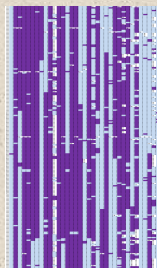


VitisGen: A Coordinated Effort to Implement Genomics Technology for Marker Assisted Breeding

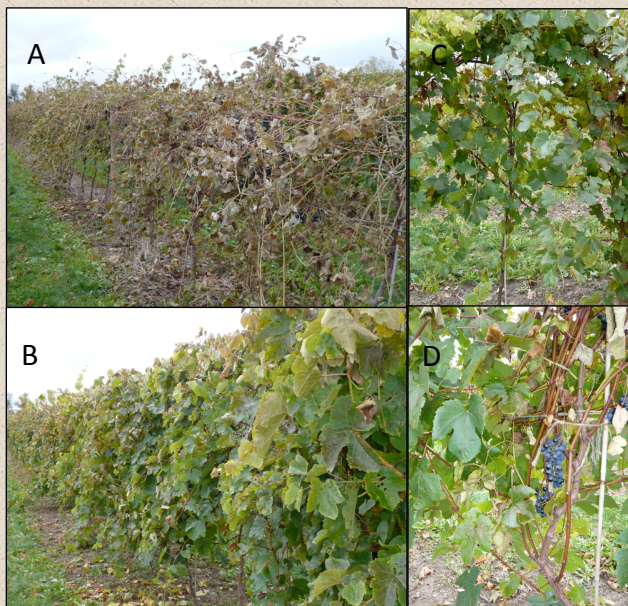


Bruce Reisch and Lance Cadle-Davidson

Qi Sun, Gavin Sacks, Anna Katharine Mansfield, David Gadoury,
Robert Seem, Peter Cousins, and 17 others

1

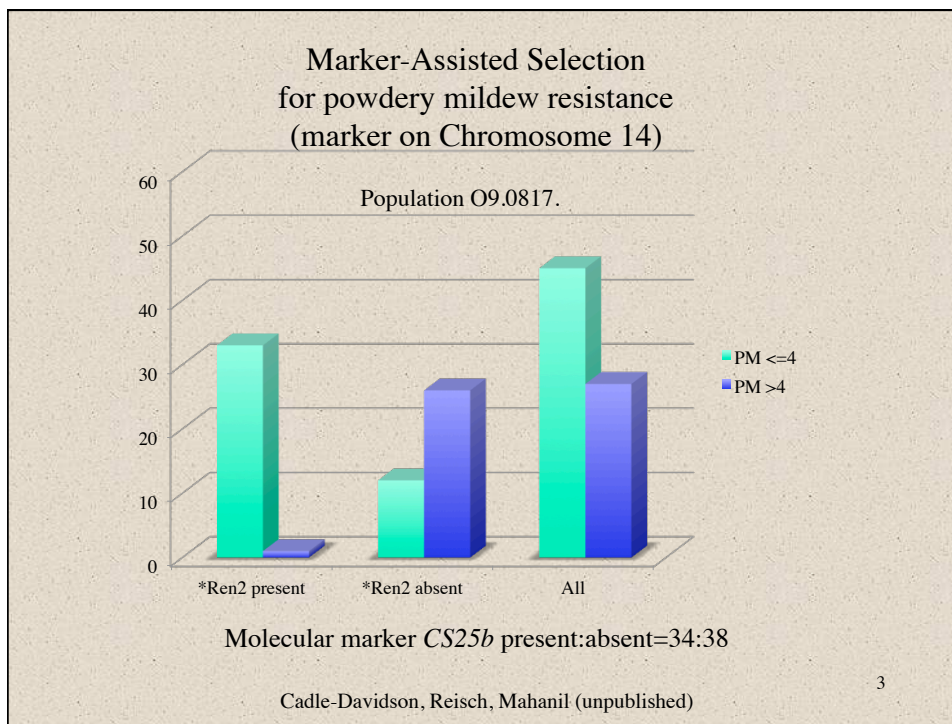
Unselected population



Run1
seedlings

Run1 population

2



Advantages to Marker-Assisted Selection (MAS) in Grape Breeding

- Pyramid (combine multiple) resistance genes
- **Early screening for fruit traits**
- For traits that are difficult to evaluate or require specialized equipment
- Selection of parents based on genes sought to combine in progeny
- More accurate than field/lab evaluation
- Narrow in on causal gene

Overall Project Goals:

Goal is to address industry needs via application of new technology to grape variety development

1. Identify top priority traits and document their value
2. Develop >30 new DNA markers linked with traits
3. Apply markers to accelerate cultivar improvement
4. Enhance communication between industry, researchers and consumers; develop educational resources in breeding and genetics



5

Huge in scope

- 5-year project, currently with 2 years of funding (~\$2 million) from USDA-NIFA Specialty Crops Research Initiative Program
- Combining expertise of breeders, geneticists, pathologists, physiologists, chemists, enologists, computational biologists, sociologists, economists, and the grape industry
- 21 project leaders, 4 collaborators, 12 institutions: (Cornell U., Cornell Coop. Extension, USDA-ARS (CA & NY), SD State, UC Davis, U. MN, MS State, OK City U., OK State U., FAMU, MO State, and Nova Scotia Agric. College)
- Industry Advisory Committee with national representation.

6

Populations and Traits

- All U.S. bunch grape breeding programs
 - End uses: Table grape, Wine, Raisin & Rootstock
- Centrally-evaluated traits
 - Powdery mildew resistance: 16 populations
 - Cold tolerance: 11 populations
 - Fruit quality: 15 populations
- 18 Mapping populations-centralized dna analysis
 - 3000 progeny * 20,000 markers = **60M data points**
- Marker application: 5000 progeny per year
 - ~15,000 progeny * 20,000 markers = **~300M data points**



Abiotic Stress Evaluation Fennell: Low Temperature

Assays performed

- 2011-12 Dec, Jan, Feb, Mar
- Viability
- Differential thermal analysis (DTA)
- Depth of dormancy



Powdery Mildew Evaluation Cornell/ARS Plant Pathology



8 isolates tested on parents
Selected isolates across 20 progeny
Coomassie microscopy for selected isolate(s)
Summer screening of entire population



Disease resistance and cold hardiness
come from wild grapevine species, e.g.

Vitis riparia



Vitis cinerea

9

Fruit Composition - Cornell/Gallo (Sacks)

- **Populations**

St. Pepin x Cabernet Franc
(Owens)

Horizon x Ill. 547-1 (Reisch)

Other populations will be added . . .



- **Assays performed**

i) Targeted analyses of known compounds of interest

- Volatiles: MPs, 'foxy' odorants, C6 compounds, other herbaceous and earthy odorants

- Non volatiles: organic acids (esp. malic), yeast assimilable nitrogen, phenolics

ii) Non-targeted volatiles analyses

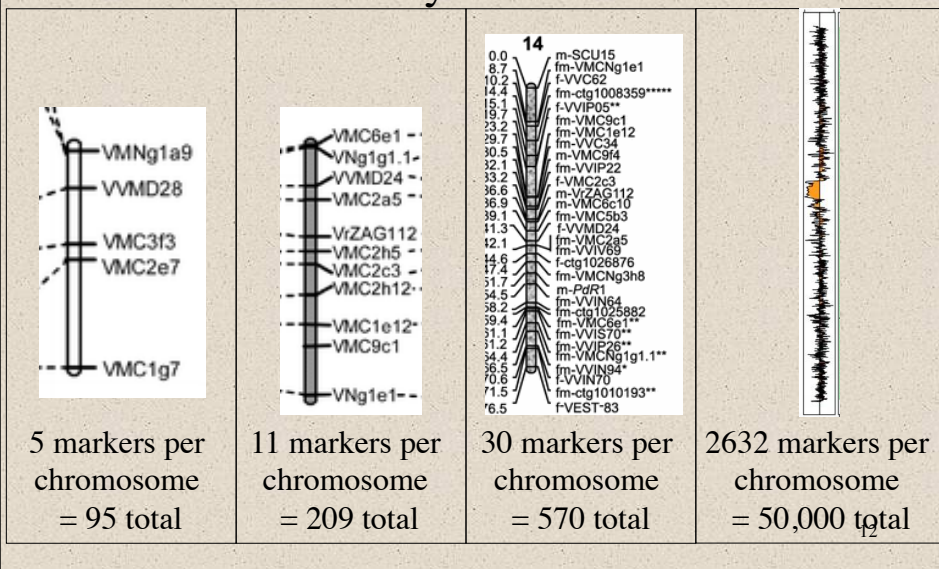
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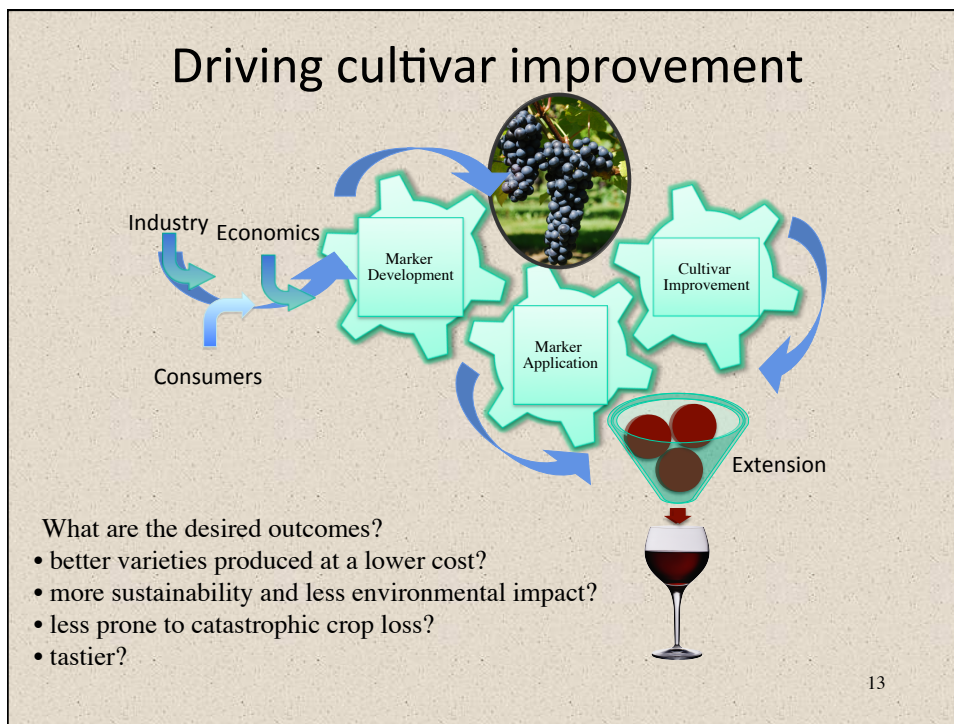
Populations and Traits

- Locally-phenotyped traits:
 - Black rot, anthracnose, phomopsis, downy mildew, bunch rot
 - Nematodes: *Meloidogyne* root knot, *Xiphinema index* dagger
 - Phylloxera: foliar and root
 - Cluster size and morphology, seedlessness, berry size, firmness, skin color, flower type
 - Dried on vine
 - Juice quality: antioxidants, secondary metabolites, muscat flavor, pigments and phenolics
 - Vine vigor and productivity
 - Phenology, critical photoperiod, dormancy, budbreak, chilling requirement



Marking traits: Marker density on a chromosome








15

Eger 99-11
(from Kozma)

(bkgnd =
rotundifolia
vinifera
+ F.H.)



Source of
Run1 and *Rpv1*
loci

Received 2000;
Crosses made in
2006

16