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# Regulation of terpene production in methyl jasmonate treated cell-cultures

Jone Echeverria[1], Chen Zhang[1], Chiara Foresti[2] Antonio Santiago[1], Luis Orduña[1], Paolo Sonego[3], Massimo Pindo[3], Sara Zenoni[2], Marco Moretto[3], José Tomás Matus[1*]

*[1] Institute for Integrative Systems Biology (I2SysBio), Universitat de València-CSIC, Paterna, 46980, Valencia, Spain*
*[2] Department of Biotechnology, University of Verona, 37134, Verona, Italy.*
*[3] Center Agriculture Food Environment (C3A), University of Trento/Fondazione Edmund Mach, via E. Mach 1, 38098, San Michele all'Adige (TN), Italy.*

**José Tomás Matus:* tomas.matus@uv.es

Terpenes are responsible for flavors and aromas of grapes, however, they also protect from radiation, participate in biotic stress and antioxidant mechanisms. The phytohormone methyl jasmonate (MeJA) mediates many of these stress responses and has been associated with increased terpene content in berries. Here, we generated transcriptomic data of *Vitis vinifera* cv. 'Gamay' cells treated with MeJA (100 µM) and cyclodextrins (50 µM) to understand these responses. Ontology analysis revealed that up-regulated genes (URGs) were enriched in jasmonic acid biosynthesis and signaling terms, as expected. Inspection of transcription factors (TFs) among URGs allowed us to study uncharacterized TFs. MapMan enrichment analysis on their TOP420 co-expressed genes (CEGs) allowed us to delimit some TFs highly enriched in jasmonate-related terms. This was the case of VviMYC2, the only grape member of the bHLH IIIe subgroup, and the best candidate for studying the regulation of jasmonate signaling. We confirmed the binding potential of *MYC2* by DAP-seq, and combining it to the list of MeJA-URGs and *MYC2*-CEGs, we generated a list of high-confidence targets that included jasmonate-related genes and TFs such as MYB24, previously found to interact with MYC2 and required for the activation of terpenoid genes. In concordance, our MeJA data showed 13 significantly induced *TPS* genes, 9 of which are bound by *MYB24*, *MYC2* or both. A few terpenoid compounds associated with the induced *TPSs* were significantly accumulated by MeJA. Our data suggests MYC2 regulates the jasmonate pathway and mediates terpene production cooperating with *MYB24* in response to MeJA.

**Keywords:** gene expression, plant cell suspensions, terpenes, methyl jasmonate, transcription factors.