

Full Length Research Paper

## Molecular cloning and tissue expression analyses of a *UF3GT* gene from *Capsicum annuum* L.

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In the present study, a novel gene designated as *UF3GT* was isolated from *Capsicum annuum* L. Sequence and structural analysis determined that the *UF3GT* protein, which contained 1401 base pairs encodes 447 amino acids and belongs to the Glycosyltransferase-GTB-type superfamily. The isoelectric point and the molecular weight of this gene are 5.97 and 49589, respectively. The deduced amino acid sequence shows highly identity with known anthocyanin synthases in other species. The phylogenetic tree analysis revealed that the *C. annuum* L. *UF3GT* has a closer genetic relationship with the *UF3GT* of petunia (*Petunia x hybrida*). The RT-PCR gene expression analysis indicated that the *UF3GT* gene was mostly expressed in pericarp, moderately expressed in stem, leaf, flower, placenta and seed, whereas no expression signal was detected in root. The study established the primary foundation for further research on this *C. annuum* L. gene.

**Key words:** *Capsicum annuum* L., semi-quantitative RT-PCR, glycosyltransferase gene, tissue expression profile analysis.

### INTRODUCTION

*Capsicum annuum* L. (commonly known as hot pepper, chili, chili pepper, and bell pepper) is a dicotyledonous flowering plant. It belongs to family Solanaceae, which includes potato, tomato, eggplant, African eggplants etc. (Knapp, 2002; Hunziker, 2001). In China, people living in Yunnan province have planted this crop for thousands of years. The whole plant is violet black, especially the fruit. Shades ranging from violet to black pigmentation in *C. annuum* L. are attributed to anthocyanin accumulation.

Anthocyanins are plant pigments widely distributed in colored fruits and flowers. They also exhibit antioxidant activities and therefore may contribute to the prevention of heart disease, cancer, and inflammatory disease (Hou,

2003; Bagchi et al., 2004; Katsube et al., 2003). They are usually localized in the vacuoles of petal epidermal cells (Goto et al., 1982; Tanaka et al., 2004) and are responsible for diverse pigmentation from orange to red, purple and blue in flowers, fruits and vegetables. Often, these compounds also occur in leaves, stems, seeds, and other tissues. Contributing to the colorful appearance of flowers, fruits and vegetables, anthocyanins help them to attract animals, leading to seed dispersal and pollination (Harborne and Williams, 2000). Mazza and Miniati (1993) reported that anthocyanins might be important in protecting plants against ultraviolet-induced damage, as well. In addition, they play roles as anti-

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oxidants and in protecting DNA and the photosynthetic apparatus from high radiation fluxes. Recently, using the known genetic sequence to synthesize primers, several genes, such as *CHS*, *CHI*, *F3H*, *DFR*, *ANS*, etc have been cloned in grapes, apples, strawberries, and other plants (Jaakola et al., 2002; Li et al., 2001).

UF3GT (UDP glucose flavonoid 3-glucosyltransferase) has been shown to be one of the key enzymes in anthocyanins biosynthesis derived from the phenylpropanoid pathway. The UF3GTs play important roles not only in modifying flower color but also in increasing the solubility and stability of hydrophobic flavonoids (Hondo et al., 1992; Yoshida et al., 2000).

UF3GT have been isolated from flowers of many ornamental plants, including *Gentiana triflora* (Tanaka et al., 1996) and *Petunia x hybrida* (Yamazaki et al., 2002). They have also been isolated from *Zea mays* (Goto et al., 1982), *Antirrhinum majus* (Martin et al., 1991), *Vitis vinifera* (Ford et al., 1998), *Hordeum vulgare* (Wise et al., 1990), *Perilla frutescens* (Gong et al., 1997) and *Fragaria ananassa* (Almeida et al., 2007). Many UF3GT genes have been cloned and heterologously expressed, which makes in-depth study of the molecular mechanism controlling anthocyanin biosynthesis possible. Semi-quantitative RT-PCR has been conducted to analyze the relative expression levels in various tissues. This study provides primary information for further understanding the biochemical functions of UF3GT in *C. annuum* L.

## MATERIALS AND METHODS

### Sample collection

All plants used in the study were derived from College of Horticulture, Yunnan Agricultural University. Yunnan Purple Pepper No.1 (*C. annuum* L.) tissues (root, stem, leaf, blossom, pericarp, placenta, and seed) were instantly frozen in liquid nitrogen and stored at  $-80^{\circ}\text{C}$  before use.

### Total RNA extraction and first-strand cDNA synthesis

Total RNA from Yunnan Purple Pepper No.1, was extracted by the Trizol procedure (TaKaRa) and cDNA was synthesized using High Fidelity PrimeScript RT-PCR Kit (TaKaRa) according to the manufacturer's protocol.

### PCR amplification

The PCR was performed to isolate the Yunnan Purple Pepper No.1 gene using the pooled cDNAs from different tissues. The 20  $\mu\text{l}$  reaction mixture contained 1.5  $\mu\text{l}$  (25 ng/ $\mu\text{l}$ ) DNA, 1  $\mu\text{l}$  2.5 mM mixed dNTPs, 2  $\mu\text{l}$  10 x Taq DNA polymerase buffer (MgCl<sub>2</sub> plus), 0.4  $\mu\text{l}$  10  $\mu\text{M}$  forward and reverse primer, 0.3  $\mu\text{l}$  5 U/ $\mu\text{l}$  Taq DNA polymerase and 13.4  $\mu\text{l}$  sterile water. The PCR program initially started with a 94 $^{\circ}\text{C}$ /4 min, followed by 35 cycles of 94 $^{\circ}\text{C}$ /1 min, 57 $^{\circ}\text{C}$ /45 s, 72 $^{\circ}\text{C}$ /90 s, and then 72 $^{\circ}\text{C}$  extension for 10 min, finally 4 $^{\circ}\text{C}$  to terminate the reaction. The mRNA and amino acid sequences for UF3GT genes from various plant species available in the databank of National Centre for Biotechnology Information

(<http://www.ncbi.nlm.nih.gov>) were used to locate conserved boxes by multiple sequence alignment through CLUSTALW 1.8 and primers with the following sequence were designed. UF3GT-F: ATGACTACTTCTCAACTTCATATT, UF3GT-R: TYAAGTARGCTTGTGACATTAA (C/T= Y, A/G= R).

### RT-PCR for expression profile

The primers of Yunnan Purple Pepper No.1 UF3GT gene which were used to perform the RT-PCR for tissue expression profile analysis was same discussed above. The 20  $\mu\text{l}$  mixture contained was: 4  $\mu\text{l}$  5xPrimeSTAR PCR Buffer, 0.4  $\mu\text{l}$  dNTP Mixture (10 mM each), 0.2  $\mu\text{l}$  of forward and reverse primer (10  $\mu\text{M}$ ), 0.2  $\mu\text{l}$  of PrimeSTAR HS DNA Polymerase (2.5 U/ $\mu\text{l}$ ) (TaKaRa), 2  $\mu\text{l}$  aliquot of cDNA and 13  $\mu\text{l}$  RNase Free dH<sub>2</sub>O water. The products of amplification were checked on a 1.5% agarose gel and visualized with ethidium bromide.

### Bioinformatics analysis

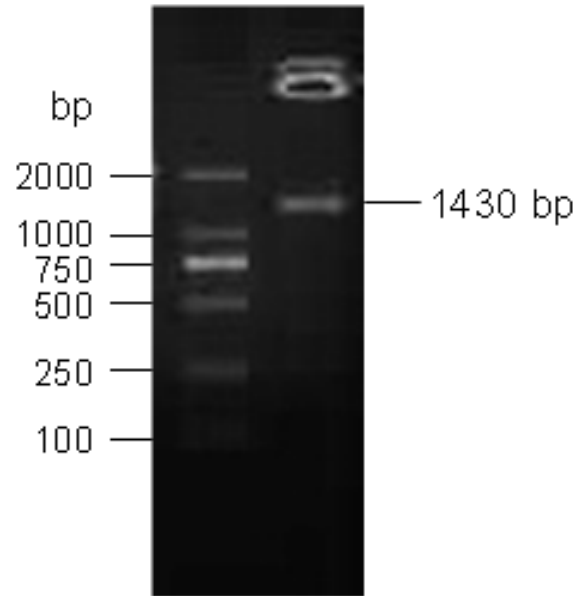
PCR amplification was repeated 5 times independently. The products were cloned into pMD18-T vector (TaKaRa) and sequenced bidirectionally. At least 10 independent clones were sequenced for each PCR product. Sequencing data were edited and aligned using DNASTAR software (DNASar Inc., Madison, Wisc.). The cDNA sequence was predicted using the GenScan software (<http://genes.mit.edu/GENSCAN.html>). Putative protein theoretical molecular weight (Mw) and isoelectric point (pI) prediction, signal peptide prediction, subcellular localization prediction and transmembrane topology prediction were performed using the Compute pI/Mw Tool ([http://us.expasy.org/tools/pi\\_tool.html](http://us.expasy.org/tools/pi_tool.html)), SignalP 3.0 server (<http://www.cbs.dtu.dk/services/SignalP/>), PSort II (<http://psort.hgc.jp/>), TMpred ([http://www.ch.embnet.org/software/TMPRED\\_form.html](http://www.ch.embnet.org/software/TMPRED_form.html)), respectively. The Blastp program and Conserved Domain Architecture Retrieval Tool were used to search for similar proteins and conserved domain, respectively (<http://www.ncbi.nlm.nih.gov/Blast>). The alignment of the nucleotide sequences and deduced amino acid sequences were computed using ClusterX, and the phylogenetic trees were computed using the ClustalX and Mega 4.0 softwares with standard parameters. Secondary structures of deduced amino acid sequences were predicted with SOPMA (<http://npsa-pbil.ibcp.fr/>). The 3D structures were predicted based on the existed 3D structures by the amino acids homology modeling on swiss server (<http://swissmodel.expasy.org/>).

## RESULTS

### RT-PCR results for *C. annuum* L. UF3GT gene

Through RT-PCR with pooled tissue cDNAs, for *C. annuum* L. UF3GT gene, the resulting PCR products were about 1430 bp long (Figure 1).

cDNA nucleotide sequence analysis using the BLAST software at NCBI server (<http://www.ncbi.nlm.nih.gov/BLAST>) revealed that this gene was not homologous to any of the known *C. annuum* L. genes. The sequence prediction was carried out using the GenScan software and the results showed that the cDNA sequences encoded 447 amino acids.



**Figure 1.** Analysis of PCR products on 1.5% agarose gels.

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ATGACTACTTCTCAACTTCATATTGCAGTTCTTGCTTTTCCTTTTGGTAGCCATGCAGTTCCTTTACTCACACTTGTCCAAAAAATCTCT
M T T S Q L H I A U L A F P F G S H A U P L L T L U Q K I S
CCATTTTACCATCAAACTCAATTTTTTCCTTCTTCAACACATCAAAATCCAACACCTCAATTTTCTCAAAAGCTCCAAACCAAGAAAAC
P F L P S N S I F S F F N T S N S N T S I F S K A P N Q E N
ATCAAGATTACATGTTTGGGATGGTGTCAAAACAAGGCAATGACACCCCTATTGTTGTGAAGCCATACAAGTCTTCATACAATCAACT
I K I Y N U W D G U K Q G N D T P I G C E A I Q U F I Q S T
CCAACTAATTTGAAAAATCAATGAAGAGGCGAGAGGAGGAATAGGTGTGAAGTTTTCTTGCATTATCAGTGCATTTTTATGGTTT
P T N F E K S M K E A E E E I G U K F S C I I S D A F L W F
TGTTGTGACTTTGCTAAGAAAATGAATGTCCCTTGGATTGCATTTTGGACTGCTGGATCATGTTCTTTGTCTGTCCATTTGTACACTGAT
C C D F A K K M N U P W I A F W T A G S C S L S U H L Y T D
TTAATTCGATCGAAGCAGGAAACATTATTAATAATTCAGGATTTTCAACAAATTAAGGATCAGTGACATGCCACAAGAAAGTTGTAGCA
L I R S N E E T L L K I P G F S T N L R I S D M P Q E U U A
CATAATTTAGAGGGGGGATTTCCATCTTTGTTATACAACATGGCCTAAATTTGCACAAAGCAGATGGTGTGTACTGAACCTCTTTCGAG
H N L E G G F P S L L Y N M A L N L H K A D G U U L N S F E
GAATGGATCCAAAAATCAACAATGATCTCAAAATCAAGCTCCAAAAGGTAATAATTTGGCCCTTTAGTCTACAGTCATCAAAAGAAA
E L D P K I N N D L K S K L Q K U L N I G P L U L Q S S K K
GTTATTTAGATGTTAATTCGATGAAGTGGATGTATCAAAATGGCTTGACAAGCAAAATGAAAAATCAGTTGTGTACTTAAGTTTGGT
U I S D U N S D E S G C I A K W L D K Q N E K S U V Y L S F G
ACTGTCACAACATTACCTCCTAATGAATTTGGCAATAGCAGAAGCATTAGAAGCCAAAAGGGTACCTTTTATTTGGTCATTAAAGAC
T U T T L P P N E I U A I A E A L E A K R U P F I W S L K D
AATGGGGTCAAGATTTTGCCTAAGGTTTTCTTGAAGGCAAAATGAATTTGGGAAAATAGTTTCTTGGGACCCCAATTTGGAATCTTG
N G U K I L P K G F L E R T N E F G K I U S W A P Q L E I L
GCACATTCACTGTGGTGTATTGTACACATTGTGGATGGAACCTATTTTGGAAAGCATATCATATGGTGTGCCTATGATATGTAGG
A H S S U G U F U T H C G W N S I L E S I S Y G U P M I C R
CCTTCTTTTGGTGACCAAAAGTTGAATAGTAGAATGGTGGGAATGTTTGGCAAAATGGTTTGCAAAATTAAGGTTGGGAATTTCACTAAA
P S F G D Q K L N S R M U E N U W Q I G L Q I E G G N F T K
AGTGGAAACAAATAGTGCATTGGATACTTTTGCATGAGGATAAAGGTAAGGTATTAAAGCAAAATGTTGAAGGGCTAAAAGAAAAGCA
S G T I S A L D T F C N E D K G K U L R Q N U E G L K E K A
TTAGAAGCTGTGAACCAAAATGGGAGTTCAACAGAAAATTTCAAGGTTCTAGTTGAGCTAATTAATGTACACCCCEACTTGA
L E A U K P N G S S T E N F K U L U E L I K C H T P T .

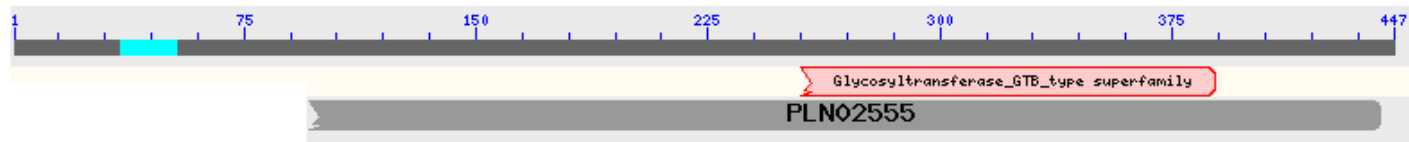
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**Figure 2.** The complete coding sequence of *Capsicum annuum* L. *UF3GT* gene and its encoding amino acids \* indicates the stop codon.

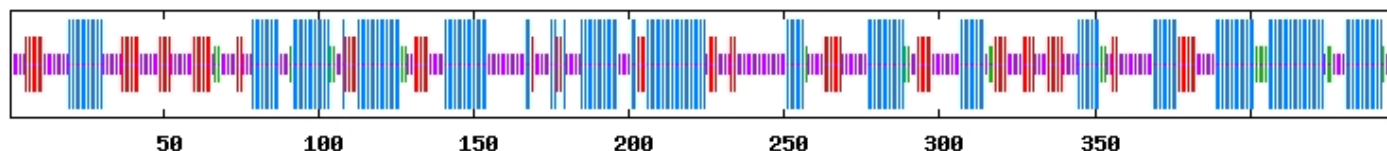
The theoretical pI and Mw of this deduced protein of this *C. annuum* L. gene was computed using the Compute pI/Mw Tool. The pI of this gene was 5.97 while molecular weight of the putative proteins was 49,589.

#### Prediction of protein properties

The complete coding sequence (CDS) of this gene and the encoded amino acids are presented in Figure 2.



**Figure 3.** The conservative domains of the protein encoded *Capsicum annum* L. *UF3GT* gene.



**Figure 4.** Secondary structure of *UF3GT* protein in *Capsicum annum* L. Helices, strands and coils are indicated, respectively, with long, middle and short vertical lines.



**Figure 5.** The tertiary structure of *UF3GT*.

The putative protein was also analyzed using the Conserved Domain Architecture Retrieval Tool of Blast at the NCBI server (<http://www.ncbi.nlm.nih.gov/BLAST>) and the conserved domain was identified as PLN02555 domain (Figure 3). According to Figure 3, we can see it belongs to Glycosyltransferase-GTB-type superfamily.

The secondary structure analysis of the deduced amino acid sequence by GOR algorithm indicated that the protein consisted of 40.94%  $\alpha$ -helix, 37.36% random coils and 17.00%  $\beta$ -sheets (Figure 4). The signal peptide prediction performed by SignalP 3.0 on the basis of a combination of several artificial neural networks and hidden Markov models revealed that *C. annum* L. *UF3GT* contained potential signal peptide with 99.9% probability (Bendtsen et al., 2004). Transmembrane topology prediction made by TMPred ([http://www.ch.embnet.org/software/TMPRED\\_form.html](http://www.ch.embnet.org/software/TMPRED_form.html)), showed that *C. annum* L. *UF3GT* had N-terminus

outside with 4 strong transmembrane helices. For subcellular localization analysis, the amino acid sequence was submitted to the PSORT program, and Reinhardt's method showed *UF3GT* was probably located in the cytoplasm with up to 76.7% probability (Nakai and Horton, 1999).

### Homology modeling

In order to better understand the detailed structures of *UF3GT*, the homology modeling was performed to estimate its 3D structure. The 3D structure of *UF3GT* (2-443AA) by homology modeling was based on template-3hbjA (chain A) with 43.1% sequence identity (Guex and Peitsch, 1997; Schwede et al., 2003; Arnold et al., 2006). The 3D structure analysis may provide a basis for further studying the relationship between structure and function of *UF3GT* (Figure 5).

Capsicum annuum	--MTTS----	-----	-----	----QLHIAU	LAPFFGSHAU	PLLLTLUQKIS	PFLPSNSIFS	FFMNSMSHTS	IFS---	KAPN	QENIKIYNWU	DGUKQGH-DT	PI								
Prunus avium	--APQPIDDD	-----	-----	HUYVEH.V.A	-----	ST.S	.T.A	IRRLA	AAS.N	TL--	--S.Q.N	L.N	TMTNL	PR...VFD.A	--PD.VYFA	GK					
Vitis labrusca	--SQTITMP	-----	-----	...U...	-----	ST.A	...AV	RRLA	AAA.H	AU...	--S.Q.A	V.HD	SMHTM	C...S.D.S	--PE.VYFA	GR					
Arabidopsis thaliana	--AKPSQPTR	-----	-----	...DS.U...	...U...	T.A	...AUT	CLA	TAA.	--TU...	...S.AR.S	LL.S	----	DI	PT...RHN.D	--PE.FUL	GN				
Petunia x hybrida	-----	-----	-----	-----	-----	L	-----	L	-----	DT.	-----	Q	----	EGSK	PD...U	-----	TET.GHK	U			
Dianthus caryophyllus	---.T.MNVEP	P-----	-----	---.RR.	C-----	T.A	---.L	ARRL	TAT.D	--TRYT	---.VER...	L.KA	IDUSU	GS...UP	---IT	LSNEAPAGP	GN				
Capsicum annuum	GCEAIQVFIQ	STPTNFESM	KEEEEEIGUK	FSCIISDAFL	W-FCCDFAKK	MNUPWIAFWT	AGSCSLSUHL	YDLIRSN--	-----	-----	-----	-----	-----	-----	-----	EETLLK----	--I				
Prunus avium	PQ.D.EL.MK	AA.H..TT.L	DACVAHT.KR	LT.L.L.T	..FGAN	LANDL	G---	LPL.L	S.LN.	..L.L.U	H...L	HTIG	---	TQSIAGL	.ME.IT	KMA	N.				
Vitis labrusca	PQ.D.EL.MR	AA.EG.RQG	UM.VA.T.RP	U...LVA...	I	FAADMA	EM	G--.A	LP...	--PN...	T.U	--E.	EKIG	---	USCIGR	.DE.N	--F.				
Arabidopsis thaliana	PQH.VEL.LE	AA.EI.RREI	.A..T.U.R	.K..LT...	...LA	ETA.AE	.KAS	.U	YVG	G.AT.	..TA...	...A.	E.UG	---	UKEUGR	M.ETIG	---	F.			
Petunia x hybrida	..L..KL..A	..A....U	..T....T	..F....F	...SY	KL.E	I	...	A.G	---	A.G	---	F	---	...	D...S	..M	---			
Dianthus caryophyllus	PWK.EE.LE	HS.GG.RRA	E.V.AHU	I.I	...	VCSDIAEE	G	LD...	L	---	TA...	...	A.	ALAS	D--	HQGECK	.DU	US	---		
Capsicum annuum	PGFSTMLRIS	DMPQEUVAH	LEGGFSLLY	NMALMLKAD	GVULMSFEEL	D--PKINMNDL	KSKLQ-KULN	IGPLUL-QSS	KK----	VIS	DUNSD	ESGCI	KW								
Prunus avium	..M.-KV..K	.L.EG.FIG	.DSU.SRM.H	Q.GQL.PR.M	A.LU.....	---ITUT...	...FM...	..L	U..FN	AAAA	SPPL	PEALTA	ADDUT--	..L	S						
Vitis labrusca	..MV-EU.FR	.LQEGI.FG	.MSL.SRM.H	R.GQU.P.T	A.FI.....	---D	SLT...	...K	TY...	..FN	ITPP	PU--	..PN	TT	----	..L	Q				
Arabidopsis thaliana	S.ME-KI.UK	.TQEG.FG	.DSU.SKT.H	Q.G.A.PR.T	A.FI.....	---T	F	R	E	FK	RY...	...A	LS	P	SQ	---	T	TLUH	PH..L	A.	
Petunia x hybrida	..ST.K..	..P..M.E	..DLPN..M..	..A.....	..T...	..K...	..U...	..PT	SP	---	KKU	LDAC	..R..	..I.							
Dianthus caryophyllus	..L..V...	..L.MGL.SGD	.DAP.SQM.H	K.GTM.P..K	U.T..V.Q...	S--	LUV...	M...K	..L	C	U..FP	TCPP	QU	---	..Y...	PDH	L	D.			
Capsicum annuum	LDKQHEKS--	UUVLSFGTUT	TLPPHEIVAI	AEALEAKRUP	FIVSLKDNQV	KILPKGFLEK	TNE---	FGKI	USWAP	QLEIL	AHSSUG	VUT	HCGVNS	SILES	IS						
Prunus avium	...K-AASS	...V...S.A	RP.EK.LM.M	.Q...SG...	..L...	SFK	TP	LNEL	UK	AS	---	M	MU	.P...	PRU..	..A..A...	....S.L.L	T	..A		
Vitis labrusca	.KERR-PTS-	..I.....	..P..A.L.L	..L...S...	...R	KAR	UH	.E...K	RC	---	V	MU	.P...	..A	U..EA..A...	....LM	..U	..U			
Arabidopsis thaliana	IE.RS--TAS	.A.IA..R.A	.P..U.L.L	.Q...SSK...	...U...	QEMM	TH	.E...D	..R	---	Q	MU	.P...	..U	L	N	EA...	...S	..G...U	..U	
Petunia x hybrida	.E..K.E--	-----	-----	-----	-----	KF	-----	I	N	T	-----	GQ	---	...	...	N..A	.....	...G	---	..G	...
Dianthus caryophyllus	..QHCP.T--	IA.I.....	.P..H..R.L	.K...GSDI	..U...	MS	SVR	AN	.ES	.I	K	IQHEPKU	-----	IKL	G.P.T	-----	...M	---			
Capsicum annuum	YGUPNICRPS	FQDQKLSRM	VENUVQIGLQ	IEGG-MFTKS	GTISALDTCF	NEDKCKULRQ	MVEGLKEKAL	EAVKP-MGSS	TENFKULVEL	IKCHTPT-											
Prunus avium	G.....F	..X.RV.A.T	.D.LE..UT	U.D..U..H	.L.KYF	.QUL	SQQR..KM.G	.INTU	LL.Q	QS.E..K..	AQ...L	LDU	..SGS	KU-							
Vitis labrusca	G...L...F	..R..G...	..D.LE..UR	..U...L	..LM	CF.QIL	SQE...K..E	.LRA	R.T.D	R..G..K...	...T..D	USKP	KDU-								
Arabidopsis thaliana	A.....I	...HAI.A.S	..A..E..UT	..SS..U..D	..FEES	..RVL	UQ.D..KMKU	..AKK	E..L.Q	...ST	K...F	..GG	.LDE	UUNFG	---						
Petunia x hybrida	C.....F	-----	..S.....	...S..I	...TM	..NQUL	ASE..EEM	K	...E..KL	E	..S..Q..G	..N...	NA	I...	..TSS	---					
Dianthus caryophyllus	T...L...I	I...E..Q.I	..IELKF	..IG	...C..Q	..TM	..NQUL	ASE..EEM	K	...E..KL	E	..S..Q..G	..N...	NA	I...	..TSS	---				

Figure 6. The alignment of the protein encoded by *C. annuum* L. *UF3GT* with *UF3GT* from other species.

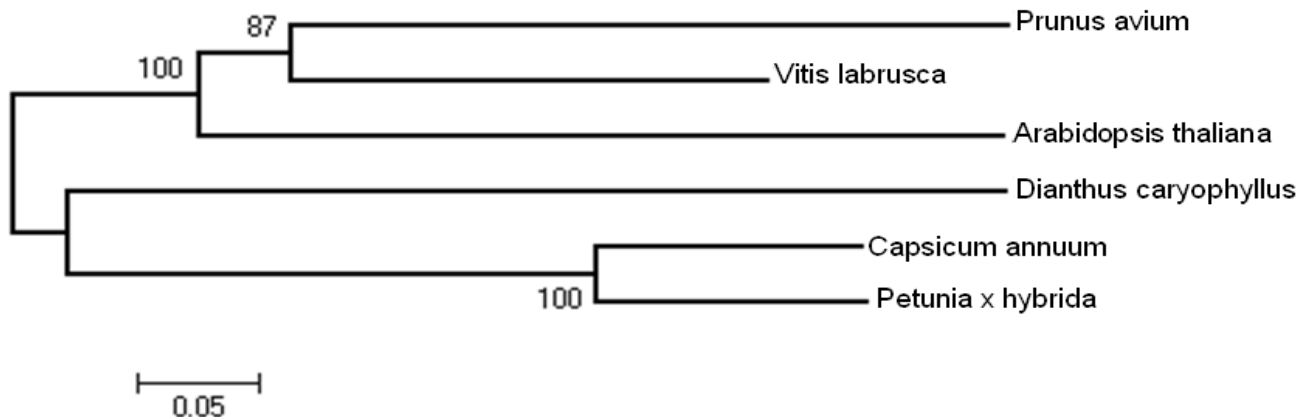


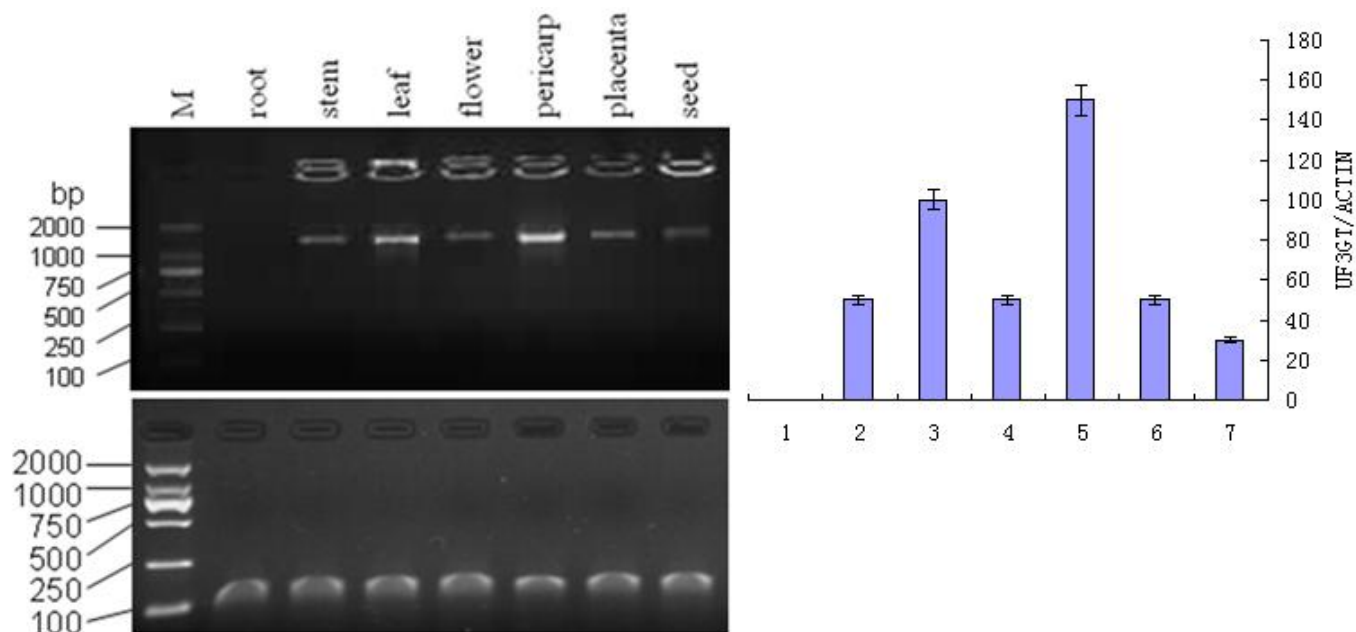
Figure 7. Phylogenetic tree analysis for selected *UF3GT* protein.

**Sequence analysis and evolutionary relationships**

Further BLAST analysis of this protein revealed that *C. annuum* L. *UF3GT* has high homology with the anthocyanin synthases protein *UF3GT* of 5 species - *Prunus avium*, *V. labrusca*, *Arabidopsis thaliana*, *Dianthus caryophyllus*, *P. x hybrida* (Figure 6).

Based on the result of the alignment of *UF3GT*, the phylogenetic tree was constructed using the ClustalW software (<http://www.ebi.ac.uk/clustalw>), as shown in Figure 7. The phylogenetic tree analysis revealed that the *C. annuum* L. *UF3GT* has a closer genetic relationship with the *UF3GT* of petunia.

Gene expression profile analysis was carried out and results revealed that the *C. annuum* L. *UF3GT* gene was highly expressed in pericarp, moderately expressed in stem, leaf, flower, pericarp, placenta and seed. There was no expression of *C. annuum* L. *UF3GT* in root (Figure 8). From the tissue expression profile analysis in our experiment it can be seen that this gene was obviously differentially expressed in some tissues and there were no expression in some tissues. As we did not study functions at protein levels yet, there might be many possible reasons for differential expression of this gene. The suitable explanation for this under current conditions is that at the same time those biological activities related



**Figure 8.** Tissue expression distribution of *C. annuum* L. *UF3GT* gene. M, DL2000 markers.

to anthocyanosides synthesis of this gene were presented diversely in different tissues.

## DISCUSSION

*UF3GT* gene have been cloned and characterized from horticulture crops, such as *Petunia* (Weiss et al., 1995; Moalem-Beno et al., 1997), *Periwinkle* (Ohlsson and Berglund, 2001), *Rose* (Zieslin et al., 1974), and a few other species. In this study, a 1430-bp full-length cDNA gene *UF3GT* was isolated from *C. annuum* L.. The deduced amino acid sequence of *UF3GT* showed extensive similarity to their counterparts in other species. Through tissue expression analyses, we detected *UF3GT* expression in stem, leaf, flower, pericarp, placenta and seed where anthocyanin was concentrated, the expression of *UF3GT* was higher in pericarp. This phenomenon is in accordance with the anthocyanin content in these tissues (data not given). These data suggest that *UF3GT* maybe a specific tissue expression gene. And it was consistent with previous research (Hughes and Hughes, 1994). Anthocyanin content might have close correlation with *UF3GT* expression levels in response to tissue specificity and genetic background.

In this report, the complete coding sequences of the *C. annuum* L. *UF3GT* gene was isolated based on the conserved sequence information of the *P. xhybrida* and some referenced *C. annuum* L. ESTs. Sequence identification further validated that comparative genomics method is one useful tool to isolate the unknown genes especially the conserve coding region of genes for *C. annuum* L. or other plants.

In conclusion, we have isolated the *C. annuum* L. *UF3GT* gene and performed necessary functional analysis and tissue expression profile analysis. This established the primary foundation for further research on *C. annuum* L. *UF3GT* gene.

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