

## Proteomic profiling of grape berry presenting early loss of mesocarp cell vitality

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### Abstract

From fruit set to ripening, the grape berry mesocarp experiences a wide range of dynamic physical, physiological, and biochemical changes, such as mesocarp cell death (MCD) and hydraulic isolation. The premature occurrence of such events is a characteristic of the Niagara Rosada (NR) variety, utilised as table grapes and winemaking. In our opinion, the onset of ripening would not cause MCD, but a down-regulation of respiratory enzymes during the early loss of cell viability, while maintaining membrane integrity. For this, we investigated three distinct developmental stages (green (E-L33), veraison (E-L35), and ripe (E-L39)) of NR berries by label-free proteomics, enzymatic respiratory activity and outer mesocarp imaging. Cell wall-modifying proteins were found to accumulate differently throughout ripening, while cytoplasmic membranes continue intact. In addition, the reduction in the mitochondria cristae density occurred simultaneously with the decrease of malate dehydrogenase and succinate dehydrogenase activities. By proteomics, we identified 956 differentially accumulated proteins, of which most were down-regulated at ripening. However, several respiratory enzymes were among the most abundant proteins at ripening, showing the maintenance of respiratory activity. Furthermore, we hypothesized that gluconeogenesis originating from malate can happen in NR berries, and that sucrose futile cycles may become an important system for storing and unloading carbohydrates. Therefore, the present data indicate that the premature loss of berry mesocarp vitality in NR was not associated with cell death. Moreover, the grape variety and cultivation region can influence protein abundance, enriching our understanding of grape berry proteome and ripening dynamics in tropical conditions.

**Keywords:** grapevine, tropical viticulture, berry maturation.