A Road Map Towards High pH Adaptability: Phenomic and Genomic Approaches to Azalea Breeding (*Rhododendron* spp.)

Alexander Q. Susko

Abstract

In ornamental plants, selection for aesthetic qualities have predominated in breeding with less focus on improving certain physiological traits such as pH tolerance. Deciduous azaleas (Ericaceae) are a prime example, where selections from the Woody Plant Breeding Program at the University of Minnesota have introduced a plethora of cold-hardy, ornately flowered plants but lack tolerance to high pH and calcareous soils common in many parts of the midwestern US. Iron deficiency chlorosis is a debilitating symptom of poor adaptation to high pH soils, manifesting as yellowed leaves with reduced photosynthetic capacity (Mengel, 1994). This results in yield losses on agronomic crops and reduced plant performance on ornamental species, limiting cultivation and resistance to other biotic and abiotic stresses. Increased iron solubility in soil and root tissue is critical to mitigating iron deficiency chlorosis, which depends on the iron atom gaining an electron (reduction): a reaction not favored at high pH or in soils of calcareous or alkaline composition (Lindsay & Schwab, 1982) (M. L. Guerinot & Yi, 1994). One way that plants make this iron reduction reaction more favorable is through rhizosphere acidification, resulting in lower soil pH near roots allowing newly soluble iron to be reduced transported into root tissues (Mary Lou Guerinot, 2001). This projects investigates rhizosphere acidification as a trait in advanced selections at the University of Minnesota and wild populations of *Rhododendron viscosum*, a deciduous azalea native to the southern US with ornamental appeal. New image analysis methods using the technical programming language MATLAB (MathWorks, Inc) were developed to measure and quantify rhizosphere acidification in tissue-cultured azaleas (genus *Rhododendron*), enabling the development of phenomic datasets for this trait. EST-SSR markers derived from the *R. viscosum* transcriptome will be used to estimate relatedness in a best linear unbiased
prediction (BLUP) model of wild and cultivated half-sib families to determine if significant genotypic variation exists in different azalea populations. This quantitative information will guide future breeding efforts by identifying azalea germplasm with increased rhizosphere acidification, improved iron efficiency, and broader pH adaptability within the genus.

References:

