

# ROSBREED

Enabling marker-assisted breeding in Rosaceae

## OBJECTIVES-ACTIVITIES 2-4

Germplasm–Phenotyping–Genomics–PBA–BIMS–  
MAB Pipeline Implementation

## GOALS, ACTIVITIES, & DELIVERABLES

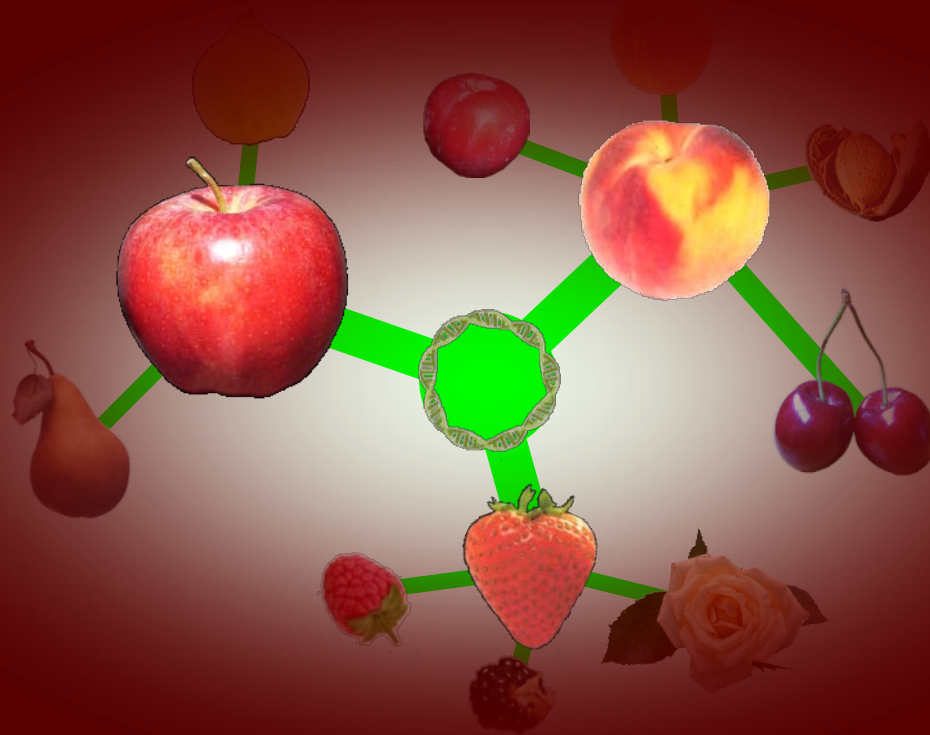
Cameron Peace, project co-director & MAB Pipeline Team leader

## Outline of Presentation

- ❖ RosBREED Components At-A-Glance
- ❖ **Germplasm:** Representation of Breeding Programs through Pedigree Connections
- ❖ **Phenotyping:** Evaluation for High-Priority Selection Targets

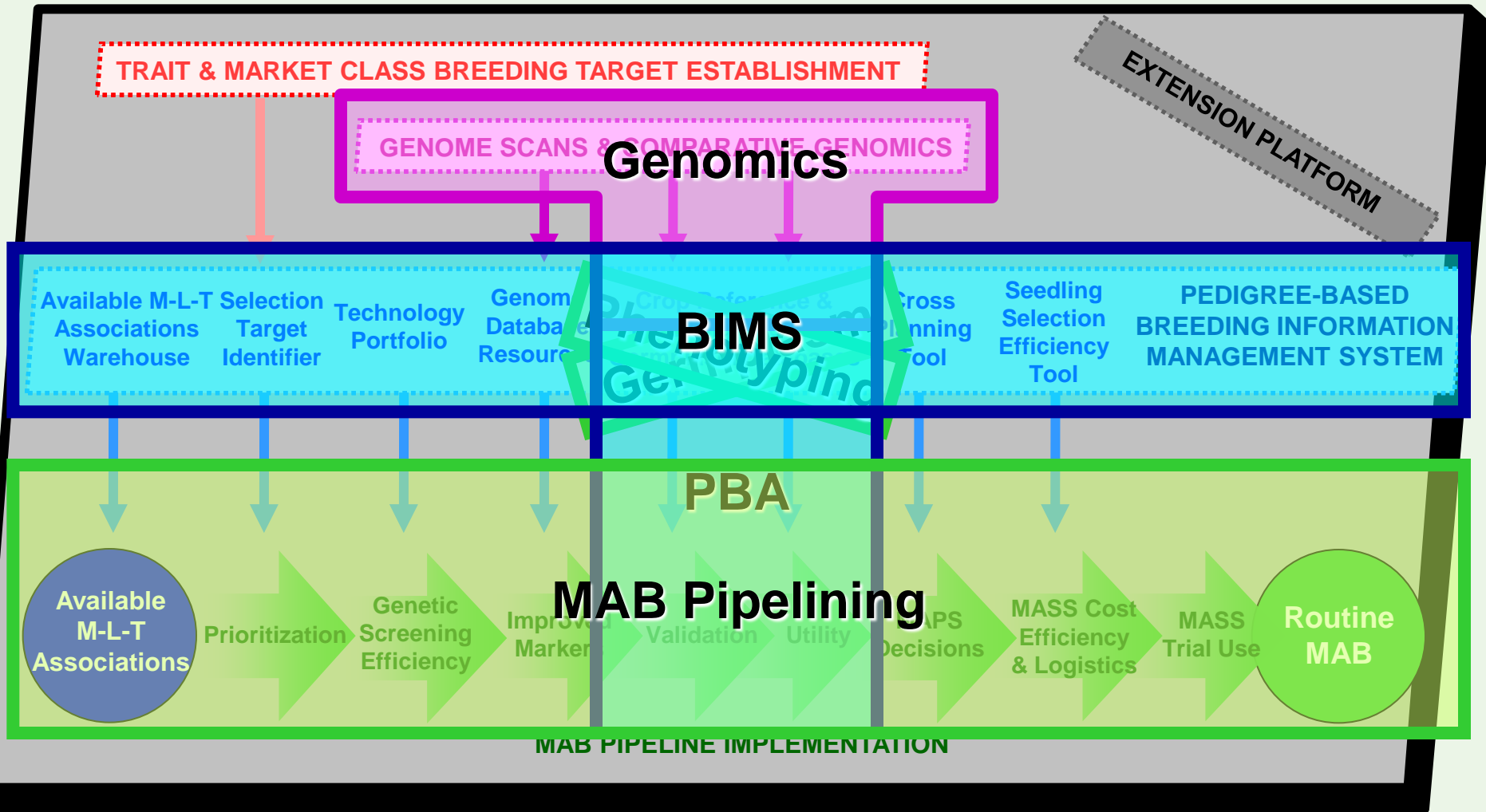
## Outline of Presentation contd.

- ❖ **Genomics:** Reference Genome-Wide Datasets
- ❖ **PBA:** A Common Analytical Framework
- ❖ **BIMS:** Collecting, Managing, and Interpreting Breeding Data
- ❖ **MAB Pipelining:** Putting It All to Use



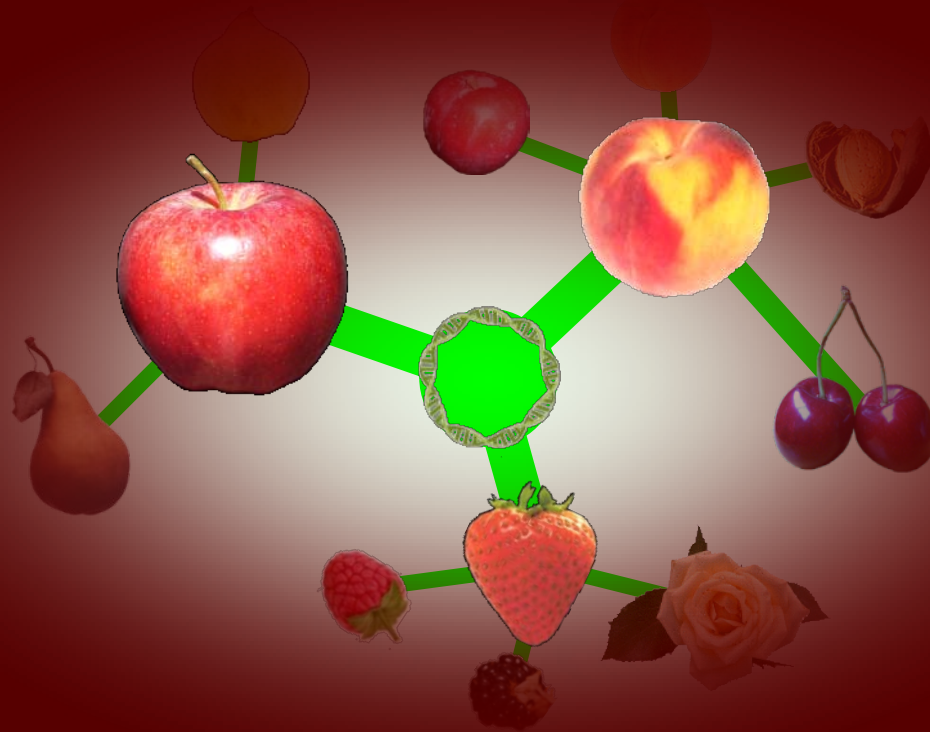
# RosBREED Components At-A-Glance

# RosBREED Components At-A-Glance



# RosBREED





# Germplasm:

Representation of Breeding Programs  
through Pedigree Connections

# Germplasm: Representation of Breeding Programs through Pedigree Connections

a. Crop Reference Sets

b. Breeding Pedigree Sets

## Goal

*Establish reference germplasm sets that enable efficient validation (crop-wide) and utility assessment (breeding program-specific) of M-L-T associations*

## Activities

## Deliverable

*Identified reference germplasm sets for apple, peach, strawberry, and cherry with sufficient founder representation*

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# a. Crop Reference Sets

*WHO:* Breeding Team, PBA Team, MAB Pipeline Team

*WHEN:* Jan – Apr 2010

- Resource for common benefit
- ~500 plants (cultivars, ancestors, founders, breeding lines, selections, and seedlings) that are fruiting in 2010-2012
- Identify common parents among programs

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# a. Crop Reference Sets contd.

- Approach:
  - Identify common parents among breeding programs
  - Trace pedigrees to founders
  - Seek tree locations
  - Calculate founder representation
- Include seedlings to adequately represent founders
  - Describe and visualize on PediMap
  - Ascertain caring and phenotyping responsibilities
  - Info (identity, pedigree, location) publicly archived

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## b. Breeding Pedigree Sets

*WHO:* Breeding Team, PBA Team, MAB Pipeline Team

*WHEN:* Jan – Apr 2010

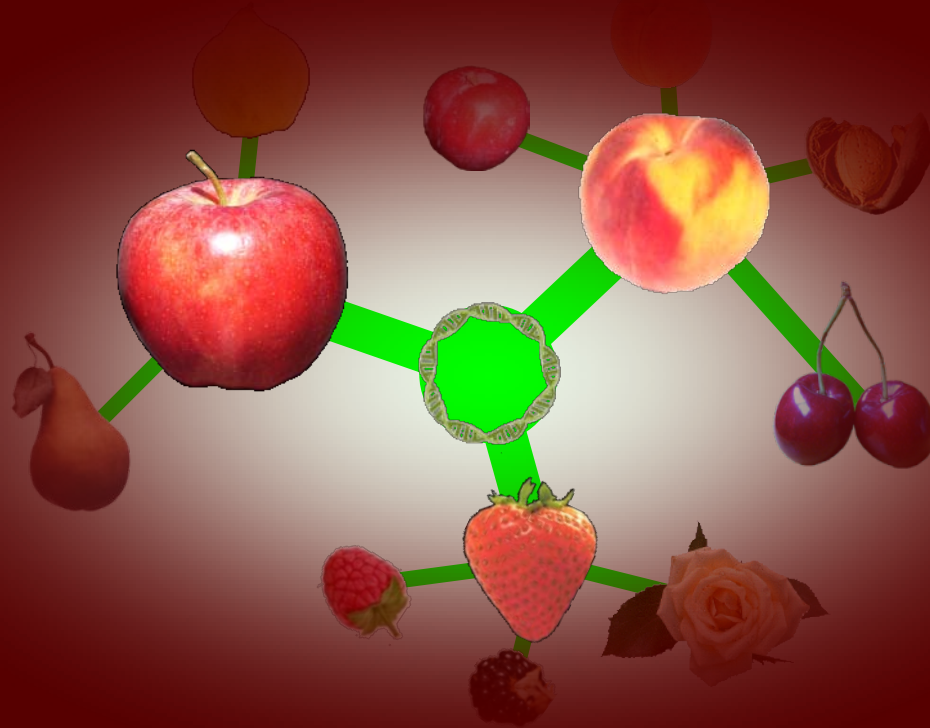
- Resource for breeding program benefit only
- ~100-300 extra plants for each breeding program that, *together with the Crop Reference Sets*, allow full representation of cultivars and founders of interest to that program
- Information may remain with each breeding program; data-sharing improves power

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# **Germplasm:** Where are we now & What's next?

- Example Crop Reference Sets were developed during proposal preparations
- True Crop Reference Sets and Breeding Pedigree Sets need to be established in next few months
- Tomorrow workshop: 10:15 am –12:15 pm

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# Phenotyping: Evaluation for High-Priority Selection Targets

# Phenotyping: Evaluation for High-Priority Selection Targets

a. Traits and standardized protocols

b. Performance evaluation

## *Goal*

*Obtain data on reference germplasm for high-priority selection targets aligned with stakeholder expectations*

## *Activities*

## *Deliverable*

*Reference phenotypic datasets of breeding-relevant traits*

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# a. Traits and standardized protocols

*WHO:* Breeding Team, SE Team, Stakeholder Advisory Panel

*WHEN:* Jan – Apr 2010

- Choose traits for each crop to be evaluated in detail for the next few years
- Standardized phenotyping protocols to be hammered out and shared to enable data pooling across locations/institutions

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## b. Performance evaluation

*WHO:* Breeding Team

*WHEN:* 2010, 2011, & 2012 seasons

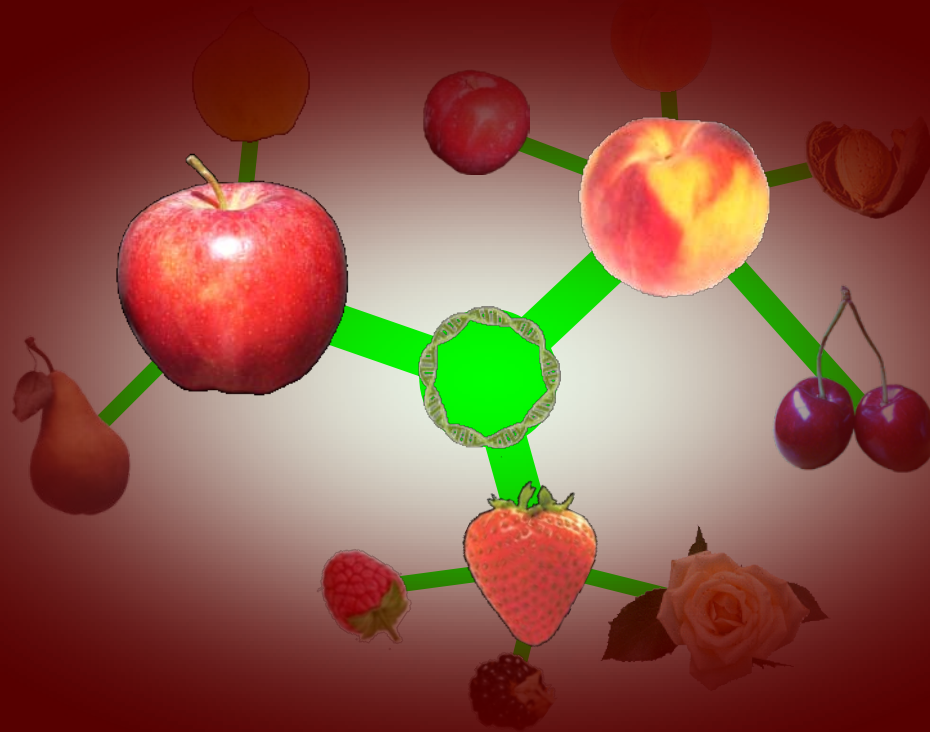
- Conduct standardized phenotyping of Crop Reference & Breeding Pedigree Sets
- Lower heritability means more seasons (2-3) of replication
- Collate data in PBA format, conduct quality control, archive

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# Phenotyping: Where are we now & What's next?

- Standardizing across programs has begun for some crops for some traits
- Traits for 2010 phenotyping need to be chosen prior to 2010 season
- 2011 & 2012 seasons will include SE data
- Previously collected data on reference germplasm plants – include where possible

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# Genomics: Reference Genome-Wide Datasets

# Genomics: Reference Genome-Wide Datasets

- a. Genome scan development
- b. Genome scan use
- c. Comparative genomics

## Goal

*Develop and implement genome scans for apple, strawberry, peach, and cherry that identify recombination events at a scale appropriate for PBA, focusing on fruit quality genes and leveraging ancestral relatedness*

## Activities

## Deliverable

*A reference dataset of genome-wide haplotype variation for Rosaceae breeding germplasm based on fruit quality genes*

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# a. Genome scan development

*WHO:* Genomics Team, Genotyping Team

*WHEN:* Sep 2009 – Sep 2010

- Choose genome-wide polymorphisms
  - To efficiently achieve 1 polymorphic marker per 5 cM in any random cross
  - Preferably in or near fruit quality candidate genes
  - Preferably common across crops
- Choose best platform for genotyping  
~4000 plants (“SNP Platform Summit”)

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## b. Genome scan use

*WHO:* Genotyping Team, Genomics Team, PBA Team

*WHEN:* Sep 2010 – Feb 2011

- Genome-scan all reference germplasm for 4 crops
- Convert data to PBA format
- Use data to confirm pedigrees
- Archive data

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## c. Comparative genomics

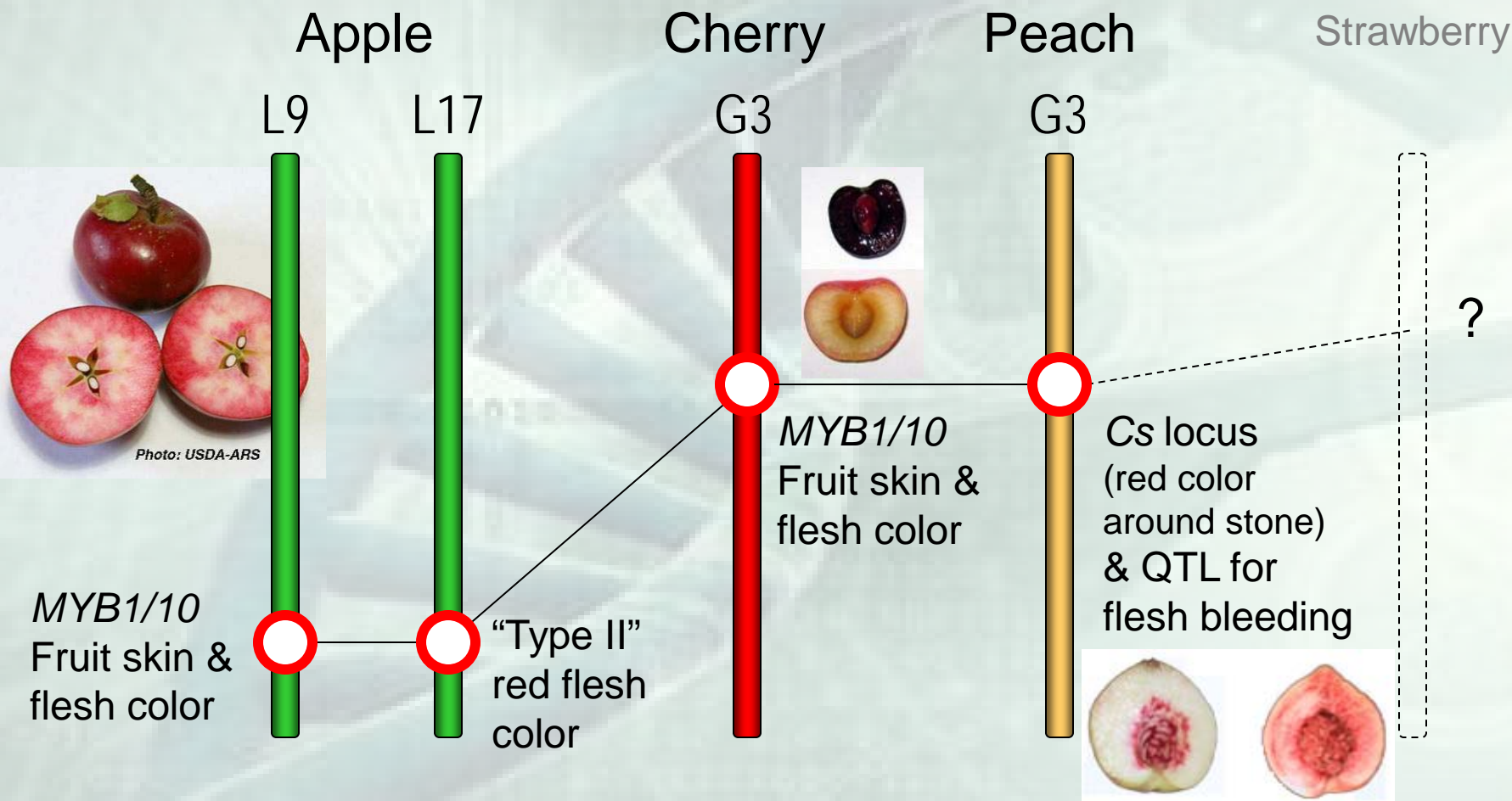
*WHO:* Genomics Team, Breeding Trainees?

*WHEN:* Jan 2011 – Aug 2013

- Align Rosaceae genomes
- Pursue opportunities to leverage ancestral relatedness
- Especially at Plant & Food Research (NZ)

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# c. Comparative genomics contd.

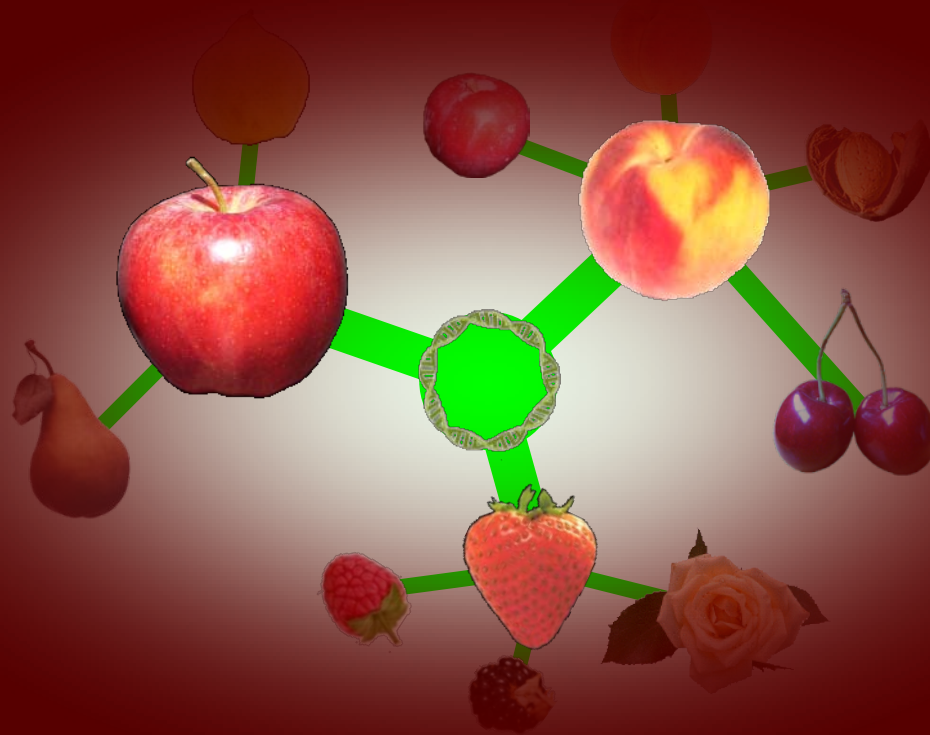


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# Genome scans: Where are we now & What's next?

- Identifying and choosing polymorphisms underway - began mid 2009
- “SNP Platform Summit” date (Aug 2010?) needs to be decided now
- Tomorrow’s Activity 3 (concurrent):  
2:00 – 4:00 pm

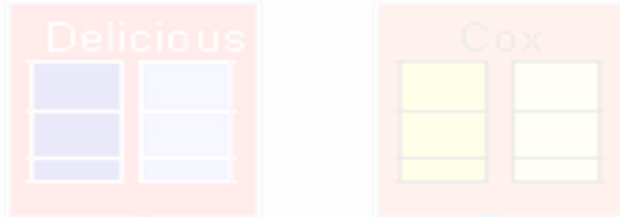
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PBA:

A Common Analytical Framework

# PBA: A Common Analytical Framework



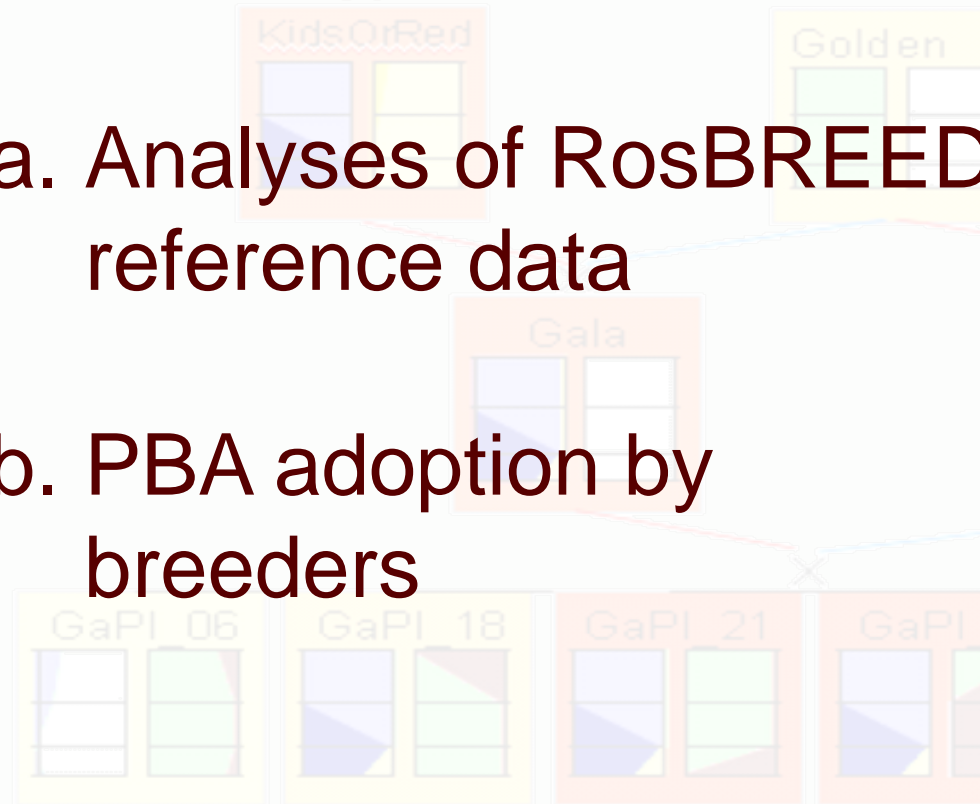
**Goal**  
*Establish and implement PBA as the common platform for marker-assisted U.S. Rosaceae breeding*

a. Analyses of RosBREED reference data

b. PBA adoption by breeders

**Activities**

**Deliverable**  
*12 Rosaceae breeding programs using PBA, synergistically gaining a better understanding of genetic potential of breeding parents and genetic control of selection targets*



# RosBREED



# a. Analyses of RosBREED reference data

*WHO:* PBA Team, BIMS Team

*WHEN:* Sep 2010–Feb 2011; Sep11–Feb12; Sep12–Apr13

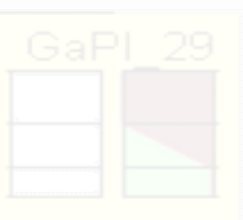
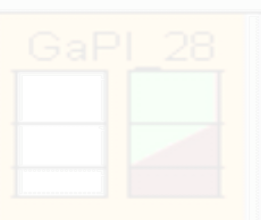
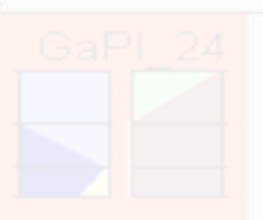
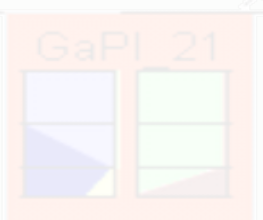
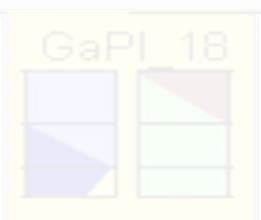
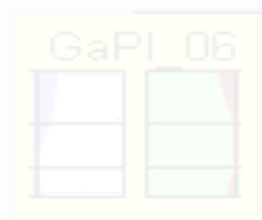
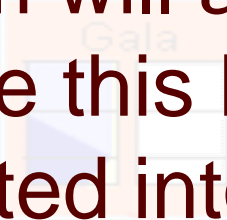
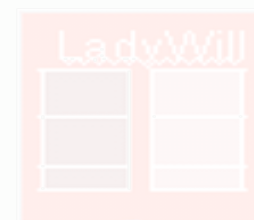
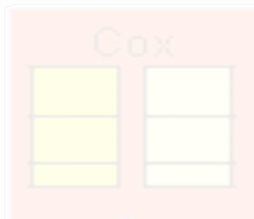
- Integration of data of genome scans and phenotypes on Crop Reference and Breeding Pedigree Sets
- This will identify and validate M-L-T associations, and characterize distribution of functional alleles in breeding parents

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# a. Analyses of RosBREED ref. data contd.

- Performed with FlexQTL™
- PBA Team will analyze data, BIMS Team will ensure this key information is incorporated into BIMS databases



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## b. PBA adoption by breeders

*WHO:* Breeding Team, PBA Team, MAB Pipeline Team, BIMS Team

*WHEN:* Jul 2010 – Feb 2011

- Software and training will be provided to breeders by PBA Team
- First dataset to analyze will be for 2010's fast-tracked M-L-T associations

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## b. PBA adoption by breeders contd.

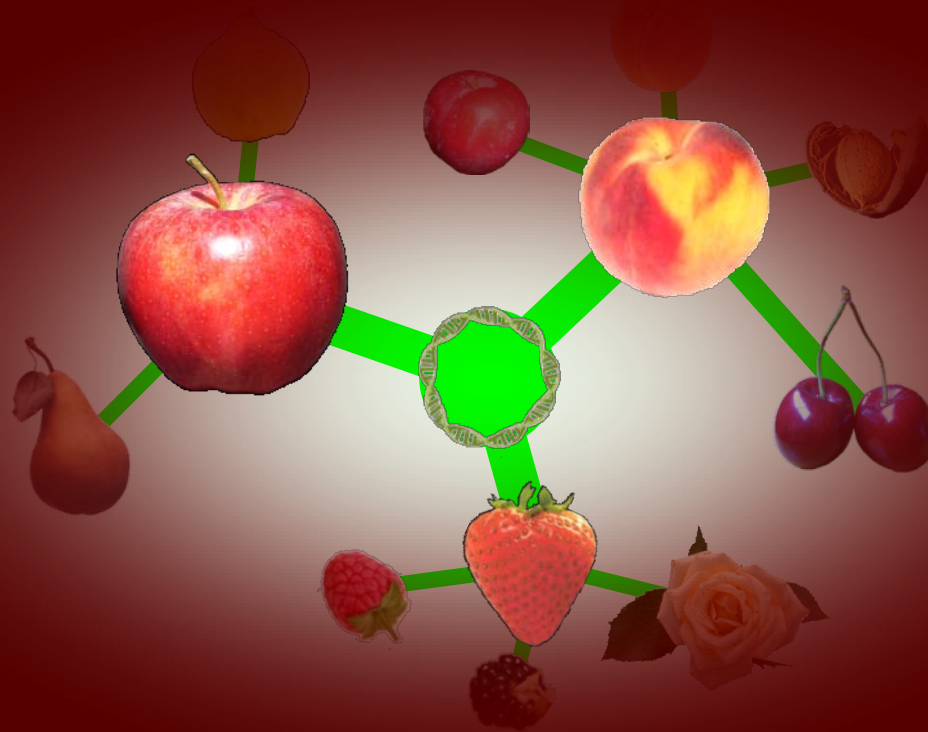
- Further PBA needs and interests of breeders to be assessed by PBA Team and new modules developed, e.g.
  - Founder representation of germplasm sets (power)
  - Polyploidy
  - Germplasm automatically annotated for QTL effects
  - Multiple QTL allele detection
  - G x E analysis
  - G x G analysis

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# PBA: Where are we now & What's next?

- Analyses await data collection
- In the meantime, breeders are becoming familiar with first software component of PBA, PediMap
- Tomorrow workshops:
  - 8:15 – 9:15 am PediMap
  - 9:15 – 9:45 am FlexQTL
  - 2:00 – 4:00 pm (Activity 1) PediMap hands-on

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# BIMS:

Collecting, Managing, and Interpreting  
Breeding Data

# BIMS: Collecting, Managing, and Interpreting Breeding Data

- a. BIMS development and improvement
- b. BIMS adoption by breeders

## *Goal*

*Establish a breeding information management system for streamlined integration of genomics and breeding data*

## *Activities*

## *Deliverable*

*Software package with seamless connections between database interfaces, analytical modules, and decision-support tools for modern breeding needs*

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# a. BIMS development and improvement

*WHO:* BIMS Team with input from all others

*WHEN:* Jan 2010 – early 2013

- Series of components: online database interfaces, analytical modules, and decision-support tools
- Primary function is ease of adoption of PBA and optimized use of PBA

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## a. BIMS development and improvement contd.

- BIMS Developer postdoc will visit each core breeding program to assess current methods and needs
- BIMS Programmer(s) will create software
- Each component of BIMS matches a stage of the MAB Pipeline

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## a. BIMS development and improvement contd.

- March 2011: release of v1.0 for alpha testing (core breeding programs to test)
- March 2012 : release of v2.0 for beta testing (all Rosaceae breeding programs)
- Early 2013: v3.0 released publicly

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## a. BIMS development and improvement contd.

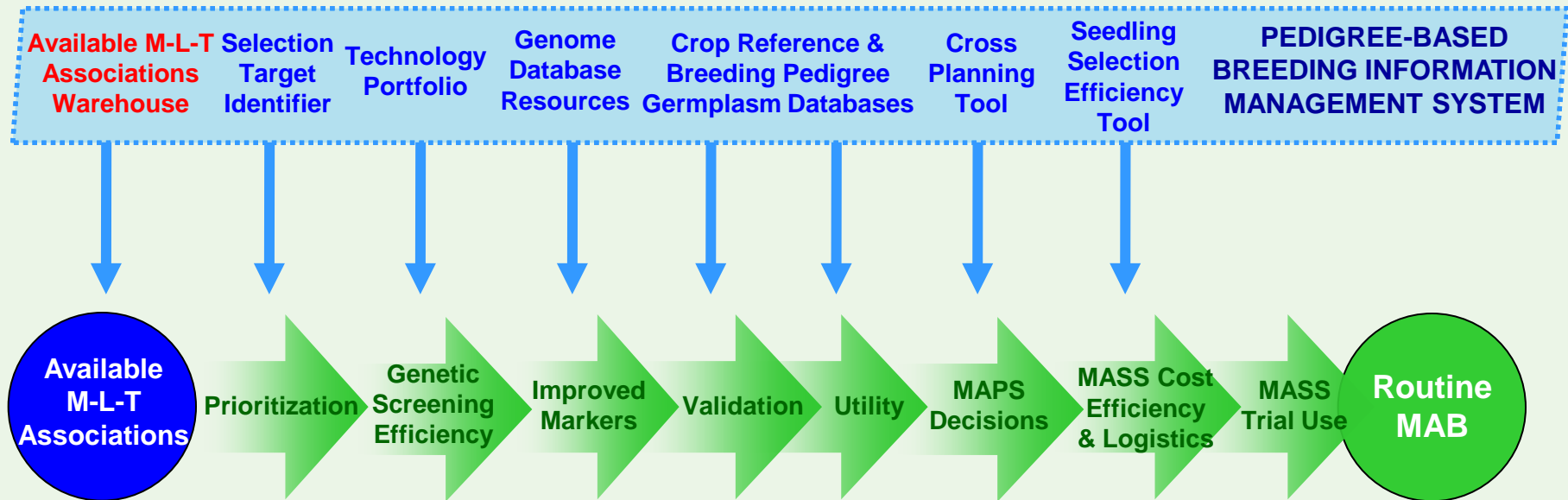
- Training (in-person, written and online manual) of breeders by BIMS Developer
- Improvement of system from feedback to BIMS Developer and Programmer
- Technology transfer to non-core breeding programs from March 2012

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# a. BIMS development and improvement contd.

## Available M-L-T Associations Warehouse

One-stop community-driven website for Rosaceae breeders to access reported marker-locus-trait associations

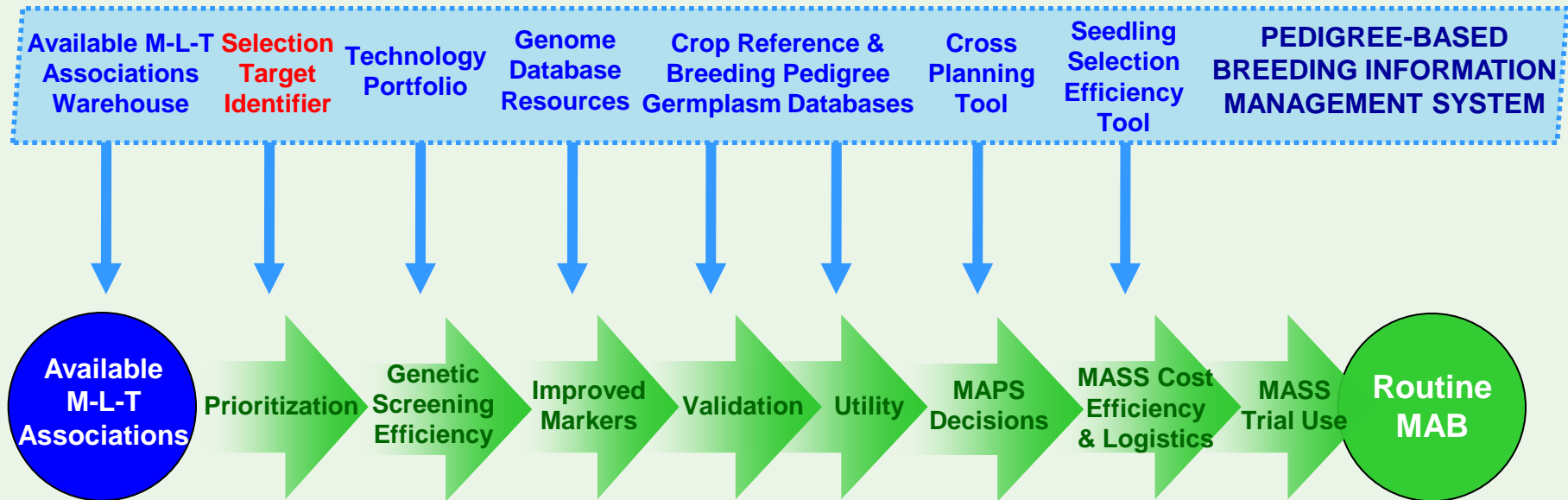


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# a. BIMS development and improvement contd.

## Selection Target Identifier

Online community-driven database of economically weighted traits, their known heritability, and available genetic variation

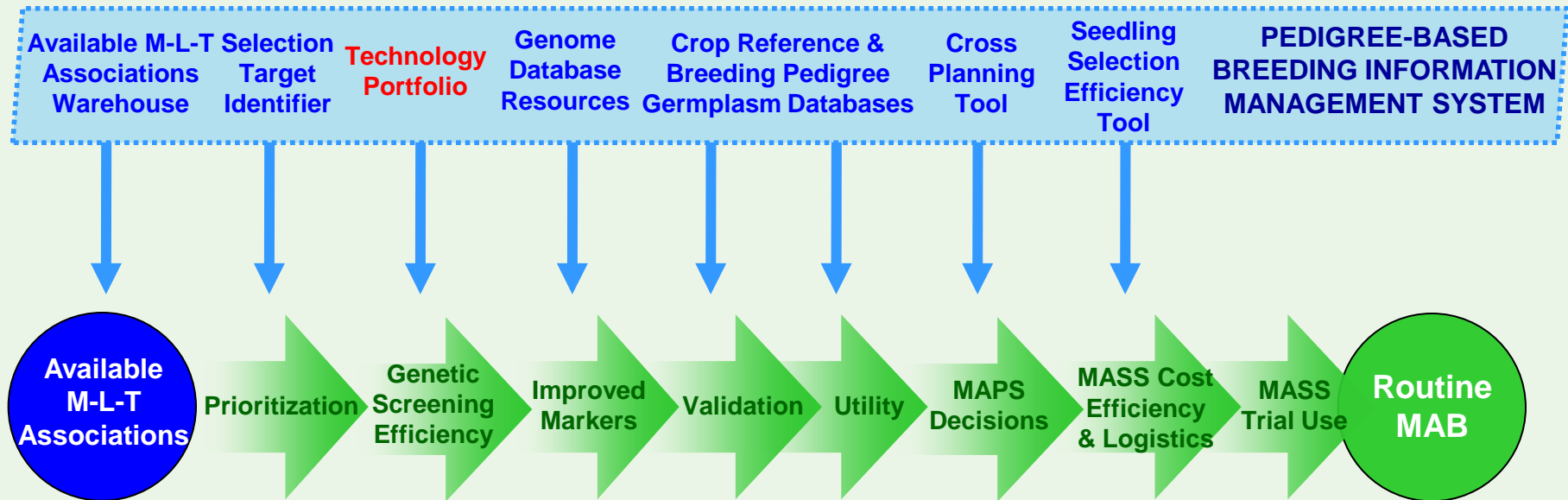


# RosBREED

# a. BIMS development and improvement contd.

## Technology Portfolio

Online community-driven website of available technologies and service centers for genetic screening in breeding

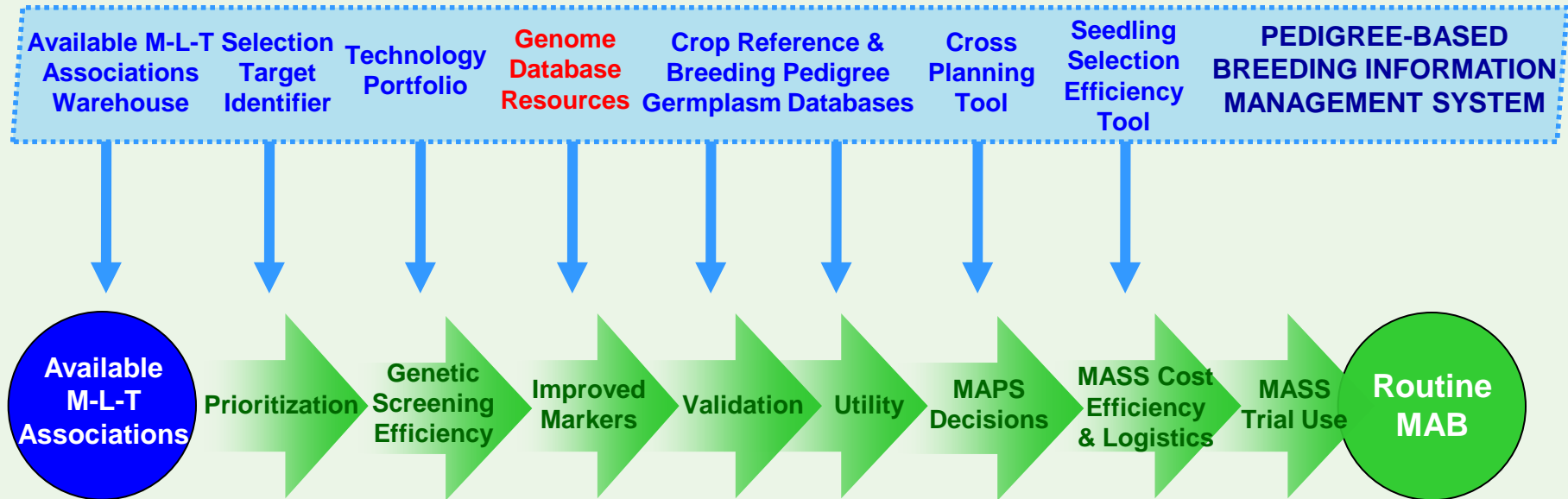


# RosBREED

# a. BIMS development and improvement contd.

## Genome Databases Resources

Interfaces that leverage publicly available genome resources for the Rosaceae family on the GDR (esp. DNA sequences)



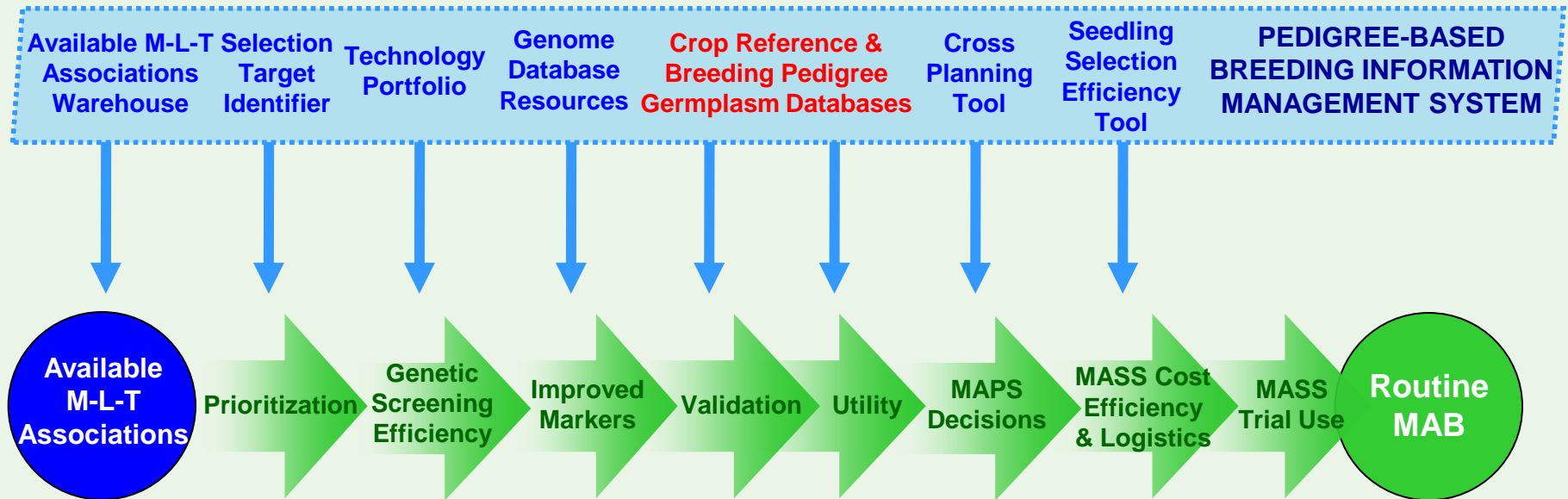
# RosBREED



# a. BIMS development and improvement contd.

## Crop Reference & Breeding Pedigree Germplasm Databases

Reference databases of phenotypic, genotypic, and pedigree data – both raw and integrated via PBA



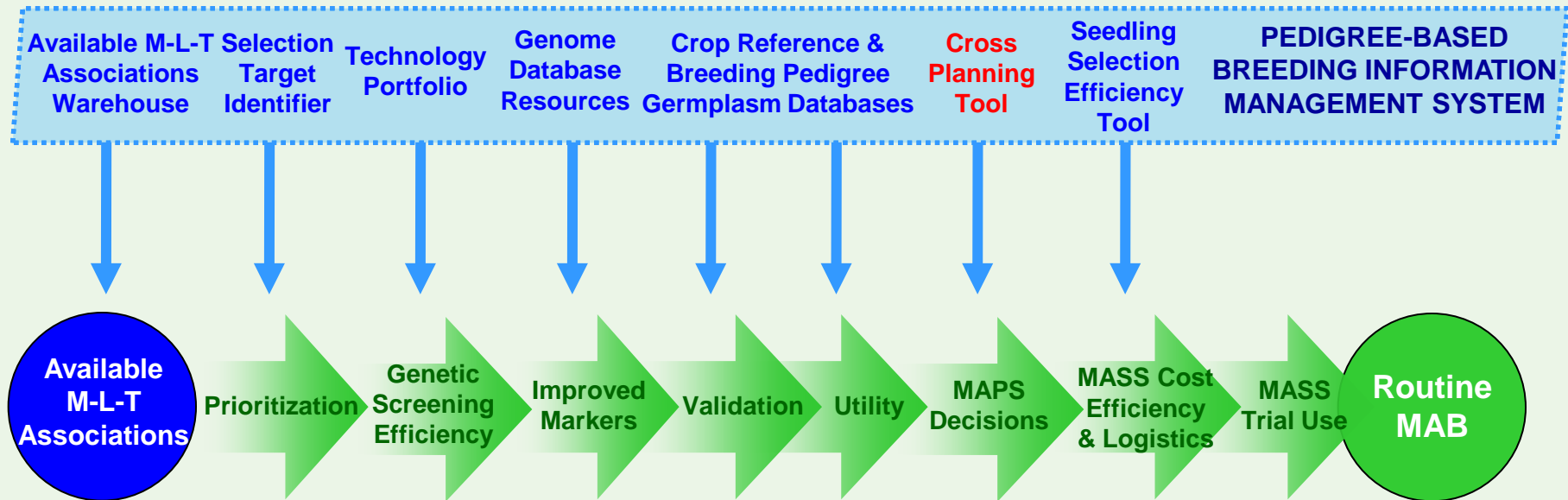
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# a. BIMS development and improvement contd.

## Cross Planning Tool

Decision-support tool for efficient combining of specific traits and alleles to achieve desired seedling outcomes



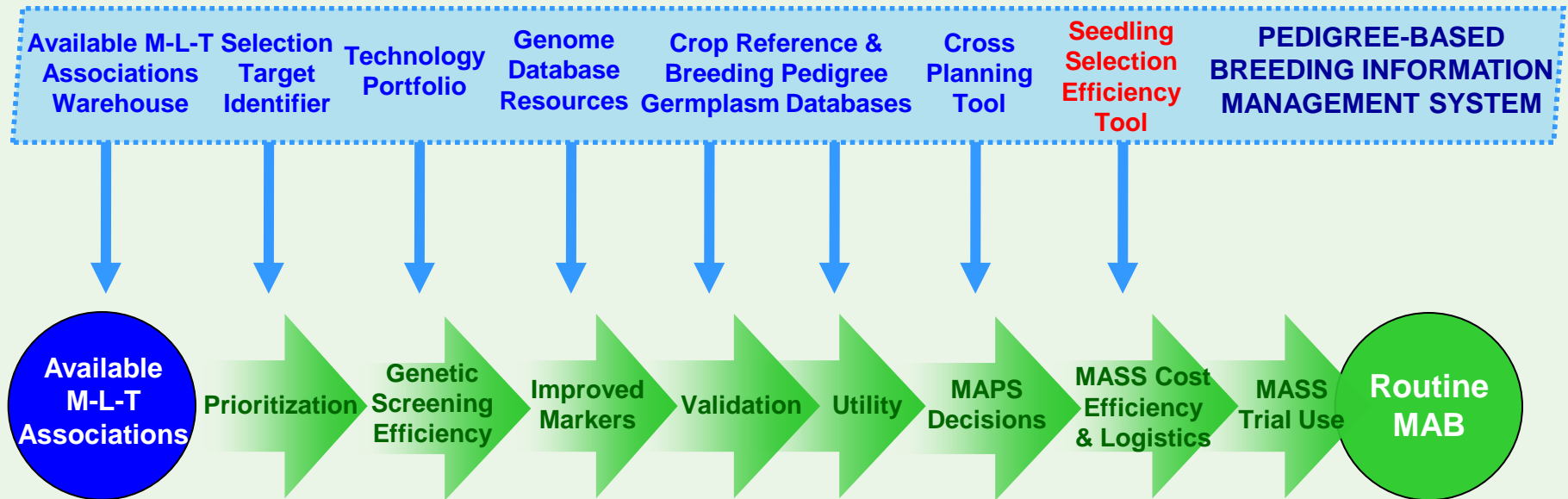
# RosBREED



# a. BIMS development and improvement contd.

## Seedling Selection Efficiency Tool

Decision-support tool for identifying economically optimal and logistically feasible seedling selection schemes



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## b. BIMS adoption

*WHO:* Breeding Team, BIMS Team, MAB Pipeline Team, Extension Team

*WHEN:* Mar 2011 onward

- Adoption of BIMS not expected to be sudden
- Advantages of this new system will be highlighted



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## b. BIMS adoption contd.

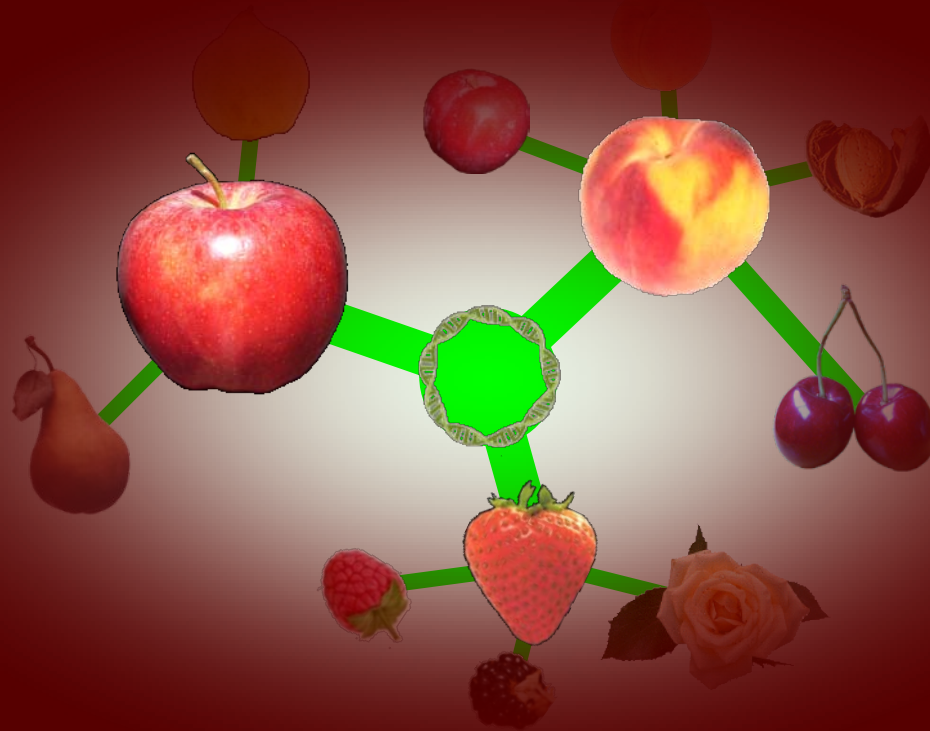
- Stepwise approach:
  1. Use of modules that address traditional needs
  2. Use of marker information to guide crossing decisions
  3. Use of marker information and genotyping services to improve seedling selection efficiency
  4. Breeder implementation of earlier components involving increasing confidence with genomics data interfacing
  5. Finally, routine use of all components, and contributions provided for further improvement

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# **BIMS:** Where are we now & What's next?

- Have prototypes for several components (Available M-L-T Associations Warehouse, Genome Database Resources, Seedling Selection Efficiency Tool)
- In recruitment process for Developer postdoc; BIMS Team will do in meantime
- Programmer already hired

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# MAB Pipelining: Putting It All to Use

# MAB Pipelining: Putting It All to Use

- a. Implementation of MAB Pipeline stages
- b. Fast-tracked pipelining in 2010

## Goal

*Implement the 8-stage MAB Pipeline in 12 core breeding programs to enable routine MAB*

## Activities

## Deliverable

*High-priority M-L-T associations identified and utilized within Rosaceae breeding programs to improve breeding efficiency. Also improve efficiency in other ways without marker use*

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# a. Implementation of MAB Pipeline stages

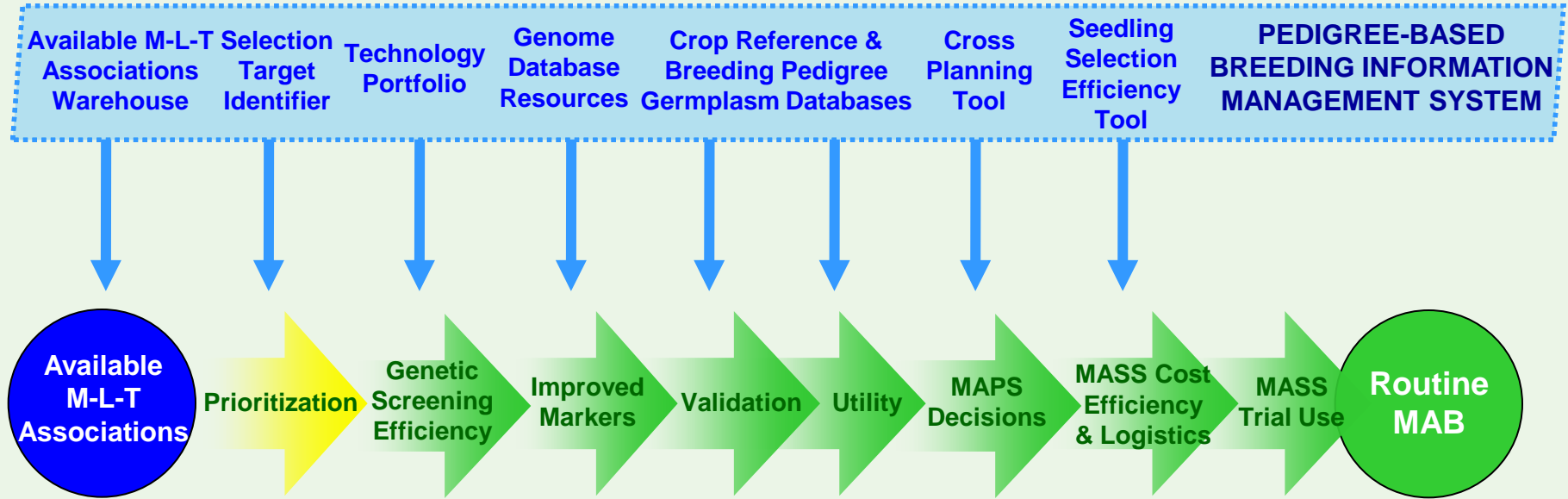
*WHO:* MAB Pipeline Team, Breeding Team, BIMS Team, PBA Team, Genotyping Team, SE Team, Extension Team

*WHEN:* Mar 2011 onward

- 8 stages of MAB Pipeline implemented by core breeding programs
- Stages are matched with BIMS components

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# a. Implementation of MAB Pipeline stages cont.

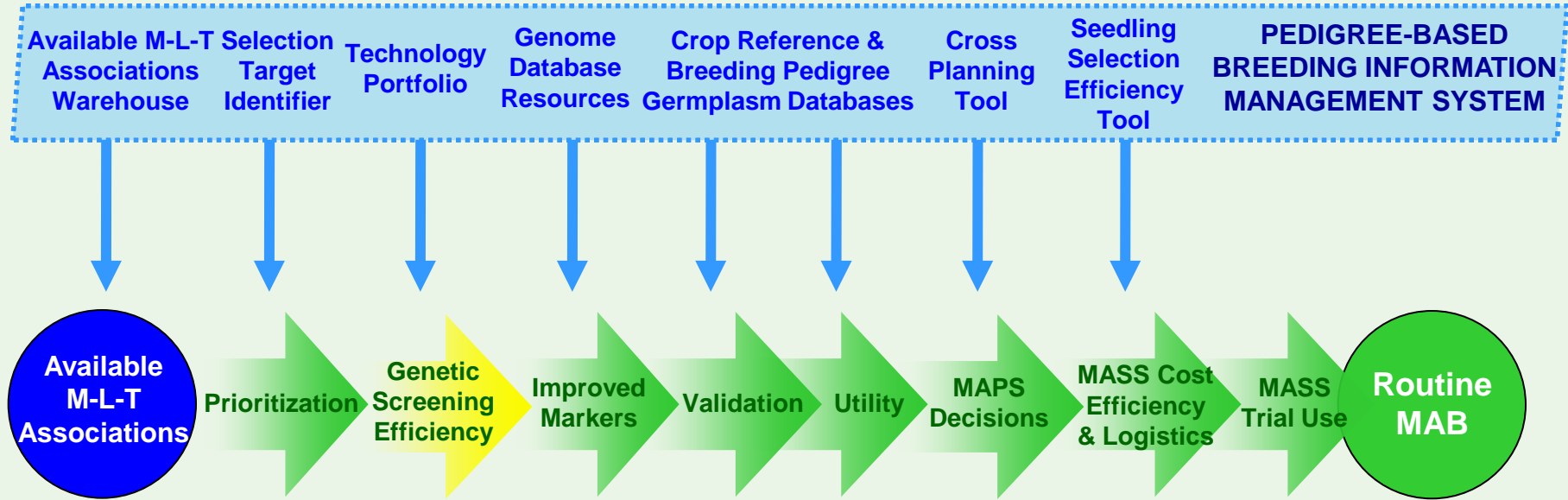


## Prioritization

Available marker-locus-trait associations are objectively prioritized for each core breeding program  $P = \$ \times H \times Vg$

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# a. Implementation of MAB Pipeline stages cont.

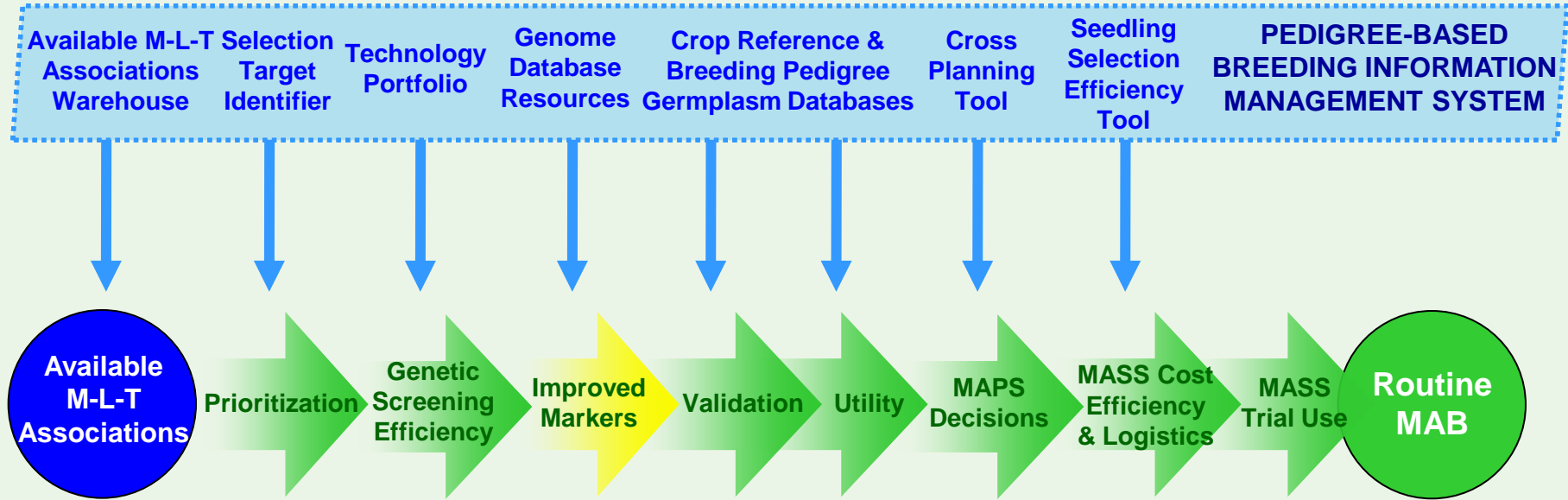


## Genetic Screening Efficiency

Efficient genetic screening technologies are identified for each breeding program

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# a. Implementation of MAB Pipeline stages cont.

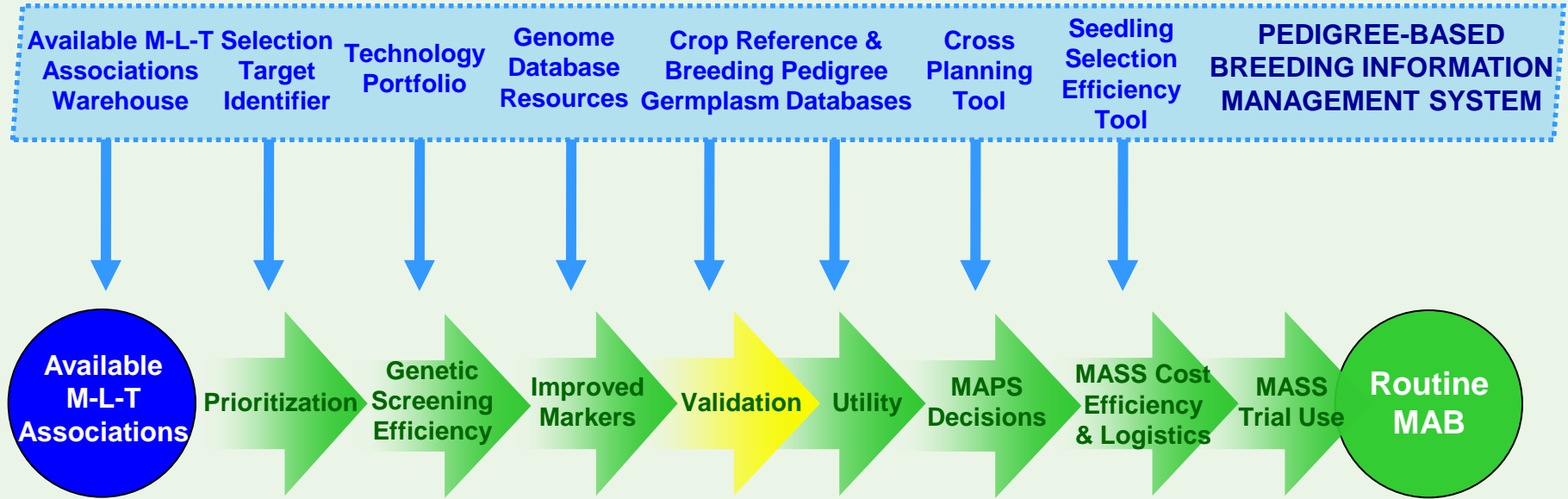


## Improved Markers

If necessary, markers are improved – converted for high-throughput screening amenability, made more reliable, etc.

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# a. Implementation of MAB Pipeline stages cont.

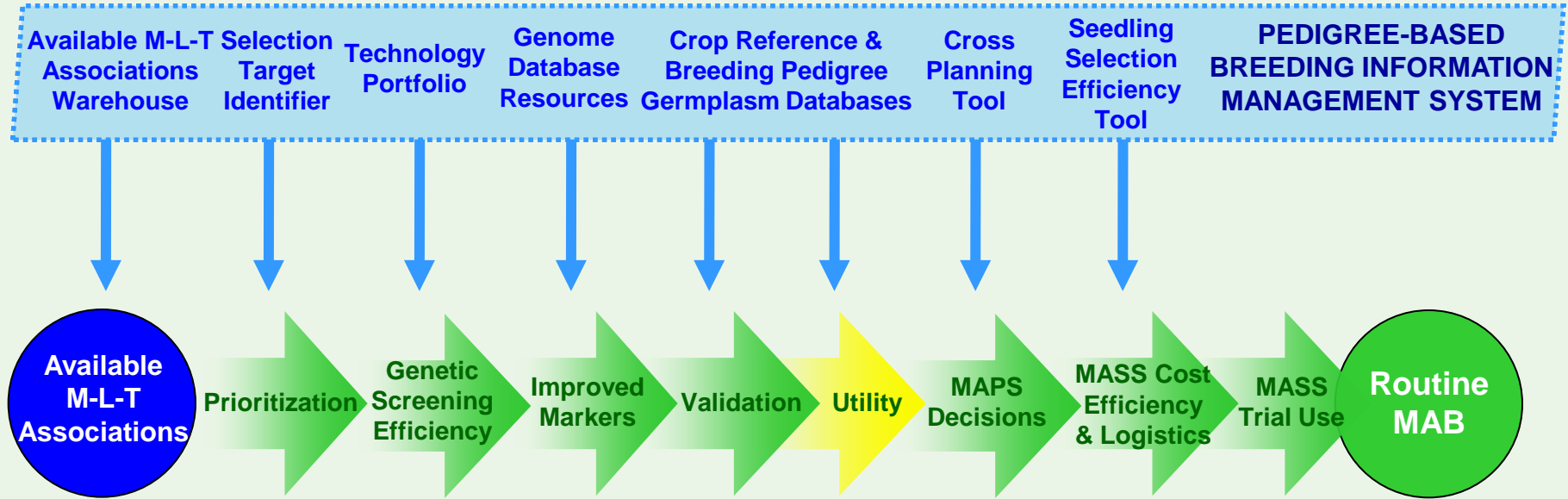


## Validation

Promising markers are individually validated on crop-wide germplasm, finding lineages where association exists

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# a. Implementation of MAB Pipeline stages cont.

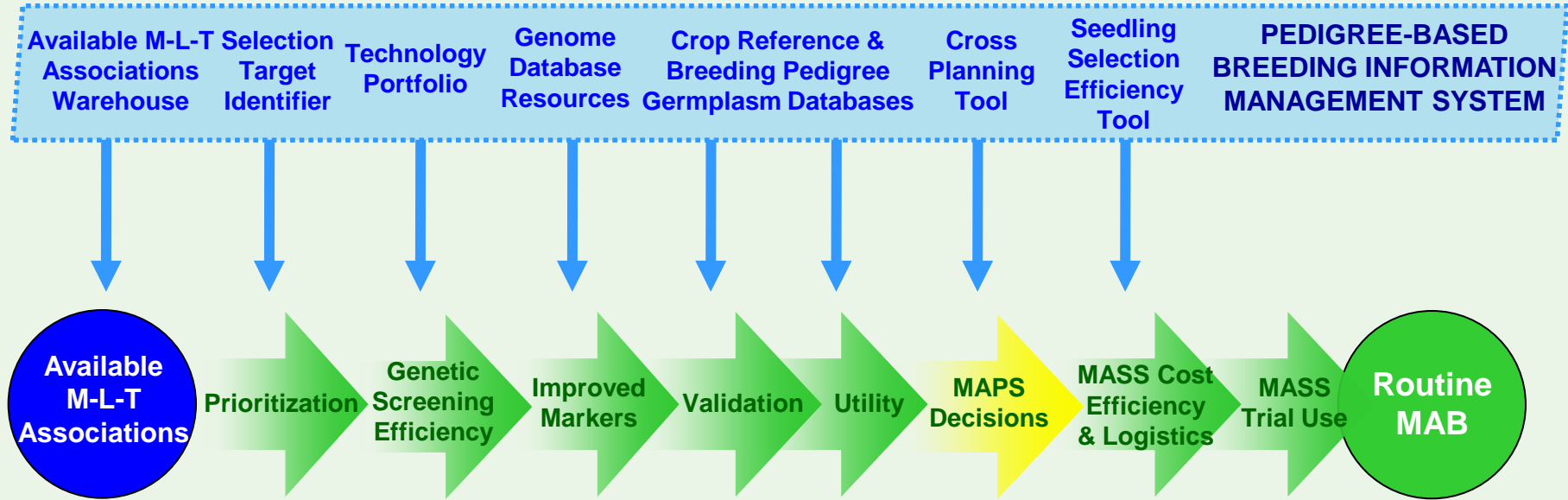


## Utility

Distribution of functional alleles within the germplasm of specific breeding programs is determined

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# a. Implementation of MAB Pipeline stages cont.

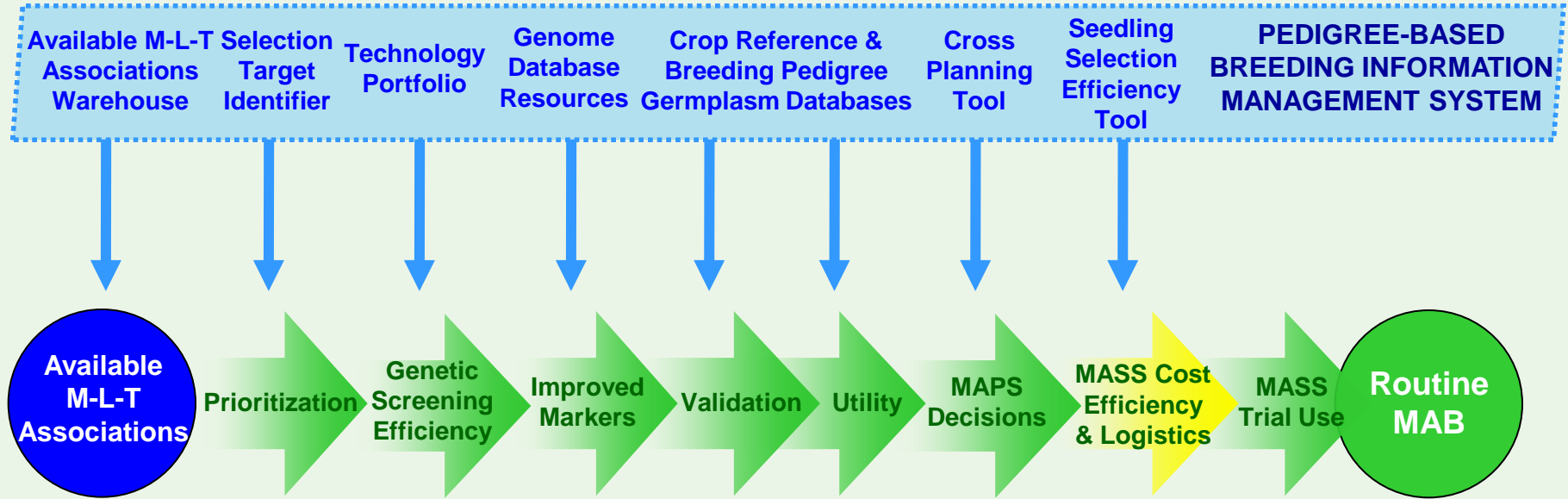


## Marker Assisted Parent Selection Decisions

Crossing decisions informed by marker data are performed (or use Cross Planning Tool modules without markers)

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# a. Implementation of MAB Pipeline stages cont.

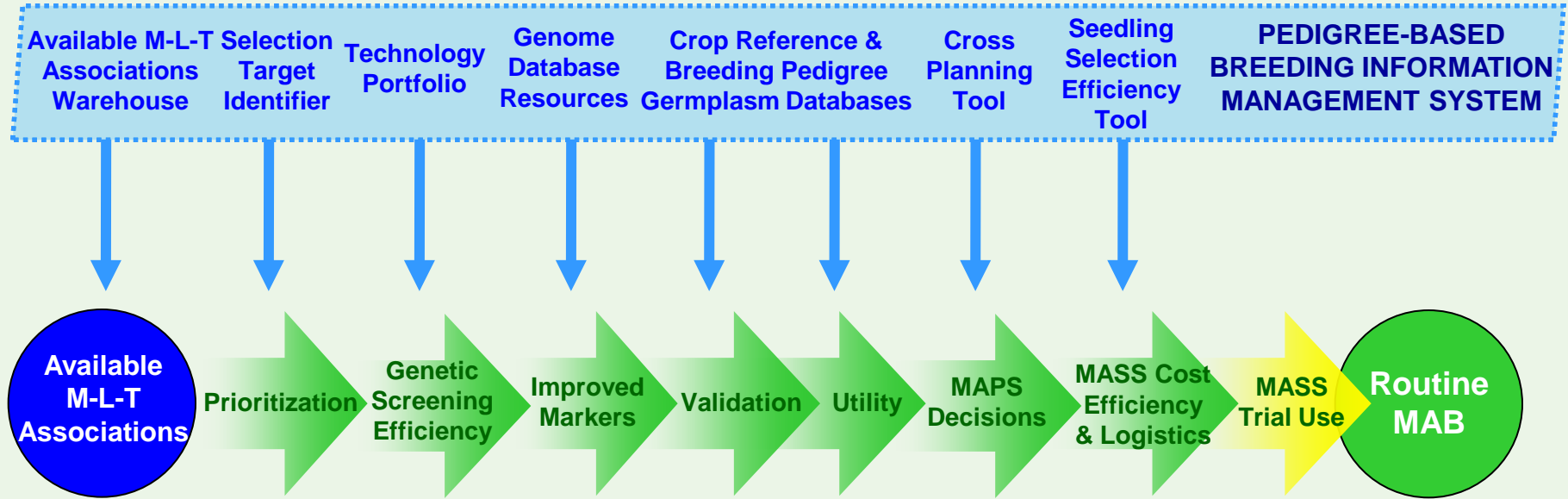


## Marker-Assisted Seedling Selection Cost Efficiency & Logistics

Efficient seedling selection schemes informed by marker data are designed

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# a. Implementation of MAB Pipeline stages cont.



## Marker-Assisted Seedling Selection Trial Use

Efficient MASS schemes are run with seedling populations to test effect on program efficiency, experience logistics, and optimize to suit idiosyncratic needs

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## b. Fast-tracked pipelining in 2010

*WHO:* Breeding Team, MAB Pipeline Team, SE Team, PBA Team, Genotyping Team, Extension Team

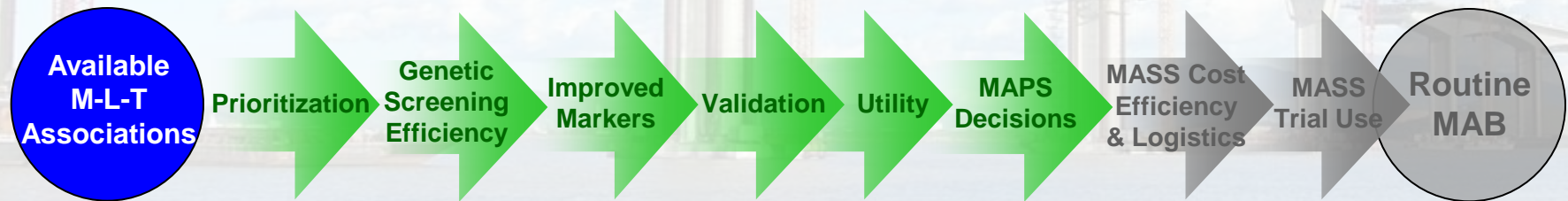
*WHEN:* Jan 2010 – Feb 2011

- Although full reference germplasm datasets (with genome scans) will not be available in 2010 and SE-facilitated trait economic weights are not yet available, potentially valuable M-L-T associations are already available for each breeding program

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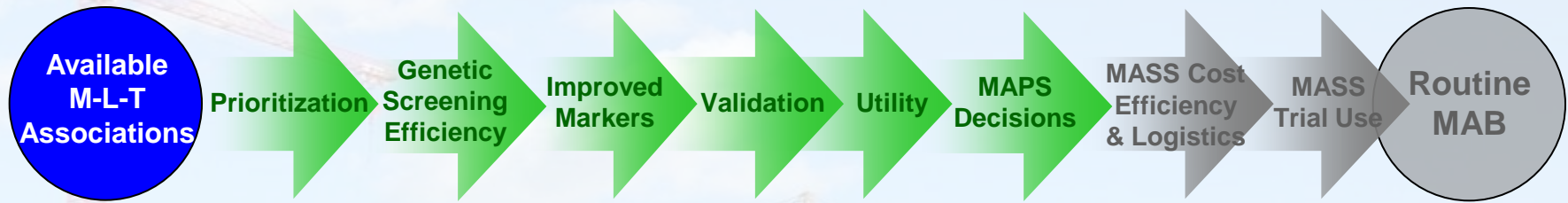
## b. Fast-tracked pipelining in 2010 contd.

- Will pipeline at least 2 promising M-L-T associations per program in 2010, to “MAPS Decisions” stage in time for 2011 crossing season



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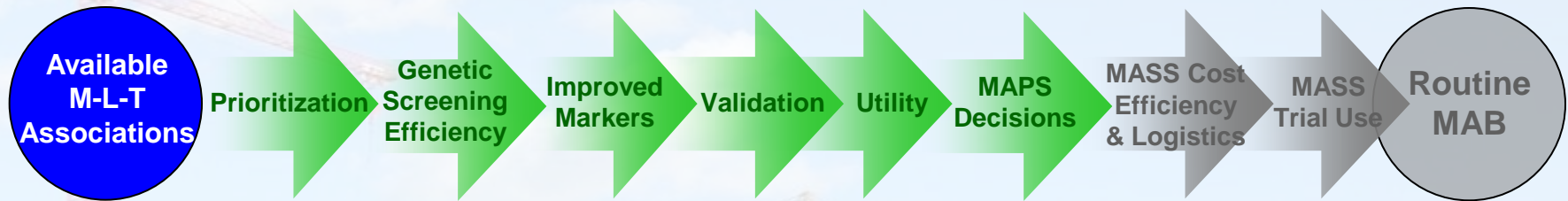
## b. Fast-tracked pipelining in 2010 contd.



- Breeders have chosen current traits of interest
- MAB Pipeline Team will seek M-L-T associations for these traits
- Genotyping Team will extract DNA and facilitate genotyping of Crop Reference and Breeding Pedigree Sets for markers

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## b. Fast-tracked pipelining in 2010 contd.



- Phenotypic data for 2010 season and anything prior will be collected
- FlexQTL™ analysis will be conducted by breeders/breeding trainees as first hands-on after July 2010 (ASHS) introduction
- Genotype information used in 2011 crossing decisions, documented by Extension Team

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# MAB Pipelining: Benefits for Breeders

- Improved breeding efficiency by use of DNA information for guiding breeding decisions to develop and apply optimal selection strategies aimed at objectively defined selection targets
- More benefits – that don't even need marker use:
  - Selection targets better aligned with stakeholder values
  - Greater stakeholder involvement in local breeding progs
  - increased germplasm availability
  - improved phenotyping protocols
  - enhanced interaction with fellow breeders

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# MAB Pipelining: Beyond Core Breeders

- Core breeders are first “technology-adopters”, “risk-takers” – to demonstrate **success stories**
- Adoption by other Rosaceae breeding programs is fundamental to RosBREED’s Mission

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# ROSBREED

Enabling marker-assisted breeding in Rosaceae

## Acknowledgements



United States Department of Agriculture  
National Institute of Food and Agriculture

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