Combining high throughput genotyping and phenotyping for the genetic improvement of table grapes in Chile

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Seedling Field Phenotyping

New plants to evaluate

Last season

CORFO
Development of agro-informatic solutions using Open Source software

- Kernel (~database) design. Software architecture adapted to grapevine breeding process.
- Tool development for data handling
  - Vine Tracker
  - Berry Analyzer
Vine Tracker

Our own mobile app for field data

Maturity assessment (16 ° Brix)
Vine Tracker

Our own mobile app for field data

Maturity assessment (16 ° Brix)

Harvest characterization
Vine Tracker

Our own mobile app for field data

Maturity assessment (16 ° Brix)

Harvest characterization

Selection
Vine Tracker
Our own mobile app for field data

Pros:
✓ Standardization
  • Better quality
  • Lower error
  • Faster
✓ Real time data synchronization
  • Team work over the field
✓ Real time data processing
  • Accuracy
  • Saves time
  • Rapid response
Berry Analyzer
Algorithm collection for trait quantification based on laboratory images

Pros:
✓ Reduce subjective evaluation
✓ Increases precision of data
✓ Faster results
✓ Wider window opportunity for decision making

✓ Tool available at:

https://berry-analyzer.agroinformatica.cl/
Correlation on berry size phenotype
Berry Analyzer vs caliper

Equatorial diameter

Polar diameter

\[ R^2 = 0.973 \]

\[ R^2 = 0.938 \]

https://berry-analyzer.agroinformatica.cl/
Correlation on rachis size phenotype
Rachis area vs rachis weight

$R^2 = 0.930$

https://berry-analyzer.agroinformatica.cl/
Correlation on cluster size phenotype
Cluster area vs cluster weight

$R^2 = 0.930$

https://berry-analyzer.agroinformatica.cl/
High throughput color phenotyping
High throughput color phenotyping: Define chromatic profiles

‘Crimson’ CLUSTER at harvest

- Green
- Yellow
- Red
- Dark blue
Chromatic profile of ‘Crimson’ BUNCH at harvest

17.7% Green
54.7% Red
20.7% Yellow
6.9% Blue
Chromatic profile of ‘Crimson’ RACHIS at harvest

VERDE: 97.70%
Green: 97.7%

ROJA: 0.42%
Red: 0.4%

PARDA: 1.88%
Brown: 1.9%
Chromatic profile of ‘Crimson’ RACHIS after 30 days cold storage

34.5% Green
3.6% Red
59.9% Brown
Chromatic profile of ‘Iniagrape-one’ RACHIS at harvest

VERDE: 91.66%
Green 91.7%

ROJA: 5.59%
Red 5.6%

PARDA: 2.75%
Brown 2.8%
Chromatic profile of ‘Iniagrape-one’ RACHIS after 30 days cold storage

78.0% Green
9.3% Red
12.8% Brown
Phenotype – genotype association (GWAS)

• Phenotype
  • Germplasm collection: one season, one location, one to three plants per genotype, six clusters per plant (harvest and postharvest), ten berries per cluster.

  • Breeding program families: one season, one location, one plant per genotype, four to six clusters per plant (harvest and postharvest), ten berries per cluster.

  • 88.143 image-derived data points acquired during the last season (finished in May!).

  • Covariates such as seed dry weight, soluble solids content, etc
Phenotype – genotype association (GWAS)

• Genotyping by sequencing 850 samples from germplasm collection and breeding families. 60k quality SNPs markers

• Work in progress.... Association mapping of 500 samples and 30k SNPs using linear mixed model with two first eigenvalues from PCA and Kinship matrix
Selección 23 progeny

‘Flame’ progeny

‘Italia’ progeny

INIA germoplasm collection
GWAS: Validation LMM using seed dry weight

Marcador
VvAGL11
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