

RosBREED

Enabling marker-assisted breeding in Rosaceae



www.rosbreed.org

RosBREED Provides DNA-Informed Opportunities for Cherry Breeding

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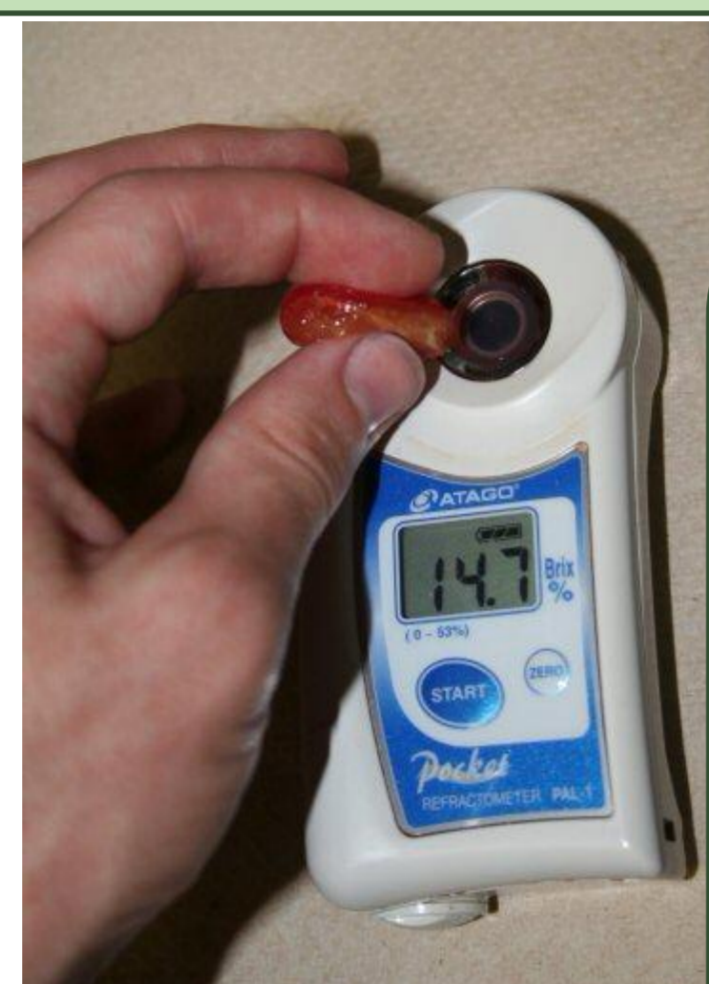
The RosBREED project and cherry genetic improvement

Fruit size, firmness, flavor, self-fertility, and yield are valuable targets for cherry genetic improvement. DNA markers for some of these traits have been previously reported but require validation in breeding germplasm under commercial conditions, beyond the experimental populations in which the marker-locus-trait associations were first discovered. Each genetic test must also be adjusted to the specific needs, capabilities, and logistics of individual breeding programs. The RosBREED project (www.rosbreed.org) is enabling cherry breeding programs to integrate DNA information into breeding decisions for more precise and efficient delivery of long-term solutions to industry challenges and consumer demands.



Performance evaluation

- The sweet and tart cherry programs follow **standardized phenotyping protocols** (www.rosbreed.org/resources/fruit-evaluation).
- Comprehensive performance evaluation for fruit quality and other valuable traits was **recently completed for the second of three seasons**.
- For sweet cherry, an earlier season of 2009 data was also included.

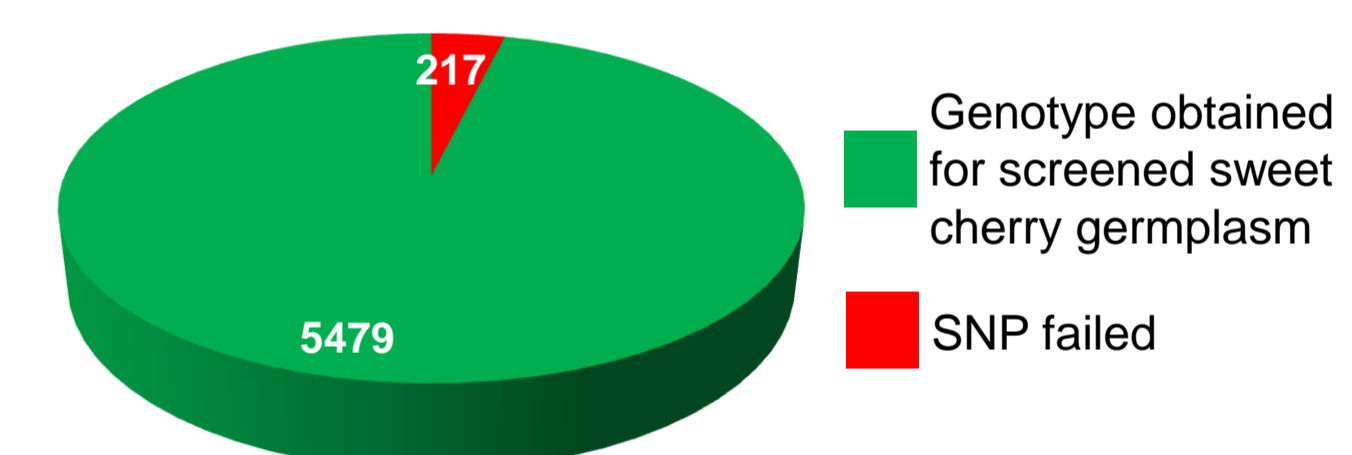
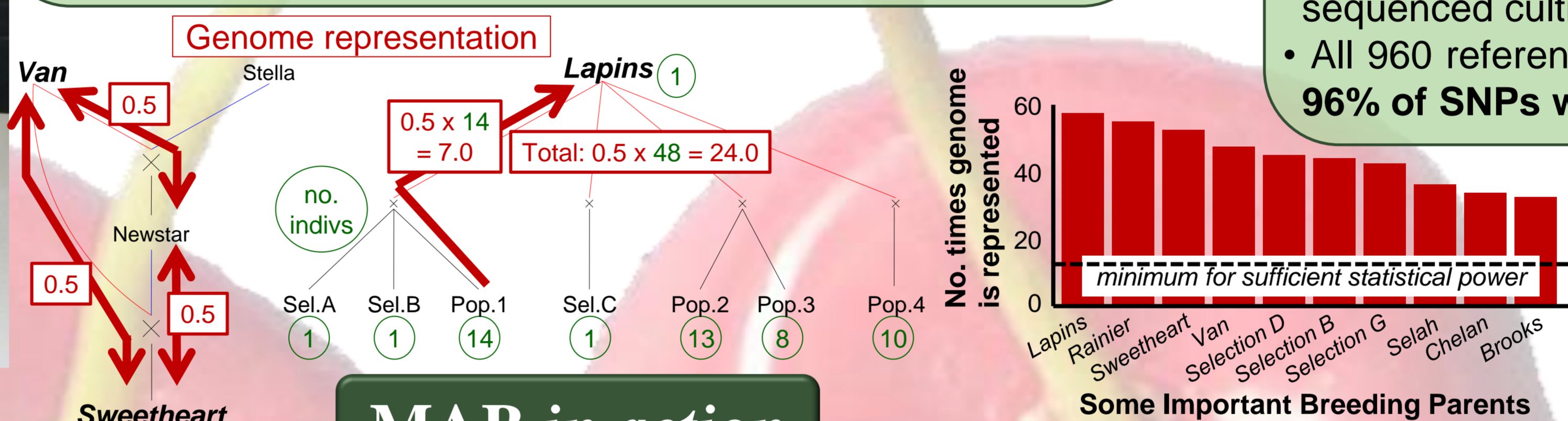


Germplasm

- Two crops are involved: **sweet cherry** (*Prunus avium*) and **tart cherry** (*P. cerasus*), with public breeding programs in Washington and Michigan, respectively.
- For each crop is a public **Crop Reference Set** (n=240 x 2), efficiently **representing the genomes of important breeding parents** with pedigree-linked cultivars, ancestors, selections, and seedling populations. **Breeding Pedigree Sets** (n=240 x 2) improve statistical power for individual breeding programs.
- The pedigree structures of cultivated cherry span **only 5-6 generations** with very few missing ancestors and low genetic diversity, facilitating our **identity-by-descent approach to detect and characterize valuable QTLs**.

SNP genome scans

- SNP-based genome-scanning capability was recently developed with a **6K cherry SNP array**.
- 4500 SNPs target the genetic diversity of sweet cherry and 1500 for tart cherry, but SNP transferability between species is expected.
- SNPs were chosen to be **evenly spaced** over the genome, anchored to the peach whole genome sequence.
- SNPs for tetraploid tart cherry** targeted differences within, not between, subgenomes via read count frequencies in 8 sequenced cultivars as a proxy for dosage.
- All 960 reference germplasm individuals are now scanned. **96% of SNPs worked** (gave a genotype) for sweet cherry.



Genetic tests for breeding

- Determination of genotypically based **breeding values** to guide cultivar development decisions will be achieved with application of the **Pedigree-Based Analysis** approach to cherry breeding germplasm.
- Such comprehensive descriptions of functional regions of the genome for any cultivar or seedling will use SNP genome scan data in **QTL analysis with FlexQTL™**, in late 2011.
- Promising **QTLs then enter the MAB Pipeline** for refinement, validation, and tailoring to individual breeding programs.
- In the meantime, available **genetic tests for fruit size and tartness** have been fast-tracked through the MAB Pipeline to provide knowledge and tools for cherry breeding decision support.

MAB in action

Marker-assisted parent selection using a **genetic test for cross-compatibility and self-fertility** has been conducted for several years, to avoid incompatible crosses and enrich for self-fruitfulness. Since 2010, **marker-assisted seedling selection at a high-throughput scale for fruit size, firmness, and self-fertility** has also improved breeding efficiency in the Washington State program.

A QTL for cherry fruit size and known genomic location of the S (*self-compatibility*) locus have already exited the MAB Pipeline, providing to breeders **knowledge** on fruit size genetic potential of prospective parents to aid crossing decisions, and **tools** for culling seedlings predicted to have small fruit. Such marker-assisted parent selection (MAPS) and marker-assisted seedling selection (MASS) is now in routine use – **MAB in action!**

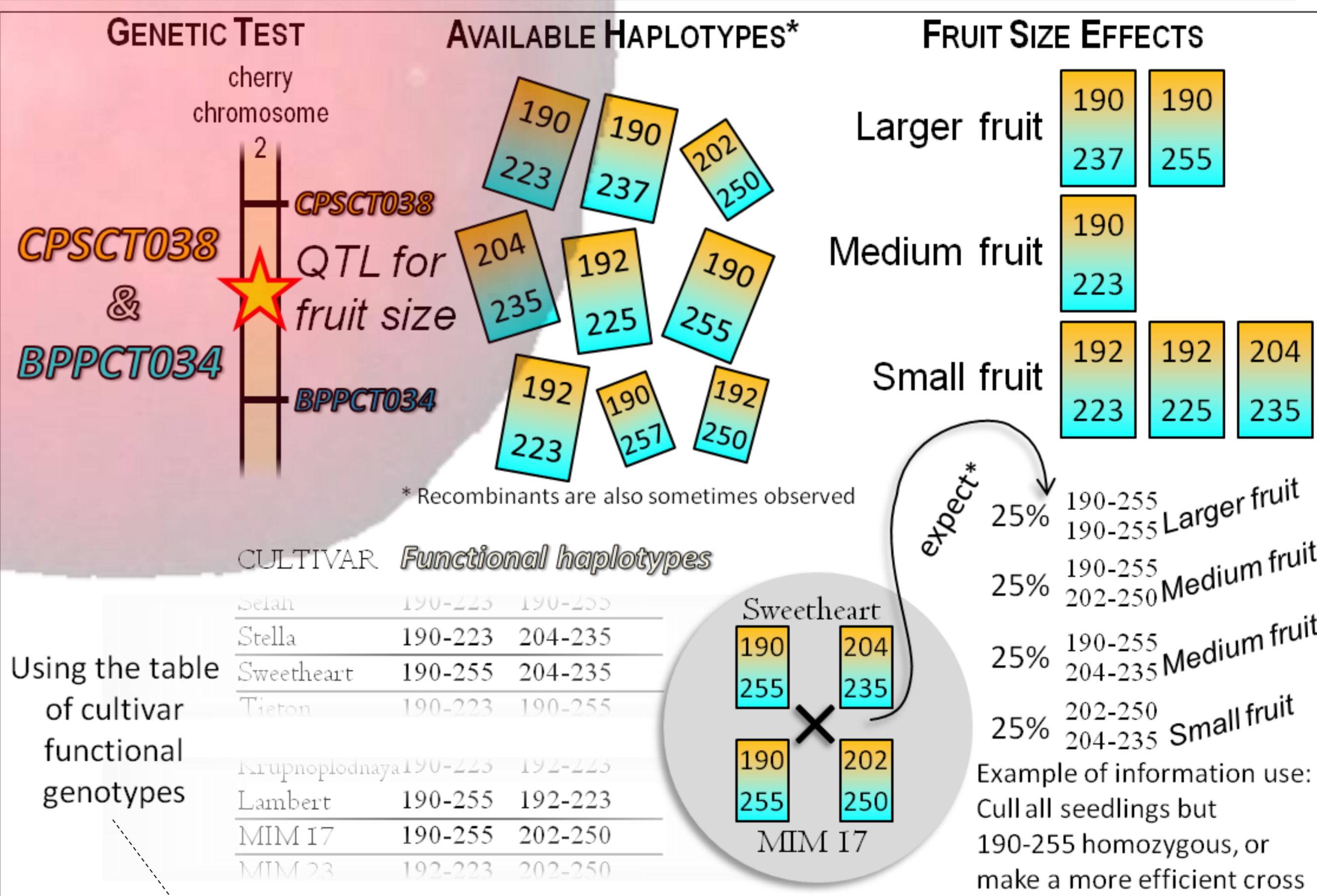


MAPS

Efficient and precise crossing designs

MASS

Efficient and precise seedling evaluation



- Carries S4' for self-fertility
- self-infertile

CONCLUSIONS

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

An unprecedented cherry breeding, genetics, and genomics initiative is underway to deliver the efficiencies and precision of MAB to new cultivar development. State University breeding programs in Washington (sweet cherry) and Michigan (tart cherry) serving the major U.S. cherry growing regions have established pedigree-linked reference germplasm sets. This germplasm, efficiently representing important breeding parents, is undergoing comprehensive performance evaluation and high-resolution SNP-based genome scans. Pedigree-Based Analysis software of FlexQTL™ integrates these community datasets to find many promising QTL targets. Then kicks in RosBREED's unique "MAB Pipeline" approach to refine and validate socio-economically valuable targets for breeding decision support. The first genetic tests are already in routine use.