

## Breeding the Next Honeycrisp Apple with Genomewide Markers

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The *Rosaceae* crop family encompasses horticultural crops such as peach, strawberry, pear, rose, and apple which are important for both their contribution to human health and well-being as well as for their economic benefits. The annual production value of crops from the *Rosaceae* family amounts to over 7 billion dollars. (Iezzoni et al., 2010). Despite this economic value, the industry struggles with sustainability and profitability. There is a need to speed up cultivar release while meeting the ever-changing demands of growers and consumers (Gallardo et al., 2015). Although there have been advances in the quality of genetic maps and markers there is still a lack of utilization of these tools by breeders (Evans et al., 2012). To address these issues, the RosBREED initiative was launched.

Across the country and around the world university breeders, including those from the University of Minnesota, were enlisted to contribute their fields of expertise to this research initiative. The fruit breeding program at the University of Minnesota is one of the oldest continuous programs on the continent (Luby, 1991). As such, researchers at the University of Minnesota were a natural fit for contributions to the improvement of genomic tools in apple breeding (Iezzoni et al., 2010). Breeders at the University of Minnesota have been responsible for the release of over 25 apple cultivars, the most well-known of which is the Honeycrisp apple (“Minnesota Landscape Arboretum,” 2016). The Honeycrisp apple appeals to consumers and producers as it excels in flavor, texture, crispness, and storage capability.

There are many traits in which an apple tree and its fruit must excel in order to be accepted commercially. There are different demands from breeders, growers, packers, shippers, and consumers and a newly released cultivar should add value to each part of this supply chain (Gallardo et al., 2015). This amounts to over 30 traits divided amongst field traits, appearance, internal traits, and sensory traits that are being evaluated in different stages of the apple breeding process (Evans et al., 2012). The incorporation of all of these traits into one cultivar, while also looking for that unique flavor profile and appearance needed in a new release, is one of the challenges faced by apple breeders.

In addition to selection on a large number of traits, apple breeders also deal with a highly heterozygous crop, long generation times and juvenile phases, and the need for asexual

propagation (Tydeman and Alston, 1964; Janick J, Cummins JN, Brown SK, 1996). As a result of these factors, out of every 30,000 seedlings germinated, only one is likely to become a commercial cultivar (Kellerhals et al., 2009). This is why it is so desirable to use marker assisted breeding (MAB), as was worked on in the first round of the RosBREED initiative (Kellerhals et al., 2009; lezzoni et al., 2010). However, markers for fruit quality and other traits are uncommon (Evans et al., 2012). For this reason, the second round of RosBREED is investigating the potential of genomewide markers in the use of genomewide selection (GWS).

GWS differs from MAB by taking into account a large set of random markers from the entire genome rather than selecting based on the presence of known markers, and there are few, for apple (Evans et al., 2012). This allows us to predict a continuum of phenotypes which is particularly useful when trying to determine which seedlings will have the best performance. The GWS approach also allows for selection of traits that are controlled by numerous small-effect quantitative trait loci (QTL), that are not easily selected for with MAB which works best when there are single, larger effect loci (Bernardo, 2010). If successful selection models can be built for apples, breeders would be able to remove the majority of inferior seedlings before field trials.

Planting and growing inferior seedlings only to discard them at fruit evaluation is one of the biggest costs to the program. The University of Minnesota has four main steps in evaluation before commercialization. The first stage is crossing and seedling growth, followed by hybrid evaluation, replicated testing, and pre-commercialization. Within our program, cost analysis indicates that approximately \$9 per seedling per year is spent growing seedlings from crossing to hybrid evaluation. Given that hybrid evaluation does not begin until approximately five years after crossing, about \$45/seedling before any fruit can be evaluated. Only one in 300 seedlings on average will then make it from hybrid evaluation to replicated testing.

The overall goal of my research is to develop GWS models that can be effectively used in apple breeding which will serve as a platform for adapting models to other *Rosaceae* crops. The three specific objectives are

- 1) Determine if including a term in the model to account for heterozygosity increases the predictive ability and accuracy of existing models
- 2) Determine if major loci can be included as fixed effects in models to increase predictive ability and;
- 3) Assess the distribution of favorable alleles across the apple genome to understand germplasm architecture for key traits

In summary, increasing the accuracy of GWS models utilizing genomewide markers will allow breeders to make efficient and informed decisions regarding which lines advance through the program. This has the potential to significantly reduce the costs associated with apple breeding. Accounting for heterozygosity and major loci may allow us to make predictions for both traits controlled by major effect QTL and those controlled by many small effect QTL.



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