

PROTEOMIC ANALYSIS OF GRAPE BERRY (*CORVINA*) RIPENING AND WITHERING

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The considerable economic impact makes wine grape one of the most important fruit species in many countries worldwide. Moreover, consumption of grapes and wine has numerous nutritional benefits for humans. For these reasons there is a great interest in studying and improving grape berry development. Molecules related to aroma and taste are produced during fruit maturation, being their synthesis profile specific for each variety. During the ripening process, changes in berry softness, pigmentation, sugar and water content contribute to confer peculiar quality characteristics. The expression analysis of grape berry (*Corvina* variety) during ripening and withering processes using a combination of transcriptomic and proteomic approaches represents the final goal of this work.

Hereby, we describe the dynamic protein expression profile of grape berry collected at seven ripening/withering stages. The comparative analysis, performed by DIGE (Differential in Gel Electrophoresis, GE Healthcare) technology, revealed that numerous soluble proteins evolve during berry development with specific distribution at different stages. A total of 800 spots were detected in the 2-DE maps, 80 protein spots resulted differentially expressed during berry withering and were identified by MS analysis. The majority of these proteins were related to metabolism, energy and defence activity.

Expression profiles at proteomic and transcriptomic level is being compared, identifying correlations and divergences.

These results may significantly contribute to the knowledge of the role played by defined proteins involved in the physiological ripening/withering process, in view of both quality improvement and varietal differentiation of grapes and wines.