Marker-assisted breeding enabled by RosBREED

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Overview

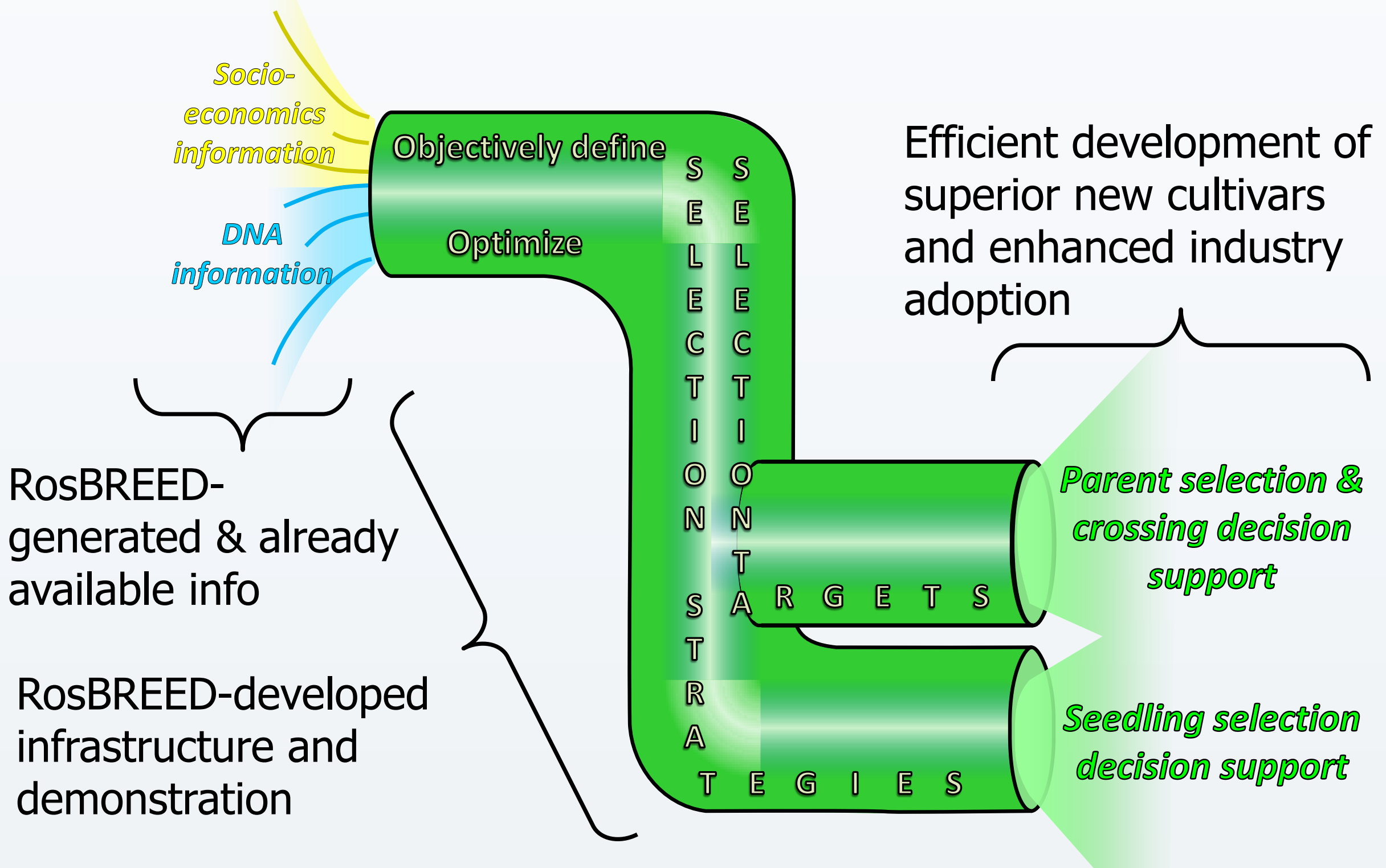
- Significant barriers limit application of marker-assisted breeding (MAB) in horticultural crops.
- Genomics knowledge is being translated into practical MAB tools and integrated into crop improvement programs.
- Breeding programs are receiving training and access to MAB tools to permanently expand capacity.
- Socio-economic factors affecting cost, benefit, technology adoption, supply chain values, and consumer preferences are being considered.
- **RosBREED focuses on fruit quality traits directly linked to consumer demand and stakeholder profitability.**

Twelve U.S. breeding programs - demonstration breeding programs, serve as initial technology adopters (Fig. 1). Other Rosaceae breeding programs are active participants (e.g. Crop Reference Set selection) and beneficiaries of RosBREED deliverables.

MAB Pipeline

- An eight-stage MAB Pipeline will exploit genomic homology across commodity boundaries (Fig. 2).
- Pipeline stages begin with economic weighting of available marker-locus-trait associations; continue through development of breeder-friendly genetic markers, crop-wide validation, and utility assessment within breeding program germplasm; and will be applied to crossing and seedling selection decisions.
- Infrastructure to integrate DNA information into routine breeding operations includes one-on-one training and the community resources of a genome-scanned, comprehensively phenotyped (for fruit quality) reference database on pedigree-linked breeding germplasm.

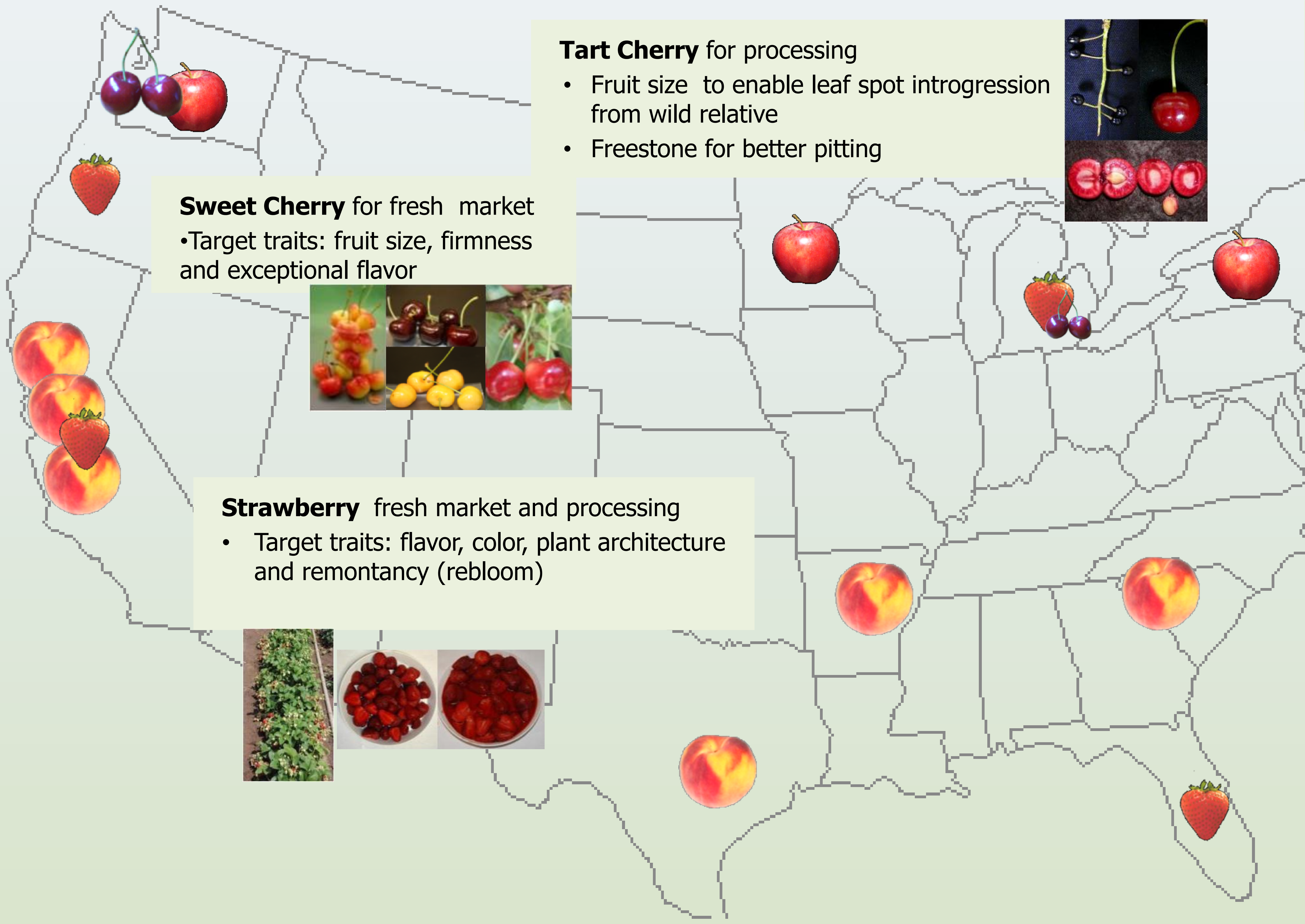
Figure 2. The Marker-Assisted Breeding Pipeline



Efficient development of superior new cultivars and enhanced industry adoption

RosBREED-generated & already available info

RosBREED-developed infrastructure and demonstration



Tart Cherry for processing

- Fruit size to enable leaf spot introgression from wild relative
- Freestone for better pitting

Sweet Cherry for fresh market

•Target traits: fruit size, firmness and exceptional flavor

Strawberry fresh market and processing

- Target traits: flavor, color, plant architecture and remontancy (rebloom)

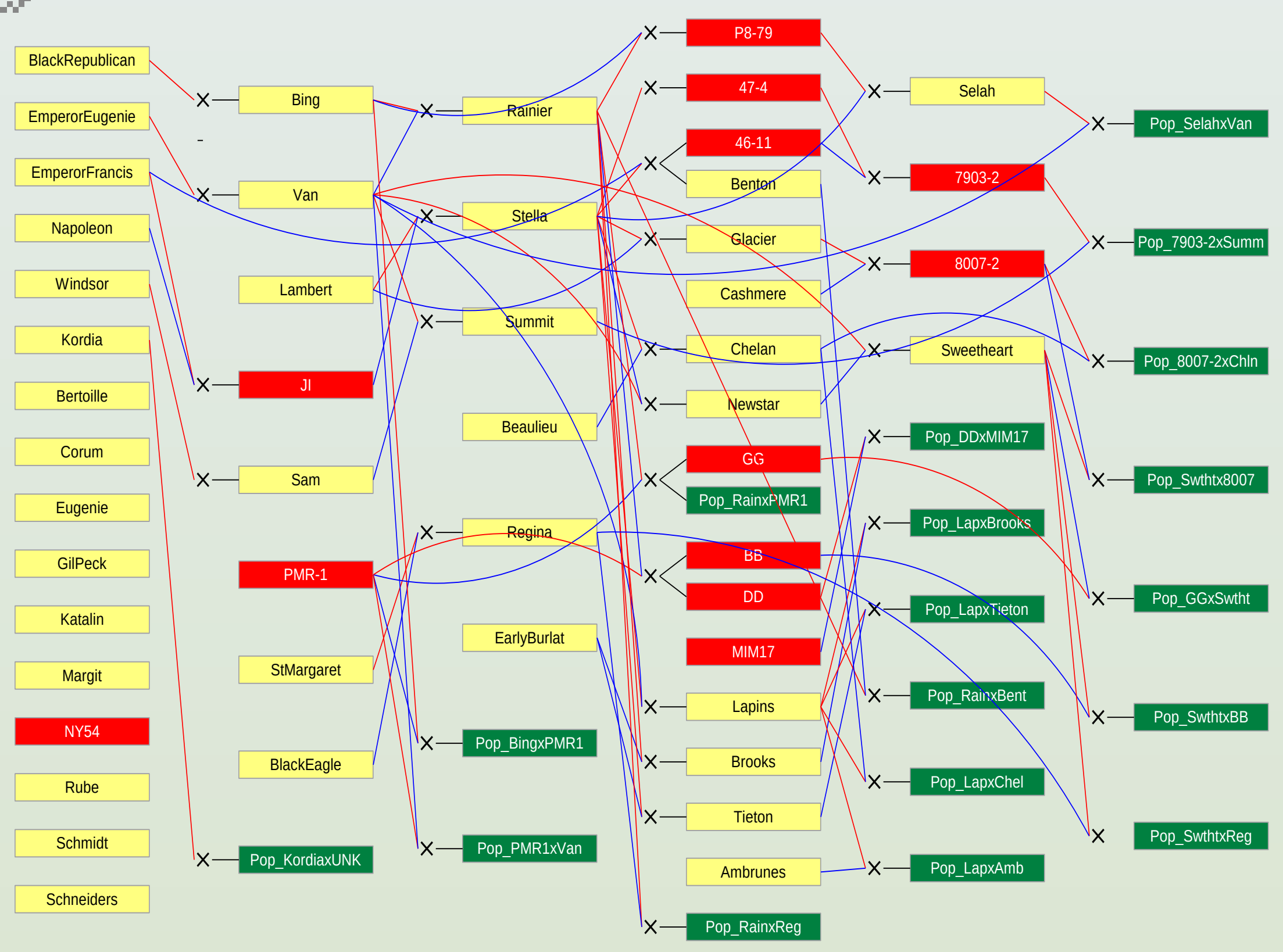
Figure 1. RosBREED demonstration breeding programs and evaluation sites

Apple for primary emphasis on fresh market

- Target traits: flavor, texture, appearance, postharvest life and resistance to storage disorders

Peach for fresh market and canning

- Target traits: flavor, texture, flesh color, size and shape, disease resistances (bacterial spot, brown rot)



- Up to 6 generations
- 49 parents and ancestors
  - 38 cultivars
  - 11 selections
- 18 crosses containing 191 offspring (5 to 24 per cross)

'Lapins' is an example of an Important Breeding Parent

Figure 3. Sweet Cherry Crop Reference Set, visualized by Pedimap software (www.plantbreeding.wur.nl/UK/software_pedimap.html)

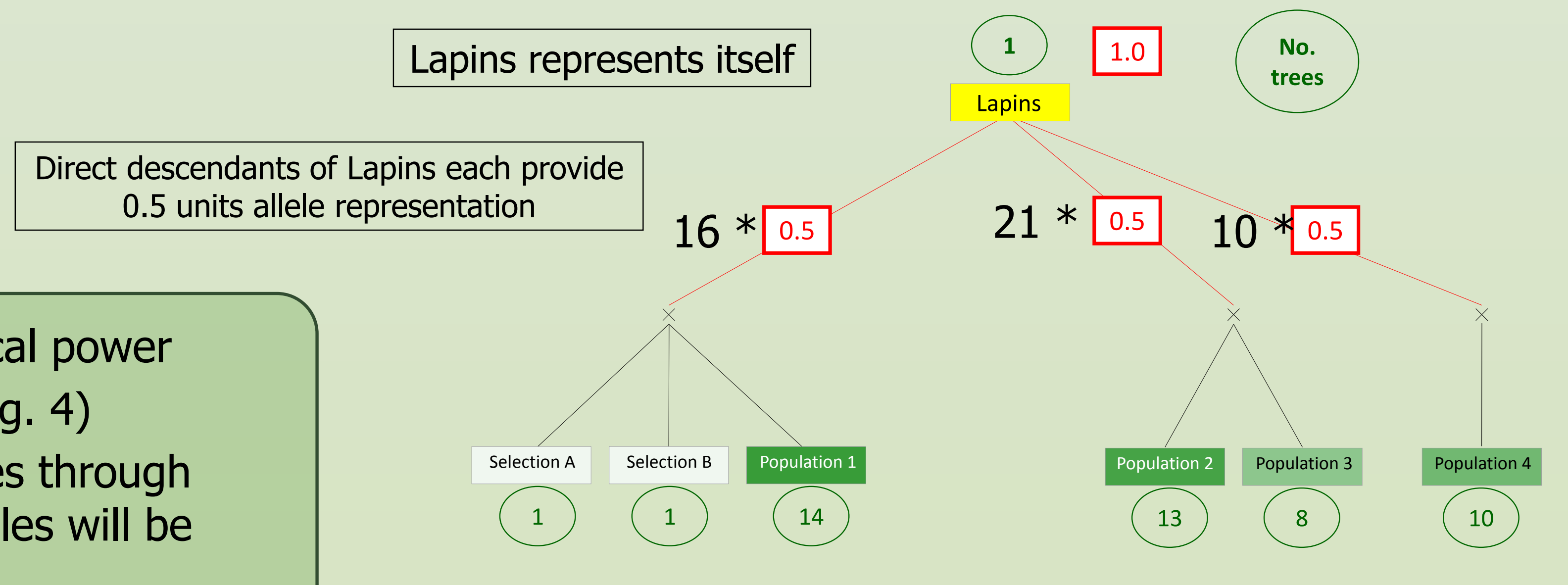


Figure 4. Representation by offspring in Crop Reference Set

Strategy for Constructing reference Germplasm Sets

- The Pedigree-Based Analysis approach will functionally characterize alleles at detected QTLs and describe parental breeding value.
- Pedigree-linked reference germplasm sets represent alleles across the genomes of Important Breeding Parents (Fig. 3).
- Each relative represents an Important Breeding Parent; goal was >12.5 representation units (e.g. 25 F_1 s) for statistical power
  - Offspring represent alleles of these Parents (Fig. 4)
  - 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

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/resources/fruit-evaluation

Crop Reference Sets (CR Sets)

- ~480 individuals (cultivars, ancestors, founders, breeding lines, selections, and seedlings) that are fruiting in 2010-2012 (Fig. 3)
- 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

Breeding Pedigree Sets (BP Sets)

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

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