

Jewels in the genome

By Amy lezzoni, 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 size is a critical fruit quality trait in which a difference of only 2 mm diameter for fresh market sweet cherries can make the financial difference between profit and loss. Therefore, although other fruit quality parameters are also important, adequate fruit size is absolutely essential. A genetic region that controls cherry fruit size has been identified near the middle of sweet cherry’s 2nd chromosome (Zhang et al. 2010). More than seven DNA types were identified for this genetic region, and those types associated with large, medium, and small fruit were identified. Unfortunately, large-fruited trees tended to be soft-fruited and firm-fruited trees tended to be small-fruited. However, using data from seedlings in the Washington State University sweet cherry breeding program, one DNA type was discovered that was associated with fruit that were large *and* firm, as well as sweet and delicious! With this valuable genetic insight, breeders can design crosses that will yield a large proportion of seedlings predicted to have large fruit while minimizing the number of seedlings that will have soft fruit. Additionally, those offspring carrying the undesirable DNA types can be weeded out at the very young seedling stage so that breeders avoid wasting resources producing and growing trees that will eventually bear small fruit.

This genetic region is very important for tart cherry breeding also as parents that are being used as donors of cherry leaf spot (CLS, see picture bottom right) resistance unfortunately also have extremely small fruit (~ 1-2 grams). With this DNA diagnostic tool, those tart cherry offspring carrying the undesirable DNA types can be weeded out at the very young seedling stage so that breeders can more efficiently combine disease resistance and large fruit size into commercial cultivar candidates. Therefore, because this cherry genetic region will lead to the more efficient breeding of large delicious cherries, it is selected as our second featured “Jewel in the Genome.”

Zhang G, Sebolt AM, Sooriyapathirana SS, Wang D, Bink MCAM, Olmstead JW, lezzoni AF. 2010. Fruit size QTL analysis in an F₁ population derived from a cross between a domesticated sweet cherry cultivar and a wild forest sweet cherry. *Tree Genetics and Genomes* 6:25-36.



Amy lezzoni evaluating a sweet cherry cultivar from Eastern Europe.



Photo courtesy of Greg Lang, Michigan State University. Pictured is his daughter Kate with a sweet cherry from the PNW.

