

## 蓝莓转录因子*VcMYB21*在果实着色及幼苗UV处理中的响应

刘中帅, 袁义杭, 张通, 张凌云\*

北京林业大学, 省部共建森林培育与保护教育部重点实验室, 北京100083

**摘要:** 本研究通过RACE-PCR从蓝莓中克隆得到一个R2R3-MYB转录因子, 命名为*VcMYB21*, 该基因全长1 373 bp, 编码区722 bp, 编码233个氨基酸。生物信息学分析发现其理论分子量为58.37 kDa, pI值为5.12, 中部有1个2Fe-2S结合域和1个EGF-like结构域, 属于膜外蛋白, 结构不稳定。酵母双杂交实验表明*VcMYB21*蛋白无自激活活性, 能自身形成同源二聚体。组织特异性表达实验显示*VcMYB21*主要在蓝莓的果皮和叶片中表达。在蓝莓果实发育过程中, *VcMYB21*基因的表达量整体呈下降趋势, 在果实发育早期表达量最高, 之后迅速下降, 全红果时期略微上升; 花青素的含量随果实发育持续上升, 在紫果期达到最大。UV-B与UV-C处理均显著诱导*VcMYB21*在蓝莓幼苗叶片组织中的表达, 其中对UV-B处理更为敏感。UV-B处理5 min以及UV-C处理10 min均能显著诱导该基因的表达, 随处理时间的延长, 基因表达量下降; 花青素的含量在基因表达量下降后迅速上升, 之后花青素分解, 积累量下降。这些研究结果表明*VcMYB21*在UV处理后叶片花青素积累过程及蓝莓果实着色过程中可能发挥着负调控作用。

**关键词:** 蓝莓; *VcMYB21*; 基因表达; 逆境响应

通过转录因子调控目的基因表达是植物调控生长发育及生理代谢的一种重要方式(陈清等2009), 大部分逆境诱导基因都受到特殊的转录因子调控(Hu等2008)。MYB是最大的植物转录因子家族成员之一(Miyake等2003), 包括R2R3-MYB、bHLH结构以及WDR蛋白, 这些蛋白通过形成MBW复合体结构激活转录, MBW复合体通过一些特定的作用元件直接作用于DNA的启动子区, 进而调控目的基因的表达。已经报道的靶基因序列包括MYB响应原件、R2R3-MYB的AC作用元件以及E-BOX或bHLH绑定区(Feller等2011; Lai等2013; Xu和Grain 2014)。植物细胞正是通过R2R3MYB、bHLH以及WDR之间复杂的相互作用来行使特定的功能(Broun 2005; Koes和Verweij 2005; Ramsay和Glover 2005)。据报道, MYB转录因子参与了细胞分化、细胞周期的调节(Payne等2000; Suo等2003)、激素和环境因子的应答(Lea等2007)、植物次生代谢以及叶片等器官形态建成(杜海等2008)等多种生物学过程。

许多研究表明, MYB转录因子参与了植物花青素的积累过程, 对果皮、果肉、叶片和花器官等各种颜色的形成具有重要作用(王华等2015; Zifkin等2012; 邢文和金晓玲2015)。随着果实的发育, 苹果中的*MdMYB10*基因过表达能使得果肉变红(Espley等2007), 杨梅中的*MrMYB1*随果实成熟着色表达量持续显著上升(Niu等2010)。花青素的生物合成不但受植物体内部遗传信息的调控, 外界环境如

紫外光处理、盐胁迫等也能诱导花青素的表达(齐艳等2014; 杨乐等2015; Yoshida等2015), 大量研究结果显示, MYB转录因子还在响应UV胁迫中发挥重要的调控作用。拟南芥的*AtMYB4*基因突变后能增加拟南芥抵抗UV胁迫的能力(Jin等2000), 而苦荞通过上调*FtMYB11*的表达抵御UV伤害(Gao等2016), 苹果果皮中的*MdMYB4*基因在UV-B处理时能显著上调, 促进果实中花青素的生物合成进而降低UV对果实的伤害(Ban等2007), 但目前其具体的调控机制有待进一步探究。

高丛蓝莓是杜鹃花科(Ericaceae)越橘属(*Vaccinium*)植物, 果实中含有丰富的花青素, 具有防止脑神经老化、强心、抗癌软化血管、增强人体免疫等功能(van der Heijden等2016)。目前调控花青素合成的MYB转录因子在葡萄、草莓等果实中研究较多, 但在蓝莓中研究报道较少; 此外, 以往研究多集中在促进花青素合成的基因上, 负调控花青素合成的研究相对较少。本研究在实验室前期蓝莓转录组测序的数据基础(Li等2016)上, 在蓝莓中克隆并鉴定了一个R2R3-MYB转录因子*VcMYB21*。通过荧光定量PCR实验测定*VcMYB21*基因在果实着色过程的差异表达, 分析其随果实着色过程的

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\* 通讯作者(E-mail: lyzhang73@sohu.com)。

表达量的变化与蓝莓果实中花青素含量的变化趋势,并进一步通过对蓝莓幼苗UV处理时*VcMYB21*基因在叶片中表达量与花青素含量的变化来分析基因的功能,以期为研究蓝莓花青素生物合成与积累机制提供分子基础。

## 材料与方法

### 1 实验材料

试验用的高丛蓝莓(*Vaccinium corymbosum* L.)果实及一年生‘日出(Sunrise)’和‘喜来(Sierra)’蓝莓苗取材于秦皇岛天硕农业科技开发有限公司。蓝莓根、茎、叶、花、果实组织分别取材于5年生的‘日出(Sunrise)’和‘喜来(Sierra)’2个蓝莓品种,选取生长健康、长势一致的植株,分别从东、西、南、北方向随机取样,经液氮处理后-80°C超低温冰箱保存。

### 2 胁迫处理

用于处理的幼苗为‘日出(Sunrise)’和‘喜来(Sierra)’组培移栽一年生苗,每3株一组做紫外光处理,共进行3次生物学重复。处理时,植株顶端距离光源约20 cm,分别在UV-B (40 W, 305 nm, 北京电光源研究所)和UV-C (40 W, 254 nm, 北京电光源研究所)照射处理0、5、10、15、20、25和30 min。处理后立即将叶片剪下用锡箔纸包好,经液氮处理后-80°C超低温冰箱保存备用。

### 3 生物信息学分析

通过Blast在NCBI在线数据库中搜索其他物种的*VcMYB21*基因的同源序列,用DNAMAN软件进行氨基酸多序列比对分析,并用ClustalX和MEGA 5.0软件构建系统发育树。用Compute pI/Mw工具预测蛋白等电点和分子质量([http://web.Expasy.org/compute\\_pi/](http://web.Expasy.org/compute_pi/)),ProParam预测该蛋白分子式及不稳

定指数(<http://web.expasy.org/protparam/>);SignalP做信号肽预测(<http://www.cbs.dtu.dk/services/SignalP/>);ProtScale分析蛋白疏水性 (<http://web.expasy.org/protscale/>);FoldIndex做无序化特征预测(<http://bip.weizmann.ac.il/fldbin/find-ex>);蛋白二级结构和三级结构则分别用SOPMA (<http://pbil.ibcp.fr/html/index.php>)和SWISS (<http://swissmodel.expasy.org>)进行预测;用ScanProsite对蛋白进行功能位点预测(<http://prosite.expasy.org/scanprosite/>)。

### 4 RNA提取及第一链cDNA合成

分别收集幼苗、花及果实等不同组织材料,通过Plant RNA Kit试剂盒(OMEGA, 北京)提取各样品的总RNA,并利用PrimeScript™ RT reagent Kit反转录试剂盒(TIANGEN, 北京)合成第1链cDNA\作为模板,分别用于基因克隆和荧光定量PCR的模板。

### 5 荧光定量PCR分析

用DNAMAN和Oligo软件设计*VcMYB21*基因的特异性表达引物,以蓝莓*UBC28*基因为内参基因,通过ABI Step One Plus荧光实时定量PCR仪检测*VcMYB21*在蓝莓根、茎、叶、花、果实和果皮等不同组织以及在UV-C与UV-B光照处理蓝莓叶片后*VcMYB21*的表达模式。其中,根、茎、叶、花和果皮是不同发育时期样品均匀混合后磨样用于测定。每个处理的样品设3个生物学重复。荧光染料使用 SYBR Green (TIANGEN, 北京),反应程序为:95°C预变性15 min;95°C变性30 s,60°C退火30 s(40个循环);引物序列见表1。

### 6 *VcMYB21*-pGADT7和*VcMYB21*-pGBKT7酵母双杂载体的构建

从蓝莓中克隆得到*VcMYB21*编码区序列,连接到PEASYT1载体(TIANGEN, 北京)上,转化大肠杆菌感受态细胞DH5 $\alpha$ ,挑选阳性菌落测序验证后,

表1 cDNA克隆及荧光定量PCR、半定量PCR和载体转化所用的引物

Table 1 Primers used in cDNA cloning, qRT-PCR, semi-quantitative PCR and vector transformation

引物名称	前引物(5'→3')	后引物(5'→3')
5' RACE	CAGTCTTAAGCTCGGGCCCCA	GTTGAGTTCGCCATAGCCCCAC
3' RACE	CTTGCTGGCATTGCAAAGTAT	CTGCCAGGAAACAGCTATGAC
ORF	ATGAGGAAGCCATGTTGTGAG	TCATGTAAAGAGAGGAAGGGTG
RT-PCR	GATTACATTCGCAGGCACGG	CCAGGAGTGCATGAAGCTTG
<i>VcMYB21</i> -pGADT7	CGGAATTCATGAGGAAGCCATGTTGTGAG	CGGGATCCTCATGTAAAGAGAGGAAGGGTG
<i>VcMYB21</i> -pGBKT7	CGGAATTCATGAGGAAGCCATGTTGTGAG	CGGGATCCTCATGTAAAGAGAGGAAGGGTG





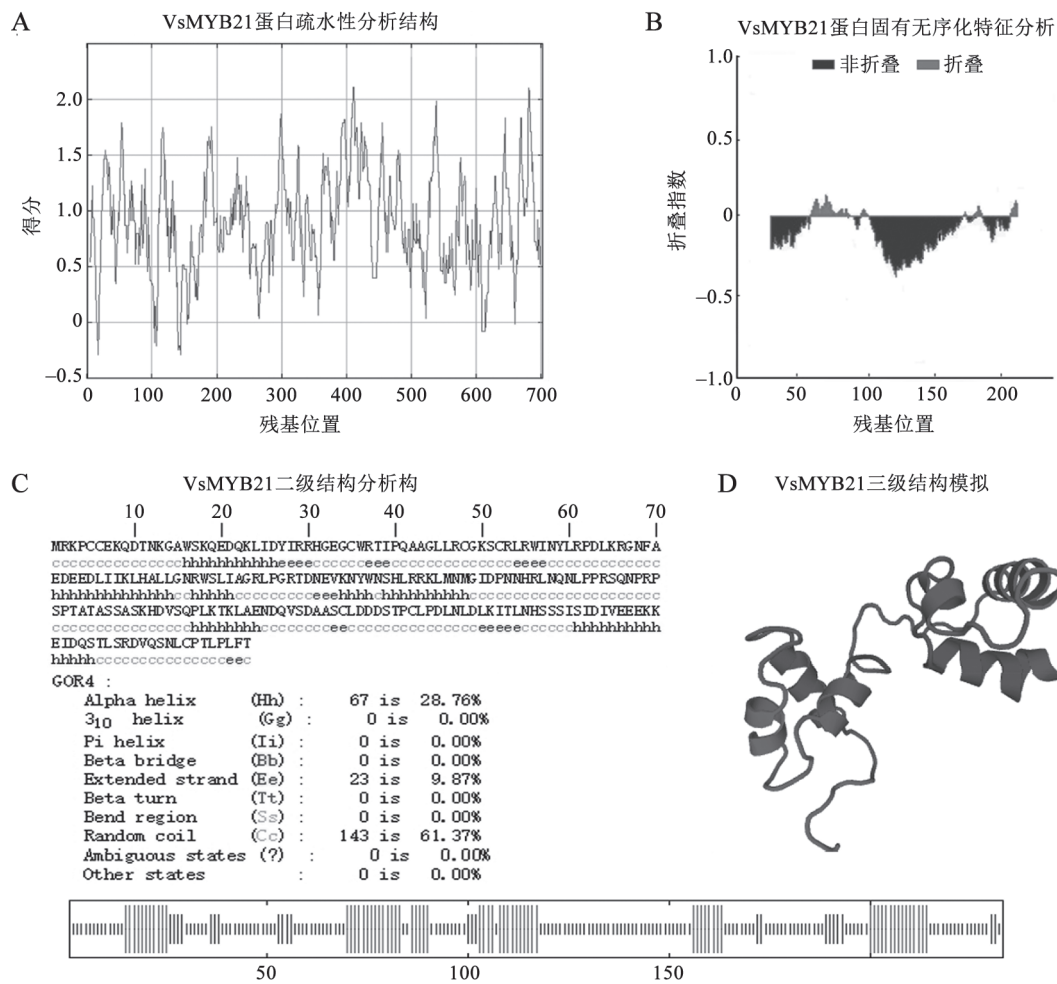


图2 VcMYB21蛋白结构及理化性质分析

Fig.2 Protein structure and chemical properties analysis of VcMYB21

VcMYB21蛋白无序化特征明显(图2-B)。VcMYB21氨基酸序列二级结构(图2-C)中 $\alpha$ 螺旋中有73个氨基酸,占总量的31.33%;无规则卷曲有137个氨基酸,占58.80%;延伸链23个,分别占9.87%,与三级结构结果相似(图2-D)。

## 2.2 VcMYB21多重序列比对与系统进化树

将VcMYB21 cDNA序列编码的氨基酸序列在NCBI的在线数据库中进行Blast分析,发现与VcMYB21一致性较高的同源蛋白有笃斯越橘(*Vaccinium uliginosum*, VuMYB2),白梨(*Pyrus × bretschneideri*, PbMYB308, LOC103948474)、苹果(*Malus × domestica*, MdMYB308, LOC103416449; *Malus hybrid cultivar*, MhMYB2)、克莱门柚(*Citrus clementina*, CcMYB)、猴面花(*Erythranthe guttatus*, EgMYB32, LOC1059-71972)、雷蒙德氏棉(*Gossypium raimondii*, GrMYB305,

LOC105782572)等。通过Clustal-X将蓝莓VcMYB21氨基酸序列与这7个物种同源蛋白多序列比对,发现VcMYB21在进化上相对保守,与笃斯越橘的MYB2基因吻合度高(图3-A),但品种间基因有个别突变。系统发育树显示蓝莓与白梨和克莱门柚的遗传距离也比较接近,用ProParam预测发现该蛋白与笃斯越橘中蛋白非常接近,为R2R3型MYB(图3-B)。

## 2.3 VcMYB21跨膜结构预测和蛋白自激活性检测

VcMYB21基因编码蛋白含有233个氨基酸残基,无典型的跨膜结构域,属膜外蛋白。

为了探究VcMYB21蛋白是否具有自激活性,分别将构建好的pGBKT7-VcMYB21与空pGADT7、pGADT7-VcMYB21与空pGBKT7、pGADT7-VcMYB21与pGBKT7-VcMYB21以及阳性对照pGBKT7-53+pGADT7-T和阴性对照pGBKT7-Lam+

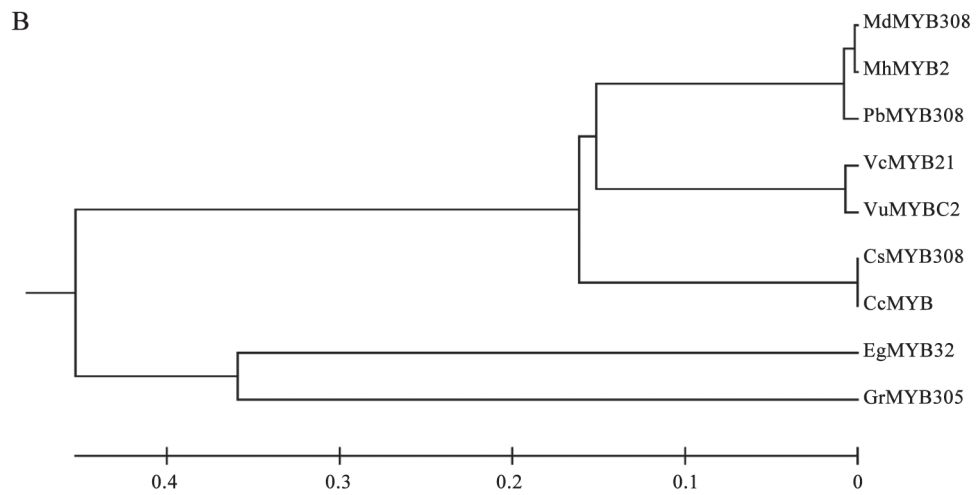
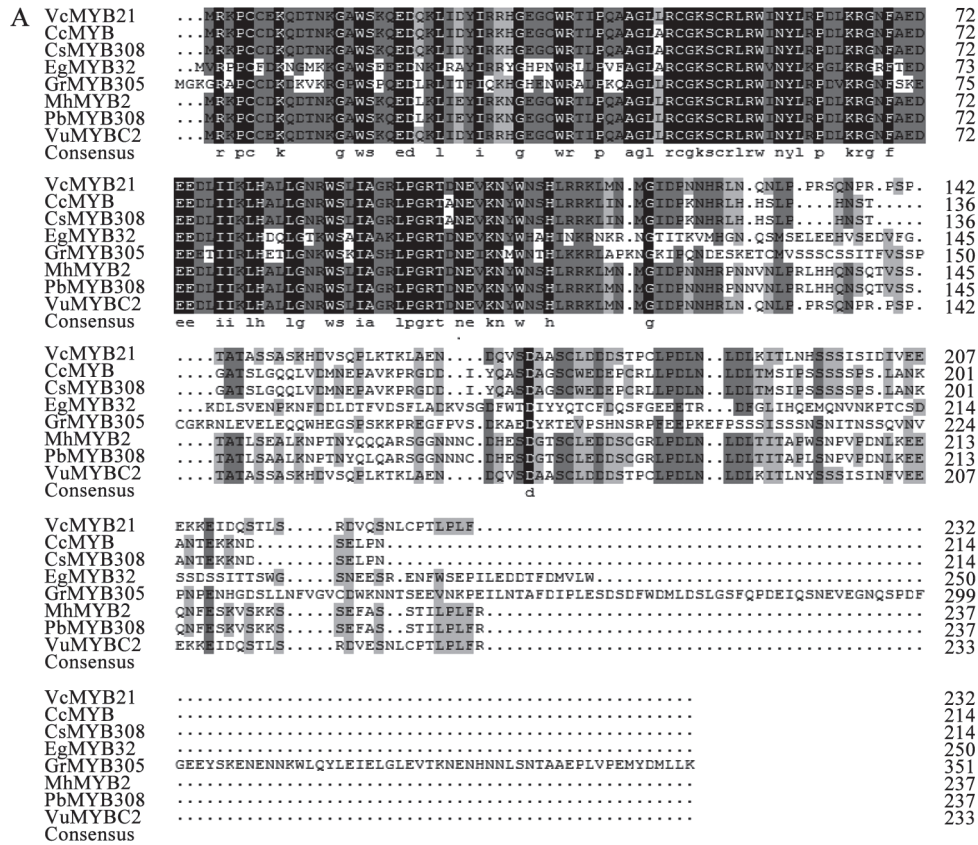


图3 VcMYB21蛋白多序列比对(A)及系统进化树分析(B)

Fig.3 Multiple protein sequence alignment result (A) and phylogenetic tree (B) of VcMYB21

pGADT7-T共转AH121酵母感受态中, 涂布于SD/-Trp/-His缺陷型培养基上, 发现均能生长证明载体成功转入酵母(图5-A)。将在SD/-Trp/-His缺陷型培养基上生长好的酵母转接到SD/-Trp/-Ade/-His/-Leu四缺培养基上时, 阳性对照能正常生长, 阴性对照不能生长, VcMYB21-pGBKT7+pGADT7也不能正

常生长, 因此显示VcMYB21蛋白没有自激活活性(图5-B)。将在SD/-Trp/-His缺陷型培养基上生长好的酵母转接到含有15 mmol·L<sup>-1</sup> 3-AT和100 μL X-a-Gal的SD/-Trp/-His/-Leu (图5-C)、SD/-Trp/-His/-Leu/-Ade (图5-D)缺陷型培养基上时, 阳性对照以及VcMYB21-pGADT7+VcMYB21-pGBKT7酵母菌株能生长并

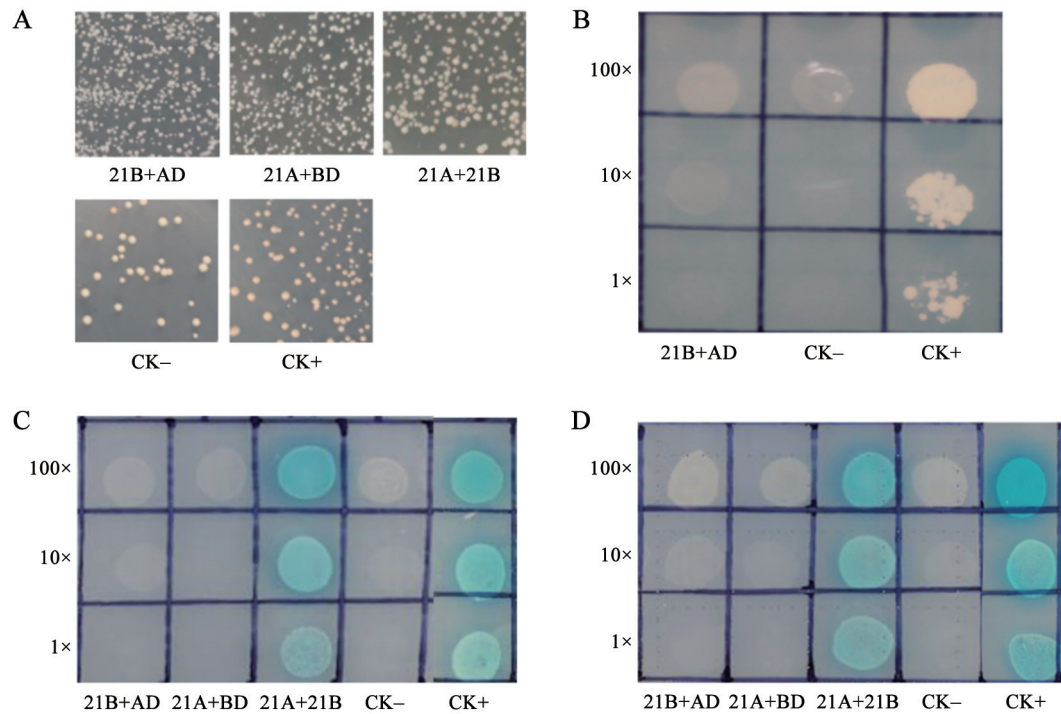


图5 pGBKT7-VcMYB21诱饵载体自激活检测和自身同源二聚体检测

Fig.5 Autoactivation of pGBKT7-VcMYB21 vector and Y2H screening

A: SD/-Trp/-His二缺培养基; B: SD/-Trp/-Ade/-His/-Leu四缺培养基; C: SD/-Trp/-His/-Leu三缺培养基; D: SD/-Trp/-Ade/-His/-Leu四缺培养基, C和D的三缺和四缺培养基中加X- $\alpha$ -gal。21B+AD为VcMYB21-pGBKT7+pGADT7, 21A+BD为VcMYB21-pGADT7+pGBKT7, 21A+21B为VcMYB21-pGADT7+VcMYB21-pGBKT7, CK+为pGADT7-T+pGBKT7-53, CK-为pGADT7-T+pGBKT7- $\lambda$ , 二缺板上的单菌落在无菌水中稀释10 (10 $\times$ )倍和100 (100 $\times$ )倍后滴在三缺和四缺培养基上

呈蓝色, 其他均不能正常生长, 说明VcMYB21蛋白能自身形成同源二聚体。

### 3 VcMYB21组织特异性表达

通过荧光定量PCR分析VcMYB21基因的组织特异性表达, 发现VcMYB21在不同品种蓝莓幼苗

各组织中的表达一致。VcMYB21在根、茎、叶、花、果实和果皮中都有表达, 其中在果皮中表达量最高, 其次是叶片, 在根部表达量最少, VcMYB21基因在果皮中的表达量是根部表达量的9倍(图6)。

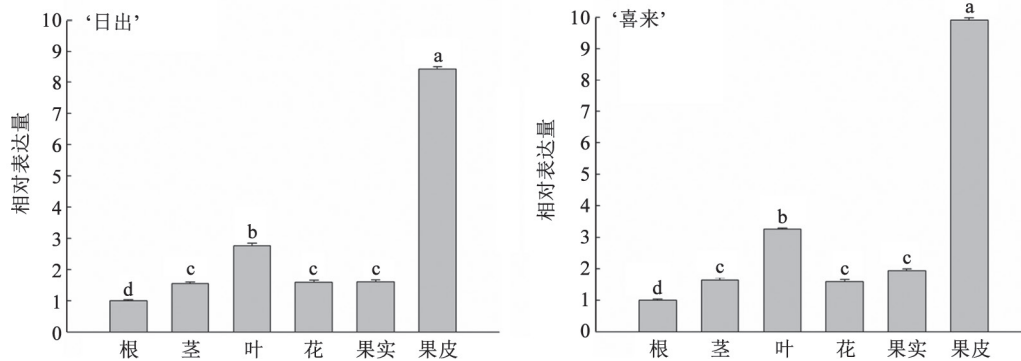


图6 ‘日出’和‘喜来’蓝莓不同组织中VcMYB21基因的表达

Fig.6 Expression analysis of VcMYB21 gene in different tissues of ‘Sunrise’ and ‘Sierra’

不同小写字母表示不同组织中VcMYB21基因表达量的显著性分析, 下图同此。

#### 4 在果实着色过程中*VcMYB21*基因表达量以及花青素含量的变化

分别选取‘日出’和‘喜来’蓝莓小绿果(花后10 d)、绿果(花后20 d)、白果(花后40 d)、半红果(花后50 d)、全红果(花后60 d)和紫果(花后75 d) 6个典型时期的果实,通过荧光定量PCR分析*VcMYB21*在此6个时期的表达量。结果(图7)显示,*VcMYB21*在‘日出’和‘喜来’品种间随果实发育的变化趋势较一致,从果实发育的整个过程来看,基因的表达量都呈现下降的趋势。在小绿果时期*VcMYB21*基因的表达量最高,之后表达量迅速下降,在全红期达略微上升但并不

显著,紫果期又下降到绿果期的水平。其中小绿果期基因表达量约为绿果期的5倍(图7)。花青素含量在‘日出’和‘喜来’中随果实着色呈上升趋势,其中,从小绿果到白果时期花青素积累迅速,在白果到全红果时期花青素合成积累速率变缓。花青素积累量都在小绿果时期最少[ $1.69 \text{ mg}\cdot\text{g}^{-1}$  (FW)],在紫果期达到最大值[ $6.93 \text{ mg}\cdot\text{g}^{-1}$  (FW)],约为小绿果期的4倍(图7)。

#### 5 *VcMYB21*基因对胁迫处理的响应

UV-B与UV-C处理均显著诱导*VcMYB21*基因在蓝莓幼苗叶片中的表达(图8)。其中*VcMYB21*基因对UV-B处理更敏感,在处理5 min时*VcMYB21*基

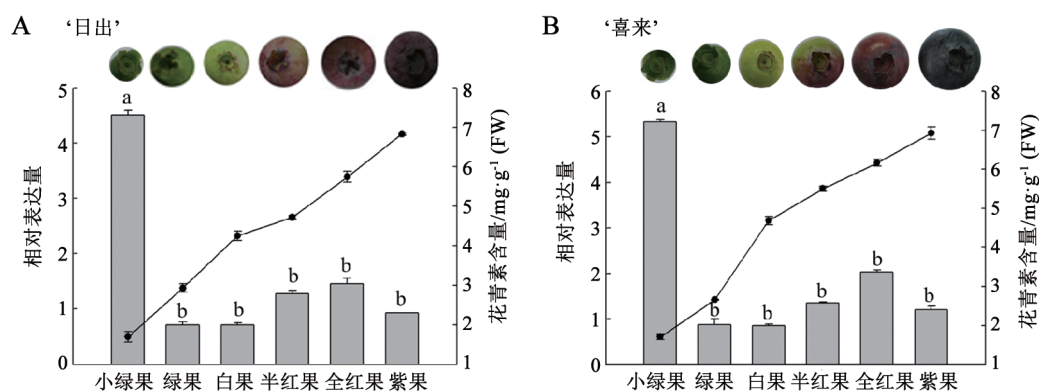


图7 ‘日出’和‘喜来’蓝莓中*VcMYB21*基因在果实不同发育时期的表达

Fig.7 Expression analysis of *VcMYB21* gene in ‘Sunrise’ and ‘Sierra’ blueberry at different developmental stages of fruit

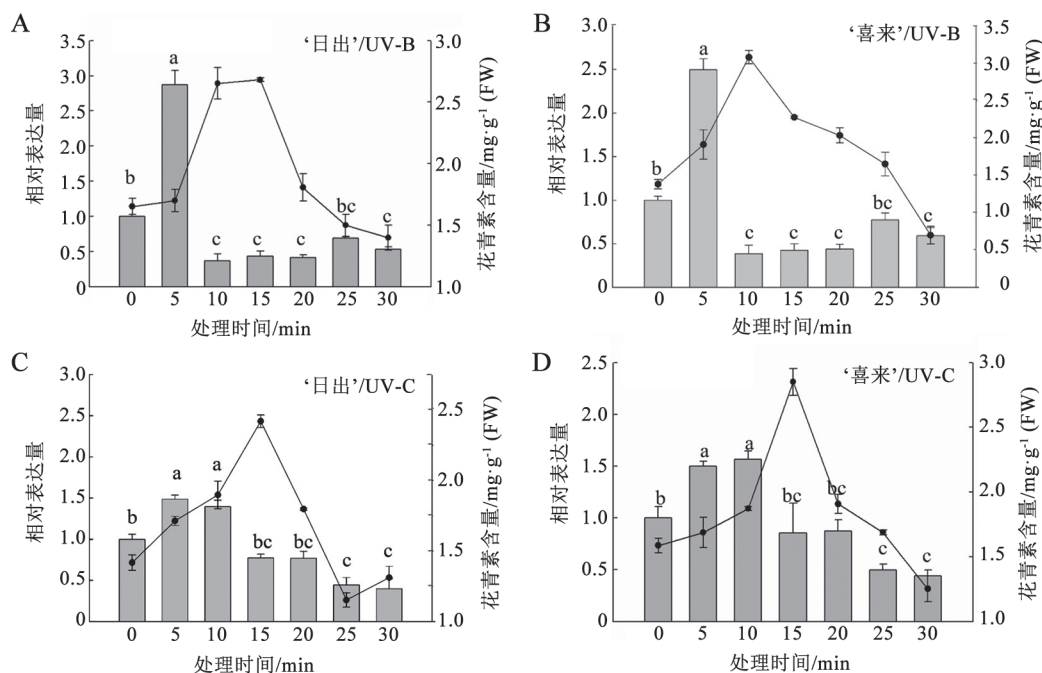


图8 UV-B和UV-C处理后*VcMYB21*基因在蓝莓幼苗叶片中的表达量变化

Fig.8 Changes in *VcMYB21* gene expression of ‘Sunrise’ and ‘Sierra’ seedlings leaves under UV-B and UV-C



因表达量达到最大;之后迅速下降到低于未处理时的表达水平;在处理25 min时略微上升,但不高于未处理时的基因表达量, *VcMYB21*基因在UV-B处理5 min时的表达量约是处理10 min时的6倍(图8-A和B)。在UV-C处理5~10 min时, *VcMYB21*基因的表达量达到最大,之后下降; *VcMYB21*基因在UV-C处理5 min时的表达量约是处理30 min时的3倍(图8-C和D)。UV-B与UV-C处理下,花青素含量在‘日出’和‘喜来’中含量变化相似。UV-B处理5 min和UV-C处理10 min后,花青素迅速增长;UV-B处理15 min和UV-C处理25 min后,花青素含量逐渐下降到低于未处理时的花青素含量(图8)。

## 讨 论

本研究在蓝莓中克隆并鉴定了一个MYB转录因子,该基因与收录在NCBI数据库中的高丛蓝莓转录因子*MYB21*的核苷酸序列相似度为99%,基因序列号为KT225483.1,所以将本研究中克隆得到的MYB转录因子命名为*VcMYB21*。生物信息学分析显示*VcMYB21*基因含有两个典型的2Fe-2S和一个EGF-like结构功能域。2Fe-2S结构复合体能结合泛醇或质体醌上的阴离子,氧化硫酸化后将离子释放到铁离子用于形成细胞色素(Harnisch等1985; Madueño等1992)。EGF-like结构域是一种表皮生长因子,与Ca离子结合、逆境响应以及细胞成熟凋亡等相关(Downing等1996; Bork等1996; Phan等2006),暗示了*VcMYB21*基因可能与细胞着色和逆境响应等生理过程相关。研究证实了这一推论,NCBI在线数据库中Blast检索结果显示笃斯越桔的*VuMYBC2*基因与本研究中的*VcMYB21*基因核苷酸序列相似度为98%,它们含有相同的2Fe-2S结构域。Primetta等(2015)研究发现*VuMYBC2*基因在笃斯越桔白化果中的表达量显著低于在正常成熟的紫色果实中的表达量。另外,Harkenrider等(2016)发现*OsWAK25*基因含有一个EGF-like结构域,在水稻中过表达该基因能显著提高水稻抗细菌和真菌病原体侵染的能力。

此外,本研究发现*VcMYB21*是一种膜外活跃的蛋白,酵母双杂交实验显示*VcMYB21*自身无自激活活性,但能形成自身同源二聚体。大量研究发现MYB基因通过形成异源二聚体发挥功能,相

对少量的研究表明MYB转录因子通过自身形成同源二聚体发挥作用(Wang等2016)。Teruaki等(1993)同样发现存在一含有锌指结构的MYB蛋白能形成同源二聚体。张志毅等(2012)研究发现同源二聚体转录因子识别螺旋相对运动存在平面摆动现象,很多转录因子被小分子或其他蛋白调控正是通过影响二聚体的形成和稳定来实现的。Farquharson (2016)研究表明, *DYT1*转录因子同源二聚体的形成受其他异源二聚体调控。因此我们推测*VcMYB21*可能在其他因子作用下改变自身构象来行使不同的功能。

本研究中蓝莓组织特异性表达实验显示*VcMYB21*基因在根、茎、叶、花、果实中都有表达,但是在果皮中表达量最高,此结果与Escarpa和González (1998)在苹果中的研究结果一致。Berardini等(2005)研究表明果皮是花青素积累的关键部位,暗示了该基因可能参与蓝莓花青素的生物合成过程。*VcMYB21*基因在小绿果时期的表达量最高,随着蓝莓果实的发育,到白果期基因的表达量迅速下降,同时伴随着花青素的大量积累;从白果期到紫果期基因的表达量略微上升的同时,花青素的积累速率随之放缓。这一研究结果与Cavallini等(2015)在葡萄中的研究结果一致,葡萄中的*VvMYBC2*基因随葡萄成熟表达量也呈现下降的趋势,过表达葡萄中的*VvMYBC2*基因会显著下调花青素的生物合成,而葡萄的*VvMYBC2*基因与本文研究的*VcMYB21*基因高度同源。这些结果表明*VcMYB21*基因的表达可能抑制了花青素的积累。

当蓝莓幼苗在UV-B和UV-C处理一段时间内,叶片中*VcMYB21*基因的表达量会迅速上调,说明该基因对UV具有一定的响应,该结果与Gao等(2016)在苦芥中的研究结果一致,苦芥*FtMYB11*基因在UV处理一段时间也显著上调;与Jin等(2000)在拟南芥中的研究结果相反,拟南芥的*AtMYB4*基因在UV处理短时间内就表现为显著下调的趋势。但是,随UV处理时间的延长, *VcMYB21*基因的表达量迅速下降,同时伴随着花青素的大量积累,这一结果不仅与本实验中随果实花青素积累基因表达量的变化趋势一致,也与杨俊枫等(2016)在蓝莓果实UV处理的结果一致,其研究结果显示蓝莓果实在UV处理10 min时花青素含量是对照的3.36倍。



以往研究表明,当植物受到外界环境胁迫,如光照、低温、盐胁迫、氧化胁迫、蔗糖及大量营养元素缺失等,都能诱导花青素的生物合成(洪雪等2014)。UV光胁迫下一定时间内在苹果和梨中花青素也出现类似的含量变化(Feng等2013; Escarpa和González 1998),但在草莓中的研究结果相反(Miao等2016; Aharoni等2001)。此外,本研究结果显示,虽然*VcMYB21*在蓝莓果皮中表达量最高,但是除果皮以外,该基因在叶片中的表达量显著高于在根、茎等其他组织中的表达量,说明该基因也可能对植物叶片响应逆境中花青素的生物合成起到一定的调节作用。

值得注意的是,蓝莓*VuMYBPA1*基因的表达量在蓝莓白化突变体的果实中下调,*VuCHS*、*VuDFR*和*VuANS*等花青素合成途径酶基因的表达量也明显下调(Primetta等2015)。推测*VcMYB21*基因可能通过调节花青素合成途径中的各种酶基因的表达来调控花青素的生物合成,模式植物拟南芥中的*MYB11*、*MYB12*等基因也证实了这一现象(Sivankalyani等2016)。Jiang等(2016)研究表明茄子果皮中花青素的合成受到*SmMYB*基因调控的同时,还受到*SmCRY1*、*SmCRY2*、*SmCOPI*、*SmHY5*等基因的共同调控,推测花青素的生物合成也受到其他调节因子的共同作用,但*VcMYB21*基因具体的调控机制有待进一步探究。

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## Expression characteristics of the transcription factor *VcMYB21* in blueberry fruit coloration and response to UV in seedling

LIU Zhong-Shuai, YUAN Yi-Hang, ZHANG Tong, ZHANG Ling-Yun\*

Key Laboratory of Forest Silviculture and Conservation of the Ministry of Education, Beijing Forestry University, Beijing 100083, China

**Abstract:** *VcMYB21* is a transcription factor of R2R3-MYB. In this study, *VcMYB21* was cloned by RACE-PCR method in blueberry. Bioinformatics analysis showed that the full length of *VcMYB21* cDNA was 1 373 bp, including the ORF 722 bp, encoding 233 amino acids. The theoretical molecular weight of *VcMYB21* was 58.37 kDa, and the value of isoelectric point (pI) was 5.12. The ScanProsite online software showed that the protein contains a 2Fe-2S and a EGF-like binding sites, and it belongs to the outer membrane with unstable structure. Yeast two-hybrid experiment showed that *VcMYB21* did not have autoactivation and had the ability to form homo-dimers itself. Tissue-specific expression showed that *VcMYB21* was mostly expressed in peel and leaves. The expression of *VcMYB21* was highest at the early development stage of fruit, and then decreased sharply with a slightly elevation in the period of whole red fruit. The anthocyanin content of fruit increased as the coloration of fruit, and reach the highest at the period of purple fruit of blueberry. Furthermore, the expression of *VcMYB21* was significantly induced under UV-B and UV-C treatment in the leaves of blueberry seedlings. The data showed that *VcMYB21* was more sensitive to UV-B treatment. The expression of *VcMYB21* was significantly induced after 5 min of UV-B treatment and 10 min of UV-C treatment. The anthocyanin content rose sharply after *VcMYB21* expression declined. Both of the expression of *VcMYB21* and the anthocyanin content decreased after 10 min of UV-B treatment and 15 min of UV-C treatment. These results indicated that *VcMYB21* played a negative role in fruit coloration and played roles during abiotic stress of UV.

**Key words:** blueberry (*Vaccinium corymbosum*); *VcMYB21*; gene expression; stress response

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\*Corresponding author (E-mail: lyzhang73@sohu.com).