

# ROSBREED

Enabling marker-assisted breeding in Rosaceae

BRIDGING THE CHASM  
BETWEEN  
GENOMICS & BREEDING:  
ENABLING MARKER-ASSISTED BREEDING

Cameron Peace, MAB Pipeline Team Leader, WSU Pullman

# The RosBREED Approach

*Socio-economics information*

Objectively define

**SELECTION TARGETS**

Optimize

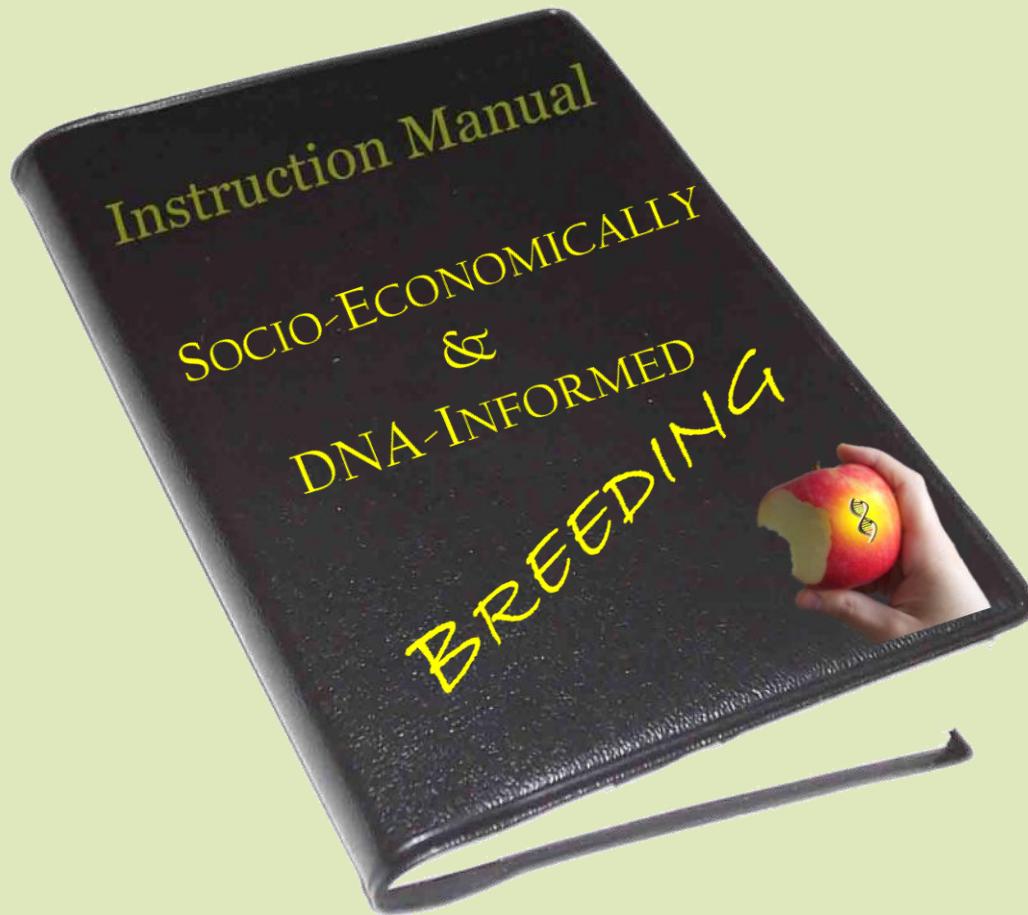
**SELECTION STRATEGIES**

**IMPROVED  
CULTIVARS**

*DNA information*



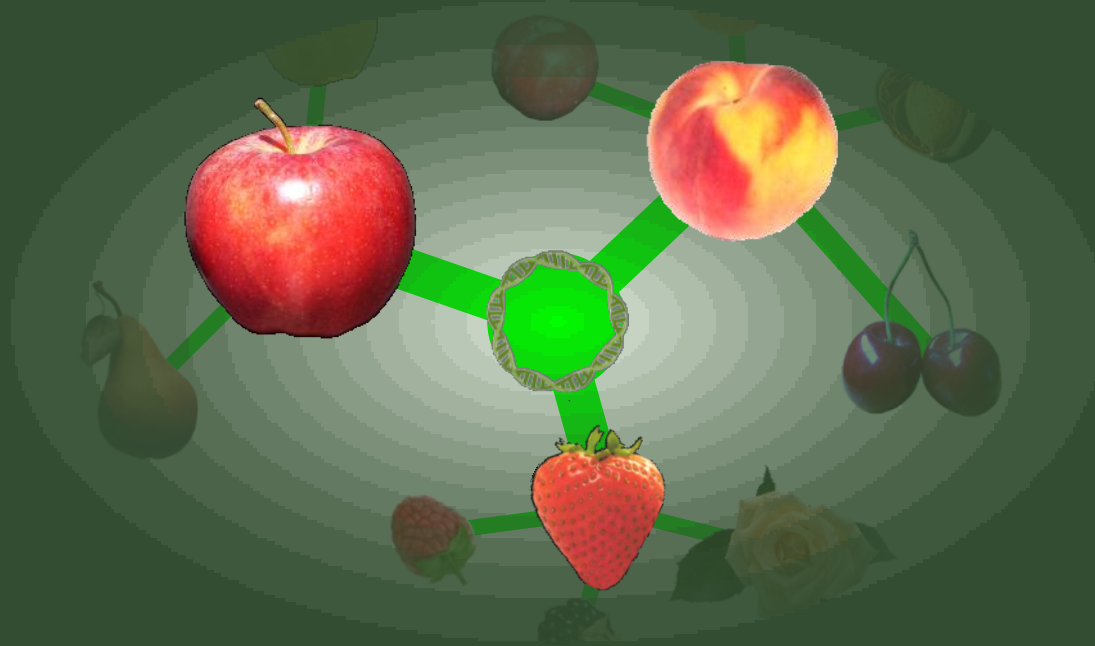
# Writing the Instruction Manual





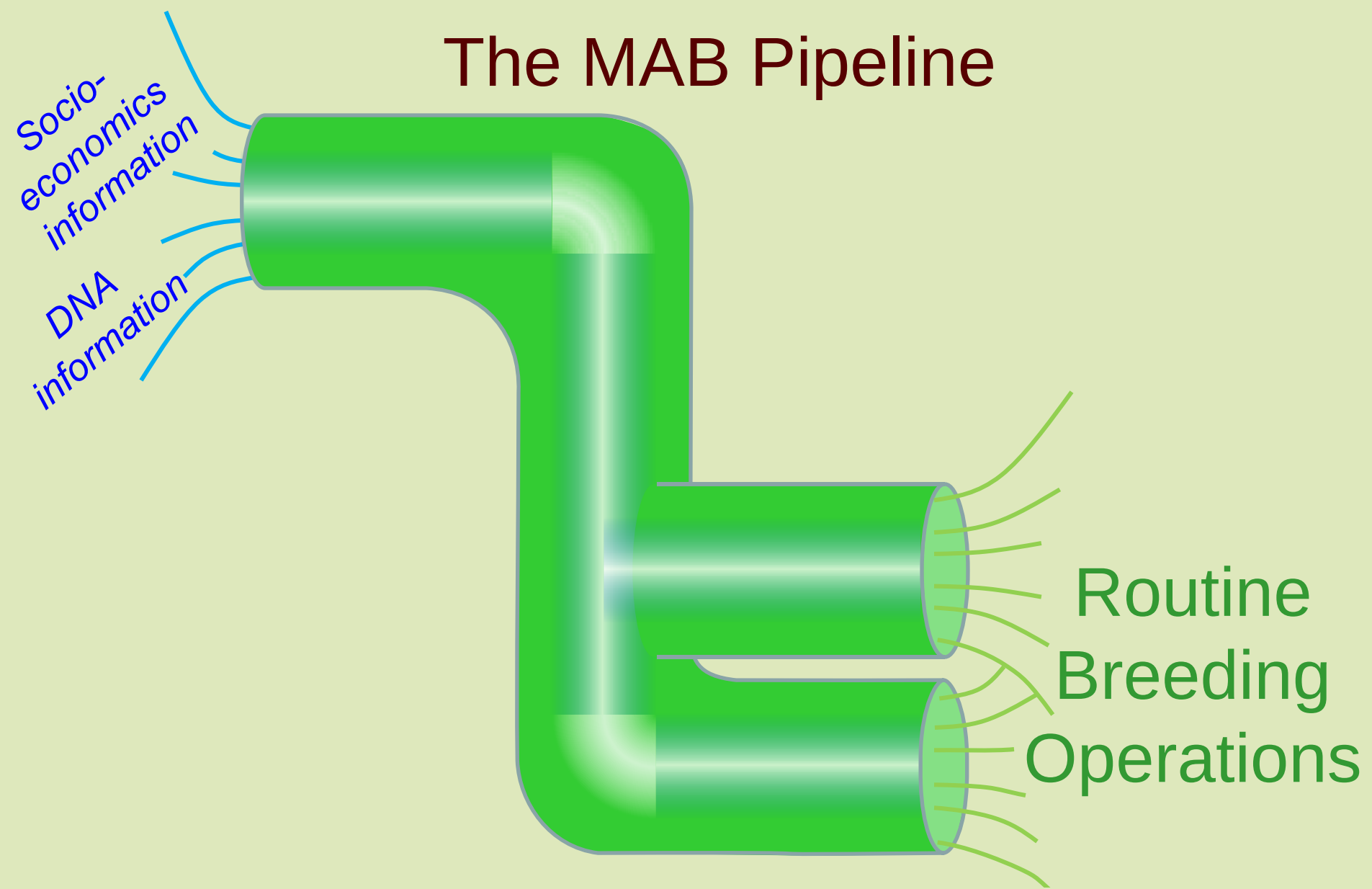
## Outline of Presentation

- ❖ The MAB Pipeline
- ❖ A High-Impact Target for Cherry Breeding
- ❖ *Example of MAB Pipelining in Action:*  
Large Fruit for Sweet Cherry



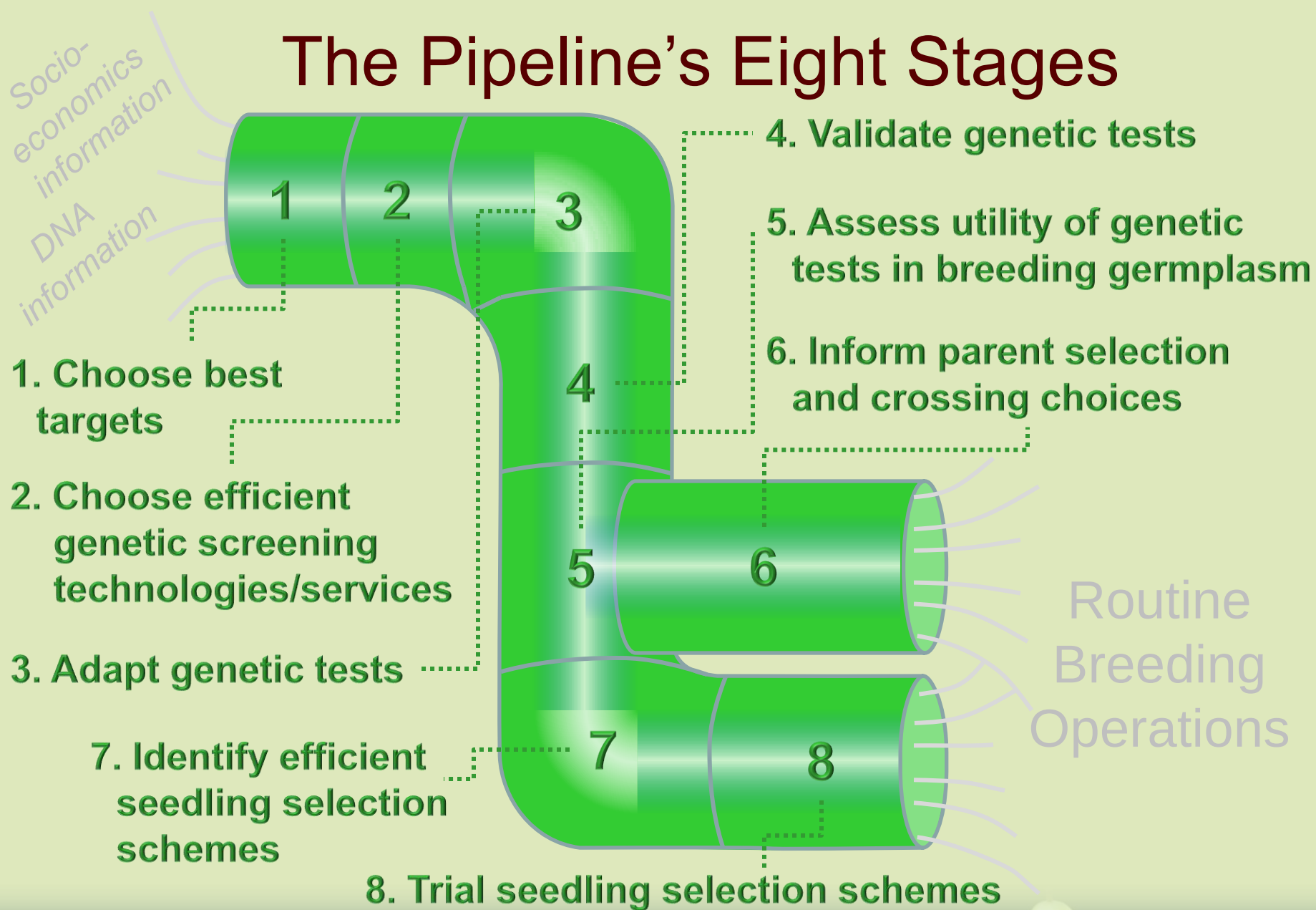
# The MAB Pipeline

# The MAB Pipeline





# The Pipeline's Eight Stages



**ROS BREED**

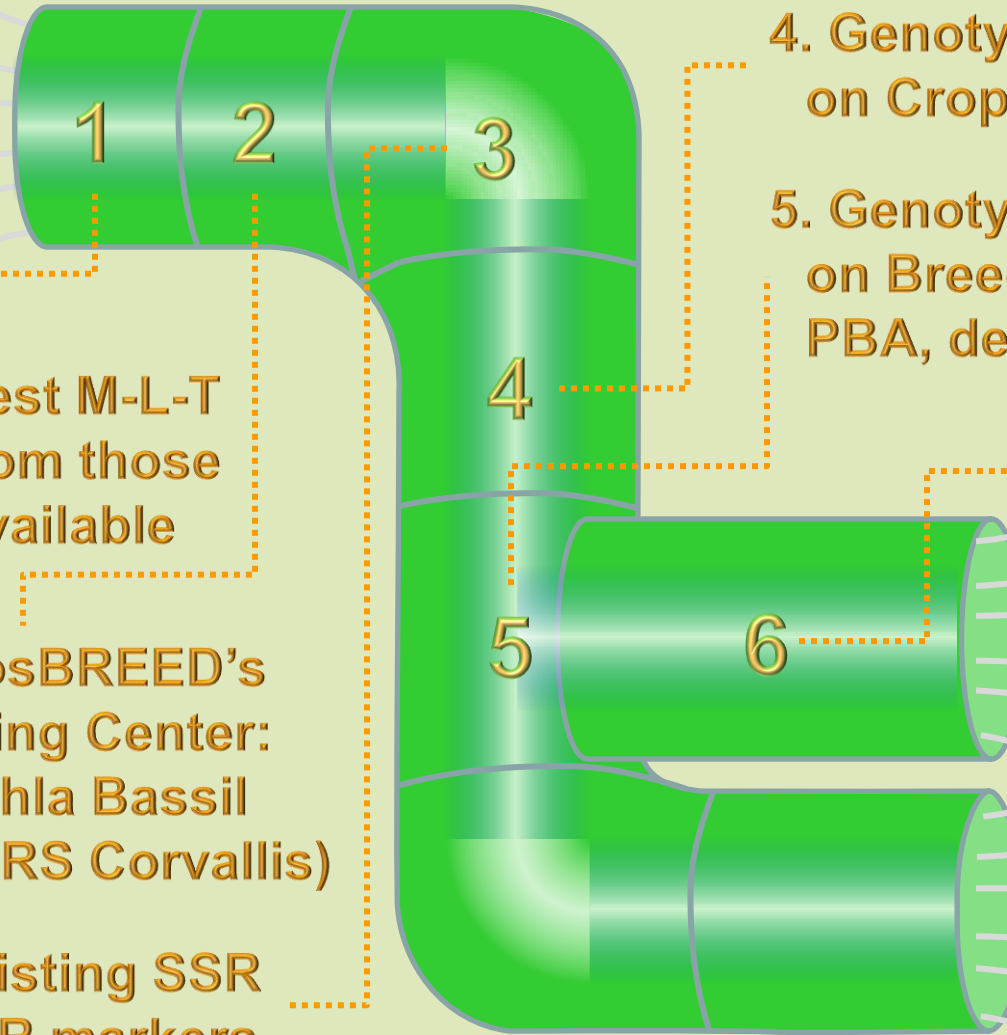
Enabling marker-assisted breeding in Rosaceae



[www.rosbreed.org](http://www.rosbreed.org)

# Fast-Track Pipelining in 2010

Socio-  
economics  
information  
DNA  
information



1. Chose best M-L-T  
assocs from those  
already available

2. Using RosBREED's  
Genotyping Center:  
lab of Nahla Bassil  
(USDA-ARS Corvallis)

3. Using existing SSR  
and SCAR markers

4. Genotyping and Phenotyping  
on Crop Reference Sets, PBA

5. Genotyping and Phenotyping  
on Breeding Pedigree Sets,  
PBA, describe parent alleles

6. Inform parent  
selection and  
crossing choices  
of 2011

Routine  
Breeding  
Operations





# Fast-Tracked Pipelining in 2010 for Fruit Quality

## Peach

1. Texture: *endoPG*  
*F-M* locus
2. Flavor: sweetness  
& acidity QTL



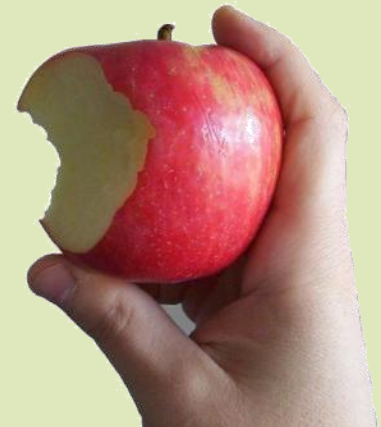
## Cherry

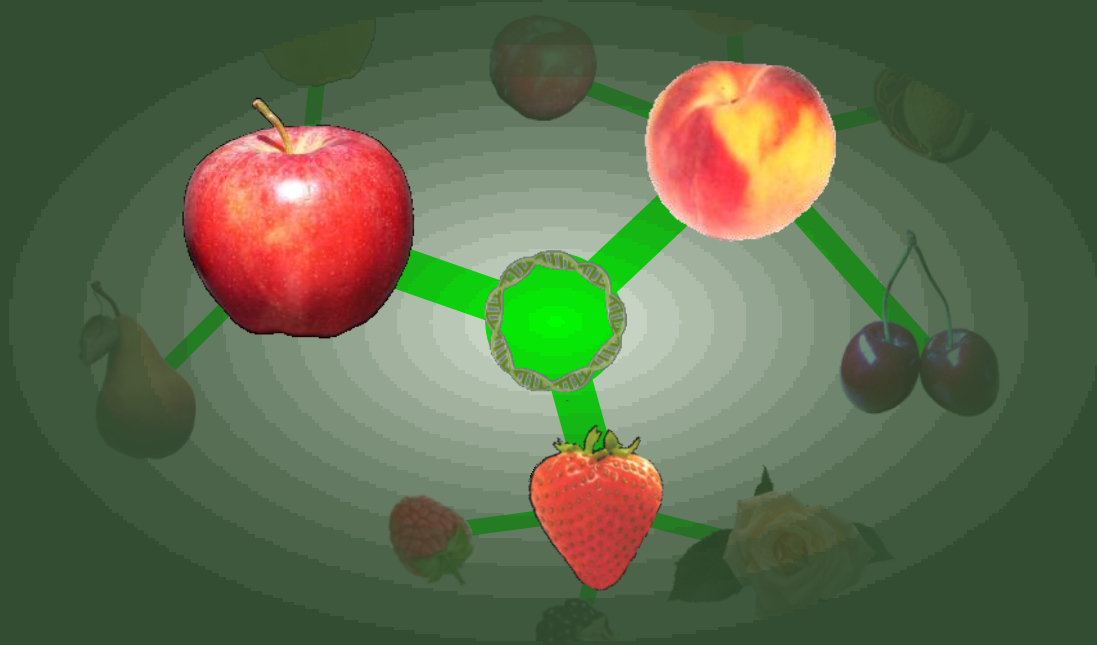
1. Fruit quality: fruit  
size and firmness  
QTL
2. Flavor: acidity QTL



## Apple

1. Flavor and Texture:  
acidity, crispness,  
juiciness QTL
2. Texture: Firmness  
QTL





A High-Impact Target  
for Cherry Breeding

# A High-Impact Target

- Fruit size for sweet cherry

Elite sweet cherry cultivars

**12 grams**

Domestication  
and breeding

**2 grams**

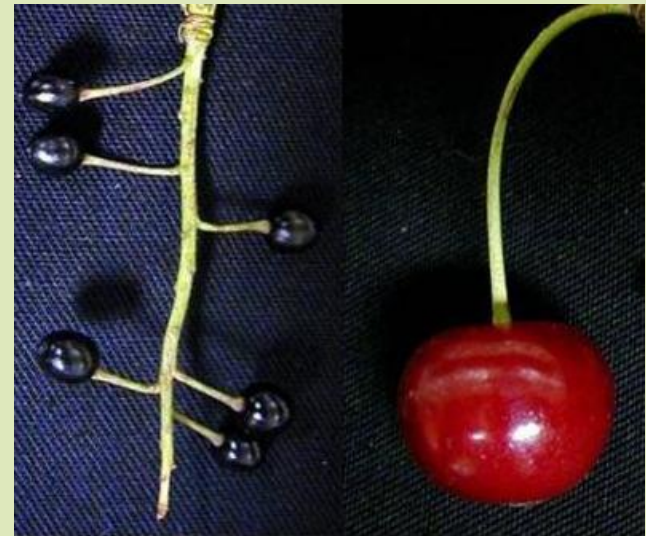
Wild forest cherries



Breeding for  
resistance

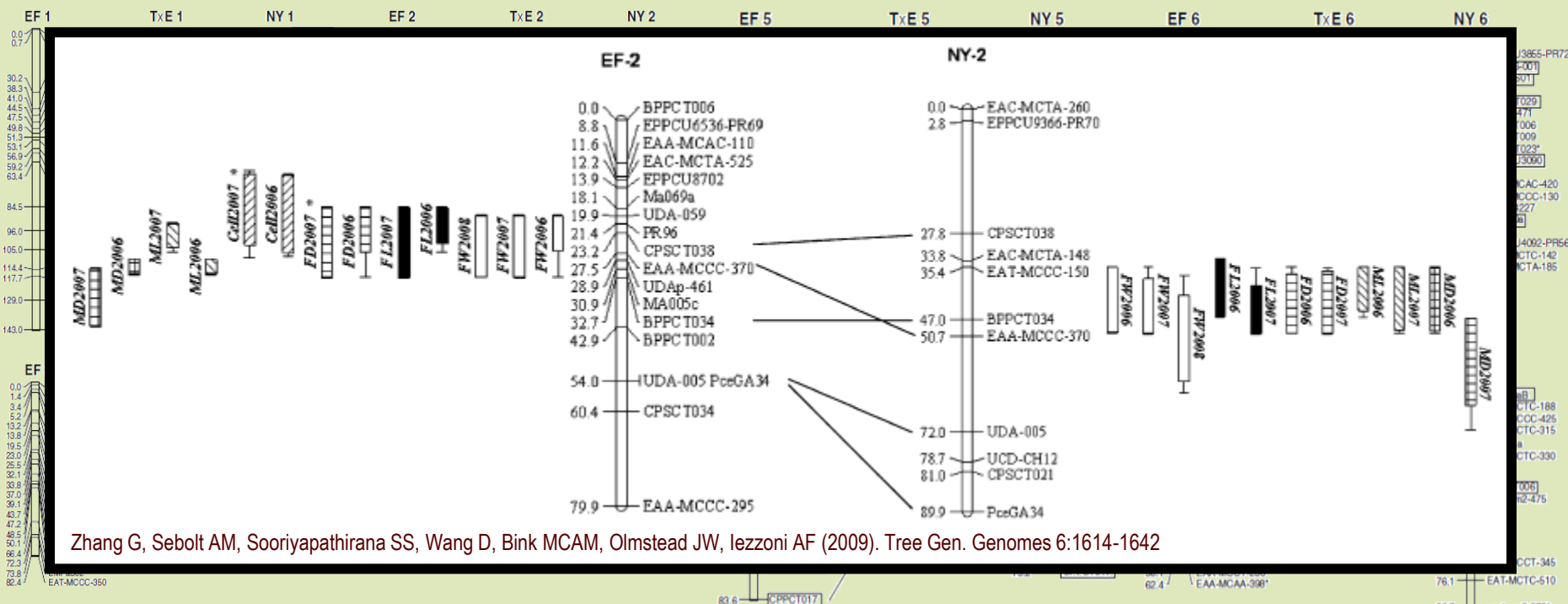
Disease  
resistant

Disease  
susceptible



# Mapping & QTL Studies

- Sweet cherry genetic map created
- Nice QTL for fruit size identified

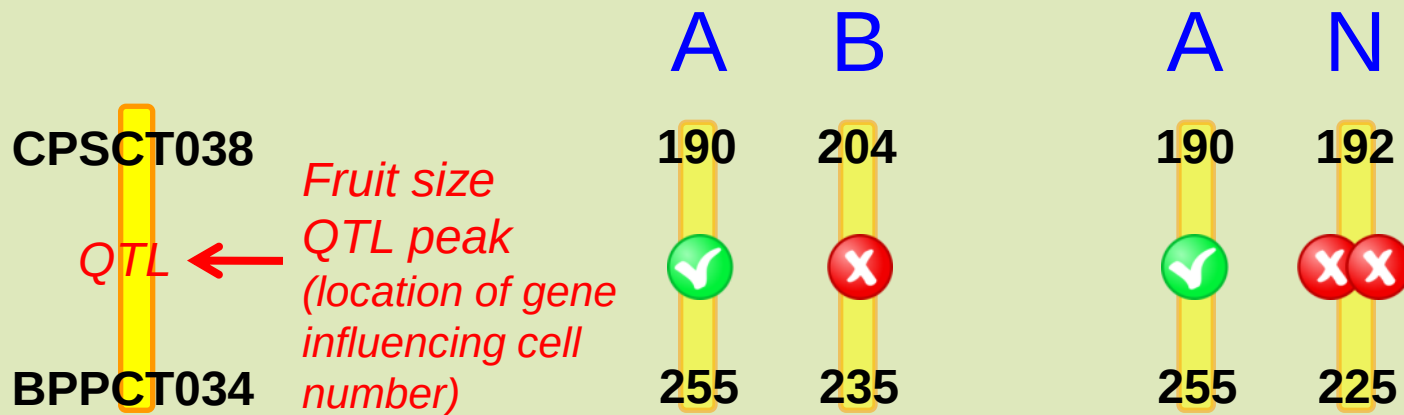
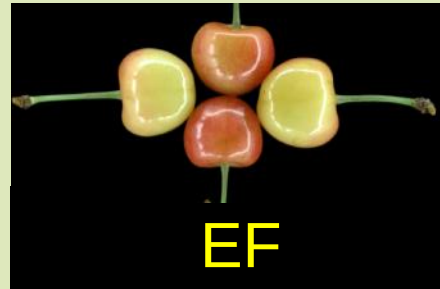


Olmstead JW, Iezzoni AF, Whiting MD (2007). Genotypic differences in sweet cherry fruit size are primarily a function of cell number. J. Amer. Soc. Hort. Sci. 132:697-703



# QTL Study

- Functional alleles reported (thanks Amy!)





# Reported M-L-T Association

- QTL paper published

Tree Genetics & Genomes  
DOI 10.1007/s11295-009-0225-x

## ORIGINAL PAPER

### Fruit size QTL analysis of an $F_1$ population derived from a cross between a domesticated sweet cherry cultivar and a wild forest sweet cherry

Guorong Zhang · Audrey M. Scholt · Suneth S. Sooriyapathirana · Dechun Wang · Marco CAM Bink · James W. Olmstead · Amy F. Jezzens

Received: 15 January 2009 / Revised: 18 June 2009 / Accepted: 24 June 2009  
© Springer-Verlag 2009

**Abstract** Maximizing fruit size is critical for profitable sweet cherry (*Prunus avium* L.) production. Yet, despite its importance, little is known about the genetic control of fruit size. This objective of this study was to identify quantitative

trait, and one QTL was identified for mesocarp cell number. Fruit size QTLs were found on linkage group 2 on the EF map (EF 2) and linkage groups 2 and 6 on the NY map (NY 2 and NY 6). On EF 2, the cell number QTL clustered





# Plenty of Reported M-L-T Associations!

## SUMMARY OF M-L-T ASSOCIATIONS IN ROSACEAE (U.S.)

| Crop           | Traits | Number of         |                   |                    | Number used in    |                   |
|----------------|--------|-------------------|-------------------|--------------------|-------------------|-------------------|
|                |        | QTLs <sup>a</sup> | MTLs <sup>b</sup> | Genes <sup>c</sup> | MAPS <sup>d</sup> | MASS <sup>e</sup> |
| Apple          | 55     | 180               | 36                | 5                  | 2                 | 1                 |
| Pear           | 5      | 7                 | 3                 | 1                  | -                 | -                 |
| Peach          | 21     | 36                | 4                 | 2                  | 1                 | -                 |
| Almond         | 10     | 8                 | 4                 | 1                  | 1                 | -                 |
| Cherry (sweet) | 1      | -                 | -                 | 1                  | 1                 | -                 |
| Cherry (tart)  | 3      | 14                | -                 | 1                  | 1                 | -                 |
| Strawberry     | 11     | 31                | 2                 | -                  | -                 | 2                 |
| Raspberry      | -      | -                 | -                 | -                  | -                 | -                 |
| Blackberry     | -      | -                 | -                 | -                  | -                 | -                 |
| Rose           | 11     | 41                | 9                 | -                  | -                 | -                 |
| <b>Total:</b>  |        | <b>117</b>        | <b>317</b>        | <b>58</b>          | <b>11</b>         | <b>6</b>          |

<sup>a</sup> QTLs = quantitative trait loci with linked markers

<sup>b</sup> MTLs = major/ trait loci with linked markers

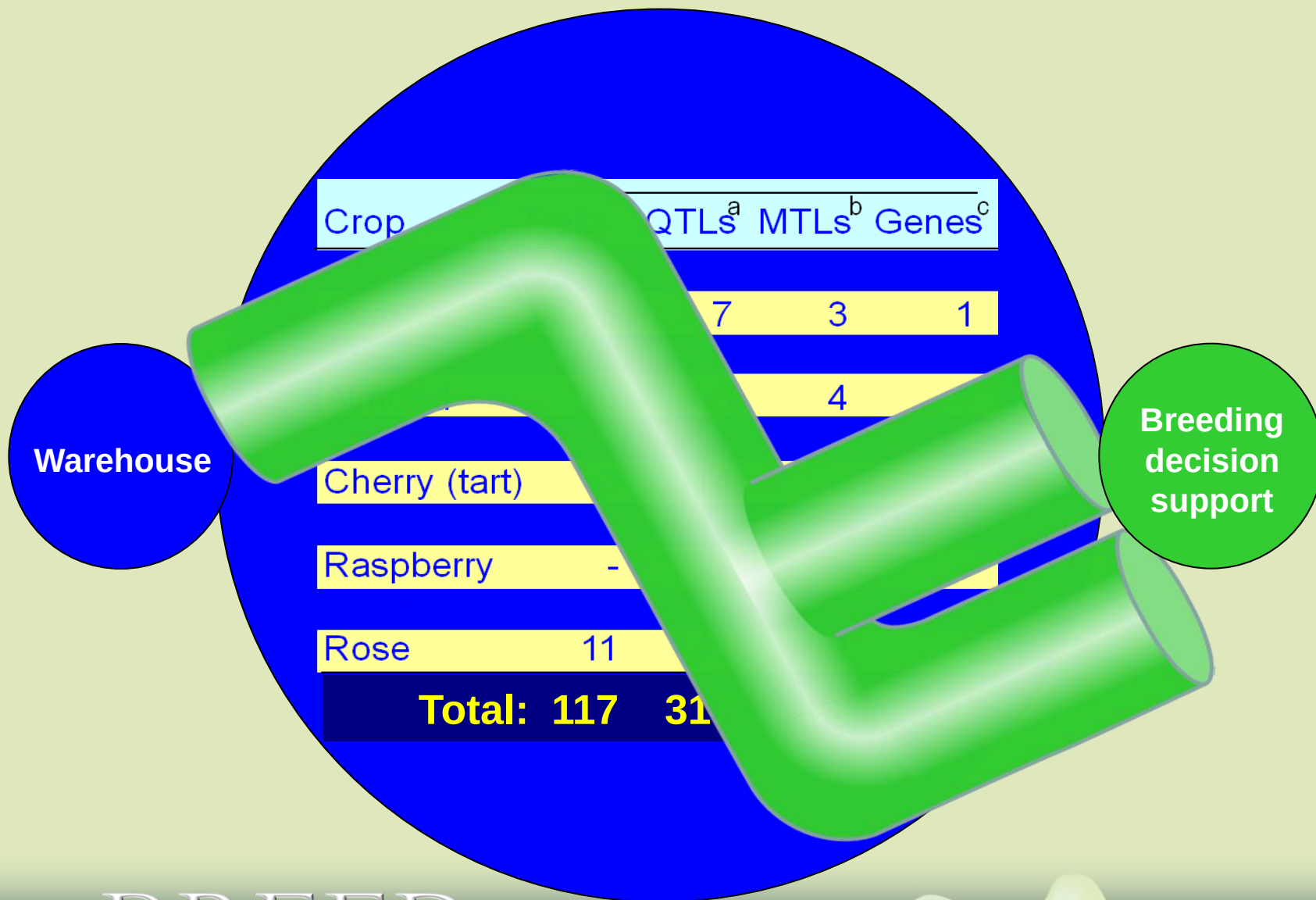
<sup>c</sup> Genes = known genes controlling a trait

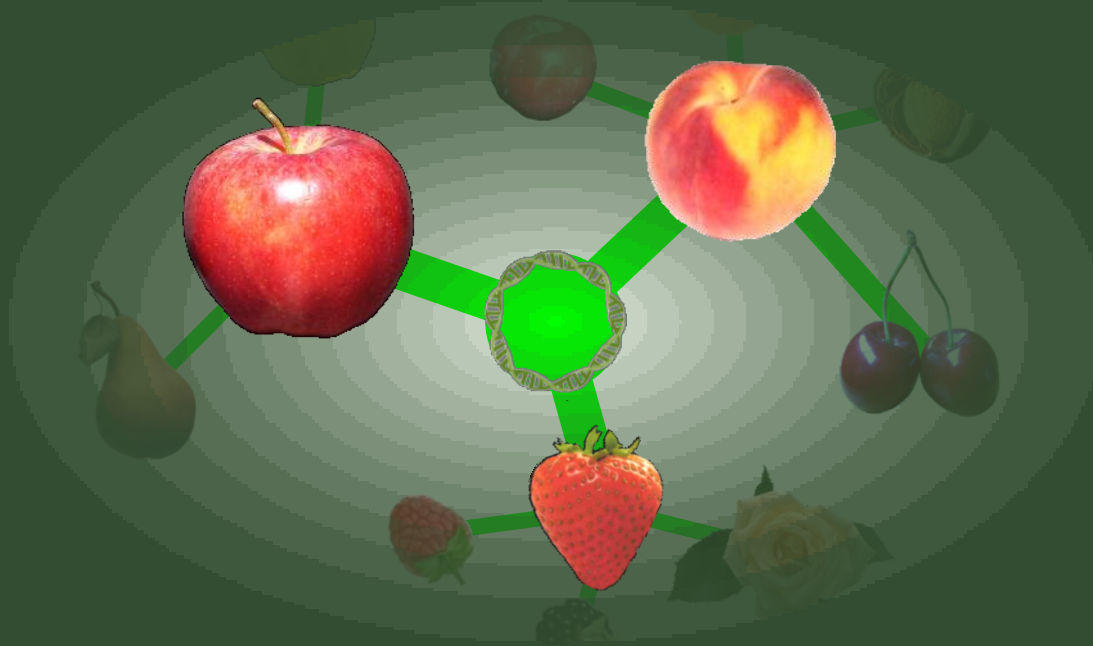
<sup>d</sup> MAPS = marker-assisted parent selection

<sup>e</sup> MASS = marker-assisted seedling selection



# “Available M-L-T Associations Warehouse”





*Example of MAB Pipelining in Action:*  
Large Fruit for Sweet Cherry

# The MAB Pipeline

*Socio-  
economics  
information*

*DNA  
information*

*Routine  
Breeding  
Operations*

**ROSBREED**  
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# The MAB Pipeline for Fruit Size

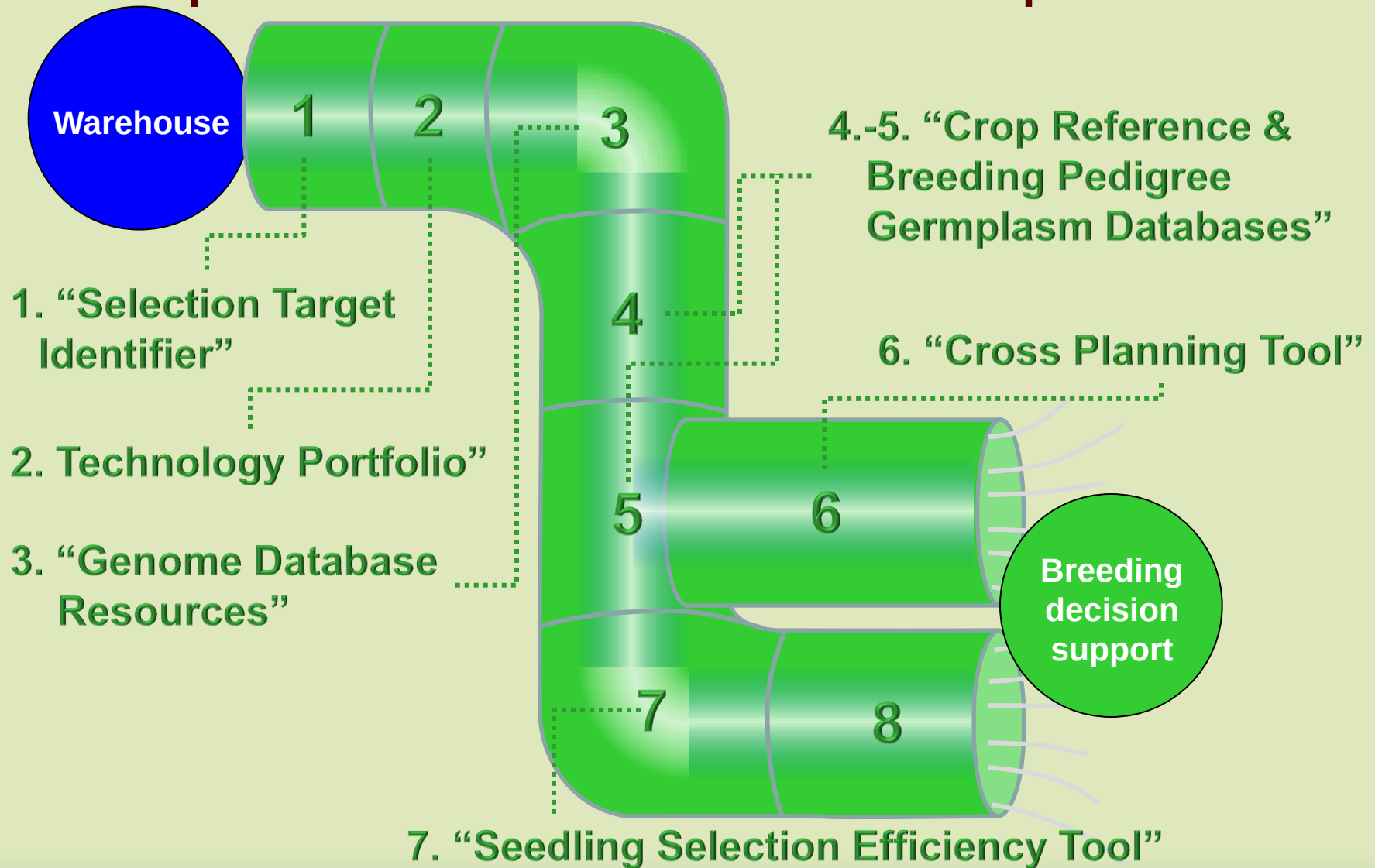
Consumer &  
industry value  
of large fruit

QTLs for  
fruit size

- Which crosses to make for efficient genetic gain in fruit size
- Efficient wild introgression
- Identify new genetic sources for large fruit
- Efficient seedling selection scheme to avoid wasting resources on small-fruited seedlings



# Pipeline Infrastructure Components





# 1. Prioritization



# 1. Prioritization

“Selection Target Identifier”

$$\text{PI} = \$ \times G \times H$$

*PRIORITY* *INDEX*



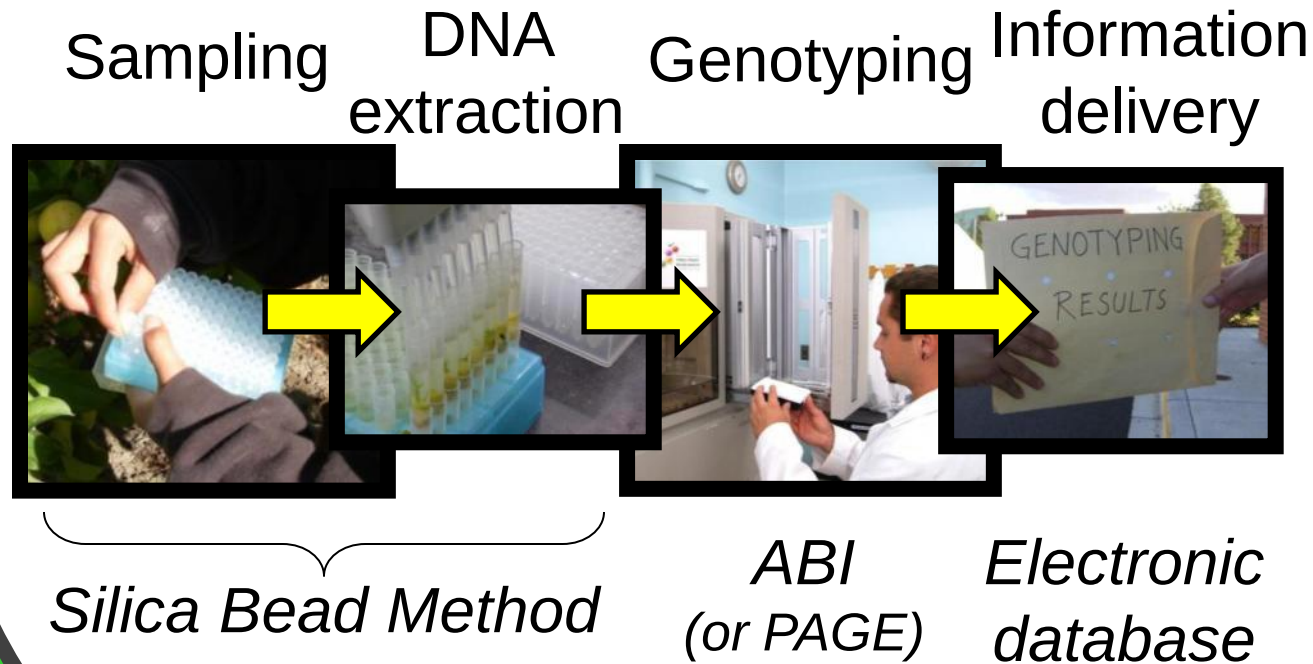
# 1. Prioritization

## “Selection Target Identifier”

| PI  | Marker-Locus-Trait Association      |
|-----|-------------------------------------|
| 9.7 | Fruit size 8-12 g                   |
| 3.1 | Fruit size 12-14 g                  |
| 1.2 | Sweetness 16-22 <sup>0</sup> Brix   |
| 1.1 | Fruit size 14 <sup>+</sup> g        |
| 1.0 | Self-fertility                      |
| 0.9 | Powdery mildew resistance           |
| 0.8 | Acidity - in balance with sweetness |



## 2. Genetic Screening Efficiency



## 2. Genetic Screening Efficiency

“Technology Portfolio”



### 3. Improved Markers

**CPSCT038** SSR, 4 alleles



*Fruit size  
QTL*



*...and fine mapping  
underway: SNPs being  
developed, controlling  
gene being sought*

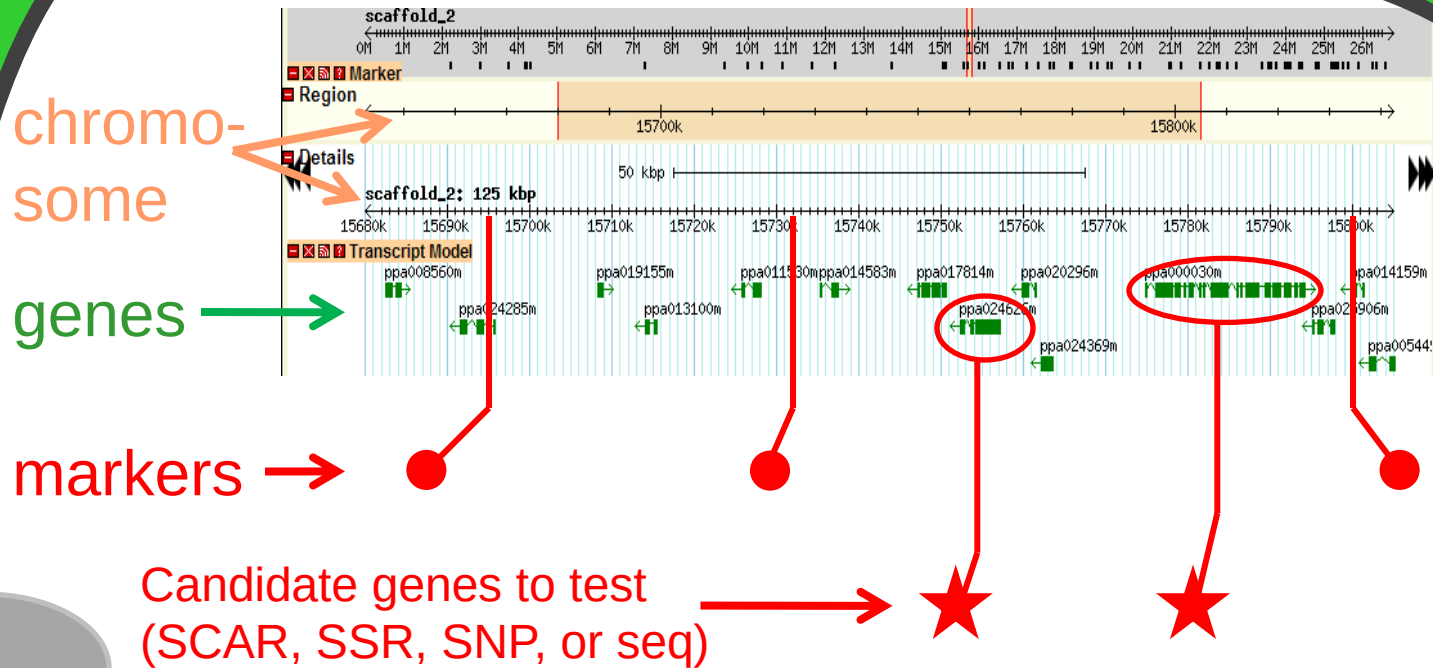
**BPPCT034** SSR, 7 alleles





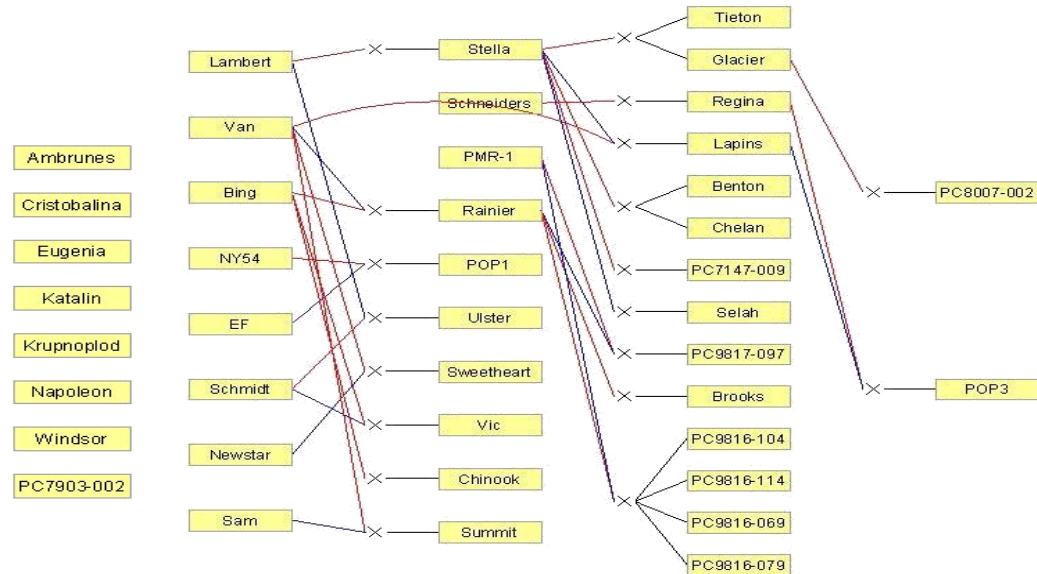
# 3. Improved Markers

## “Genome Database Resources”



# 4. Validation

## Validation on “Pedigree Set”

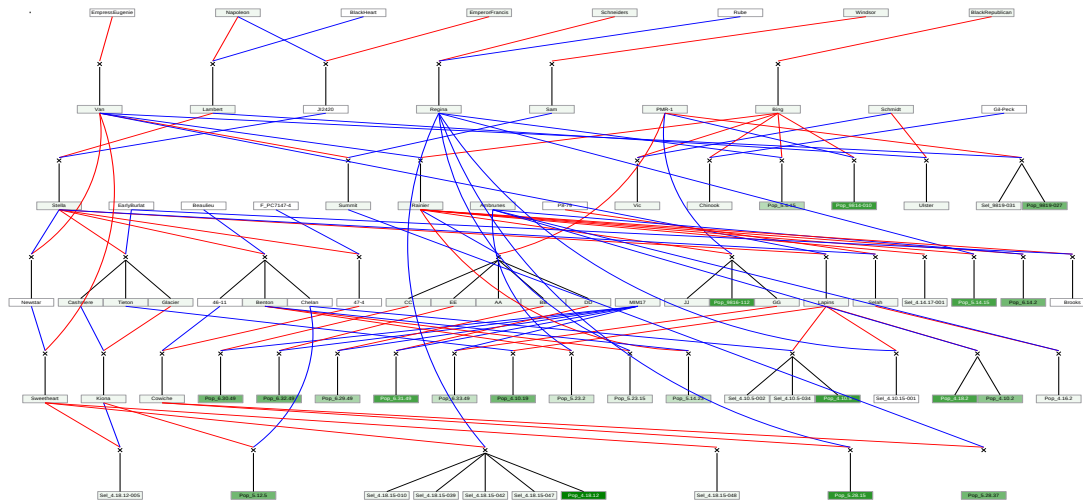


41 cultivars and 3 populations (417 seedlings)

# 4. Validation

## “Crop Reference Germplasm Databases”

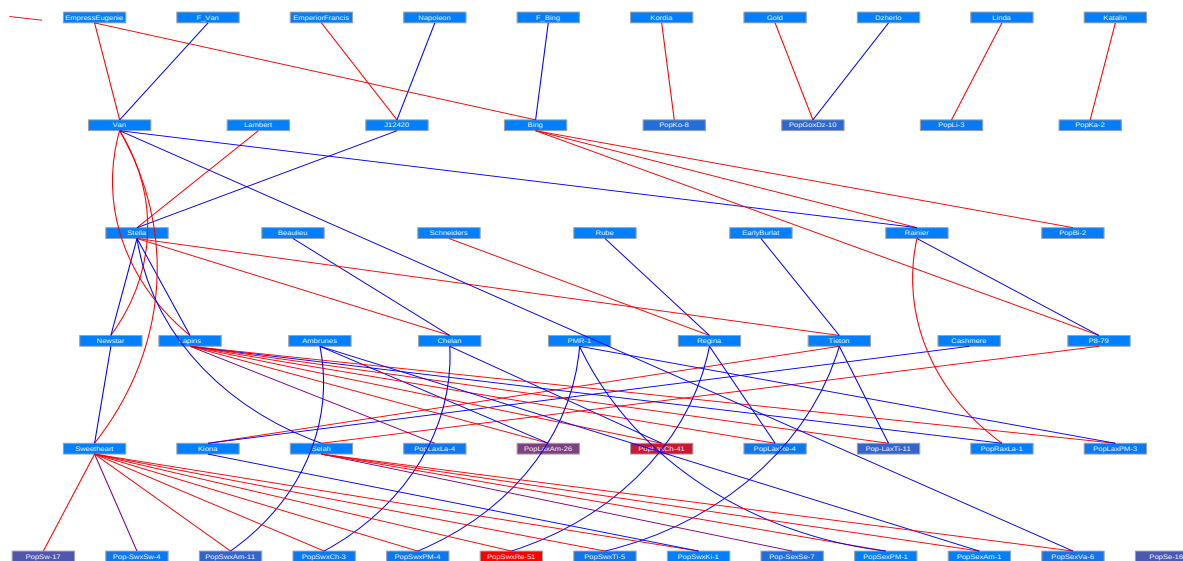
### Sweet Cherry Crop Reference Set



57 cultivars and 23 populations (183 seedlings)

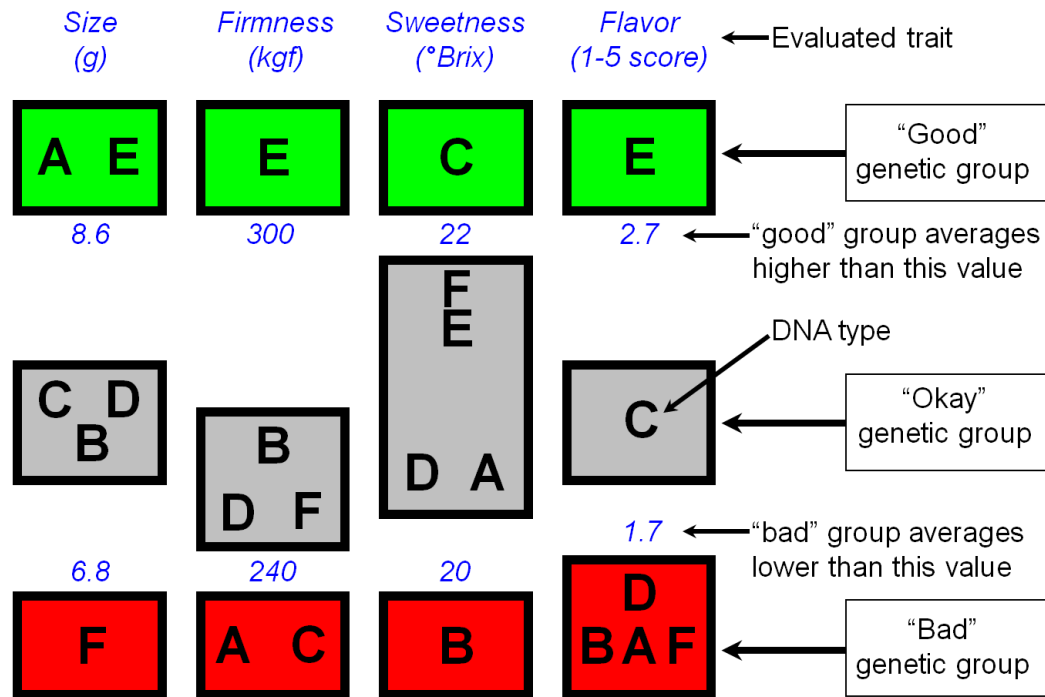
# 5. Utility

## Utility assessment on fruiting seedlings



22 populations (219 seedlings)

# 5. Utility



E = large, firm

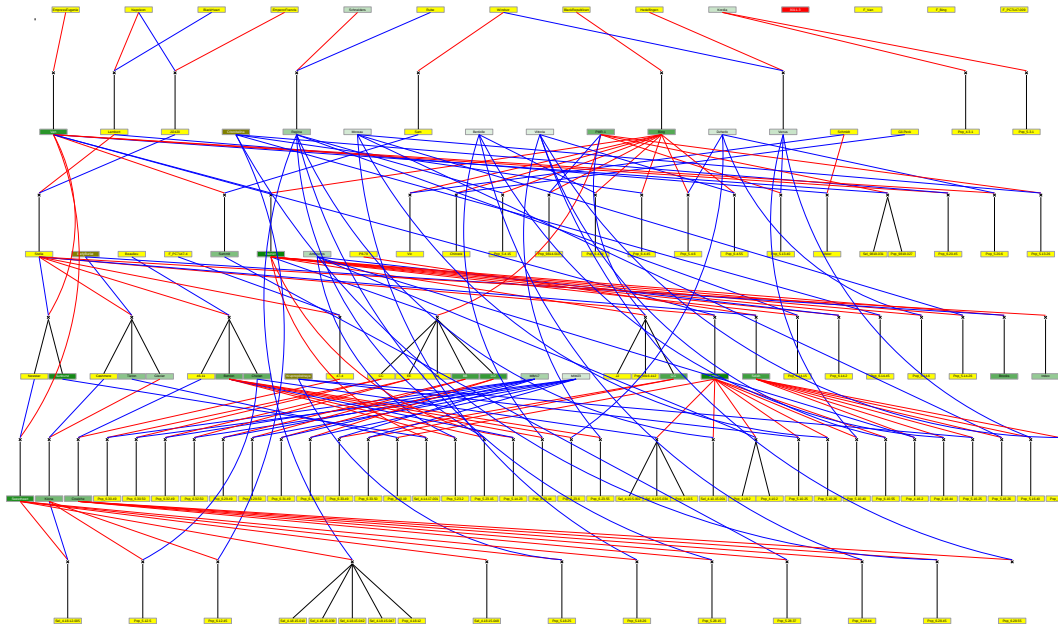
A = large, soft

B, C, D, F  
= small

# 5. Utility

## “Breeding Pedigree Germplasm Databases”

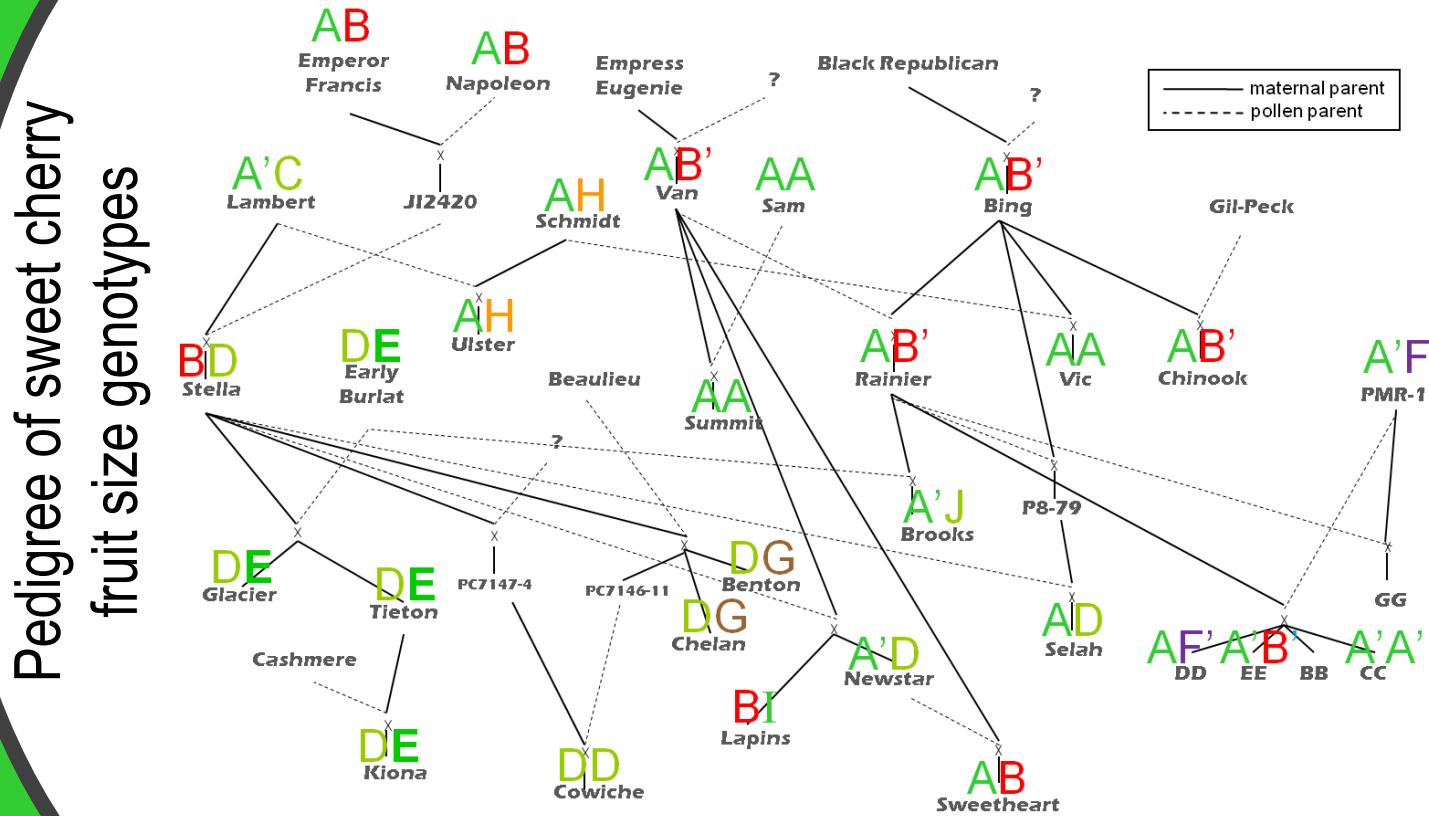
### PNWSCBP Breeding Pedigree Set



66 cultivars and 59 populations (414 seedlings)

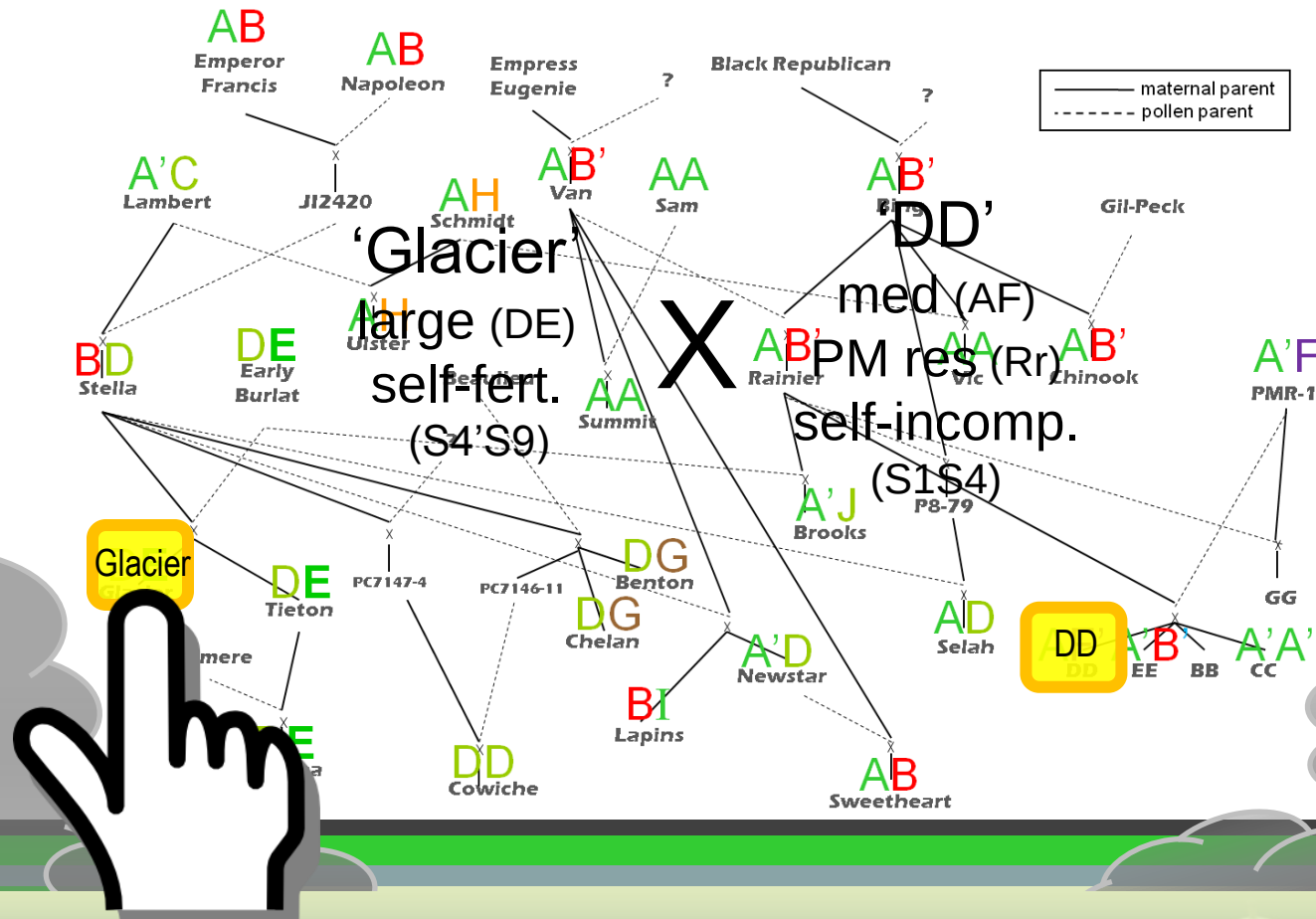


## 6. Parent Selection Decisions



# 6. Parent Selection Decisions

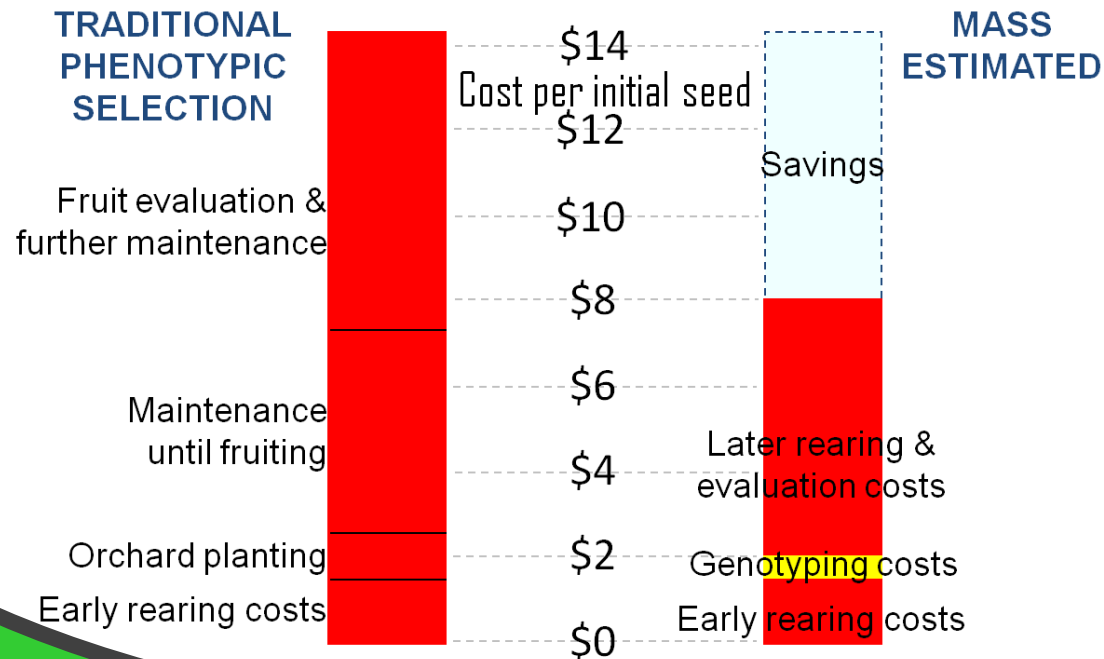
“Cross Planning Tool”



# 7. Seedling Selection Cost Efficiency & Logistics

Spreadsheet tool:

Predicted savings for 1 marker, 50% cull



# 7. Seedling Selection Cost Efficiency & Logistics

“Seedling Selection Efficiency Tool”



## 8. Trial Use

Fall 2010: Genotype ~1000 seedlings for fruit size, cull predicted small-fruited





# The MAB Pipeline for Fruit Size

Consumer &  
industry value  
of large fruit

QTL for  
fruit size

The most efficient use of  
SE and DNA information!

- Which crosses to make for efficient genetic gain in fruit size

- Efficient wild introgression

- Identify new genetic sources for large fruit

- Efficient seedling selection scheme to avoid wasting resources on small-fruited seedlings

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A man with short dark hair, wearing sunglasses, a light yellow short-sleeved button-down shirt, and blue cargo shorts, stands in a cherry orchard. He is holding two large, dark red cherries in his right hand and a bunch of three large, dark red cherries in his left hand. The orchard has rows of cherry trees with green leaves on either side of a dirt path. The ground is covered with dry leaves and some green weeds. The lighting is bright, suggesting a sunny day.

Dr. Nnadozie Oraguzie,  
sweet cherry breeder

Breeding  
orchard

Fruits of our labor



# Acknowledgements



United States Department of Agriculture  
National Institute of Food and Agriculture

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Food and Agriculture



# Questions?

