

RosBREED

Enabling marker-assisted breeding in Rosaceae



www.rosbreed.org

RosBREED Enables Marker-Assisted Breeding for Apple

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The RosBREED project and apple genetic improvement

U.S. apple breeders primarily target consumer-preferred traits of excellent texture, flavor, and appearance. The ability to retain superior fruit quality after storage is a particular focus so that a year-round domestic supply of nutritious apples is available to the public. Also considered are traits valued by industry sectors, especially suitability to local production environments. DNA information, if gathered, validated, deployed, and routinely used in breeding decision-making, offers the opportunity for apple genetic improvement to become more efficient and precise in delivering long-term solutions to industry challenges and consumer demands. The multi-institutional RosBREED project (www.rosbreed.org) is enabling such marker-assisted breeding (MAB) for apple.

Performance evaluation

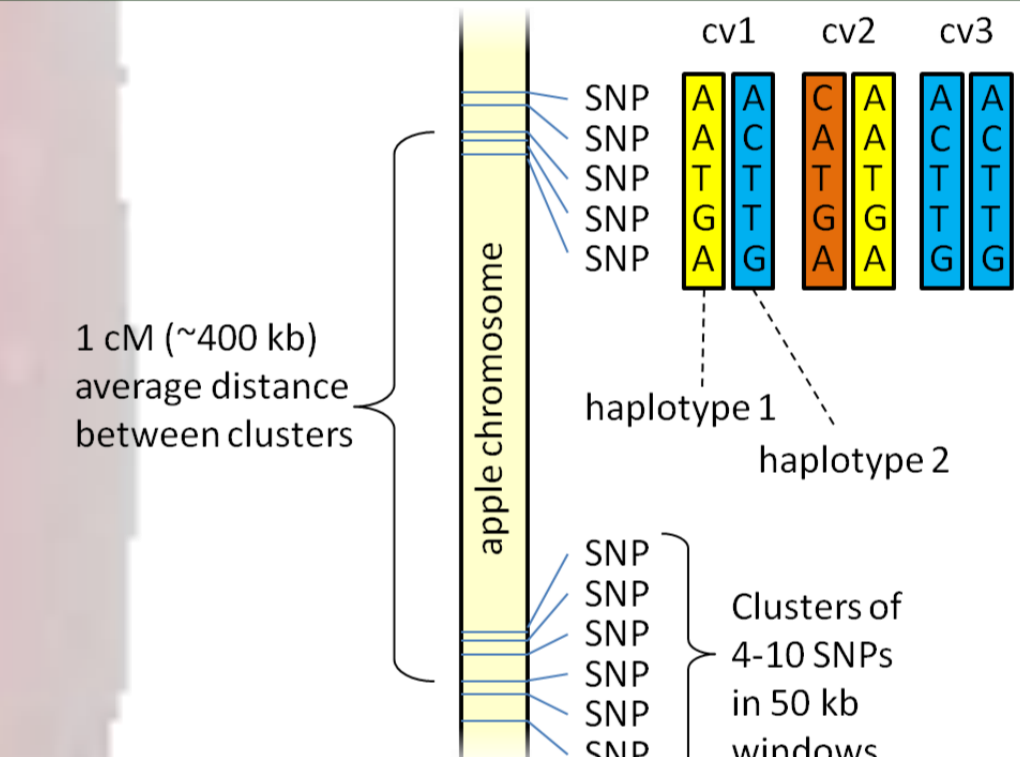
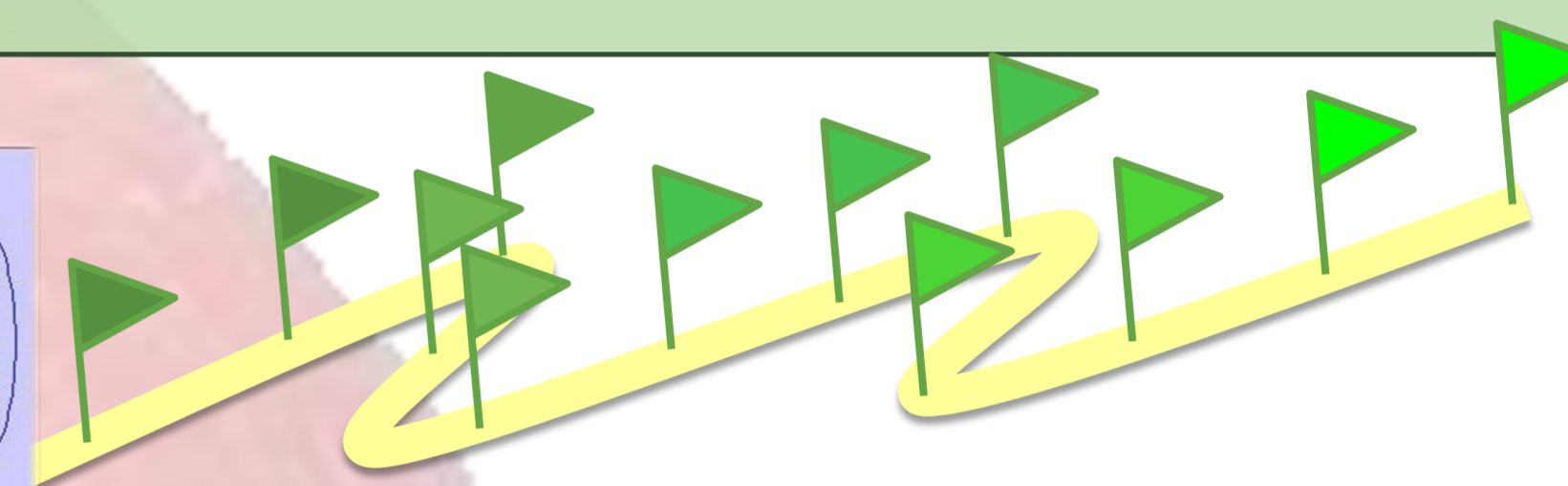
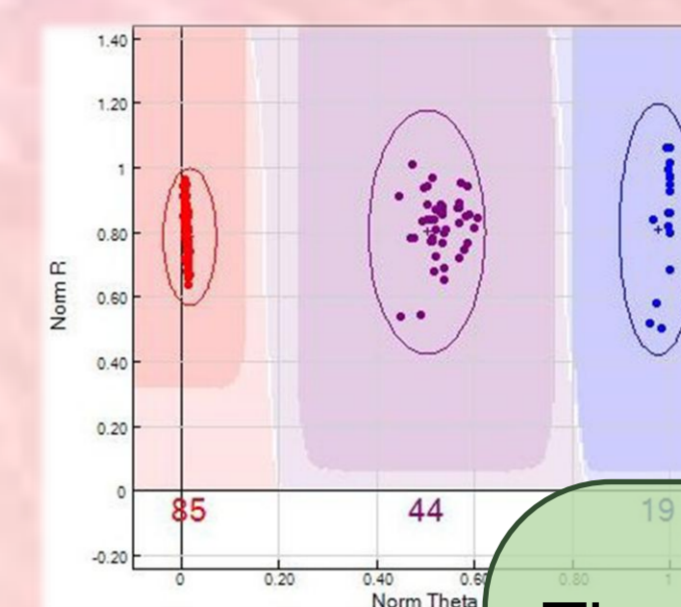
- Standardized phenotyping protocols for fruit quality evaluation (www.rosbreed.org/resources/fruit-evaluation) were collaboratively developed.
- Performance evaluation at **multiple, nation-wide breeding locations** was conducted since 2010 for many fruit quality and productivity traits.
- Access data at: www.rosaceae.org/breeders_toolbox

Germplasm

- The **apple Crop Reference Set** has a complex pedigree structure across eight generations of cultivated germplasm.
- Together with program-specific **Breeding Pedigree Sets** for a total of ~1000 apple individuals, this germplasm represents the genomes of each of 65 important breeding parents at least 12X – for statistical power in determining effects of their alleles.
- Multi-generational flow of marker alleles, linkage blocks, and phenotypes for all or subsets of these pedigree connections are **visualized with Pedimap**, Pedigree-Based Analysis software.

SNP genome scans

- The International RosBREED SNP Consortium apple 8K SNP array v1 comprises **clusters** of 4-10 SNPs spaced **every 1 cM** along the apple genome.
- The clustering strategy **streamlines haplotyping** and readily achieves our target of **≥1 heterozygous SNP per 5 cM** along the chromosomes of any genome-scanned individual to maximize recombination tracking.

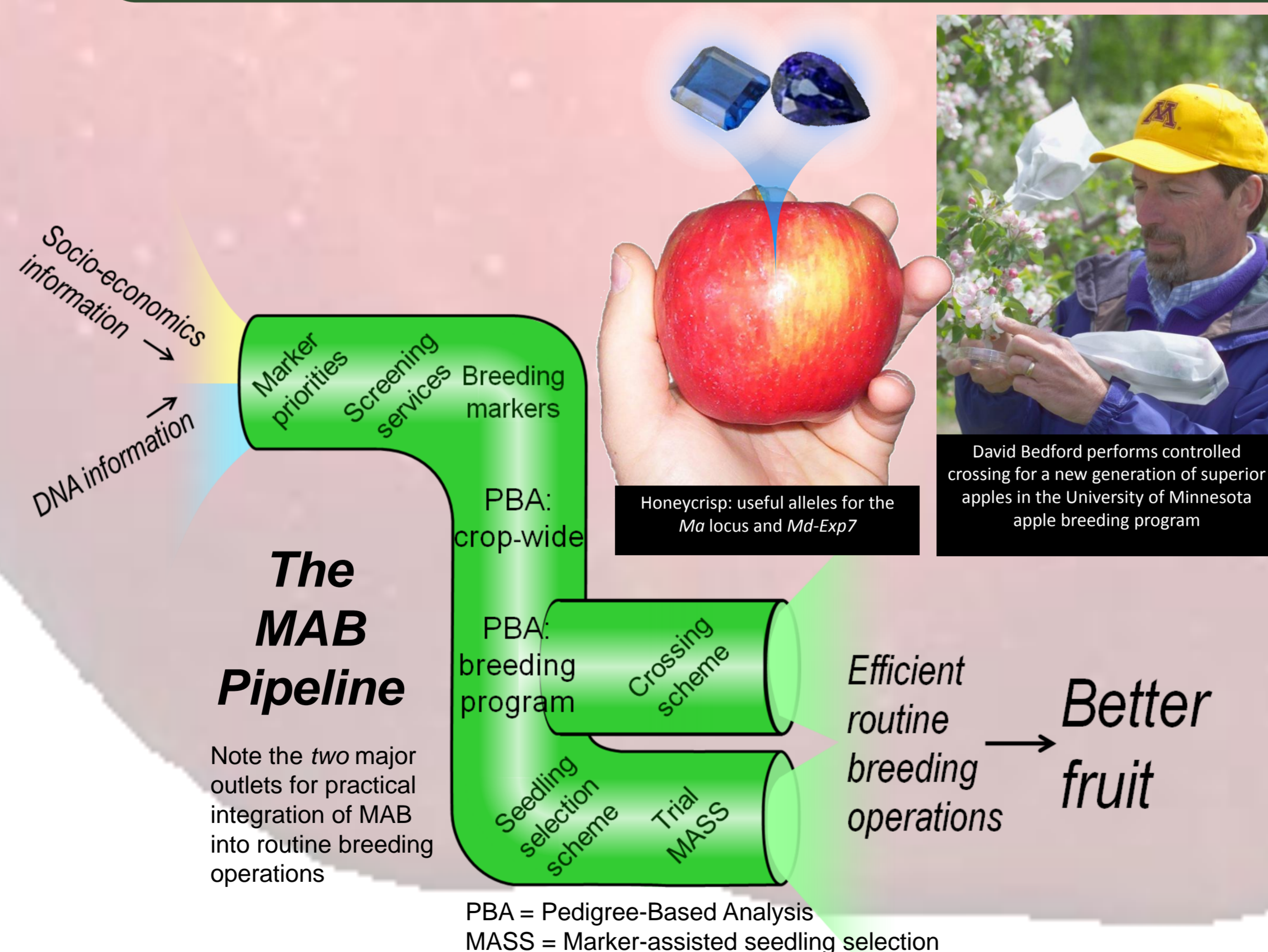


Genetic tests for breeding

- RosBREED uses the 8-stage “MAB Pipeline” to **translate QTLs into breeding tools and knowledge**.
- Pipelining began with **two promising available genetic tests**, for fruit texture and flavor components (*Ma* locus and *Md-Exp7*).
- **Functional alleles** were revealed for important breeding parents – such as Honeycrisp, Braeburn, Gala, and Fuji.
- Added benefits of screening hundreds of individuals with the three SSRs include **verification of pedigrees** and **identification of incorrect records**, with some deductions of likely pedigrees.
- Once genome scan data is ready in late 2011, we anticipate Pedigree-Based Analysis will identify and characterize **hundreds of promising QTLs**.
- Each QTL will then enter the MAB Pipeline.
- Those genetic tests with proven utility for individual breeding programs will be used to **support parent and seedling selection decisions and actions**.

MAB in action

Genetic tests for apple fruit storability have assisted the Washington apple breeding program since 2010 to cull inferior seedlings prior to expensive field maintenance and evaluation. **Most powerfully**, DNA information on fruit texture and flavor is **informing crossing decisions** of U.S. apple breeders, delivering new knowledge to efficiently **enrich the next generations of apples with the genetics for superior fruit quality**.



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

**** 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
Siren	12	22
Splendour	22	12
Sundowner	12	22
Wendland	12	22

Using the table of cultivar functional genotypes

Gala × 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

CONCLUSIONS

Table available at: www.rosbreed.org/breeding/jewel-5

MAB is a reality for apple, and is undergoing major advances. Major public apple breeding programs in Washington, Minnesota, and New York have united to establish a germplasm set comprehensively representing U.S. cultivated germplasm. Three years of large-scale phenotyping of the reference germplasm is underway. High-resolution SNP-based genome scans are providing an unprecedented view of cultivated apple functional genetic diversity. A new era in QTL discovery for valuable traits will arrive in late 2011 when genome scans are integrated with phenotypic performance using FlexQTL™ software. In the meantime, promising genetic tests for fruit texture and flavor were fast-tracked through RosBREED’s “MAB Pipeline”. MAB is now in routine operation in U.S. apple breeding, for efficient development of new cultivars with superior fruit quality.