

## **P73 – Identification of genetic determinants associated to cluster architecture and plant fitness in table grapes using genome-wide association studies**

Reyes-Impellizzeri, Sofía<sup>1</sup>; Meneses, Marco<sup>1</sup>; Tapia, Patricio<sup>1</sup>; Iribarra, Juan Pablo<sup>2</sup>; Salazar, Carolina<sup>2</sup>; Salazar, Erika<sup>2</sup>; Barba, Paola<sup>2</sup>; Hinrichsen, Patricio<sup>2</sup>; Muñoz-Espinoza, Claudia<sup>1\*</sup>

<sup>1</sup>Universidad Andrés Bello, Center for Plant Biotechnology, Santiago, Chile

<sup>2</sup>Instituto de Investigaciones Agropecuarias, INIA La Platina, Santiago, Chile

\*camunoz2009@gmail.com

### **Abstract**

Grapevine (*Vitis vinifera* L.) is one of the most economically relevant fruit crops in the world. Grapevine phenology and physiology are highly dependent of environment fluctuations, which alter the progression of phenological states and interfere with plant physiology, being fruit development one of the most severely affected traits. Since the fresh consumption is one of the most profitable markets, the characterization of the genetic architecture of traits related to cluster structure and berry development, and the further determination of associated genetic markers, is highly relevant for the development of breeding selection tools. To elaborate on this, a diverse panel of 116 grapevine varieties containing table, wine and mixed-use varieties as well as segregant lines from INIA's breeding program, were used to perform a genotyping-by-sequencing (GBS) experiment. Subsequently, biallelic polymorphisms were filtered by MAF (>5%) and missing data (<5%) following a VCF pipeline, resulting in the identification of ca. 210,000 high-quality single nucleotide polymorphisms (SNPs), later annotated using SnpEff 12X.2 assembly and VCost3 annotation. In parallel, this panel was phenotyped over three seasons at harvest, including traits such as cluster weight (CW), rachis weight, berry fresh weight (BFW), leaf area index (LAI), photosynthetic efficiency, the latter two as vigour and fitness indicators, among others. Genome-wide association analysis (GWAS) were performed using TASSEL software and GLM /MLM models. Our preliminary results point to the identification of chromosomal regions associated with CW, BFW, LAI and photosynthetic efficiency, among others. Further studies, including experimental validation with transcript and metabolite characterization, are currently under development. Our ultimate goal is to identify markers with association to cluster architecture and plant fitness. These will be validated using amplicon sequencing to evaluate their relevance and potential application in MAS breeding programs.

Financed by FONDECYT/ANID Chile grants 11190936 and 1221410.

**Keywords:** SNPs, GWAS, molecular markers, cluster architecture, plant fitness, grapes, plant breeding.