

Foundations for a modern grape breeding program

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WISCONSIN
UNIVERSITY OF WISCONSIN-MADISON







Historically, grape breeding has focused on single-gene traits



Pierce's disease (PdR1)



Powdery mildew

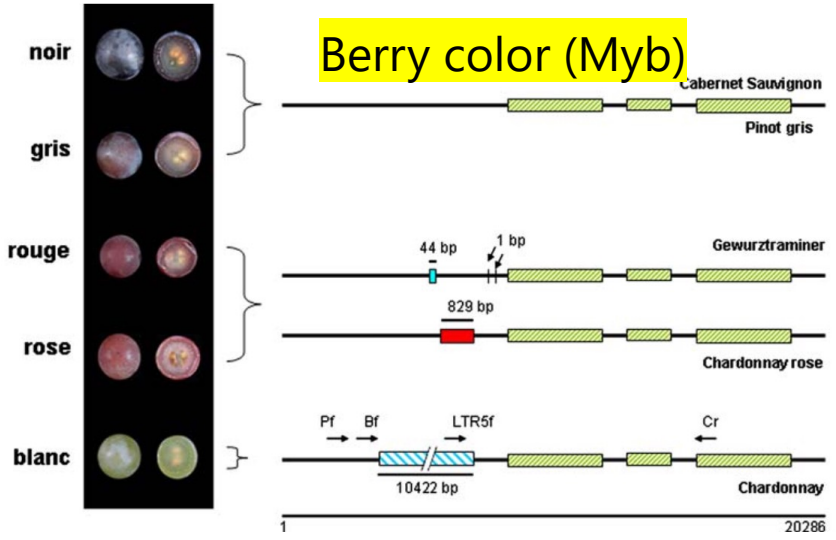
UC Statewide IPM Project
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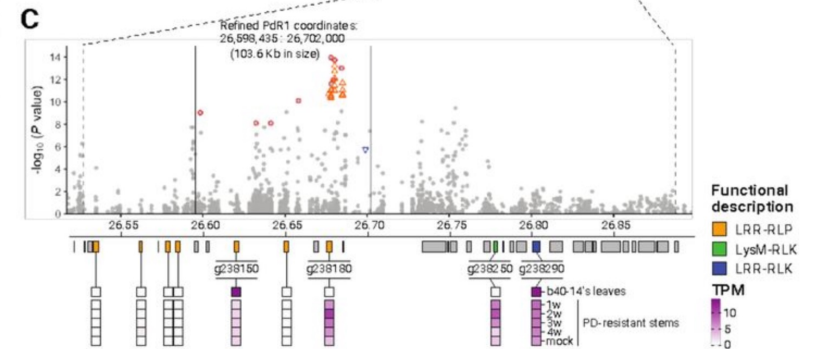
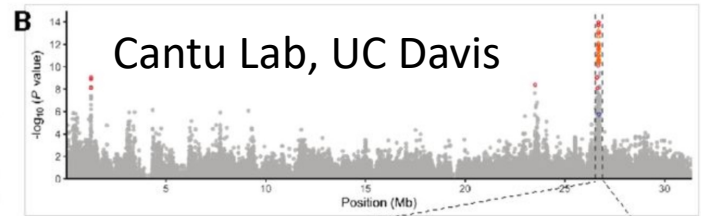
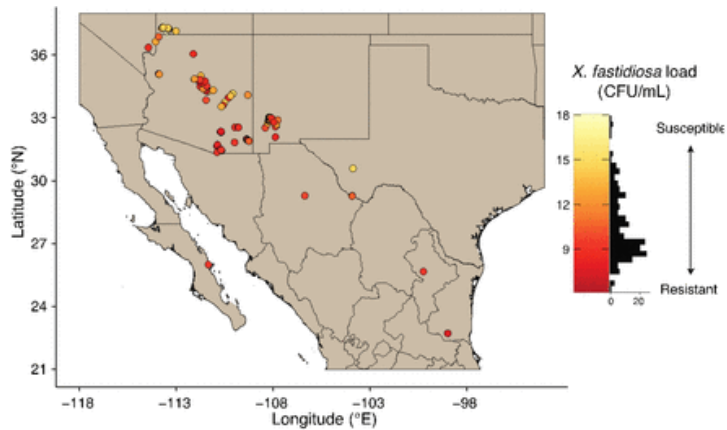


Muscat aroma (DXS gene)



phylloxera





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New PD-Resistant Wine Grape Varieties Named and Released

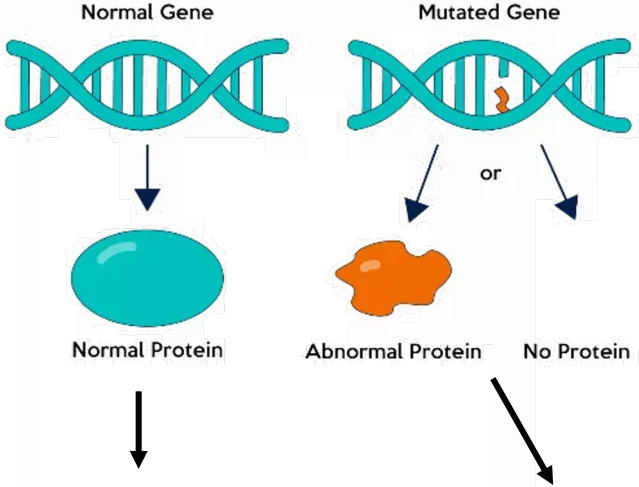
Patents Filed for Walker-bred Cultivars Developed at UCD

by [Ted Rieger](#)

Dec 3, 2019



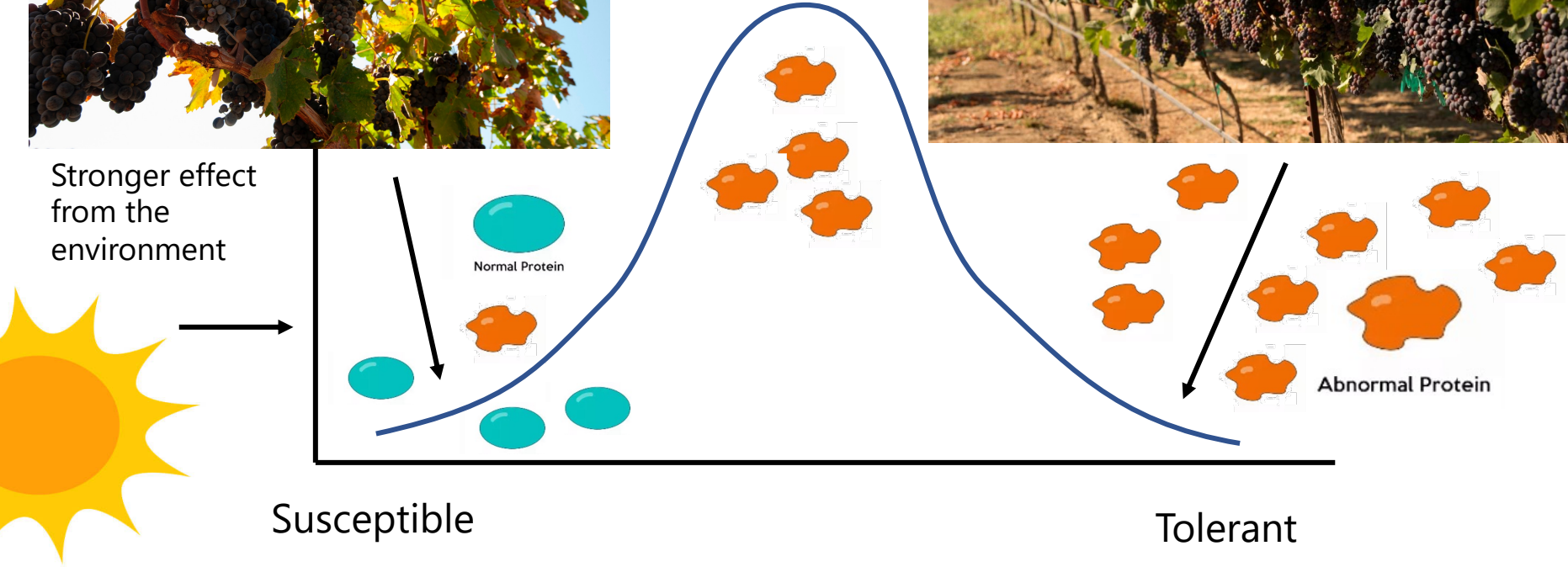
Single-gene traits: A mutation produce an observable and significant phenotype



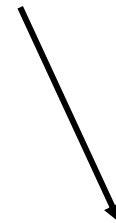
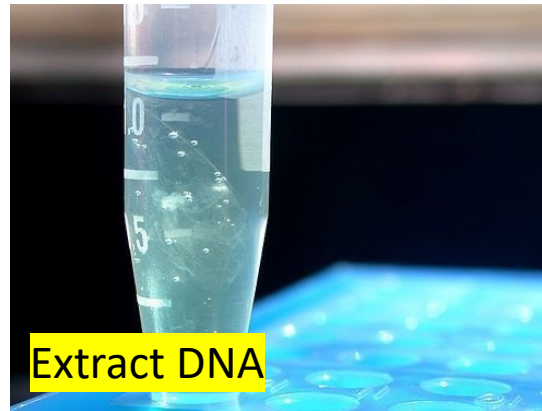
Less effect from the environment



Quantitative traits: a phenotype is the result of many genes

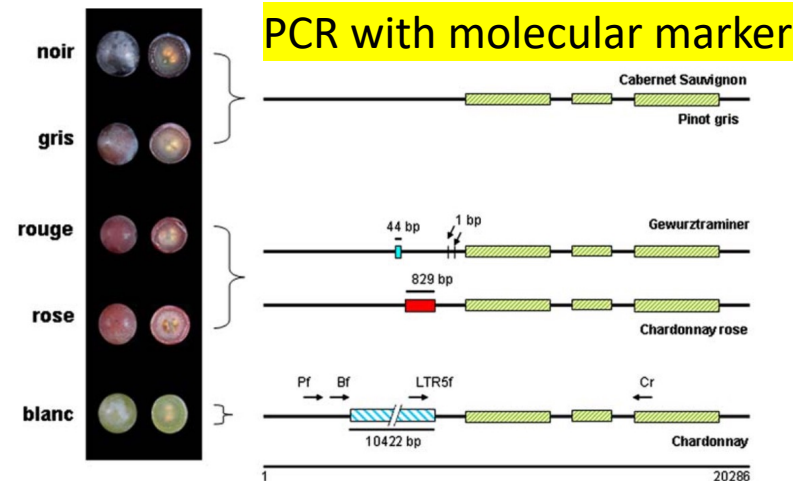
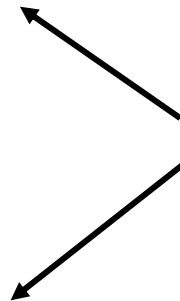


Marker-assisted selection works on single-gene traits only



If amplified fragment is longer = white

If amplified fragment is smaller = red



Breeding for quantitative traits is difficult as increments in genetic gain are small

- Complex traits: Difficult to measure
- Further genetic improvement on “single-gene traits” requires increasing small-effect additive genes
- The breeder’s equation:

$$\Delta G = \frac{\overset{\text{(Selection intensity)}}{i} \times \overset{\text{(Accuracy)}}{r_{TI}} \times \overset{\text{(Genetic variation)}}{\sigma_A}}{\underset{\text{(Generation interval)}}{L}}$$

$$\begin{array}{c}
 \uparrow \Delta G \\
 \text{(Genetic gain)}
 \end{array}
 = \frac{
 \begin{array}{c}
 \text{(Selection intensity)} \\
 i
 \end{array}
 \times
 \begin{array}{c}
 \text{(Accuracy)} \\
 r_{TI}
 \end{array}
 \times
 \begin{array}{c}
 \text{(Genetic variation)} \\
 \sigma_A \uparrow
 \end{array}
 }{
 \begin{array}{c}
 \downarrow L \\
 \text{(Generation interval)}
 \end{array}
 }$$

- ✓ **Selection intensity (i)** can be increased by increasing the number of plants we evaluate
- ✓ **Accuracy (r_{TI})** can be increased by replicating our experiments more, or by phenotyping very accurately
- ✓ Reducing the **generation interval (L)** depends on the plant itself, however, identifying superior-performing plants earlier allow recycling them as parents sooner

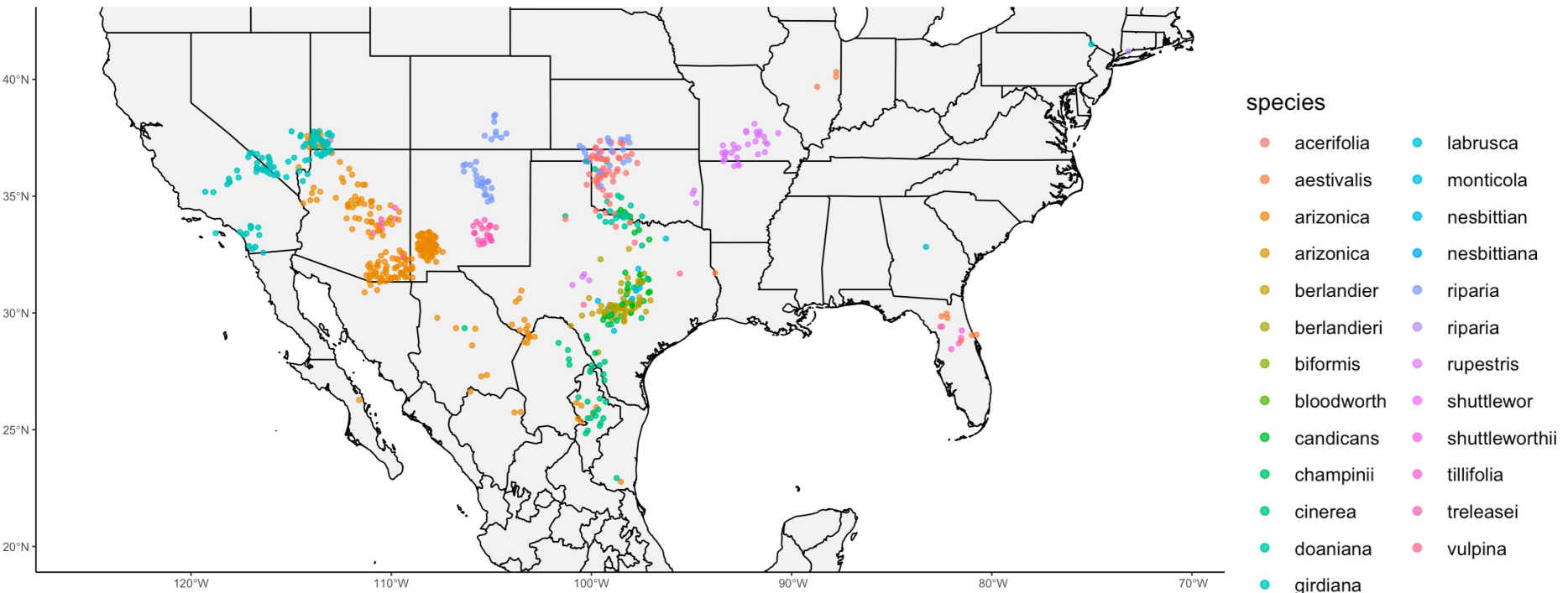
UC Davis grape breeding program: Current state

$$\Delta G = \frac{\overset{\text{(Selection intensity)}}{i} \times \overset{\text{(Accuracy)}}{r_{TI}} \times \overset{\text{(Genetic variation)}}{\sigma_A}}{\underset{\text{(Generation interval)}}{L}}$$

Mapping populations

Advanced materials with multiple sources of tolerance to powdery mildew and Pierce's disease

9,298 accessions in a ~100-acre field: 43.2 million possible crosses



The breeder's equation can be optimized using high-throughput phenotyping (HTP) methods

$$\Delta G = \frac{\overset{\text{(Selection intensity)}}{i} \times \overset{\text{(Accuracy)}}{r_{\text{TI}}} \times \overset{\text{(Genetic variation)}}{\sigma_A}}{\underset{\text{(Generation interval)}}{L}}$$

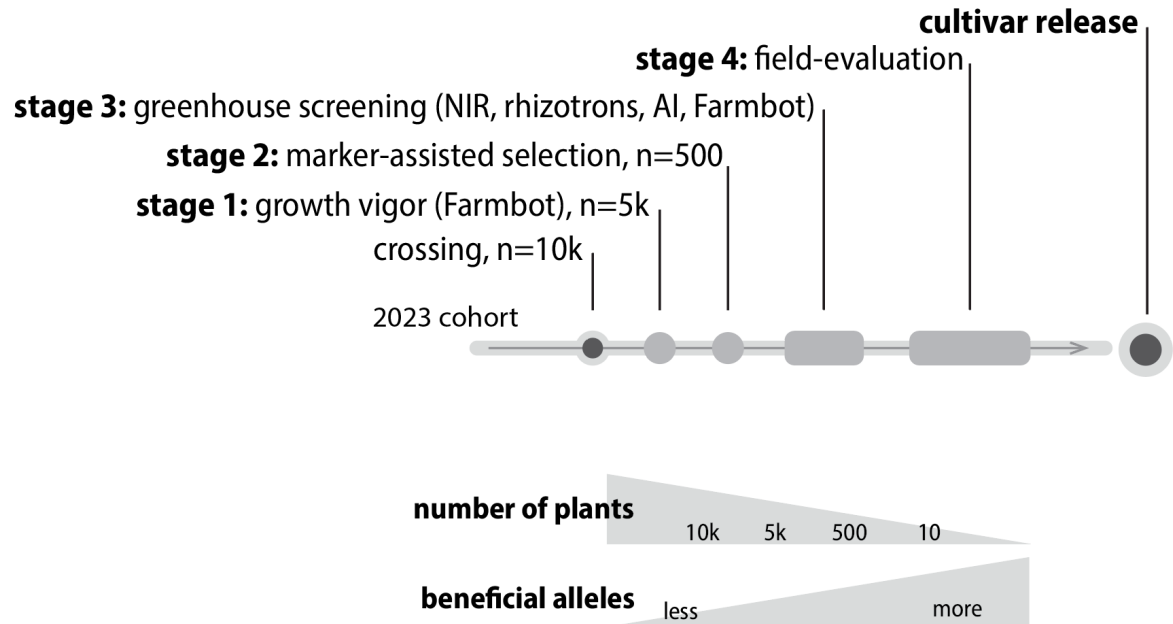
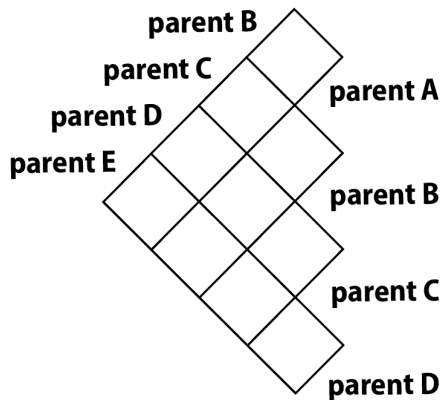
- Defining “high-throughput”:
 - Fully (or mostly) automated data collection
 - Scalable
 - Automated data processing



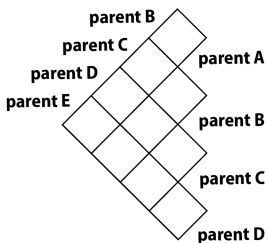
Incorporating HTP methods in the grape breeding program

Goal: rapidly identify superior-performing candidates for field evaluation

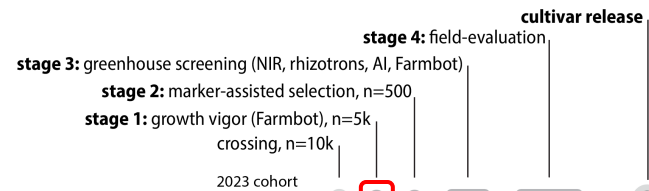
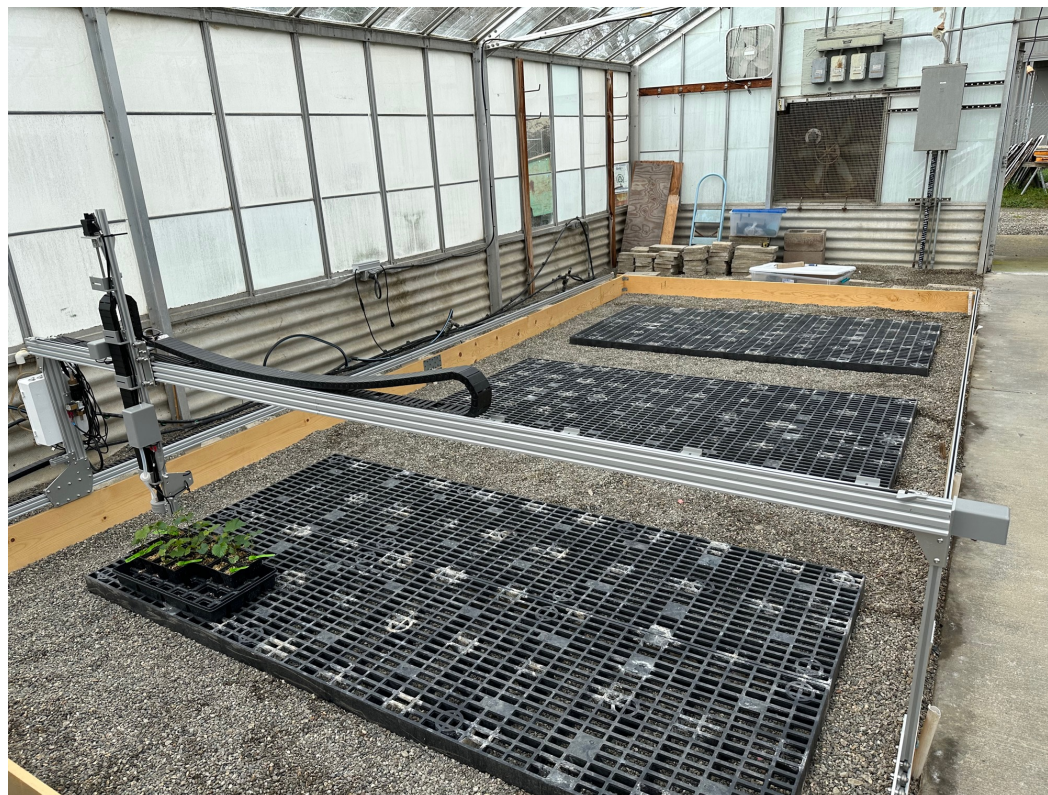
Crossing scheme



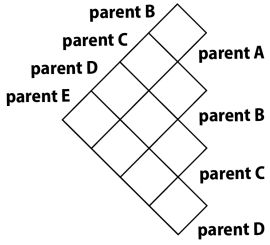
Incorporating HTP methods in the grape breeding program



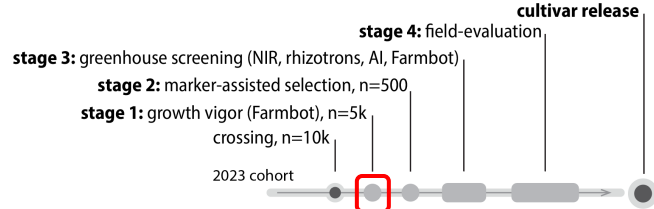
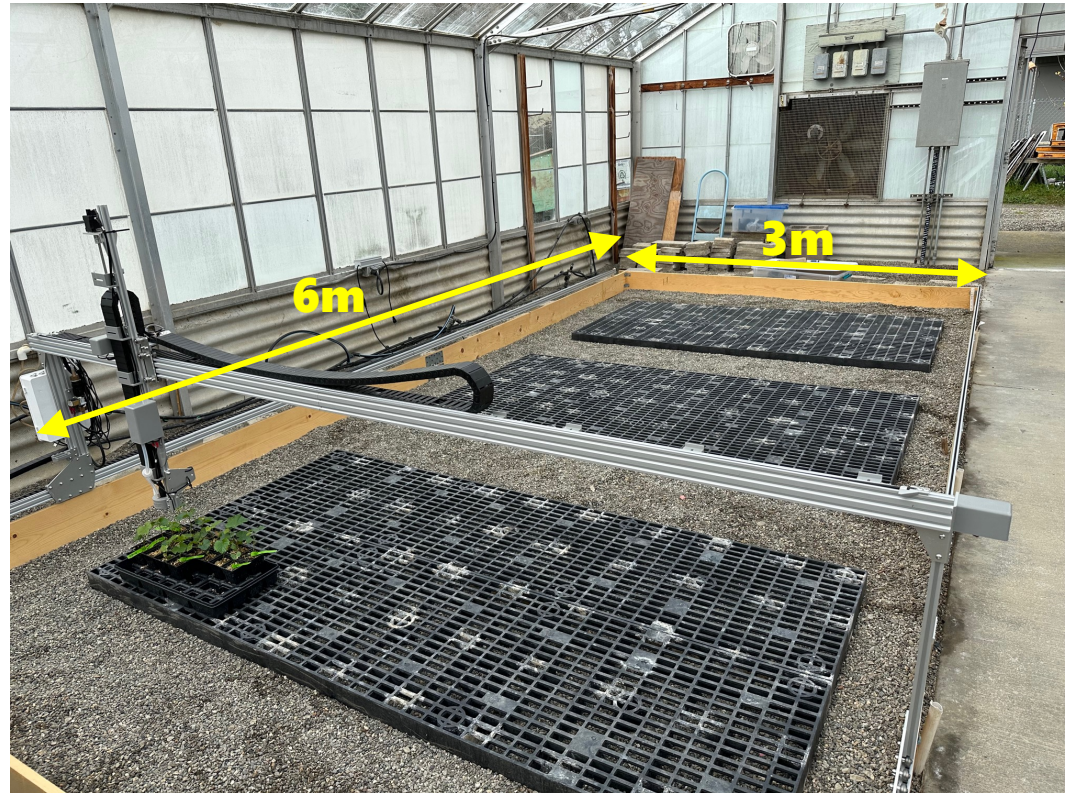
10,000 seedlings



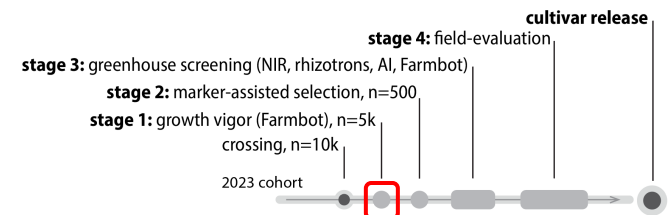
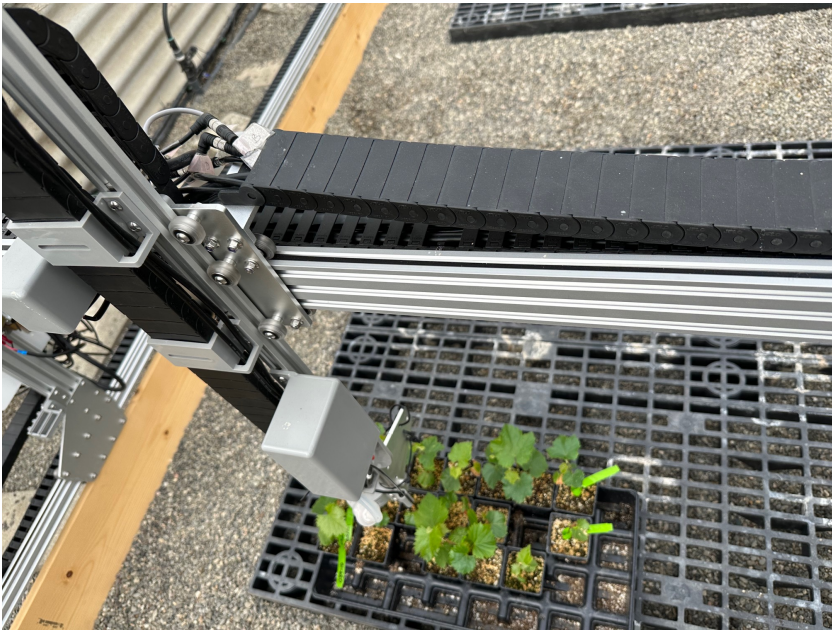
Incorporating HTP methods in the grape breeding program



10,000 seedlings

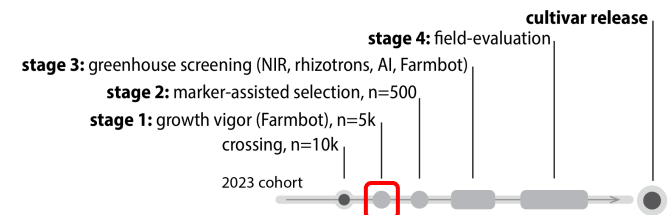


Incorporating HTP methods in the grape breeding program



Incorporating HTP methods in the grape breeding program

Identifying green tissue, track over time



Marker assisted selection to enrich "beneficial genes"

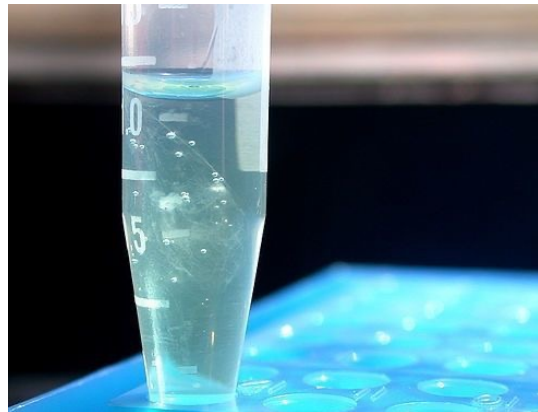


5,000 stronger seedlings

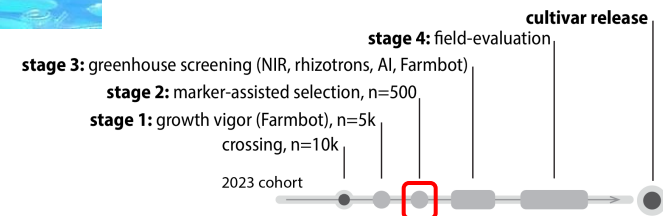


Pierce's disease
Phylloxera
Dagger nematode (Xi)
Flower sex

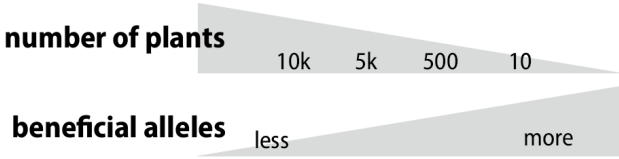
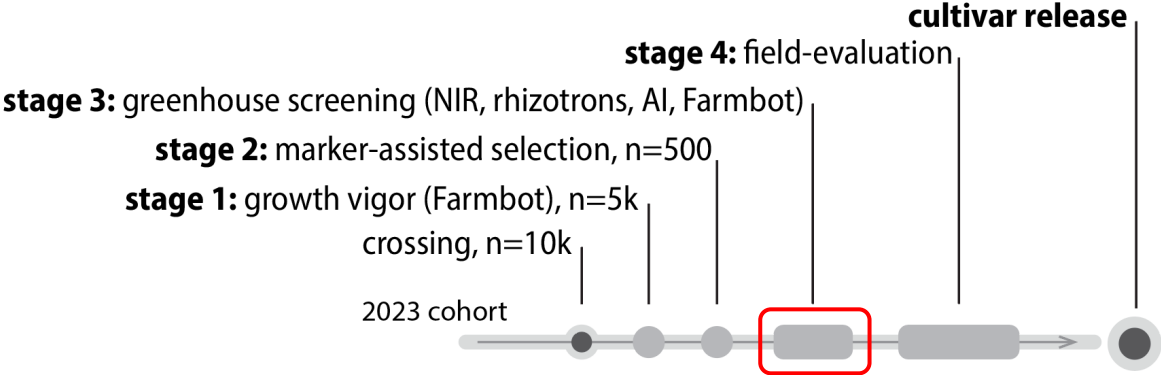
Powdery mildew (>4 markers)
Pierce's disease
Flower sex
Methoxypyrazines IBMP
Muscat flavor
Seedless
Skin color



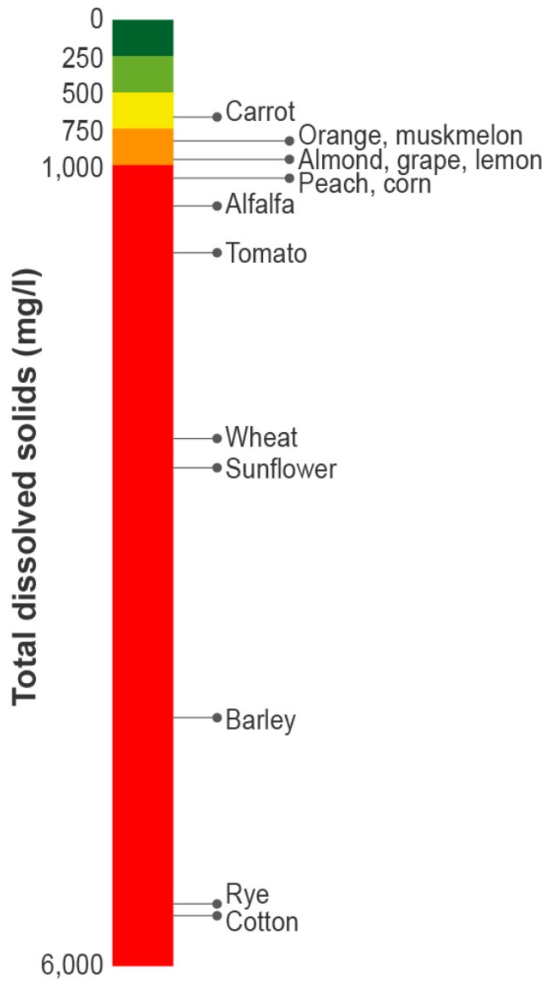
100-500



2-3 years to identify superior-performing materials

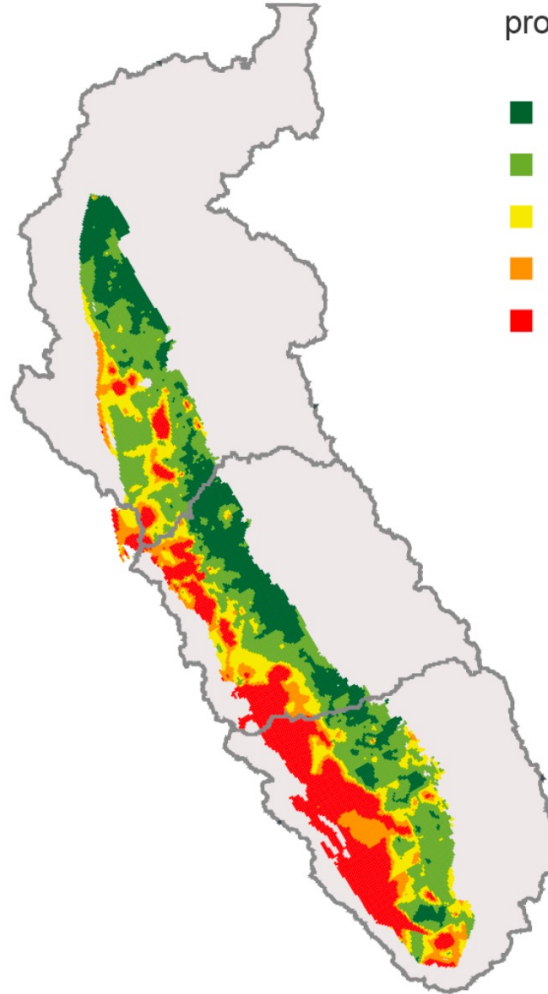
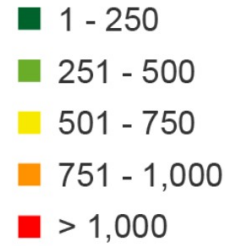


A) Salinity thresholds at which crop yields start to decline

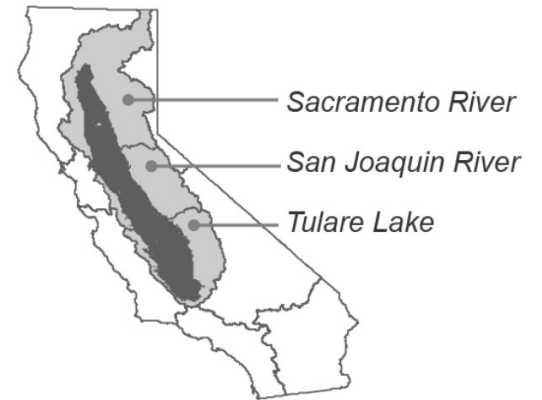


B) Shallow groundwater salinity

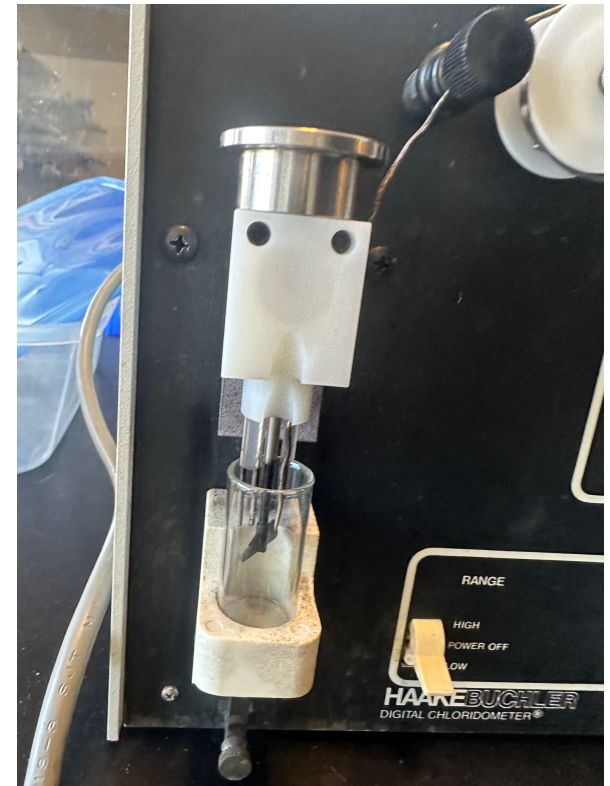
Total dissolved solids in the production zone (mg/L)



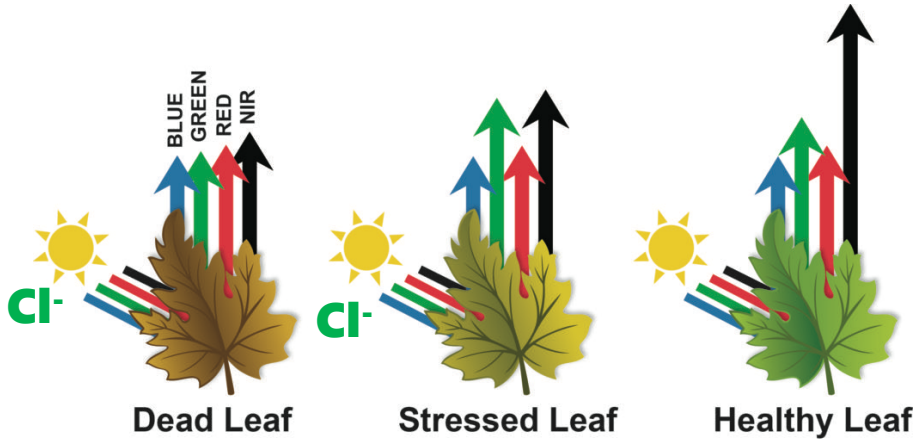
Hydrologic regions shown



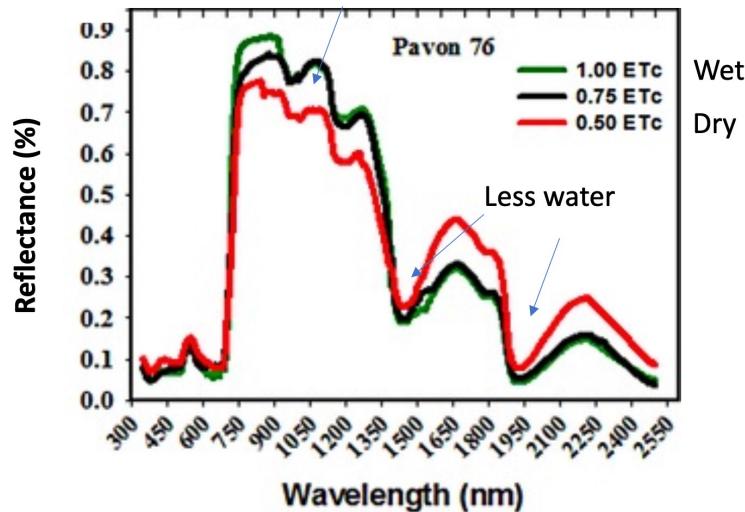
Traditional methods to measure salt toxicity are time-consuming



Hyperspectral imaging detects changes in foliar structure produced by salt and water deficits



Denser mesophyll



Handheld spectrometers

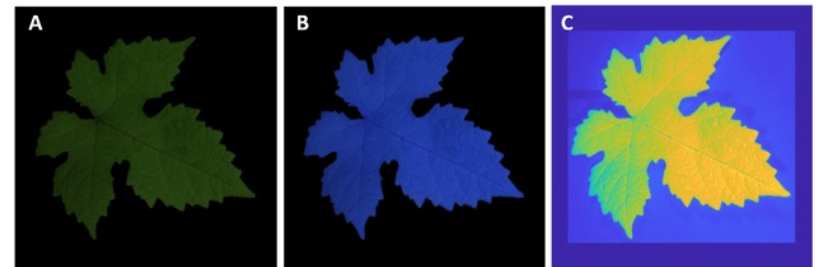
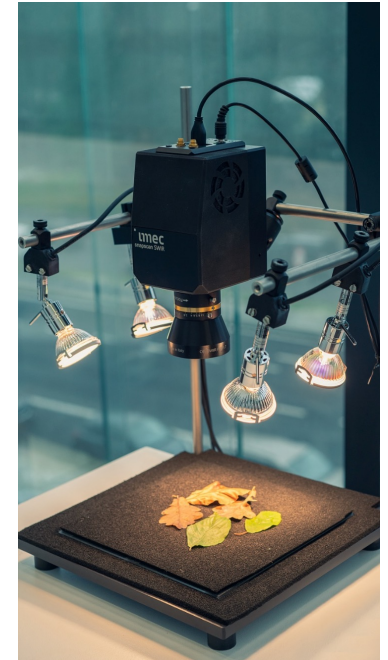


800-1400nm

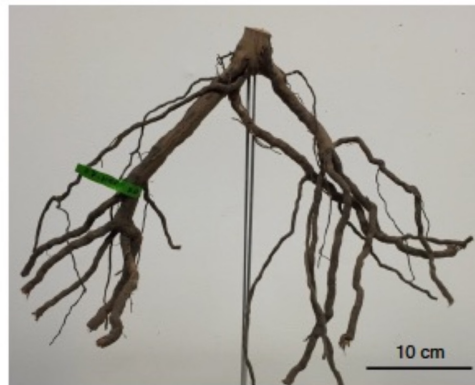


1400-2300nm

IMEC Multispectral camera
400-900nm



Drought tolerance is related to root architecture and foliar properties



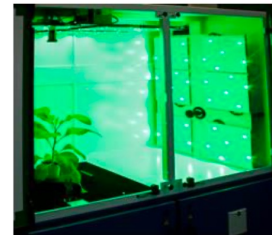
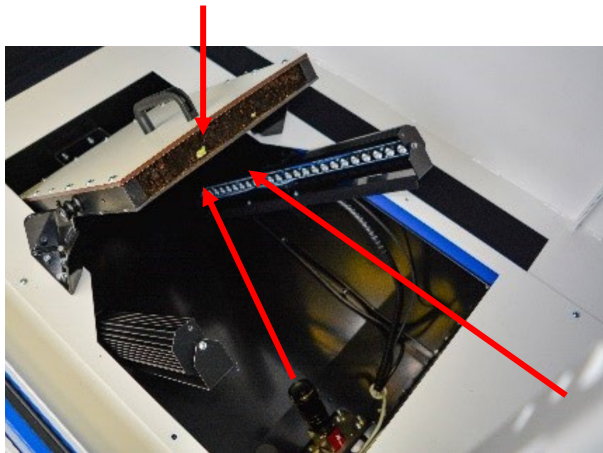
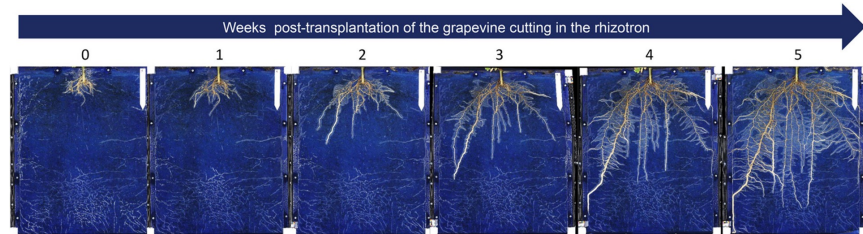
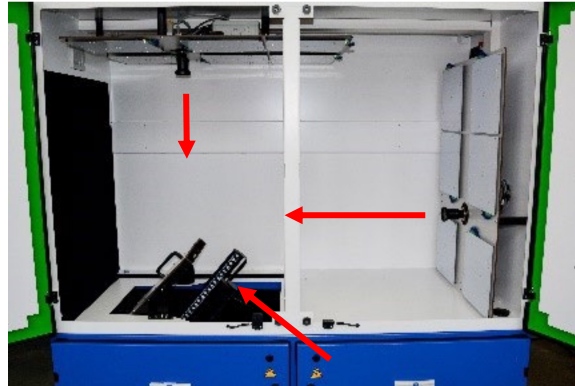
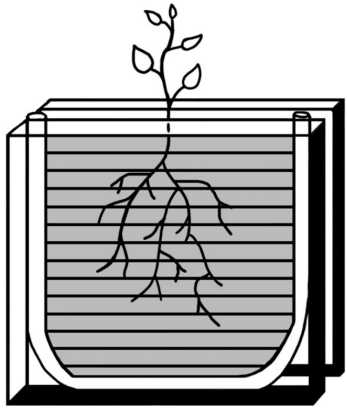
110R produces thick main roots with limited lateral branching.

101-14 Mgt produces finer main roots and abundant lateral branching.



Large-scale phenotyping of root systems is difficult

Semi-automated imaging using rhizotrons



Illumination with different wavelengths



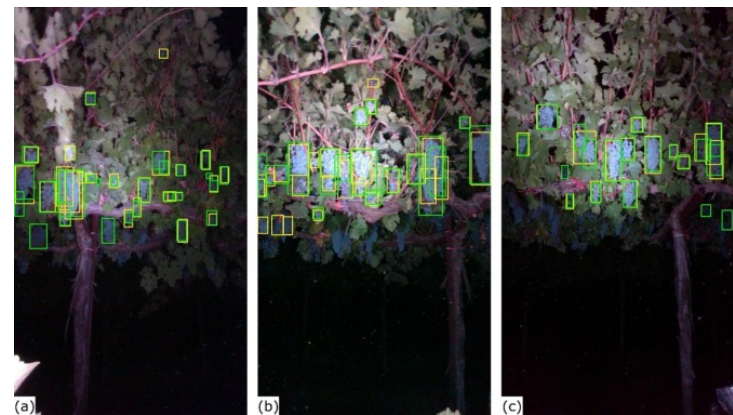
Krzyzaniak et al. 2021



Image analysis + machine learning to track root growth over time and identify galls



Deep learning to estimate grape yield



Predicted Labeled

Predicted Count: 25

Labeled Count: 27

Predicted Area: 15,637 px

GT Area: 14,779 px

Predicted Count: 27

Labeled Count: 16

Predicted Area: 21,657 px

GT Area: 23,786 px

Predicted Count: 15

Labeled Count: 19

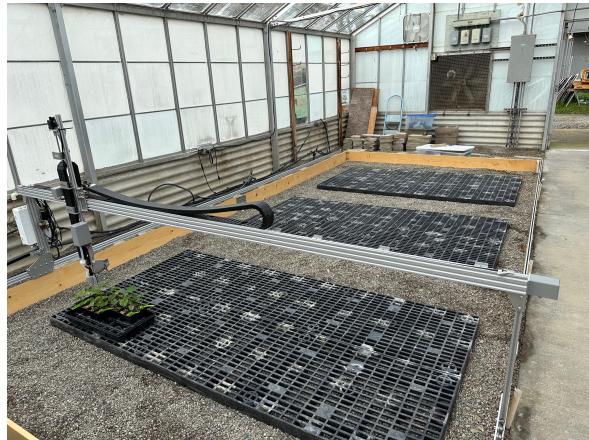
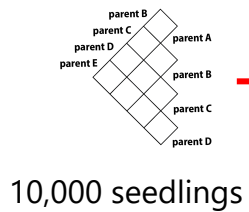
Predicted Area: 13,188 px

GT Area: 13,212 px

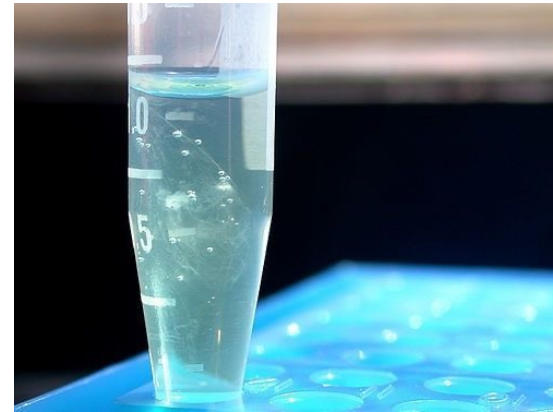
Mason Earles



Breeding pipeline integration

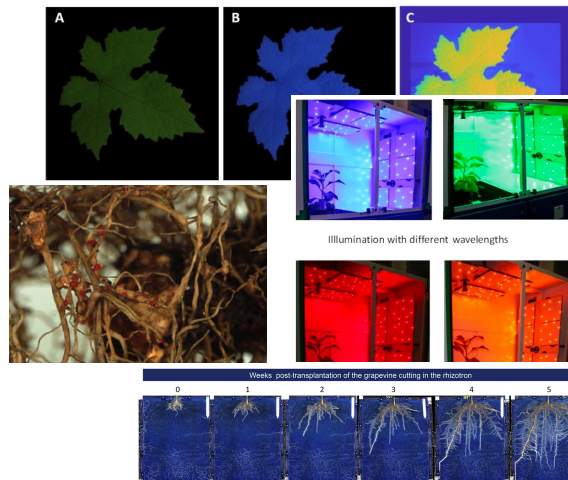
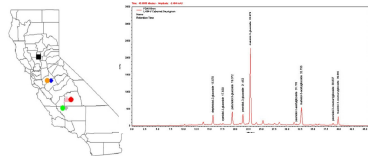


5000 stronger plantlets



500 after MAS

5-20 for field evaluation

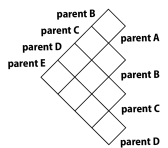


Propagation



Breeding pipeline integration

Increasing selection intensity

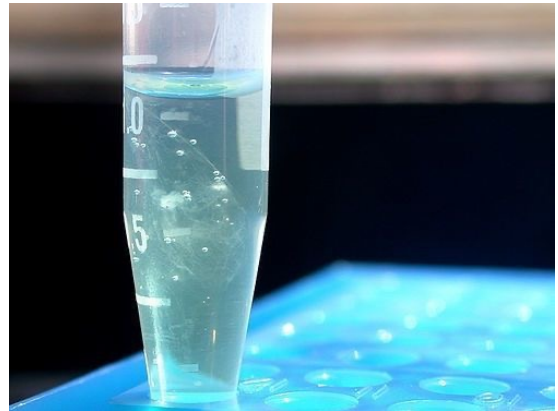


10,000 seedlings

Recycling parents



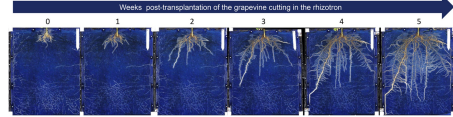
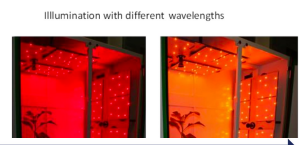
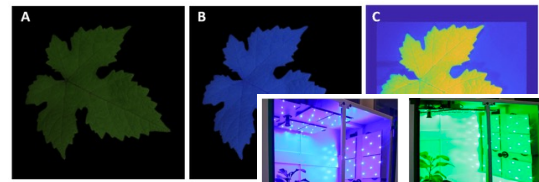
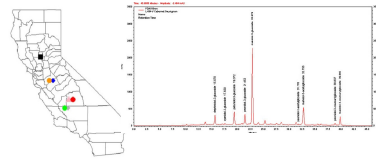
500 after MAS



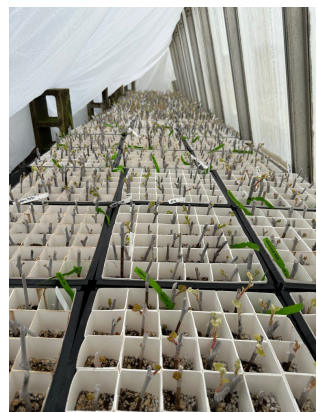
Reducing interval time

Increasing selection accuracy

5-20 for field evaluation



Propagation



And for the next trick...

