Domesticated apple (*Malus x domestica*) is one of the most popular and economically and culturally significant fruits in the United States and the world. It is a temperate fruit in the family Rosaceae and is grown commercially in many different countries and states of the US. Apple breeding goals are multi-faceted and shaped by consumers, growers, and processors. US market demand for fresh apples out of the local apple harvest season has driven the adoption of cultivars with enhanced storage qualities (Costa et al., 2005) as well as the development of new cold storage technologies (Kupferman, 1997) and the importation of apples from other countries. Popular UMN apple breeding program release ‘Honeycrisp’ is well known for having outstanding texture, as well as the ability to retain its texture following cold storage (Tong et al., 1999). However, it is also susceptible to some storage disorders such as soft scald and soggy breakdown (Tong et al., 2003; Watkins et al., 2005).

Apple soft scald, or ribbon scald, is characterized by distinct brown and often longitudinal lesions on the fruit and can lead to secondary infections in the fruit. Soggy breakdown is an internal disorder where the cortex of the fruit becomes brown, soft, spongy, and often wet. These disorders are particularly nefarious to growers and sellers of apples because fruit that develop the disorders are unmarketable and the disorders develop after investing a considerable amount of money growing, storing, and/or shipping the apples. Though the exact physiological causes of soft scald and soggy breakdown are not completely understood, previous studies have found that both soft scald and soggy breakdown are more likely to develop when fruit is harvested at advanced maturity and stored at temperatures close to 0°C (Tong et al., 2003; Watkins 2004; Watkins, 2005, Johnston et al., 2009). Many other studies show little consensus, other than the fact that there appears to be a high year and location effect on scald incidence (Johnston et al., 2009; Robinson & Lopez, 2012; Tong et al., 2003; Watkins et al., 2005). Only Alspach et al. (2000) has reported genetic parameters for soft scald and soggy breakdown incidence, where they estimated heritabilities ranging from 0.73 to 1.07 for soft scald and 0.10 – 0.39 for soggy breakdown. Segregation for incidence of these disorders has been observed among families from UMN apple breeding program. Considering the importance of ‘Honeycrisp’ in breeding at UMN and elsewhere, knowing the genetics underlying these disorders would be valuable.
The purpose of my research is to investigate the genetic and phenotypic variation of soft scald and soggy breakdown in the UMN apple breeding program with the objectives of discovering marker-trait associations for the disorders, determining haplotype effects, and creating selectable markers for use in marker-assisted breeding. The objectives of my research are to 1. Determine occurrence and variability of soft scald and soggy breakdown, 2. Determine correlations between storage disorders and other traits that may explain variation in incidence of soft scald and soggy break down, 3. Identify marker-trait associations for soft scald and SBD, and 4. Identify functional haplotypes for identified QTL.

Two different apple populations will be used in this research: one is composed of the UMN portion of the population used in RosBREED (Peace et al. 2014) and additional UMN selections, and the other is a group of 5 families with ‘Honeycrisp’ as their common parent. Both populations will be genotyped using the apple 8K SNP array (Chagné et al. 2012) and phenotyped between 2013 and 2015. Soft scald and soggy breakdown phenotypic data will be compared to additional phenotypic trait measurements (ex. Starch-Iodine level; a measure of apple maturity at harvest) in an effort to account for non-target trait phenotypic variance which will be used to lower environmental/year variation in the target traits for use in marker-trait analyses. Marker-trait analyses will be conducted using the pedigree-based software FlexQTL®, which uses a Bayesian approach to detecting marker-trait analyses (Bink et al. 2014), and G-Model (Bernardo 2013), which uses a model that accounts for all marker effects and uses multiple linear regression for identifying marker-trait associations. Haplotypes will be identified and their mean effects will be determined and compared via Tukey’s HSD. The ultimate goal of this research is to develop selectable markers from identified QTL to use in marker-assisted breeding in the UMN apple breeding program.

Literature cited:


