







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

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Gobierno de Chile
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Fondo Nacional de Desarrollo Científico y Tecnológico
Iniciación 11161044
BIOFRUTALES
Genetic Fruit Improvement

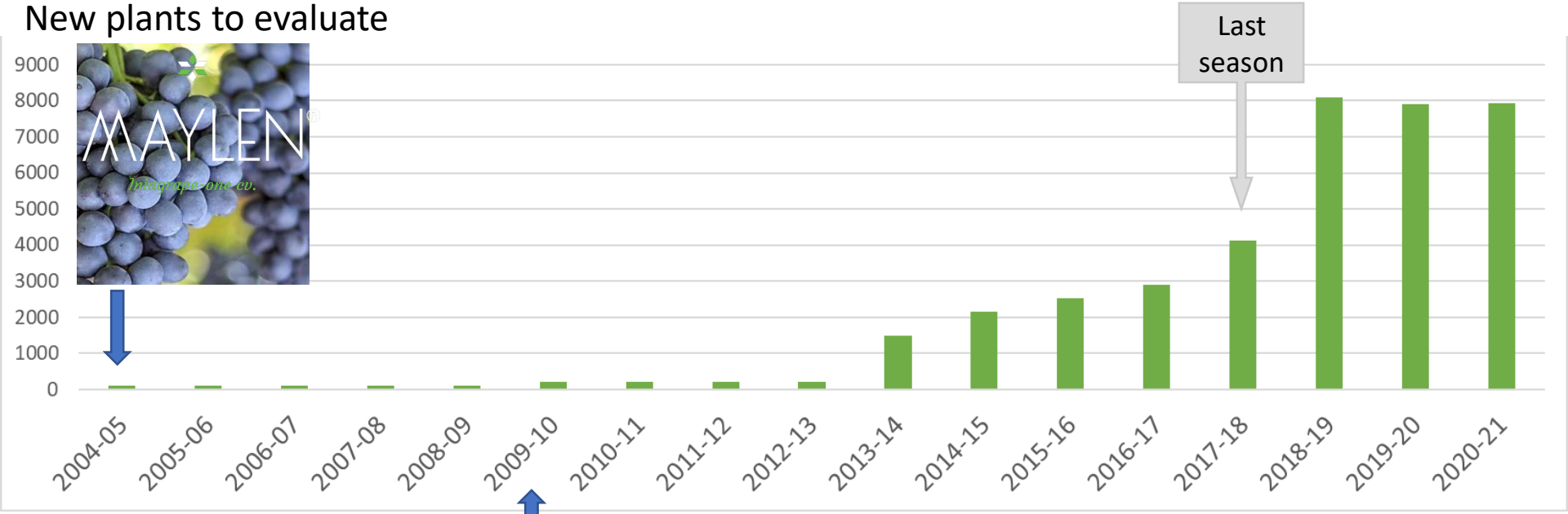
MAYLEN®

Iniagrape-one cv.

Uquillas, Carolina, et al. "'Iniagrape-one', a New Chilean Table Grape Cultivar." *HortScience* 48.4 (2013): 501-503.

Seedling Field Phenotyping

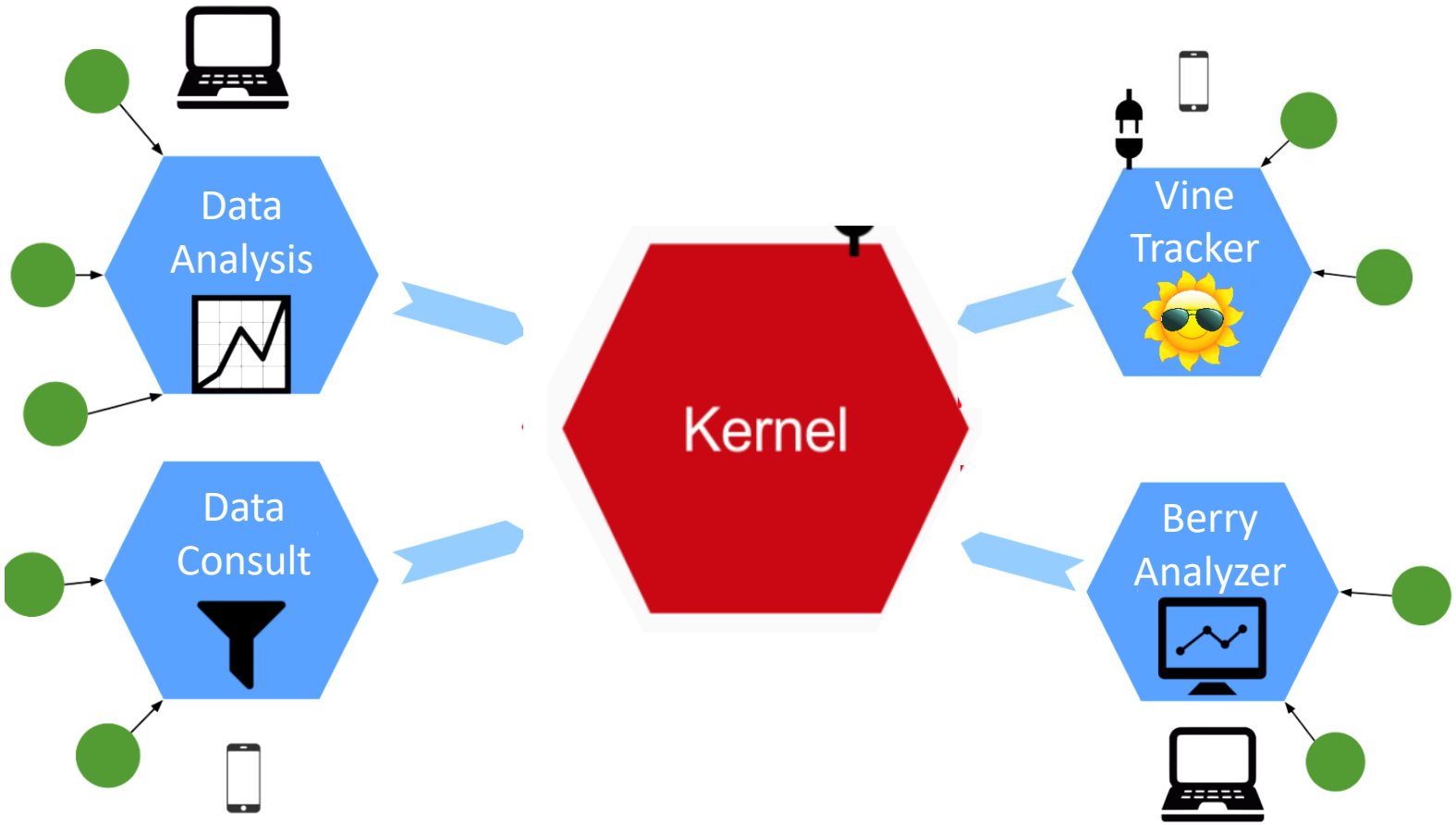
New plants to evaluate



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

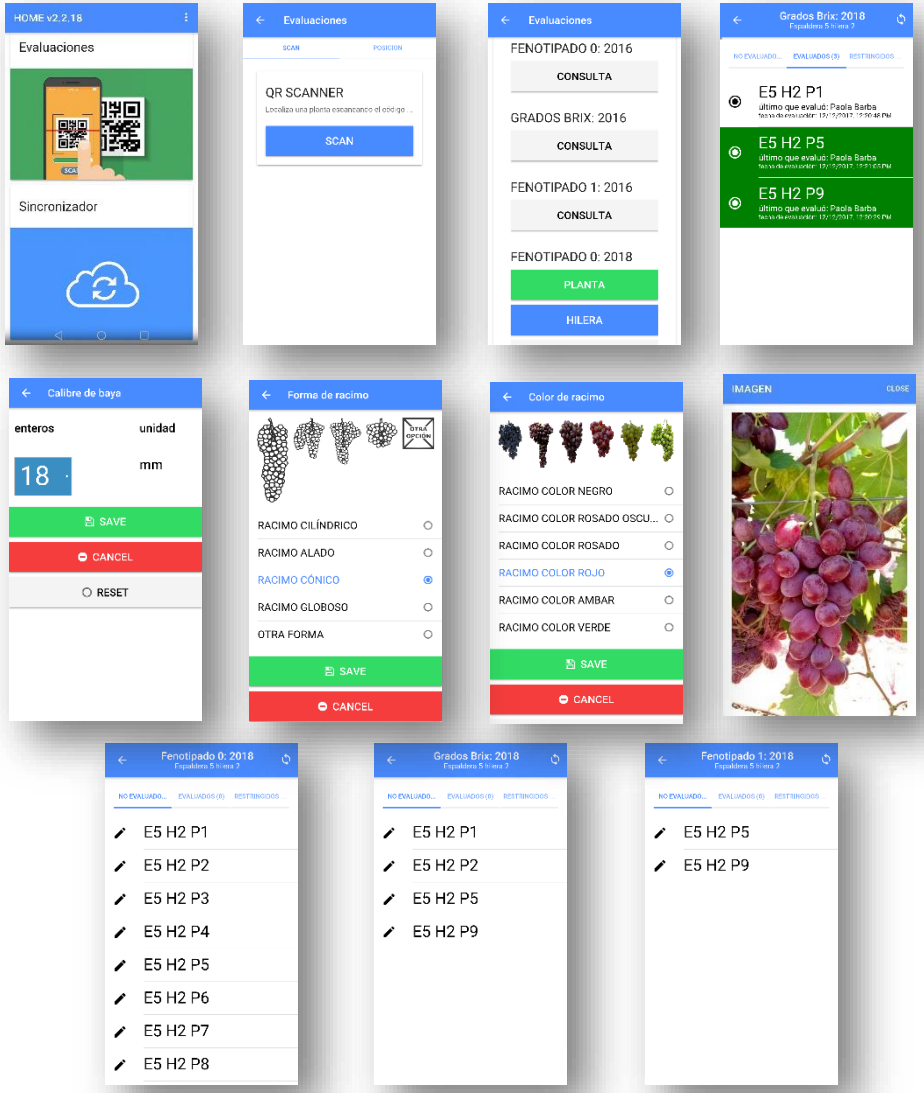
Maturity assessment (16 ° Brix)

Harvest characterization

Selection

Vine Tracker

Our own mobile app for field data

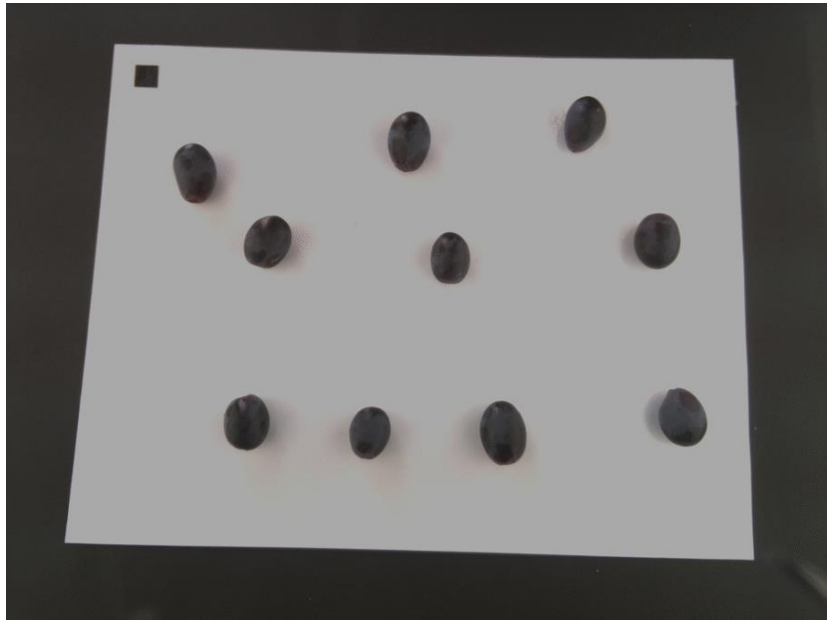


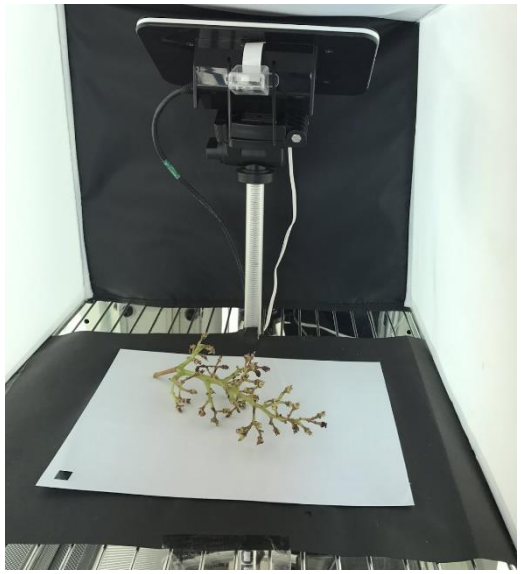
Pros:

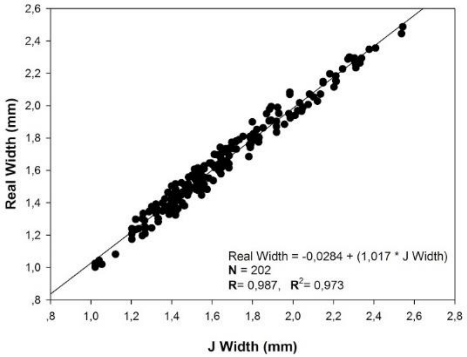
- ✓ Standardization
  - Better quality
  - Lower error
  - Faster
- ✓ Real time data synchronization
  - Team work over the field
- ✓ Real time data processing
  - Accuracy
  - Saves time
  - Rapid response

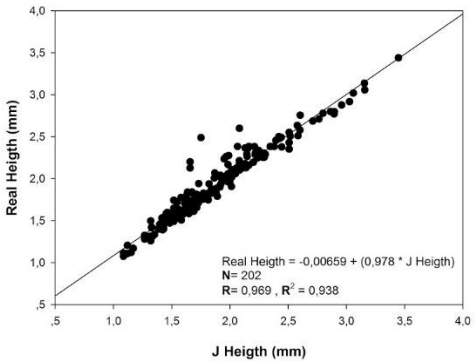
Berry Analyzer

Algoritm collection for trait quantification based on laboratory images









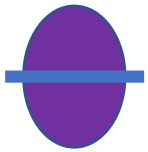
Pros:

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

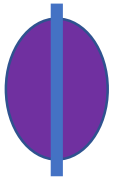
- ✓ Tool available at:

https://berry-analyzer.agroinformatica.cl/

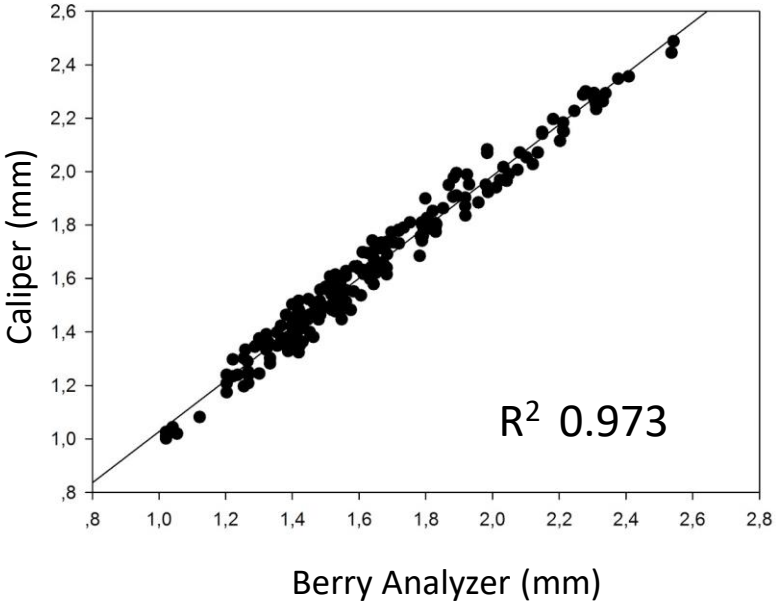
Correlation on berry size phenotype
Berry Analyzer vs caliper

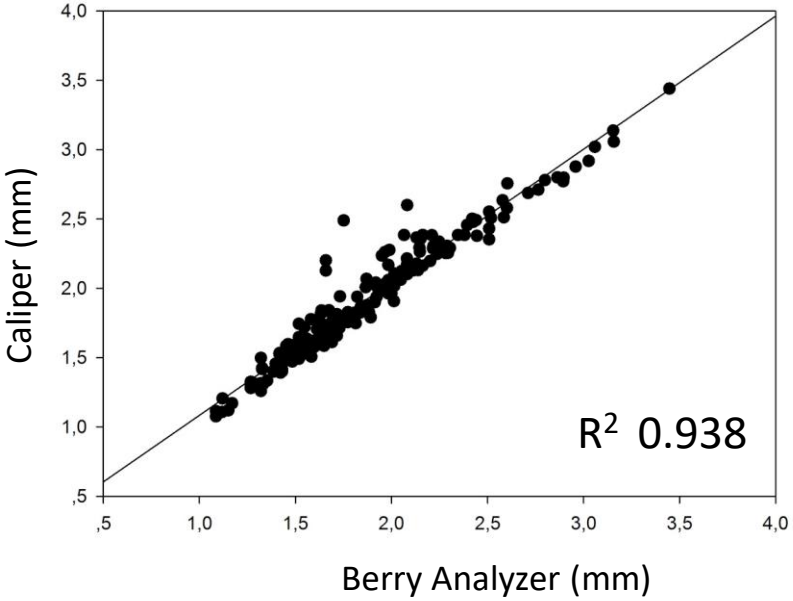


Equatorial diameter



Polar diameter

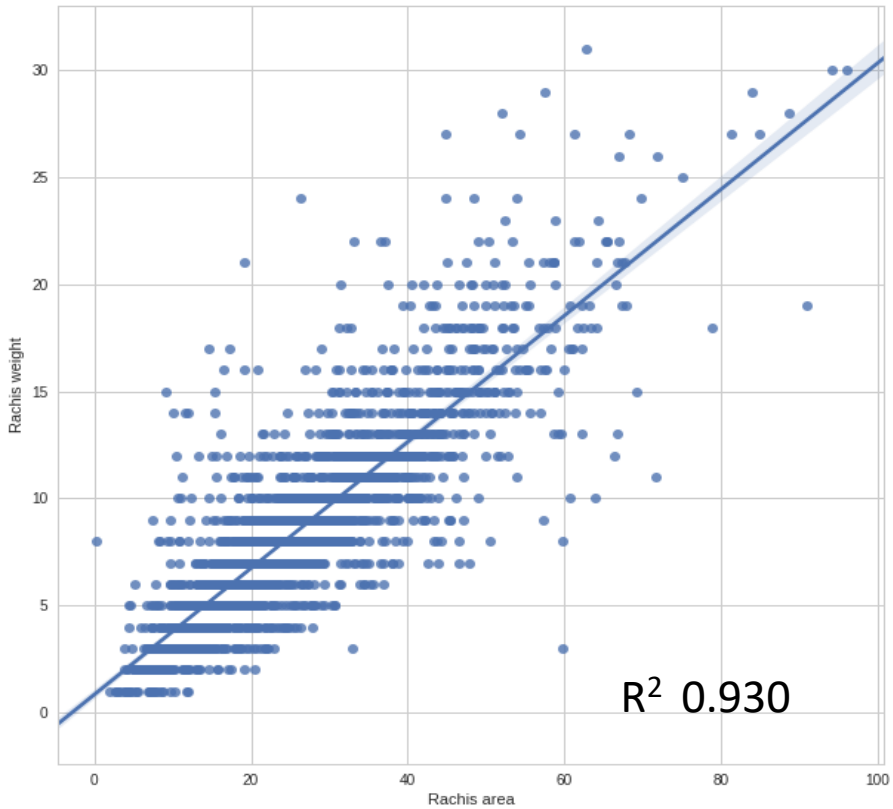


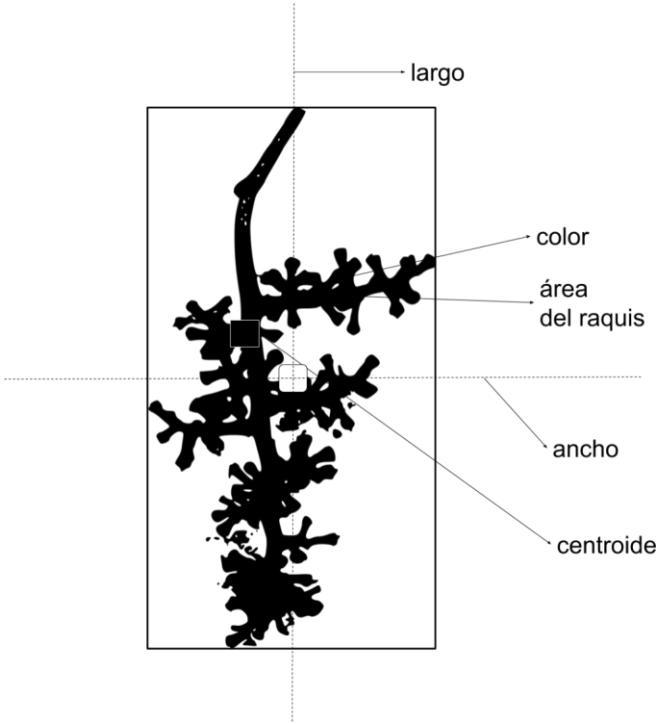


INIA

https://berry-analyzer.agroinformatica.cl/

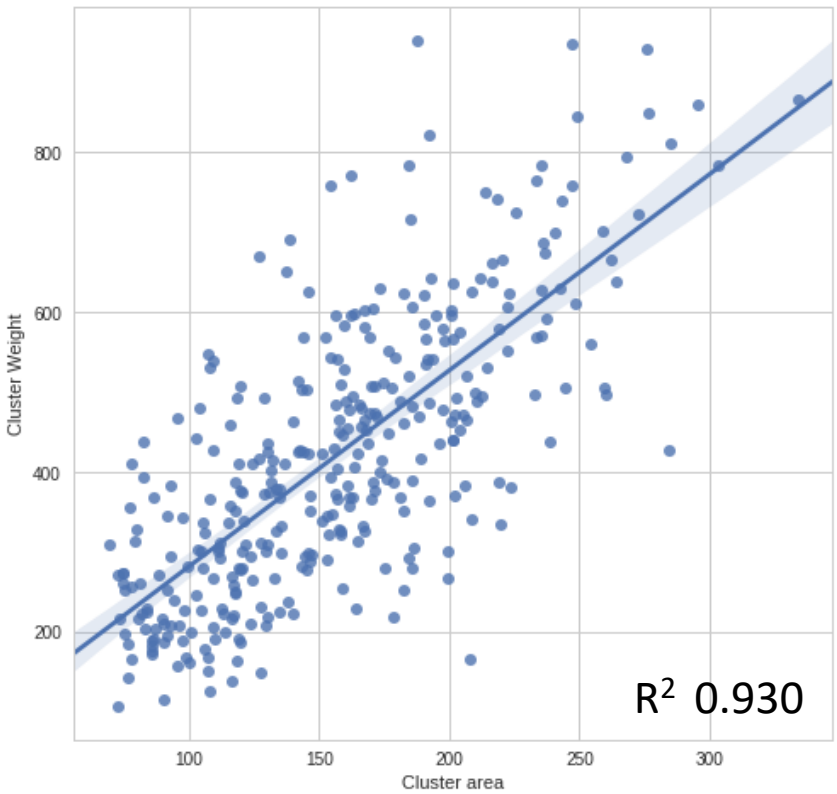
Correlation on rachis size phenotype
Rachis area vs rachis weight





https://berry-analyzer.agroinformatica.cl/

Correlation on cluster size phenotype
Cluster area vs cluster weight



https://berry-analyzer.agroinformatica.cl/

High throughput color phenotyping

6.807 colors

High throughput color phenotyping: Define chromatic profiles

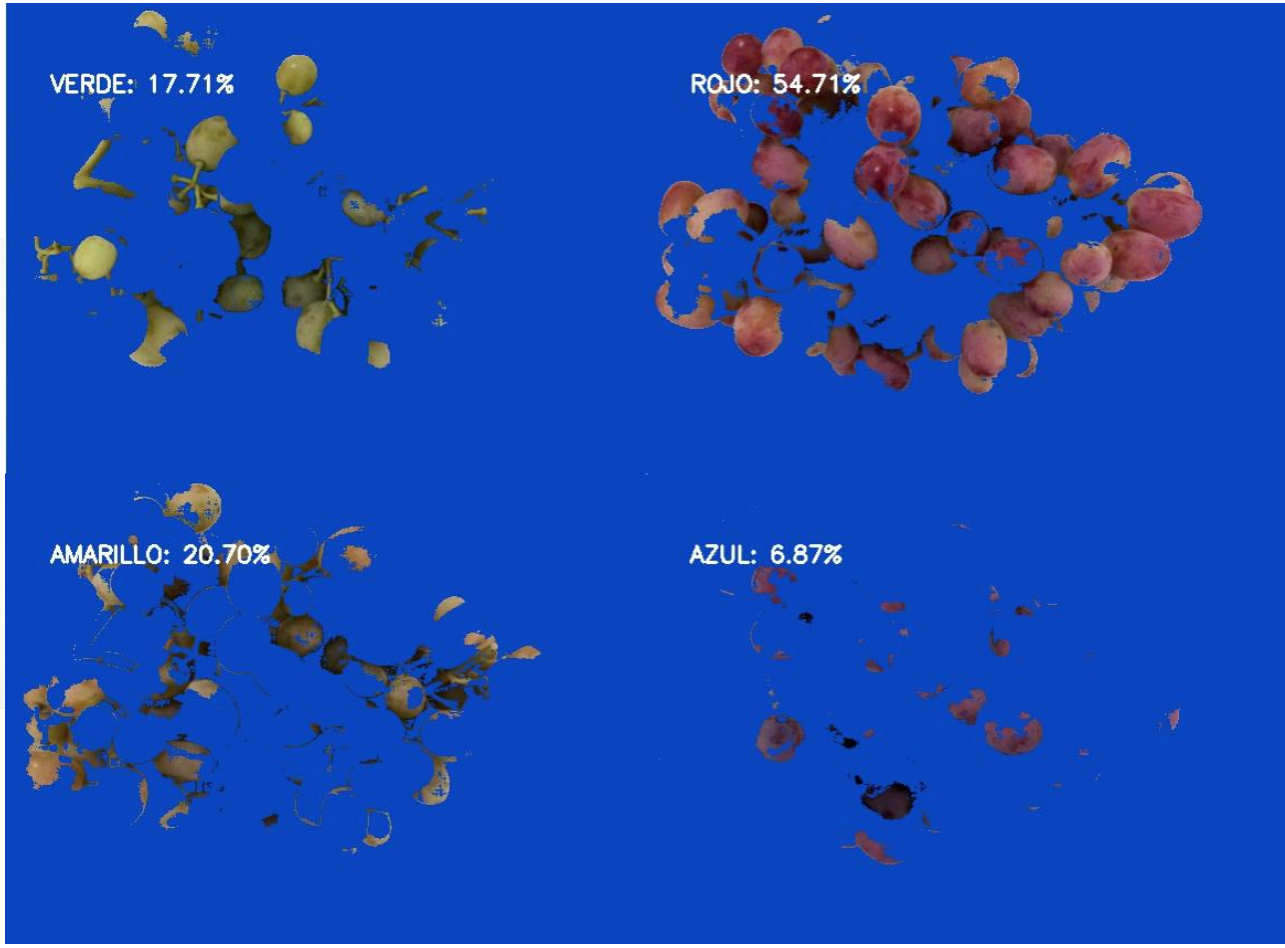
- Green
- Yellow
- Red
- Dark blue

‘Crimson’ CLUSTER at harvest

Chromatic profile of ‘Crimson’ BUNCH at harvest

17.7%
Green

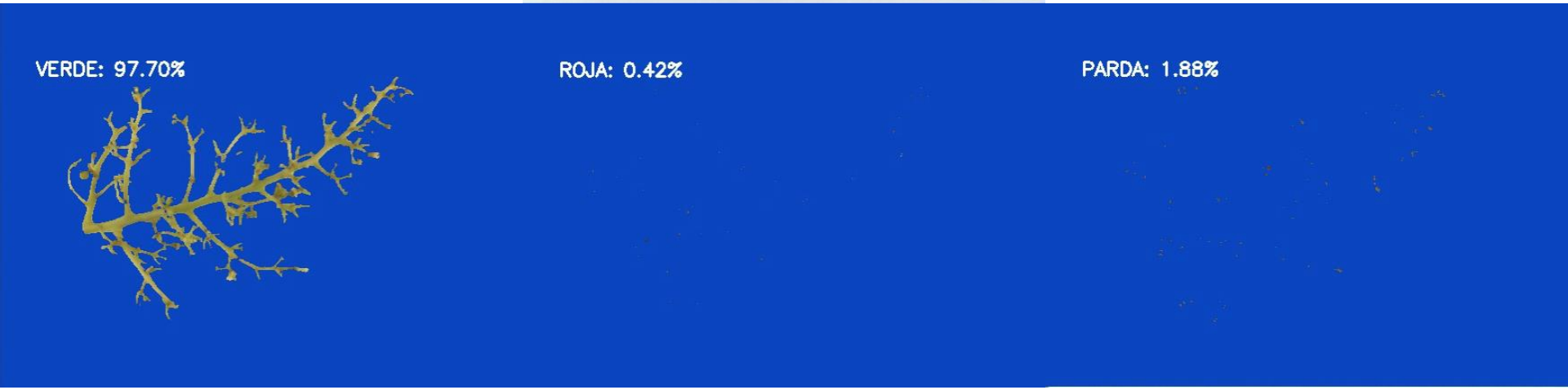
54.7%
Red



20.7%
Yelllow

6.9%
Blue

Chromatic profile of ‘Crimson’ RACHIS at harvest



97.7%
Green

0.4%
Red

1.9%
Brown

Chromatic profile of ‘Crimson’ RACHIS

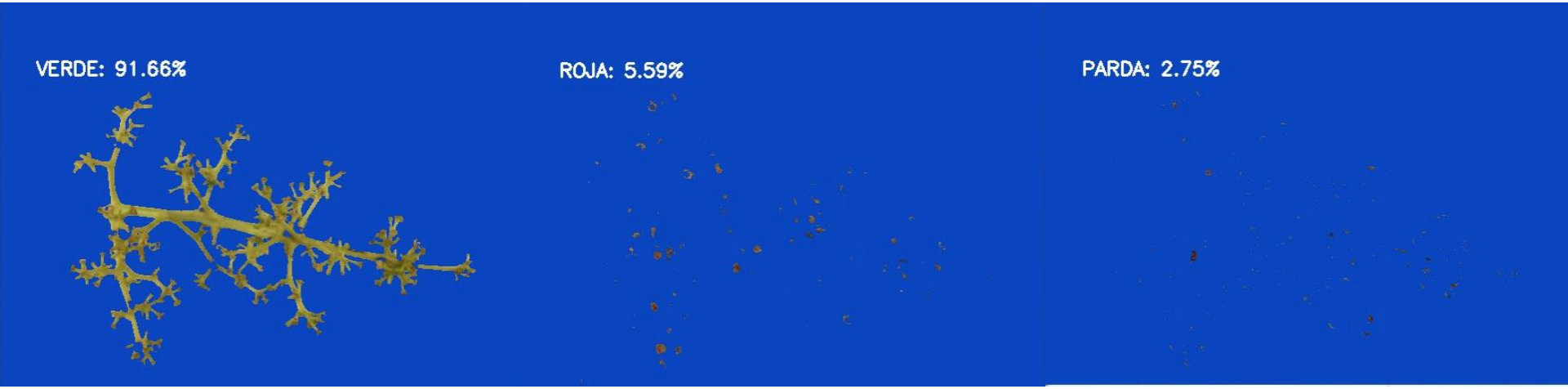
after 30 days cold storage

34.5%
Green

3.6%
Red

59.9%
Brown

Chromatic profile of ‘Iniagrape-one’ RACHIS at harvest



91.7%
Green

5.6%
Red

2.8%
Brown

Chromatic profile of ‘Iniagrape-one’ RACHIS after 30 days cold storage

78.0%
Green

9.3%
Red

12.8%
Brown

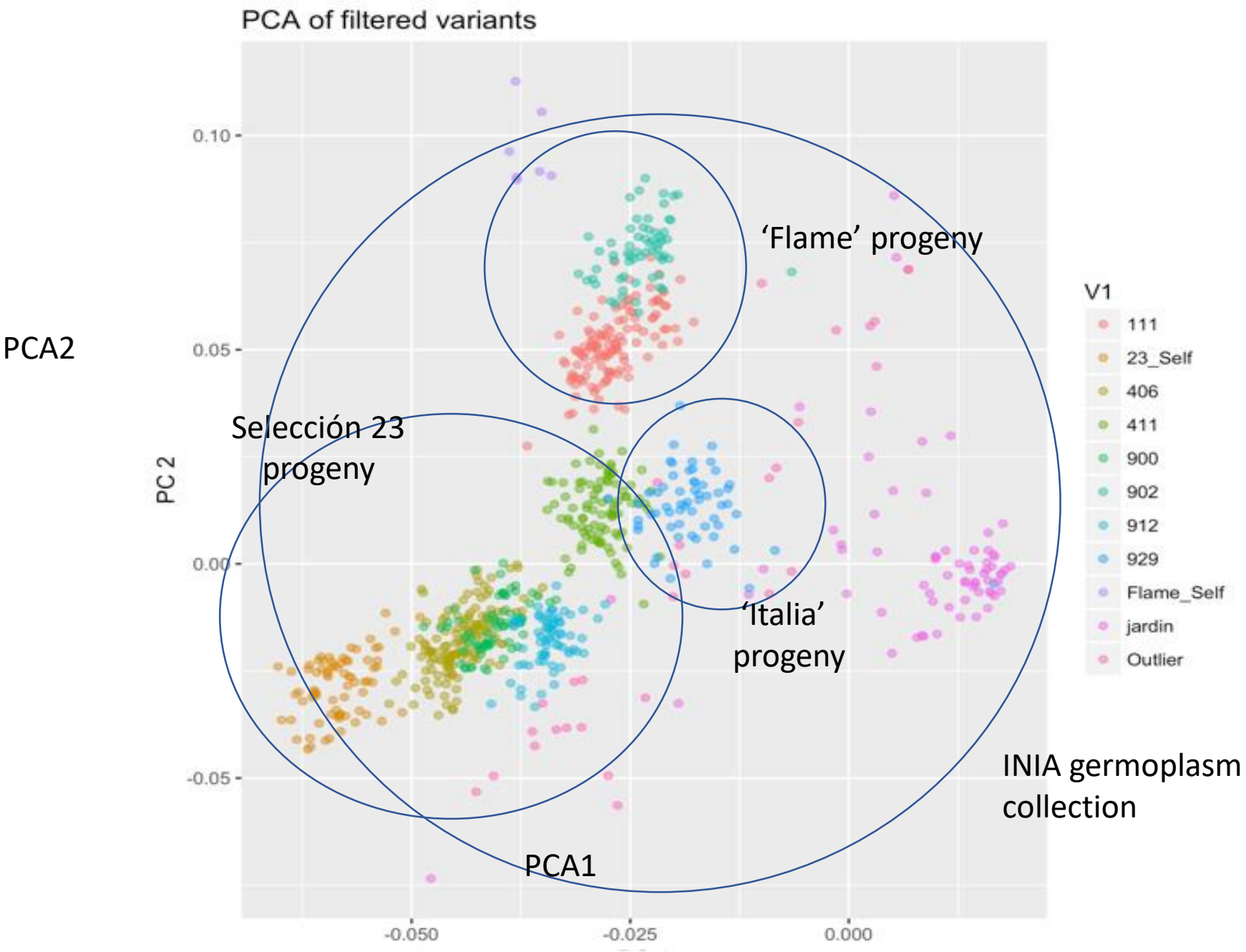
Phenotype – genotype association (GWAS)

- 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 por 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

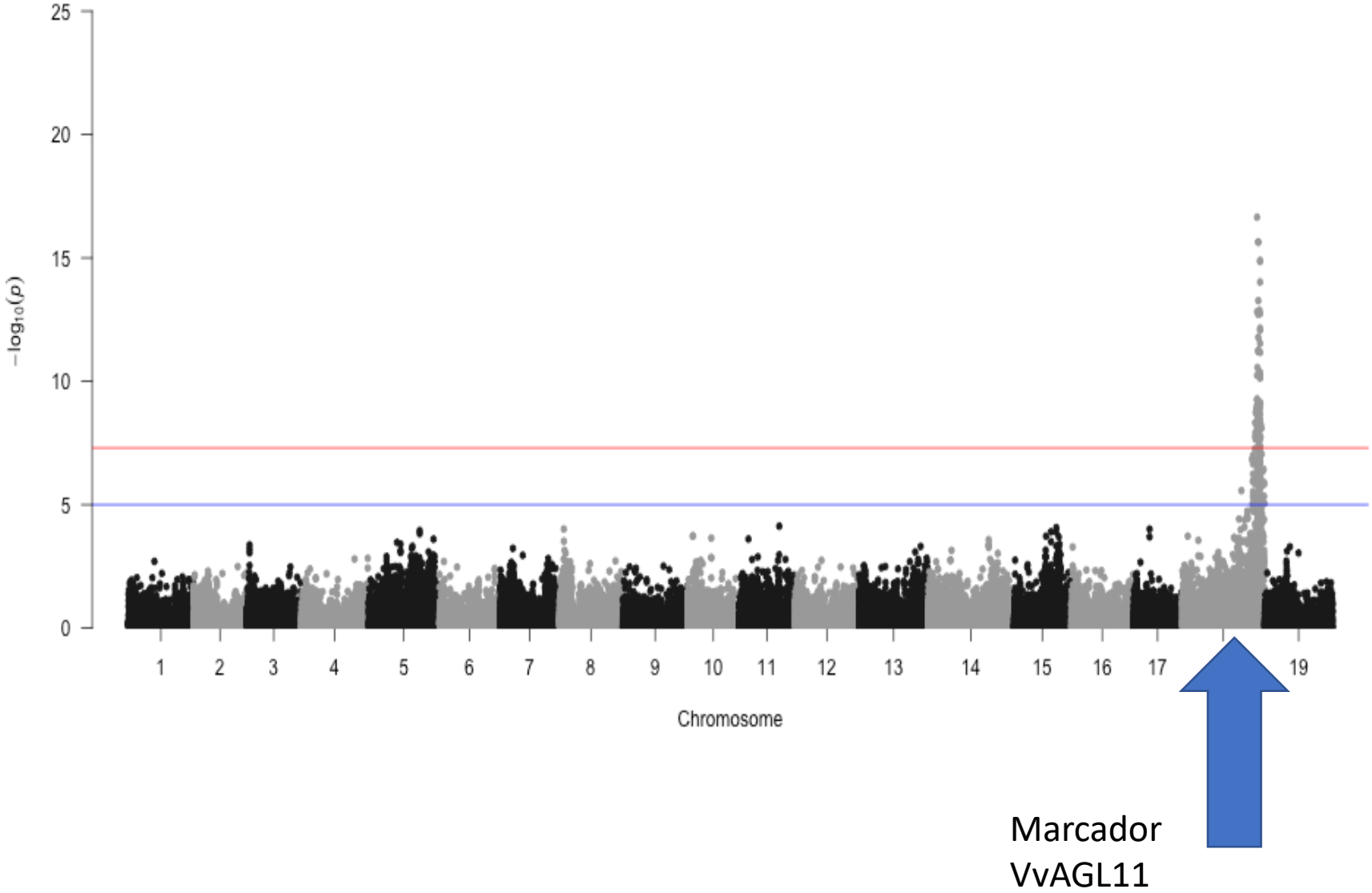
Phenotype – genotype association (GWAS)

- 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


PCA of filtered variants
PCA2
PC 2
0.10
0.05
0.00
-0.05
-0.050
-0.025
0.000
'Flame' progeny
Selección 23 progeny
'Italia' progeny
INIA germoplasm collection
PCA1
V1
111
23_Self
406
411
900
902
912
929
Flame_Self
jardin
Outlier

GWAS: Validation LMM using seed dry weight



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Iniciación 11161044

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