

TRANSCRIPTOME CHARACTERIZATION OF PHENOTYPIC PLASTICITY IN *VITIS VINIFERA*

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Phenotypic plasticity, the ability of an individual to change its phenotype in response to changes in the environment, is common among plants owing to their sessile lifestyle. It has been deeply studied in plants, both for its agronomical significance as well as its ecological and evolutionary implications. However, mechanisms determining plastic changes are still mostly unclear especially for plants cultivated in open fields, where the simultaneous challenge of different environmental signals leads to complex responses in terms of gene expression, metabolic rearrangements and epigenetic mechanisms.

Vitis vinifera spp is one of the most plastic plants known, a single genotype being able to produce berries with different quality, thus different wine qualities, depending on the micro-environment where it is cultivated. Moreover, plastic responses in grapevine are one of the causes of excellent-to-poor wine vintages.

In this study, plastic rearrangements of the transcriptome of a single clone of *Vitis vinifera* cv Corvina (48) were analyzed. Berries of different developmental stages were harvested from 11 vineyards during 3 consecutive years. A total of 171 hybridizations were performed using a NimbleGen microarray system designed on the new V1 grapevine genome annotation.

More than 5% of the whole Corvina transcriptome was estimated to be used for plastic reorganization of the gene expression during berry development. Plastic dynamics were also assessed in light of seasonal changes, highlighting transcripts expressed during standard meteorological trends and those expressed under unfavorable weather conditions. Differential gene expression was further correlated with metabolic and enological data as well as central micro-environmental and agricultural features revealing how human-imposed conditions rather than natural environment might trigger plastic reactions in ripe berry transcriptome.