

RosBREED

Enabling marker-assisted breeding in Rosaceae



www.rosbreed.org

RosBREED Facilitates Peach Genetic Improvement via Marker-Assisted Breeding

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The RosBREED project and peach genetic improvement

New cultivar development for peach in the U.S. can be divided into two types according to usage of fruit: fresh market and processing market. Objectives common to all peach breeding programs include improving and maintaining fruit quality (flavor, firmness, and appearance), productivity, size, and extending the season. These trait targets are complemented with emphases on ease of processing, disease and pest resistance, a greater diversity of fruit types, and adaptation to low-chill zones in individual programs. Despite being one of the best characterized Rosaceae crops, with genomic resources that include a whole genome sequence, a reference genetic map, EST libraries, and a growing list of marker-locus-trait associations, application of these resources in peach breeding is still limited. The RosBREED project (www.rosbreed.org) aims to bridge this chasm by providing markers and simplified technologies to enable peach marker-assisted breeding (MAB) for fruit quality and other critical traits.

Performance evaluation

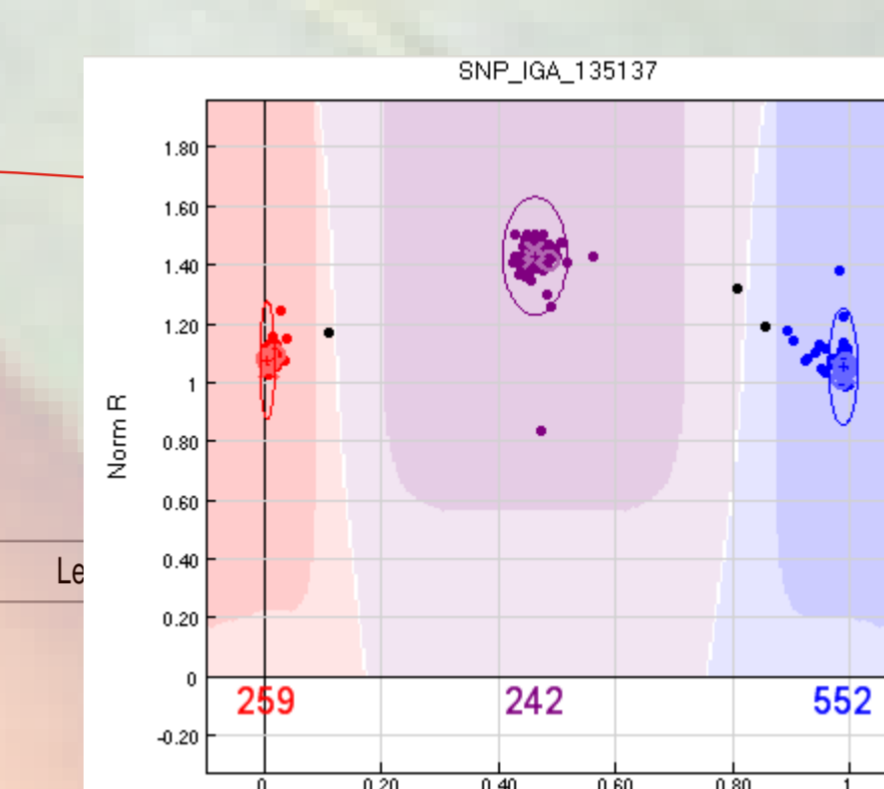
- Standardized phenotyping protocols for peach fruit quality evaluation (www.rosbreed.org/resources/fruit-evaluation) were collaboratively developed.
- Performance evaluation began in 2010 for 13 fruit quality and 3 productivity traits at multiple, nation-wide breeding locations.



- ZinDai
- ChineseCling
- EarlyCrawford
- F_JHale
- Quetta
- Lippiatt
- JulyEiberta
- F_EarlySunGrand
- Lola
- F_Arp_Beauty
- Hiley
- LukensHoney
- Strawberry
- Peento
- Mayflower

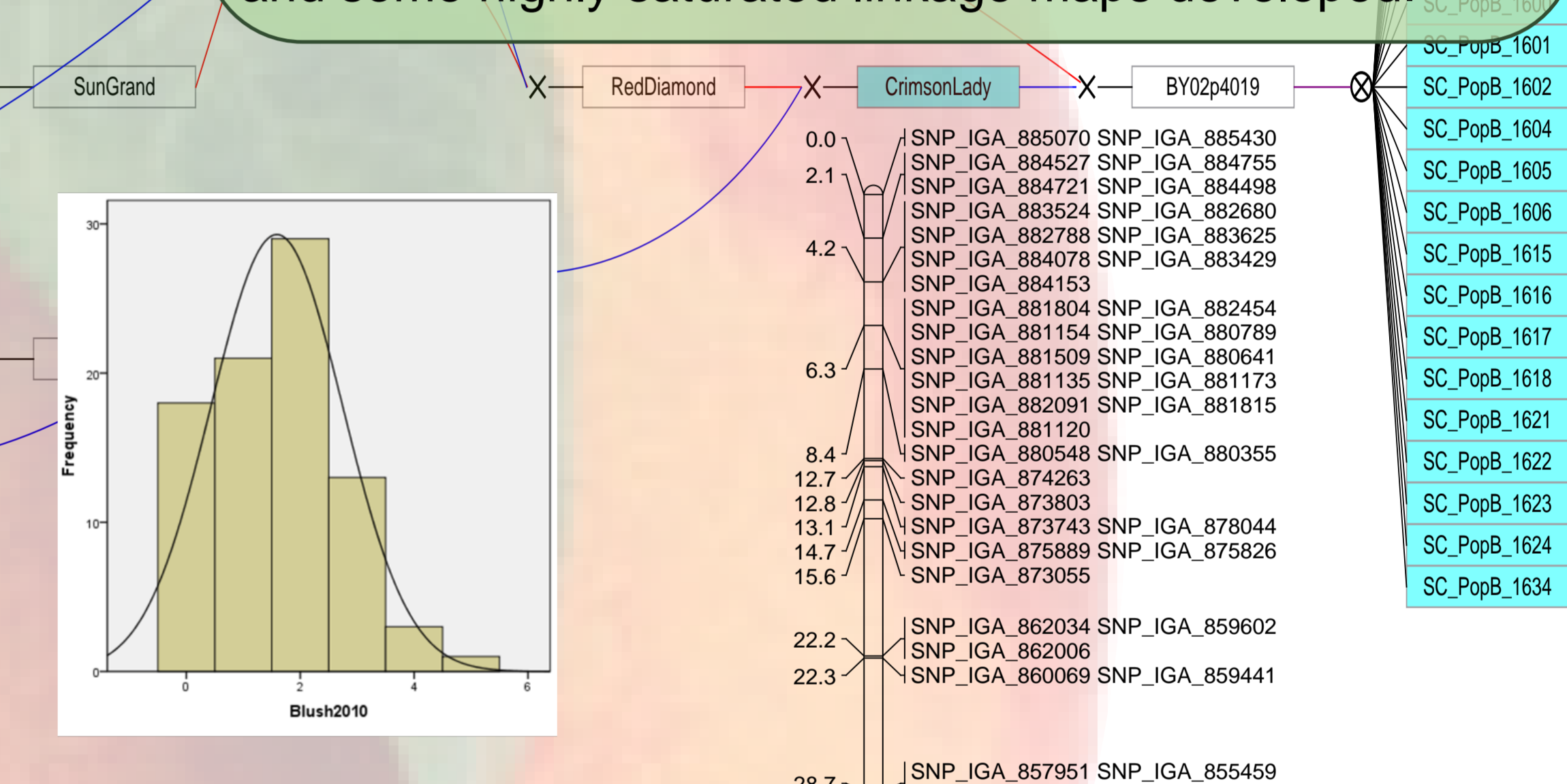
Germplasm

- The peach Crop Reference Set has a very complex structure, for which pedigree records stretch across eighteen generations!
- Together with program-specific Breeding Pedigree Sets for a total of ~1000 peach individuals, this germplasm represents the genomes of important breeding parents
- Pedimap software is used to visualize flow of marker alleles, linkage blocks, and phenotypes across these pedigree connections, and has revealed unrealized fractions of shared genomes.



SNP genome scans

- High-resolution SNP-based genome scanning capability with an 9K array was developed for peach.
- SNPs are evenly spread over the genome to readily track recombination events in breeding germplasm.
- Genome scanning of ~1000 peach accessions underway, for use in QTL discovery via the PBA approach.
- Additional uses: pedigree relationships are being resolved, and some highly saturated linkage maps developed.

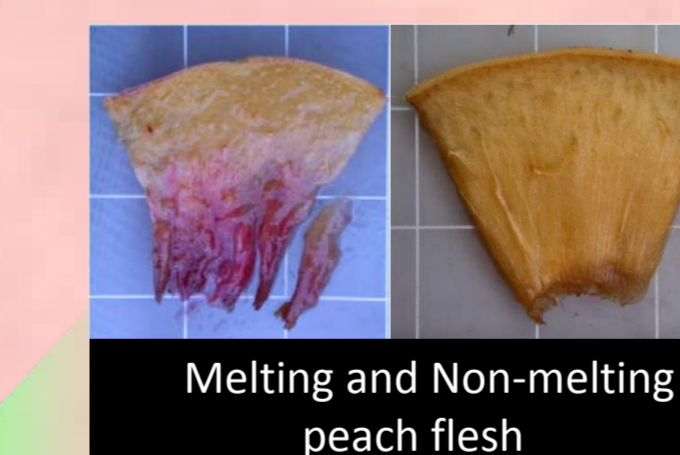
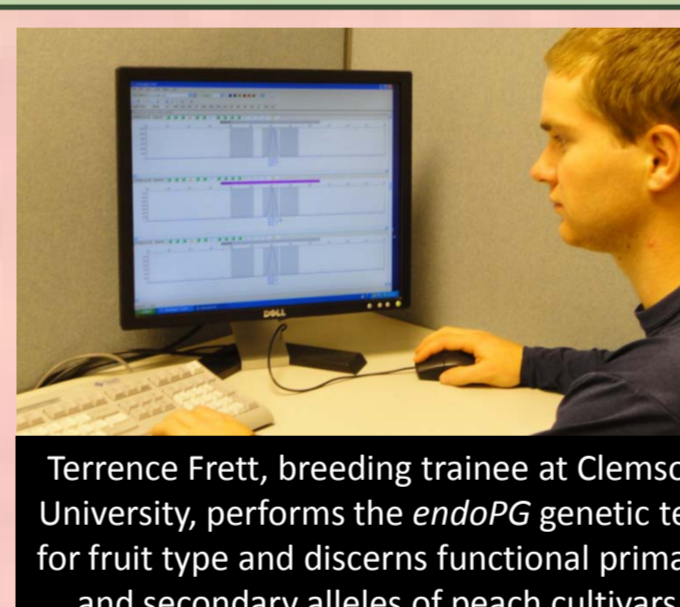
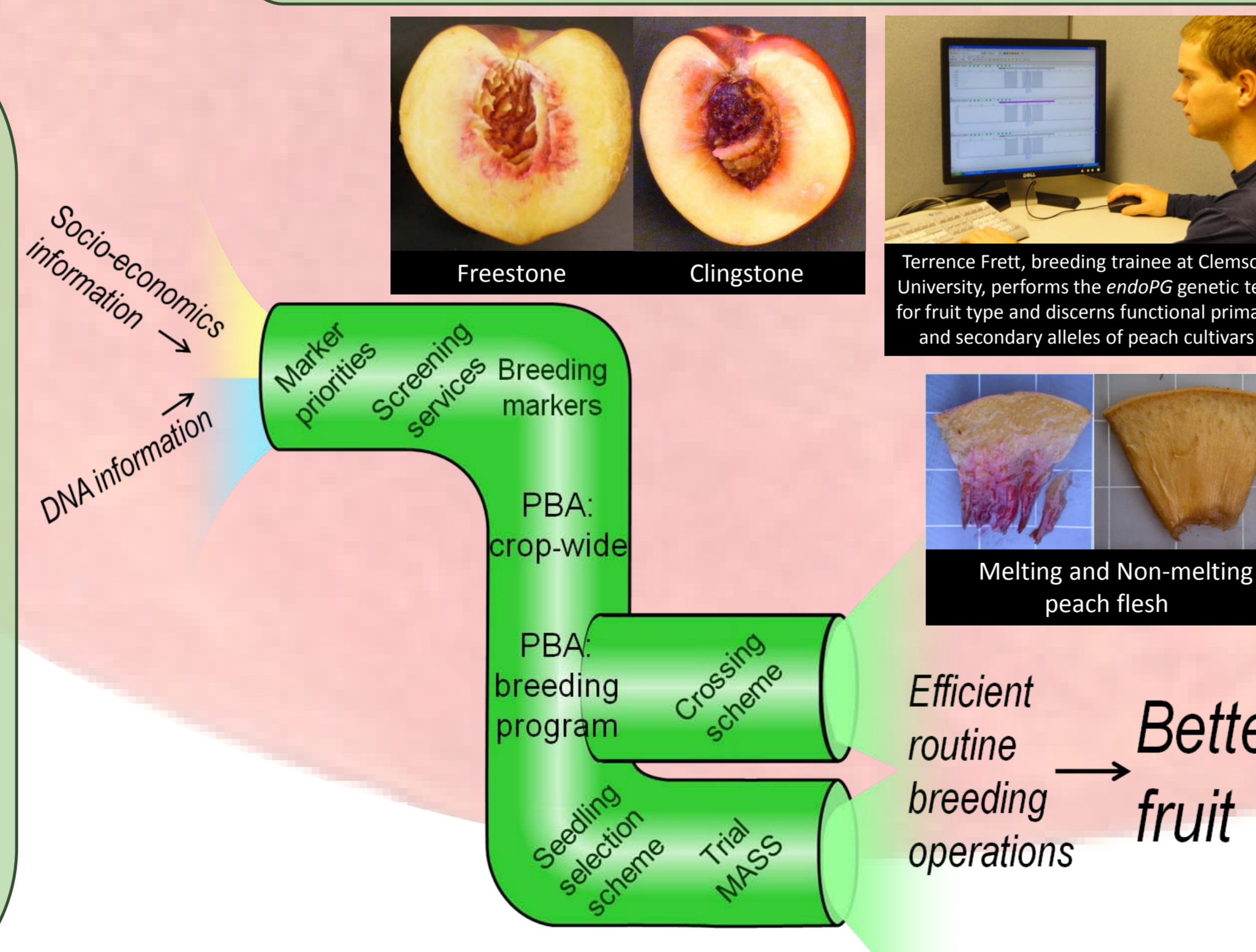


MAB in action

Genetic tests for promising trait targets were recently fast-tracked through RosBREED's "MAB Pipeline". Imminently, DNA information on fruit type (melting vs. non-softening vs. non-melting; freestone vs. clingstone) will inform crossing decisions of U.S. peach breeders, enabling more efficient breeding and development of the next generations of peaches destined for fresh market or canning.

Genetic tests for breeding

- Peach is model genome for the Rosaceae family.
- Has an excellent whole genome sequence, a reference genetic map, and bin set available.
- Many fruit quality QTLs have been detected and mapped in peach but MAB has yet to be routinely implemented in U.S. peach breeding programs.
- The *endoPG* genetic test facilitated identification of incorrect records, validation of phenotypic data, and provided valuable information for crossing decisions in 2012.
- Genome-wide SNP data will facilitate Pedigree Based Analysis.
- FlexQTL™ software will enable detection of QTLs associated with fruit quality traits, with direct validation in breeding germplasm to facilitate rapid integration of new DNA information into breeding.



GENETIC TEST	AVAILABLE ALLELES		FRUIT TEXTURE EFFECTS		FRUIT TEXTURE TYPE CODE
	PRIMARY	SECONDARY	STONE-FLESH ADHESION	FLESH SOFTENING TYPE	
<i>endoPG</i>	F (dominant)	F ₁₀₉ , F ₂₀₃ , F ₂₀₅ , F ₂₀₇ , F ₂₃₁	freestone	melting	FMF
	f (recessive)	f ₂₀₉ , f ₂₁₁ , f ₂₁₃ , f ₂₁₅ , f ₂₂₇ , f ₂₂₉ , f ₂₃₃ , f ₂₃₅ , f ₂₃₇ , f ₂₇₇ , + many from other species	clingstone	melting	CMF
	f1	f ₁₁₉₉ , f ₁₂₀₁	clingstone	non-melting	CNMF
	f2	f _{2null}	clingstone	non-softening	CNSF

CULTIVAR	Functional genotype Primary	Secondary
China Pearl	F F	F ₂₀₅ F ₂₀₇
Chinese Cling	f f	f ₂₂₉ f _{2null}
Clayton	F f	F ₂₀₅ f
Compass	F F	F ₂₀₅ F ₂₀₇
Eight Sweet	f f	f ₂₁₁ f
BY01P6245	F f1	F ₂₀₅ f ₁₂₀₁
Carmen	F f	F ₂₀₅ f
Cherry	f f	f ₂₀₅ f

Using the table of cultivar functional genotypes

Chinese Cling f₂₂₉ f_{2null} × BY01P6245 F₂₀₅ f₁₂₀₁

expect 50% FMF F₂₀₅ f₂₂₉ / F₂₀₅ f_{2null}
25% CMF f₂₂₉ f₁₂₀₁
25% CNMF f₁₂₀₁ f_{2null}

Example of information use: For fresh-market breeding, cull CNMF seedlings or make a more efficient cross

CONCLUSIONS

Four public peach breeding programs in California, Texas, South Carolina, and Arkansas, representing a range of breeding objectives, have established a comprehensive reference germplasm set representing important breeding parents, containing about 500 popular cultivars, ancestors, breeding selections, and breeding populations. Three years of phenotyping this germplasm for more than 20 traits is underway. High-resolution SNP-based genome scans with more than 3.5 million data points provide genome-wide tags to determine chromosome regions containing genetic variation that control complex traits such as flavor in peach. The promise of MAB in peach is finally being realized through the established RosBREED MAB Pipeline and information database ("Breeders' Toolbox") now being demonstrated for routine operation by the four U.S. public breeding programs. The chasm is being bridged and genomics-age promise of more efficient breeding in peach is now a reality.