

Leaf elemental composition in a replicated hybrid grape progeny grown in distinct climates

Jesse Krokower¹, Courteny Coleman¹, Courtney Duncan¹, Zachary Harris², Samantha Mazumder², Anne Fennell³, Allison Miller², Jason Londo⁴, Misha Kwasniewski⁵, Laszlo Kovacs^{1*}

¹ Department of Biology, Missouri State University, Springfield, MO USA

² Donald Danforth Plant Science Center, St. Louis, MO USA

³ Department of Plant Science, South Dakota State University, Brookings, SD USA

⁴ School of Integrative Plant Science, Cornell University, Geneva, NY USA

⁵ Department of Food Science, Pennsylvania State University, University Park, PA USA

*Corresponding author: LaszloKovacs@MissouriState.edu

The elemental composition (the ionome) of grape leaves is an important indicator of nutritional health, but its genetic architecture has received limited scientific attention. In this study, we analyzed the leaf ionome of 131 interspecific F1 hybrid progeny from a *Vitis rupestris* (♀) X *Vitis riparia* (♂) cross. The progeny were replicated in New York, South Dakota, Southwest Missouri and Central Missouri, and the concentration of 20 elements were measured in their leaves at three different phenological stages during the growing season. In leaves collected at the apical node at anthesis, elemental concentrations correlated in a consistent manner ($p < 0.05$) across all four geographic locations. In subsequent phenological stages, elemental ratios in the apical-node leaves remained consistent across the South Dakota and New York sites, but not across the Missouri sites. In leaves collected at the basal and middle nodes, correlations varied greatly across all locations. Varimax-rotated PCA performed on the leaf ionome separated the two Missouri vineyards from their New York and South Dakota counterparts, even though the first two principal components accounted for only 27.8% of the variance. Using a GBS-based linkage map and the concentration of individual elements as phenotype, we were able to map nine QTL which could be detected at more than one vineyard locations. We were also able to detect a QTL when we applied ionomic profile-derived PC1 scores as phenotype. Interestingly, this PCA-derived QTL mapped to the same locus as the QTL for potassium concentration.

Keywords: Ionome, mineral nutrition, quantitative trait loci, *Vitis rupestris*, *Vitis riparia*