RosBREED

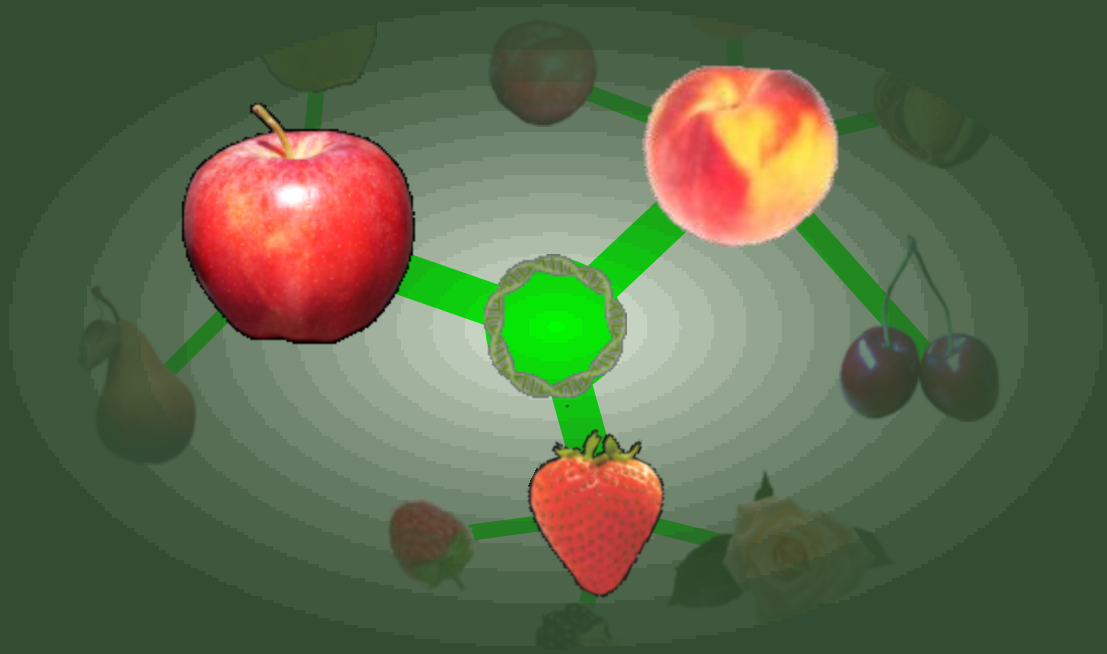
Enabling marker-assisted breeding in Rosaceae

RosBREED Demonstration Breeding Programs

Jim Luby, Breeding Team Leader, Univ. of Minnesota

Outline of Presentation

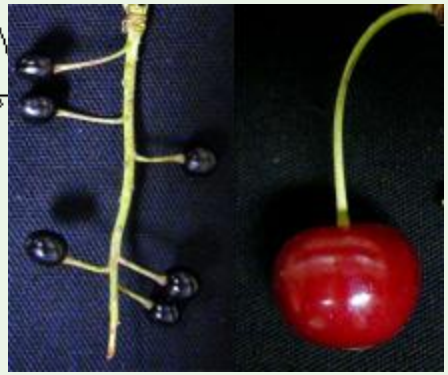
- Intro to Demonstration Breeding Programs and Traits for each RosBREED Crop
  - Strawberry
  - Peach
  - Tart Cherry
  - Sweet Cherry
  - Apple
- Reference Germplasm Sets

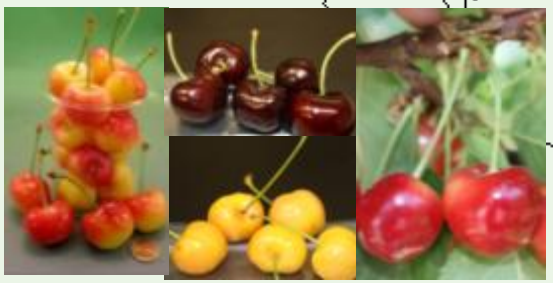


Tart and Sweet Cherries

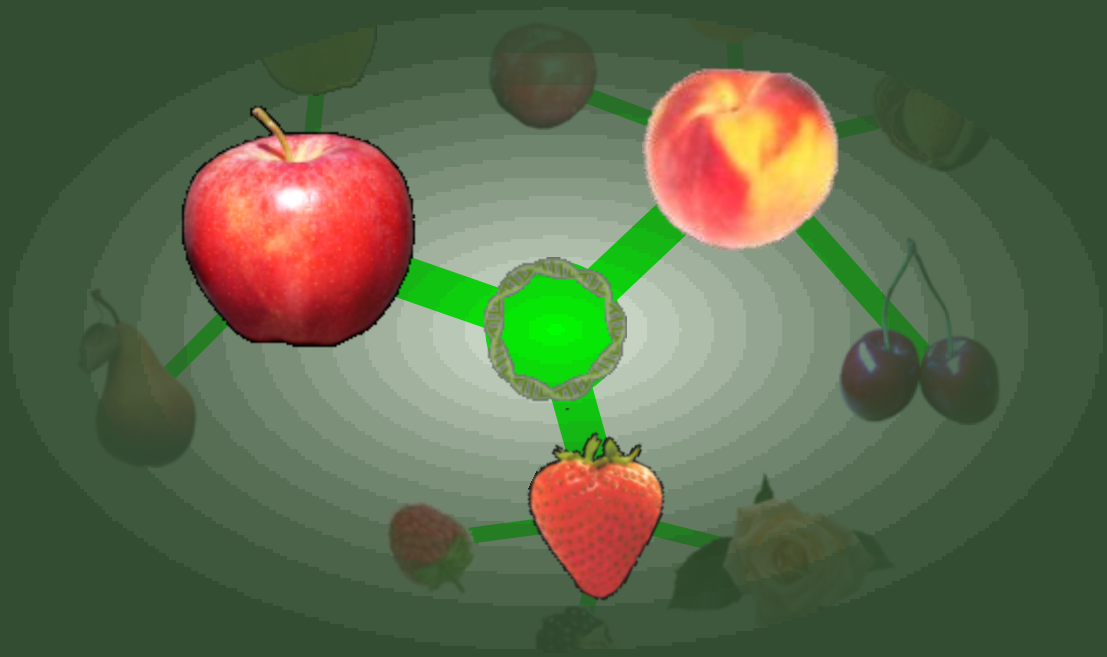
- Tart Cherry - Amy Iezzoni
  - Michigan State University
- Sweet Cherry - Nnadozie Oraguzie
  - Washington State University

RosBREED Cherry Phenotyping





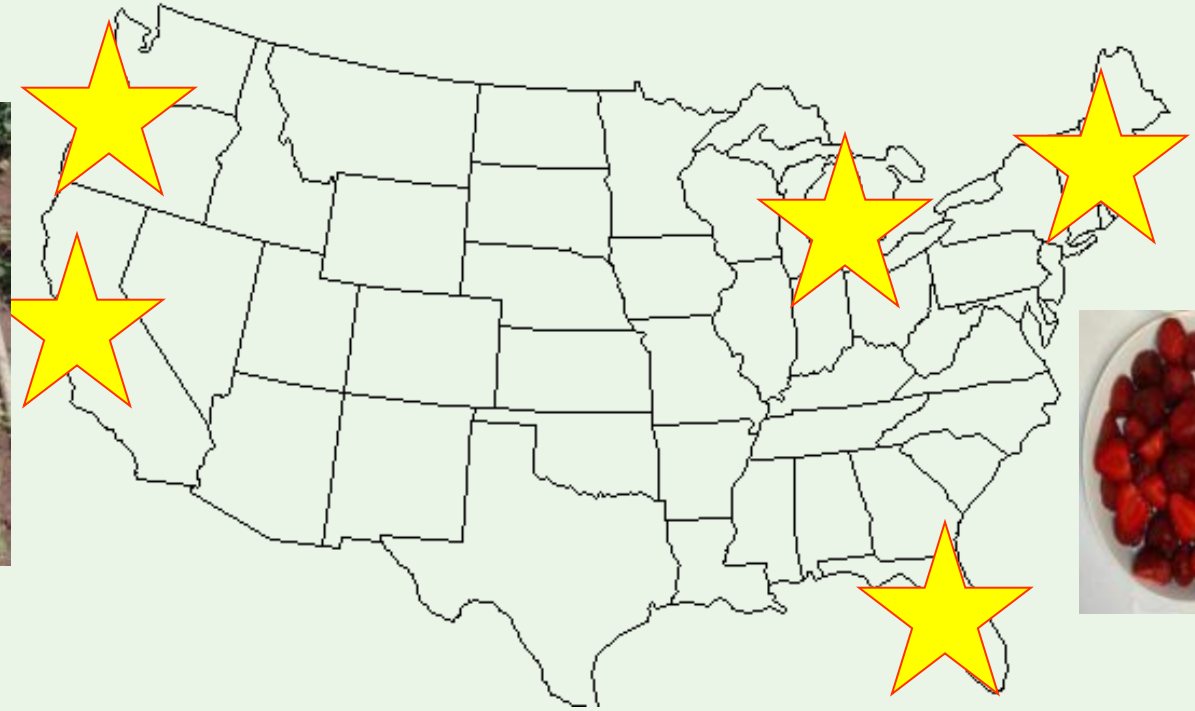
- Sweet Cherries for Fresh Market in Pacific Northwest with firmness and a range of colors
- Tart Cherries for Processing in Michigan
  - Fruit size genes to enable leaf spot introgression from wild relative
  - Freestone for better pitting



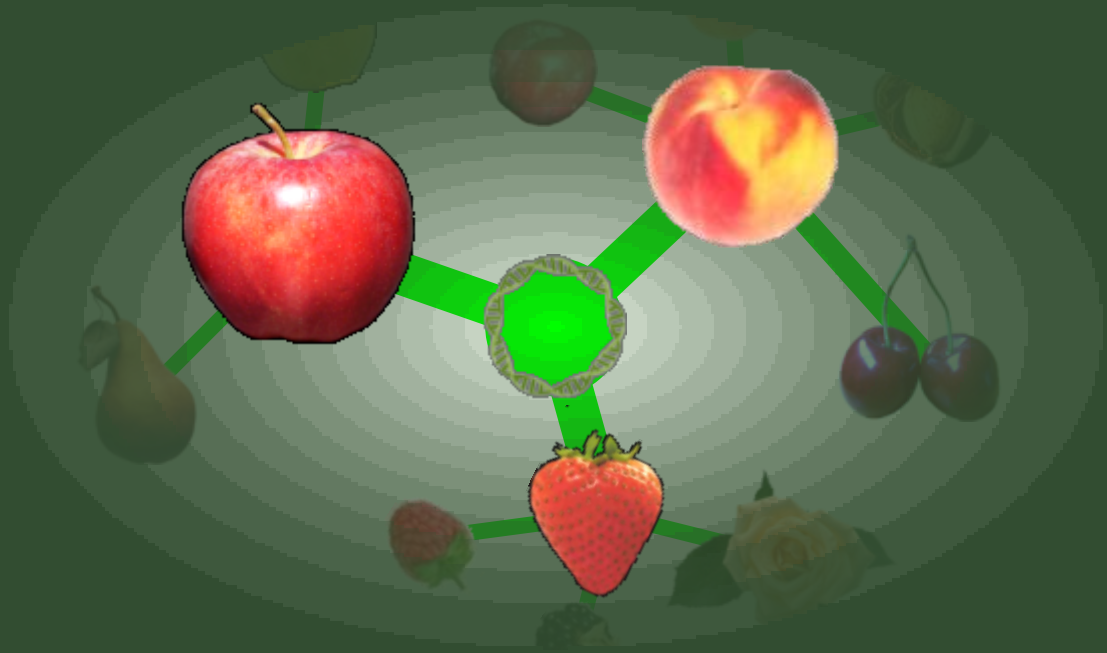
Strawberry

- Chad Finn - USDA-ARS, Corvallis, OR
- Jim Hancock - Michigan State University
- Tom Davis - University of New Hampshire
- Phil Stewart - Driscoll Strawberry Associates

RosBREED Strawberry Phenotyping



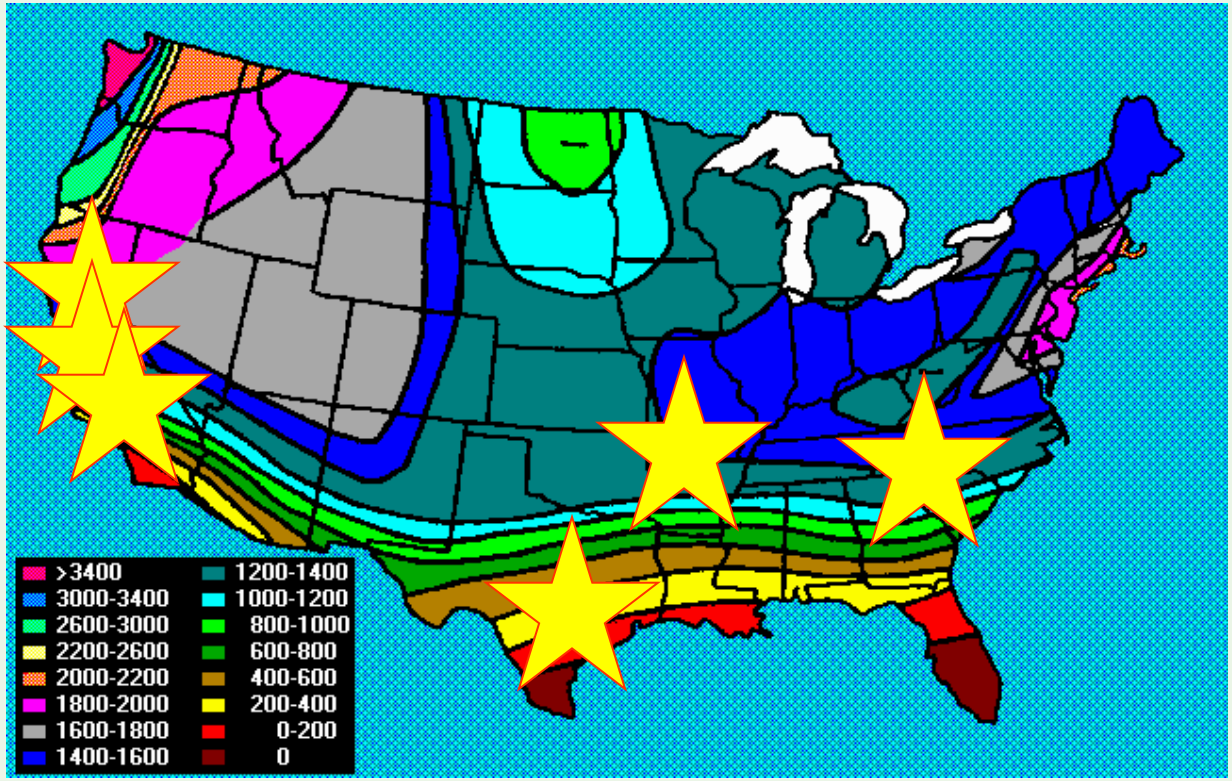
- Entire germplasm set evaluated at multiple locations
- Allows for dissection of GxE effects in PBA
- Includes fresh market and processing fruit traits
- Plant architecture and remontancy (rebloom)



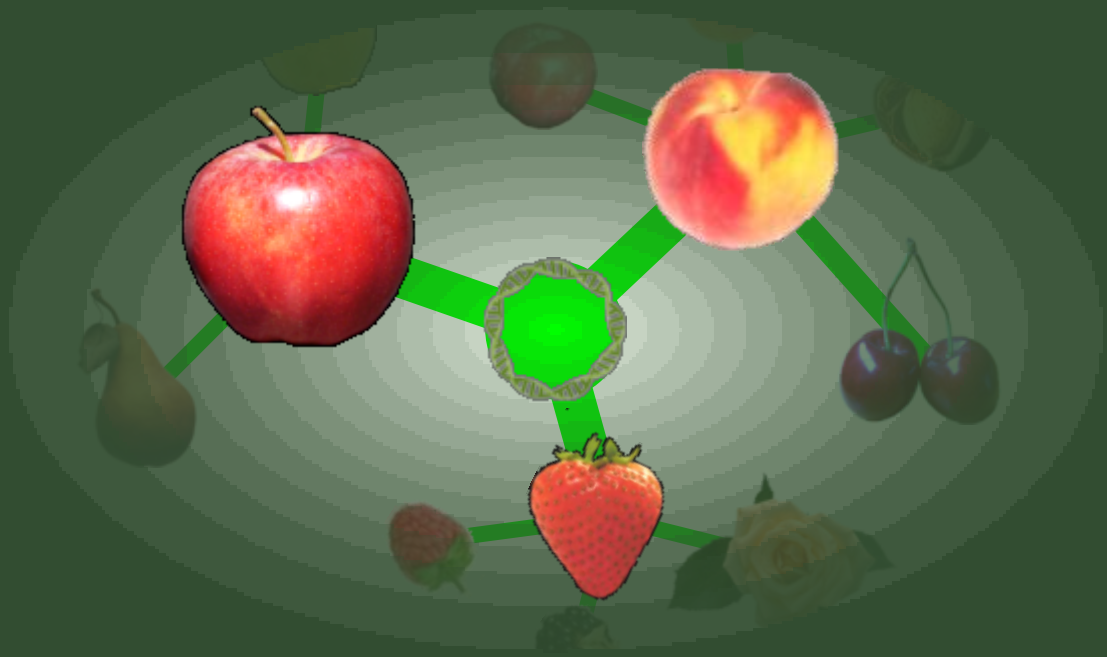
Peach

- Ksenija Gasic - Clemson University
- Tom Gradziel – UC-Davis
- John Clark - University of Arkansas
- Dave Byrne - Texas A&M University

RosBREED Peach Phenotyping



- Covers southern and western geography of US peach production, range of chilling zones
- Several market types
  - Fresh, Processing
  - Nectarine, acidity/sugar, flesh color, shape
- Disease resistances (bacterial spot, brown rot)



Apple

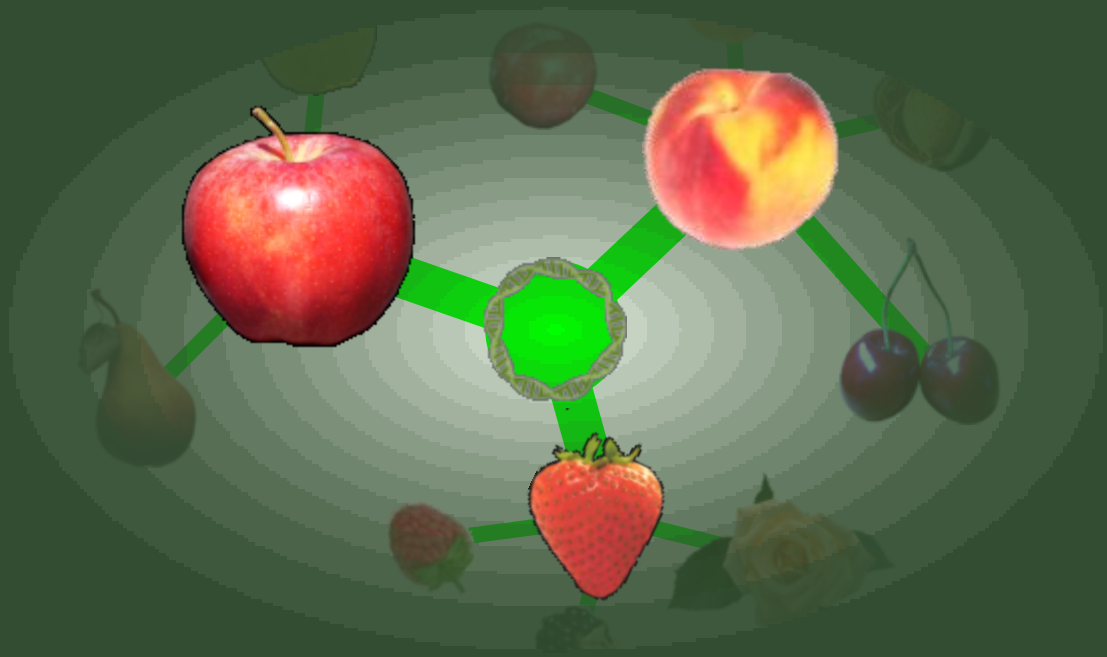
- Kate Evans - Washington State Univ.
- Susan Brown - Cornell University
- Jim Luby - University of Minnesota

RosBREED Apple Phenotyping

- Primary emphasis on fresh market traits
- Components of Flavor, Texture and Appearance
- Postharvest life and storage disorders

Traits and Standardized Phenotyping Protocols

- Identify critical fruit quality traits and other important traits
- Develop standardized phenotyping protocols to enable data pooling across locations/institutions
- Protocols available at www.RosBREED.org
  - "Fruit Evaluation"



Reference Germplasm Sets

Crop Reference Set (CR Set)

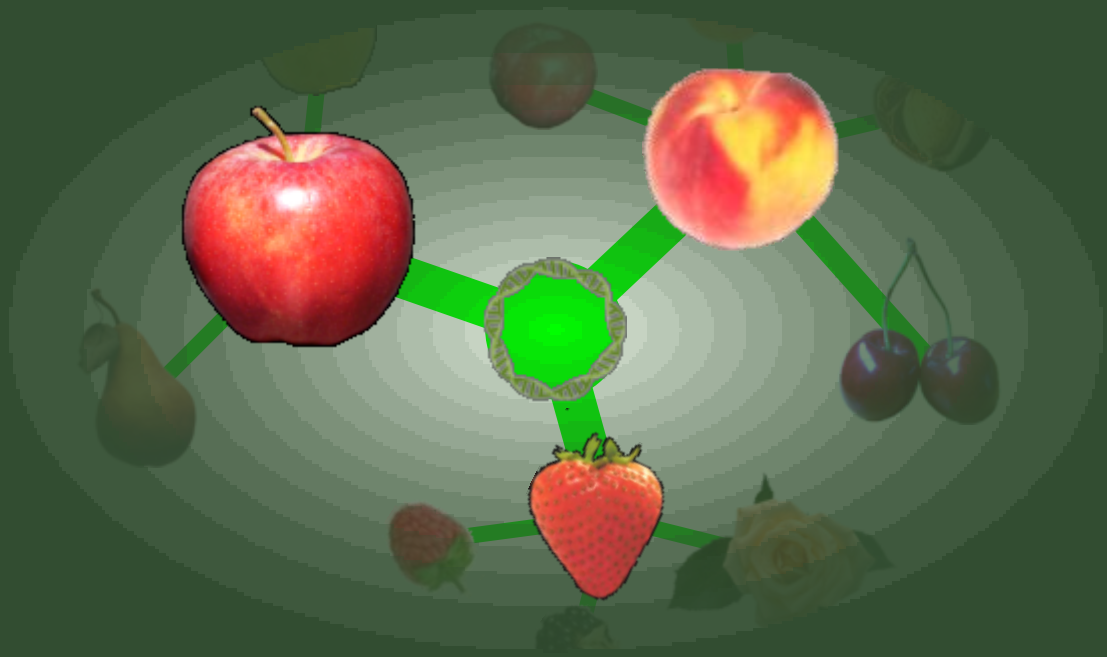
Breeding Pedigree Set (BP Set)

Crop Reference Set (CR Set)

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

Breeding Pedigree Sets (BP Set)

- ~100-300 extra plants for each breeding program that, together with the CR Set, allow full representation of important parents in that program
- Information may remain proprietary with each breeding program; data-sharing improves power

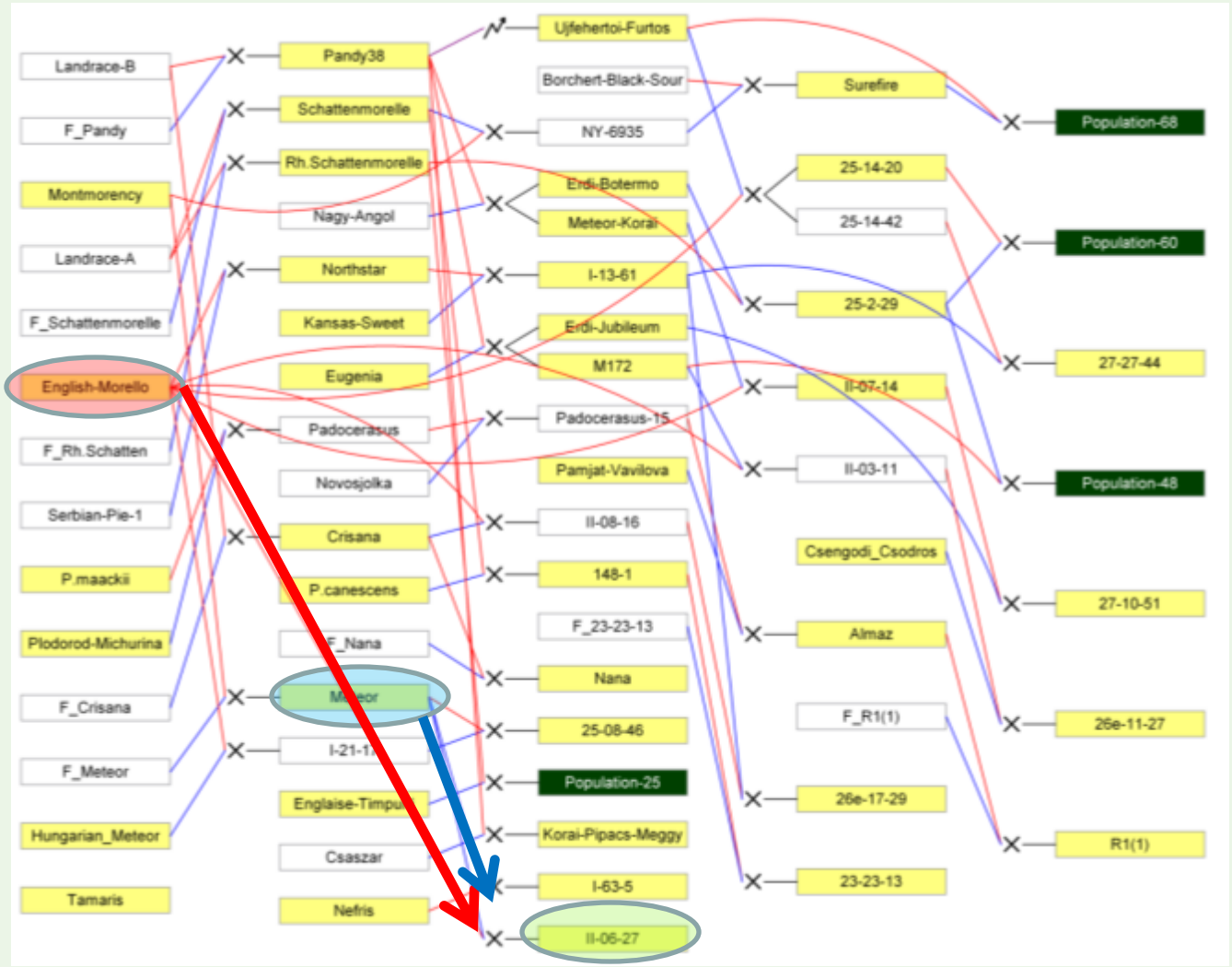


Crop Reference Set

Visualizing Structure in a Breeding Program with PediMap™

Tart Cherry Crop Reference Set:

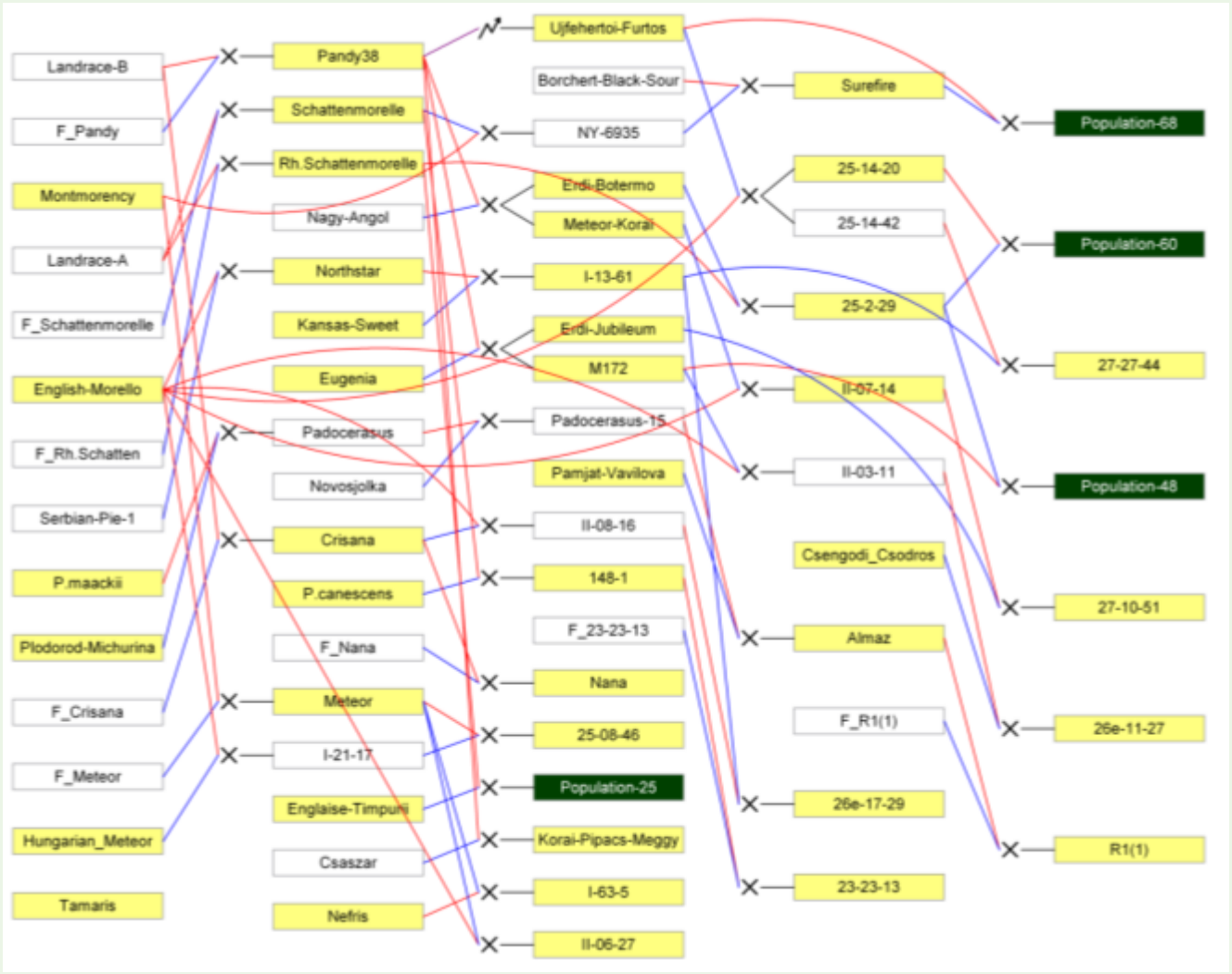
Visualizing a Breeding Program



- Up to 5 generations
- Important ancestors:
  - English Morello
  - Meteor
- Pedigree linkage

Tart Cherry Crop Reference Set:

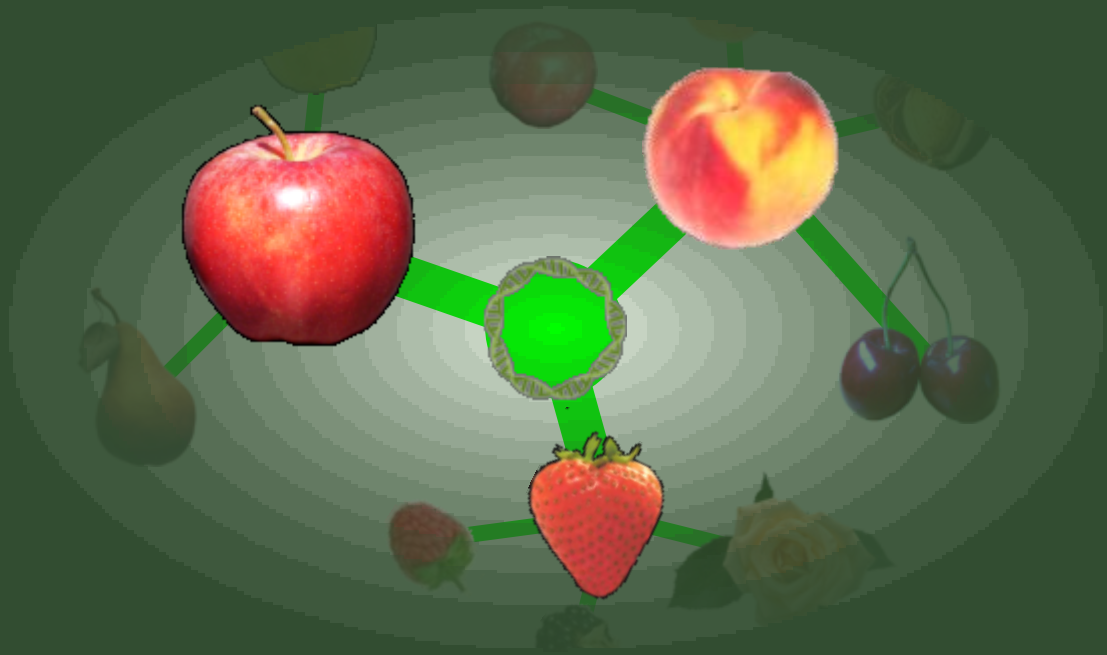
Visualizing a Breeding Program



39 individuals
Half are selections

4 crosses containing 201 individuals provide representation of important parents

20 Ancestors unavailable



Crop Reference Set

Allele Representation

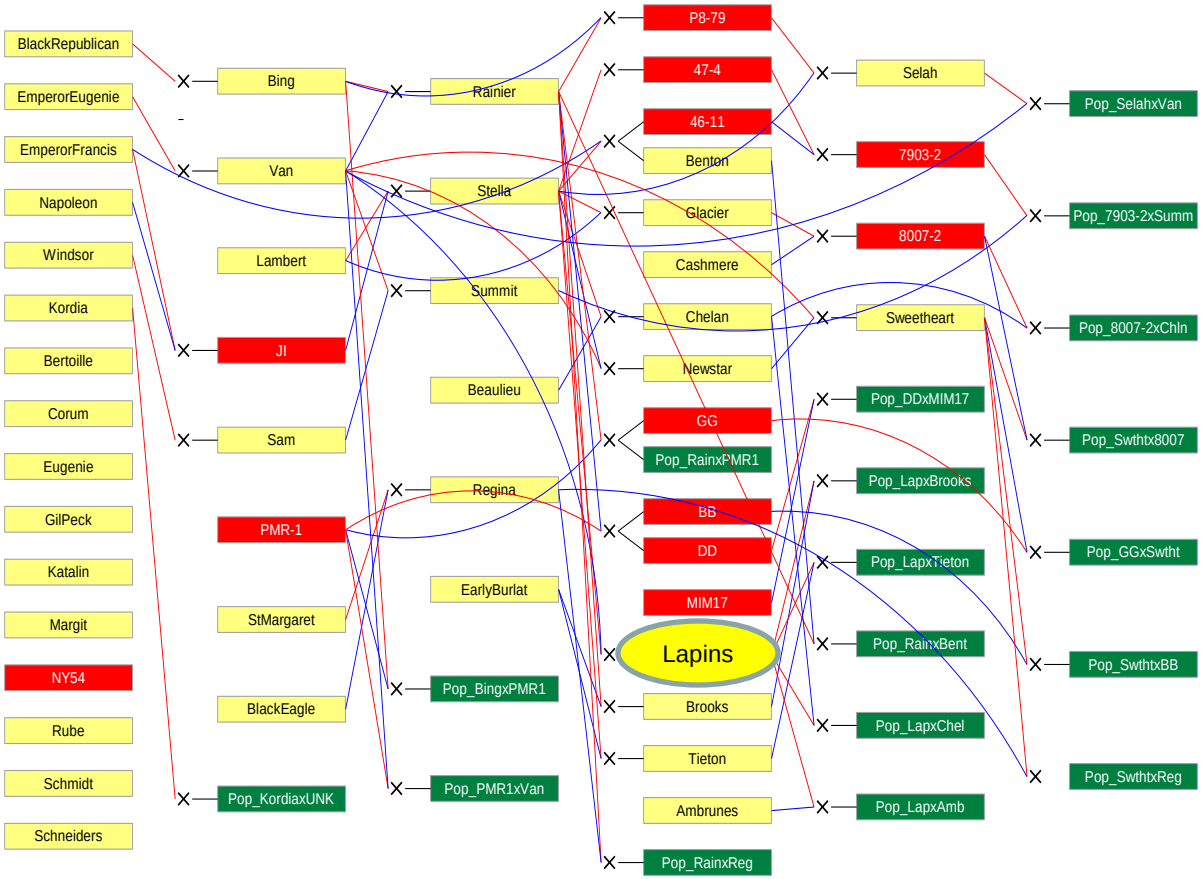
Strategy for Constructing Reference Germplasm Sets

- Pedigree-linked reference germplasm sets represent alleles across the genomes of Important Breeding Parents

- Each relative represents an Important Parent; goal was >12.5 representation units (e.g. 25 F_1 s) for statistical power
  - Offspring represent alleles of these Parents
  - Other relatives can also represent Parent alleles through shared ancestors (because a proportion of alleles will be Identical By Descent)

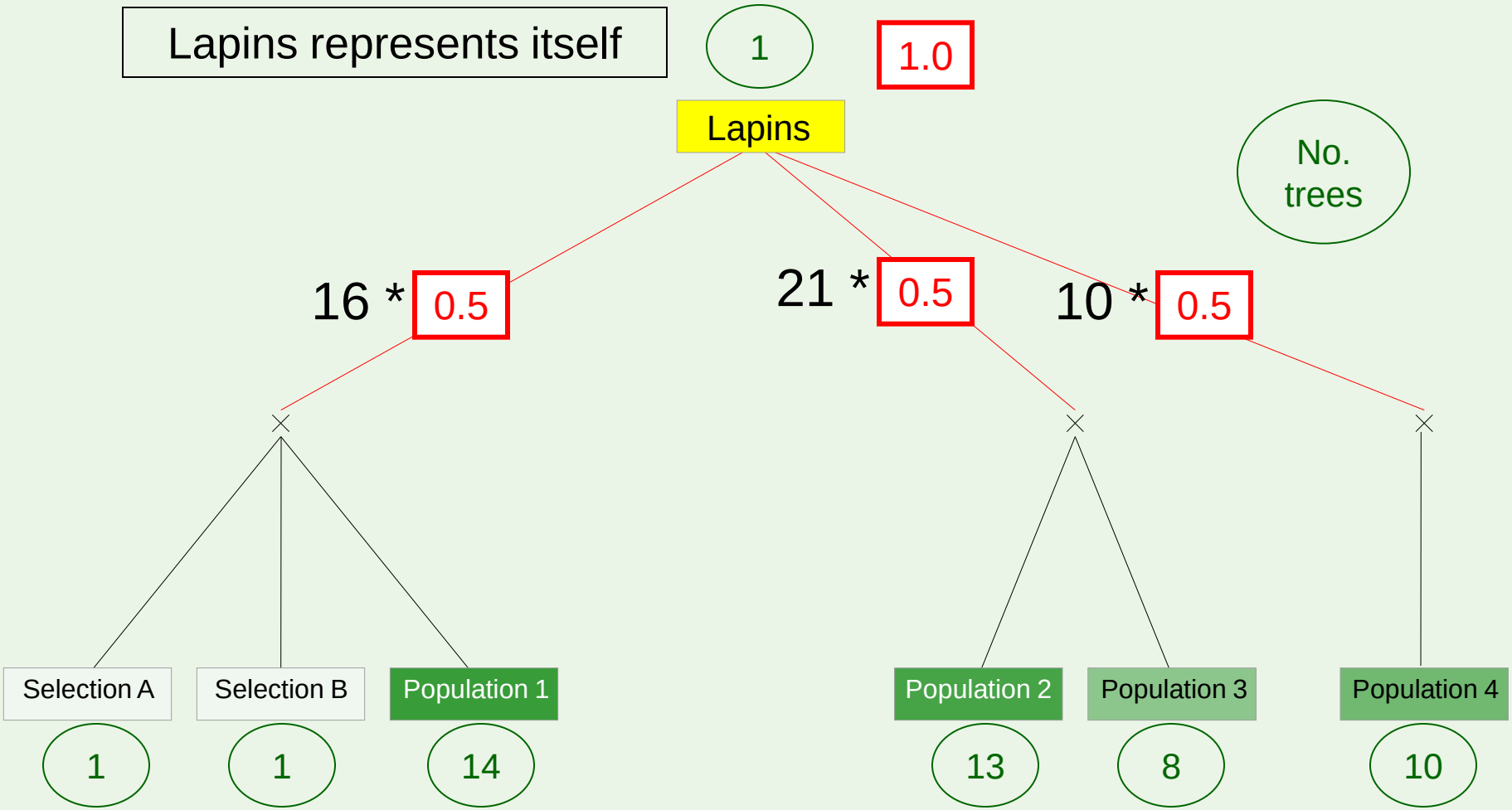
- F_1 offspring, full-sibs, and parents provide best genome coverage

Sweet Cherry Crop Reference Set



- Up to 6 generations
- 49 individuals
  - 38 cultivars
  - 11 selections
- 18 crosses containing 191 individuals (5 to 24 per cross)
- ‘Lapins’ is an Important Parent

Representation by offspring in CRS

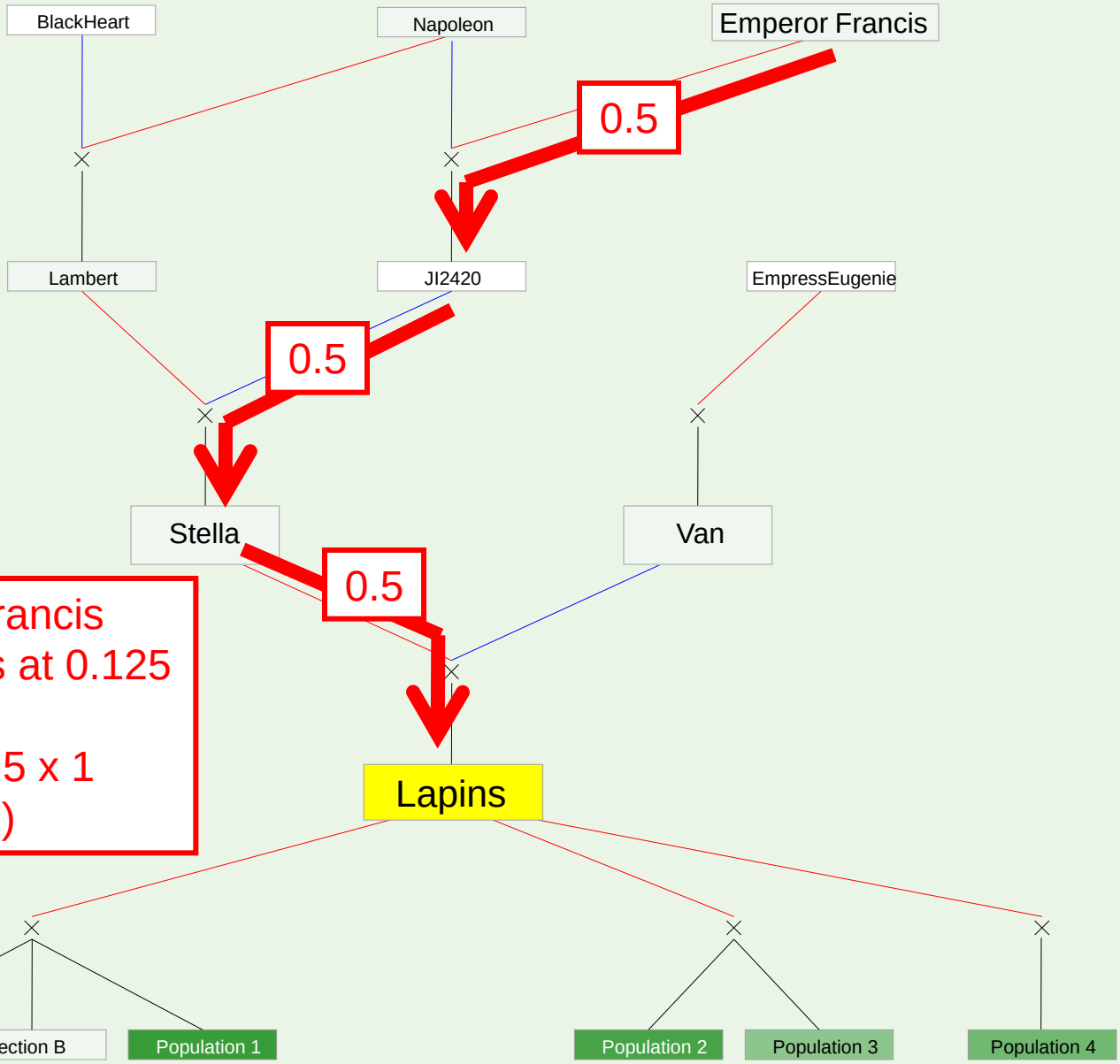


Direct descendants of Lapins each provide 0.5 units allele representation

Pedigree diagrams are outputs of Pedimap program

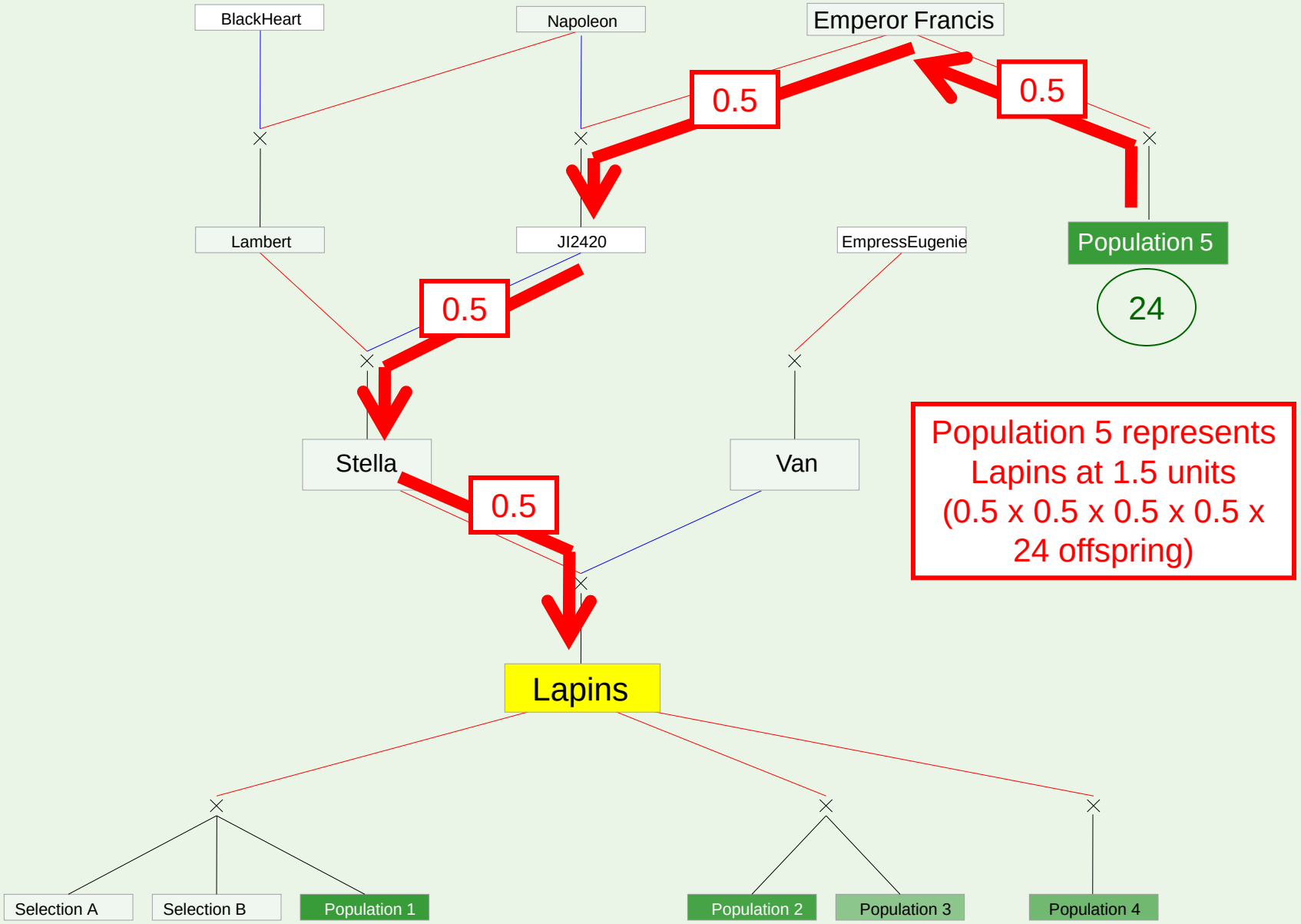
Representation by other relatives

Immediate ancestors of Lapins



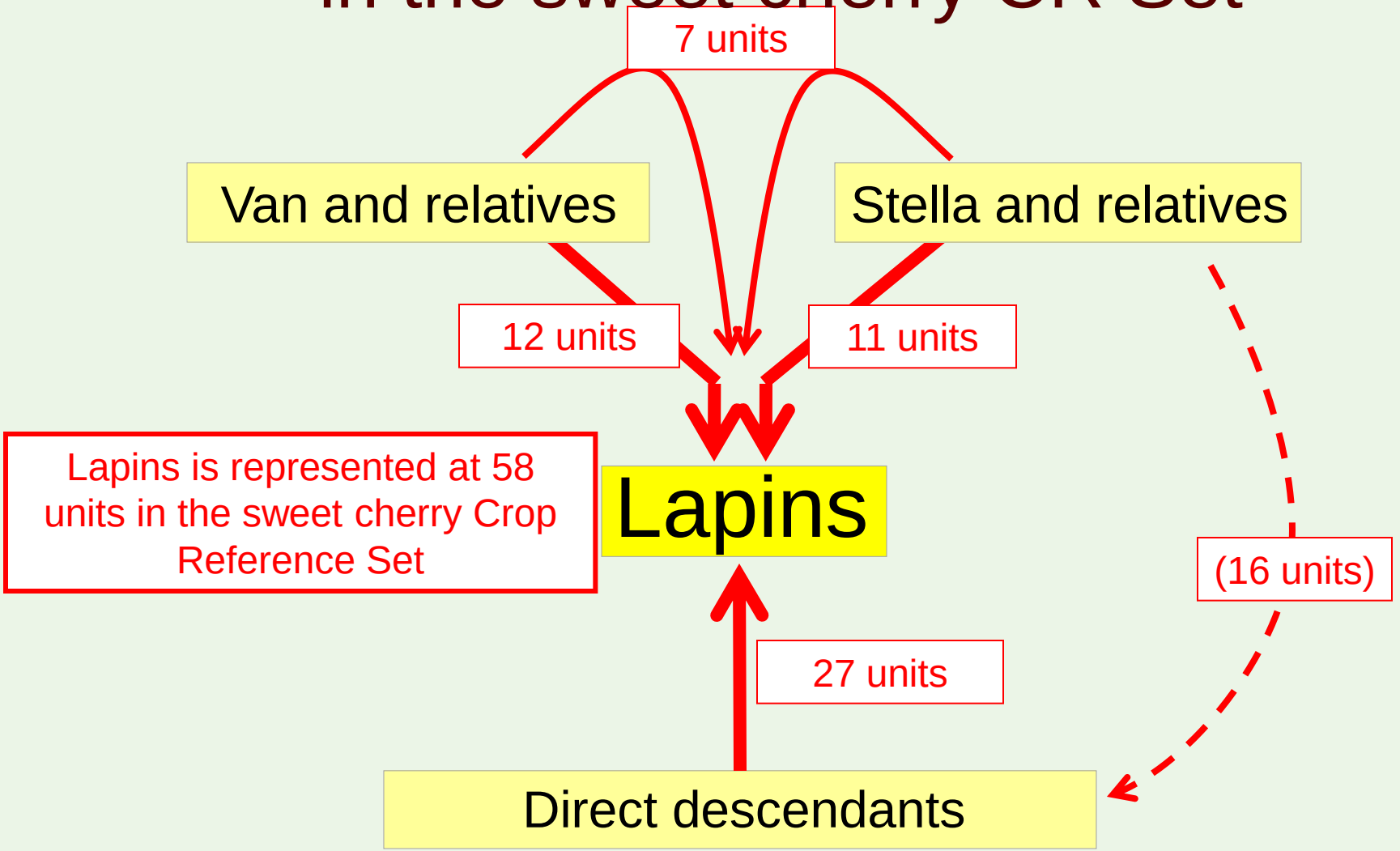
cv Emperor Francis represents Lapins at 0.125 units
(0.5 x 0.5 x 0.5 x 1 individual)

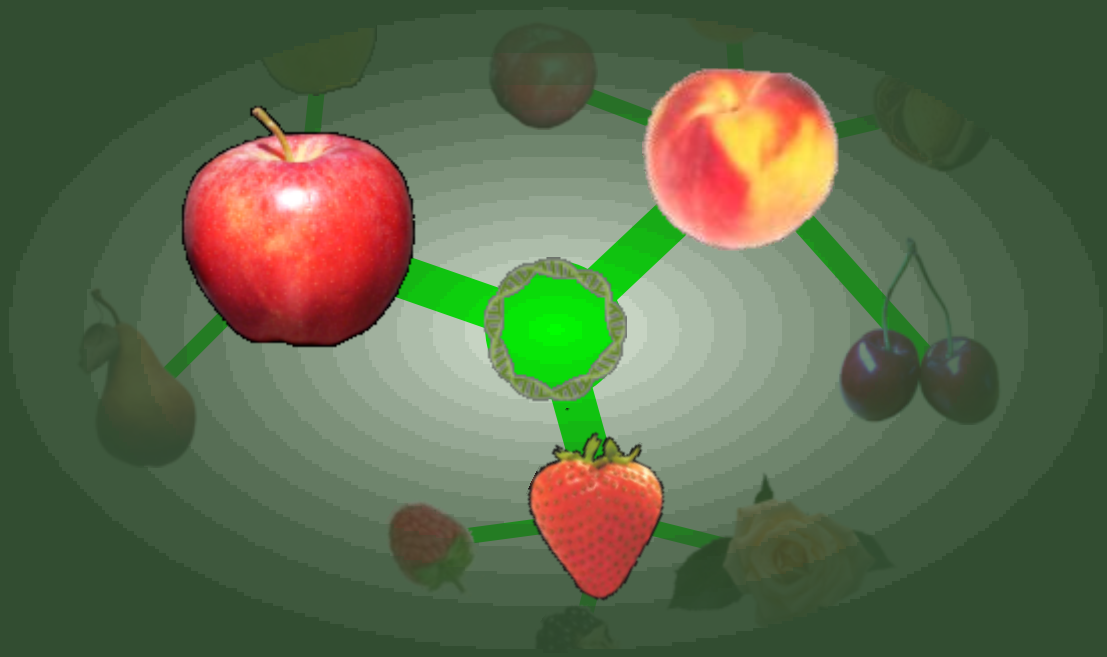
Representation by other relatives



Population 5 represents Lapins at 1.5 units (0.5 x 0.5 x 0.5 x 0.5 x 24 offspring)

Total representation of Lapins in the sweet cherry CR Set





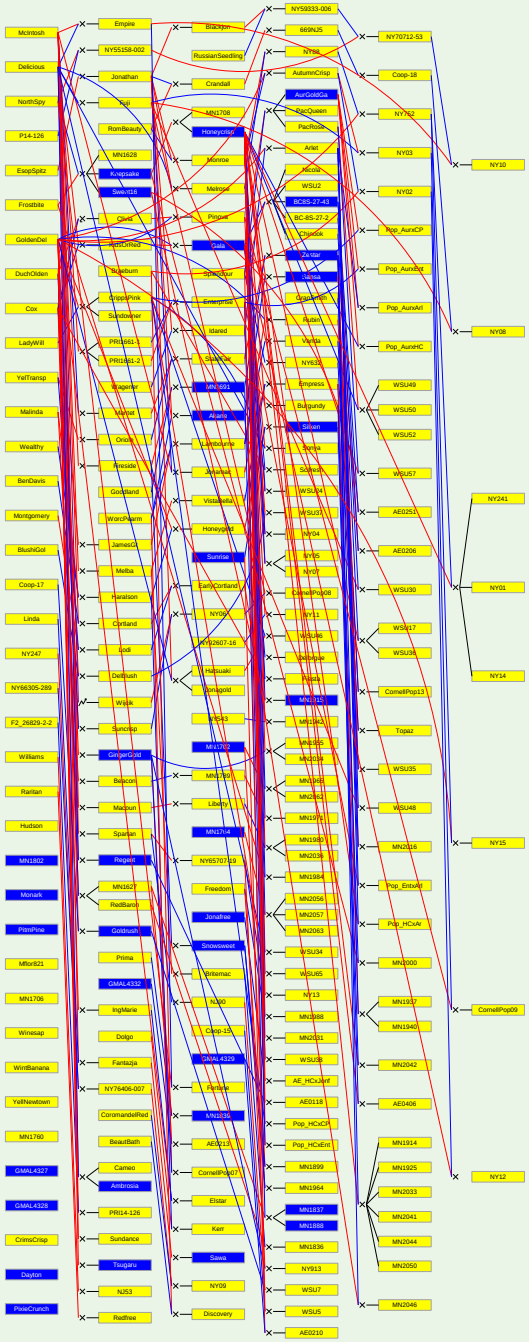
Crop Reference Set
Integrating Multiple Breeding Programs

Apple Peach Strawberry

Apple Crop Reference Set

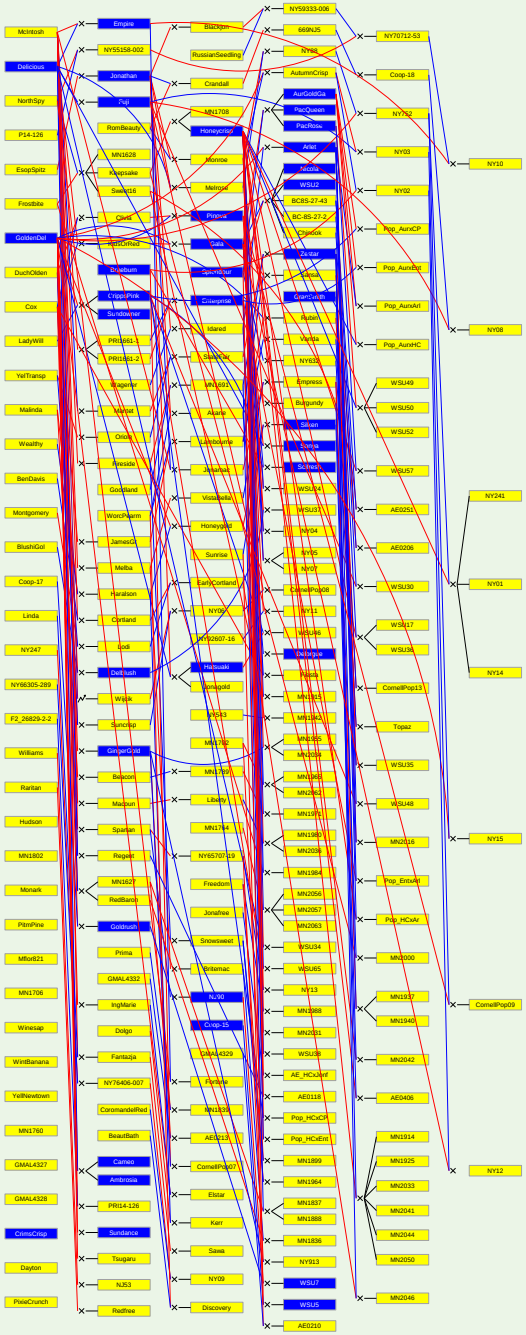
- Need to integrate 3 breeding programs
- Much overlap of Important Parents among 3 breeding programs
- Maximum 6 generations
- Results in CR Set with much commonality and high pedigree connectedness
- Allows transfer of information among breeding programs

Apple Crop Reference Set



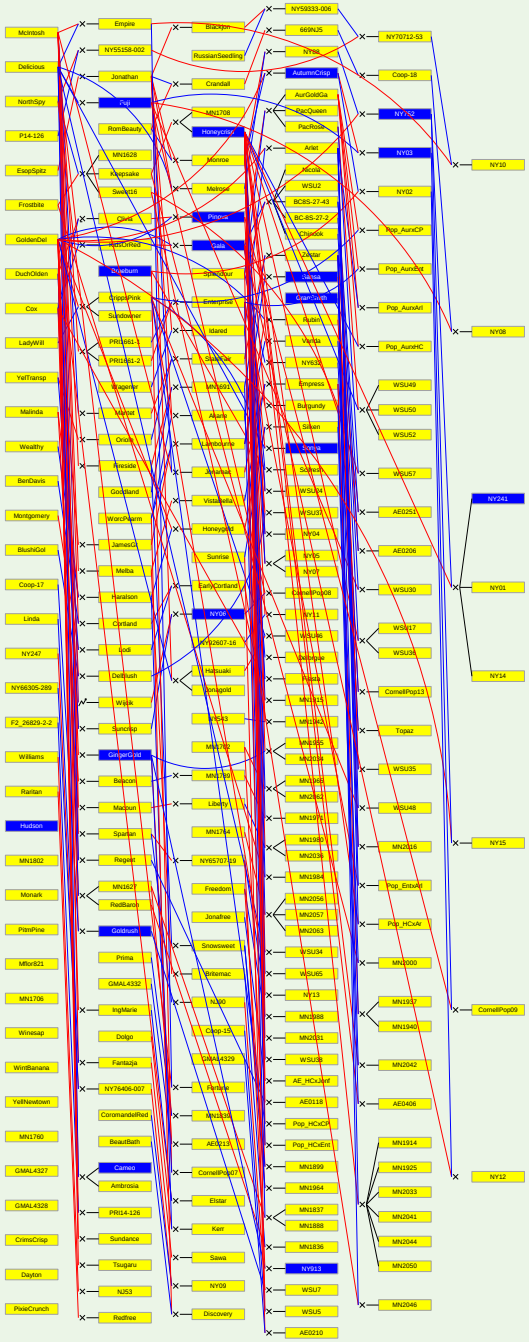
U of MN 35 Important Parents

Apple Crop Reference Set



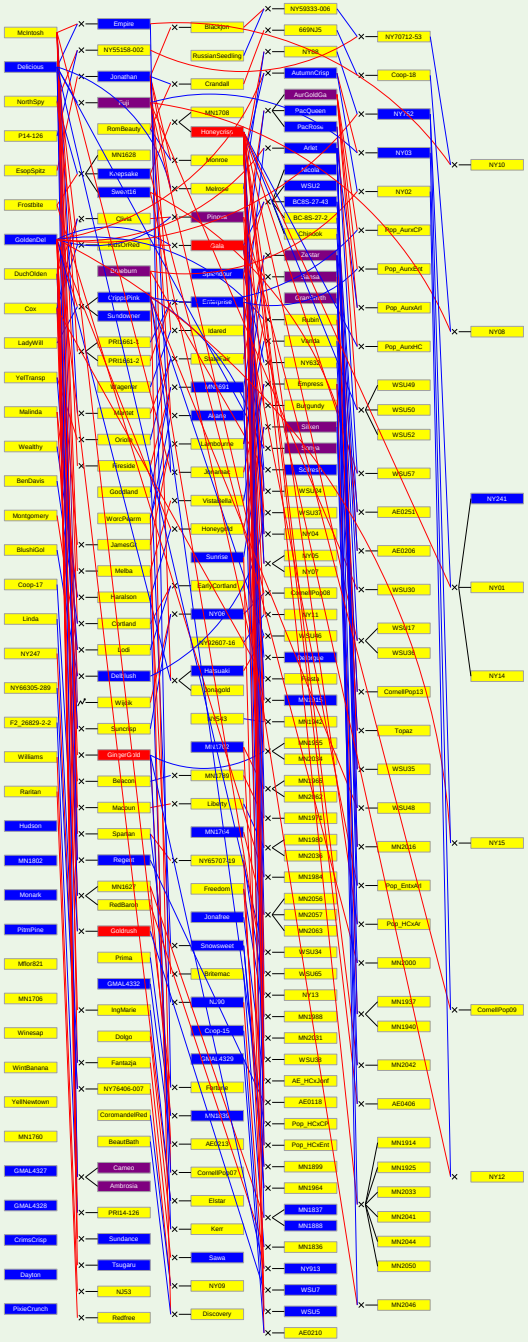
Wash. State 38 Important Parents

Apple Crop Reference Set



Cornell 18 Important Parents

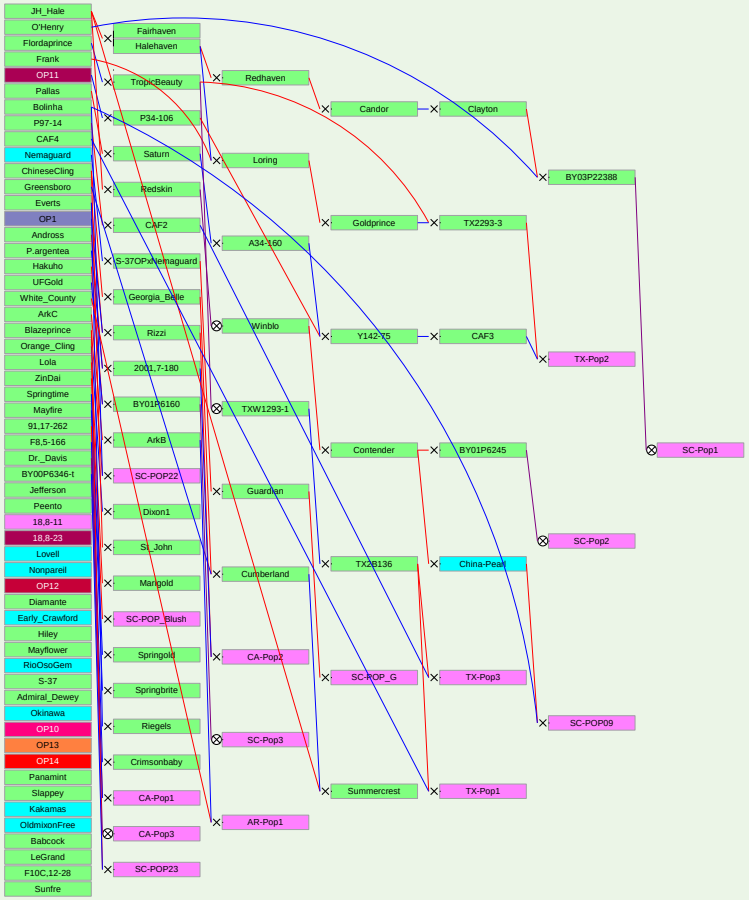
Apple Crop Reference Set



All Programs' 72 Important Parents

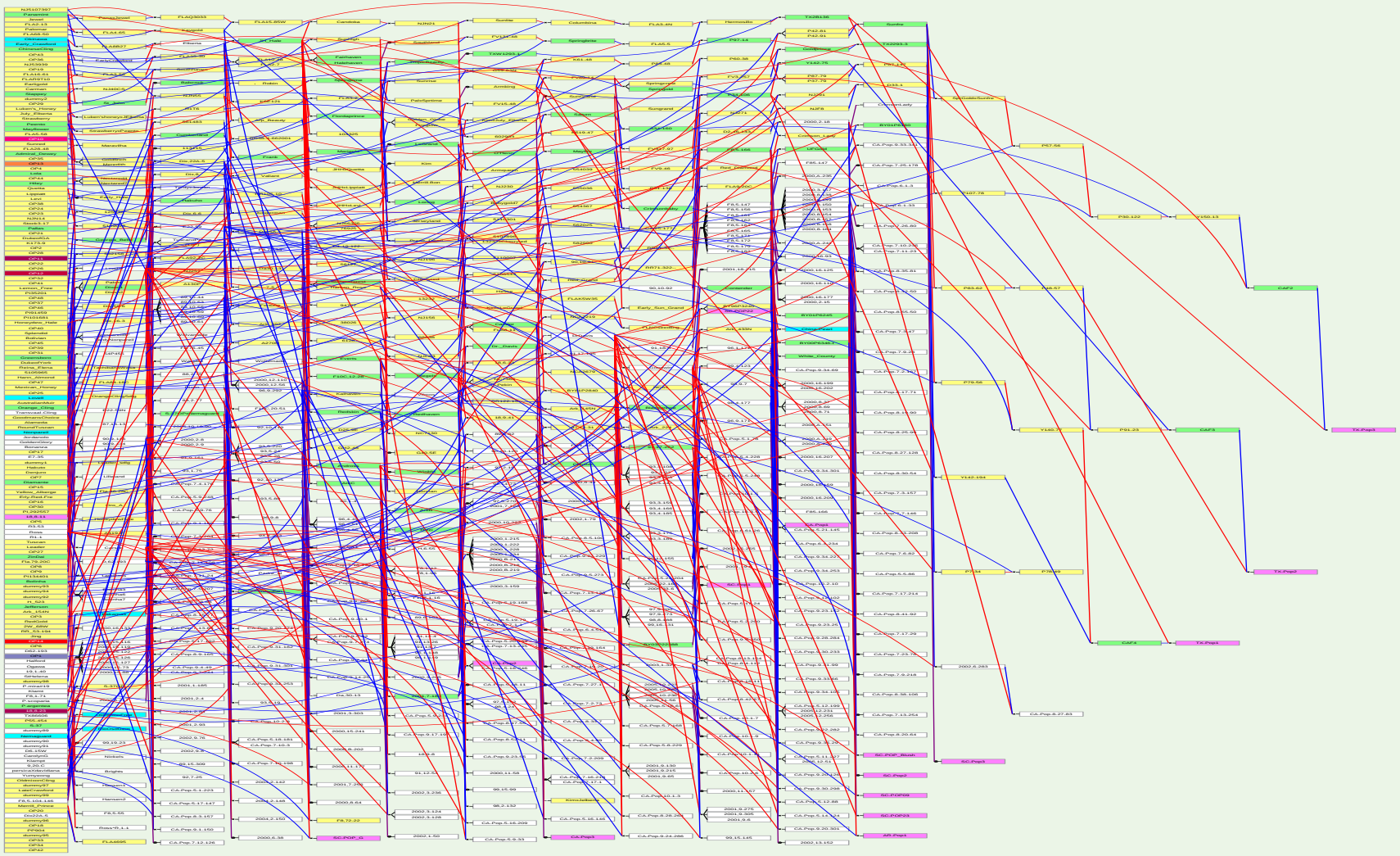
Peach Crop Reference Set

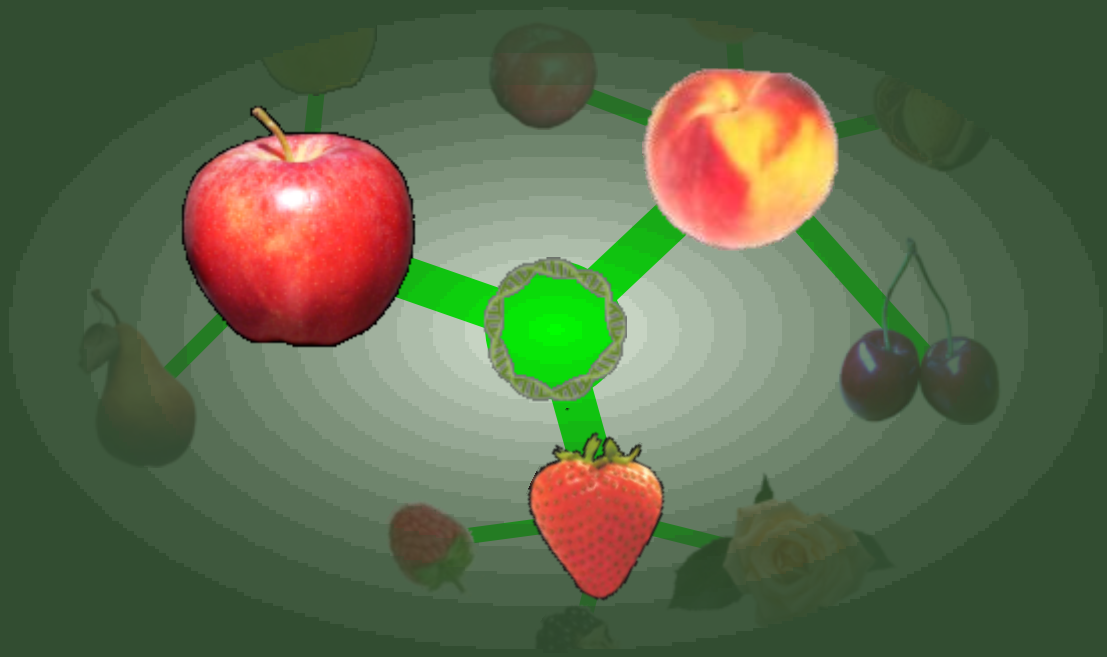
- 4 Breeding programs
  - Limited overlap of germplasm between market types
- 118 cultivars and selections
- 373 progeny in 23 crosses
- Up to 11 generations



Peach Crop Reference Set

Complete Pedigree

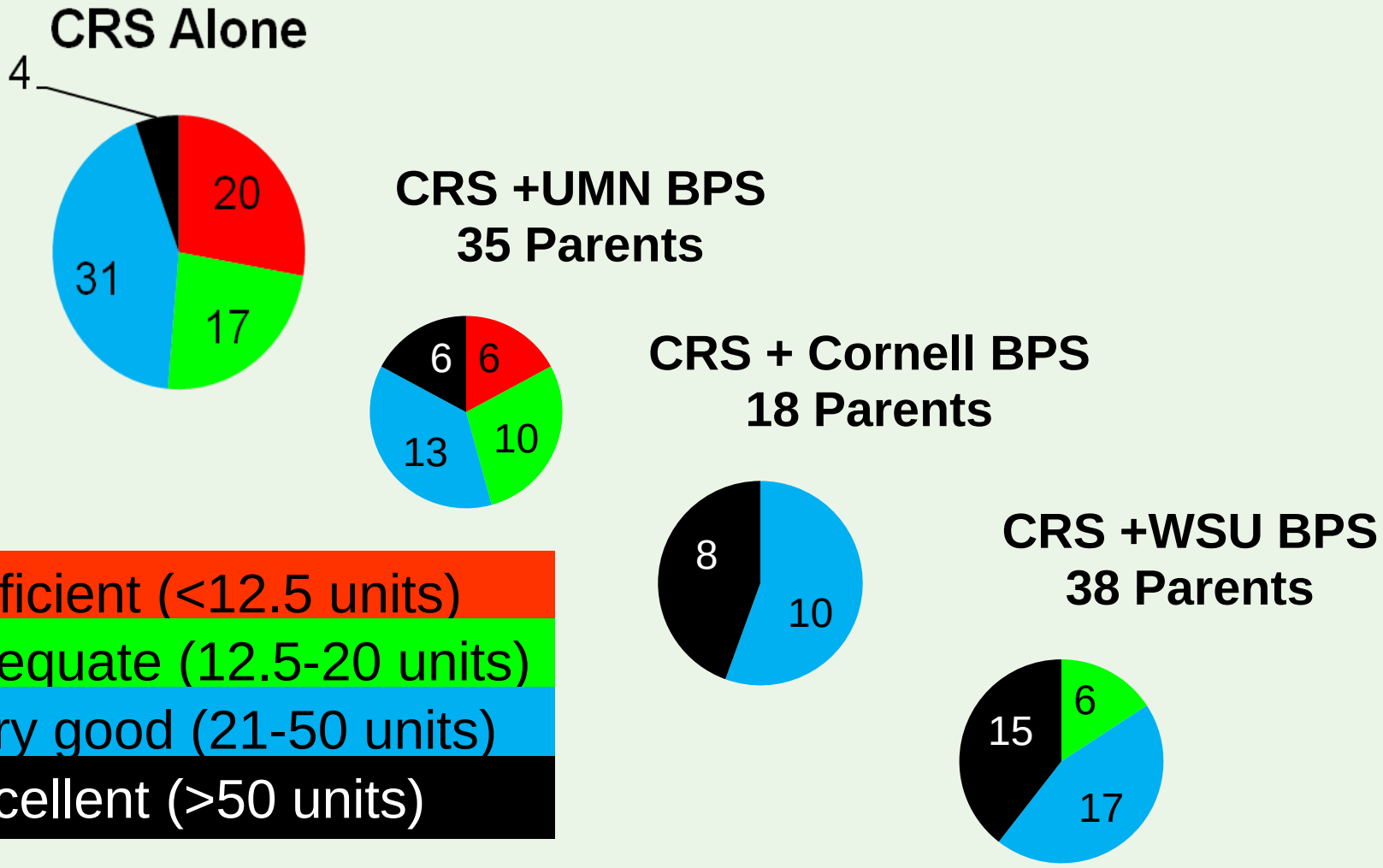


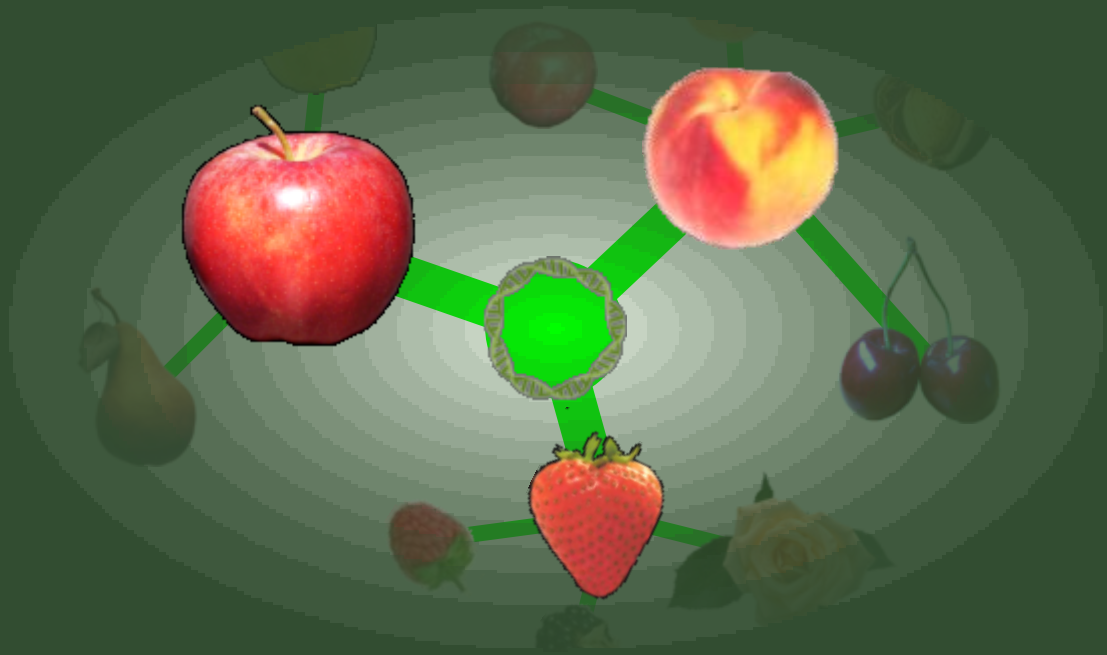


Crop Reference and Breeding Pedigree Sets

Allele Representation of Important Parents in Multiple Breeding Programs

Allele Representation of 72 Important Parents in Apple Germplasm Set





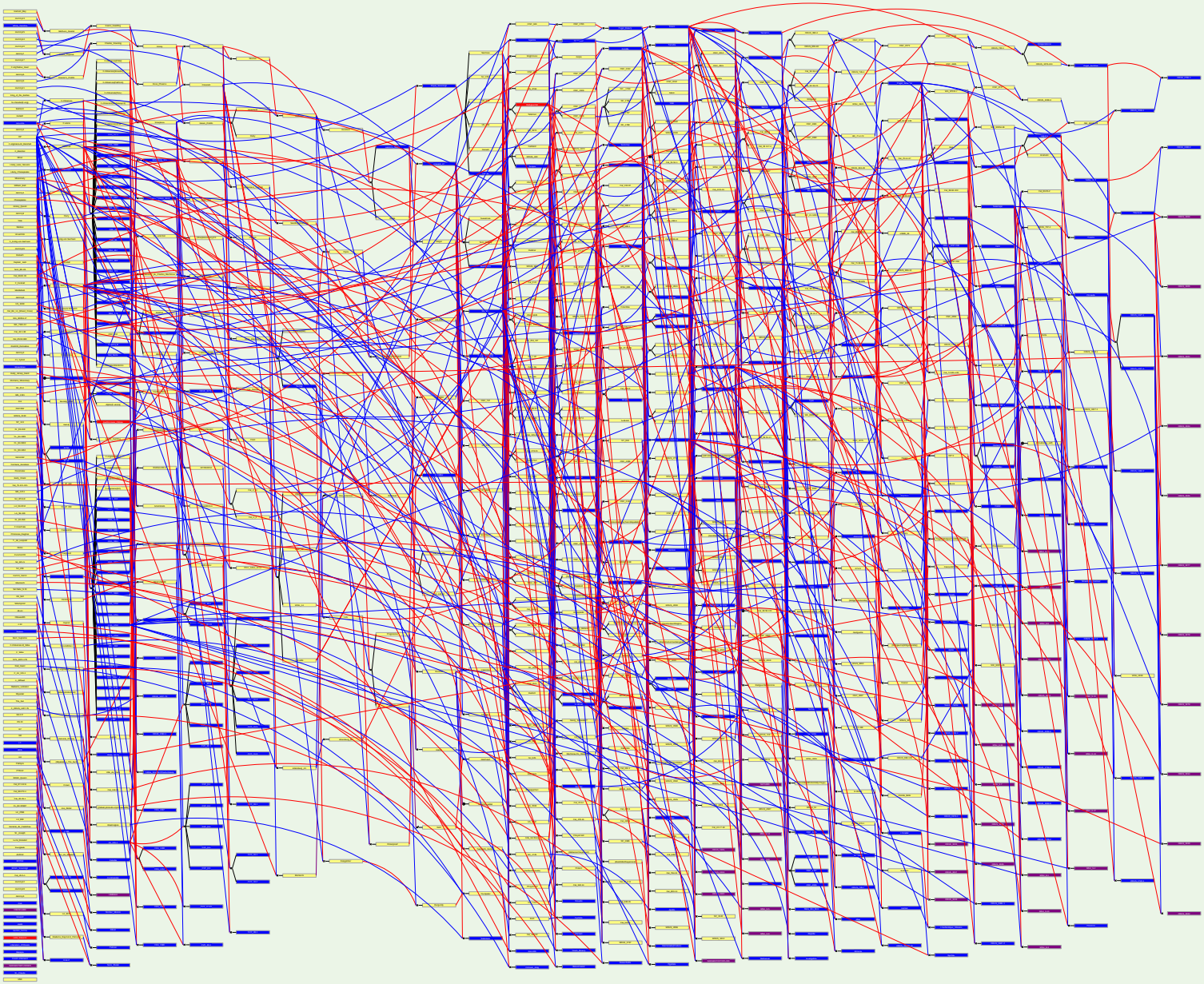
Strawberry

Large Integrated Crop Reference and Breeding Pedigree Set

Strawberry Crop Reference Set

- 26 generations
- Covers several germplasm groups
  - CA, PNW, Eastern US, Europe, Wild
- 209 cultivars and selections
- 78 wild strawberries
  - *F. virginiana*, *F. chiloensis* or *F. virginiana* x *chiloensis*
- 618 seedlings in 44 crosses
- Results in CRS with much commonality and high pedigree connectedness

Strawberry Crop Reference Set



Acknowledgements

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

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

Questions?