stages in the breeding process. However, the cost of genetic testing may present a burden for some programs, and markers often struggle to accurately predict quantitative traits. Recent advances in high throughput, high-dimensional data have provoked investigation into the use of high-dimensional phenomics as a low-cost addition to the grape breeder's toolkit that may offer advantages in predicting quantitative traits. High-dimensional secondary trait (HDST) data has been employed in annual crops for prediction of agriculturally important traits such as yield. To explore the potential of HDST data in grapes, 1618 grapevine seeds and seedlings from six populations were evaluated using hyperspectral and high-dimensional HSV color data. We show that HDST data are variable within seed populations. To start, we explore correlations of HDST data with early life stage traits, demonstrating potential to develop predictive models. Our work utilizes low-cost, high throughput data which has the potential to supplement genomic selection, allowing breeders to make decisions at the earliest stage in the breeding cycle. This work lays a foundation for the use of HDST data from seeds to predict traits in grapevine.

Keywords: phenomic selection, high throughput phenotyping, high-dimensional data