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Poster Communication Abstract – 4.10

GENETIC AND DEVELOPMENT FACTORS AFFECT THE EXPRESSION OF GENES INVOLVED IN FATTY ACID AND PHENYLPROPANOID BIOSYNTHESIS AND IN LIGHT SIGNAL TRANSDUCTION IN OLIVE FRUITS

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Olive oil, for its beneficial proprieties in terms of high content of healthy antioxidant compounds, such as well-balanced fatty acids (FAs) and secondary metabolites, like phenylpropanoids playing a role in the irradiation and protection from oxidative stress of plants, is a high commercial valuable product for Mediterranean countries.

Fruit development has a significant effect on the accumulation of these metabolites which vary significantly depending on the cultivar, therefore, it is very important to investigate differentially expressed genes (DEGs) of the genetic network of FAs and phenylpropanoids relating to the different ripening phases.

For this purpose, olive drupes from three olive cultivars, ‘Cellina di Nardò’, ‘Ruveia’ and ‘Salella’, very different in FAs and phenylpropanoids content, were selected and studied at two ripening stages corresponding at the beginning and end of fruit maturation.

Targeted RNA-Sequencing approach, based on a custom panel of about 250 genes, was therefore performed for the first time in olive. Forty-eight genes are involved in the regulation of phenylpropanoids pathway, 112 in FAs metabolism and 97 in photoperception and light signal transduction.

Gene expression analysis confirmed, for all the three cultivars, a decrement of phenylpropanoids transcript levels in olives at complete maturation. A similar behaviour was observed for the genes involved in FAs pathway.

The transcripts of many genes, implicated in both FAs and phenylpropanoid pathways, resulted down-regulated during ripening only in ‘Salella’, characterized by the lowest oleic acid and total phenols levels, in respect of ‘Cellina di Nardò’ and ‘Ruveia’.

On the other hand, a member of the MYB transcription factors, RVE8, a transcriptional activator of evening

element containing clock-controlled genes, resulted relevantly overexpressed in ‘Salella’. From the results observed, this study gives additional insight into the regulation of secondary metabolites in olive fruits and a major impact of development processes in the control of gene expression, as well as genotype-dependent transcriptional control mechanisms on photoperception-related traits.

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