Table 1 Suppl. List of primers used for isolation of the flavonoid biosynthesis-related genes of *Tricyrtis* spp.

Gene	Analyzes	Position	Sequence (5'→3')
TrMYB1	3'RACE	forward	GATGAGGAGGACCTCATTATCAGG
	5'RACE (reverse transcription)	reverse	GGTCGAGCTTGTGGTTTG
	5'RACE (1st PCR)	forward	GAACTACTGGAACTCACATTGG
	5'RACE (1st PCR)	reverse	GTCCTACCGGGAATTCGACCGG
	5'RACE (2nd PCR)	forward	GCTGGAGATAAGATTGATGG
	5'RACE (2nd PCR)	reverse	GGACCACCTGTTCCCTAAAAG
TrbHLH2	3'RACE (1st PCR)	forward	GTGACAAGGAGCAGTCCAC
	3'RACE (2nd PCR)	forward	AGTCTTCTGCAGAACCATTCTCG
	5'RACE (reverse transcription)	reverse	GTCACACTAGTAG
	5'RACE (1st PCR)	forward	AGTCTTCTGGCAGAACCATTCTCG
	5'RACE (1st PCR)	reverse	TCGACAGTCACCTCCATTGG
	5'RACE (2nd PCR)	forward	AGTCTTCTGCAGAACCATTCTCG
	5'RACE (2nd PCR)	reverse	AGAACCACACTTGACCTCTCGTG
TrWDR1	3'RACE (1st PCR)	forward	GTGACAAGGAGCAGTCCAC
	3'RACE (2nd PCR)	forward	GTTGTGGTGCTGGATATACG
	5'RACE (reverse transcription)	reverse	ATCGCAATCCAATCG
	5'RACE (1st PCR)	forward	GTTGTGGTGCTGGATATACG
	5'RACE (1st PCR)	reverse	CTGGACTTACTGTTGTTCAGCACG
	5'RACE (2nd PCR)	forward	GTTGTGGTGCTGGATATACG
	5'RACE (2nd PCR)	reverse	GTGGAACATGAGCTTGGTGG
TrCHI	3'RACE	forward	CTTCAAGGCGGAGACC
	5'RACE (reverse transcription)	reverse	CCTTTCTAGCATCCTC
	5'RACE (1st PCR)	forward	CGATAACAAAGCTCTTTCAGAC
	5'RACE (1st PCR)	reverse	CGAACCATCCTTCGAGAATCC
	5'RACE (2nd PCR)	forward	GTCCATCATTGGTGAGCACGGCGTG
	5'RACE (2nd PCR)	reverse	GTGAACCGGAAGGGGAGTGGGTG
TrF3H	3'RACE	forward	GGTGAAGCAGTGCAAGATTGG
	5'RACE (reverse transcription)	reverse	CTTAAGCTTGGCAAGCTCGATG
	5'RACE (1st PCR)	forward	TCAAGAATGCCGACCACCAG
	5'RACE (1st PCR)	reverse	GGTATGAGAAGTACGTCACTATCTCC
	5'RACE (2nd PCR)	forward	AGCCGATTACTTTCAGCGAGATG
	5'RACE (2nd PCR)	reverse	TGAAATATCCCCCAGTCCTCG
TrF3'H	3'RACE	forward	GAGGAGGAGGATGAGGCAAAC
	5'RACE (reverse transcription)	reverse	TGGGTGGCGGATCAA
	5'RACE (1st PCR)	forward	CCCAACCTCCCATTCCTAC
	5'RACE (1st PCR)	reverse	CGTGTCTGTTCCTGCTGTG
	5'RACE (2nd PCR)	forward	AACTCTCCTGGTTAACGTTTGG
	5'RACE (2nd PCR)	reverse	CAAGAAACGCATCCATCCTC
TrFLS	3'RACE	forward	CTSRABYTGRTCDCCRATRTC
	5'RACE (reverse transcription)	reverse	ATATGCTGAGCAAAGGTTCG
	5'RACE (1st PCR)	forward	TTGAGCAATGGGAGGTACAAG
	5'RACE (1st PCR)	reverse	GTCACCTATGTGGATGACAAGAG
	5'RACE (2nd PCR)	forward	CAAGAATGTCATGGCCTGTG
	5'RACE (2nd PCR)	reverse	GACATGTCAGTATGTGCCAC
TrDFR	3'RACE	forward	CGTCAAGATGACTGGATGGATG
	5'RACE (reverse transcription)	reverse	GTCACACTAGTAG
	5'RACE (1st PCR)	forward	TCAAGTATGAGTACACCGTGGAG
	5'RACE (1st PCR)	reverse	GTCCTACCGGGAATTCGACCGG
	5'RACE (2nd PCR)	forward	TGTTTGATGACGGAATCCAG
	5'RACE (2nd PCR)	reverse	GCGGTTATCATACTGGGTGG
TrANS	3'RACE	forward	GGGCAGTGTTTCGTGAGCCGCCAAAGG
	5'RACE (reverse transcription)	reverse	ATATGCTGAGCAAAGGTTCG
	5'RACE (1st PCR)	forward	GCTCACCTTCCTGCTCACC
	5'RACE (1st PCR)	reverse	GGCTAGCTCTGGTTGTGG
	5'RACE (2nd PCR)	forward	AGCGGAGCCTGCTAGGTTC
	5'RACE (2nd PCR)	reverse	CTCCTTTGTCCCTCCGTATAC
	common primer for 3'RACE	reverse	CTGATCTGAGGTACCGGTCC

Table 2 Suppl. List of genes used for the phylogenetic analysis.

Group	Gene	Plant species	Accession No.	Identity [%]	Similarity[%]
R2R3-MYB	*AmROSEA1*	*Antirrhinum majus*	DQ275529	41.4	54.4
	AtPAP1	*Arabidopsis thaliana*	AF325123	38.8	50.8
	AtTT2	*Arabidopsis thaliana*	NM_122946	33.7	46.6
	GhMYB10	*Gerbera* sp.	AJ554700	39.5	52.5
	InMYB2	*Ipomoea nil*	AB234211	42.4	56.8
	LhMYB6	*Lilium hyblid*	AB534587	42.4	56.5
	LhMYB12	*Lilium hyblid*	AB534586	43.5	57.3
	LjTT2a	*Lotus japonicus*	AB300033	31.5	45.3
	OgMYB1	*Oncidium* sp.	EF570115	36.8	48.9
	PhAn2	*Petunia hybrida*.	AF146702	42.4	51.9
	VvMYBA1	*Vitis vinifera*	AB097923	40.4	50.2
	ZmPI	*Zea mays*	L19495	35.4	45.5
	ZmC1	*Zea mays*	X52201	35.5	44.0
bHLH	*AtTT8*	*Arabidopsis thaliana*	AJ277509	40.9	54.1
	AtEGL3	*Arabidopsis thaliana*	NM_105042	30.8	50.0
	InbHLH1	*Ipomoea nil*	AB232774	32.5	51.2
	InbHLH2	*Ipomoea nil*	AB232775	46.1	61.8
	LhbHLH1	*Lilium* sp.	AB222075	31.8	50.1
	LhbHLH2	*Lilium* sp.	AB222076	59.6	70.1
	LjTT8	*Lotus japonicus*	AB490778	49.4	63.7
	LjGL3	*Lotus japonicus*	AB492284	32.7	50.2
	PhAN1	*Petunia hybrida*.	AF260919	46.2	62.1
	PhJAF13	*Petunia hybrida*.	AF020545	30.1	49.7
	TfbHLH1	*Tulipa fosteriana*	KC256778	32.7	51.1
	TfbHLH2	*Tulipa fosteriana*	KF924736	56.8	70.1
	ZmIN1	*Zea mays*	U57899	42.1	54.6
	ZmLc	*Zea mays*	M26227	28.3	47.4
WDR	*AaTTG1*	*Anthurium amnicola*	GDJX01022041	74.6	85.2
	AtTTG1	*Arabidopsis thaliana*	NM_180739	66.9	81.1
	InWDR1	*Ipomoea nil*	AB232779	69.3	82.8
	LjTTG1	*Lotus japonicus*	AB490777	67.3	81.1
	PhAN11	*Petunia hybrida*.	U94748	70.9	84.9
	PeWDR1	*Phalaenopsis equestris*	KF769483	59.8	73.3
	RrTTG1	*Rosa rugose*	JX878895	71.0	83.2
	VvWDR1	*Vitis vinifera*	DQ517913	72.4	84.6
	ZmPAC1	*Zea mays*	AY115485	63.5	75.7
CHI	*AmCHI1*	*Antirrhinum majus*	AB861648	63.2	76.1
	AtCHI	*Arabidopsis thaliana*	AJ418046	54.9	70.3
	CgCHI	*Canna generalis*	DQ160232	62.6	75.7
	CmCHI	*Chrysanthemum morifolium*	JF834891	57.6	72.5
	DpCHI	*Dahlia pinnata*	AB591827	60.4	76.2
	GmCHI2-A	*Glycine max*	NM_001249839	50.4	68.8
	LhCHI	*Lilium* sp.	KJ784468	70.3	83.1
	NtCHI	*Narcissus tazetta*	JN227884	62.6	76.8
	PhCHI	*Petunia hybrida*.	Y00852	57.4	73.1
	TfCHI	*Tulipa fosteriana*	JX878398	69.9	81.8
	VvCHI	*Vitis vinifera*	NM_001281104	60.4	79.6
	ZmCHI1	*Zea mays*	NM_001150530	64.0	77.5
	AtF3H	*Arabidopsis thaliana*	AF064064	63.3	68.9
	CaF3H	*Curcuma alismatifolia*	GU140081	62.8	69.4
	EgF3H	*Eustoma exaltatum*	AB078956	64.7	70.0
	GmF3H	*Glycine max*	NM_001249868	58.1	67.2
	LhF3H	*Lilium* sp.	AB699160	65.0	69.9
	NtF3H	*Narcissus tazetta*	JQ388493	63.0	69.3
	PhF3H	*Petunia hybrida*.	LQ275617	60.9	68.3
	PhF3H	*Phalaenopsis* sp.	JX162553	60.5	67.3
	TfF3H	*Tulipa fosteriana*	JX863898	65.8	71.6
	VvF3H	*Vitis vinifera*	EF192467	62.8	70.2

	ZmFHT1	*Zea mays*	NM_001136803	61.7	67.8
F3’H	*AtF3’H*	*Arabidopsis thaliana*	AF271650	62.1	77.2
	CmF3’H	*Chrysanthemum morifolium*	AB523844	64.1	77.6
	DpF3’H	*Dahlia pinnata*	FJ216428	65.0	79.0
	GmSF3'H1	*Glycine max*	NM_001250086	63.2	77.9
	InF3’H	*Ipomoea nil*	AB113261	64.2	77.4
	LhF3’H-1	*Lilium* sp.	AB699161	78.2	84.1
	PhF3’H	*Petunia hybrida*.	AF155332	64.1	78.1
	PeF3’H	*Phalaenopsis equestris*	KF769465	50.5	63.2
	SbF3’H	*Sorghum bicolor*	AY675075	62.9	76.7
	ThF3’H	*Torenia* sp.	AB057672	60.5	75.6
	TfF3’H	*Tulipa fosteriana*	JX878399	75.4	85.0
	VvF3’H	*Vitis vinifera*	KT216254	67.5	79.2
DFR	*ApDFR*	*Agapanthus praecox*	AB099529	70.1	82.8
	AtDFR	*Arabidopsis thaliana*	AK221622	59.2	76.2
	CaDFR	*Curcuma alismatifolia*	GU126388	66.7	81.2
	CgDFR	*Cyclamen graecum*	AB517921	60.7	77.3
	ChDFR	*Cymbidium* sp.	AF017451	66.7	77.8
	GhDFR	*Gossypium hirsutum*	FJ713480	58.3	76.3
	IhDFR	*Iris hollandica*	AB332098	69.8	82.0
	LhDFR	*Lilium* sp.	AB058641	78.0	87.0
	PhDFR	*Petunia hybrida*.	AF233639	58.1	75.2
	RhDFR	*Rosa* sp.	AY780885	60.4	77.7
	TfDFR	*Tulipa fosteriana*	JX401219	65.4	75.8
	ZmDFR	*Zea mays*	NM_001158995	65.1	79.5
FLS	*AcFLS1*	*Allium cepa*	AY221247	74.0	86.9
	AmFLS	*Antirrhinum majus*	DQ272591	66.4	80.7
	AtFLS1	*Arabidopsis thaliana*	NM_001203337	63.4	76.8
	DaFLS1	*Dioscorea alata*	KJ022640	73.2	84.5
	EgFLS	*Eustoma grandiflorum*	AB078965	66.3	81.2
	GmFLS1	*Glycine max*	NM_001250490	64.7	77.2
	NtFLS	*Narcissus tazetta*	JX467719	71.9	85.1
	PhFLS	*Petunia hybrida*.	Z22543	64.4	79.0
	RrFLS1	*Rosa rugosa*	KM099095	62.4	76.7
	TfFLS	*Tulipa fosteriana*	KF924735	80.5	88.6
	VvFLS1	*Vitis vinifera*	AB086055	63.6	76.4
	ZmFLS1	*Zea mays*	NM_001147443	57.1	72.3
ANS	*AcANS*	*Allium cepa*	AY585678	63.3	78.4
	AaANS	*Anthurium andraeanum*	EF079869	65.7	82.1
	AtANS	*Arabidopsis thaliana*	JF681791	63.5	79.1
	EgANS	*Eustoma grandiflorum*	AB551412	61.7	77.7
	GhANS	*Gerbera* sp.	AY997842	63.0	77.6
	GmANS	*Glycine max*	AY382828	67.7	81.2
	InANS	*Ipomoea nil*	AB073920	64.1	78.6
	LhANS	*Lilium* sp.	KP857572	81.2	88.4
	PeANS3	*Phalaenopsis equestris*	KF769463	57.4	75.1
	TfANS	*Tulipa fosteriana*	JX401218	76.8	86.5
	VvANS	*Vitis vinifera*	EU156063	66.0	80.1

Table 3 Suppl. List of primers used for the real-time semi-quantitative PCR analysis.

Gene	Position	Sequence (5'→3')	PCR conditions
TrMYB1	forward	TCTATTACTTGATGAGGAGTCGAAC	annealing temperature: 60°C
	reverse	GTTCTTAGTGCCAGTTCTTCTTG	cycle number: 32
TrbHLH	forward	CTACTCCCGGAGATGCGTTGAGAACC	annealing temperature: 60°C
	reverse	CAGTCCTACCGGGAATTCGACCGGC	cycle number: 32
TrWDR	forward	CTACTCCCGGAGATGCGTTGAGAACC	annealing temperature: 60°C
	reverse	CAGTCCTACCGGGAATTCGACCGGC	cycle number: 32
TrCHS	forward	TGGAGGTTAAGTTGGCGTTG	annealing temperature: 60°C
	reverse	CGCTTCCTCATCTCATCCAG	cycle number: 30
TrCHI	forward	CCCTCCTGGTGCCTCCATCCTCTTC	annealing temperature: 60°C
	reverse	CGCTAATGGCAATTGGCTCCTTAGC	cycle number: 30
TrF3H	forward	GGCGCTCGCATGCAAGCTCTTGGG	annealing temperature: 60°C
	reverse	GGCACCACGACGGGCTTGACAG	cycle number: 30
TrF3'H	forward	GCGGCGGAGGAGTTTAAGGAGATGG	annealing temperature: 60°C
	reverse	GGCCCATTCTACTGTGCTCGAGG	cycle number: 30
TrFLS	forward	ATGGAGGTCGAGAGAGTCCAAG	annealing temperature: 60°C
	reverse	ACTCTATGGCAGCCTCAGTTATG	cycle number: 30
TrDFR	forward	CAATGCCACCCAGTATGATAAACC	annealing temperature: 60°C
	reverse	CATGAAAAGAACACATATATCTCCC	cycle number: 32
TrANS	forward	GACAATTGTGTTGAAGCCGTTGG	annealing temperature: 60°C
	reverse	GGGCTCCACCGAAGATTTTATTG	cycle number: 30
TrAct2	forward	TGCCATGTATGTTGCCATTCAG	annealing temperature: 60°C
	reverse	AGGGAGTCGGTCAGGTCTCTG	cycle number: 30

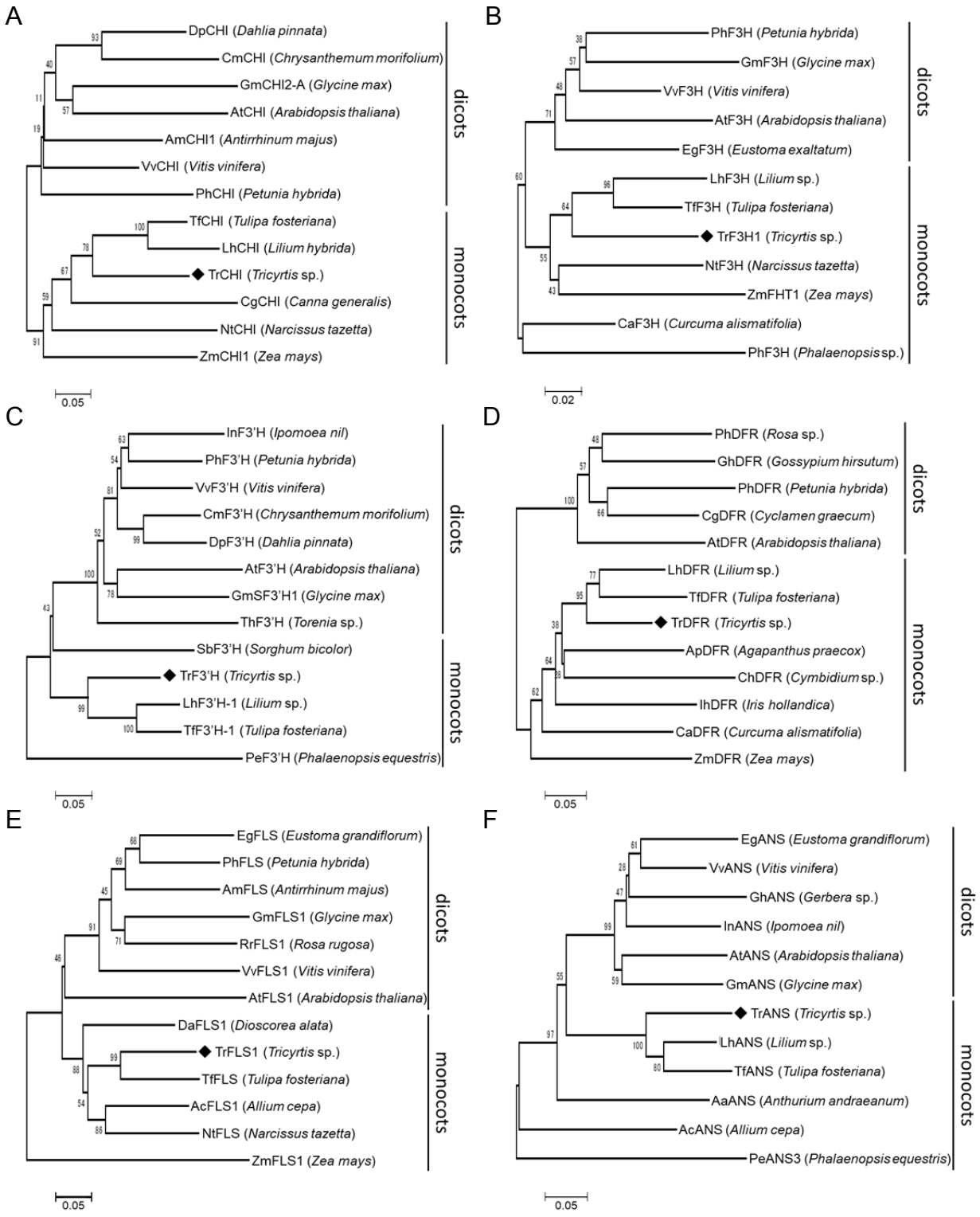

Fig. 1 Suppl. Molecular phylogenetic trees of the deduced amino acid sequences of flavonoid biosynthesis genes. CHI, chalcone isomerase (*A*); F3H, flavanone 3-hydroxylase (*B*); F3'H, flavonoid 3'-hydroxylase (*C*); DFR, dihydroflavonol 4-reductase (*D*); FLS, flavonol synthase (*E*); ANS, anthocyanin synthase (*F*).

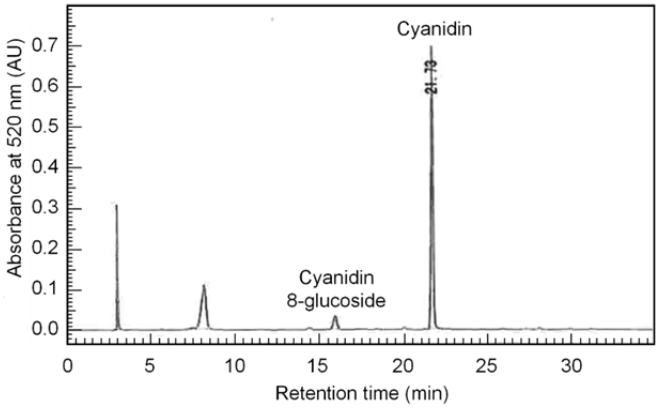

Fig. 2 Suppl. HPLC profile for the accumulation of anthocyanidins in outer tepals of stage 5 flowers.