微生物学报
Acta Microbiologica Sinica
2016, 56(11): 1680-1690
http://journals.im.ac.cn/actamicrocn
DOI: 10.13343/j.cnki.wsxb.20160089

Mini-Review 小型综述

八氢番茄红素脱氢酶的研究进展

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摘要：类胡萝卜素是一类超过700种的萜烯基团类不饱和化合物的总称，根据结构可分为胡萝卜素族和叶黄素族，具有较高的营养价值。八氢番茄红素脱氢酶是类胡萝卜素生物合成途径中的首要限速酶，它参与催化无色的八氢番茄红素转变成有色类胡萝卜素，发挥着中心调控作用。不同生物源的八氢番茄红素脱氢酶在功能上呈现多样性，在大多数蓝细菌，藻类和高等植物的类胡萝卜素生物合成途径中，由CrtP，CrtQ和异构酶CrtH或PDS，ZDS和异构酶Z-ISO、CrtISO共同参与番茄红素的形成，而在大多数微生物中只有CrtI-type一种酶来完成八氢番茄红素的脱氢反应，且根据脱氢步骤的不同分别可生成链孢红素、番茄红素或脱氢番茄红素。本文阐述了不同生物源八氢番茄红素脱氢酶的基因分离与鉴定，功能多样性及表达调控机制等最新研究进展，并进行了进化分析，为八氢番茄红素脱氢酶的深入研究及利用基因工程策略生产类胡萝卜素的应用提供重要信息。

关键词：类胡萝卜素，八氢番茄红素脱氢酶，功能多样性，进化分析，调控机制

类胡萝卜素是自然界中广泛存在的一种类异戊二烯物质，具有许多重要的生物学功能，例如它们可以作为维生素A的前体物质，具有抗衰老以及潜在的抗癌抗肿瘤功能等[1]。在自然界中，所有的光合生物(包括细菌，藻类和高等植物)和一些非光合生物能合成类胡萝卜素，其中绝大部分类胡萝卜素属于C40和C30类[2]。环境中的许多微生物可以合成类胡萝卜素，例如三孢布拉霉(*Blakeslea trispora*)[3]，固氮红细菌(*Rhodobacter azotoformans*)[4]和地中海嗜盐古菌(*Haloferax mediterrane*)[5]等。在植物中，类胡萝卜素主要位于细胞膜和质体，参与光捕获和抗氧化等功能，并赋予茎、叶、花和果实等器官丰富颜色[6]。研究发现，绿色阔嘴鸭(*Calyptomena viridis*)羽毛[7]中，三文鱼(Salmon)[8]和纳滨对虾(*Litopenaeus vannamei*)[9]体中也含有类胡萝卜素。

微生物类胡萝卜素生物合成主要步骤如图1：乙酰辅酶A在3-羧基-3-甲基戊二酸单酰辅酶A酶的

基金项目：国家自然科学基金面上项目(31271818)；沈阳市科技创新农业科技攻关专项(F13-143-3-00)；中国博士后科学基金项目(2012M510836，2013T60299)

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收稿日期：2016-03-06；**修回日期：**2016-04-15；**网络出版日期：**2016-05-05

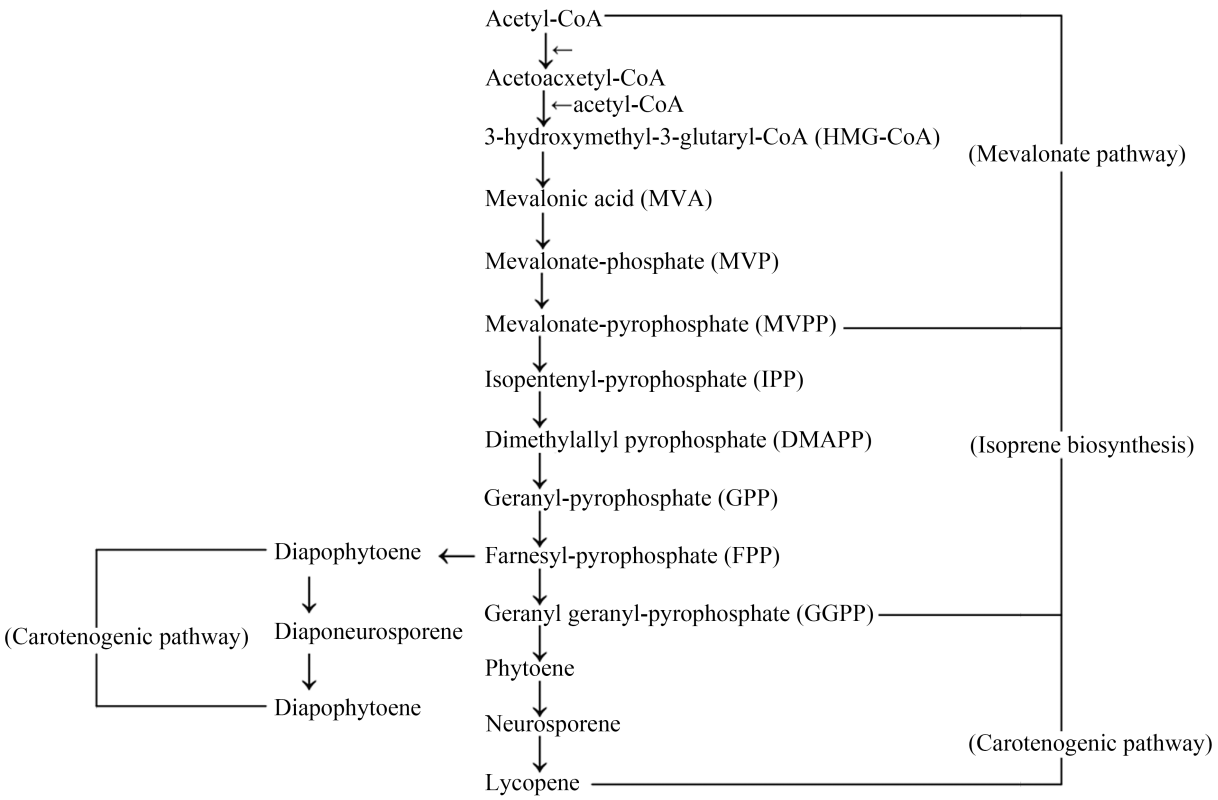

图 1. C40和C30番茄红素生物合成参考途径

Figure 1. Biosynthesis pathways of lycopene and diapolycopene in carotenoid-synthesizing organisms.

催化下变为3-羟基-3-甲基戊二酰辅酶A(HMG-CoA)，然后再进一步转变为甲羟戊酸(MVA)，其在甲羟戊酸激酶的作用下形成异戊稀焦磷酸(IPP)，IPP异构化成二甲丙烯焦磷酸酯(DMAPP)，DMAPP在牛儿基牛儿基焦磷酸合成酶作用下与3个IPP缩合，依次生成牛儿基焦磷酸(GPP)、法尼基焦磷酸(FPP)和牛儿基牛儿基焦磷酸(GGPP)，两分子的GGPP在八氢番茄红素合成酶的作用下生成C40八氢番茄红素(phytoene)[10]，两分子的FPP缩合形成C30八氢番茄红素(diapophytoene)[2]。

其中，八氢番茄红素脱氢酶是类胡萝卜素合成途径中的首要限速酶，它们可催化无色C40八氢番茄红素生成ζ-胡萝卜素(ζ-carotene)，链孢红素(neurosporene)，番茄红素(lycopene)、3,4-脱氢番茄红素(3,4-didehydrolycopene)，3,4,3’,4’-脱氢番茄红素(3,4,3’,4’-tetradehydrolycopene)或3,4-脱氢链孢红素(3,4-didehydroneurosporene)，或者催化C30八氢番茄红素(diapophytoene)生成diapo-ζ-carotene，diaponeuroporene，diapolycopene[11]。八氢番茄红素脱氢酶催化产物是类胡萝卜素生物合成途径中的重要的前体物质和分支点，其脱氢产物通过环化、甲基化以及加入不同的含氧基团等反应形成其它类型的类胡萝卜素。八氢番茄红素的脱氢产物类型决定了后续合成反应的产物类型，因此八氢番茄红素脱氢酶在生物类胡萝卜素生物合成途径中扮演了重要的角色。

1 八氢番茄红素脱氢酶基因的分离与鉴定

目前，类胡萝卜素代谢途径中的一些关键酶

的基因已经被成功的分离与鉴定，例如：GGPP合成酶、八氢番茄红素合成酶、八氢番茄红素脱氢酶、番茄红素环化酶和双功能八氢番茄红素合成酶/番茄红素环化酶(CrtYB)等。八氢番茄红素脱氢酶基因的研究较为广泛(表1)，例如，枸杞(*Lycium chinense*)的*pds*和*zds*[12]，雨生红球藻(*Haematococcuspluvialis*)的*pds*[13]，海洋红冬孢酵母(*Rhodosporidium diobovatum*)的*crtI*[14]，固氮红细菌(*Rhodobacter azotoformans*)的*crtI*[4]和蓝细菌(Cyanobacteria)的*crtP*和*crtQb*[15]等。在微生物中，一般都存在着单拷贝的八氢番茄红素脱氢酶基因，而黄色黏球菌(*Myxococcus xanthus*)中则存在2个同源的*crtI*基因：*crtIa*和*crtIb*[16]，绿硫细菌(*Chlorobium tepidum*)中也存在2个同源的*crtP*和*crtQ*[17]，这与高等植物，藻类和蓝细菌(除*Gloeobacter violaceous*外)类似，有关古菌八氢番茄红素脱氢酶基因的研究较少，目前只在嗜盐古菌(*Haloarcula japonica*)中发现了“3,4-位”脱氢酶基因*c0507*，*c0506*，和*c0505* (*crtD*)，它们与细菌*crtI*同源[18]。

八氢番茄红素脱氢酶基因是最早被分离与鉴定的类胡萝卜素生物合成关键酶基因之一，且该基因的鉴定主要是在大肠杆菌原核表达体系中利用异源互补检测法完成的。大肠杆菌可以合成GGPP的前体FPP，当外源GGPP/FPP合成酶基因(*crtE*)和八氢番茄红素合成酶基因(*crtB*)在大肠杆菌细胞内表达时便可合成八氢番茄红素(phytoene)，待鉴定八氢番茄红素脱氢酶基因转化该菌株时，便可通过产物判断该基因的功能特性。

2 八氢番茄红素脱氢酶功能多样性与进化

2.1 CrtI-type八氢番茄红素脱氢酶

多项研究表明，不同生物源CrtI-type八氢番茄红素脱氢酶呈现功能多样性(表2)。绝大部分真菌具有催化四步脱氢功能的八氢番茄红素脱氢酶，可直接将无色顺式八氢番茄红素(15-*cis*-phytoene)脱氢转化为粉红色全反式番茄红素(all-*trans*-lycopene)，例如三孢布拉霉(*Blakeslea trispora*)，法夫酵母(*Xanthophyllomyces dendrorhous*)

表1. 部分八氢番茄红素脱氢酶基因的分离与鉴定

Table 1. Isolation and identification of partial phytoene dehydrogenase genes

Gene name	Organism	Metabolic product	Identification means	Reference
pds	*Lycium chinense*	ζ-carotene	Heterologous complementation	[12]
pds	*Haematococcuspluvialis*	ζ-carotene	*In vitro* validation	[13]
zds	*Lycium chinense*	Lycopene	Heterologous complementation	[12]
crtI	*Rhodosporidium diobovatum*	Lycopene	Heterologous complementation	[14]
crtI	*Rhodobacter azotoformans*	Neurosporene	Heterologous complementation	[4]
crtP	Cyanobacteria	ζ-carotene	*In vivo* validation	[15]
crtQb	Cyanobacteria	Lycopene	*In vivo* validation	[15]
crtP	*Chlorobium tepidum*	ζ-carotene	*In vivo* validation	[17]
crtQb	*Chlorobium tepidum*	Lycopene	*In vivo* validation	[17]
crtIa	*Myxococcus xanthus*	ζ-carotene	*In vivo* validation	[16]
crtIb	*Myxococcus xanthus*	Lycopene	*In vivo* validation	[16]
crtD	*Haloarcula japonica*	Isopentenyldehydrorhodopin or Bisanhydrobacterioruberin	*In vivo* validation	[18]

表2. CrtI-type八氢番茄红素脱氢酶功能多样性

Table 2. Functional diversity of CrtI-type phytoene dehydrogenase

Enzymes	Dehydrogenation ability	Substrates	Products	Reference
Synechocystis CrtD	1-step	Neurosporene or Lycopene	3,4-didehydrolycopene or 3,4-didehydroneurosporene	[24]
M. xanthus CrtIa	2-step	Phytoene	ζ-carotene	[16]
M. xanthus CrtIb	2-step	ζ-carotene	Lycopene	[16]
R. capsulatus CrtI	3-step	Phytoene	Neurosporene	[20]
R. azotoformans CrtI	3,4-step	Phytoene	Neurosporene and Lycopene	[21]
R. diobovatum CrtI	4-step	Phytoene	Lycopene	[14]
S. aureus CrtN	4-step	Diapophytoene	Diapolycopene	[11]
N. crassa Al-1	5-step	Phytoene	3,4-didehydrolycopene	[19]
P. ananatis $CrtI_{14}$	4 - or 6-step	Phytoene	Lycopene or 3,4,3',4'-tetradehydrolycopene	[23]
R. gelatinosus CrtI	3,4-or 6-step	Phytoene	Neurosporene and Lycopene; or 3,4,3',4'-tetradehydrolycopen	[22]

和海洋红冬孢酵母(*R. diobovatum*)等，而粗糙脉孢菌(*Neurospora crassa*)八氢番茄红素脱氢酶AL-1则可催化顺式八氢番茄红素的五步脱氢生成全反式"3,4-脱氢番茄红素"(all-*trans*-3,4-didehydrolycopene)[19]。脱氢反应中，细菌八氢番茄红素脱氢酶常以FAD作为受氢体[20]，而粗糙脉孢菌(*N. crassa*)则以NAD作为受氢体，这是否是导致AL-1具有独特5步脱氢功能的原因有待进一步的研究。

细菌源八氢番茄红素脱氢酶与真菌类似，大多属于CrtI-type，但功能具有多样性。例如，荚膜红细菌(*Rhodobacter capsulatus*)八氢番茄红素脱氢酶可以催化顺式八氢番茄红素三步脱氢反应生成全反式链孢红素(all-*trans*-neurosporene)，这是第1个被鉴定具有三步脱氢功能的八氢番茄红素脱氢酶[20]，固氮红细菌(*R. azotoformans*)[4]和胶状红环菌(*Rubrivivax gelatinosus*)八氢番茄红素脱氢酶均可以催化顺式八氢番茄红素的三步和四步脱氢反应生成全反式链孢红素和番茄红素[21]，欧文氏菌(*Pantoea ananatis*)八氢番茄红素脱氢酶可以催化顺式八氢番茄红素的四步脱氢反应生成全反式番茄红素。Stickforth等对胶状红环菌(*R. gelatinosus*)八氢番茄红素脱氢酶CrtI的酶促反应动力学研究发现，高CrtI酶浓度或低底物浓度条件更有利于最大限度脱氢反应的进行，条件适宜甚至会催化顺式八氢番茄红素6步脱氢生成全反式3,4-3',4'-脱氢番茄红素(all-*trans*-3,4,3',4'-tradehydrolycopene)[22]，另外，通过点突变得到的欧文氏菌(*P. ananatis*) $CrtI_{14}$也能够催化顺式八氢番茄红素的六步脱氢反应[23]。在黄色黏球菌(*M. xanthus*)中，CrtIa可催化顺式八氢番茄红素生成全反式ζ-胡萝卜素(all-*trans*-ζ-carotene)，CrtIb则催化全反式ζ-胡萝卜素生成全反式番茄红素，CrtIa和CrtIb序列相似度较高，属于CrtI-type [16]。

集胞藻(*Synechocystis* sp. strain PCC 6803)细胞内存在着1种"3,4位"脱氢酶CrtD，它可以分别催化番茄红素和链孢红素生成3,4-脱氢番茄红素(3,4-didehydrolycopene)和3,4-脱氢链孢红素(3,4-didehydroneurosporene)[24]。特别的，蓝细菌*Gloeobacter violaceous*八氢番茄红素脱氢酶也属于CrtI-type[25]。金黄色葡萄球菌(*Staphylococcus aureus*) CrtN，与CrtI-type同源，可催化Diapophytoene (C30)四步脱氢生成Diapolycopen (C30)[11]。

2.2 CrtP/CrtQ-type和PDS/ZDS-type八氢番茄红素脱氢酶

CrtI-type八氢番茄红素脱氢酶可直接将顺式八氢番茄红素(15-*cis*-phytoene)转化为全反式番茄红素(all-*trans*-lycopene)，而在蓝细菌(除*Gloeobacter violaceous*外)，藻类和高等植物中，顺式八氢番茄红素(15-*cis*-phytoene)转化为全反式番茄红素(all-*trans*-lycopene)的反应过程一般涉及2个脱氢酶CrtP/PDS，CrtQ/ZDS(表3)和顺反异构酶CrtH/Z-ISO，CrtISO[1]。例如，在蓝细菌中，首先由CrtP和CrtQb分别催化顺式八氢番茄红素的前、后两步脱氢反应生成顺式番茄红素(7,9,7',9'-tetra-*cis*-lycopene)，随后在异构酶CrtH的催化下生成全反式番茄红素。在藻类和高等植物中，首先由PDS，Z-ISO和ZDS催化顺式八氢番茄红素生成顺式番茄红素，再经CrtISO催化最终生成全反式番茄红素。念珠藻(*Nostoc* sp. PCC 7120)中CrtP催化顺式八氢番茄红素的前两步脱氢反应生成顺式ζ-胡萝卜素(9,9'-di-*cis*-ζ-carotene)，后者又经CrtQa催化最终生成全反式番茄红素，而不需要CrtH的参与[26]。细菌通常具有CrtI-type八氢番茄红素脱氢酶，不同于大多数的细菌，绿硫细菌没有典型的CrtI-type八氢番茄红素脱氢酶，而具有2个同源的CrtP和CrtQb。

有关CrtI-type，PDS/ZDS-type和CrtP/CrtQ-type八氢番茄红素脱氢酶参与的类胡萝卜素代谢途径如图2所示。

2.3 八氢番茄红素脱氢酶的进化分析

根据蛋白序列同源检索将不同生物源的八氢番茄红素脱氢酶构建系统发育树(图3)，并对该酶进化途径进行分析(图4)。细菌源CrtI-type单酶(Single-enzyme)可能是八氢番茄红素脱氢酶的"共同祖先"，分别进化为嗜盐古菌CrtI-type八氢番茄红素脱氢酶(图4-a)，真菌源CrtI-type八氢番茄红素脱氢酶(图4-b)，以八氢番茄红素为常见底物，构成非光合微生物八氢番茄红素脱氢酶的主要类型。另外，在细菌八氢番茄红素脱氢酶进化过程中，表现出底物特异性改变，如金黄色葡萄球菌(*S. aureus*)八氢番茄红素脱氢酶CrtN催化C30八氢番茄红素(diapophytoene)生成C30番茄红素(diapolycopene)(图4-c)，黄色黏球菌CrtIa催化八氢番茄红素生成ζ-胡萝卜素(图4-d)，CrtIb催化ζ-胡萝卜素生成番茄红素，CrtIb很可能是由CrtIa通过复制(图4-l)形成的CrtIa/CrtIb双酶(Double-enzyme)系统，革兰氏阳性菌(*Brevibacterium linens*, *Brevibacterium flavum*) CrtU催化β-胡萝卜素类胡萝卜素的脱氢反应(图4-g)，集胞藻(*Synechocystis* sp. strain PCC 6803) 3,4位脱氢酶CrtD催化番茄红

表3. PDS/ZDS-type, CrtP/CrtQ-type八氢番茄红素脱氢酶功能多样性

Table 3. Functional diversity of PDS/ZDS-type and CrtP/CrtQ-type phytoene dehydrogenases

Enzymes	Dehydrogenation ability	Substrates	Products	Reference
C. tepidum CrtP	2-step	Phytoene	ζ-carotene	[17]
C. tepidum CrtQb	2-step	ζ-carotene	Lycopene	[17]
L. chinense PDS	2-step	Phytoene	ζ-carotene	[12]
L. chinense ZDS	2-step	ζ-carotene	Lycopene	[12]
Cyanobacteria CrtP	2-step	Phytoene	ζ-carotene	[15]
Cyanobacteria CrtQb	2-step	ζ-carotene	Lycopene	[15]
Nostoc sp. CrtP	2-step	Phytoene	ζ-carotene	[26]
Nostoc sp. CrtQa	2-step	ζ-carotene	Lycopene	[26]

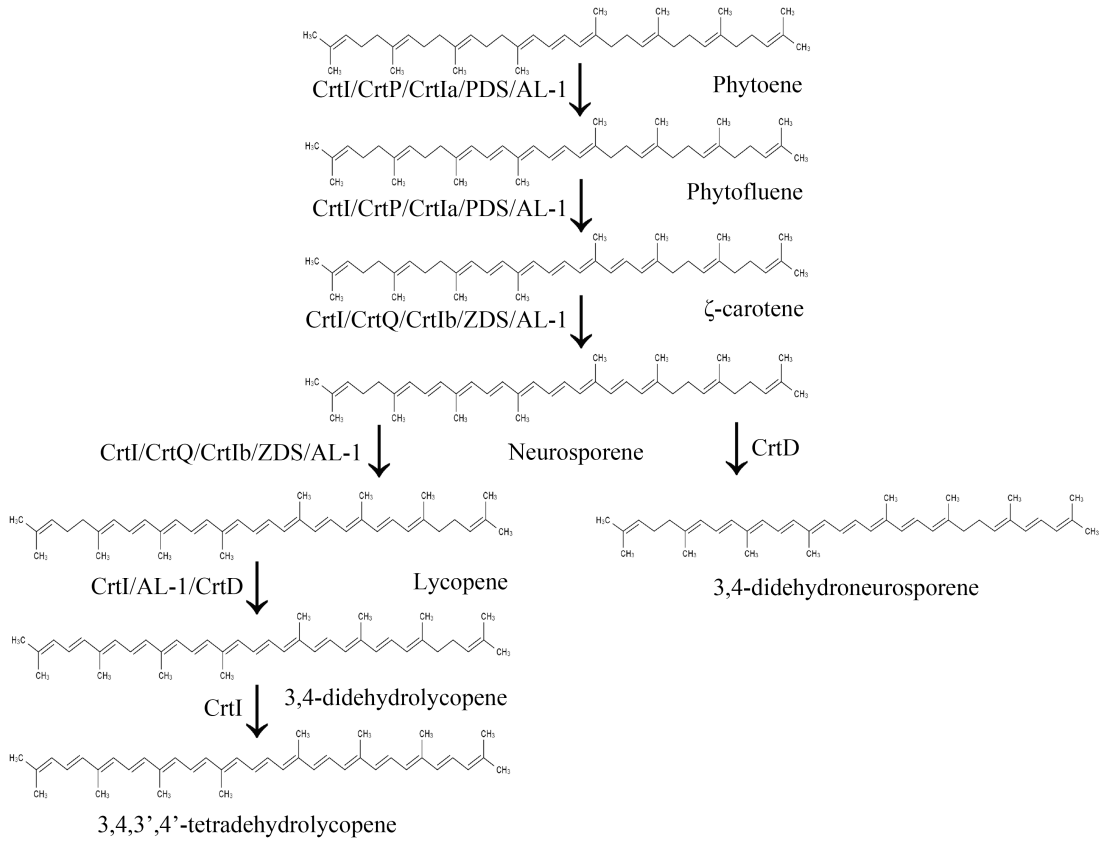

图 2. 八氢番茄红素脱氢酶参与的类胡萝卜素生物合成途径

Figure 2. Natural biosynthesis pathways of C40 carotenoids involved in phytoene dehydrogenases.

素和链孢红素生成3,4-脱氢番茄红素和3,4-脱氢链孢红素(图4-e)。

念珠藻CrtP和CrtQa分别与自革兰氏阳性菌的β-胡萝卜素类脱氢酶CrtU的C末端(C-terminal)[27]，以及细菌源CrtI-type八氢番茄红素脱氢酶同源性较高，说明念珠藻CrtP和CrtQa分别由革兰氏阳性菌CrtU (图4-h)和细菌源CrtI-type进化而来(图4-f)，形成了念珠藻CrtP/CrtQa双酶系统。随后念珠藻CrtP进化为蓝细菌源CrtP (图4-j)，蓝细菌源CrtP又经过复制得到了CrtQb (图4-k)，念珠藻CrtQa进化为蓝细菌顺反异构酶CrtH (*cis*-to-*trans*)(图4-i)，从而形成了蓝细菌源CrtP/CrtQb/CrtH-type三酶(Triple-enzyme)系统。绿硫细菌(*C. tepidum*)通过基因转移等方式获得了蓝细菌源CrtP/CrtQb/CrtH-type (图4-m) 三酶系统。蓝细菌源CrtP/CrtQb/CrtH-type三酶系统又经进化而形成更加复杂的植物源PDS/ZDS/Z-ISO/CrtISO-type (图4-n)四酶(Quadruple-enzyme)系统。以上分析过程是从分子水平了解八氢番茄红素脱氢酶系统发育关系并分析了其进化历程。

3 八氢番茄红素脱氢酶基因表达调控

3.1 基因转录调控

八氢番茄红素脱氢酶基因的转录受多种因素调控，其中类胡萝卜素合成相关结构基因调控、转录因子调控、响应胁迫压力调控和受其他代谢途径调控是主要的调控方式。类胡萝卜素合成其他相关基因的过表达，能够诱导八氢番茄红素脱氢酶基因的表达并促进类胡萝卜素的积累，例如

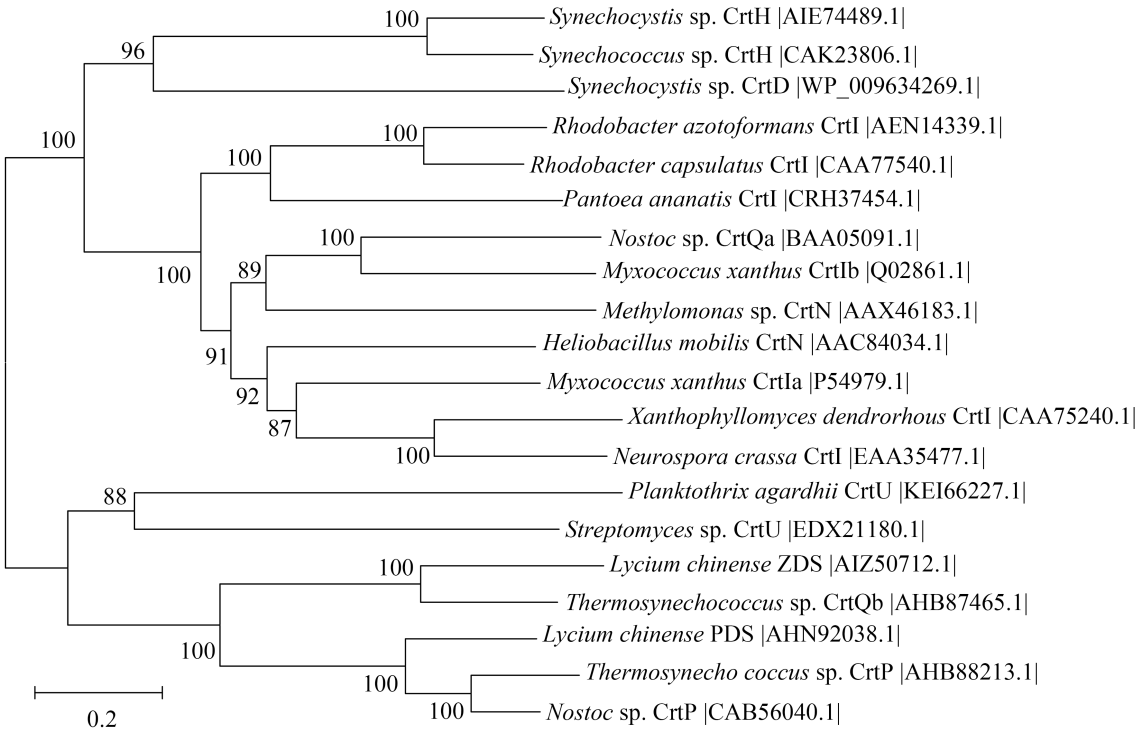

图 3. 基于八氢番茄红素脱氢酶蛋白序列及Neighbor-Joining法构建的系统发育树

Figure 3. Phylogenetic tree analysis of phytoene dehydrogenases based on the amino acid sequences by the Neighbor-Joining method.

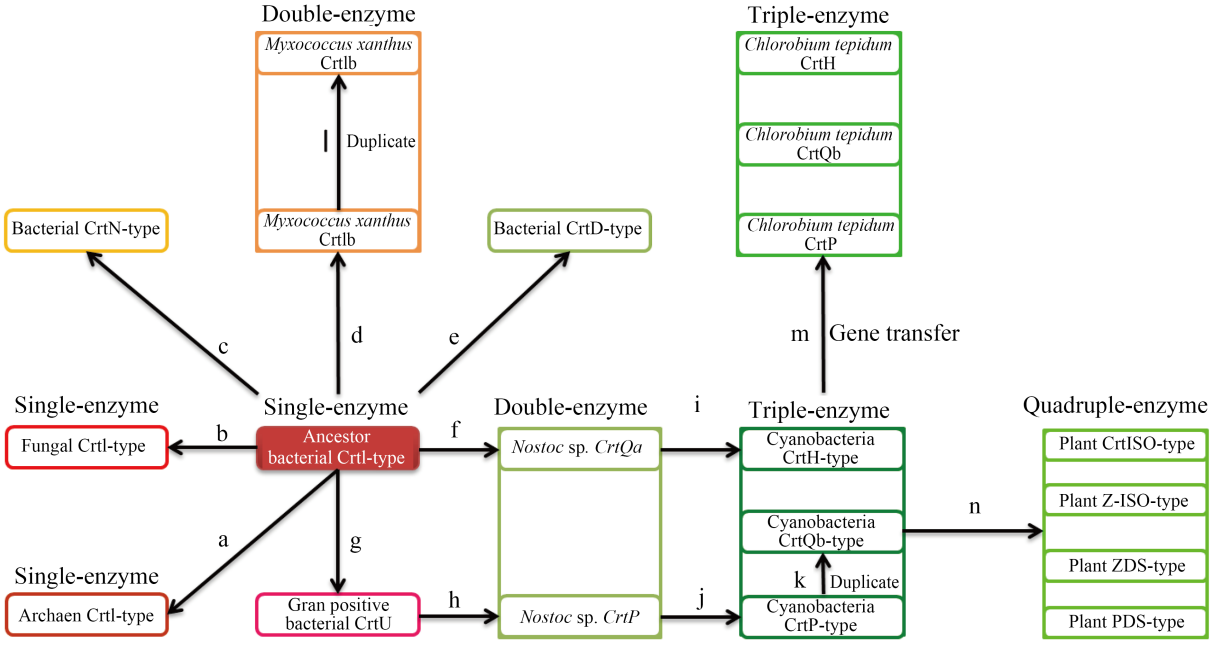

图 4. 八氢番茄红素脱氢酶进化途径分析

Figure 4. Evolutionary pathway analysis of phytoene dehydrogenases.

Chi等研究发现，在法夫酵母突变株MK19细胞中高表达虾青素合成酶基因*crtS*时可诱导八氢番茄红素脱氢酶等类胡萝卜素合成相关基因上调，使重组菌株CSR19的虾青素产量提高33.5%[28]。

目前，有关微生物类胡萝卜素生物合成的转录因子调控的报道较少。相关研究大多集中在高等植物领域，转录因子能直接或间接的调控八氢番茄红素脱氢酶基因的表达，导致整个类胡萝卜素合成途径发生显著变化。大多数植物*pds*和*zds*启动子上存在ATCTA顺式作用元件，该元件可直接受光照调控而影响八氢番茄红素脱氢酶基因的表达，例如葡萄柚愈伤组织中的*pds*和*zds*的转录在白光光照条件下受到抑制[29]。Sanz等[30]研究发现蓝光可以刺激须霉(*Phycomyces blakesleeanus*)胞内八氢番茄红素脱氢酶基因等相关基因转录水平提高，因为蓝光可将阻碍八氢番茄红素脱氢酶基因转录的转录因子结合蛋白复合物HMC (high mobility gel retardation complex)暂时性失活，这是细胞提高类胡萝卜素产量以抵抗光氧化胁迫而进化产生的适应机制。

类胡萝卜素的生物合成是一个既相对独立又相互联系的复杂网络系统，当遭遇氧化胁迫时，机体通常会产生一些应急响应机制，其中就包括高产类胡萝卜素，在这过程中相关基因的表达水平将发生变化，整个代谢途径也将做出相应的调整。例如Kathiresan等[31]研究发现，氯化钠和醋酸钠胁迫可诱导重组β-胡萝卜素酮化酶(BKT)基因的雨生红球藻细胞中八氢番茄红素脱氢酶基因*pds*及相关基因上调，促使虾青素产量提高，此现象的诱因包括*pds*终产物的锐减和盐胁迫条件产生了较多活性氧(ROS)而迫使细胞合成更多类胡萝卜素用于抵抗氧化胁迫。与上述研究类似，Coesel等[32]研究发现，营养不足，氯化钠和光照胁迫均可诱导盐生杜氏藻(*Dunaliella salina*)细胞中基因*pds*/*zds*的高表达及β-胡萝卜素高产。本课题组前期从草莓果实上分离得到了1株掷孢酵母(*Sporidiololus pararoseus* CGMCC 2.5280)，主要积累β-胡萝卜素(β-carotene)，圆酵母素(torulene)和红酵母红素(torularhodin)，并发现细胞在低浓度氯化钠(1.0 mol/L)和高温(35 °C)胁迫下圆酵母素和红酵母红素所占总类胡萝卜素产量的比例提高，同时八氢番茄红素脱氢酶基因显著上调，说明该基因在细胞抵抗氯化钠和高温胁迫方面起到了关键的作用，此过程与上述胁迫条件下的响应模式较相似，但其调控机制尚不明确。

3.2 基因转录后调控

在类胡萝卜素的生物合成过程中，相关基因的转录后调控也将对代谢途径产生重要影响。Schledz等[33]研究发现在黄水仙(*Narcissus pseudonarcissus*)质体中游离状态的PDS并不具有生物活性，只有当其与相应的膜结构结合后酶活才能被激活，且近期有研究表明蓝细菌(*Synechocystis* sp. PCC6803)细胞中的CrtQb主要位于质膜和类囊体膜上[15]，水稻(*Oryza sativa*) PDS[34]和菠萝泛菌(*Pantoea ananatis*) CrtI[35]都属于膜结合蛋白，说明八氢番茄红素脱氢酶应是一类生物膜结合蛋白。

Shi等[36]研究发现，低温(20 °C)使重组法夫酵母(*Phaffia rhodozyma*)类胡萝卜素合成基因的酿酒酵母(*Saccharomyces cerevisiae*)工程菌株高产β-胡萝卜素，而其八氢番茄红素脱氢酶基因并没有上调。本课题组在研究掷孢酵母抗低温(18 °C)胁迫时也发现了类似现象，说明低温不能使八氢番茄红素脱氢酶基因高表达，因为低温胁迫不会在细胞内产生过多的活性氧(ROS)以诱导相关基因上调。在植物中，八氢番茄红素脱氢酶也是多种除草剂的目的结合蛋白，如氟草敏和氟啶酮等，这些除草剂与PDS/ZDS结合后抑制其酶活，使八氢番茄红素大量积累，导致叶绿素不能稳定的存在于植物细胞，失去光合作用能力而停止生长[37]。迄今为止，有关八氢番茄红素脱氢酶基因的转录

后调控机制研究尚处于初级阶段，但随着研究的不断深入，将八氢番茄红素脱氢酶应用于基因工程手段以调控类胡萝卜素的生物合成将成为可能。

4 问题与展望

随着人们对利用微生物合成类胡萝卜素关注度的逐渐提高，八氢番茄红素脱氢酶的研究已越来越受到重视。目前，针对八氢番茄红素脱氢酶的研究主要集中于编码基因的分离与鉴定。虽然人们对八氢番茄红素脱氢酶基因参与的类胡萝卜素生物合成途径已有大致的了解，但其调控机制仍不够清晰，正逐渐成为研究热点。然而，不同生物源八氢番茄红素脱氢酶序列中决定脱氢反应功能分化的区域，特定功能位点，蛋白亚细胞定位和微进化等方面尚需进一步研究阐明。高通量测序等技术的迅猛发展使得全面系统地分析不同生物源的八氢番茄红素脱氢酶成为可能，研究者可根据大量基因和蛋白信息综合分析，利用遗传学、分子生物学及生物信息学等手段探索八氢番茄红素脱氢酶的功能多样性和调控机制，为有目的地应用八氢番茄红素脱氢酶的多样性特征，合成种类丰富的类胡萝卜素产品，提供理论指导。

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Advances in phytoene dehydrogenase - A review

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Abstract: Carotenoids, as a group of over 700 valuable unsaturated terpene compounds classified as carotene and xanthophyll family, are endowed with powerful nutritional value. Phytoene dehydrogenase is the key rate-limiting enzyme in carotenoids biosynthesis pathway, involved in catalyzing the conversion from colorless hydrocarbon phytoene to other pigmented carotenoids, and plays an essential central regulation role. The function of phytoene dehydrogenases from different organisms exist diversity. CrtP, CrtQ and isomerase CrtH are essential for the formation of lycopene in most Cyanobacteria, whereas PDS, ZDS and isomerase Z-ISO, CrtISO are in charge of producing lycopene in most algae and plants. Nevertheless, there is only one CrtI-type for the formation of neurosporene, lycopene or dehydrolycopene in most bacteria and fungi. In this review, isolation, characterization, functional diversity, transcription regulatory mechanisms and phylogenetic analysis of phytoene dehydrogenase from different organisms are illustrated. This paper will provide insights into phytoene dehydrogenase and may facilitate the optimization of carotenoids production in genetic engineering strategy.

Keywords: carotenoids, phytoene dehydrogenase, functional diversity, phylogenetic analysis, regulatory mechanisms

(本文责编：李磊)

Supported by the National Natural Science Foundation of China (31271818), by the Special Fund Project for Technology Innovation of Shenyang City (F13-143-3-00), and by the Postdoctoral Science Foundation of China (2012M510836, 2013T60299)

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Received: 6 March 2016; Revised: 15 April 2016; Published online: 5 May 2016