



Expression of carotenoid biosynthesis genes during carrot root development

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Titre	Expression of carotenoid biosynthesis genes during carrot root development
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Auteur	Clotault, Jérémie [1], Peltier, Didier [2], Berruyer, Romain [3], Thomas, Mathieu [4], Briard, Mathilde [5], Geoffriau, Emmanuel [6]
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Mots-clés	Carotenoid accumulation [7], <i>Daucus carota</i> [8], Gene Expression [9], root development [10] Carotenogenesis has been extensively studied in fruits and flower petals. Transcriptional regulation is thought to be the major factor in carotenoid accumulation in these organs. However, little is known about regulation in root organs. The root carotenoid content of carrot germplasm varies widely. The present study was conducted to investigate transcriptional regulation of carotenoid biosynthesis genes in relation to carotenoid accumulation during early carrot root development and up to 3 months after sowing. HPLC carotenoid content analysis and quantitative RT-PCR were compared to quantify the expression of eight genes encoding carotenoid biosynthesis enzymes during the development of white, yellow, orange, and red carrot roots. The genes chosen encode phytoene synthase (PSY1 and PSY2), phytoene desaturase (PDS), ζ -carotene desaturase (ZDS1 and ZDS2), lycopene α -cyclase (LCYE), lycopene β -cyclase (LCYB1), and zeaxanthin epoxidase (ZEP). All eight genes were expressed in the white cultivar even though it did not contain carotenoids. By contrast with fruit maturation, the expression of carotenogenic genes began during the early stages of development and then progressively increased for most of these genes during root development as the total carotenoid level increased in coloured carrots. The high expression of genes encoding LCYE and ZDS noted in yellow and red cultivars, respectively, might be consistent with the accumulation of lutein and lycopene, respectively. The results showed that the accumulation of total carotenoids during development and the accumulation of major carotenoids in the red and yellow cultivars might partially be explained by the transcriptional level of genes directing the carotenoid biosynthesis pathway.
Résumé en anglais	

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Liens

- [1] <http://okina.univ-angers.fr/jeremy.clotault/publications>
- [2] <http://okina.univ-angers.fr/didier.peltier/publications>
- [3] <http://okina.univ-angers.fr/romain.berruyer/publications>
- [4] [http://okina.univ-angers.fr/publications?f\[author\]=24055](http://okina.univ-angers.fr/publications?f[author]=24055)
- [5] [http://okina.univ-angers.fr/publications?f\[author\]=166](http://okina.univ-angers.fr/publications?f[author]=166)
- [6] <http://okina.univ-angers.fr/geoffriau/publications>
- [7] [http://okina.univ-angers.fr/publications?f\[keyword\]=20414](http://okina.univ-angers.fr/publications?f[keyword]=20414)
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