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Comparative analysis of plant lycopene cyclases

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ABSTRACT

Carotenoids are essential isoprenoid pigments produced by plants, algae, fungi and bacteria. Lycopene cyclase (LYC) commonly cyclize carotenoids, which is an important branching step in the carotenogenesis, at one or both end of the backbone. Plants have two types of LYC (β-LCY and ε-LCY). In this study, plant LYCs were analyzed. Based on domain analysis, all LYCs accommodate lycopene cyclase domain (Pf05834). Furthermore, motif analysis indicated that motifs were conserved among the plants. On the basis of phylogenetic analysis, β-LCYs and ε-LCYs were classified in β and ε groups. Monocot and dicot plants separated from each other in the phylogenetic tree. Subsequently, *Oryza sativa* Japonica Group and *Zea mays* of LYCs as monocot plants and *Vitis vinifera* and *Solanum lycopersicum* of LYCs as dicot plants were analyzed. According to nucleotide diversity analysis of *β-LCY* and *ε-LCY* genes, nucleotide diversities were found to be π: 0.30 and π: 0.25, respectively. The result highlighted *β-LCY* genes showed higher nucleotide diversity than *ε-LCY* genes. LYCs interacting genes and their co-expression partners were also predicted using String server. The obtained data suggested the importance of LYCs in carotenoid metabolism. 3D modeling revealed that depicted structures were similar in *O. sativa*, *Z mays*, *S. lycopersicum*, and *V. vinifera* β-LCYs and ε-LCYs. Likewise, the predicted binding sites were highly similar between *O. sativa*, *Z mays*, *S. lycopersicum*, and *V. vinifera* LCYs. Most importantly, analysis elucidated the V/IXGXGXXGXXXA motif for both type of LYC (β-LCY and ε-LCY). This motif related to Rossmann fold domain and probably provides a flat platform for binding of FAD in *O. sativa*, *Z mays*, *S. lycopersicum*, and *V. vinifera* β-LCYs and ε-LCYs with conserved structure. In addition to lycopene cyclase domain, the V/IXGXGXXGXXXA motif can be used for exploring LYCs proteins and to annotate the function of unknown proteins containing lycopene cyclase domain. Overall results indicated that a high degree of conserved signature were observed in plant LYCs.

1. Introduction

With more than 600 different structures, carotenoids are common isoprenoid pigments synthesized by various organisms including plants, certain algae, fungi and bacteria (Alquezar et al., 2009). These are structurally localized in the thylakoid membrane and play a key role as accessory molecules for harvesting light, prevention from photo damage, and as antioxidants under stress conditions (Gao et al., 2010; Demmig-Adams et al., 1996; Cui et al., 2011). Carotenoids also provide the yellow, orange or red coloration characteristic of many flowers and fruits to attract animals and insects for pollination or for the dispersal of seeds (Bartley and Scolnik, 1995). The attractive colors and beneficial health effects of caretonoids, especially β-carotene, have received attention (Alquezar et al., 2009). In addition, β-carotene is a substrate for the biosynthesis of other carotenoids such as zeaxanthin, xanthphylls, neoxanthin, violaxanthin (Hugueney et al., 1995). Vitamin A is also synthesized from β-caroten (Rock and Zeevaart, 1991). Thus, vitamin A is not only fundamental for plants but also beneficial for human and animal nutrition.

Toward the end of metabolic processes of carotenoids, they are commonly cyclized at one or both ends of backbones by lycopene cyclase (Mohamed and Vermaas, 2006). Lycopene cyclization is a crucial branching point in the carotenogenesis (Alquezar et al., 2009). Lycopene cyclization is caused by β-LCY (EC:5.5.1.19) using NADP(H) or FAD as a co-factor (Hornero-Méndez and Britton, 2002; Yu et al., 2010). β-LCY alone produces β-carotene whereas two enzymes, β-LCY and ε-LCY (EC: 5.5.1.18), together form

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α-carotene (Beyer et al., 1991; Hornero-Méndez and Britton, 2002; Moreno et al., 2013).

β-LCYs of plants and bacteria have a conserved dinucleotide binding motif. Furthermore, several conserved domains such as conserved region β-LCY's, β-LCY specific motif, cylase motif I and II (CMI and CMII), β-LCY CAD (catalytic activity domain) and a charged region are highly conserved in plants (Moreno et al., 2013; Hugueney et al., 1995). β-LCY CAD is essential for β-LCY activity

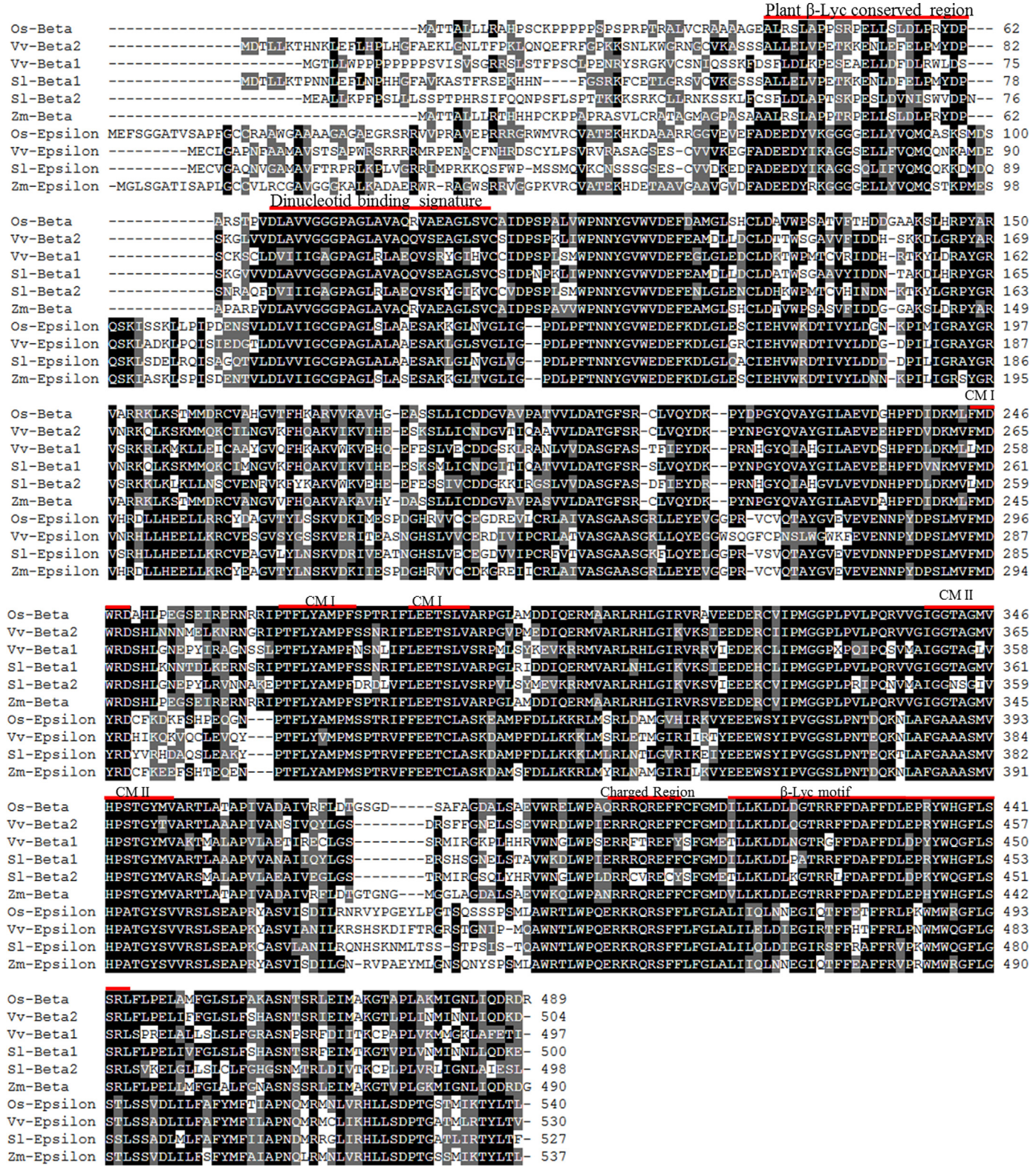

Fig. 1. Aligment of the amino acid sequences of β-LCY and ε-LCY proteins in *O. Sativa*,*V. Vinifera*, *S. Lycopersicum*, and *Z. mays* via ClustalW. The numbers on the left indicate the number of amino acids. Residues identical for all sequences in a given position are indicated with white text on a black background. Illustration was made by using BoxShade server. Characteristic regions of LCYs indicated on the sequences; Plant β-LCY conserved region, dinucleotide binding signature, cyclase motif (CM I and CM II), charged region, and β-LCY motif.