

TOP-DOWN AND BOTTOM-UP QUANTITATIVE PROTEOMIC APPROACHES TO CHARACTERIZE THE DEVELOPMENT OF GRAPE BERRY TISSUES

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Grapevine (*Vitis vinifera*) is one of the economically most important fruit crops. The berry components that compose the final quality traits of both table and wine grapes, such as sugars, acids, flavours, anthocyanins, tannins, etc., are synthesized or accumulated along the different grape berry development stages. Thus the proteomic profiles along berry development have to correlate with the biochemical and physiological changes known to occur in the grape berries. The grape berry development has been characterized to some extent at biochemical and molecular levels, and semi-quantitative proteomic approaches have been undertaken to better characterize and understand this biological process of agro-economical relevance.

We have taken advantage of top-down (DIGE) and bottom-up (iTRAQ) quantitative proteomic approaches to characterize both large and subtle, but statistically significant quantitative changes in proteins along the grape berry development. In pre-veraison stages the pericarp was analyzed as a single tissue, while from veraison to full ripening the pericarp was divided into flesh and skin and analyzed separately. A suite of bioinformatic and statistical tools were used to group proteins into abundance patterns, to rank proteins according to abundance levels and to determine the ontologies associated to each cluster and each developmental stage.

Results correlate quite well with known physiological, biochemical and molecular changes, thus giving a proof of concept of our proteomic analysis. Then new proteins not previously associated to developmental stages could be described.