RosBREED

Enabling marker-assisted breeding in Rosaceae

RosBREED's approach to bridging the gap between genomics knowledge and breeding application.

Amy Iezzoni
Project Director & Tart Cherry Breeder
www.rosbreed.org

NIFA

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

Our Dream

Ultra-crisp tasty apples
sweet juicy peaches
flavorful cherries
luscious strawberries

Consistent quality, available & affordable

Enjoyed by consumers, regularly

Sustainably produced throughout the U.S.

Our Vision

Integration of modern genomics tools with traditional breeding approaches will transform crop improvement in Rosaceae, significantly improving profitability and sustainability of U.S. rosaceous crop industries & contribute to the increased consumption and enjoyment of these fruit, nut and floral products.

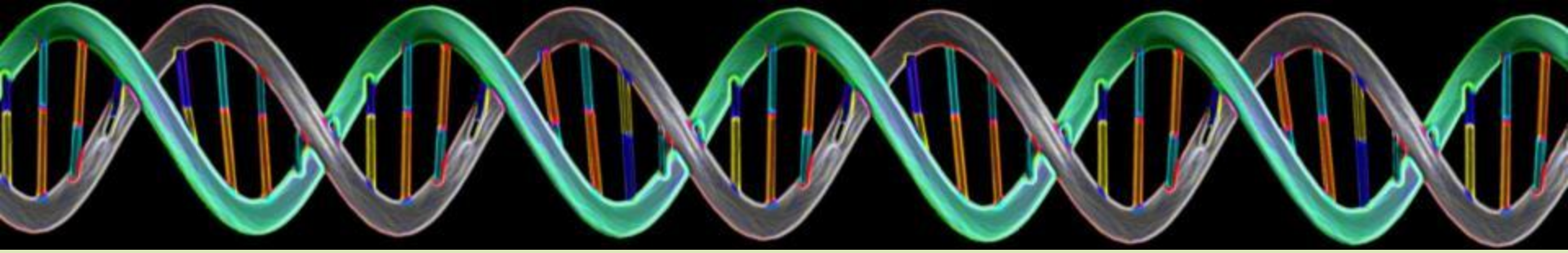
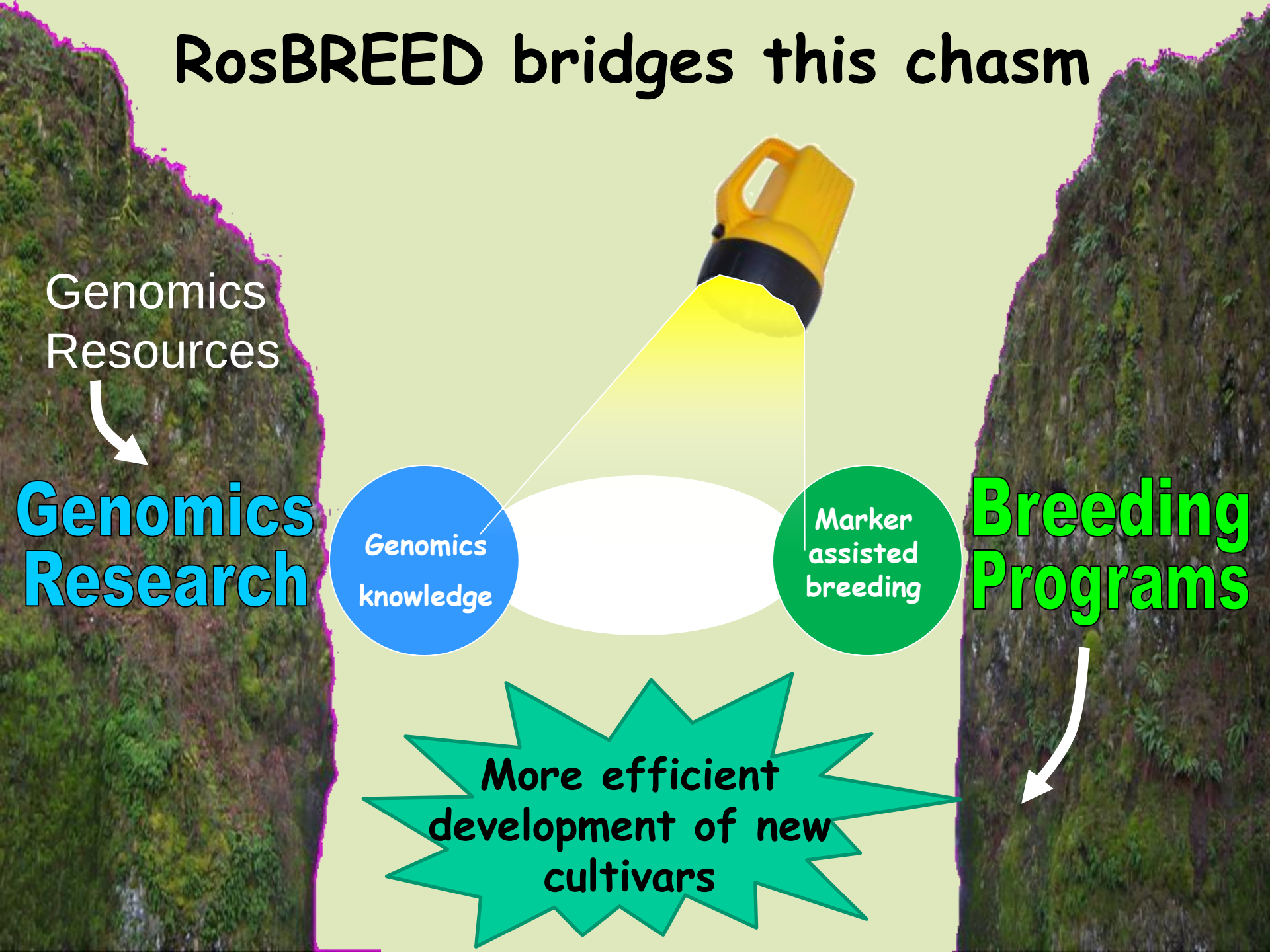


Image courtesy of NSF

Why now?
Apple, peach & diploid strawberry genome sequences are available!

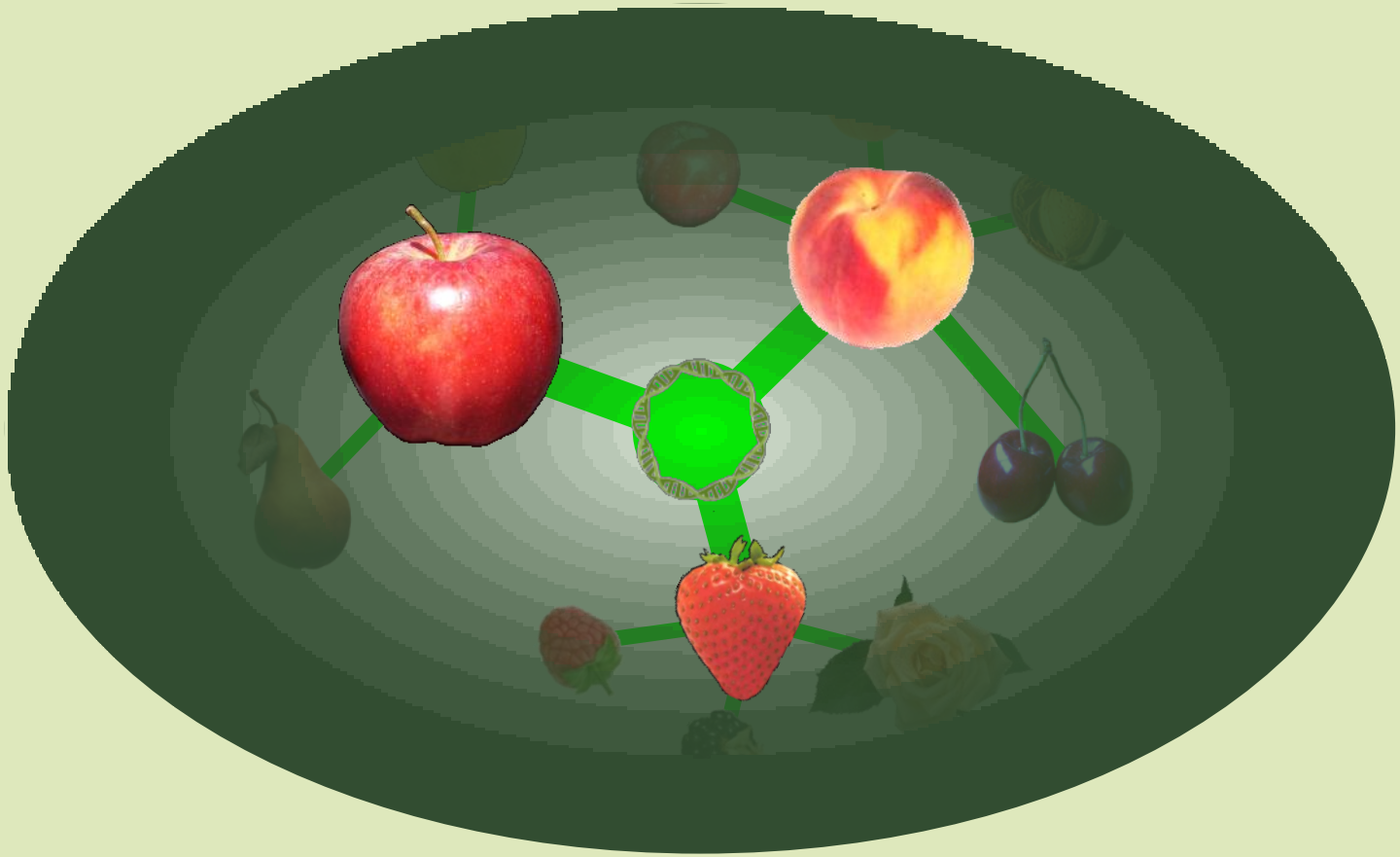
Images courtesy of www.beakandskiff.com, www.ehow.com, Jim Hancock

RosBREED bridges this chasm



Rosaceous Crops Included in RosBREED

Five crops were selected for this initial project: apple, strawberry, peach and sweet & tart cherry.



IMPACT: Focus on fruit quality: Demand from consumers and processors for premium cultivars.









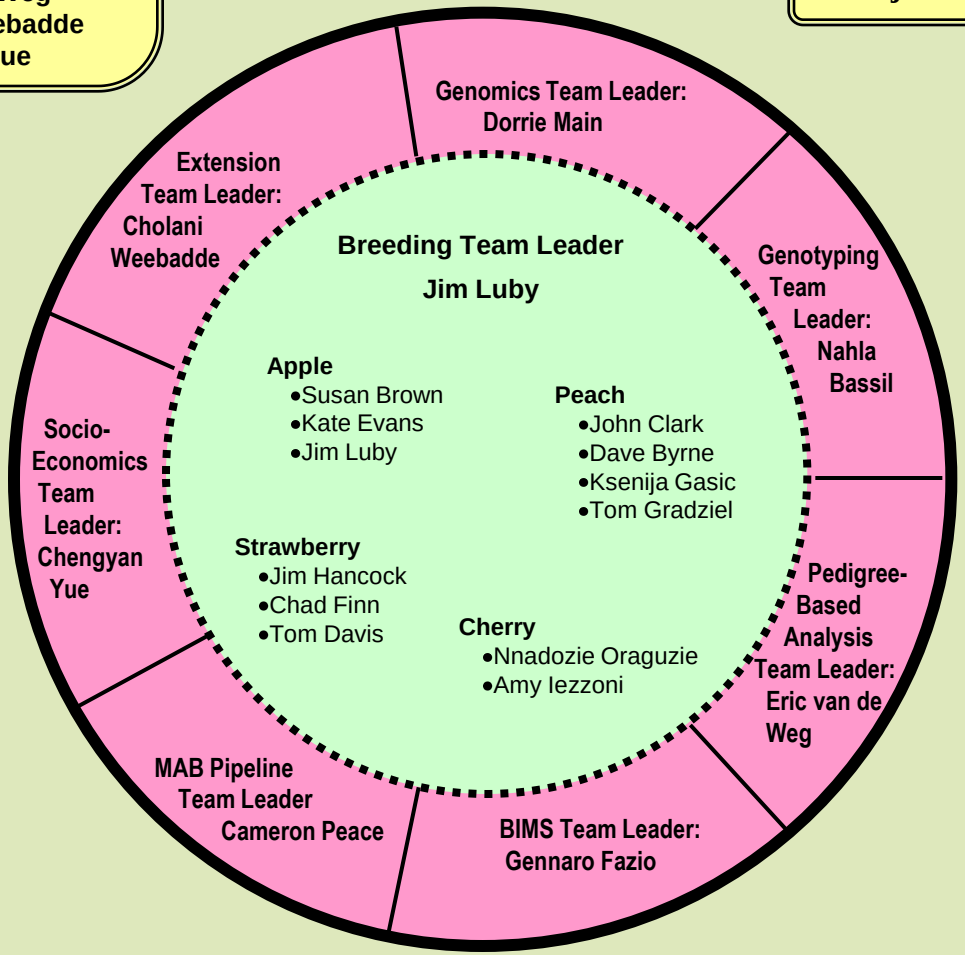



RosBREED Organization

Executive Committee
- Cameron Peace
- Nahla Bassil
- Gennaro Fazio
- Jim Luby
- Dorrie Main
- Jim McFerson
- Eric van de Weg
- Cholani Weebadde
- Chengyan Yue

Project Director
Amy Iezzoni

Project Assistant



RosBREEDs International Partners.

Plant Research Intl., NL
East Malling Research, UK
INRA – Bordeaux, Avignon & Angers
CRA-FRU Rome

Andres Bello University, Chile
ARC, SA
Plant & Food Research, NZ

MISSION STATEMENT

We will develop and apply marker-assisted breeding, based on improved knowledge of industry value and consumer preferences, to accelerate and increase the efficiency of rosaceous cultivar release and successful cultivar adoption.

Amy Iezzoni, Michigan State Univ
Cameron Peace, WA State Univ

4 yrs
$7.2M federal
$7.2M matching

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

This project is supported by the Specialty Crops Research Initiative of USDA's National Institute of Food and Agriculture

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Overview of RosBREED deliverables

Market trait values assessed from:	Germplasm data sets (Crop Reference Sets):	Enabling technologies
* Breeders * Market Intermediaries * Producers * Consumers	* Plant material * Phenotypic data * Genotypic data	* Statistical software * Genotyping platforms * MAB Pipeline

Trait and Market Class Breeding Target Establishment





Use knowledge of trait values & preferences from

producers, processors, & consumers

to prioritize breeder targets so that new cultivars will be more quickly accepted and have an enhanced commercial and consumer impact.

Trait Impact: Focus on fruit quality

Target trait selection: utilize improved knowledge of industry value & consumer preferences.

Are red fleshed peaches & nectarines high priority breeding targets?
Would this fruit type have value in the marketplace?
What is the economic weight for this fruit color trait?

Photos courtesy of Dr. Byrne (nectarine & peach)

What trait is my next breeding target?

We like disease resistant apple trees!

We like firm tart cherries that pit well!

I like tasty strawberries!

Breeder survey 2010

Producer survey Fall 2011/Winter 2012

Market Intermediary survey Fall 2010

Household data analysis 2010
Consumer survey 2012

RosBREED's Socio-Economics Team will determine trait values

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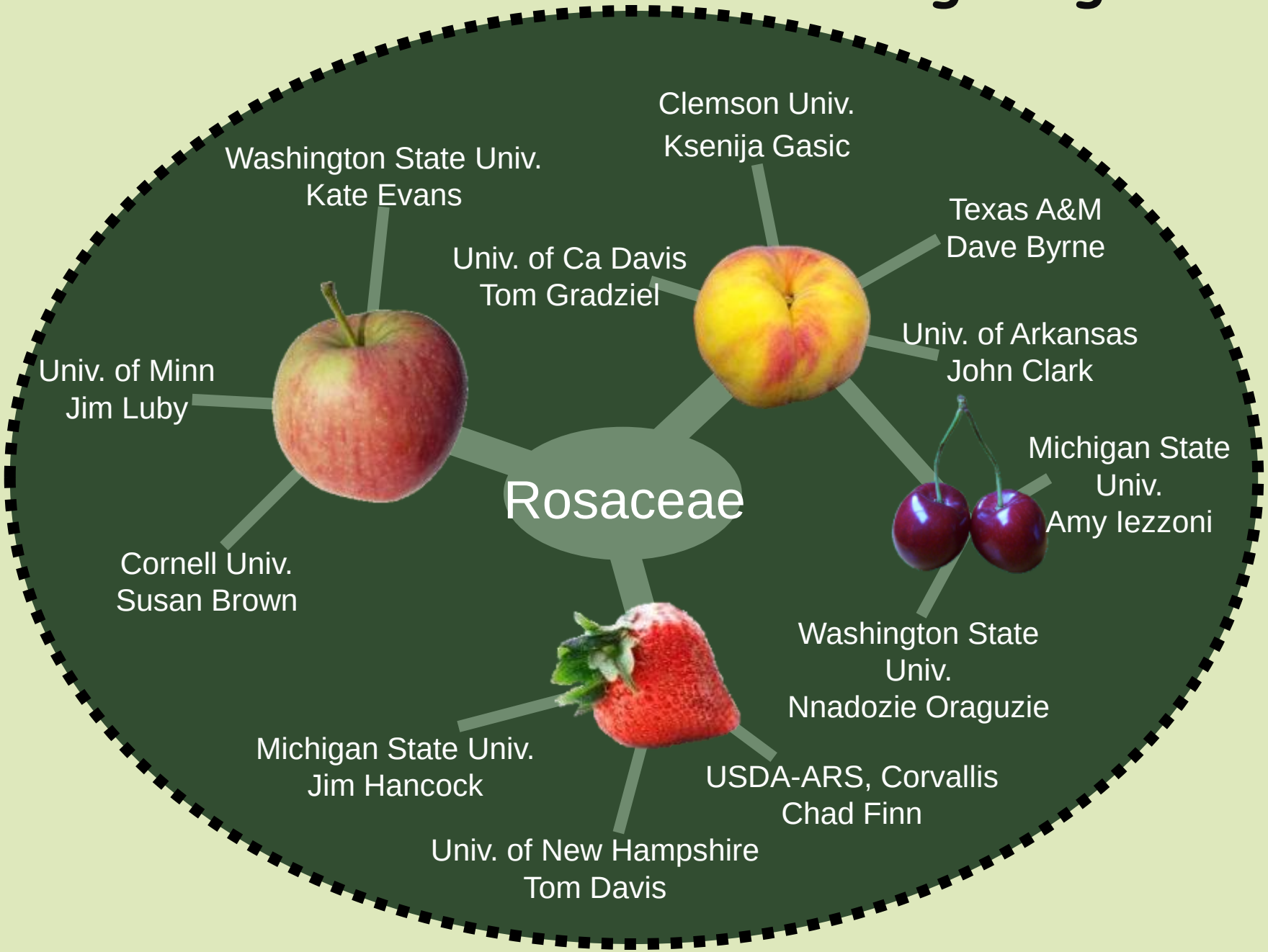
RosBREED Demonstration Breeding Programs



Plant Material

Develop crop sets that represent the parental allele diversity across multiple breeding programs.

Crop Reference Sets




Crop Reference Sets

- 480 individuals (cultivars, ancestors, founders, breeding selections and seedlings) that fruit in 2010-2012
- Genotyped genome-wide with SNP markers & phenotyped for fruit quality traits and other high-impact traits.
- Enable efficient validation and utility assessment of Marker-Locus-Trait associations
- Resource for common benefit

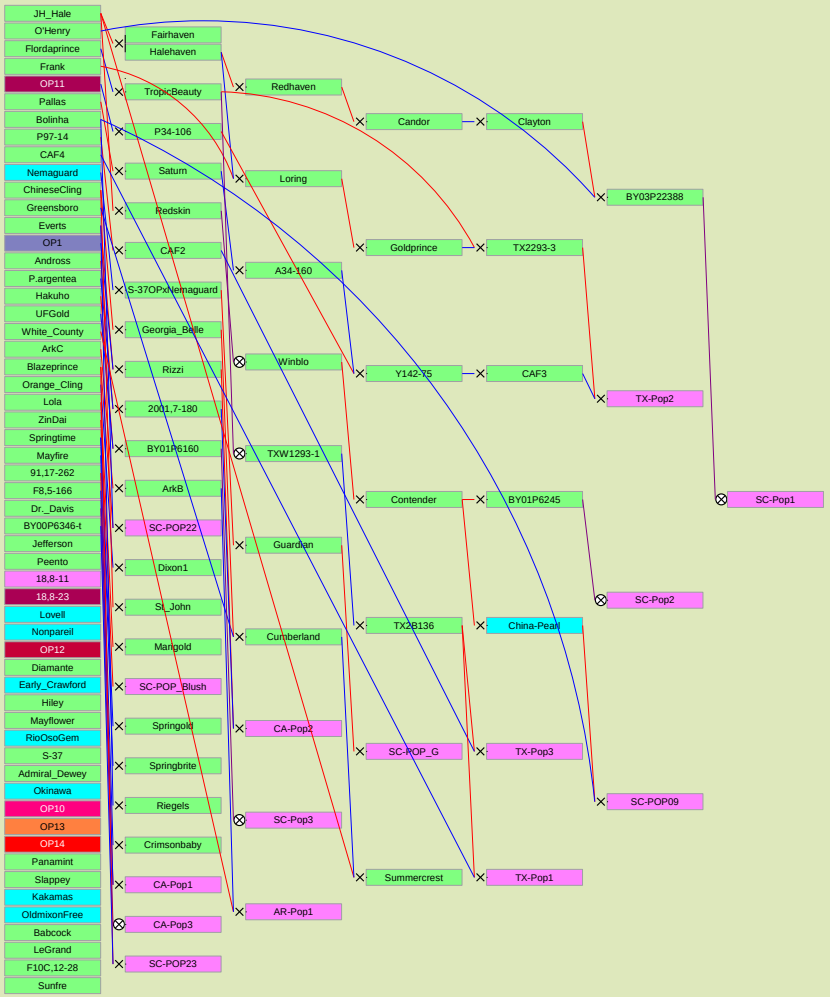
Peach Crop Reference Set

- 4 Breeding programs
  - Limited overlap of germplasm between market types

- 118 cultivars and selections

- 373 progeny in 23 crosses

- Up to 11 generations

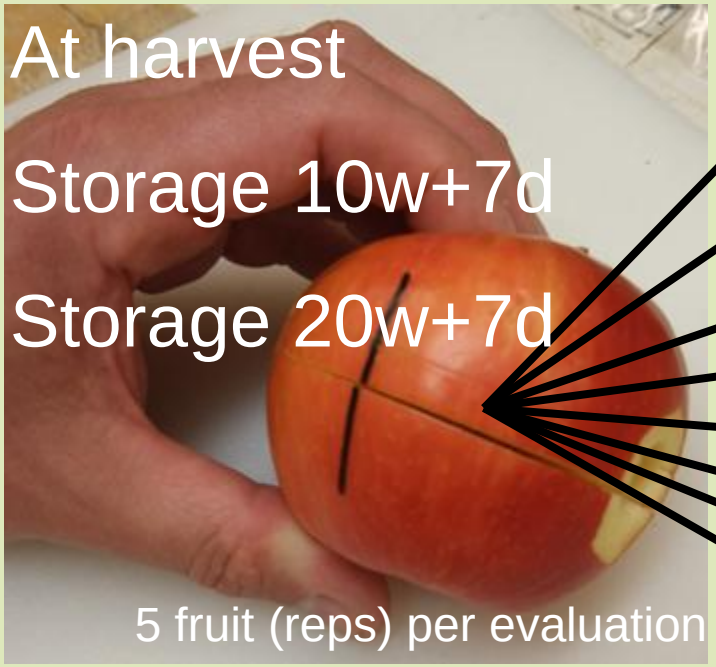


Phenotyping of the Crop Reference Sets

- Standardized phenotyping protocols were developed.
- Phenotypic data for apple, peach, and cherry was taken in 2010.




Apple Standardized Phenotyping



Firmness, Crispness – Instrumental, Sensory

Sweetness, Acidity – Intstrumental, Sensory

Color, Appearance, Juiciness, Aroma – Sensory

Cracking, Russet, Sunburn

Maturity

Fruit size

Postharvest disorders

Harvest date, Crop, Dropping

RosBREED

Intranet

Home | About | Breeding | Socio-economics | Resources | News | Events | Contact Us | Search this website... | SEARCH

Downloads

RosBREED: Enabling marker-assisted breeding in Rosaceae

RosBREED will create a national, dynamic, sustained ... [Read More...]

Slideshow

Enabling marker-assisted breeding in Rosaceae Click ... [Read More...]

Resources

Project Description

Integration of modern genomics tools with traditional breeding approaches will transform crop improvement in Rosaceae, significantly improving ... [Read More...]

Marker-Locus-Trait Associations

A marker-locus-trait (M-L-T) association is a predictive genetic marker developed for specific locus that contribute to genetic variation for ... [Read More...]

News

RosBREED releases the May issue of their newsletter (05/26/10)

Enhancing the RosBREED network at professional meetings: International Fruit Tree Association (IFTA) Grand Rapids, MI RosBREED project will use every opportunity to link with its Advisory Panel (AP) ... [Read More...]

ASHS RosBREED Workshop has been scheduled for August 4th, 2010

RosBREED will be hosting a workshop at the 2010 ASHS Annual Conference in Palm Desert, CA. The workshop will be Wednesday, August 4th 8-10 am. For more information please visit the ASHS RosBREED ... [Read More...]

Peach genome sequence has been released!! (04/01/2010)

On 1 April 2010 at 9 pm PST, the peach genome sequence was released on GDR. Please visit this website for more information. ... [Read More...]

Welcome to the RosBREED Project

Funded by the 2009 USDA NIFA Specialty Crops Research Initiative, 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. [Read More...]

Highlights

Amy Iezzoni presents at the ...

.

Upcoming Events

› August 4, 2010
ASHS RosBREED Workshop has been scheduled for August 4th, 2010
Palm Dessert
More Info

View All Events

You can access these standardized phenotyping protocols by visiting our website:

Resources

Genotyping of the Crop Reference Sets

- Genotyping to validate the first sets of marker-trait associations is underway.
- DNAs for the genome-wide SNP genotyping have been extracted and are awaiting development of the genotypng platform.

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

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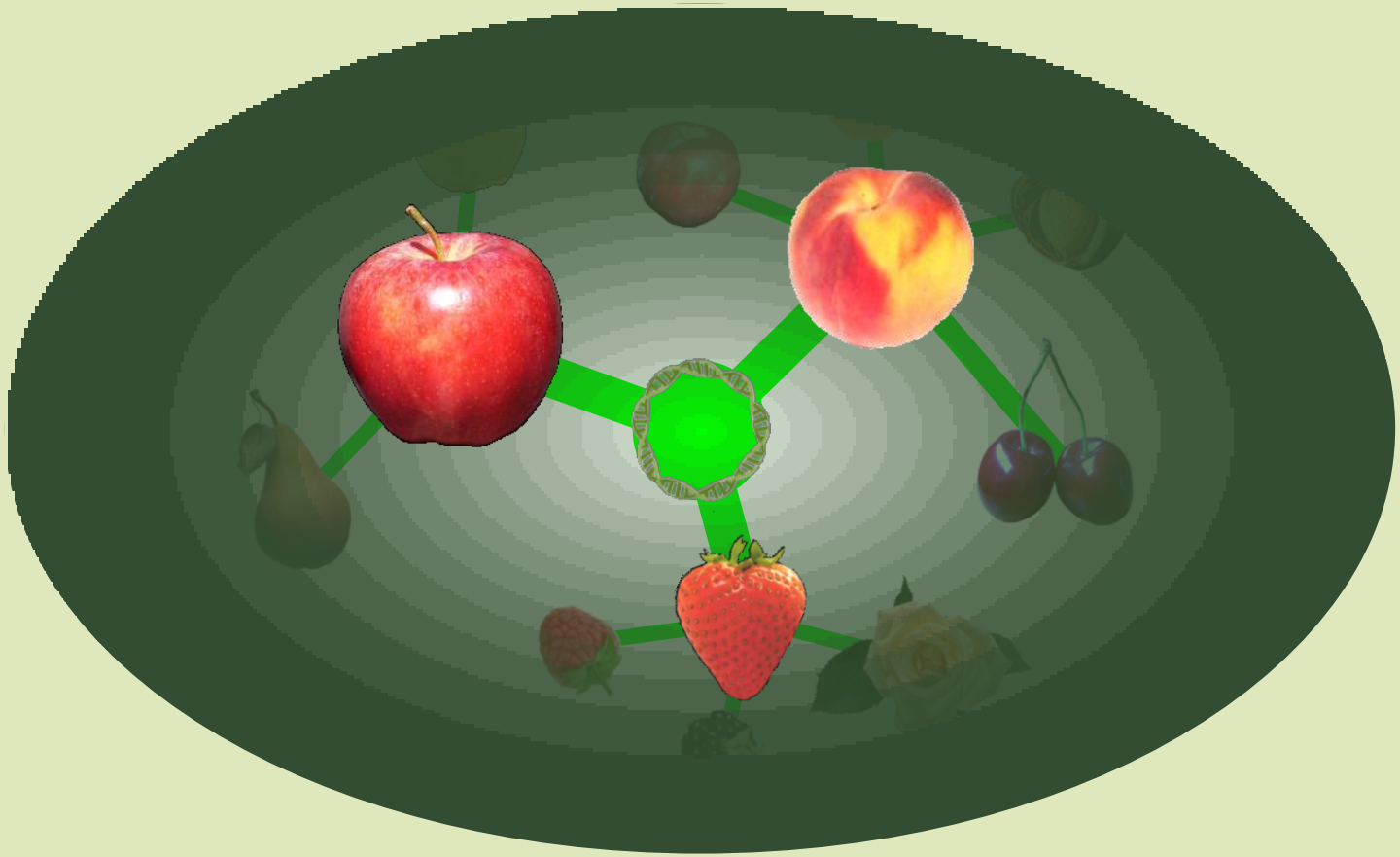
Pedigree Based Analysis

QTL discovery and validation and estimation of breeding values.



Identity-By-Descent (IBD): FlexQTL™

Jonathan X **Golden**

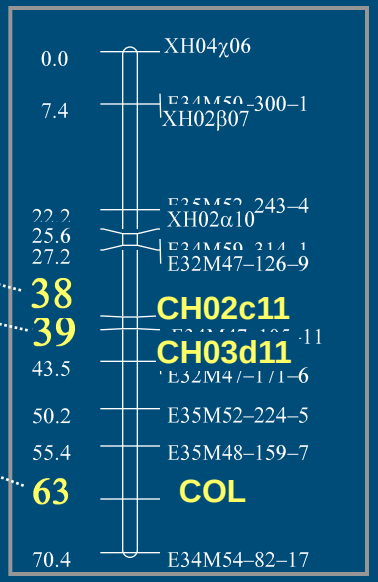
Jonathan		Golden	
231	**237**	221	235
125	121	121	0
232	230	232	222

Septer X **Cox**

Septer		Cox	
231	221	219	219
125	121	127	121
232	232	230	230

Elise

Elise	
221	219
121	121
232!	230



Elise: 219 descents from Cox

⇒ **I**dentical **B**y **D**escent

Elise: 221 descents from **GD**

WAGENINGEN UR
For quality of life

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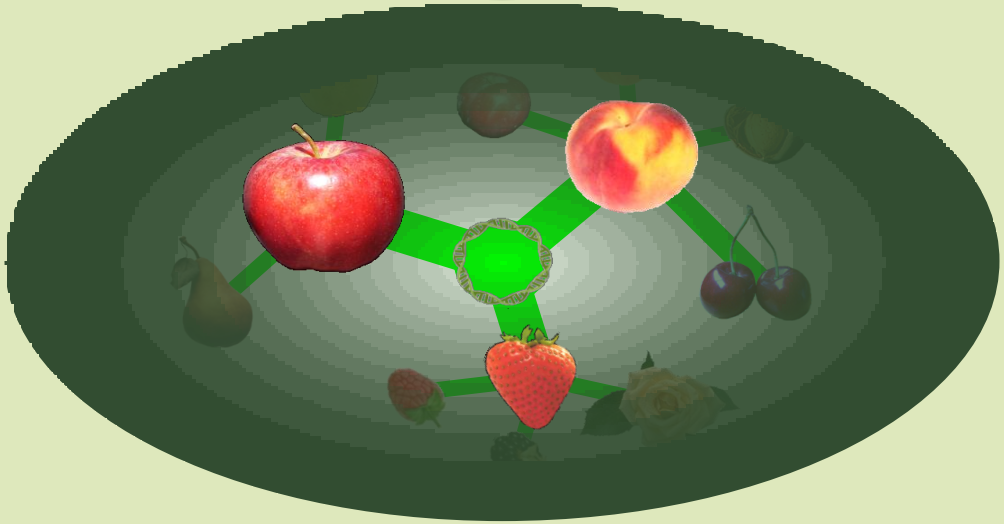
SNP Genotyping Platforms

Develop and utilize high throughput genotyping platforms in collaboration with a newly formed Illumina SNP consortium to implement a 9K Infinium chip for each of apple and peach and a 6K chip for cherry



Peach SNP Detection Panel

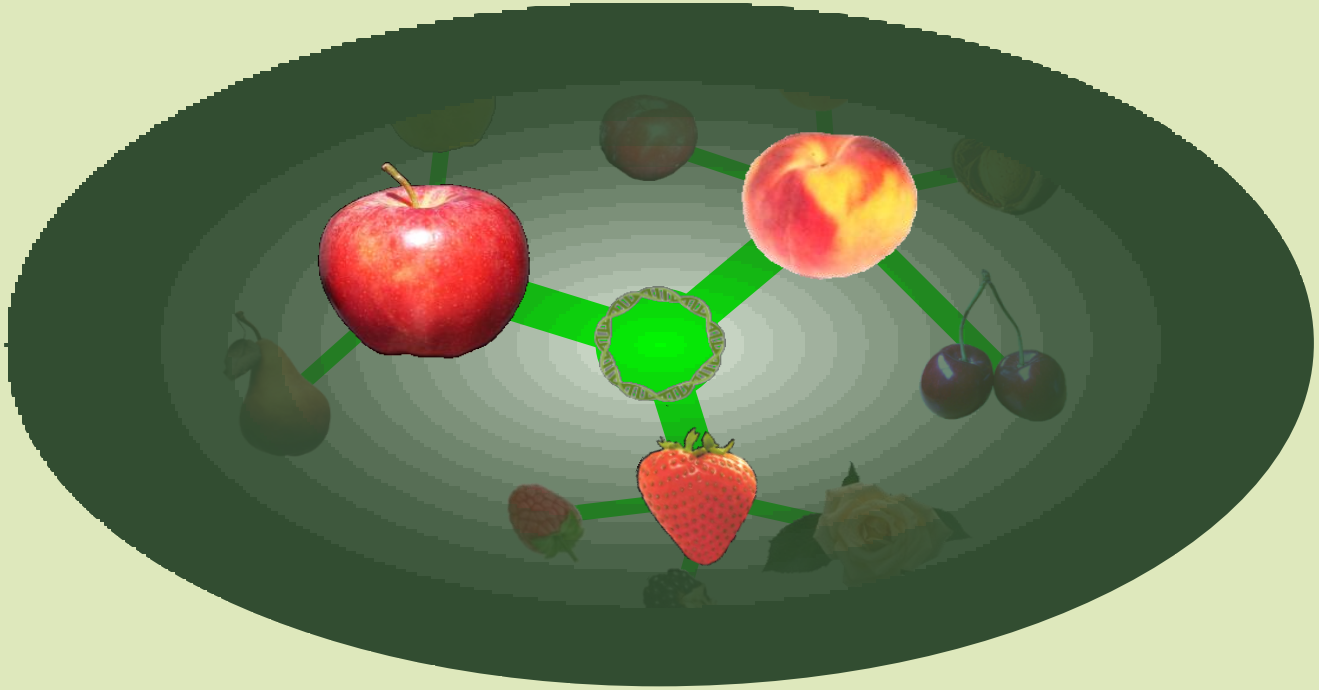
Peach Cultivar	Read Count (M)	Genome Coverage	SNP Frequency
Admiral Dewey	2.4	0.9	23
Slappey	2.0	0.7	19
Babcock	3.2	1.2	21
Elberta	0.6	0.2	46
Carmen	1.7	0.6	22
Chinese Cling	2.5	0.9	14
Mayflower	1.3	0.5	29
Bolinha	3.5	1.3	16
Yellow St. John	1.4	0.5	68
J.H. Hale	3.2	1.2	13
Rio Oso Gem	2.6	0.9	15
Diamante	2.1	0.8	22
Dixon	1.3	0.5	40
Early Crawford	3.9	1.4	18
Florida Prince	1.8	0.7	20
Nonpareil	2.5	0.9	41
Dr. Davis	2.3	0.8	25
O'Henry	4.3	1.6	11
Okinawa	2.2	0.8	20
Nemaguard	2.4	0.9	19

20 accessions in 5 multiplexes generated

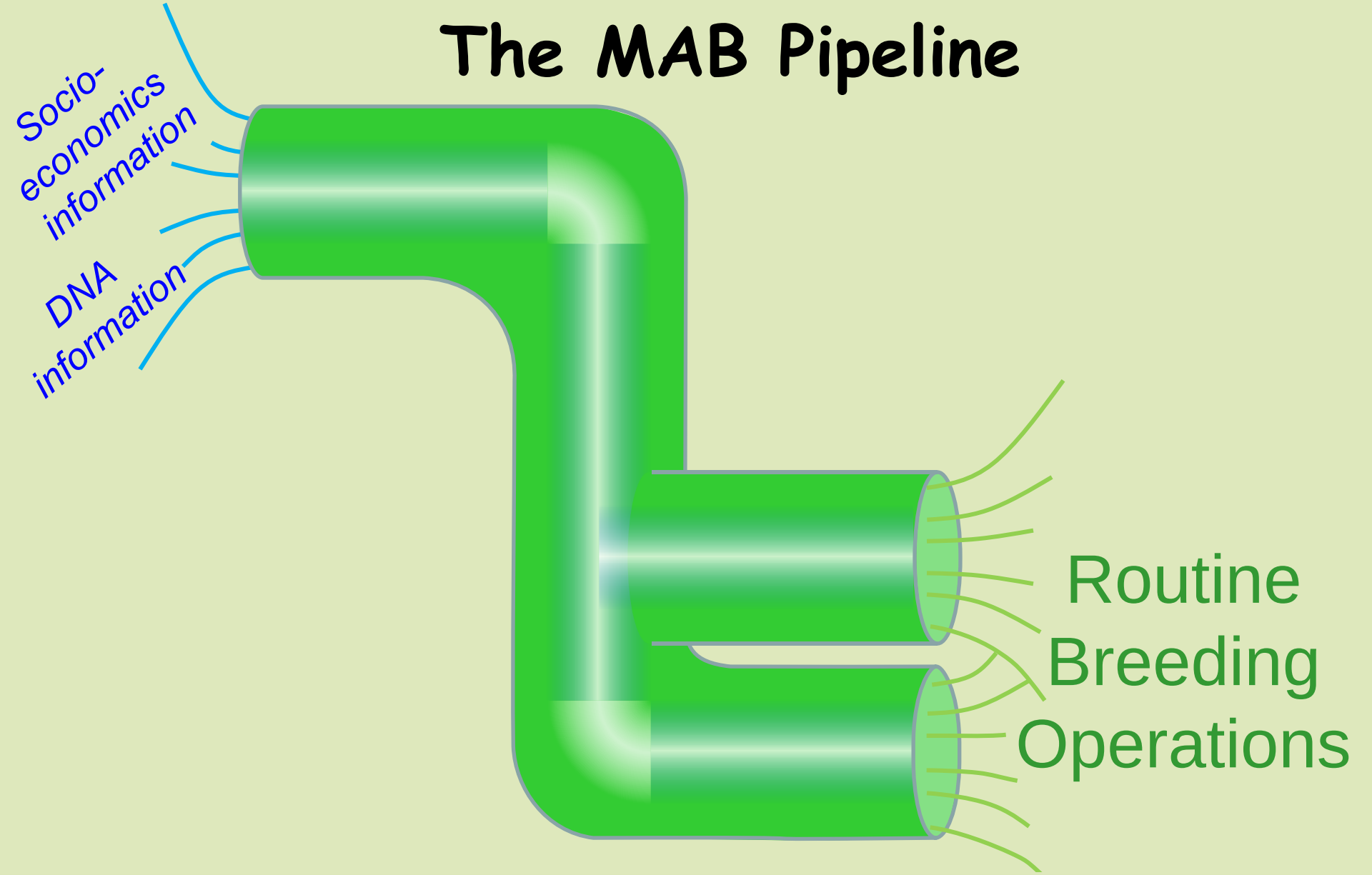
- 3.8 Gb
- 2.3 Gb aligned
- 0.9 x coverage, on average

Marker Assisted Breeding Pipeline

Put MAB into practice.



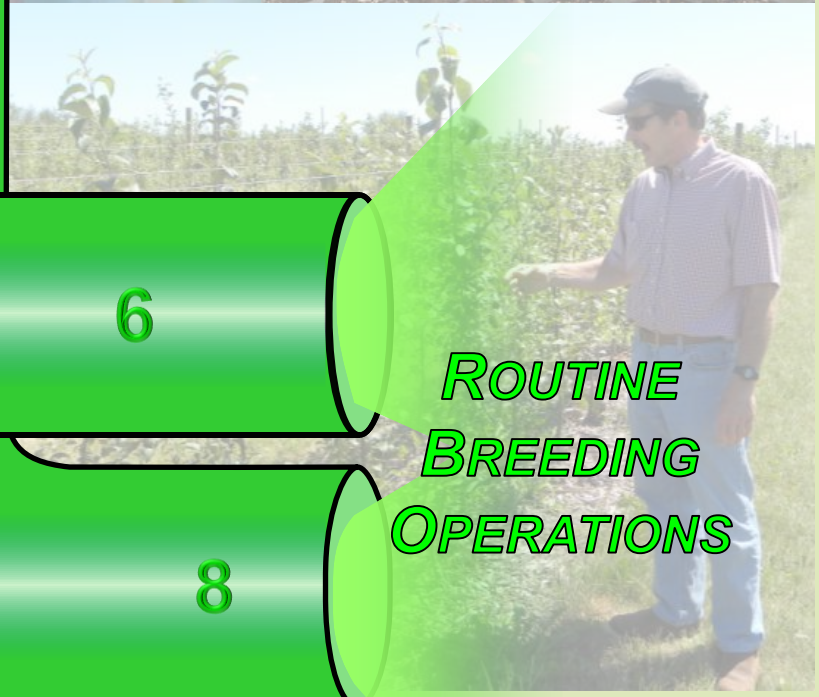
The MAB Pipeline



RosBREED's MARKER-ASSISTED BREEDING PIPELINE

SOCIO-ECONOMICS INFORMATION

DNA INFORMATION



Pipeline Stages

1. Choose valuable, impactful targets
2. Choose efficient genetic screening technologies and service providers
3. Adapt reported genetic tests to local genetic screening approach
4. Validate genetic tests across crop
5. Assess utility of genetic tests for breeding germplasm
6. Inform parent selection and crossing
7. Identify efficient seedling selection schemes
8. Trial seedling selection schemes

ROUTINE BREEDING OPERATIONS

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Marker-Assisted Breeding Outcomes

Four year project outcomes

Increased genetic knowledge flow across taxonomic boundaries in the Rosaceae

Implementation of MAB by breeding programs

Increased gain in fruit quality per breeding cycle due to improved parent selection and improved mean progeny value

Long-term outcomes

More rapid availability of new cultivars with genetically superior fruit quality

Improved profitability and sustainability of US rosaceous fruit, nut, and floral crops with increased consumption and enjoyment

What's next?

RosEXEC: U.S. Rosaceae Genomics, Genetics, & Breeding Executive Committee

It's not too early to identify knowledge gaps and goals for a second project… and add collaborators.

Polyploidy?, High resolution phenotyping?

RosBREED Co-PDs

MSU
Amy Iezzoni (PD)
Jim Hancock
Dechun Wang
Cho Weebadde

WSU
Cameron Peace
Dorrie Main
Kate Evans
Karina Gallardo
Raymond Jussaume
Vicki McCracken
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Alexandra Stone

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Nahla Bassil
Gennaro Fazio
Chad Finn

Texas A&M
Dave Byrne

Plant Research Intl, Netherlands
Eric van de Weg
Marco Bink

Cornell
Susan Brown
Kenong Xu

Clemson
Ksenija Gasic
Gregory Reighard

Univ. of Arkansas
John Clark

Univ. of CA-Davis
Tom Gradziel
Carlos Crisosto

Univ. of New Hamp.
Tom Davis

International Project Participants

ARC Jasper Rees

Dan Sargent

Herman Silva & Lee Meisel

INRA (Bordeaux, Angiers, Avignon)

David Chagné

Ignazio Verde

Questions?