

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 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.”

Crisp, juicy apples with pleasing acidity are highly desirable for the fresh market. However, obtaining the optimum combination of these desirable textural and taste attributes has been challenging as soft, mealy and poor tasting apples frequently occur in breeding populations. In apple (and many other fruits), malic acid is a major contributor to fruit acidity. The locus that controls malic acid level in apple, named *Ma*, is located near the top of apple linkage group (LG) 16 (Maliepaard et al. 1998). Interestingly, this same region on LG 16 also contains gene(s) that influence apple crispness and juiciness (King et al. 2001).

Alleles for the *Ma* locus in apple are associated with a wide range of eating quality. For example, some types appear to be associated with desirable tart crisp juicy apples, other types with just crisp or tart apples, and some with poor quality for all these traits (Fig. 1). This locus is currently under detailed investigation in RosBREED (Fig. 2), and is already revealing much wider diversity in U.S. breeding germplasm than the alleles originally reported in European apple populations.

With genetic knowledge of *Ma* locus alleles in their germplasm, breeders can harness this wide array of genetic diversity to make desirable parental combinations and select seedlings with superior performance prior to field planting. Using this DNA information is particularly powerful as it simultaneously provides predictions for three high priority traits (acidity, crispness and juiciness). Therefore, because the *Ma* locus will lead to more efficient breeding of apples with desirable eating quality, it is chosen as our sixth featured “Jewel in the Genome.”

King GJ, Lynn JR, Dover CJ, Evans KM, and GB Seymour. 2001. Resolution of quantitative trait loci for mechanical measures accounting for genetic variation in fruit texture of apple (*Malus pumila* Mill.). *Theor Appl Genet* 101: 1227-1235.

Maliepaard C, Alston FH, van Arkel G, Brown LM, Chevreau E, Dunemann F, Evans KM, Gardiner S, Guilford P, van Heusden AW, Janse J, Laurens F, Lynn JR, Manganaris AG, den Nijs APM, Periam N, Rikkerink E, Roche P, Ryder C, Sansavini S, Schmidt H, Tartarini S, Verhaegh JJ, Vrielink-van Ginkel M, and GJ King. 1998. Aligning male and female linkage maps of apple (*Malus pumila* Mill.) using multi-allelic markers. *Theor Appl Genet* 97: 60-73.

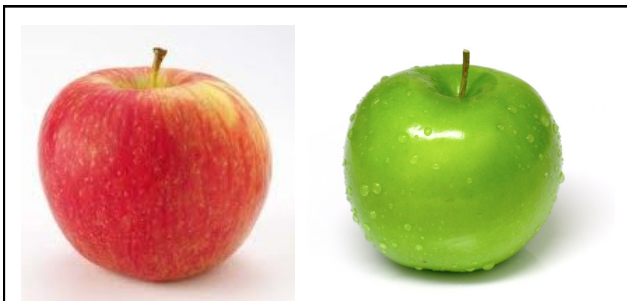


Figure 1. Unusual allelic combinations at the *Ma* locus for Honeycrisp (left) and Granny Smith (right), may contribute to their extreme fruit quality attributes.



Figure 2. Evaluating crispness with a Mohr Digi-Test.