

RosBREED

Enabling marker-assisted breeding in Rosaceae

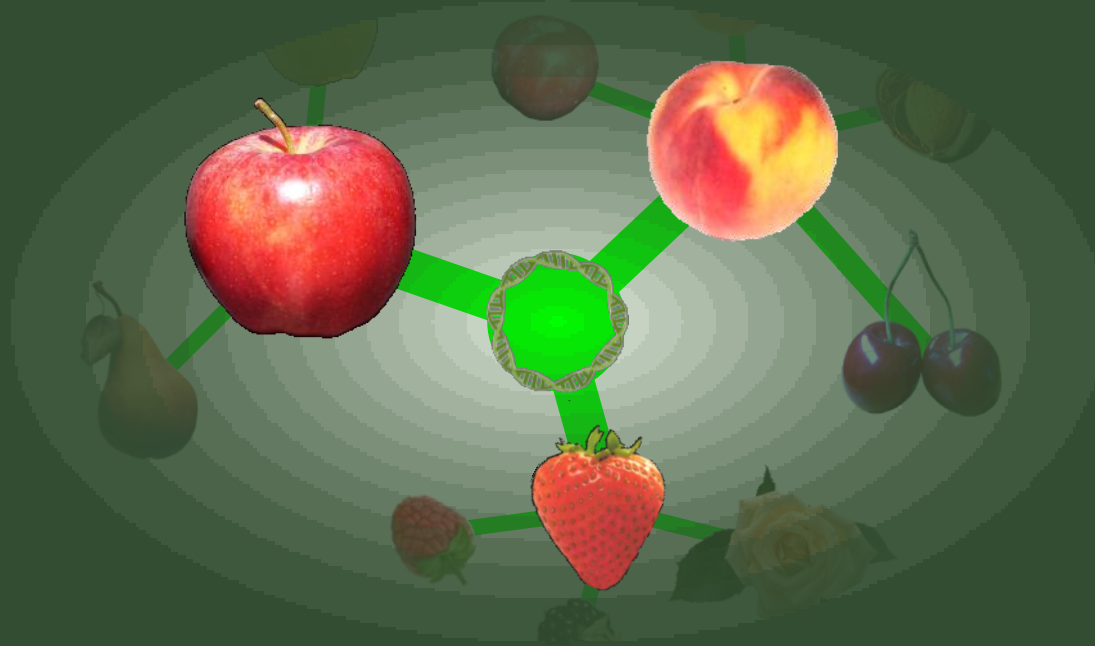
Germplasm Sets and Standardized Phenotyping Protocols for Fruit Quality Traits in RosBREED

Jim Luby, Breeding Team Leader

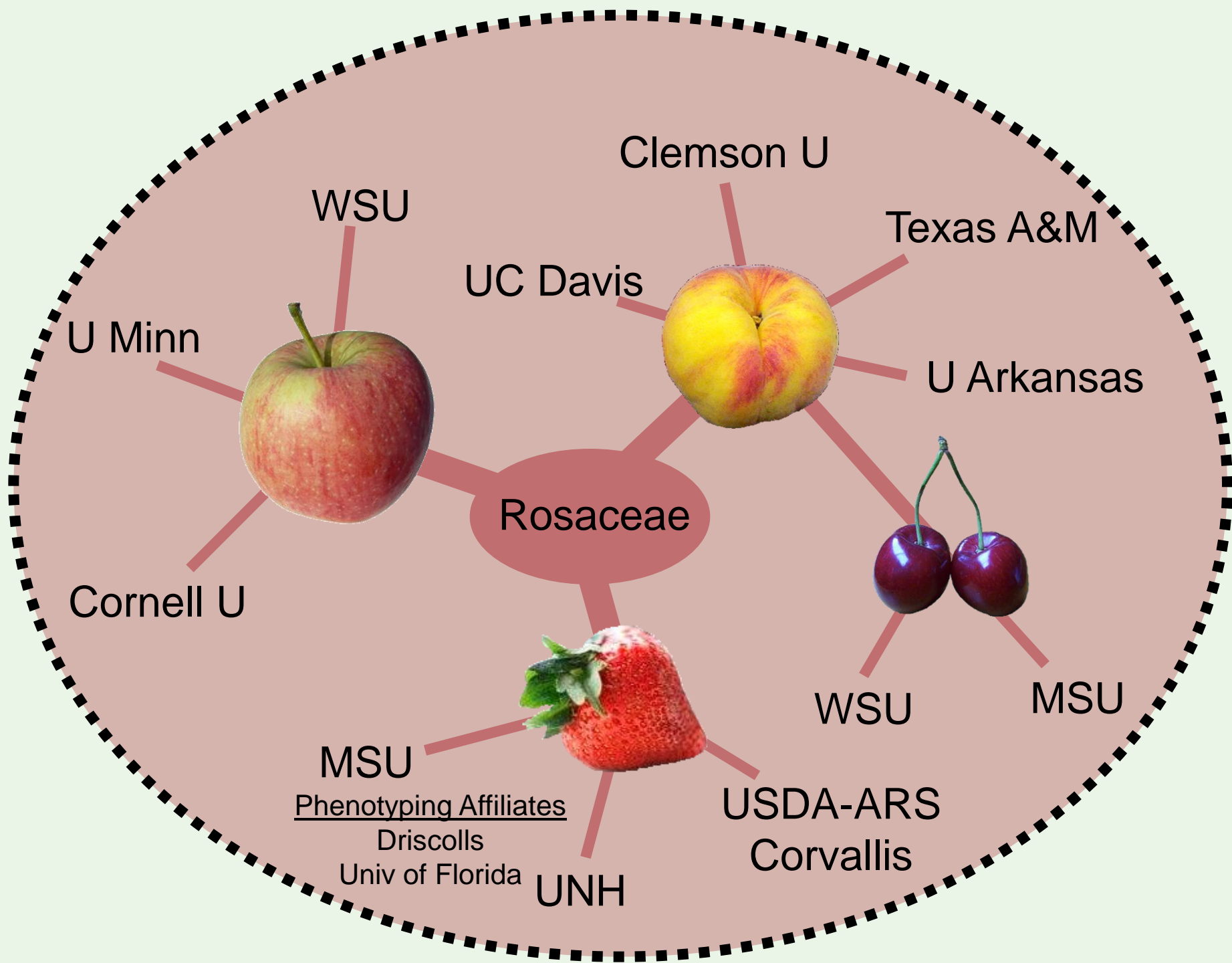


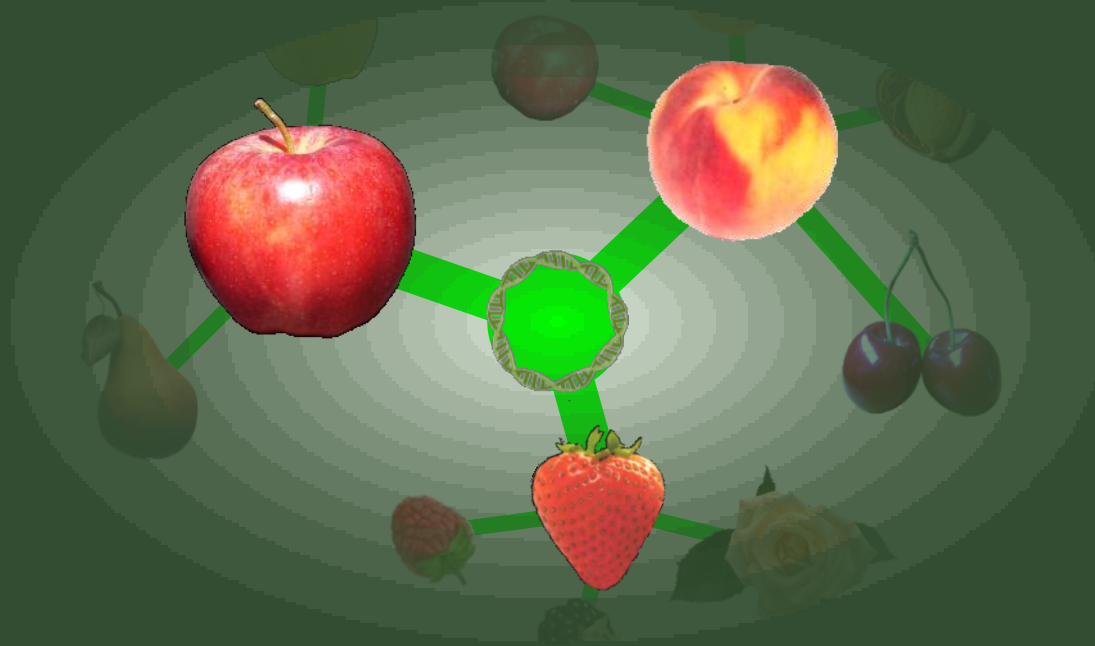
Outline of Presentation

- ❖ RosBREED Demonstration Breeding Programs
- ❖ Standardized Phenotyping Protocols
- ❖ Reference Germplasm Sets
 - ❖ SNP Detection Panels
 - ❖ Crop Reference Set
 - ❖ Breeding Pedigree Set



RosBREED Demonstration Breeding Programs





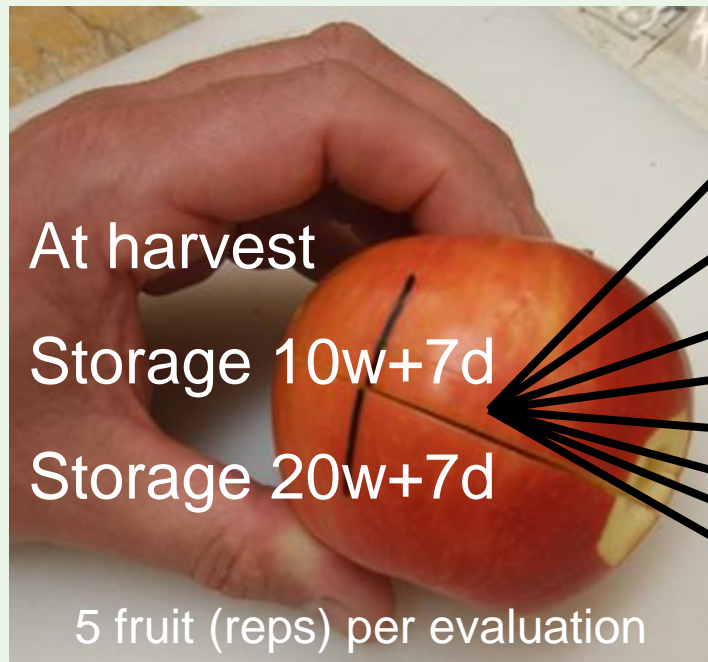
Standardized Phenotyping Protocols

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



Apple Standardized Phenotyping



Firmness, Crispness

– Instrumental, Sensory

Sweetness, Acidity –

Instrumental, Sensory

Color, Appearance,

Juiciness, Aroma – Sensory

Cracking, Russet, Sunburn

Maturity

Fruit size

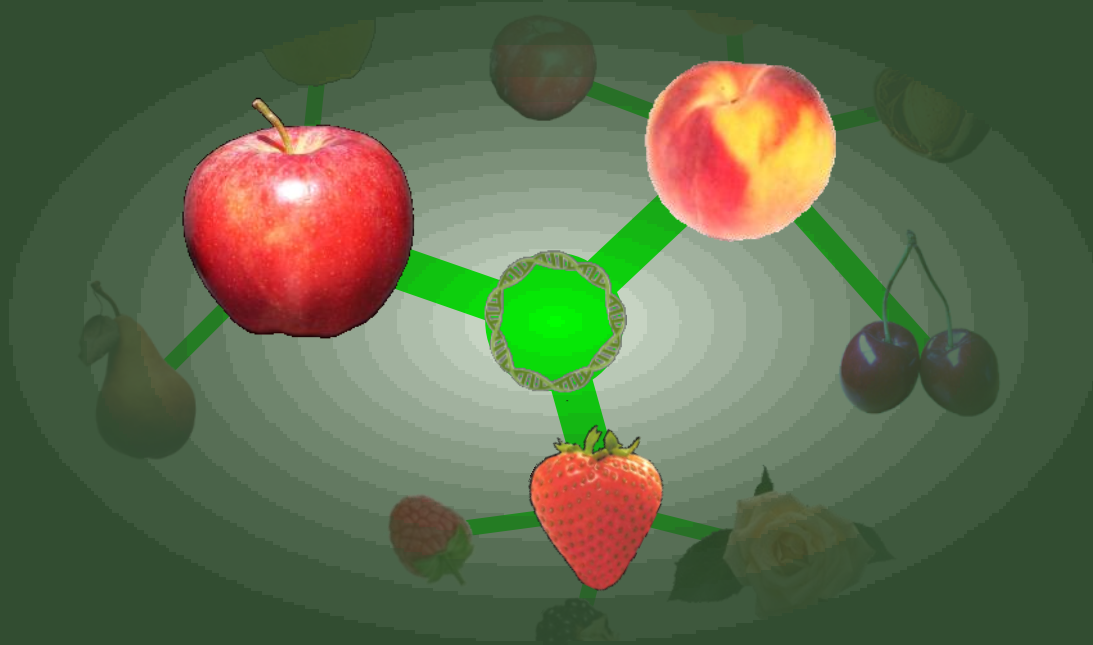
Postharvest disorders

Harvest date, Crop, Dropping

RosBREED Apple Phenotyping Locations



- One location for all evaluations would reduce variation among instruments and evaluators
- Local evaluations more sustainable and relevant for future efforts at each institution
- Conduct standardized phenotyping of Germplasm Sets at respective sites over multiple (2-3) seasons
- Collate data in PBA format, conduct quality control, archive



Reference Germplasm Sets

Crop Reference Set
Breeding Pedigree Set
SNP Detection Panel

Crop Reference Sets

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



Breeding Pedigree Sets

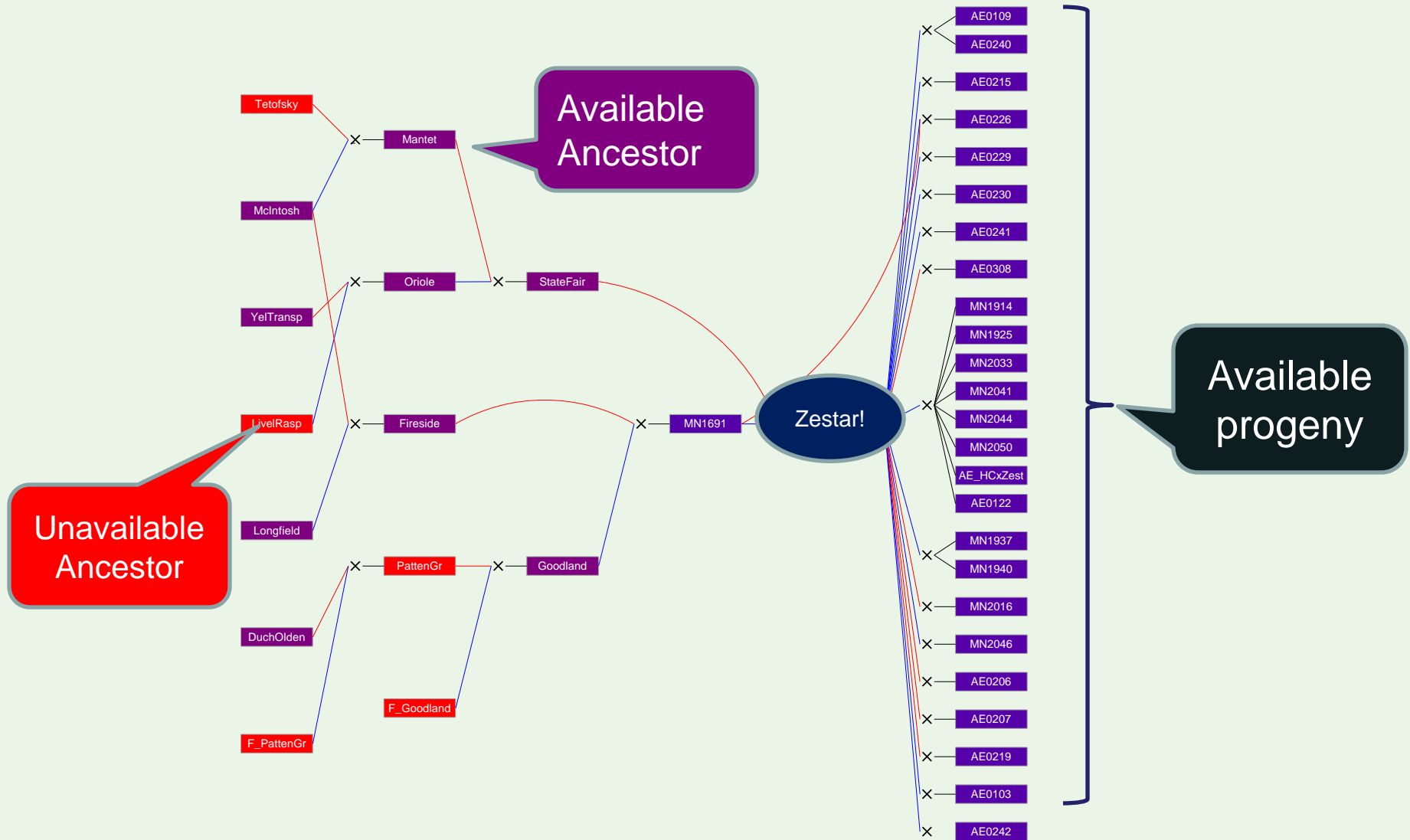
- Resource for proprietary benefit of breeding program benefit only
- ~100-300 extra plants for each breeding program that, together with the Crop Reference Sets, allow full representation of founders of interest to that program
- Information may remain with each breeding program; data-sharing improves power

Reference Germplasm Sets

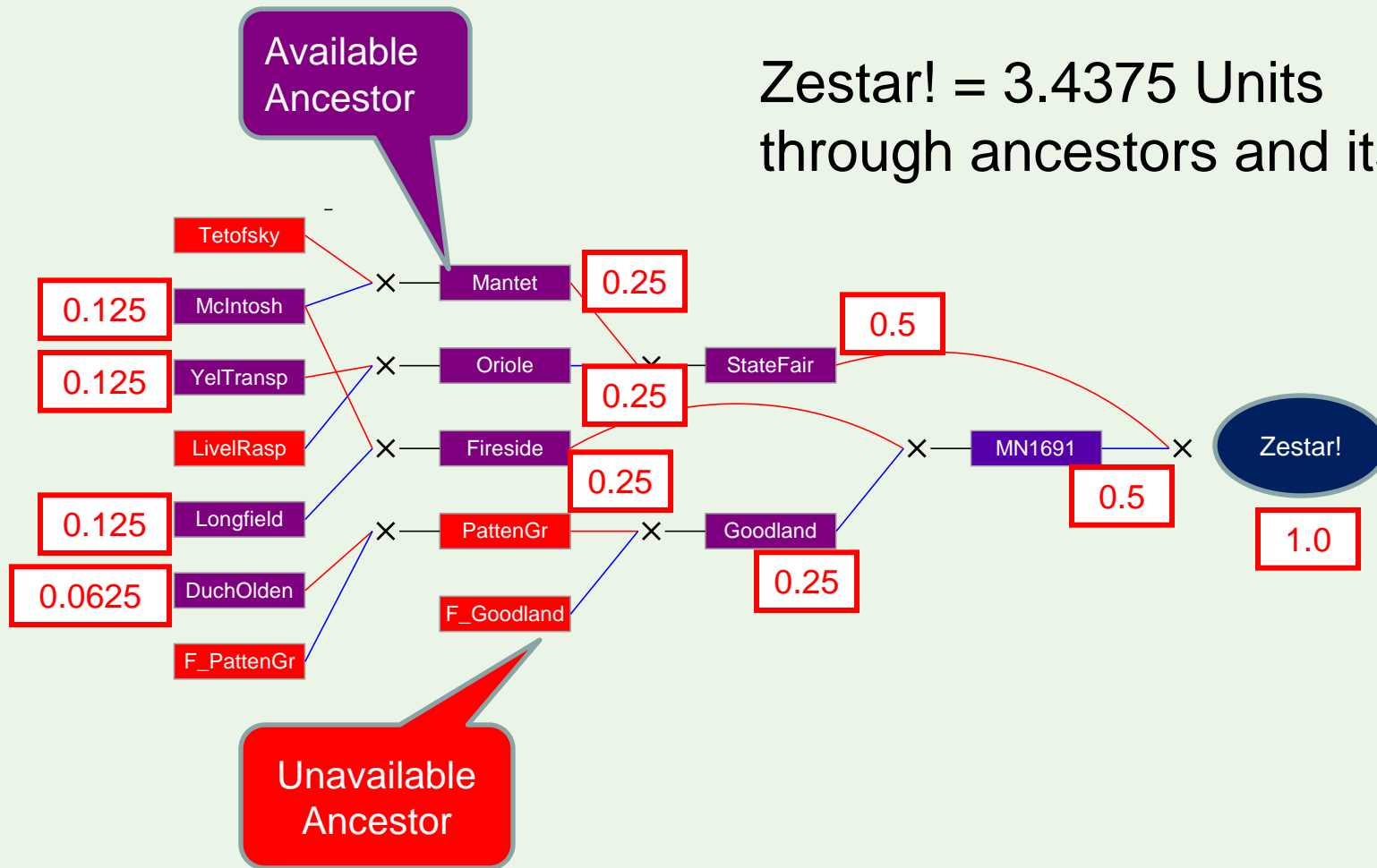
- Approach:
 - Identify important parents among breeding programs
 - Trace pedigrees to founders and identify available founders and intermediates
 - Identify progeny available in breeding programs
 - Use PediMap™ to visualize pedigree relationships
 - Calculate allele representation of important parent back through available founders and intermediates
 - Include progeny to adequately represent important parents
 - Crop Reference Sets will be publicly archived

Identify Important Parent, Ancestors, Progeny

Example at U of Minn: Zestar!



Calculate allele representation of important parent back through available ancestors

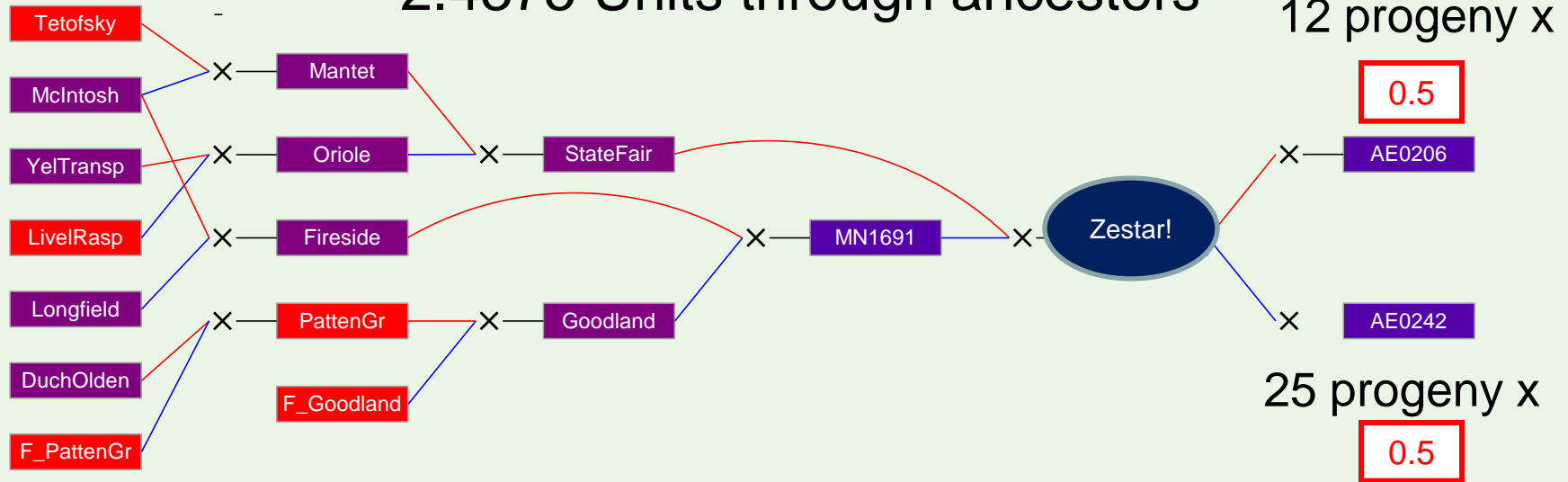


Include progeny to adequately represent important parents

Goal = 12.5 units minimum

1.0 unit through itself

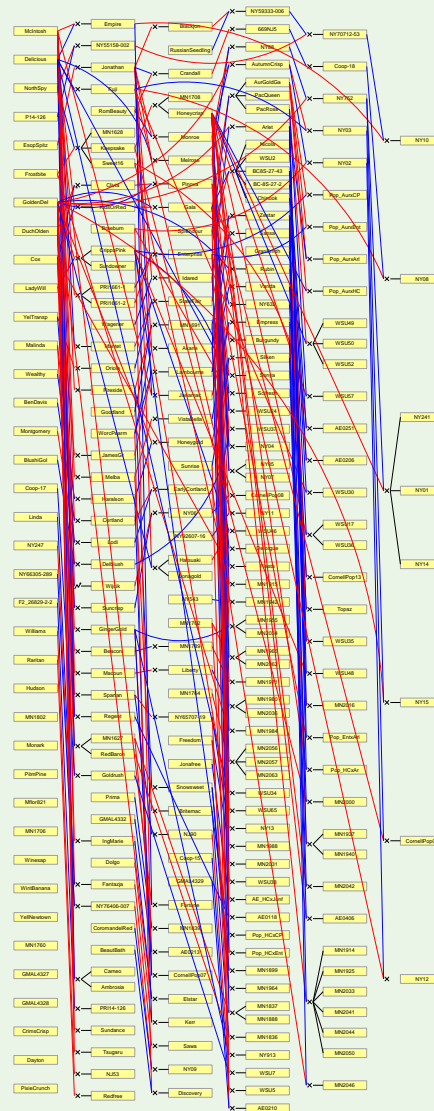
2.4375 Units through ancestors



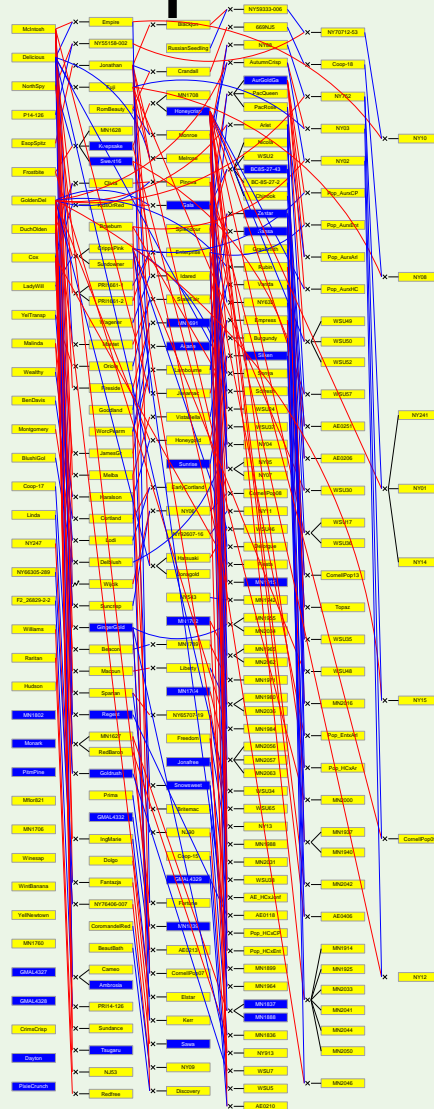
18.5 units through 37 progeny

Zestar! allele representation = ~22 units

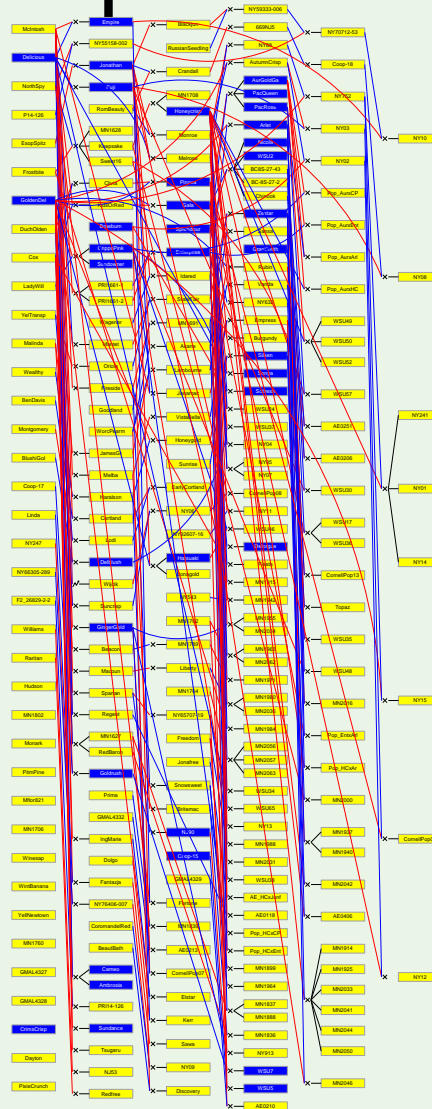
Apple Crop Reference Set



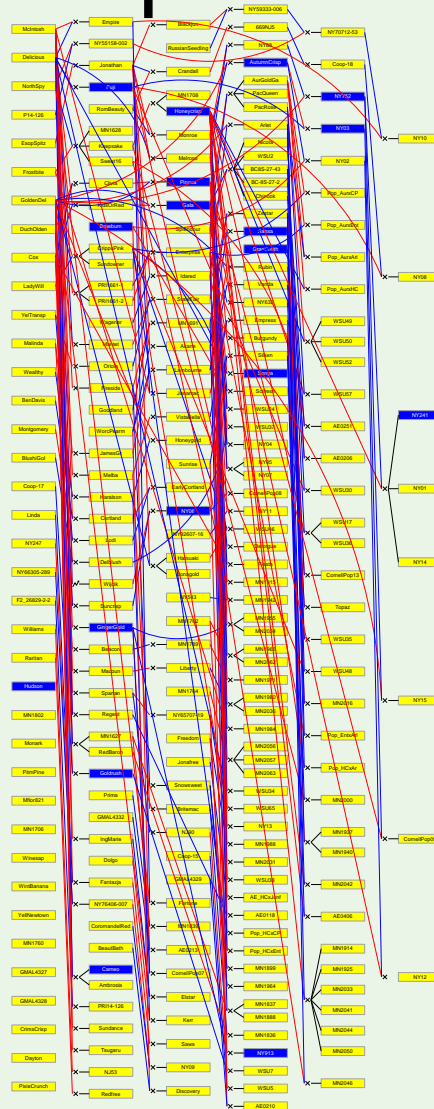
Apple Crop Reference Set: U of MN Important Parents



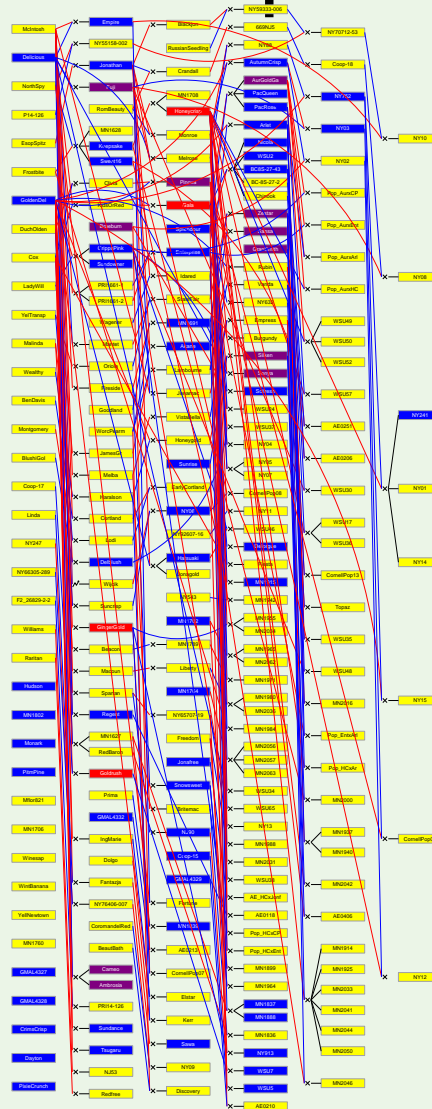
Apple Crop Reference Set: WSU Important Parents



Apple Crop Reference Set: Cornell Important Parents



Apple Crop Reference Set: All Programs' Important Parents



SNP Detection Panel

- Used for genome scans to identify SNPs distributed along genome
- Up to 20 individuals from Crop Reference Set
- Includes Diverse Key Founders or Intermediate Ancestors

Apple SNP Panel

Founders

Intermediate
Ancestors

Delicious

Golden Delicious

McIntosh

Jonathan

Cox's Orange Pippin

Rome Beauty

Northern Spy

Dolgo

Duchess of Oldenburg

Wagener

Cripp's Pink

Fuji

Honeycrisp

Zestar!

Goldrush

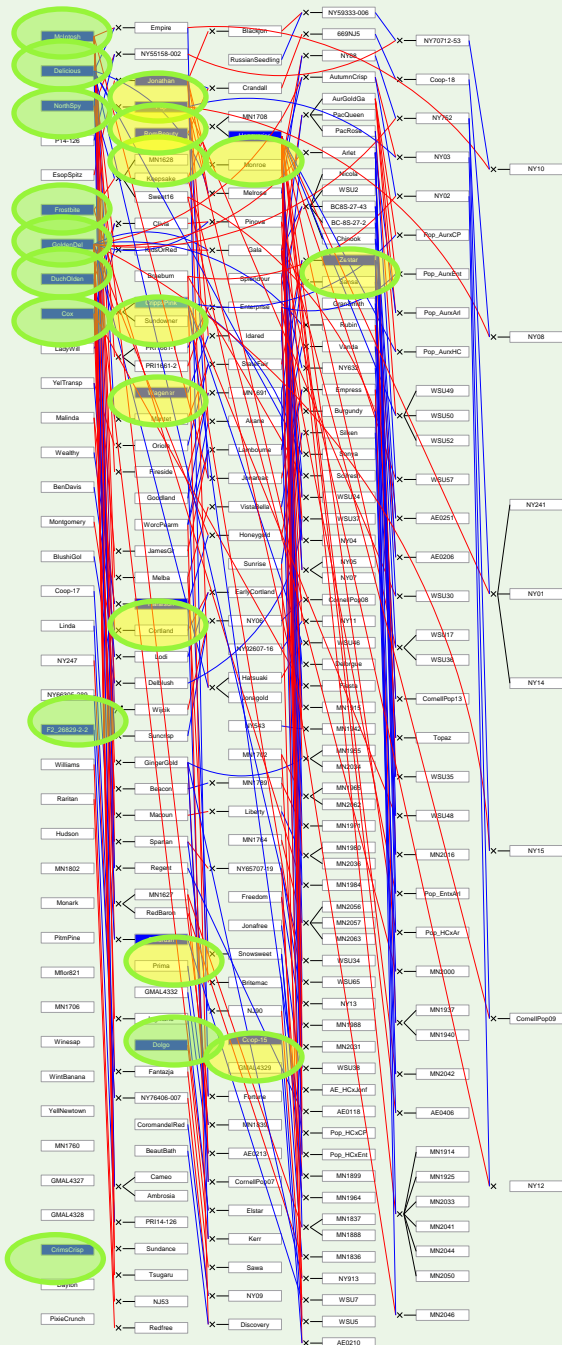
CrimsonCrisp

Coop-15

F2 2689-2-2

Frostbite

Haralson



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Questions?

