

INSIGHTS INTO FRUIT SENESCENCE REGULATORY NETWORKS IN A TOMATO LANDRACE WITH LONG SHELF-LIFE

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Fruit senescence has a great impact on fruit quality and storability thereby generating product loss during long term storage. Currently, molecular networks underlying regulation of this process are poorly understood. Furthermore, the boundary between fruit ripening and senescence is still unclear. Tomato (*Solanum lycopersicum* L.) is, at the moment, the best model to study ripening in climacteric fleshy fruit. The Italian landrace Lucariello (LUC), recognized as 'Pomodoro del Piennolo del Vesuvio', is characterized by a long shelf-life reaching more than 150 days after harvest. LUC represents both an excellent model to investigate the relationship between ripening and senescence and, likely, a genetic resource to transfer its long shelf-life to other cultivars. For this reason, the genome of LUC was re-sequenced, assembled and annotated.

In this work, LUC was characterized following a multi-omics approach. Coding and non-coding RNAs, DNA methylation, and histone post-translational modifications (H3K4me3, H3K27me3, H3K9K14ac) were analyzed in fruit pericarps at the red ripe stage, and at 60 and 150 days in post-harvest. More than 10,000 genes were found to be differentially expressed across the time points (DEGs) and many are coding for transcription factors related to fruit ripening. About 2000 putative miRNAs were predicted as anti-correlated to DEG targets. Differentially enriched regions for H3K4me3, H3K27me3, H3K9K14ac and differentially methylated regions were identified pivoting around the transcription start site and correlated with gene expression. An integrated analysis is now being carried out to find activator and/or repressor candidates regulating senescence process in tomato fruits. All the genomic and epigenomic datasets are gathered into a dedicated and user-friendly web-based platform.