

RosBREED



Enabling Marker-Assisted Breeding In Rosaceae

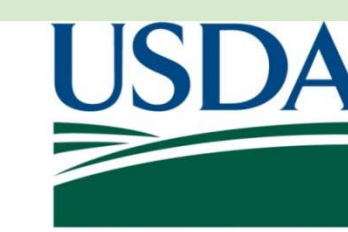
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ABSTRACT

RosBREED will create a national, dynamic, sustained effort in research, infrastructure establishment, training, and extension for applying marker-assisted breeding (MAB) to deliver improved plant materials more efficiently and rapidly. The Rosaceae family (including apple, peach, sweet and tart cherries, and strawberry) provides vital contributions to human health and well-being, and collectively constitutes the economic backbone of many U.S. rural communities. Rosaceae genetics and genomics are developing rapidly but have not been translated to routine practical application. Specific objectives are to:

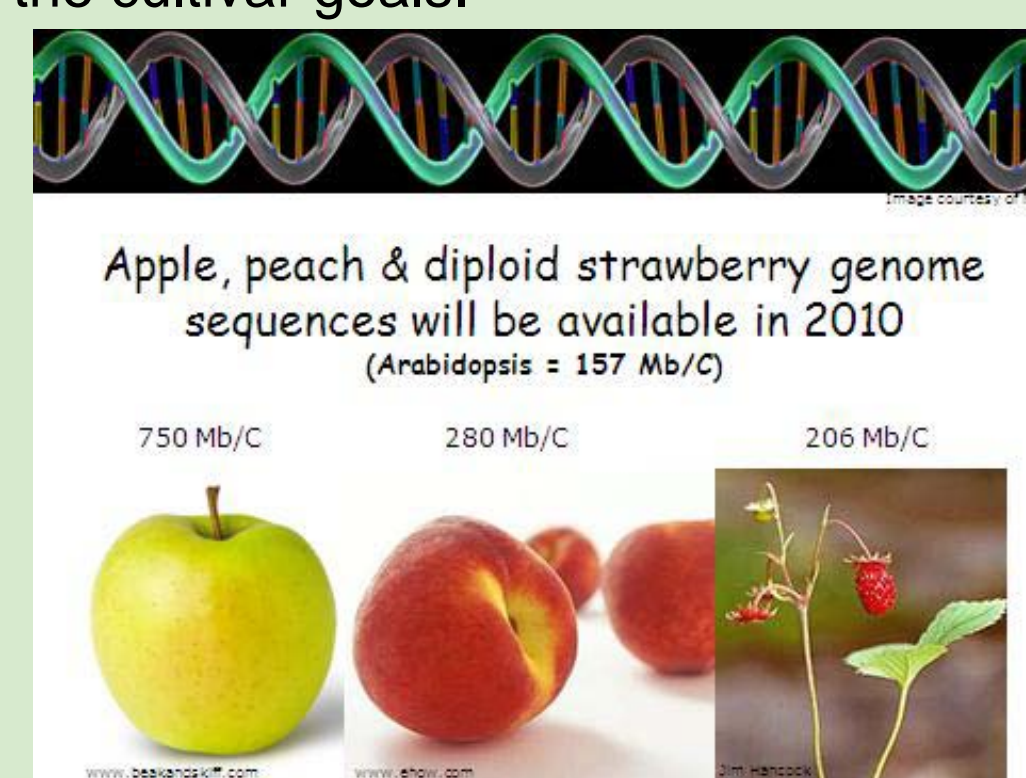
- (1) Socio-economics: Enhance the likelihood of new cultivar adoption, enlarge market potential, and increase consumption of rosaceous fruits by using socio-economic knowledge of stakeholder values and consumer preferences to inform breeding;
- (2) Genomics: Establish sustainable technical infrastructure for an efficient MAB Pipeline in Rosaceae, including crop-specific SNP genome scan platforms for breeding-relevant germplasm exploiting the shared ancestry of Rosaceae crops;
- (3) Breeding information management system: Integrate breeding and genomics resources by establishing a user-friendly U.S.-wide standardized statistical framework and breeding information management system;
- (4) Marker-assisted breeding pipelining: Implement MAB in core RosBREED breeding programs with a common focus on fruit quality traits; and
- (5) Outreach: Enhance sustainability of cultivar development by transferring MAB technologies to the public and private community of U.S. Rosaceae breeders through training current and future breeders as well as engaging the production, processing and marketing sectors, allied scientists, and consumers.

What need does RosBREED address?

The U.S. Rosaceae crop industries face numerous limitations to profitability and sustainability. Overcoming these barriers requires rapid development and deployment of new cultivars with improved characteristics to meet dynamic industry and market needs and consumer preferences. This project will utilize genomics information and knowledge of what consumers value to increase the efficiency of cultivar development and deployment.

Why now?

2010 is a watershed year for the Rosaceae with the anticipated publication of the peach, apple and strawberry genome sequences. In addition, over 250 genes and marker-trait associations have been identified in rosaceous crops. Yet, a huge gap exists as this DNA-based information is rarely used to improve plant breeding. RosBREED will bridge this gap and ensure that future breeding efforts leverage this genomics and genetics information to more efficiently reach the cultivar goals.

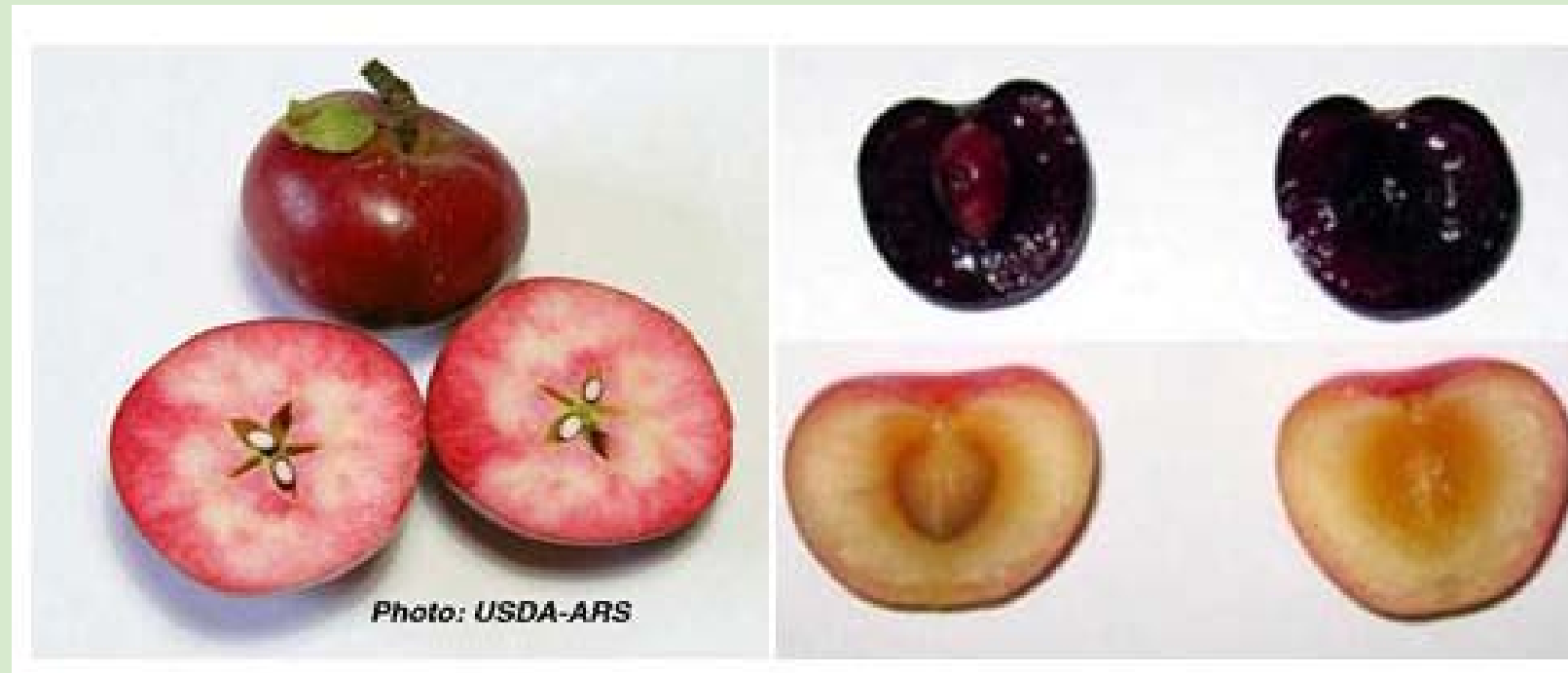


Status and utilization of genetic information in rosaceous crops.

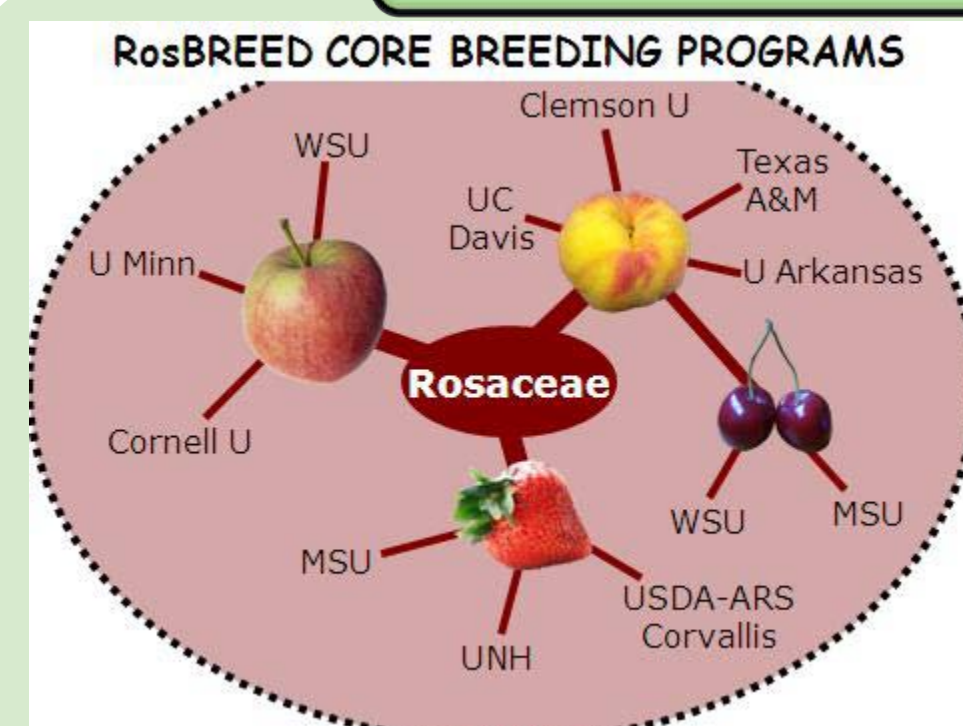
Crop	Number of M-T Associations (USA)			Number of M-T Associations (World)		
	Total	Quality	Yield	Total	Quality	Yield
Apple	55	150	36	5	2	1
Peach	5	7	3	1	0	0
Strawberry	21	36	4	2	1	0
Cherry (sweet)	10	5	4	1	1	0
Cherry (sour)	1	0	0	1	1	0
Strawberry	11	31	2	0	0	2
Raspberry	0	0	0	0	0	0
Blackberry	0	0	0	0	0	0
Rose	11	51	2	0	0	0
Total	117	358	45	10	4	3

Why are we working together as a crop group?

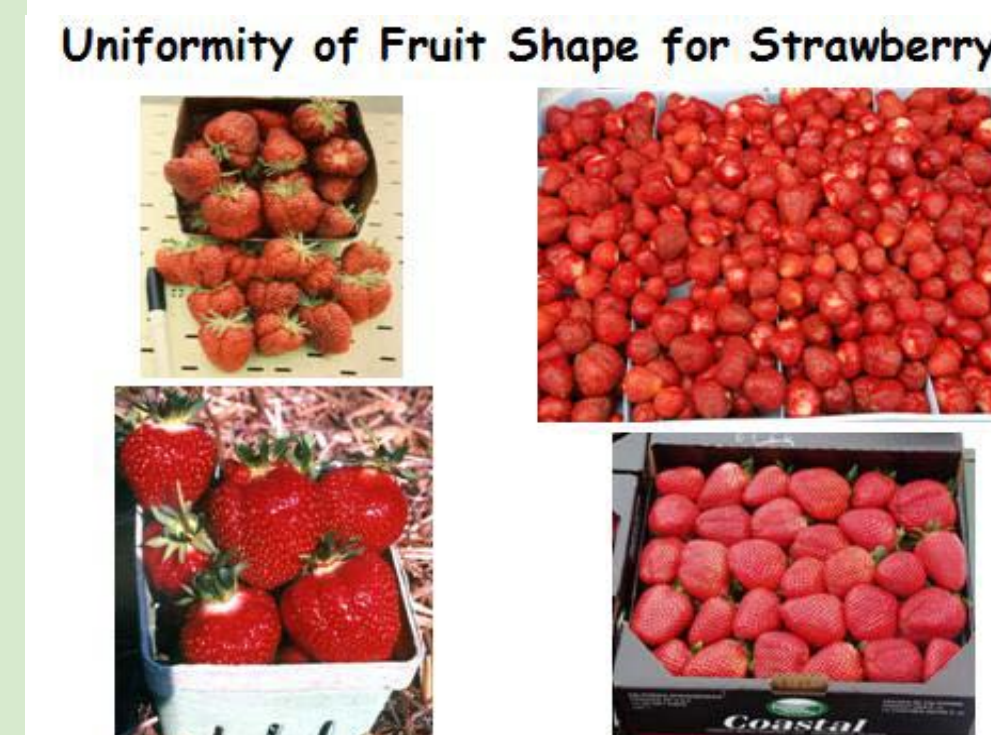
RosBREED is rooted in our vision that the common ancestral origin of the diverse rosaceous genera can be harnessed to leverage knowledge and resources across commodity boundaries. For example, the same transcription factor that controls the presence of red pigment in apple, likely controls the presence of red pigment in cherry.



What rosaceous crops and traits will be targeted in RosBREED?

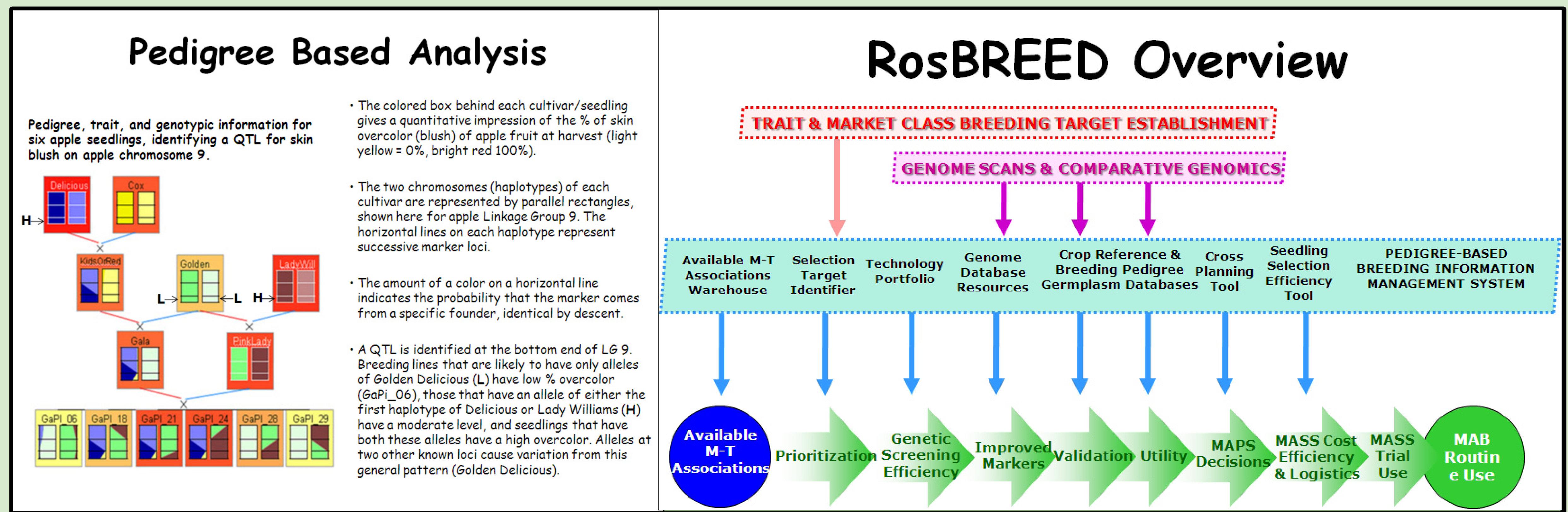


RosBREED will focus on fruit quality traits for four rosaceous crops; apple, peach, cherry and strawberry. Market-based information will be used to objectively quantify the importance of fruit quality traits that will be targeted for marker-assisted breeding.



What technology will be developed and adopted?

The central technology to be used in this project is marker-assisted breeding (MAB). An eight-stage MAB Pipeline will be established, and demonstrated with markers for high impact traits, to assist breeders in improving the efficiency of their programs. RosBREED will develop the community resource of a genome-scanned, comprehensively phenotyped (for fruit quality) reference database on pedigree-linked breeding germplasm. Pedigree-Based Analysis will be used to functionally characterize alleles at detected QTLs, describing the genotypic value of breeding parents. The genome scans for each of the major crop groups (apple, peach, strawberry, and cherry) will exploit ancestral genomic relationships across Rosaceae, and focus on shared fruit quality genes. Software will be developed for breeder access to databases and decision-support analytical tools, incorporating such features as trait economic values, cost-efficiency calculation of (marker-assisted) seedling selection schemes, cross planning, and breeder-friendly interfacing of genomics information.



How will project results be communicated with stakeholders?

An extension platform of workshops, web-based communications and publications will be delivered to stakeholders on how the use of genomics information can be harnessed to develop new varieties that meet market needs and consumer preferences.

The Rosaceae Specialty Crops Planning Workshop (22-23 June 2007)

Year 1 Activities				
Timeline	Meeting	Location	Target Audience	Theme
YR 1	RosBREED I	San Diego, CA Jan 7 th - Jan 8 th , 2010	RosBREED Participants, Advisory Panel Members, & Collaborators	RosBREED Orientation & Planning
	SNP Summit	Seattle, WA May 2010	RosBREED Genomics team participants & Collaborators	Design genotyping platforms in coordination with international partners.
	ASHS	Palm Springs, CA August 2010	Non-core breeders & AP Members	RosBREED Introduction to non-core Rosaceous crop breeders

What are the targets for success?

Marker-assisted breeding will be adopted by the core breeders as a cost effective strategy for improving the efficiency of their programs. Breeders will use economic weighting of traits for selection for marker-assisted breeding. Stakeholders will appreciate how the use of genomics information can be harnessed to develop new varieties that meet market needs and consumer preferences.

Please visit our website at: www.rosbreed.org