

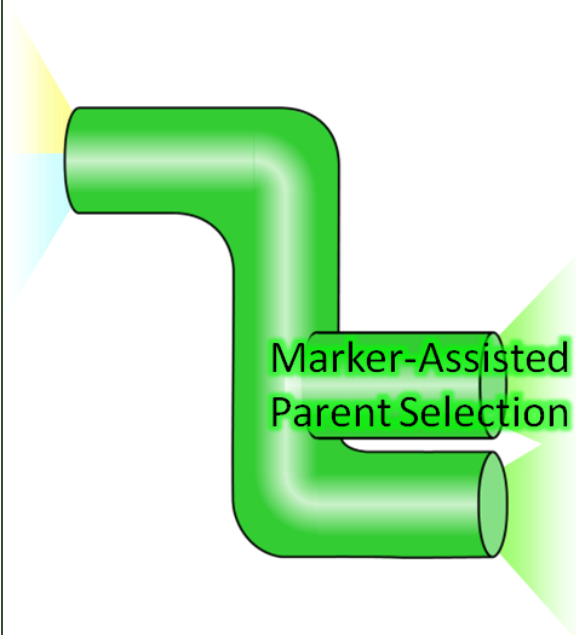
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The Marker-Assisted Breeding Pipeline: Channeling socio-economic and DNA information into routine breeding operations

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In this issue:

Informing crossing decisions in Rosaceae crop breeding



Crossing is arguably the most influential, far-reaching decision that Rosaceae crop breeders can make. The breeder has in mind the next generation – thousands of plants that must be cared for and evaluated to find those few offspring on which the future industry will be based. In preparation for the pollination period, a plethora of possible pairwise parental permutations are pondered. The breeder must decide the set of cross combinations to make and the target number of seed for each. While the best offspring should carry the best attributes of their two parents, most will probably be only as good as one parent or the other, or combine some or all of the worst traits of each! The fewer redeeming features a potential parent has, and the harder it is to pass those features to the next generation, the poorer its value as a parent and the larger a population must be for a decent chance of spotting a rare elite seedling.

Breeders thus often talk of “breeding value” when considering the suitability of parenthood for individual varieties (cultivars, advanced selections, specialized breeding lines, or germplasm collection accessions). If a variety has many redeeming features that its offspring readily inherit, it is said to have a good “general combining ability”, which follows the same concept as breeding value. In other cases, certain parents may shine only when crossed with certain others, and are then said to have good “specific combining ability”, at least for those specific cross combinations. Breeding values and combining abilities for multiple or single traits can be objectively calculated with well designed crossing experiments, about a decade of dedicated trait evaluation, and advanced training in quantitative genetics. Instead, most Rosaceae breeders have relied on their own experience and a honed breeding instinct – more subjective but nevertheless effective, judging by the extent to which modern cultivars support vibrant industries.

Molecular genetics in the form of *DNA-informed breeding* offers the means of supporting crossing decisions with more direct measures of breeding value than those supplied by quantitative genetics parameters, and provides objective explanations to breeders’ gut feelings. How? Heritable traits are controlled by genes and genetic tests can be developed that monitor the presence and dosage of alleles contributing to the trait. Use of the tests for any age of any plant, from world-famous cultivar to new seedling, will predict what functional alleles the plant carries. This gives a direct window onto its genetic potential for performance and its breeding value. Kate Evans, apple breeder at Washington State University in Wenatchee and RosBREED Demonstration Breeder, is a DNA-informed breeder. For several years, Kate has used DNA-based knowledge of fruit quality retention (at least for firmness) to inform her crossing decisions (Figure 1, next page). The DNA information is not the only factor that Kate takes into account in her crossing decisions, but does assist her decisions – thus the term “marker-assisted”.

Marker-assisted parent selection requires at least one genetic test that a breeder can trust. To date, only a few tests have been available to Rosaceae breeders, such as those highlighted in Amy Iezzoni’s ongoing

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Jewels in the Genome Newsletter articles. To dispel a myth, there is no need to wait until many predictive tests are available for all the traits a breeder is considering, nor until the genetic tests are 100% predictive of individual traits. DNA information *adds to*, rather than replaces, other information sources considered for crossing, such as each potential parent's performance in field trials and its tendency to pass on useful traits from past crossing experience.

Each genetic test provides useful information that adds to breeders' decision factors at little or no cost to breeders. The predictive genotypes of prospective parents are determined by publicly funded researchers and the knowledge is placed in the public domain. Still, such knowledge can be scattered and garbled in scientific publications that were not written with immediate use by breeders in mind. On the RosBREED Community Breeders webpage, we will compile this rapidly accumulating public domain knowledge on the functional alleles carried by varieties and translate it into forms that you can use. If you would like to gain the genotypic information about your own program's prospective parents, we will also describe the steps for you to obtain it so that the information remains confidential with you.

In coming articles we will describe other examples of Rosaceae breeders using DNA information to help support their critical crossing decisions. What we describe here is just the beginning of a revolution. RosBREED is poised to stock a huge warehouse of predictive genetic tests for you to choose from and enhance your crossing decisions. We will detail the successes and learning experiences of Demonstration Breeders as they shop from this warehouse, while providing the same knowledge accessibility and tools to all of you for con-

Figure 1. Marker-assisted parent selection in apple using gene markers for apple fruit storability. A table of functional genotypes for various apple cultivars can be found at www.rosbreed.org/breeding/jewel-use/

GENE MARKERS	AVAILABLE ALLELES	ETHYLENE PRODUCTION	BREEDING UTILITY
<i>Md-ACS1</i>	1	normal	- softening
	2	low	+ less softening
<i>Md-ACO1</i>	1	low	+ less softening
	2	normal	- softening

Allelic variation at these two genes does not completely predict storability. Research is underway to refine our knowledge of allelic effects and interactions with other genes. But their use in guiding crossing decisions increases genetic potential for storability in resulting populations.

**** Implications for breeding: Enrich for positive alleles and avoid negative alleles, especially in homozygosity ****

CULTIVAR	<i>Md-ACS1</i>	<i>Md-ACO1</i>
Fuji	22	11
Gala	22	12
Golden Delicious	12	22
Honeycrisp	12	22
Silken	12	22
Splendour	22	12
Sundowner	12	22
Sunrise	12	22

Using the table of cultivar functional genotypes

Gala

22 12

×

22 12

Splendour

expect

25% 22 11

50% 22 12

25% 22 22

e.g.

Pac. Beauty 22 11

Pac. Rose 22 12

WA 2 22 22

Aurora 22 22