Using R/qtl to Map Yield and Relevant Quantitative Traits in a Cranberry (*Vaccinium macrocarpon*) Outcross F1, Biparental Population

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A native to North America, cranberry (*Vaccinium macrocarpon*) is a diploid woody perennial in the Ericaceae family with, until recently, limited genetic resources. In cranberry, the recent development of a high-density genotype-by-sequencing (GBS), multi-pedigree composite map has enabled QTL-mapping, GWAS, and genomic selection. As cranberry suffers from a fragmented breeding history and a long breeding cycle due to lengthy establishment (2-4 years) and longer evaluation periods (4-5 years) because of its biennial-bearing nature, the utility of these maps to molecular-assisted breeding methods or genomic prediction has the potential to make a big impact.

From 2011-2013, the Zalapa lab undertook an extensive effort to phenotype relevant cranberry fruiting upright traits in an F1-population derived from an outcross of two unrelated, elite cultivars, *Mullica Queen* x *Crimson Queen (CNJ02, n=154).* Fruiting upright traits assessed included berry mass, berry length, berry width, total berry mass, number of berries per upright, rebud, and berry shape parameters. Genomic heritabilities and breeding values were estimated using a mixed model approach with the *sommer* R package, using an additive relationship matrix derived from GBS markers in the linkage map. Using the estimated breeding values, the *R/qtl* package `scanone()` and `stepwiseqtl()` methods were applied to map additive QTLs and estimate their effects. An interactive circos visualization was constructed to display the utility of such an approach in exploring these QTLs and to look for consistency between the methods. Preliminary results show significant QTLs in linkage group 11 for yield-related traits of berry length, berry width, berry mass, and total berry mass, with variance explained by these QTLs ranging from 18.6 to 42.9 percent. Although these variances are likely an overestimate of the real marker variance, their locations are consistent with other mapping studies of similar traits in this population and express the utility of *R/qtl* for mapping QTLs in an outcrossed F1 cranberry population. Future directions include converting this mapping effort to use *R/qtl2*,

taking advantage of its new features in interactively assessing QTLs and their effects.