

these genes showed dynamic regulation during fruit development and differential expression among genotypes. The peak expression of auxin transporter MdPIN1-1 correlated with the detection of the transcripts of a pre-climacteric ethylene biosynthesis gene MdACS3. Both transcript profiles during maturation and tissue-specific expression features for these genes suggested that auxin transport and homeostasis are important in regulating the timing of ethylene pathway activation and therefore may contribute to distinct ripening processes among apple genotypes.

Phenolic profile of different red and yellow raspberry varieties during ripening

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Rubus species, including raspberries, have been used since ancient times for the treatment of wounds, diarrhea, colic pain, diabetes, etc.[1]. Being among the fruits with higher antioxidant contents, raspberries are receiving increasing attention as a source of potentially healthy compounds that can help prevent cardiovascular disease and diabetes mellitus [2]. A large part of the health effects attributed to berries is supposed to be due to polyphenolic compounds. The majority of raspberries polyphenols are ellagitannins, but they also contain large amounts of anthocyanins (in red raspberries) and smaller amounts of hydroxycinnamic acids, flavonols, flavan-3-ols and proanthocyanidins [3]. Yellow raspberries, which lack anthocyanins at all, seem to be as effective or even more effective than their red counterparts at inhibiting enzymes with potential impact on chronic diabetes or hypertension [4, 5]. From the biosynthetic point of view there is as yet no information on where the block of the anthocyanin pathway in yellow raspberries could be. In this study a targeted UPLC-MS/MS method recently developed by our lab was used to screen 140 phenolic compounds including benzoates, phenylpropanoids, coumarins, stilbenes, dihydrochalcones and flavonoids, using MRM transitions for accurate quantification. The fruits of different plants of 4 red and 6 yellow raspberry varieties, at different ripening stages (green, turning and ripe) were analyzed. Around 34 phenolic compounds were detected above the quantification limit at the different ripening stages.

This allowed to obtain not only a profile of the phenolic composition of the different raspberry varieties, at different stages, but also to highlight the different tendencies in the variation of concentration of each of the different compounds during ripening. Furthermore, a general biosynthetic scheme and a prediction of the mechanism underlying the loss of anthocyanin in yellow raspberries can be predicted

[1] G. Rocabado, L. Bedoya, M. Abad, P. Bermejo, Natural Product Communications, 3 (2008) 423-436.

[2] J. Beekwilder, R.D. Hall, C.H.R. de Vos, Biofactors, 23 (2005) 197-205.

[3] A.V. Rao, D.M. Snyder, Journal of Agricultural and Food Chemistry, 58 (2010) 3871-3883.

[4] S. Cheplick, Y.-I. Kwon, P. Bhowmik, K. Shetty, J Food Biochemistry, 31 (2007) 656-679.

[5] L. Zhang, J. Li, S. Hogan, H. Chung, G.E. Welbaum, K. Zhou, Food Chemistry, 119 (2010) 592-599.

The Role Of MYB Factors In Fruit Color

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Fruit quality traits included color are major breeding targets in the Rosaceae. In order to have better knowledge on genetic control of fruit color, we analysed a segregating population and genetic resources in the cultivated octoploid strawberry for skin fruit color. In addition, color of the juice was measure with a spectrophotometer. Results highlighted one region, in which in several QTL linked to fruit color co-localized. Based on the genome *Fragaria* sequence, the QTL region included two MYBs that were not yet studied. Expression patterns and transitory expression of these MYB were performed. Results suggested the role of one these MYB in the control of fruit color. Considering the level of ploidy of strawberry, only one allele out of the eight present in the parent may control the QTL linked to color. In addition, using a marker linked to the region that included the MYB, we showed an association between this marker and fruit color assessed visually in genetic resources. We believe that the mechanisms unraveled in the present study may play a crucial role in the variations of fruit color in other Rosaceous species.