



Expression analysis of *LCY1* gene in *Solanum lycopersicum* (tomato) in various organs and developmental stages using microarray data sets

Zahra Zinati

Department of Agroecology, College of Agriculture and Natural Resources of Darab, Shiraz University, Iran

*Corresponding Author: Zahra.zinati@yahoo.com

Abstract

LCY1 (Gene ID: 544104) encodes lycopene β -cyclase, chloroplastic in *Solanum lycopersicum* (tomato) which is involved in the β -carotene and β -zeacarotene biosynthesis pathways. Although previous studies proposed the principal role of *LCY1* in controlling the lycopene transformation, the expression patterns of *LCY1* is still lacking. In the current study, *in-silico* expression profile of *LCY1* gene in tomato was analyzed at developmental levels and anatomical parts using the anatomy tool, and the developmental tool via retrieving the expression values from affymetrix array database of Genevestigator response viewer (<https://www.genevestigator.com/gv/>). Based on the Genevestigator analysis of the anatomical parts of the samples, the highest expression of the gene was found in seedling followed by shoot, inflorescence, roots, and fruits, respectively. In terms of developmental stages, the highest expression of *LCY1* was noticed in the flowering stage, main shoot growth stage and fruit formation followed by a moderate expression during an inflorescence visible stage, fruit ripening complete stage, ripening stage respectively. This study provides a bioinformatics background for the expression pattern of the *LCY1* in tomato that may be contributing to create improved varieties.

Keywords: expression pattern, *LCY1*, tomato

Introduction

Tomatoes (*Lycopersicon esculentum* Mill.) are the major dietary source of lycopene, which is a carotenoid, and is highly effective in combating some diseases such as the heart disease and the cancer (Wan *et al.*, 2007). Cyclisation of lycopene results in β -carotene, through the action of a β -cyclase (Ralley *et al.*, 2016). In tomato, two lycopene cyclase, including *LCYB* (*LCY1*) and *CYCB* are present. *LCY1* is suggested to be the most important in the vegetative carotenoids formation, while the *CYCB* gene exhibits ripening specific expression and *CYCB* is so related to production of β -carotene over ripening (Pecker *et al.*, 1990). Suppressing the of *Lcy* gene expression, the principal gene controlling the lycopene transformation, is a convenient and practical approach to increase the lycopene content. It has been reported that regulating biosynthetic enzyme in the carotenoid pathway using RNAi-mediated *Lcy* gene silencing can enhance the lycopene content of plant-derived products (Wan *et al.*, 2007). Although previous studies proposed the principal role of *LCY1* in controlling the lycopene transformation, the expression pattern of *LCY1* is still lacking. In the current study, *in-silico* expression profile of *LCY1* gene in tomato was analyzed at developmental levels and anatomical parts to provide valuable information about *LCY1* expression patterns in tomato that may be contributing to create improved varieties.

Material and methods

Expression analysis of *LCY1* gene in *Solanum lycopersicum* (tomato) in various organs, and developmental stages

In the current study, *in-silico* expression profile of *LCY1* gene in tomato was analyzed at developmental levels and anatomical parts using the anatomy tool, and the developmental tool via retrieving the expression values from affymetrix array database of Genevestigator response viewer (<https://www.genevestigator.com/gv/>). The Anatomy tool displays how strongly genes of interest are expressed in different anatomical categories, including cell cultures from primary cells, tissues, and organs. The Development tool sums up the gene expressions across distinct developmental stages of the life cycle of an organism. Affymetrix Tomato Genome Array was chosen for the analysis of microarray data.

Results and discussion



The expression analysis of *LCY1* gene in different plant anatomical features demonstrated that the *LCY1* expression was ubiquitous in almost all tissues. The highest expression of the gene was found in seedling followed by shoot, inflorescence, roots, and fruits, respectively (Fig. 1). These findings are consistent with the results of previous studies (Pecker et al., 1990) indicating that (*LCY1*) is predominate in the formation of vegetative carotenoids.

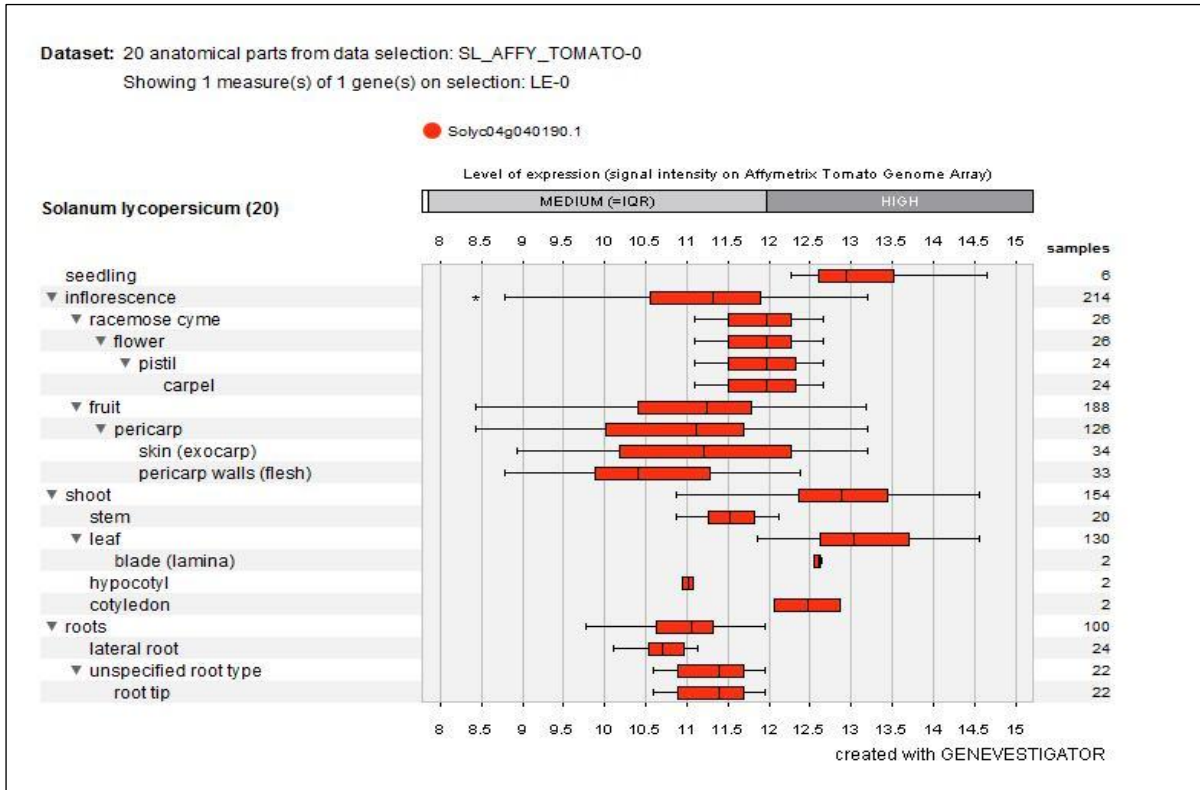


Fig. 1- Expression analysis of *LCY1* gene in various organs of tomato

The highest expression of *LCY1* was noticed in the flowering stage, main shoot growth stage and fruit formation followed by a moderate expression during an inflorescence visible stage, fruit ripening complete stage, ripening stage respectively (Fig. 2). This study provides a bioinformatics background for the expression pattern of the *LCY1* in tomato that may be contributing to create improved varieties.



Dataset: 6 developmental stages from data selection: SL_AFFY_TOMATO-0
Showing 1 measure(s) of 1 gene(s) on selection: LE-0

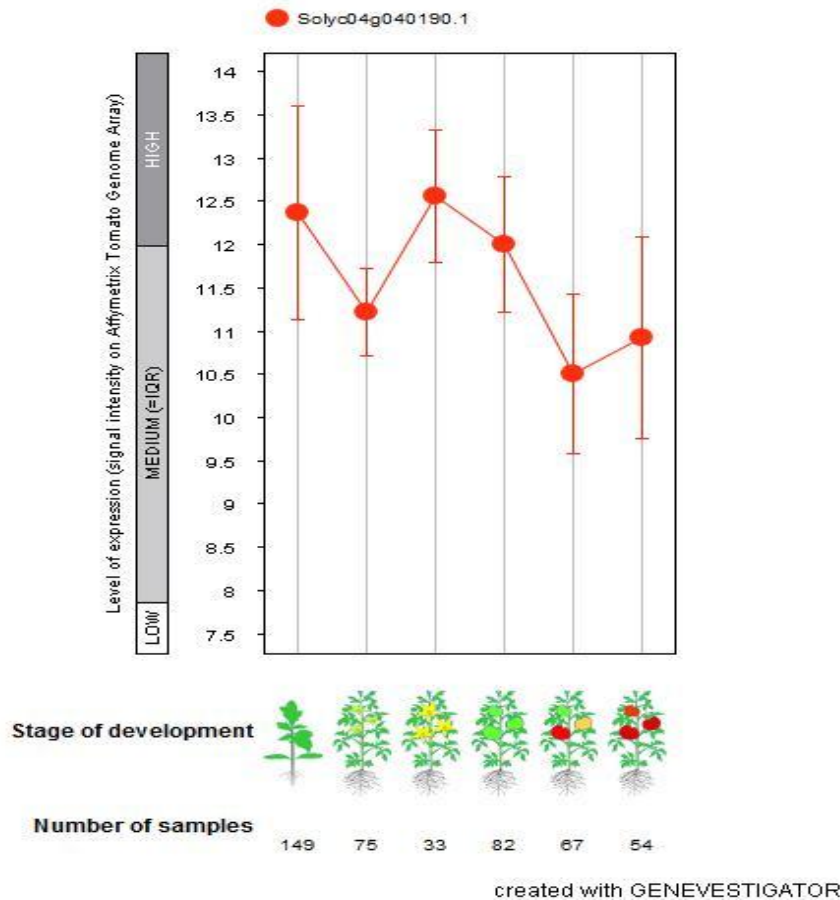


Fig. 2- Expression analysis of *LCY1* gene in developmental stages of *tomato*

References

- Wan Q., Zhang X.G. and Song M., 2007. Fruit-specific RNAi-mediated Lcy gene enhances content of Lycopene in tomatoes silencing. *Sheng wu Gong cheng Xue bao*, 23(3): 429-433.
- Ralley L., Schuch W., Fraser P.D. and Bramley P.M. 2016. Genetic modification of tomato with the tobacco lycopene β -cyclase gene produces high β -carotene and lycopene fruit. *Z Naturforsch*, 71(9-10): 295-301
- Pecker I., Gabbay R., Cunningham F.X. and Hirschberg J. 1990. Cloning and characterization of the cDNA for lycopene β -cyclase from tomato reveals a decrease in its expression during fruit ripening. *Plant Molecular Biology*, 30: 807-19.
- Zimmermann P, Hirsch-Hoffmann M, Hennig L, Gruissem W. 2004. GENEVESTIGATOR Arabidopsis microarray database and analysis toolbox. *Plant Physiology*. 136: 2621-2632.