Oral presentations

Differences on the transcriptomic profiles explain clonal phenotypic variation in *Vitis vinifera* L. ‘Malbec’

Calderón, Luciano[1*]; Carbonell-Bejerano, Pablo[2,3]; Muñoz, Claudio[1,4]; Bree, Laura[5]; Sola, Cristobal[5]; Bergamin, Daniel[5]; Gomez-Talquenca, Sebastian[6]; Ibañez, Javier[2]; Martinez-Zapater, José Miguel[2]; Weigel, Detlef[4]; Lijavetzky, Diego[1**]

[1]Instituto de Biología Agrícola de Mendoza (CONICET-UNCuyo), GenoVid, Chacras de Coria, Argentina
[2]Instituto de Ciencias de la Vid y del Vino, Vitigen, Logroño, Spain
[3]Max Planck Institute for Biology, Molecular Biology Department, Tübingen, Germany
[4]Facultad de Ciencias Agrarias (UNCuyo), Cátedra Fitopatología, Chacras de Coria, Argentina
[5]Vivero Mercier Argentina, Perdriel, Argentina
[6]Instituto Nacional de Tecnología Agropecuaria, Plant Virology Laboratory, Mendoza, Argentina
*lucianocalderon@yahoo.com.ar; **dlijavetky@gmail.com

Abstract

Cultivated grapevines are clonally propagated, mainly to maintain phenotypic traits of productive interest; this practice turns particularly relevant in the wine industry to preserve the varietal typicity. Nonetheless, a wide clonal phenotypic diversity has been reported for several cultivars. Malbec is appreciated for producing high-quality red wines and recognized world-wide as the flag cultivar of the Argentine viticulture. Previous analyses demonstrated a notorious clonal phenotypic diversity for Malbec, in technologically relevant traits. On the other hand, clonal genetic diversity was shown to be scarce, affecting mostly the intergenic regions. Aiming to dissect the molecular bases of the reported phenotypic diversity, we studied 27 clonal accessions grown under the same environmental and cultural conditions at *Vivero Mercier Argentina* experimental vineyard. Phenotypic analyses were performed on berries at technological maturity (~23º Brix), during two consecutive seasons (2017-2019). More precisely, we meassured: i) phenolic composition, ii) analytical profile and iii) skin weight. Afterwards, we chose the six accessions exhibiting extreme contrasting values for the evaluated features. Whole RNA extractions were performed from veraison berries (75% colored), from the six selected clones. Illumina stranded paired-end reads (150 bp in length) were obtained, totaling ~122 Gb of transcriptomic data for 18 samples (6 clones x 3 biological replicates). In order to perform differential gene expression (DEG) and gene ontology (GO) enrichment analyses, the obtained transcriptomic data was aligned to a Malbec reference genome, assembled *de novo* in a truly-phased fashion and annotated by our group. After performing a discriminant analysis including all RNA-seq data, clone Cot-595 exhibited a highly differentiated transcriptomic profile. Moreover, this clone showed the highest total polyphenols and anthocyanins concentration, while clones Mb-506 and Cot-596 showed the lowest concentrations. Therefore, we focused the fore coming DEG and GO analyses to pairwise comparisons among the three mentioned accessions. Consistently, Cot-595 exhibited GO enrichment for genes involved in the anthocyanins biosynthesis pathways, while Mb-506 and Cot-596 showed enrichment for genes involved in metabolic pathways that regulate vegetative growth. These results suggest that phenotypic diversity observed among Malbec clones, might have solid ground on the described differences at the transcriptomic level.

Keywords: Intra-cultivar diversity, RNA-seq, Phenotyping, Malbec