Community Breeders' Page

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

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"Fast-tracked" MAB Pipelining

What's in a byline?

Enabling marker-assisted breeding in Rosaceae. What does it mean? "Enabling" means we are not just touting the promise but providing the instructions for implementation. "Marker-assisted breeding" (MAB) means integration of socio-economic and DNA information into routine breeding operations, supporting breeding decisions with supplemental knowledge. "In Rosaceae" means across the crops belonging to this diverse plant family, such as almond, rose, pear, and raspberry, in addition to the crops included for demonstration purposes of peach, cherry, strawberry, and apple. Scion or rootstock breeding, at public or private institutions – all are our target beneficiaries. Knowledge, tools, and skills obtained for one Rosaceae crop breeder are often applicable to others.

The MAB Pipeline in action in 2011

We enable MAB with the MAB Pipeline. The MAB Pipeline is a systematic process for identifying and conducting efficient breeding schemes. Each stage is illuminated to light the way to successful MAB. Over its four-year duration, RosBREED is establishing powerful infrastructure for each stage to enable MAB. But rather than waiting until the whole edifice is built before implementing efficient parent and seedling selection schemes, "fast-tracked pipelining" is underway to bring to fruition several marker-locus-trait associations that are available, very promising, yet unused in Rosaceae breeding… until now. With jewels in the genome that excite our Demonstration Breeders, 2011's goal for the MAB Pipeline Team has been to inform parent selection decisions as soon as possible. Achieving this goal requires rapid progress of promising markers through Pipeline stages 1-6 (Figure 1, next page).

Fast-tracked pipelining is positively benefiting apple breeding *now*. In Minnesota, breeders Jim Luby and David Bedford used DNA information in the form of functional haplotypes for the *Ma* locus (this issue's Jewel in the Genome) to choose exciting cross combinations and avoid certain others. Spin-off benefits of the translated marker data included confirming pedigree records for most Minnesota selections, detecting some incorrect records, deducing likely pedigrees in certain cases, and providing confidence in the genetic potential and identity of elite selections on the path to commercial release or in use as parents. A second targeted trait locus for fast-tracking, *MdExp7* for fruit firmness, also revealed useful functionality for Minnesota apple breeding and was incorporated in parent selection decisions this May. Jim and David, welcome to the rank of DNA-informed breeders!

Jim Luby and David Bedford, University of Minnesota, tasting crisp, delicious apples from their breeding program

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Fast-tracked MAB Pipelining...

RosBREED's MARKER-ASSISTED BREEDING PIPELINE in action!

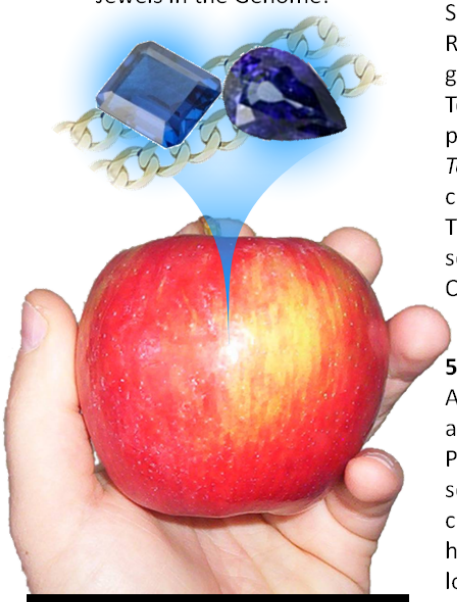
1. Prioritization
Two promising fruit quality trait loci for each crop were chosen from literature and experience (*MAB Pipeline and Breeding Teams*). These targets addressed trait priorities identified in Breeder surveys (*SE Team*). The *Ma* locus* was one of the target trait loci for apple, reportedly influencing acidity, crispness, and juiciness.

2. Genetic Screening Efficiency
For internal project purposes, the reliable, capable, and dedicated lab of Dr. Nahla Bassil at USDA-Corvallis, Oregon, is the default service provider for genetic screening (*Genotyping Team*).

3. Improved Markers
Previously reported markers for the target trait loci were tested, and all worked fine (*Genotyping Team*). For the *Ma* locus, two flanking SSRs were used. Although one is ~14 cM from the locus, it still contributes to informative haplotypes.

David Bedford performs controlled crossing for a new generation of superior apples in the University of Minnesota apple breeding program

* See this issue's Jewels in the Genome!



Honeycrisp: useful alleles for the *Ma* locus and *Md-Exp7*

4. Validation
So far so good. But now came the real work. Crop Reference Set individuals were DNA-extracted and genotyped with the trait locus markers (Genotyping Team). In the meantime, the same germplasm was phenotyped for fruit quality and databased (*Breeding Team*). Finally, the FlexQTL™ program was run to confirm QTL presence (*PBA and MAB Pipeline Teams*). The *Ma* locus markers revealed >20 haplotypes segregating in apple breeding pedigrees. Significant QTLs for several traits were confirmed at this locus.

5. Utility
Analyses were refined (so far only for apple) to specific breeding locations. Performance levels associated with each segregating haplotype were calculated and compared (*MAB Pipeline Team*). Functional haplotypes were detected for the *Ma* locus, some associated with desirable trait levels and others with poor performance.

6. Parent Selection Decisions
The integrated and translated socio-economics and DNA information was offered to RosBREED's Demonstration Breeders – at least to apple breeders who still had time before the pollination season to incorporate the new information on genetic potential of their parents in their crossing plans (*Breeding Team*).

Figure 1: "Fast-tracked" MAB pipelining efforts in 2010 - 2011 have integrated socio-economics and DNA information to support breeding decisions