

ROSBREED

Enabling marker-assisted breeding in Rosaceae

Planned Year 2 Deliverables

Socio-Economics Team I

1. What

- Survey of trait priorities for breeders of rosaceous fruit crops – analyzed, interpreted, and reported

To whom

- U.S. Rosaceae industries, U.S. Rosaceae genomics, genetic, and breeding community

Intended impact

- Knowledge of breeder trait priorities gained and considered by breeders in comparison with priorities of other industry sectors



Socio-Economics Team II

2. What

- Survey of trait priorities for market intermediaries for peaches, cherries, apples and strawberries – developed, distribution, analyzed, interpreted, and reported

To whom

- U.S. Rosaceae industries, U.S. Rosaceae genomics, genetics, and breeding community

Intended impact

- Knowledge of trait priorities and economic value for traits by marketing intermediaries gained and used to help objectively define Rosaceae breeding selection targets



Socio-Economics Team III

3. What

- Survey of trait priorities for growers of apples, peaches, cherries, and strawberries – developed, disseminated, analyzed, interpreted, and reported

To whom

- U.S. Rosaceae industries, U.S. Rosaceae genomics, genetics, and breeding community

Intended impact

- Knowledge of trait priorities and economic values for traits by growers gained and used to help objectively define Rosaceae breeding selection targets



Breeding Team I

1. What

- Phenotypic data for the reference germplasm sets of apple, peach, sweet and tart cherry, and strawberry for 2011 season
 - collected, combined with prior phenotypic data, and archived

To whom

- U.S. Rosaceae genomics, genetics, and breeding community



Breeding Team I

Intended impact

- Enable validation and utility assessment of known QTLs, and discovery of new QTLs;
 - collaborations result in knowledge gained of useful genetic diversity conferred by important breeding parents



Breeding Team II

2. What

- Pedigree-Based Analysis (PBA) using accumulated pedigree, phenotypic, and genotypic data on Crop Reference and Breeding Pedigree Sets
 - conducted by Demonstration Breeders with much PBA Team help

To whom

- Demonstration and Community Breeders



Breeding Team II

Intended impact

- Knowledge gained by breeders in the use of PBA software;
 - With feedback, PBA and the Breeder Information Management system (BIMS) can be optimized for breeder use and breeding programs will be enabled to perform future PBA on their own



Breeding Team III

3. What

- Initial attempts at marker-assisted parent selection (MAPS) and/or marker-assisted seedling selection (MASS) in Demonstration Breeding programs using QTL predicted from PBA – conducted and reported

To whom

- Community Breeders

Intended impact

- Knowledge gained in the utility, efficacy, and challenges of MAPS and MASS in rosaceous fruit breeding programs



Pedigree-Based Analysis Team I

1. What

- New software modules and functionalities to improve QTL analysis and understanding of germplasm developed

To whom

- Demonstration Breeders and breeding trainees

Intended impact

- Enhanced utility and use of PBA software permitting breeders to make informed decisions based on genetic knowledge of their germplasm



Pedigree-Based Analysis Team II

2. What

- Use of PBA – further training of Demonstration Breeders and breeding trainees

To whom

- RosBREED breeding teams at a 2.5-day workshop on Pedimap FlexQTL™ (Mar 2011) and subsequent sustained support provided by the U.S.-based PBA consulting center



Pedigree-Based Analysis Team II

Intended impact

- Participants gain a good understanding and hands-on experience in using FlexQTL™ for QTL discovery and breeding applications. Specifics include:
 - Understanding consequences of parameter settings on outcomes; familiarity with major FlexQTL™ outputs regarding QTL discovery;
 - Evaluating overall quality of FlexQTL™ outputs on QTL effects, positions, intervals, functional genotypes, and distribution over germplasm, linkage phase between QTL alleles and marker alleles, genotype-based breeding values, IBD estimates in the presence of semi-founders,
 - Selection of the best combining parents



Pedigree-Based Analysis Team III

3. What

- Protocols for and first examples of validating and characterizing fruit quality QTLs in breeding germplasm within the context of MAB Pipelining – developed, provided, and described

To whom

- Demonstration and Community Breeders

Intended impact

- Breeders are enabled to use PBA to translate genomics outputs into breeding language so that DNA-based information can be used in selection decisions



Breeding Information Management System Team I

1. What

- Database structure of breeding data – modeled for initial core of Demonstration Breeders (Evans, Finn, Oraguzie)

To whom

- BIMS Team

The screenshot displays the GDR Genome Database for Rosaceae interface. A table with columns for various genetic markers (APP, SWE, AROM, SEED, COGN, CRIP, GDR, GDRCOL, HARD, HUS, JUC, LEVE, LEWA) is visible. A 'Download' dialog box is open, asking 'Do you want to open or save this file?' with options for 'Open', 'Save', and 'Cancel'. Below the table, there are links to download results in Excel 2003 and Excel 2007 formats. The footer includes logos for Washington State University and Clemson University, along with funding information from the 2009 USDA NIFA Specialty Crop Research Initiative Program.



Breeding Information Management System Team I

Intended impact

- Knowledge gained on breeding data structure will be used to guide development of the first version of the BIMS software package to translate DNA information into breeding application



Breeding Information Management System Team II

2. What

- BIMS v1.0 (the first version of the BIMS software package) – developed, released, and tested by breeders

To whom

- Demonstration Breeders

Intended impact

- Breeders gain experience testing the interface and operability of BIMS and provide feedback on further needs



Breeding Information Management System Team III

3. What

- Breeding data of remaining Demo Breeders – continue loading into BIMS v1.0

To whom

- Demonstration Breeders

Intended impact

- Conversion of data in individual breeding programs to the BIMS format will enable all Demo Breeders to readily test v1.0 in Years 2 and 3 to facilitate improvement of this critical software package



Breeding Information Management System Team IV

4. What

- Community Breeder survey – developed, disseminated, analyzed, and interpreted

To whom

- Community Breeders and BIMS Team

Intended impact

- Knowledge gained on general community breeding database needs and desires



Genotyping Team I

1. What

- Genotypic data of reference germplasm sets for high-priority markers
 - obtained and used by Demonstration Breeders to verify pedigrees and analyze these marker-locus-trait associations in the reference germplasm sets

To whom

- Demonstration Breeders, Community Breeders, PBA Team, MAB Pipeline Team, and genetics researchers



Genotyping Team I

Intended impact

- Demo Breeders gain knowledge of the use of markers to verify pedigrees and predict breeding values in breeding germplasm;
 - this exercise will provide Demo Breeders with their first MAB Pipelining opportunities



Genotyping Team II

2. What

- SNP Validation for apple, peach, sweet cherry, and tart cherry – conducted; crop-specific genome-scan platforms designed and commercially available

To whom

- Genomics Team, International SNP Consortium members, and International Rosaceae genomics, genetics, and breeding community



Genotyping Team II

Intended impact

- Knowledge gained on the criteria to optimize performance of each crop's final SNP arrays and used to develop 9K apple and peach SNP arrays and 6K cherry arrays; research community has access to high-throughput genome-scan technology for apple, peach, and cherry



SPECIAL EARLY ACCESS PRICING					SPECIAL EARLY ACCESS PRICING				
9,000 Attempted BeadTypes	Tier A	Tier B	Tier C	Tier D	6,000 Attempted BeadTypes	Tier A	Tier B	Tier C	Tier D
Number of Samples in multiples of 48 (Total Purchase Orders Received)	<2,016	2,016+	4,032+	6,000+	Number of Samples in multiples of 48 (Total Purchase Orders Received)	<2,016	2,016+	4,032+	6,000+
Price per Sample* (USD)	\$100	\$75	\$65	\$60	Price per Sample* (USD)	\$70	\$65	\$60	\$55



Genotyping Team III

3. What

- Genome-wide genotypic data for the apple, peach, and cherry Crop Reference Sets – obtained, reviewed for quality control and loaded in publicly accessible archived database

To whom

- PBA Team, Genomics Team, BIMS Team, Demonstration Breeders



Genotyping Team III

Intended impact

- Analysis of this dataset, combined with pedigree and phenotypic datasets, will enable systematic and streamlined validation and characterization of marker-locus-trait associations for use in breeding



Genotyping Team IV

4. What

- DNA samples for Crop Reference Sets and Breeding Pedigree Sets – replenished and strawberry added

Intended impact

- Assured stocks for trait marker genotyping and genome scans

To whom

- Genotyping Team, Demonstration Breeders



Genotyping Team V

5. What

- A strategy for high-throughput genome scans for octoploid strawberry via targeted genome sequencing and analysis – developed

To whom

- Strawberry breeders and genomics researchers

Intended impact

- Implementation of a strategy for genome-scan capability in octoploid strawberry will facilitate the ability to conduct marker-assisted breeding



MAB Pipeline Team I

1. What

- MAB Pipeline used for QTL “Validation”
(Stage 4, crop-wide validation of marker-locus-trait associations)
- fast-tracked targets of interest to each Demo Breeder

To whom

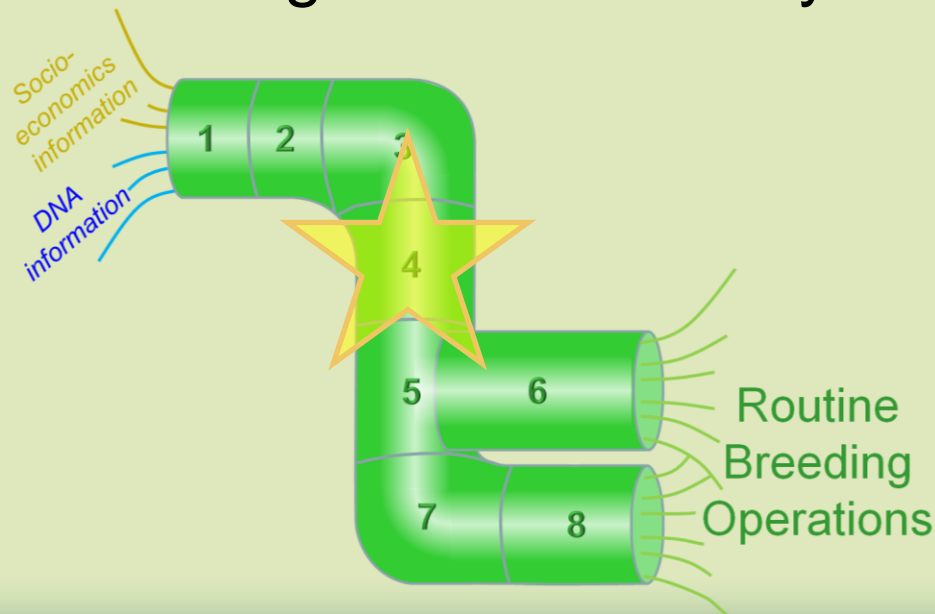
- Demonstration Breeders



MAB Pipeline Team I

Intended impact

- Breeders gain experience in using Pipeline Stage 4
- Breeders access crop-wide reference germplasm data
- Breeders conduct Pedigree-Based Analysis



MAB Pipeline Team II

2. What

- MAB Pipeline used for QTL “Utility”
(Stage 5, utility assessment of markers in breeder’s own germplasm)
- fast-tracked targets of interest to each Demo Breeder

To whom

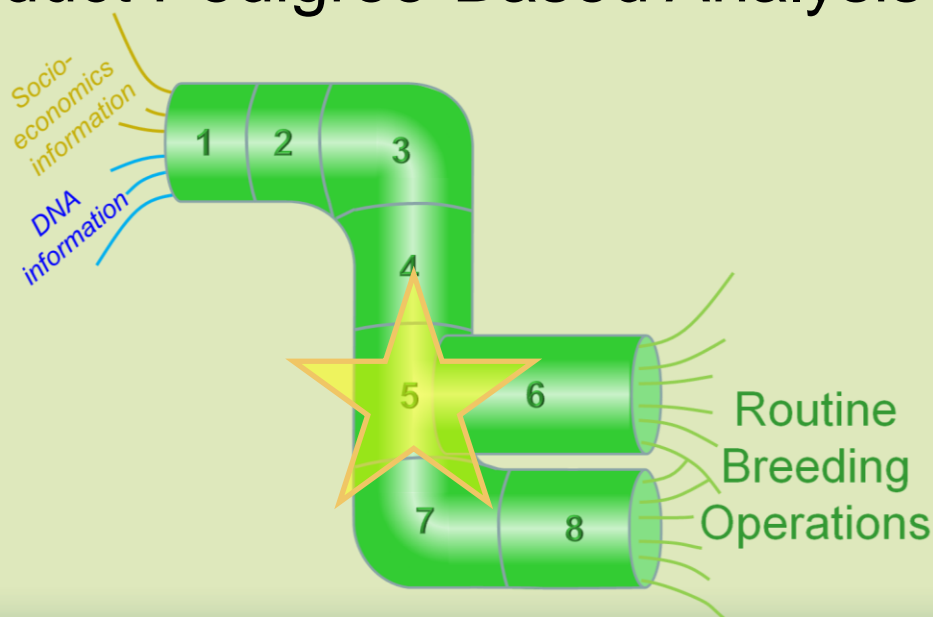
- Demonstration Breeders



MAB Pipeline Team II

Intended impact

- Breeders gain experience in using Pipeline Stage 5
- Breeders access crop-wide reference germplasm data
- Breeders conduct Pedigree-Based Analysis



MAB Pipeline Team III

3. What

- MAB Pipeline used for “Marker-Assisted Parent Selection Decisions” (Stage 6, using DNA info on parents to support crossing decisions)
 - fast-tracked targets of interest to each Demo Breeder

To whom

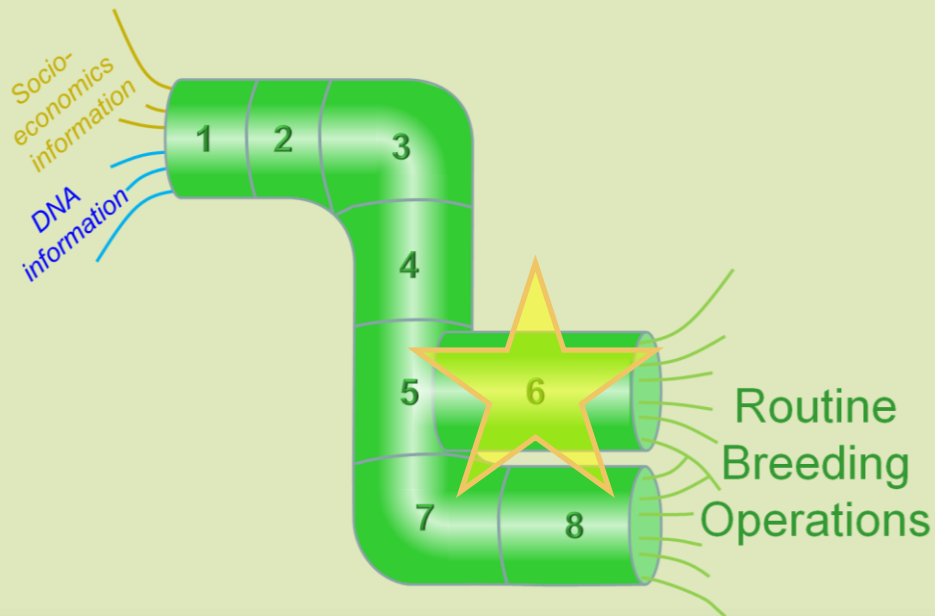
- Demonstration Breeders



MAB Pipeline Team III

Intended impact

- Use of genetic information on prospective breeding parents results in breeding populations enriched for favorable alleles



Genomics Team I

1. What

- Genome scan platforms for apple, peach, cherry, and strawberry – created, promoted, and used

To whom

- International Rosaceae genomics, genetics, and breeding community; Genotyping, PBA, BIMS, and other RosBREED Teams

Intended impact

- New QTLs for apple, peach, cherry, and strawberry discovered and characterized by researchers



Genomics Team II

2. What

Database templates for the first stages of the Marker-Assisted Breeding (MAB) Pipeline – created. [Pipeline infrastructure components include: “Available Marker-Locus-Trait Associations Warehouse”, “Selection Trait Identifier Database”, and “Technology Portfolio”, and further breeder-oriented features in “Genome Database Resources”]

To whom

- Breeding, BIMS, Genotyping, and MAB Pipeline Teams



Genomics Team II

Intended impact

- Infrastructure and functionality of these Pipeline components enables MAB in Rosaceae breeding programs



Genomics Team III

3. What

- Reference germplasm set databases compatible with the Breeding Information Management System (BIMS) and the MAB Pipeline – establish and curate

To whom

- Breeding, BIMS, and MAB Pipeline Teams

Intended impact

- Data necessary for breeders to make genetically informed decisions, and allied scientists to query, is seamlessly integrated and accessible



Extension Team I

1. What

- Partnerships with extension specialists and industry members – create and foster (e.g., attend grower meetings and field days, strategic industry visits)

To whom

- SE and Extension Teams, Demonstration Breeders, extension agents, industry



Extension Team I

Intended impact

- A better communication conduit established between industry and extension specialists and between the Extension and SE Teams for more efficient achievement of Extension and SE Teams' goals



Extension Team II

2. What

- Highlight & deliver results from the Marker-Assisted Breeding (MAB) Pipeline Team as a key component to the success of RosBREED's Demonstration Breeding Programs

To whom

- Demonstration and Community Breeders

Impact

- Comprehension by breeders of what they can and need to do to be able to conduct routine MAB



Extension Team III

3. What

- RosBREED materials (descriptions, data, deliverables, impacts, etc.)
 - publish using media connections. Connections have been established with industry trade journals Good Fruit Grower and American/Western Fruit Grower. More connections should be sought

To whom

- Industry, Community Breeders, growers



Extension Team III

Impact

- Knowledge of RosBREED goals, activities, upcoming events and surveys, successes disseminated



RosBREED

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www.rosbreed.org



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