RosBREED's MARKER-ASSISTED BREEDING PIPELINE
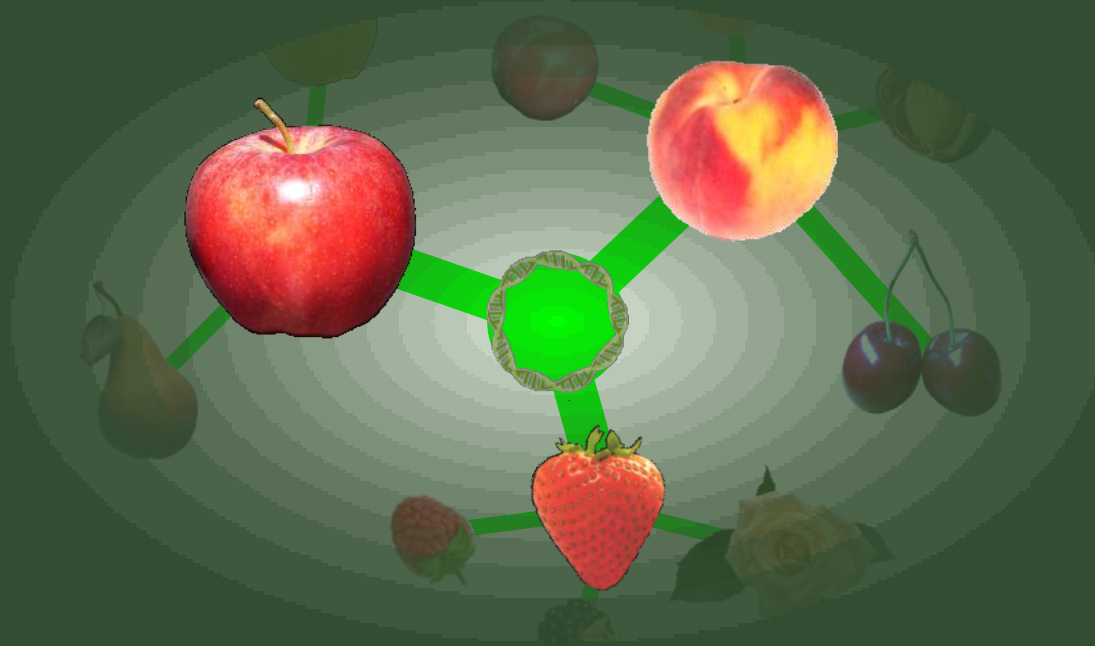
Cameron Peace, MAB Pipeline Team Leader, WSU Pullman

Outline of Presentation

❖ The RosBREED Project

❖ Bridging the Chasm

❖ The MAB Pipeline

❖ Fast-Tracked Pipelining in 2010

The RosBREED Project

The RosBREED Project

- **PI**: Amy Iezzoni, Michigan State University

- 4 years, Sep 2009 – Aug 2013

- Funded by SCRI (USDA-NIFA's Specialty Crops Research Initiative)

- $14.4 M ($7.2 M SCRI, $7.2 in-kind Partners)

The RosBREED Project

- Centered on breeders & breeding programs

- U.S.-wide and international collaboration

- 10 Teams (Socio-Economics, Industry, Breeding, Pedigree-Based Analysis, Breeding Information Management System, Genomics, Genetics, Marker-Assisted Breeding Pipeline, Extension, Administration)

- 32 members of 3 Advisory Panels (Stakeholder, Extension, Scientific)

RosBREED
Enabling marker-assisted breeding in Rosaceae
www.rosbreed.org

The RosBREED Project

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 and contributing to increased consumption and enjoyment of these fruit, nut, and floral products.

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The RosBREED Project

Mission

We will create a dynamic, sustained program in research, infrastructure establishment, training, and outreach for developing and applying 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.

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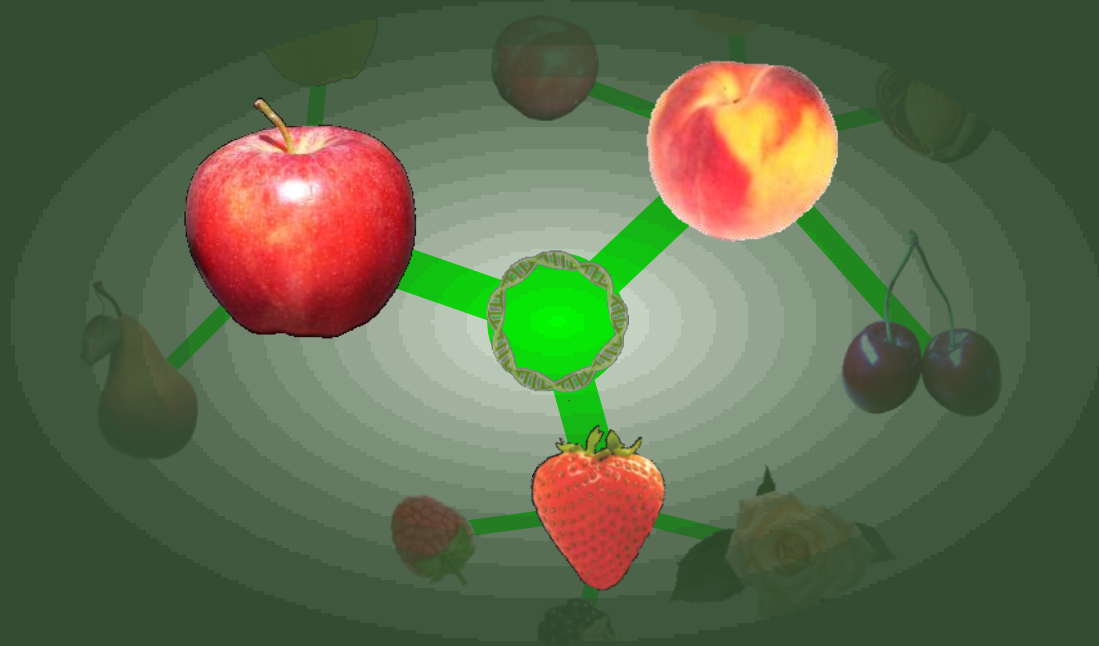
Bridging the Chasm

Rosaceae Breeding = Genetic Improvement

of peach, apple, strawberry, cherry, almond, pear, raspberry, apricot, plum, nectarine, blackberry, rose…

- Successful breeding raises the bar for what new cultivars can produce

- Breeding involves lots of decisions!
  - Choosing parents carrying desirable traits
  - Crossing parents for efficient combinations
  - Selecting the best-performing seedlings
  - Commercially releasing the very best

- Industry also decides which cultivars to produce

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Rosaceae Breeding = Genetic Improvement

of peach, apple, strawberry, cherry, almond, pear, raspberry, apricot, plum, nectarine, blackberry, rose…

- Breeding (and industry) decisions can be supported by:

  Socio-economics information
  (trait values)

  DNA information
  (molecular genetics & genomics)

→ To allow more informed and objective decisions

Genomics Research = Breeding Support

GENOMICS RESOURCE DEVELOPMENT
Whole genome sequences
Genetic maps
Marker systems
Expressed gene libraries
DNA fragment libraries
Transformation systems
Stats & programs
Databases

GENOMICS RESEARCH
Structural Genomics
Comparative Genomics
Functional Genomics

…to elucidate genetic control of horticultural traits

INDUSTRY & CONSUMERS

BREEDING INNOVATION

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Genomics Research = Breeding Support

- Genomicists seek underlying genetic control of traits

- Mendelian/major trait loci (MTLs)   and   Quantitative trait loci (QTLs)

  *Genes with allelic variation in available germplasm that explain/predict **most** phenotypic variation*

  *…explain/predict **some** phenotypic variation*

- Marker-locus-trait (M-L-T) associations

  Genetic <u>markers</u> at specific <u>loci</u> associated with particular <u>traits</u>

Term coined by Fred Bliss, 2010 (*Marker-assisted breeding in horticultural crops*. Acta Horticulturae 859:339-350. Proceedings of the ISHS Symposium on Molecular Markers in Horticulture, Corvallis, Oregon, USA, 29 Jul - Aug 1 2009)

Genomics Research = Breeding Support

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

Crop	Traits	Number of		
		QTLs[a]	MTLs[b]	Genes[c]
Apple	55	180	36	5
Pear	5	7	3	1
Peach	21	36	4	2
Almond	10	8	4	1
Cherry (sweet)	1	-	-	1
Cherry (tart)	3	14	-	1
Strawberry	11	31	2	-
Raspberry	-	-	-	-
Blackberry	-	-	-	-
Rose	11	41	9	-
Total:	**117**	**317**	**58**	**11**

[a] QTLs = quantitative trait loci with linked markers
[b] MTLs = major trait loci with linked markers
[c] Genes = known genes controlling a trait

Genomics Research = Breeding Support

- Geneticists convert genomics knowledge into *genetic tests* enabling prediction of performance

- Breeders use genetic tests to support decisions (DNA information)

Genomics Research = Breeding Support

DOES THIS REALLY HAPPEN??

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Genomics Research = Breeding Support

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[a] QTLs = quantitative trait loci with linked markers
[b] MTLs = major trait loci with linked markers
[c] Genes = known genes controlling a trait
[d] MAPS = marker-assisted parent selection
[e] MASS = marker-assisted seedling selection

OPPORTUNITIES AVAILABLE

OPPORTUNITIES EXPLOITED

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Some Reasons for the Chasm

Mkr-loc-trait associations

Decision support

M-L-T association itself:
Trait low priority / low value
Weak linkage
Different germplasm
Unknown functional alleles
Unknown genetic action
Unknown environ. effects
Unknown linkage drag

Genomics Research

Breeding Programs

No local genotyping service
Not believed to be cost efficient
No training in routine DNA testing
Acronyms…

2009-2010: Building The Bridge
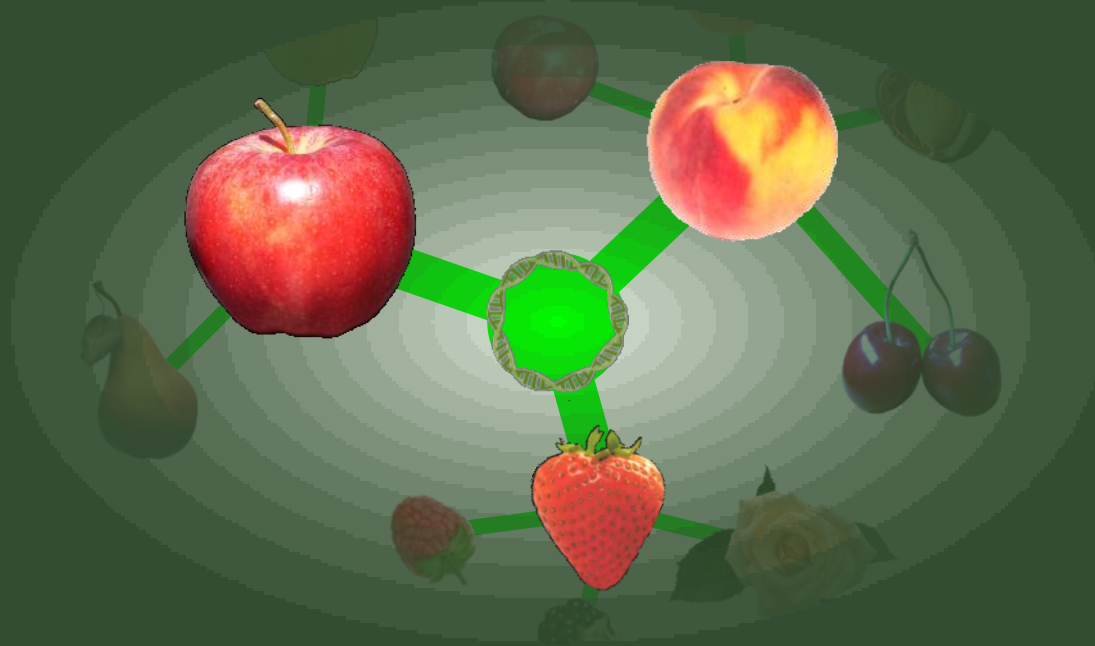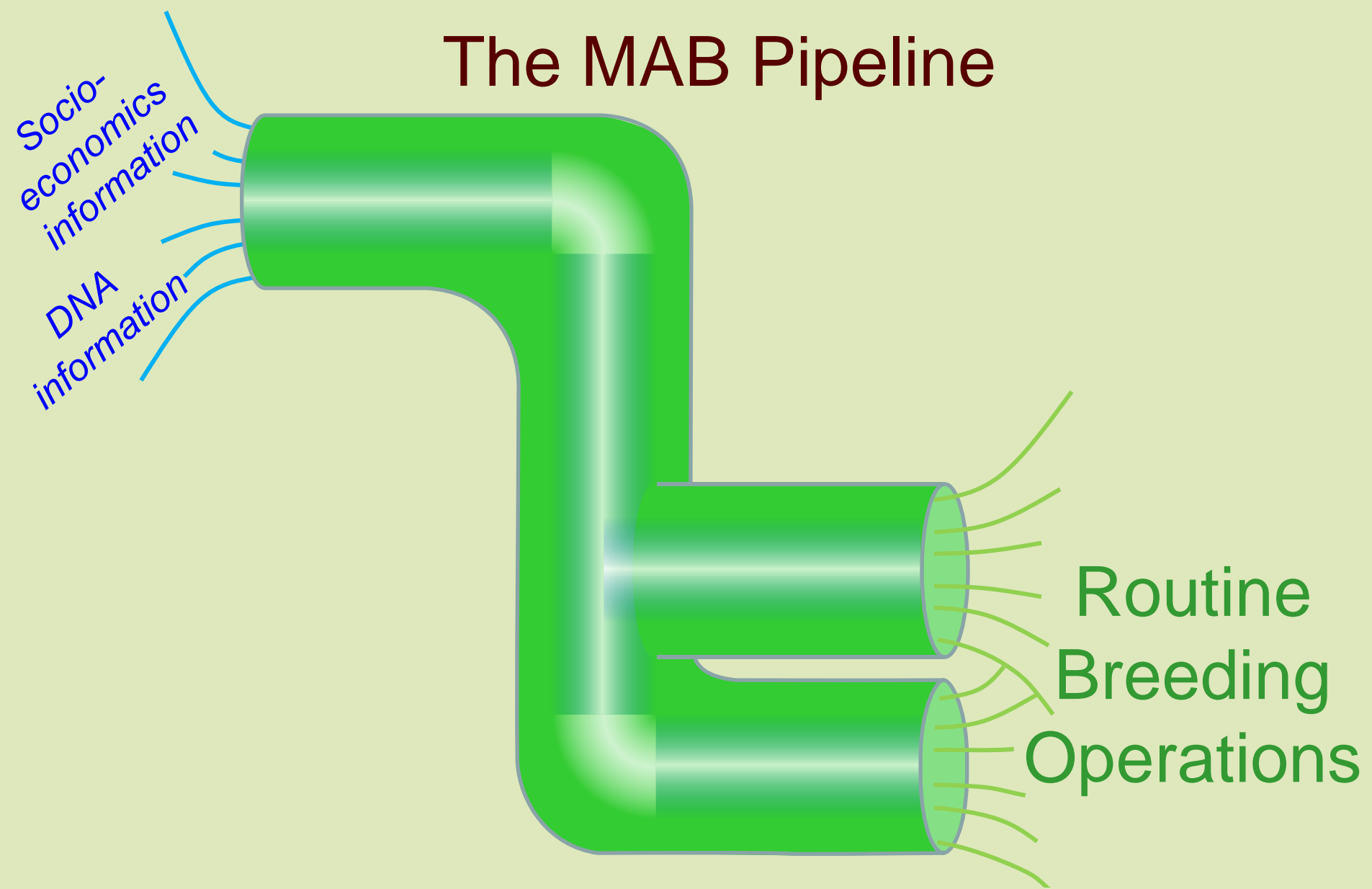
The MAB Pipeline

The Pipeline's Eight Stages

1
2
3
4
5
6
7
8

4. Validate genetic tests

5. Assess utility of genetic tests in breeding germplasm

6. Inform parent selection and crossing choices

1. Choose best targets

2. Choose efficient genetic screening technologies/services

3. Adapt genetic tests

7. Identify efficient seedling selection schemes

Routine Breeding Operations

8. Trial seedling selection schemes

The MAB Pipeline

- Example of the Pipeline in practice:
  9:00 am Wed, during *Workshop 14*, 8-10am

- Next slides: General pipeline components

Pipeline Components

- Reference sets of breeding germplasm

- Standardized phenotyping protocols

- Common statistical platform for validating (and identifying) utility of M-L-T associations for specific breeding programs and lineages = Pedigree-Based Analysis (PBA)

Pipeline Components

- Breeding decision-support tools, e.g.…

    - Pedigree viewer
      (Pedimap: www.plantbreeding.wur.nl/UK/software_pedimap.html)

    - Cross planner

    - Calculators: heritability, breeding value, inbreeding index, genetic distance

    - Seedling selection efficiency tool

  All above also integrated with DNA info

Pipeline Packaging and Delivery

- Breeding Information Management System (software package) that integrates all these components

- Tailoring to each breeding program

- Step-wise introduction of Pipeline components to breeders
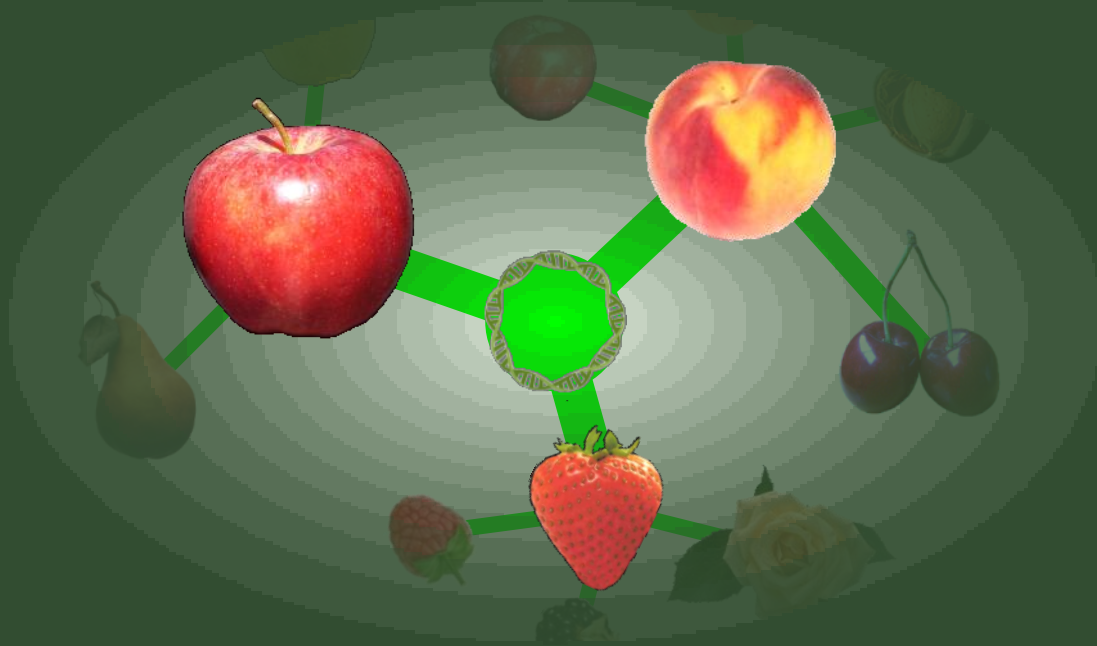
Fast-Tracked Pipelining in 2010
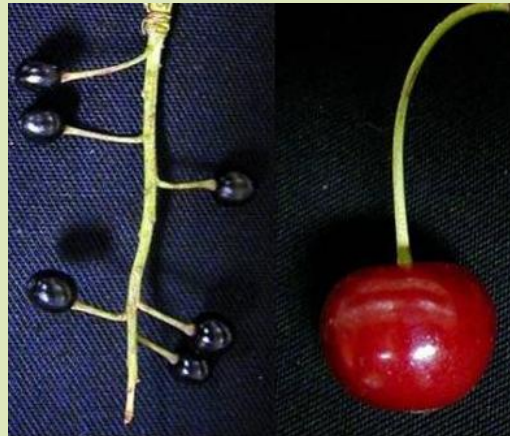
Fast-Tracked Pipelining in 2010

- Peach

   1. Texture: Freestone/Clingstone, Melting/Non-melting, fruit softening rate, softening location
      – *endoPG F-M* locus

   2. Flavor: sweetness and acidity
      – QTL, linked to *F-M* locus

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Fast-Tracked Pipelining in 2010

- Cherry (sweet and tart)
  1. Fruit quality: fruit size, fruit firmness
     – QTL (linked to sweetness QTL)
  2. Flavor: acidity
     – QTL (linked to fruit color MTL)

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Fast-Tracked Pipelining in 2010

- Apple
  1. Flavor and Texture: acidity, crispness, juiciness
     - QTL (*Ma* locus)
  2. Texture: Firmness
     - QTL (*Md-Exp7* gene)

www.solo.be
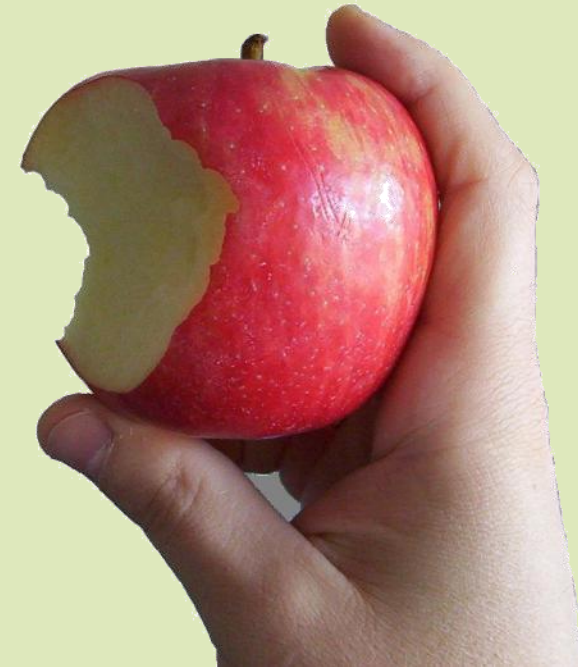
Fast-Tracked Pipelining in 2010

- Strawberry

  Lack of available fruit quality M-L-T associations

  Using instead:

  1. Red stele root rot resistance
     – unpublished QTL (PRI, Netherlands)

  Meeting at IHC to discuss more associations

www.omafra.gov.on.ca

www.forestryimages.org

www.urbanext.illinois.edu

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Fast-Tracked Pipelining in 2010

Socio-economics information

DNA information

1
2
3
4
5
6
7
8

4. Validating and then Genotyping and Phenotyping on Crop Reference Sets, PBA

5. Applying and genotyping on Breeding Pedigree Sets, PBA, describe parent alleles

Genotyping of germplasm as Breeding Pedigree Sets

1. Choose 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 tests markers (SSR, SCAR)

6. Inform parent selection and crossing choices of 2011

Routine Breeding Operations

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2011 And Beyond

- Don't expect to run out of targets in the future…

- ➤ Genome scans of Crop Reference Sets and Breeding Pedigree Sets in 2010-2011

- ➤ Standardized phenotyping of Sets in 2010-2012

- ➤ Integrated with Pedigree-Based Analysis…

2011 And Beyond

- …To stock the shelf with new tools & info – helping breeders to *adjust the genetics of their populations*

www.hand-tools.us

www.storewall.com

www.nzno.org.nz

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Acknowledgements

Questions?