

DEEP SEQUENCING OF OLIVE (*OLEA EUROPAEA* L.) SHORT RNAS IDENTIFIES MICRORNAS TARGETING INVOLVED IN DRUPE RIPENING

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The ripening process of olive fruits is associated with chemical and/or enzymatic specific transformations making them particularly attractive to animals and humans. Usually, there is a progressive chromatic change characterized by a final red-brown color of both epidermis and mesocarp. This event has an exception in the *Leucocarpa* cultivar, in which we observed the destabilization in the equilibrium between the metabolism on chlorophyll and that of the other pigments, particularly the anthocyanins, whose switch-off during maturation promotes the white coloration of the fruits.

Recently, transcription profiling of ripening olives from ‘*Leucocarpa*’ and ‘*Cassanese*’, through an Illumina RNA-seq approach, has provided some information about genes involved in fruit maturation as flavonoid and anthocyanin transcripts.

To study the possible gene differences involved in flavonoids and anthocyanins biosynthetic pathways during ripening possibly caused by small nuclear RNA (snRNA) in olive drupes, the snRNA libraries of fruit ripening from ‘*Leucocarpa*’ and ‘*Cassanese*’ were constructed with RNAs from drupes at 100 and 130 DAF (Days After Flowering) and sequenced by Illumina approach. Comparing sequence information, 130 conserved microRNAs (miRNA) in the *Viridiplantae* were detected belonging 14 miRNA families. For the remaining read not-matched with known miRNAs in the *Viridiplantae*, we combined secondary structure and minimum free energy to discover novel olive miRNAs. Based on these analyses, 492 miRNAs were considered as putative novel. To increase insights into the functions of known and putative novel miRNA in olive, putative target genes were computationally predicted by alignment with the olive drupe transcripts obtained from the same samples. A total of 32 and 186 transcripts were predicted as targets of 130 known and 492 putative novel miRNA, respectively. The identified target genes are involved in a broad range of biological processes.

Interestingly, some genes involved in negative regulation of anthocyanin metabolic process, were identified as target of miR168 suggesting that this miRNA family is likely operative during color transition in olive.