

# Jewels in the Genome

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## What is a “Jewel in the Genome?”

- An individual’s genome is the full complement of genetic information inherited from its parents. Within this vast repertoire of genetic information, individual genes are being discovered that control critical production and fruit quality traits. As valuable rosaceous gene discoveries are made and put into breeding applications, we describe them as “Jewels in the Genome.”

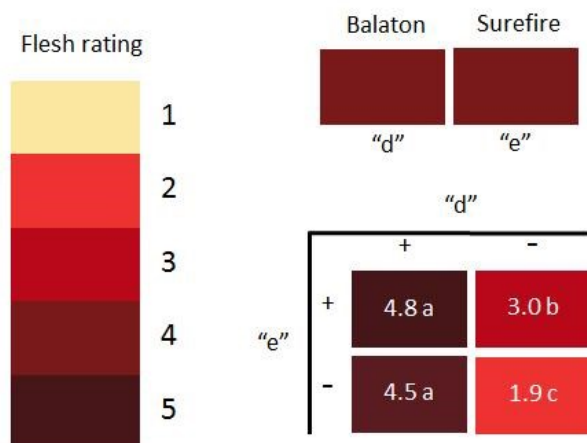
Tart cherry **skin and flesh color** varies widely from dark purple skin and flesh to orange skin and colorless flesh due to differences in anthocyanin pigmentation. Fruit flesh color variation is used to define market types with dark red-purple flesh types called “Morello” and clear fleshed types called “Amarello”. As tart cherries are primarily used for processing, individual food manufacturers frequently have a color preference. The clear-fleshed ‘Montmorency’, the dominant cultivar in the U.S., is preferred for cherry pie, while dark-fleshed types are preferred in Europe for processed products such as juice, jam and compote. In apple and sweet cherry (and many other fruits), members of an anthocyanin-activating group of genes called MYB transcription factors control this variation for red skin and flesh color (Chagné et al., 2007; Espley et al., 2007; Sooriyapathirana et al., 2010). It was hypothesized that the same MYB gene may control fruit skin and flesh color in tart cherry because sweet cherry is a progenitor species of tart cherry. Addressing this hypothesis was complicated by the fact that tart cherry is genetically more complex than sweet cherry as it possesses twice as many chromosomes that pair somewhat erratically at meiosis. Therefore, unlike sweet cherry individuals where two alleles are present at the MYB locus, each tart cherry cultivar or seedling has four alleles at the MYB locus.



Clear fleshed cultivar, ‘Montmorency’, left, and a dark fleshed European cultivar, right.

Thirteen alleles of the MYB locus in tart cherry germplasm were defined based on 17 polymorphic DNA markers that span a ~7 cM region (T. Stegmeir, pers. comm.). Four of these alleles, observed in various combinations in breeding germplasm, were found to be predictive of increased pigmentation. In contrast, the clear-juiced ‘Montmorency’ was found not to possess any of these four dark color alleles. Most importantly, allele combinations associated with the fruit color desired by U.S. processors, i.e., bright red skin and flesh, were also identified.

Genetic knowledge of the MYB alleles allows the tart cherry breeder to discard seedlings predicted to have very dark fruit flesh color prior to incurring the expense of field planting. Therefore the seedling population in the breeding orchard will be enriched for individuals with the desired fruit flesh color.



Inheritance of red flesh color illustrated with progeny from the cross ‘Balaton’ × ‘Surefire’. Left: Phenotypic scale used to rate flesh color. Top: ‘Balaton’ and ‘Surefire’ each have one copy of a MYB allele, termed allele “d” and “e”, respectively, that contribute to dark red flesh color. Bottom right: Progeny mean flesh scores with the presence or absence of the “d” and “e” color alleles. Different letters following mean scores represent statistical differences ( $P > 0.05$ ). Image courtesy of Travis Stegmeir.

This example illustrates how the common ancestry of rosaceous fruit crops can be used to accelerate discoveries across species boundaries. Furthermore, it demonstrates that the genetic tools developed in the RosBREED project (Peace et al., 2012) can be effectively used to dissect the genetic complexity of the MYB locus in this complicated polyploid. The duplicated MYB locus in tart cherry is chosen as the 13<sup>th</sup> “Jewel in the Genome” because knowledge of this region is leading to more efficient breeding of tart cherry.

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