MOLECULAR RESPONSE TO DIFFERENT SOILS AND ROOTSTOCKS IN GRAPEVINES

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Grapevine is an ancient culture that constitutes one of the most economically important fruit species worldwide. Soil conditions and rootstocks are two of the main causes that can influence quality and wine production. In this work the transcriptome variation to different soils and two different rootstocks in Vitis vinifera was investigated through Affymetrix GeneChip® microarray technology. The grapes cv. Pinot noir were grown in greenhouse with three different soils: sand, turf and vineyard soil from Asti. The plants were grafted with two different rootstock: 101/14, a weak rootstock and 1103 Paulsen, a vigorous one that enhances the growing rate, than the leaves samples were collected during two subsequent years. The results from the large-scale analysis of mRNA expression profiles in vegetative tissues of grapevine show that a mRNA abundance changes in response to different grafting and soil conditions is active. A greater number of transcripts are mainly involved in physiological and molecular processes as primary metabolism, secondary including phenylpropanoid, flavonoid and lignan biosynthesis, energy, cellular transport and communication as signal transduction mechanisms and biogenesis of cellular components. The transcript profiling pointed out genes and metabolic pathways regulated by soils and rootstocks conditions in specific manner in two different years. The object of this work is to identify the genes and the molecular bases that explain the soils and rootstocks role in grapevine development.