

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.”

Fruit texture in peaches (and nectarines), characterized by differences in flesh softening and flesh adherence to the pit, defines industry market classes (fresh market or canning) and strongly influences consumer appeal. We know the controlling gene!

“Melting flesh” types, which soften rapidly to a smooth buttery texture, are most desirable for the fresh market. Melting peaches can be freestone or clingstone, which describes whether flesh fibers detach from the stone (seed, pit) when fruit are ripe. Melting types also have the possibility of becoming mealy (dry and grainy, which no one likes!) if they also carry other genetic susceptibility factors and are picked and stored incorrectly.

“Non-melting flesh” types soften gradually to a rubbery texture, and are the mainstay of peaches used for canning. Non-melting types are always clingstone. Two other types soften even less: “clingstone non-softening flesh” and “stony hard” peaches, and both are suitable for fresh eating because flesh remains crisp. All these firmer types do not become mealy.

The gene controlling melting/non-melting and freestone/clingstone is known, residing at the so-called *Freestone-Melting flesh* locus on stone fruit chromosome #4. This gene (*endoPG*) encodes the cell wall pectin-cleaving enzyme known as endopolygalacturonase that also plays a major role in fruit softening in many other fruit crops like pear, avocado, and melon. Twelve *endoPG* variants (alleles) have already been detected in peach. Upon hunting through the USDA’s *Prunus* stone fruit collection in Davis, California, in peach’s stone fruit relatives (plum, apricot, almond, etc.) more than 200 alleles were found! Commercially exploitable differences in peach fruit softening profiles have been associated with these different *endoPG* alleles. For example, one breeding line contains a unique allele associated with gradual softening over a week to a pleasing melting texture. In contrast, there are alleles from wild sources associated with immediate mushiness and others where fruit splits too easily along the suture – undesirable and mostly bred out of the modern industry, but useful to have a genetic handle on for rapid elimination from breeding populations when breeders seek to introduce valuable traits like disease resistance from wild relatives.

With genetic knowledge of the *endoPG* variants in their plant material, breeders can harness this wide array of genetic and trait diversity to create desirable parental combinations and select superior seedlings prior to field planting. Therefore, because this *endoPG* locus will lead to the more efficient breeding of peaches and nectarines with desirable texture, it is selected as our third featured “Jewel in the Genome.”

