

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.”

Maturity date for peach cultivars is a critical factor considered by growers so that they can provide a continuum of ripe peaches for an extended production season. Having a range of maturity dates not only benefits growers by spreading out market risks and production costs, but it also benefits consumers seeking a continual summer supply of peaches. Peach breeders therefore target cultivar development for specific maturity dates to fill gaps held by less desirable cultivars.

Having genetic knowledge of which crosses will yield a higher percentage of seedlings predicted to be in the targeted maturity date classes would help breeders more efficiently reach their maturity date goals. Many genetic studies have reported genomic regions containing genes influencing maturity date in peach (Etienne et al. 2002; Verde et al. 2002; Eduardo et al. 2011; and Dirlwanger et al. 2012); however, there is one consistently detected region that has been confirmed with RosBREED data to be important in U.S. breeding germplasm. This trait locus is on peach chromosome 4 at ~44 cM (based on the *Prunus* T×E reference map) and a putative candidate gene has been identified at ~10.5 Mbp based on v.1 of the peach genome sequence (Dirlwanger et al. 2012). In individual crosses, this trait locus has been shown to be associated with up to 70% of the genetic variation for maturity date. Peach chromosome 4 also contains trait loci for fruit texture, fruit stone-flesh adhesion, and bloom time, making this one of the most important genomic regions for peach breeders to consider.

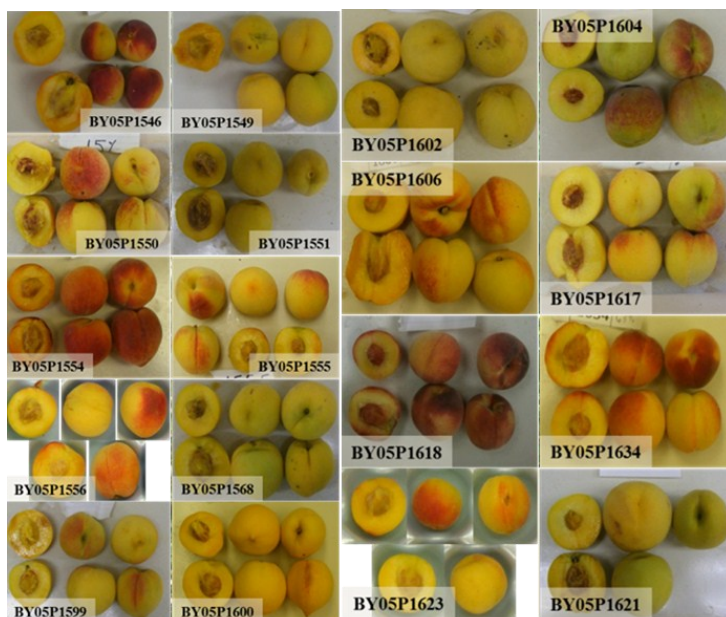
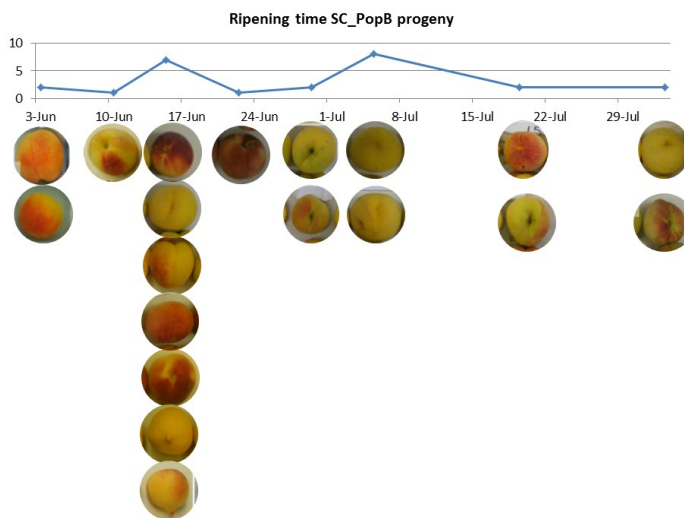
With genetic knowledge of what peach seedlings will ripen at specific maturity dates, breeders can plan crosses to maximize the probability of obtaining cultivars that target these maturity dates. Such an approach helps redirect resources to be spent on other critically important consumer-related traits such as the wonderful fruit flavors. Therefore, because knowledge of this genetic region will lead to the more efficient breeding of peach varieties, it is chosen as one of RosBREED’s “Jewels in the Genome.”

Dirlwanger E, Quero-Garcia J, Le Dantec L, Lambert P, Ruiz D, Dondini L, Illa E, Quilot-Turion B. 2012. Comparison of the genetic determinism of two key phenological traits, flowering and maturity dates in three *Prunus* species: peach, apricot and sweet cherry. Heredity doi:10.1038/hdy.2012.38.

Eduardo I, Pacheco I, Chietera G, Bassi D, Pozzi C, Vecchiotti A, Rossini L. 2011. QTL analysis of fruit quality traits in two peach intra-specific populations and importance of maturity date pleiotropic effect. Tree Genet Genomes 7:323-335

Etienne C, Rothan C, Moing A, Plomion C, Bodenes C, Dumas LS, Cosson P, Pronier V, Monet R, Dirlwanger E. 2002. Candidate genes and QTL for sugar and organic acid content in peach (*Prunus persica* (L.) Batsch). Theor Appl Genet 105:145–159

Verde I, Quarta R, Cerdrola C, Dettori MT. 2002. QTL analysis of agronomic traits in a BC1 peach population. Acta Hort 592:291–297



Top photo: range of ripening dates for a Clemson University population. Bottom photo: peach hybrids from the same parentage exhibit a wide range of ripening dates. Photos courtesy of Terrence Frett.