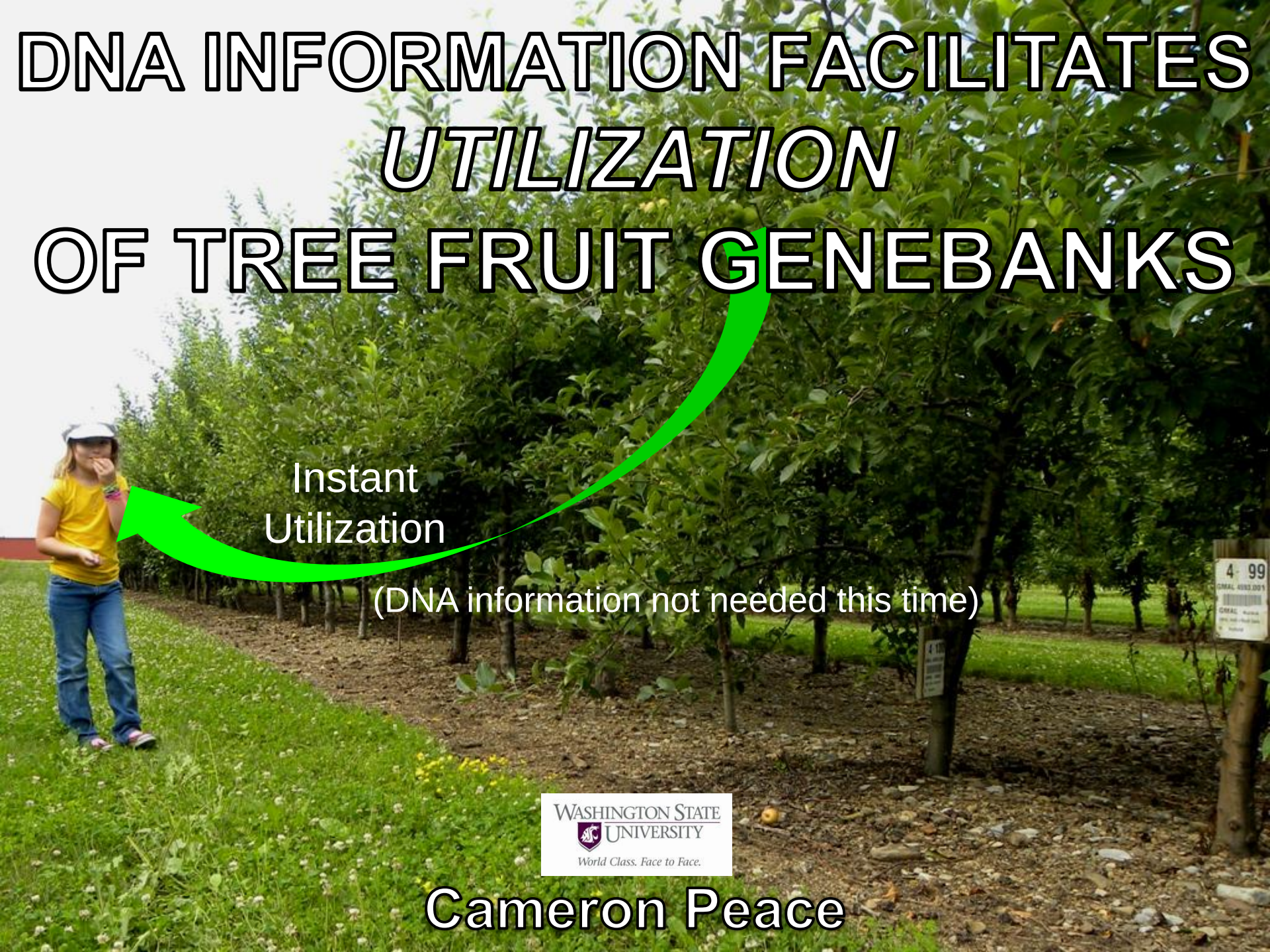
DNA INFORMATION FACILITATES *UTILIZATION* OF TREE FRUIT GENEBANKS



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Cameron Peace

TAKE HOME MESSAGE

To Facilitate Utilization of Tree Fruit Genebanks:

1. ~~Think like a curator~~
   →Think like a breeder
2. ~~Static collections~~
   →Segregating descendant populations
3. ~~Descriptors~~
   →Comprehensive and standardized performance information
4. ~~Phenotypes~~
   →Performance-predictive DNA information

WHO IS THIS GUY?

Asst Prof
Tree Fruit Genetics

WASHINGTON STATE UNIVERSITY
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College of Agricultural, Human, and Natural Resource Sciences
Horticulture and Landscape Architecture

Chair, *Prunus* CGC
Member, Apple CGC

USDA ARS
United States Department Of Agriculture
Agricultural Research Service
National Plant Germplasm System

Co-Project Director
MAB Pipeline Team Leader

RosBREED
www.rosbreed.org

ACKNOWLEDGEMENTS

Breeders: Tom Gradziel, Amy Iezzoni, Jim Olmstead, Kate Evans, Nnadozie Oraguzie, Jim Luby

Germplasm curators: Phil Forsline, Gennaro Fazio, Ed Stover, John Preece

Germplasm DNA evaluators: Gayle Volk, Nahla Bassil, Malli Aradhya

Co-PIs and participants of NRI project “Candidate genes for fruit softening in *Prunus*”

Co-PIs and participants of NRI project “Functional gene markers for Rosaceae tree fruit texture”

Co-PIs and participants of SCRI project “RosBREED: Enabling marker-assisted breeding in Rosaceae”

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Washington Tree Fruit Research Commission

USDA
United States Department of Agriculture
National Institute of Food and Agriculture

NIFA

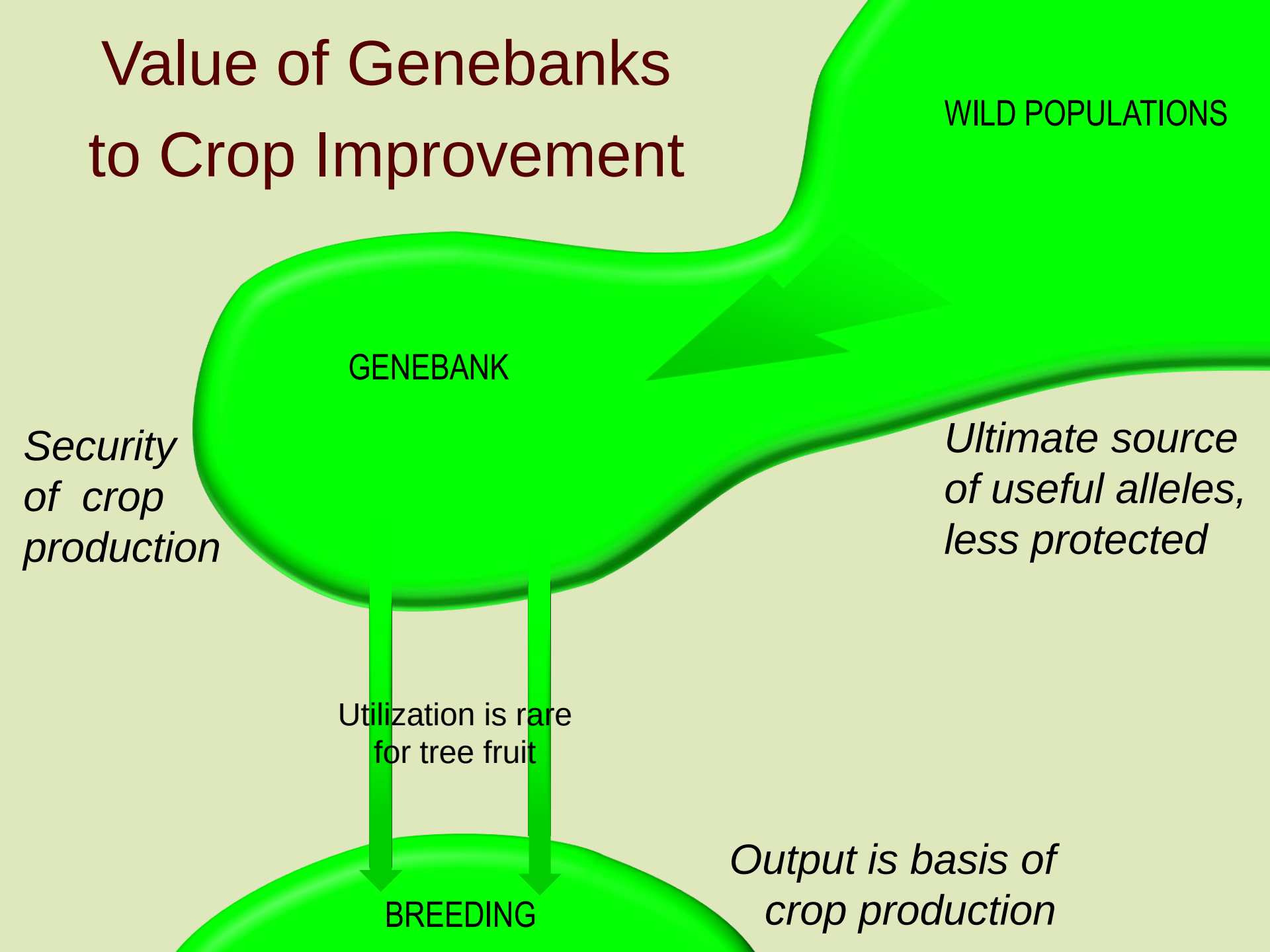
Outline of Presentation

- Value of Genebanks to Crop Improvement
- Think Like a Breeder
- Segregating Descendant Germplasm
- Comprehensive & Standardized Performance Information
- Performance-Predictive DNA Information
- Genebanks as Conduits to Utilization

Value of Genebanks to Crop Improvement

Pullman
Corvallis
Aberdeen
Davis
Ft. Collins
Parlier
Riverside
Ames
Urbana
Sturgeon Bay
Geneva
Columbus
Beltsville
Washington
Stuttgart
College Station
Mayaguez, PR

Value of Genebanks to Crop Improvement



Value of Genebanks to Crop Improvement

- Allelic diversity is not useful if not used
- Primary users for crop improvement = BREEDERS
- Encourage utilization by breeders!


Think Like a Breeder

Think Like a Breeder

Select parents

Cross

Select seedlings

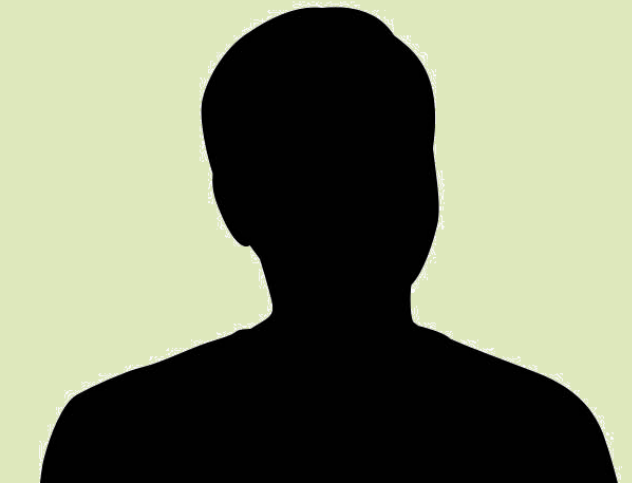
Release commercially

Think Like a Breeder

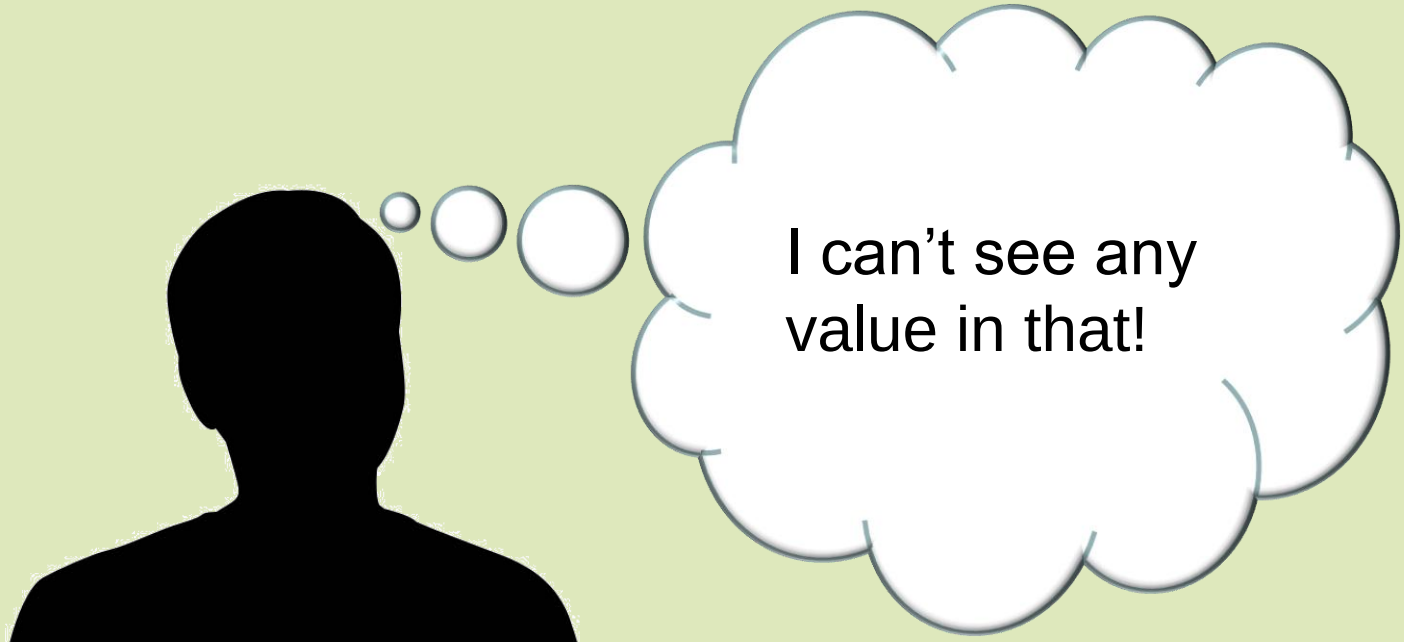
Select parents

Genebank accessions

Cultivars and selections



Think Like a Breeder



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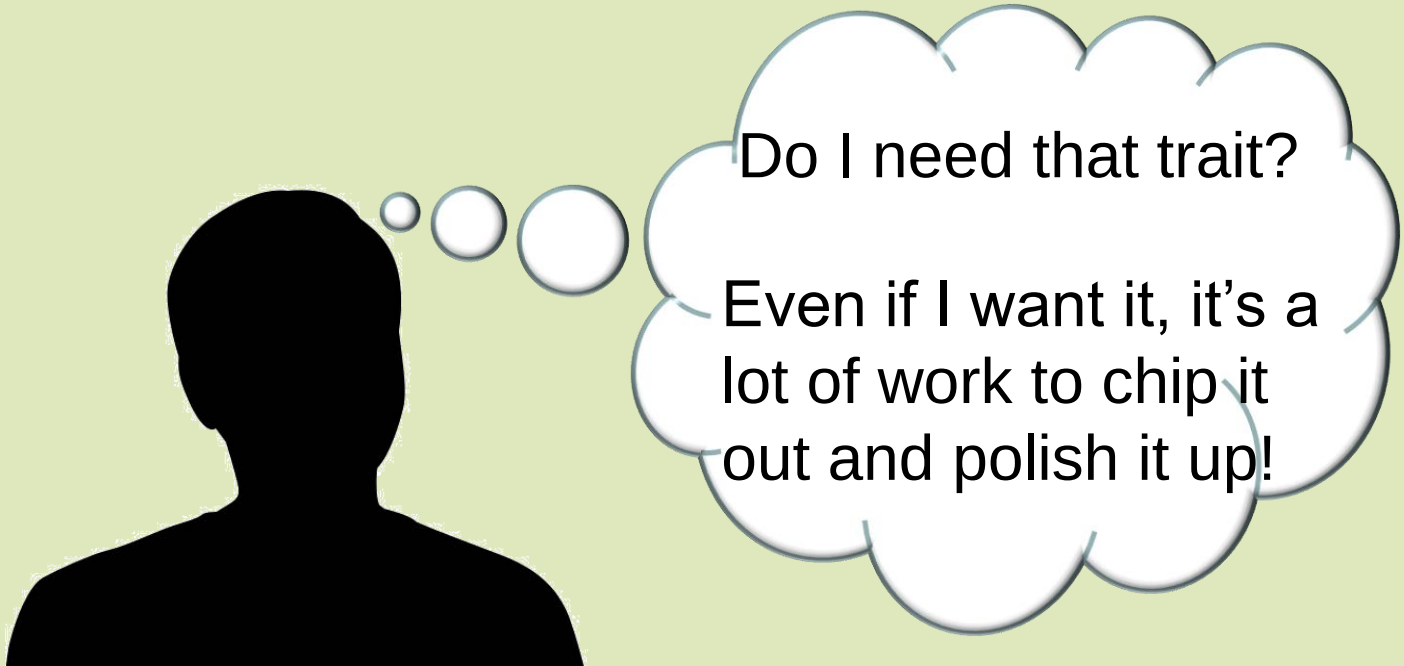
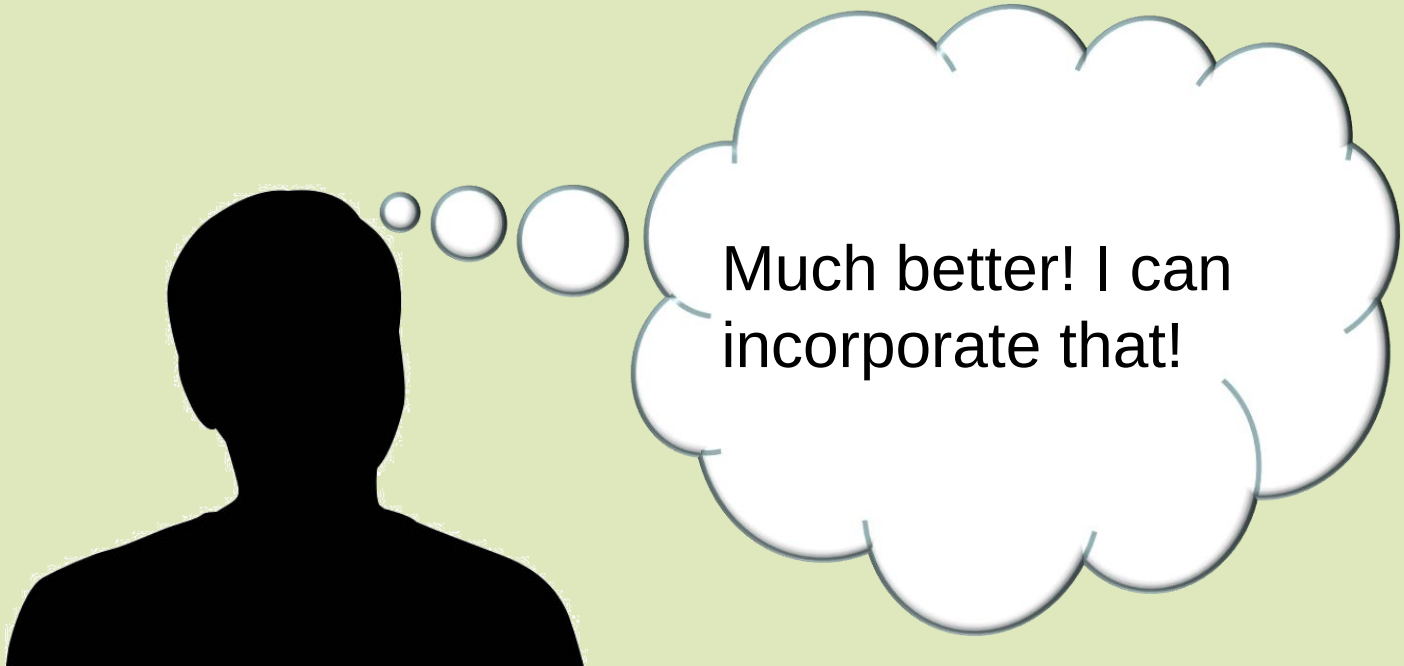


Think Like a Breeder



Think Like a Breeder

Select parents

Genebank accessions

Cultivars and selections

Think Like a Breeder

Select parents

Genebank accessions

Cultivars and selections

Think Like a Breeder

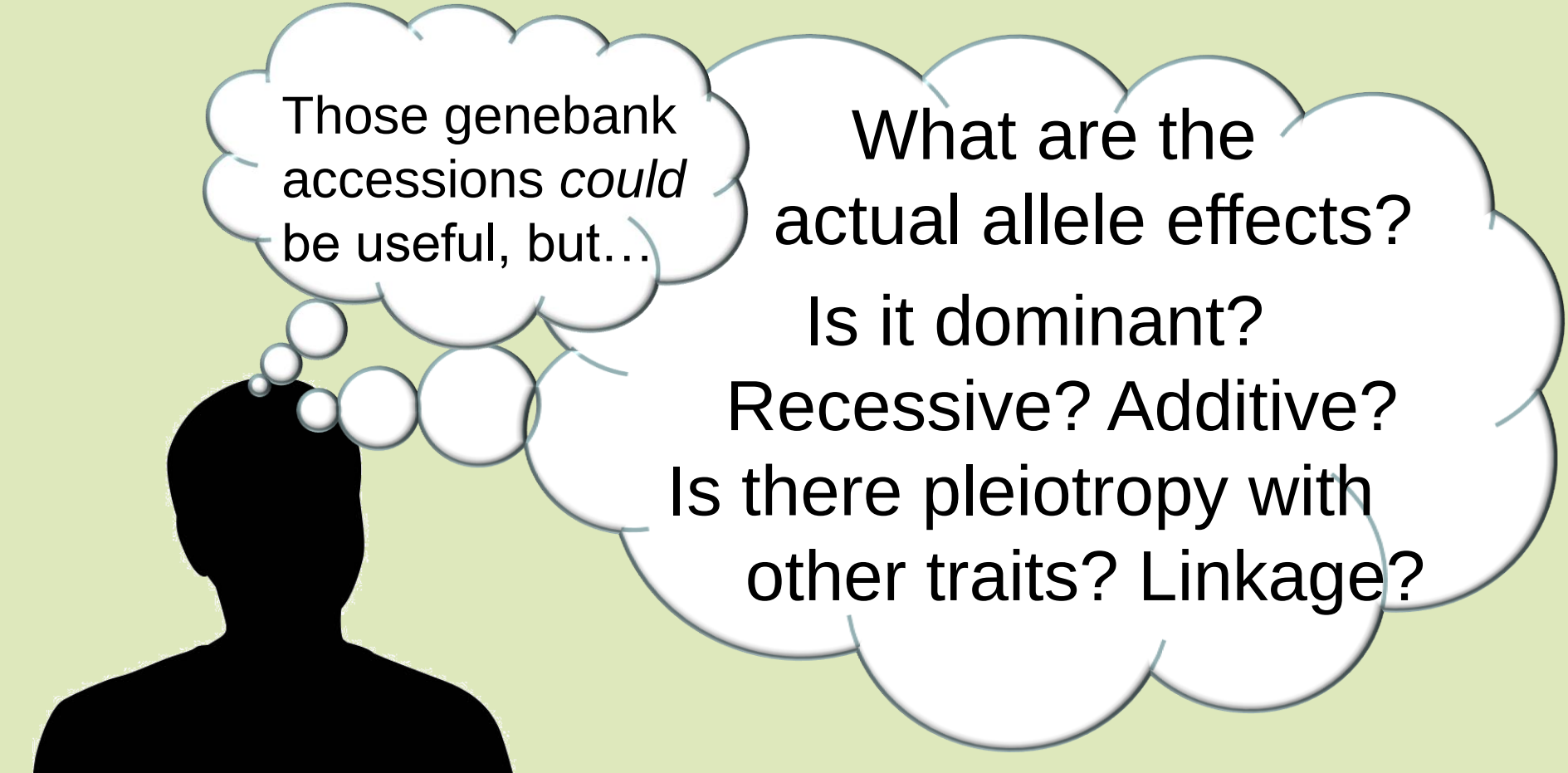
Select parents

Genebank accessions

Cultivars and selections

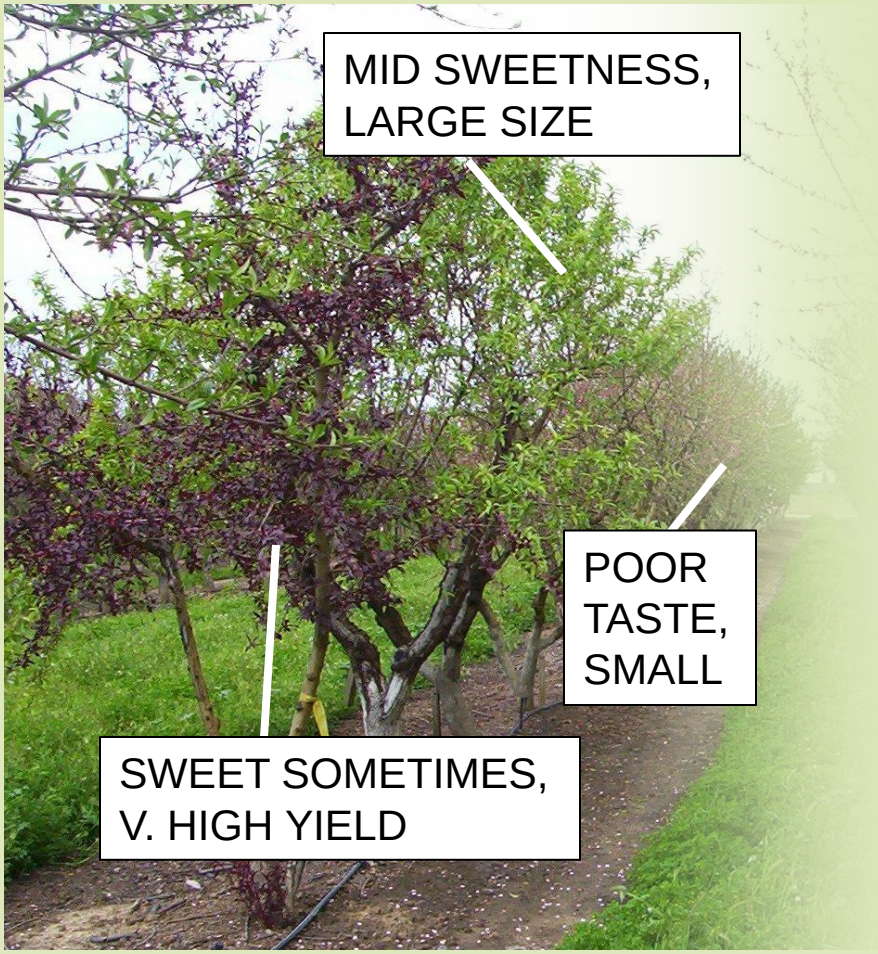
Think Like a Breeder

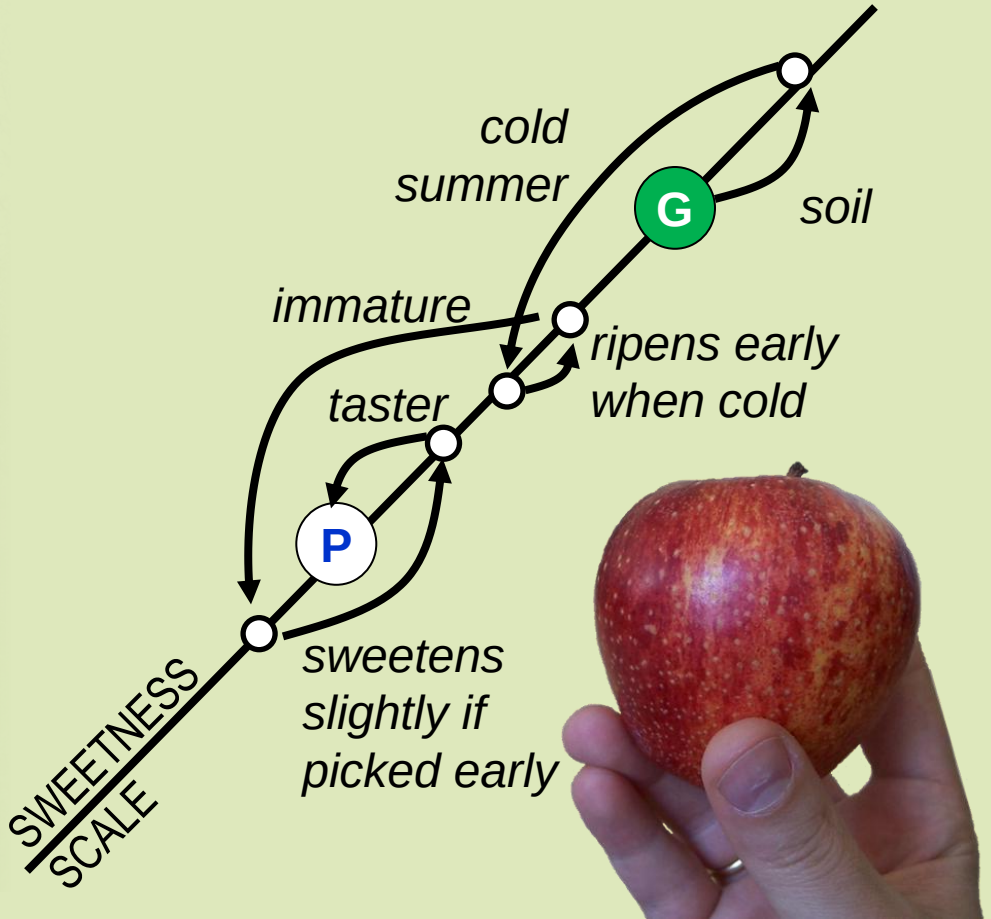
- To support “Use as parent/Ignore” decisions (and encourage “Use”), need to get into breeders’ heads!



Think Like a Breeder

- Phenotype is an incomplete predictor of underlying genetics





Think Like a Breeder

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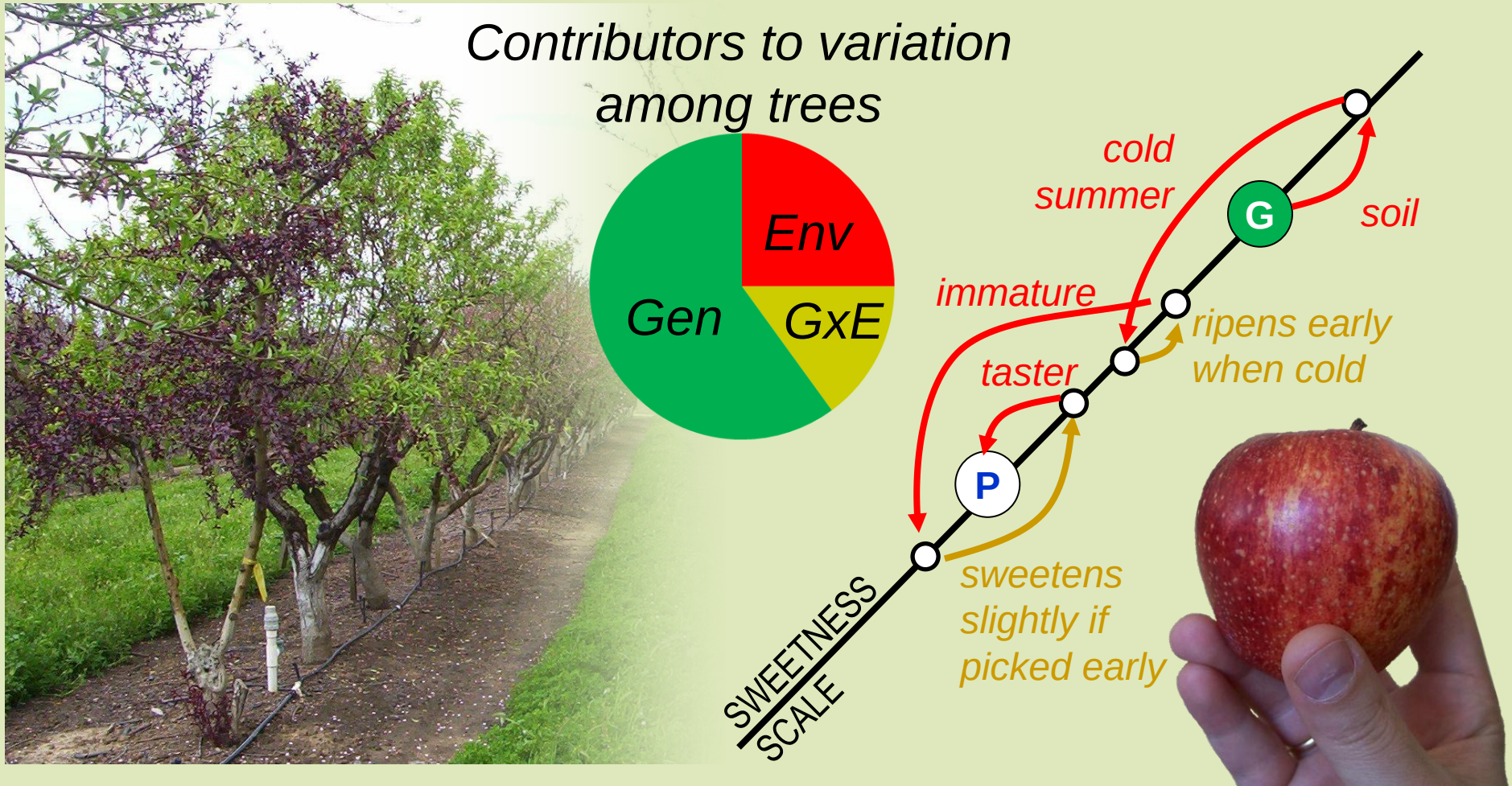
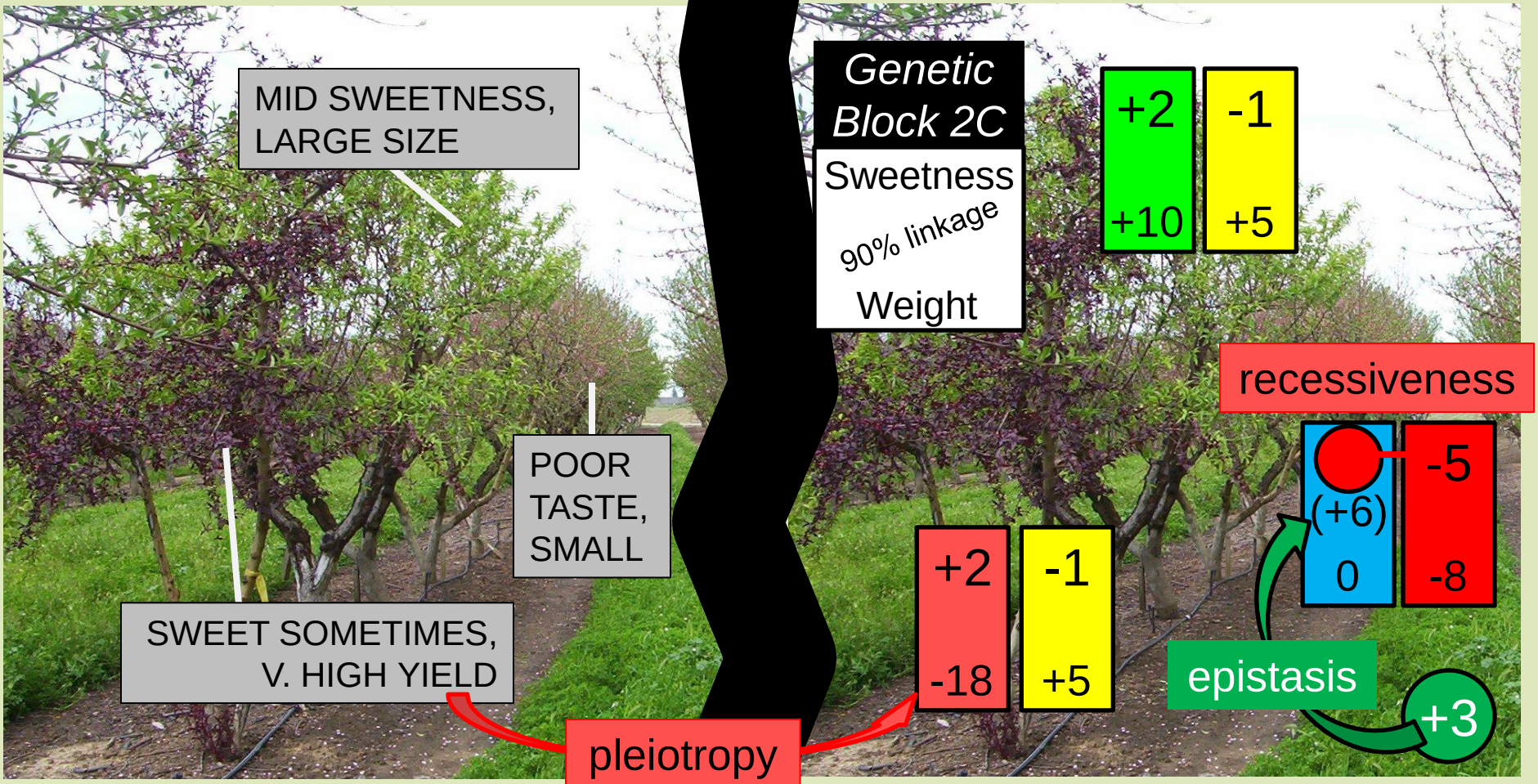


Think Like a Breeder



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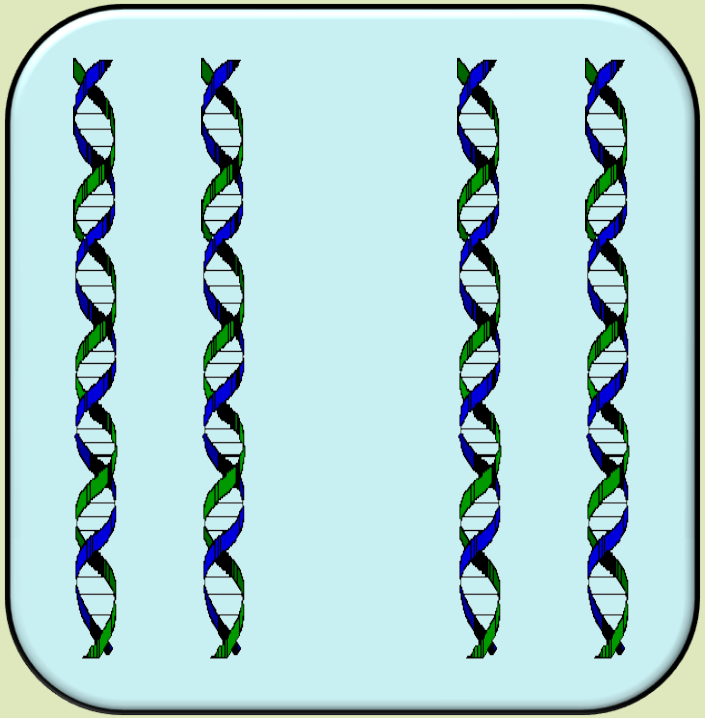
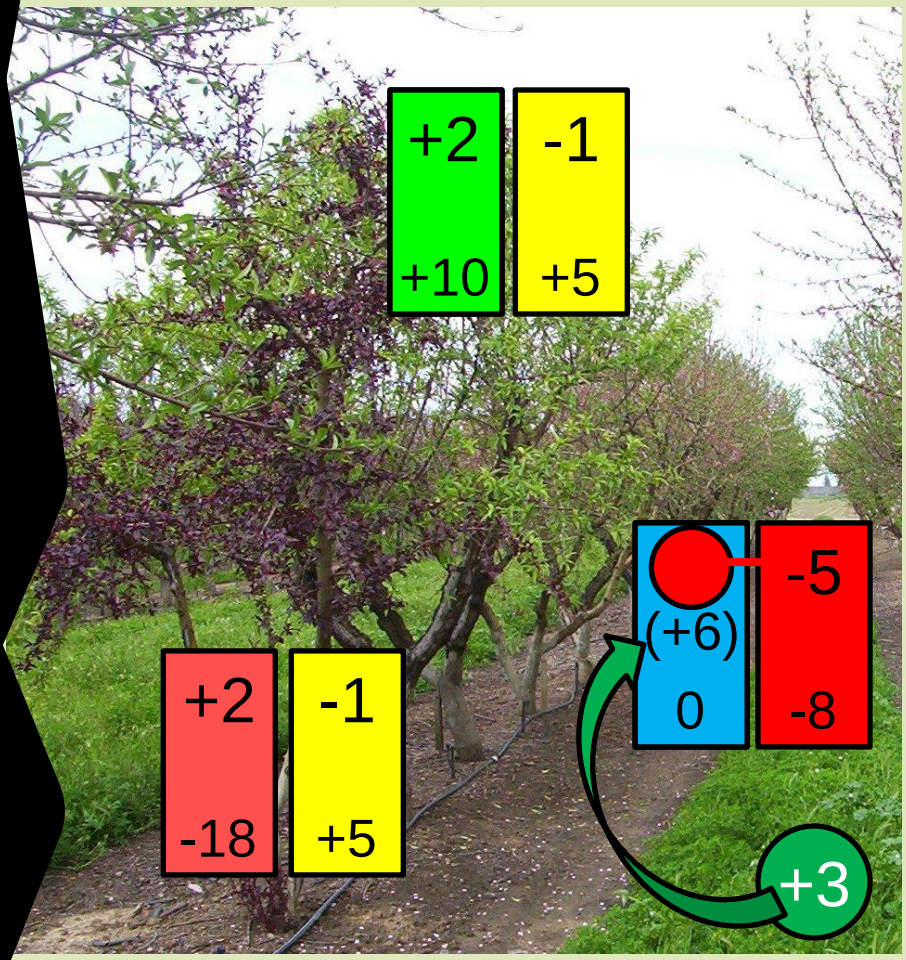
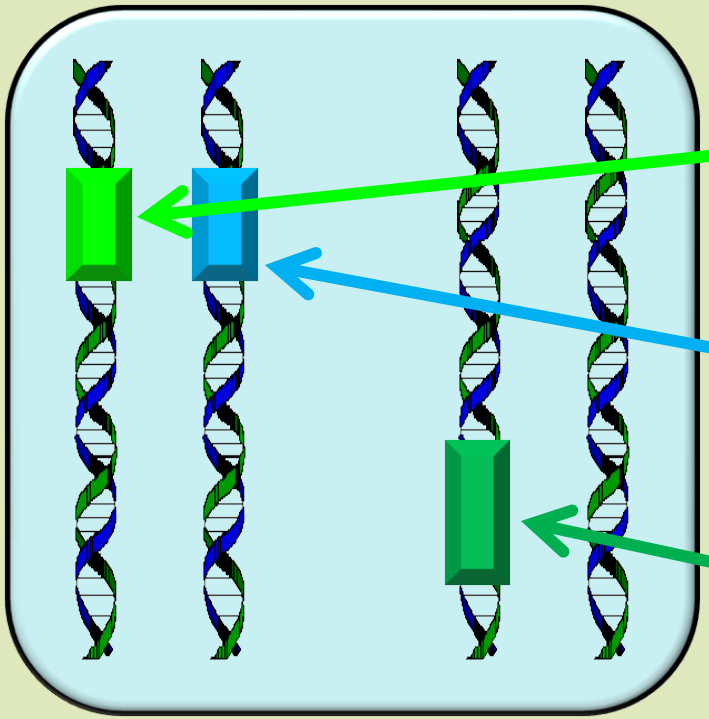


Breeders' optimal view



Think Like a Breeder

Putting the jewels together…



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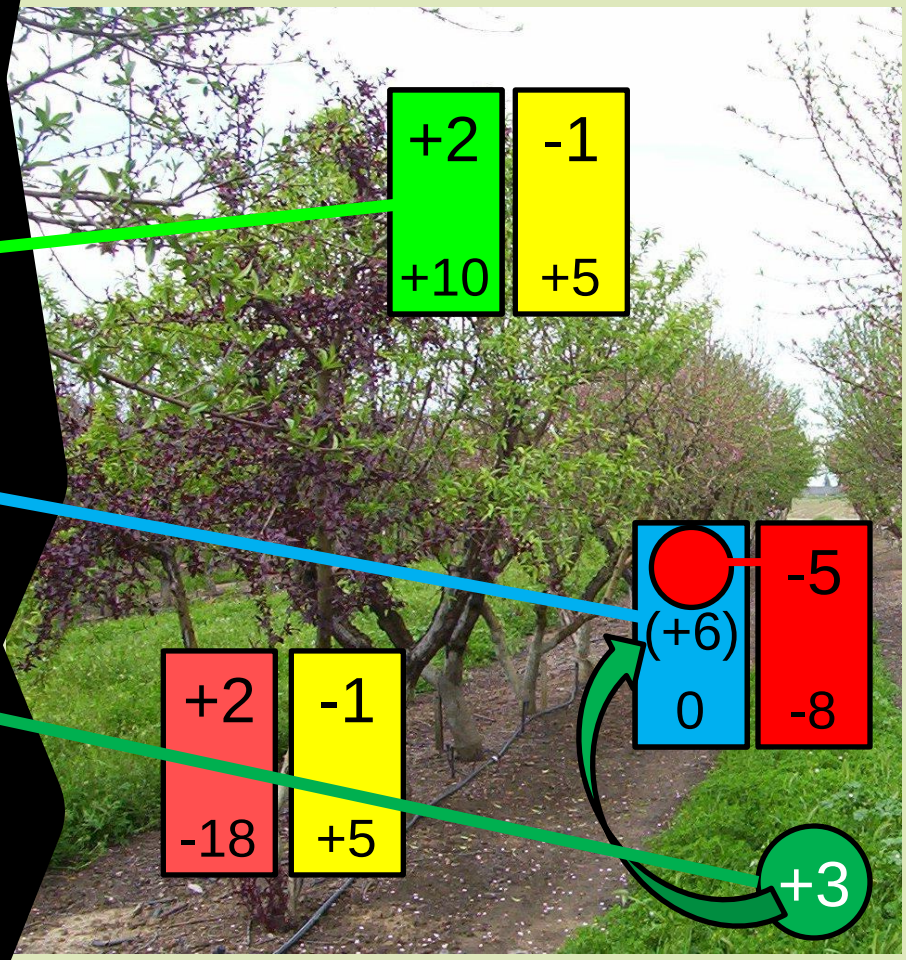
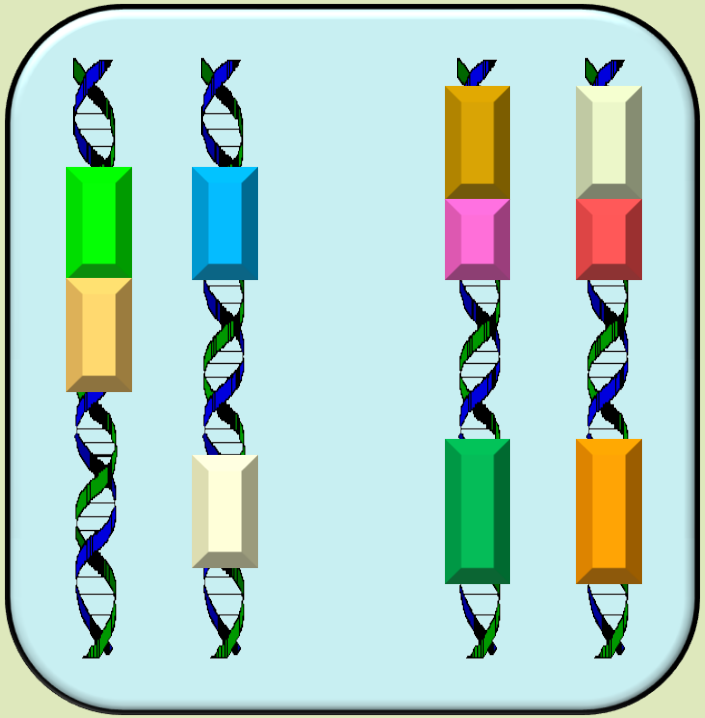


Think Like a Breeder

Putting the jewels together…



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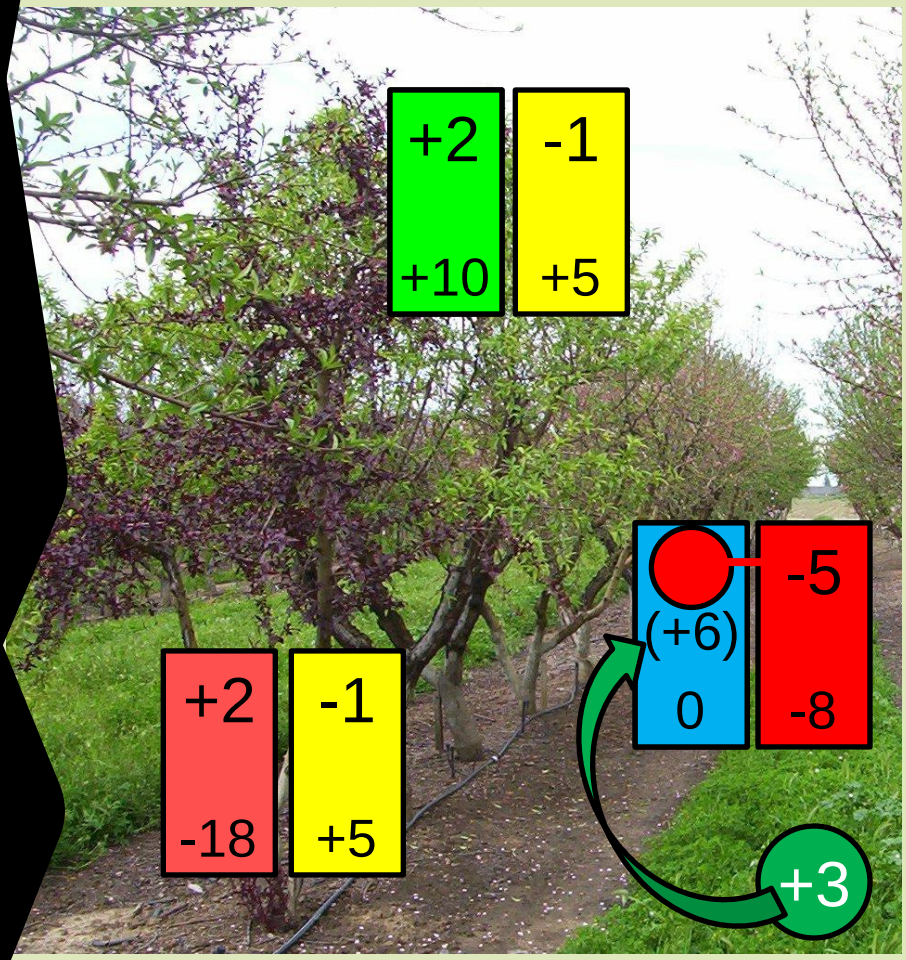



Provide
Segregating
Descendant Germplasm

Provide Segregating Descendant Germplasm

1. Marker-trait association approaches require enough contrasting individuals for statistical power

e.g. Red flesh and the *MYB10* gene in apple

✓ F_1 mapping population: 516 seedlings

✓ NPGS genebank: >50 accessions (>30 red)

(red-flesh allele dominant)

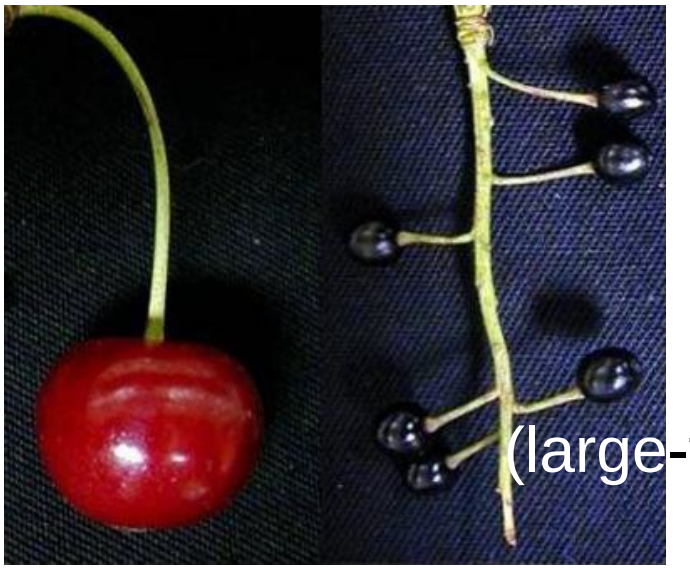
Plant & Food RESEARCH
RANGAHAU AHUMĀRA KAI

Provide Segregating Descendant Germplasm

2. Cryptic alleles – not detected by phenotype

If favorable allele is recessive or epistatic, then
- not detected, or
- mistaken for dominance or additive effect

Typical cultivar | Wild forest cherry



e.g. Fruit size in sweet cherry

QTL study found a tiny-fruited wild cherry accession contains common large-fruit allele at major locus

(large-fruit allele masked by another locus)

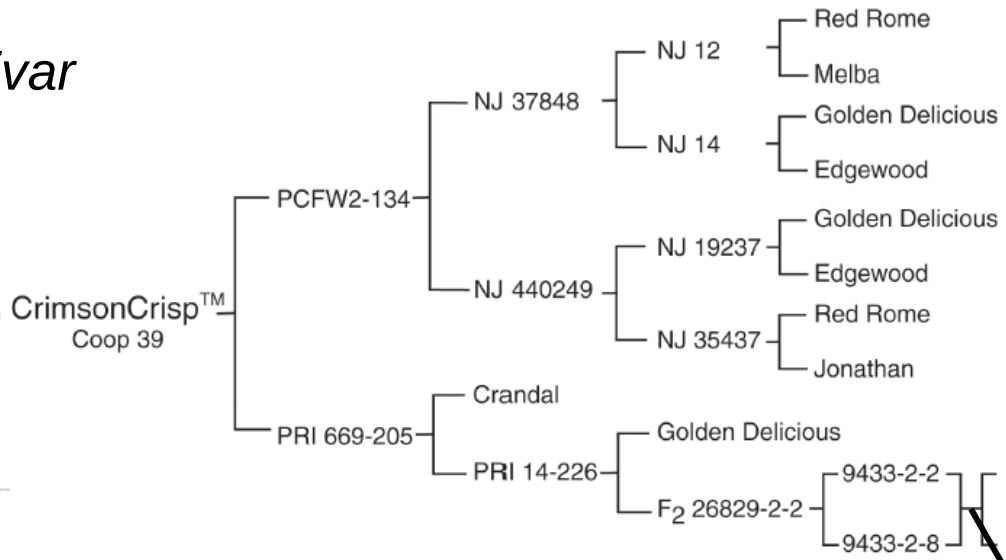
MICHIGAN STATE UNIVERSITY

Provide Segregating Descendant Germplasm

3. Wild germplasm, even if carrying wonderful alleles, is far from being cultivar-producing parents. *How can breeders rapidly respond??*

   e.g. *Malus floribunda*-derived disease resistance in apple

A modern cultivar



Scab-resistant wild relative

<- - - - - 5 generations

First cross made <1940

Disease Resistant Apple Breeding Program

Purdue University
Rutgers University
University of Illinois

Provide Segregating Descendant Germplasm

SOLUTION

- Genebanks need to have, or else energetically facilitate, availability of descendant segregating germplasm

→ *Enough contrasting individuals* } Useful alleles easier to find

→ *Reveal cryptic alleles* } Useful alleles easier to extract

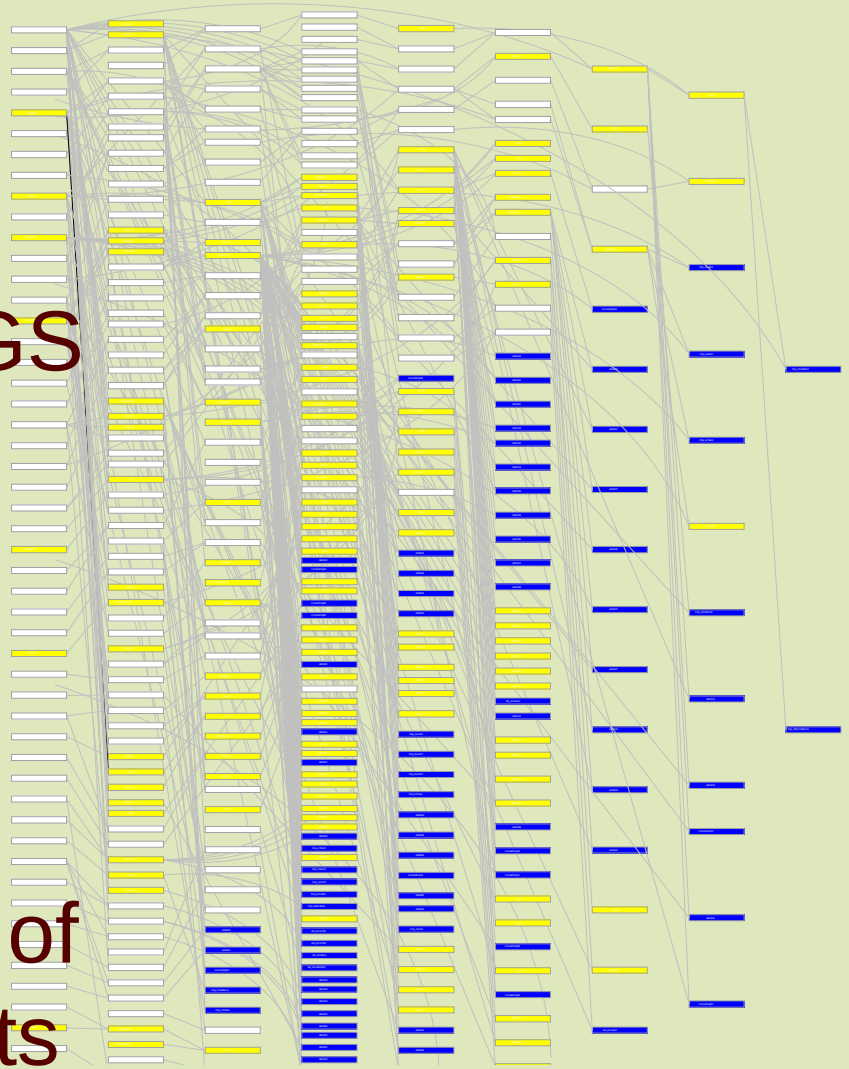
→ *Closer to elite*

Provide Segregating Descendant Germplasm

- RosBREED's reference germplasm set of apple merges breeding & NPGS

85	NPGS accessions
135	cultivars (breeding progs)
260	seedlings (breeding progs)

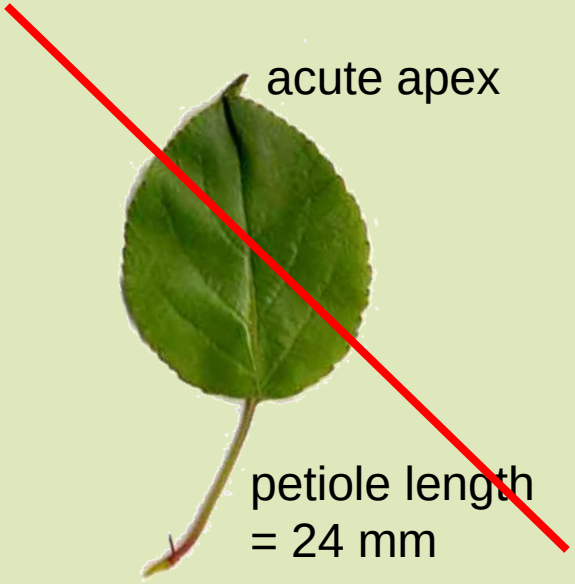
- NPGS accessions = ancestors. Allow joining of many populations in stats




Provide
Comprehensive & Standardized
Performance Information

Provide Comprehensive & Standardized Performance Information

- Phenotypic evaluation: performance, not descriptors



Firmness
– Instr, Sens

Crispness
– Instr, Sens

Juiciness
– Sens

Harvest date

Maturity

Fruit size

Sweetness

Acidity

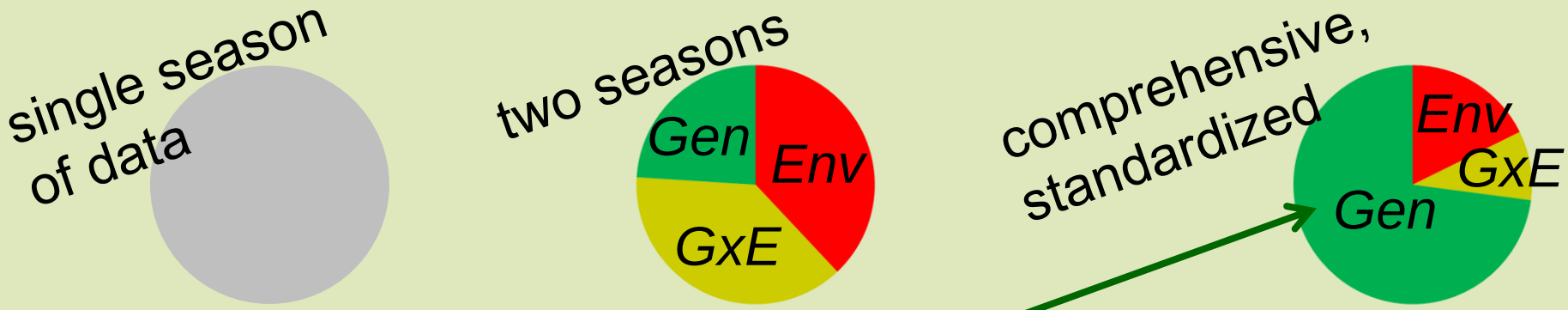
Internal ethylene conc

→ *Relevant to breeding*

Provide Comprehensive & Standardized Performance Information

- Excellent quality phenotypic information (and available in GRIN) is critical
  → *Reduces unpredictable components of performance*

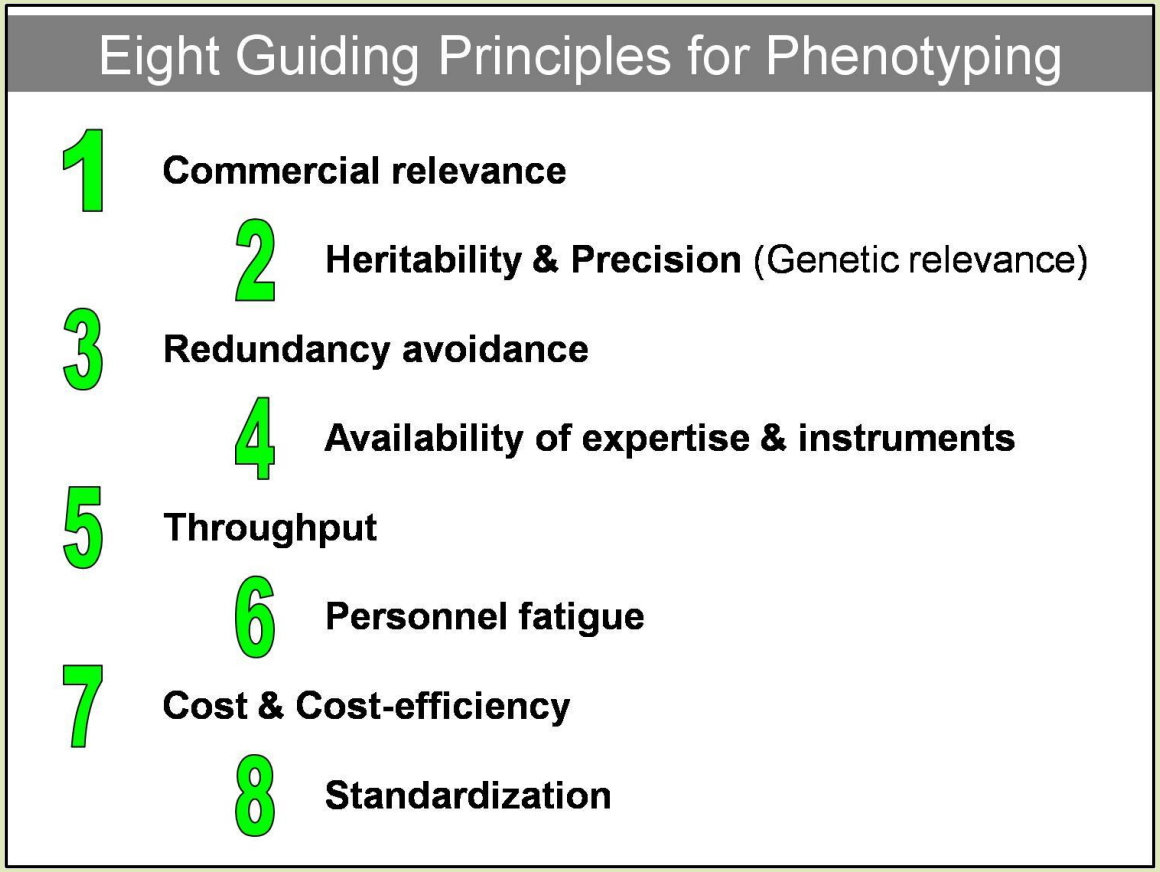
Contributors to variation among trees



…needed by researchers to develop excellent quality genetic tests for performance

Provide Comprehensive & Standardized Performance Information

- Standardized phenotyping for Rosaceae (led by Gayle Volk, USDA-ARS Fort Collins)



For:

- Genebanks
- Breeding programs
- Research programs

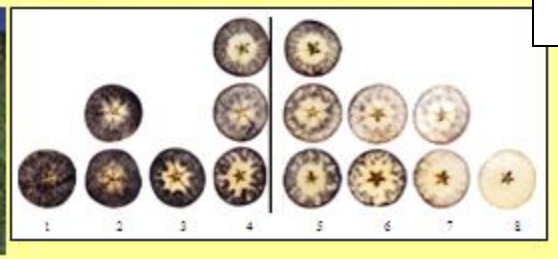
First presented at ASHS July 2009

Provide Comprehensive & Standardized Performance Information

- **Protocols**
  www.rosbreed.org/resources/fruit-evaluation/

Fruit Maturity and Harvest

- Check trees weekly for fruit color changes that indicate onset of fruit maturation – changes in background color (from green to cream or light yellow) and brightening in red blush color development.
- When the tree looks like it may be ready for the first harvest sampling, select 1-2 fruit with the most advanced maturity appearance and conduct a starch-iodine test. **Aim for a maturity indicator of SPI 3-5** on the 1-8 Cornell (Blanpied) Chart below (available at http://ecommons.library.cornell.edu/bitstream/1813/3299/2/Predicting%20Harvest%20Date%20Window%20for%20Apples.pdf) or **1.5-2.5 on a 0-6 starch pattern chart as a generic harvesting 'go date'**. This is equivalent to commercial harvest, and is a good intermediate range where it is unlikely for any trees to be too immature or over-mature.
- If the SPI indicates onset of maturation for a tree, visually evaluate the remaining fruit on the tree for their range in maturity. If ~50 % of the fruit have a 'harvest-mature' appearance (roughly similar to the SPI-tested fruit), take the sample of 15-40 fruit selectively picked to be at the correct harvest maturity. 15 fruit is minimum to cover all evaluation stages (5 fruit x 3 evaluation times), and extra fruit provides some backup in case of fruit rot in storage.



Free Stone continued

Rating of 5

Rating of 1

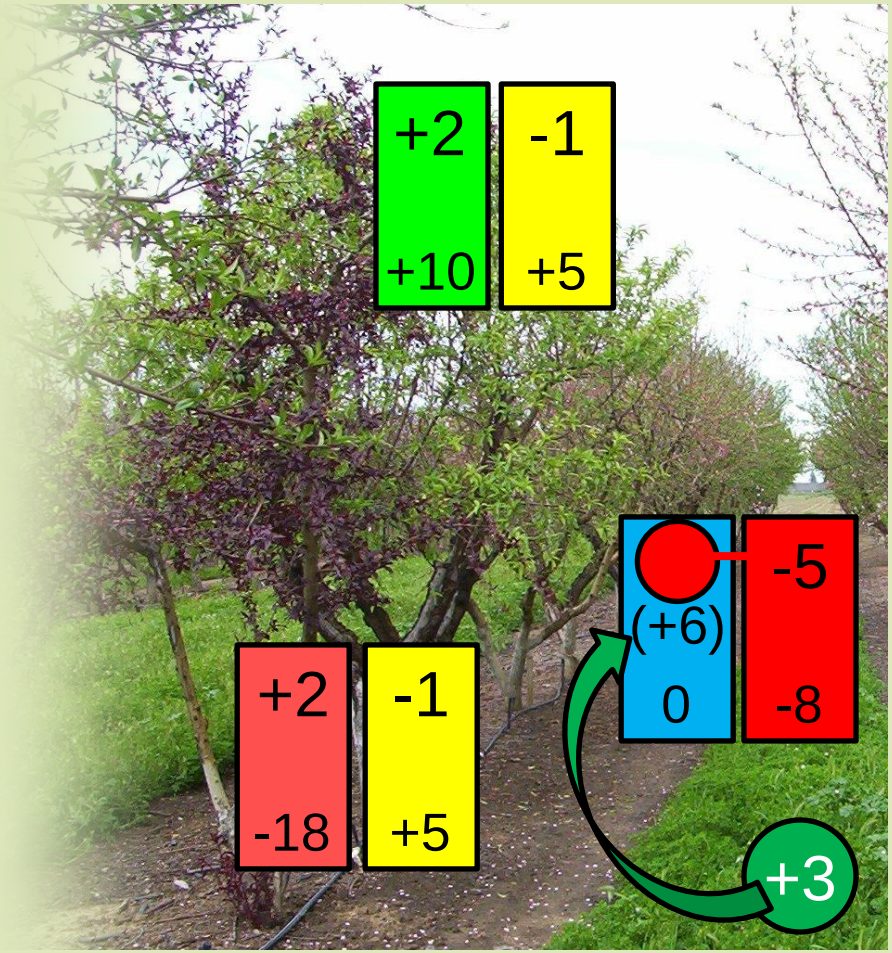
Crop Germplasm Committees: trait priorities -> + protocols?


Provide
Performance-Predictive
DNA Information

Provide Performance-Predictive DNA Information

- Research required to develop genetic tests that provide functional genotypes for valuable traits

Breeders' optimal view

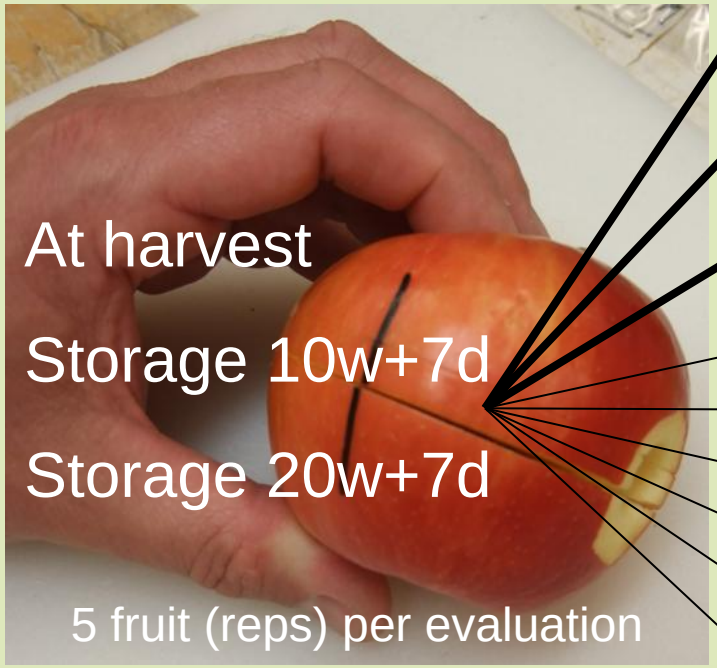


Provide Performance-Predictive DNA Information

- Target appropriate traits

Provide Performance-Predictive DNA Information

- Need excellent quality phenotypic data



Firmness – Instr, Sens

Crispness – Instr, Sens

Juiciness – Sens

Harvest date

Maturity

Fruit size

Sweetness

Acidity

Internal ethylene conc

Multiple harvests

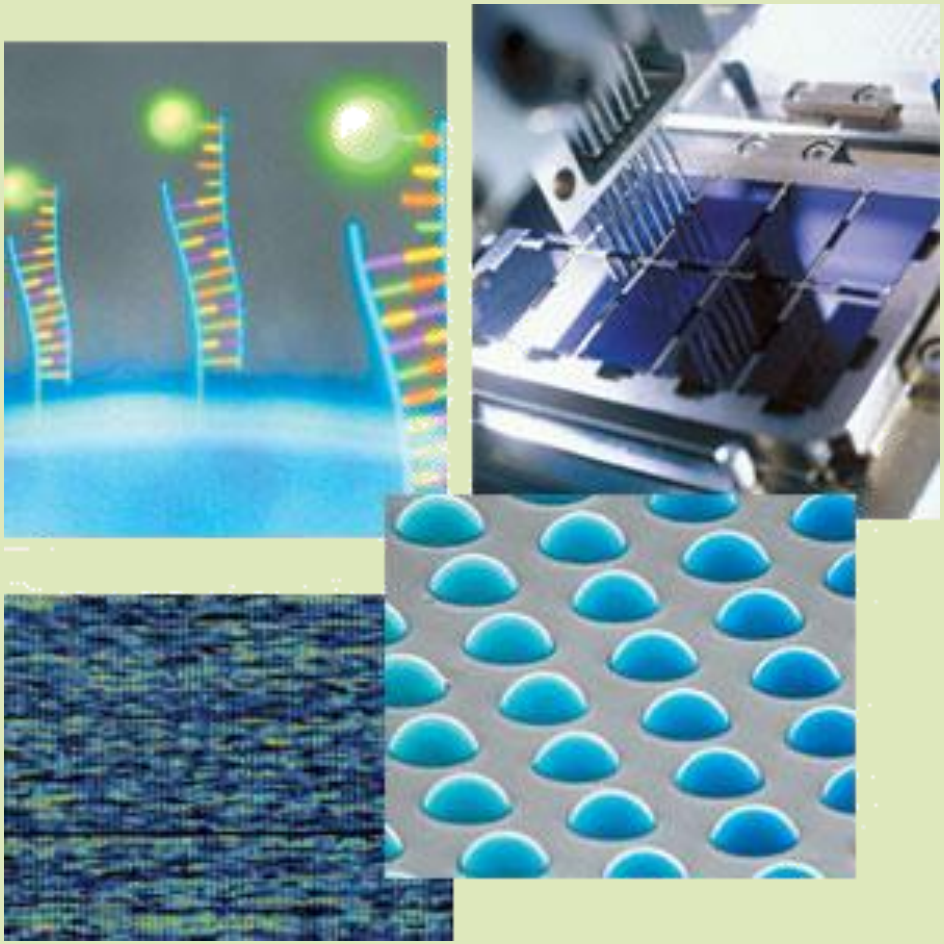
Multiple locations

Multiple years

Multiple tree reps

Provide Performance-Predictive DNA Information

- Need efficient DNA technologies



Provide Performance-Predictive DNA Information

- Need appropriate germplasm

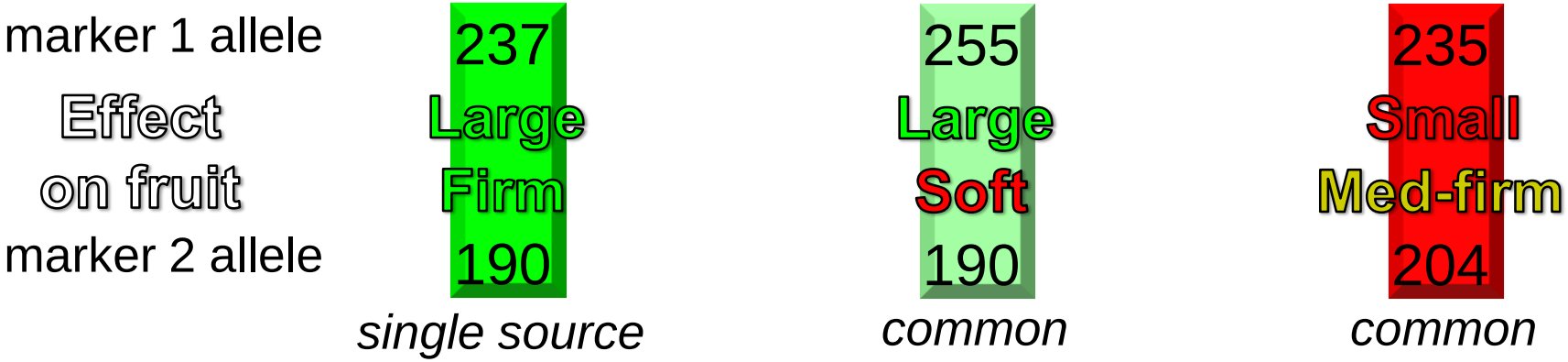
  → *Segregating descendant germplasm*

  - Associations are discovered and characterized in training set(s)
  - Then extrapolated to the rest of the crop – breeding material, repositories, wild populations

Provide Performance-Predictive DNA Information

- A jewel for sweet cherry

Some functional genotypes (haplotypes) in cultivars



single source *common* *common*

→ *Using already in breeding*

→ *Screening Davis Repository cherries*

- *further sources of the good haplotype?*
- *new useful haplotypes?*
- *tag bad haplotypes (avoid in introgression)*

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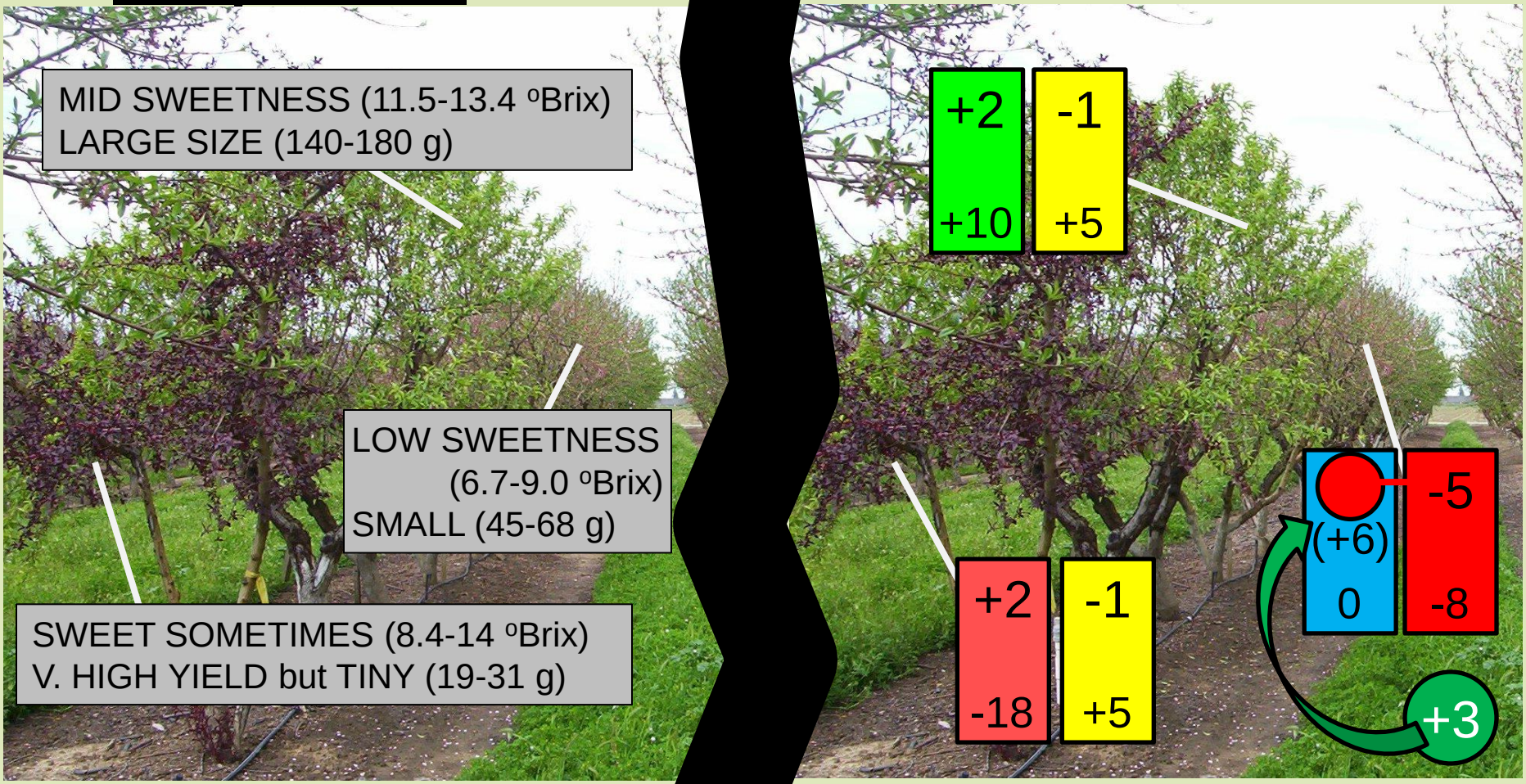
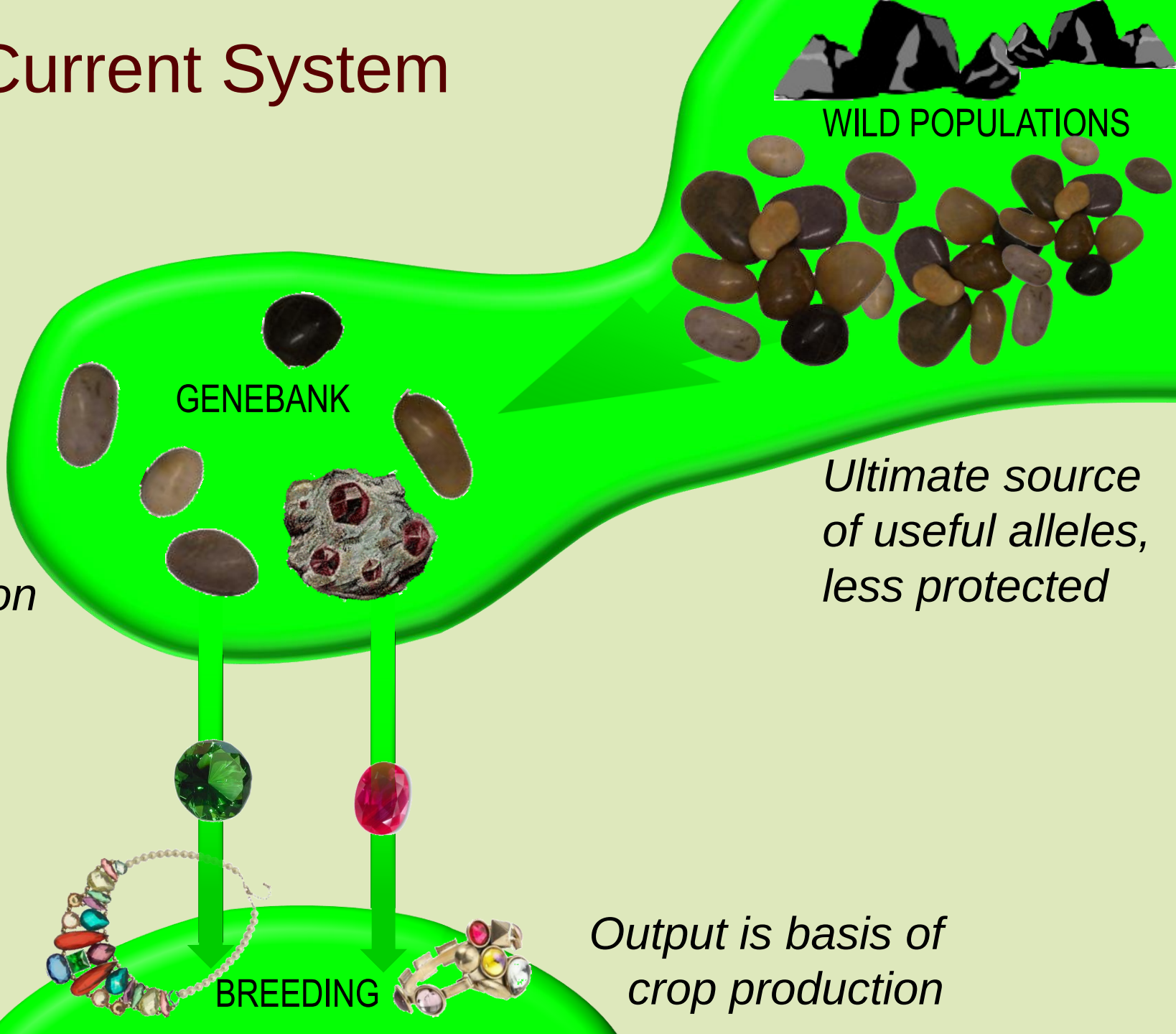
Provide Performance-Predictive DNA Information

→ *Replace this* *…with this*




Genebanks as Conduits
to Utilization

The Current System



Security of crop production

Ultimate source of useful alleles, less protected

Output is basis of crop production

4. Provide performance-predictive DNA information

WILD POPULATIONS

GENEBANK

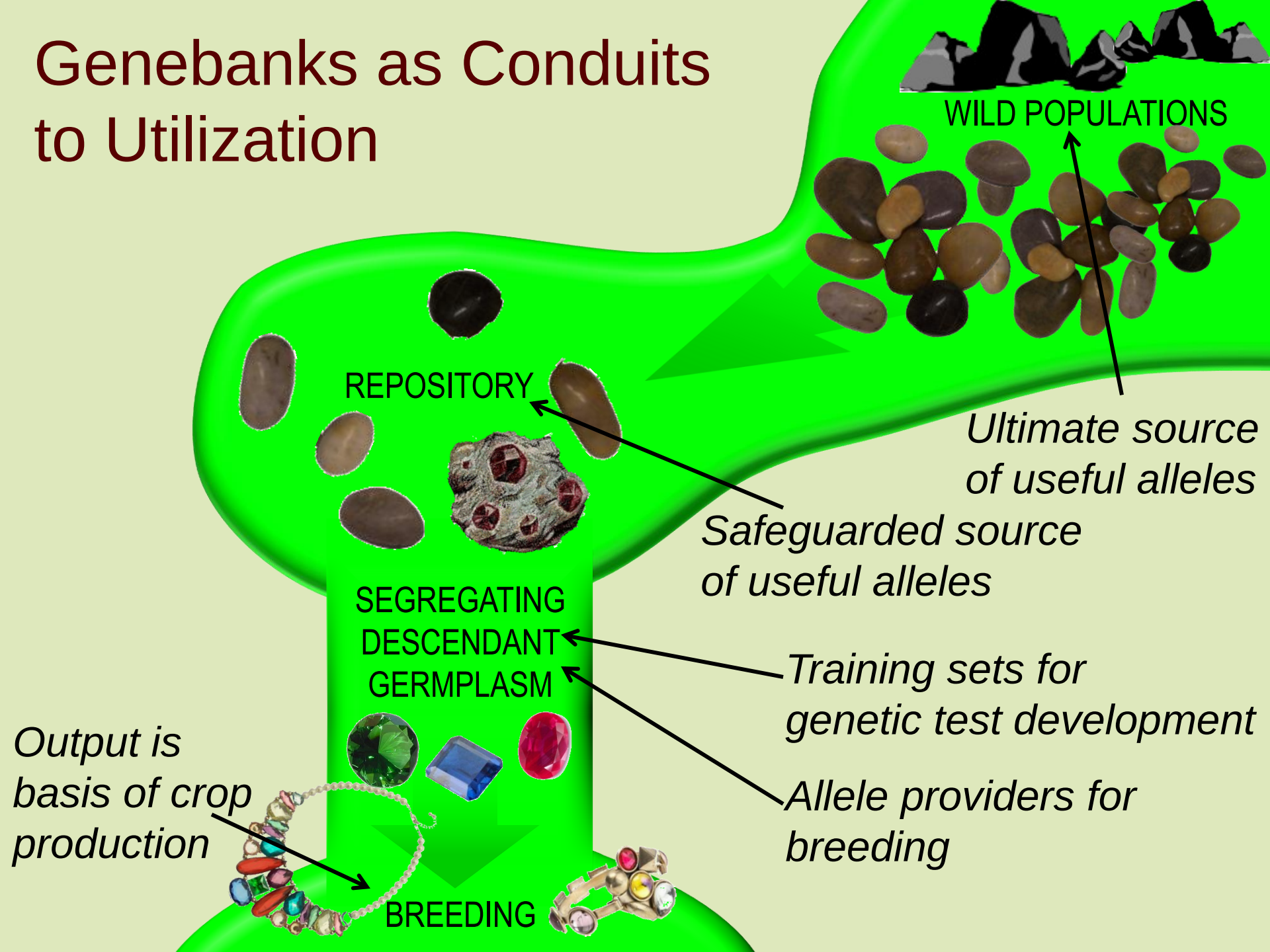
2. Provide segregating descendant populations

3. Provide comprehensive & standardized performance information

1. Think like a breeder

BREEDING

Genebanks as Conduits to Utilization



Genebanks as Conduits to Utilization

WILD POPULATIONS

REPOSITORY

BREEDING

SEGREGATING
DESCENDANT
GERMPLASM