P35 – Multi-site QTL analysis of rootstock-scion interactions across varied climates

Fennell, Anne[1]*; Londo, Jason P.[2]; Miller, Allison[3]; Kovacs, Lazlo[4]; Kwasniewski, Misha[5]

[1]South Dakota State University, Agronomy, Horticulture, and Plant Science, Brookings, SD, USA
[2] Cornell AgriTech, Horticulture, School of Integrative Plant Science, Geneva, NY, USA
[3]Saint Louis University and Danforth Plant Science Center, Biology, St. Louis, MO, USA
[4]Missouri State University, Biology, School of Integrative Plant Science, Springfield, MO, USA
[5]PennState University, Food Science, University Park, PA, USA
*anne.fennell@sdstate.edu

Abstract

What is the genetic basis of rootstock modulation of scion phenotypes? Rootstock and environment contribute to scion phenotypic variability. Understanding and improving the genetics of rootstock scion interactions is essential to maintain sustainable grape production, particularly in the face of climate change. To determine the genetic underpinnings of rootstock affects on scion phenotype, a multi-site QTL mapping study was established. An F1 rootstock mapping population (200 individuals) derived from *V. rupestris* ('B38', seed parent) and *V. riparia* ('HP-1', pollen parent) was studied as ungrafted F1 vines and grafted with a common scion 'Marquette'. Contrasting phenotypes between these species include differences in leaf senescence, cold acclimation, dormancy length, budbreak date, sprawling versus climbing habitat, lateral versus primary meristem dominance, deep versus shallow rooting, fruit ripening, leaf shape, leaf ion concentration, and gene expression. To understand genotype-by-environment effects and rootstock-mediated scion plasticity, the segregating rootstock population was clonally replicated and the ungrafted and grafted populations were planted in a common garden arrangement in three climatically diverse regions of the US (New York, South Dakota, Missouri). Morphological, physiological, berry metabolite, leaf ionome and carbon isotope, and transcriptomic traits are explored to understand genetic and genotype by environment effects modulating scion phenotypes. An integrated GBS and rhampSeq map was used to identify the genetic basis of rootstock-scion interaction and amplitude of scion phenotypic modulation.

Keywords: QTL, rootstock, *V. rupestris*, *V. riparia*, phenotype, GxE