

Transcriptome analysis and postharvest behavior of the kiwifruit ‘*Actinidia deliciosa*’ reveal the role of ethylene-related phytohormones during fruit ripening

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Abstract

Kiwifruit are climacteric fruit, so they must be harvested before they are fully ripe, allowing for the extension of their shelf-life via cold storage. Therefore, an adequate knowledge about how ethylene-induced fruit senescence is required to avoid significant economic losses. The main goal of the present study was to investigate the kiwifruit ripening process at the physiological and molecular levels by RNA-seq after 1-methylcyclopropene (1-MCP, ethylene inhibitor) and Ethrel® (ethylene stimulator) treatments. The results showed that Ethrel® (ethephon) treatment induced more accelerated fruit ripening, leading to rapid fruit senescence, meanwhile 1-MCP caused a slowing flesh softening, and thus a longer shelf-life period. The RNA-seq was carried out on the fruit after 4 and 13 days, considering day 4 as the most determinant in terms of differentially expressed genes (DEGs). The sequencing achieved 70.7% alignment with the ‘Hongyang’ genome, obtaining 18,036 DEGs. The protein-protein interaction (PPI) network shows the interaction between different pathways in two main clusters: (1) pentose and glucuronate interconversions, citrate cycle, glycolysis and gluconeogenesis or starch, and sucrose metabolism and (2) porphyrin and chlorophyll metabolism. The first cluster is mainly interconnected by G6PD1 (pentose pathway); E1 ALPHA and ACLB-2 (citrate cycle); Achn209711 (pentose and glucuronate); LOS2 (glycolysis); HKL1 and HXK1 (glycolysis—starch and sucrose); and PHS2 (starch and sucrose). In the second cluster, GUN5 through PORA is interacting with CRD1 and NYC1 which were overexpressed by 1-MCP in the porphyrin and chlorophyll metabolism. In addition, genes linked to PSBY and PSBP photosynthesis-linked proteins in

photosystem 2 were overexpressed by 1-MCP which is undoubtedly related to chlorophyll degradation and fruit senescence. These results suggest that in kiwifruit, the main pathways that are regulated by ethylene-induced senescence comprise sugar catabolism and chlorophyll degradation.