

## Jewels in the Genome

By Amy Iezzoni, Project Director

What is a “Jewel in the Genome?”

- An individual’s genome is the full complement of genetic information that it 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 these valuable rosaceous gene discoveries are made and put into breeding applications, we will describe them in this column as “Jewels in the Genome.”

The pattern of apple skin color differs widely among commercial cultivars and unique patterns are associated with major market cultivars. For example, the cultivars Granny Smith and Golden Delicious have no red overcolor on the skin in contrast to other cultivars that have a medium or high proportion of overcolor. The popular cultivar Honeycrisp exhibits some red overcolor whereas Empire and Jonathan often have complete cover. The pattern of red overcolor on the fruit can also vary. Fruit of cultivars such as Pink Lady have a red blush that is seamlessly blended with a yellow ground color. In comparison, other cultivars such as strains of Red Delicious, have red pigment “painted” in a striped pattern on the fruit. Furthermore, the color of the blush or stripes can be orange to pink to red to almost purple, depending on the cultivar.

In apple (and many other fruits), members of an anthocyanin-activating group of genes called MYB transcription factors control this variation for red color. Rosaceae-wide MYB gene was selected [as our 5<sup>th</sup> Jewel in the Genome](#) because of its importance in controlling apple and cherry fruit and skin color. In apple, the morphological locus is known as *Red fruit*, with the partially dominant *Rf* allele conditioning the high skin overcolor proportion and cultivars like Granny Smith and Golden Delicious being homozygous for the *rf* allele. Genotypes at the *Rf* locus can therefore be used to predict the proportion of overcolor on apple skin in cultivars, selections, seedlings, and arising from cross combinations. Variations of the two primary alleles, detected as unique SNP haplotypes, were recently detected in RosBREED investigations. These secondary alleles appear to be associated with subtle differences in skin color attributes and other traits such as sunburn incidence (presented at the 2012 6<sup>th</sup> Rosaceae Genomics Conference, Mezzocorona, Italy).

However, the *Rf* locus does not act alone. Additional loci are being detected from Pedigree-Based Analysis of RosBREED datasets. For example, another locus on chromosome 2, nicknamed the “blush” locus (*Bl*), influences how this overcolor is “painted” on the apple fruit surface. Those apple selections with two dominant *Bl* alleles are more likely to have a red (or orange or pink) blush blended across the fruit surface, while those selections that have two recessive *bl* alleles are more likely to have the overcolor appear as stripes.

Genetic knowledge of alleles at the *Rf* and *Bl* loci will allow apple breeders to design crosses and select seedlings that are more likely to have desired skin color amounts and patterns, perhaps including new appearances not seen in common cultivars. Therefore, the *Rf* and *Bl* loci are selected as one of RosBREED’s “Jewels in the Genome” because it will lead to more efficient breeding of apples with desirable appearance.

