



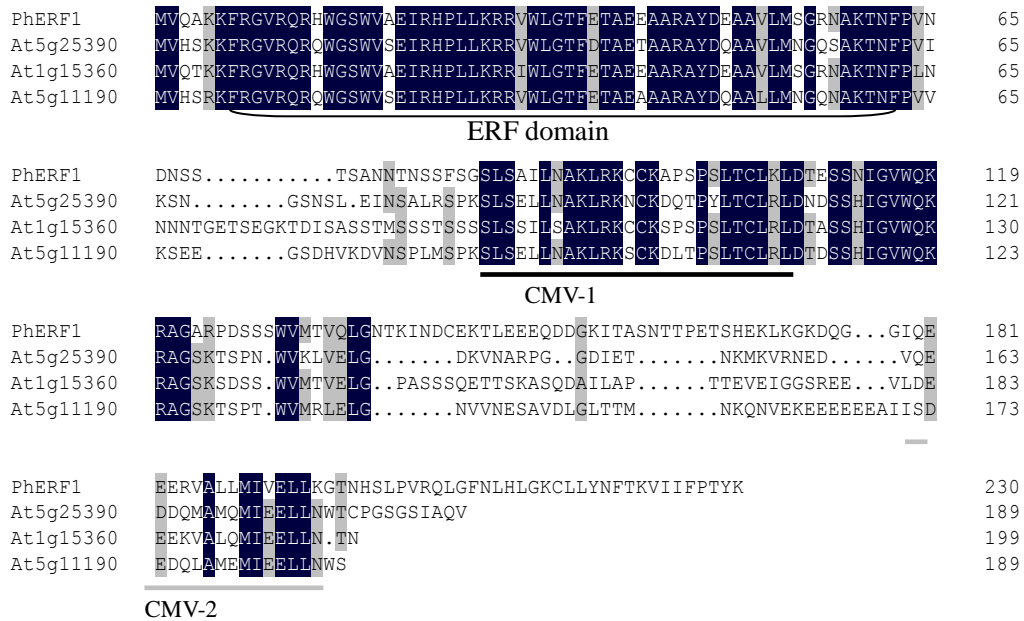
Identification and expression analysis of *ERF* transcription factor genes in petunia during flower senescence and in response to hormone treatments

Juanxu Liu*, Huinan Wang*, Jingyu Li, Zhaodi Fu, Juan Liu and Yixun Yu 

College of Horticulture, South China Agricultural University, Guangzhou 510642, China

 Yixun Yu

E-mail: yuyixun@scau.edu.cn



Supplementary Fig. S1a: Amino acid sequence alignment of Group V ERFs that includes PhERF1, At1g15360/SHN1, At5g11190/SHN2, and At5g25390/SHN3 using DNAMAN program. Conserved residues are shaded in black. Grey shading indicates similar residues in three out of four of the sequences. The filled black bar below the sequences represents the CMV-1 motif and the gray bar below the sequences represents the CMV-2 motif.

At1g53910	MCGGAIISDFIPPPRS.LRVVTSEFIWP..DLK...KNLKSGSKSSKNRSNFFDFDAEF EADFQGF	59
At3g14230	MCGGAIISDFIPPPRS.LRVVTNEFIWP..DLK...NKVKASKKRSNKRSDFFDLDDD EADFQGF	59
PhERF2	MCGGAIISDYIPNRTSRRLTAELLWGRS.DLSKSKNPNPNYHSKPLR.SQIVDLDDD EADFQGF	64
PhERF3	MCGGAIISDLVPSRRTSRRLTADLLWGS.DLK...KNPNYHSKPLRSKFFIDLDF EADFQGF	62
PhERF4	MCGGAIISDLIP..RRDRRASSTDLWP.....TSADFWPNASFSPKPTSSL	44
CMVII-1		
At1g53910	KDDSSIDCDDDFDVGDFADVKEFVFTSTPKPAVS..AAEAGSVFGKVTGLDGDAAEKSANRKRK	122
At3g14230	KDDSAFDCEDD...DDVFVNVKPFVFTATTKPVASAFVSTVGSAYAKKTVE SAEQAEKSSKRKRK	121
PhERF2	KD....FSDD.....EDVKEPFAFSA PKQST.....GSKSVKSADS.EKDADSSSKRKRK	108
PhERF3	S.....DDIKPEFGSKSVKSAD.....ANCEEADKSSKRKRK	93
PhERF4	S.....TQKVEVTPKRAQPTT.....EQIEKSKKRQRK	72
At1g53910	NOYRGIRQRPWGKWAAEIRDPRKRGARLWLGTFKTAEEAARAYDAAARRIRGSKAKVNFPEE.NMK	186
At3g14230	NOYRGIRQRPWGKWAAEIRDPRKGSREWLGTFTAEAAARAYDAAARRIRGSKAKVNFPEEKNPS	186
PhERF2	NOYRGIRQRPWGKWAAEIRDPSKGVVWVWLGTFNTAEAAARAYDVEARRIRGNKAKVNFPEE..AP	171
PhERF3	NOYRGIRQRPWGKWAAEIRDPRKGRVWVWLGTFNSAEAAARAYDVEARRIRGNKAKVNFPEE..TP	156
PhERF4	NLYRGIRQRPWGKWAAEIRDPRKGVVWVWLGTFNTAEAAARAYDSEARRIRGNKAKVNFPEE....	133
ERF domain		
At1g53910	ANSQKR.SVKAN.LQKPVAKPN.....PNPSPALVQNSNISFEN...MCFMEEKHQVSNNNNN	239
At3g14230	VVSQKRPSAKTNNLQKSVAKPNKSVTLVQQPPHLSQQYCNNSFDNSFGDMSFMEEKPQMYNN...	248
PhERF2	VPSSRR.AVKVN.PQKVLPSLD...SVQPDTTVMNNLRNGYYDS...LGFLEEKPVAKQYGYE	226
PhERF3	VSASRR.TVKQN.PQKVEESSN...TVQLNTFNFCNNLDSGCYDS...LDFVEEKPTAKQYAYE	211
PhERF4	...DNHYSTHPQ.PQRSIGYDS.....YDTCYNS.....HEVNNS...	164
At1g53910	QFGMTNSVDAG.....CNGYQYFSSDQGSNSFDCSEFGWSDQAPITPDISSAVINNNNS..AL	295
At3g14230	QFGLTNSFDAGG.....NNGYQYFSSDQGSNSFDCSEFGWSDHGPKTPEISSMLVNNNE...AS	304
PhERF2	DGGST.SVDIGFDSFAPSAGADIYFNSDVGSNSFDCSDFGWGEPCTRTPEISSVLSAAIESNEAQ	290
PhERF3	DVCIT.AGDMGLGSFSPSAGADVYFTSDEGSNTFDCSDFGWGEPGSRTPEISSVLSAVAENGQTQ	275
PhERF4YG.....IIENTEPVNNNDQNCQLKEQEKEENEVEKISEELMAYES...LMK	207
At1g53910	FVEEANPAKKLK.....SMDFETPYNNTEWDASLD.....FLNEDAVTTQD.....	336
At3g14230	FVEETNAAKKLPNSDESDDLMAFLDNALWDTPLEVE.....AMLGADAGAVTQ.....	353
PhERF2	FVEDARPEKKLSDPNNPVADDGNTVNSELSAFESEMFLQIPYLEGNWDASADTFLNLT SAT	355
PhERF3	FVEDASPAKRLKSCTNNSVQR	296
PhERF4	FYEIPYVDGQSV AATMNPAAEA.....	229
At1g53910	.NGANPMDLWSIDEIHS MIGGVF	358
At3g14230	.EEENPVELWLSLEINFMLE GDF	375
PhERF2	QDGENAMDLSFDVPSLMGGVY	378
PhERF3		
PhERF4	.MGGGMDLWSFDVSPVSPAH	251

Supplementary Fig. S1b: Amino acid sequence alignment of Group V ERFs that includes PhERF2, PhERF3, PhERF4, At1g53910/RAP2.12 and At3g14230/RAP2.2, using DNAMAN program. Conserved residues are shaded in black. Grey shading indicates similar residues in four out of five of the sequences. The filled black bar below the sequences represents the CMVII-1 motif.

At1g28370	MPNITMGLKPDVPAPTNPTHHESNAAKEIRYRGVRRKPWGRYAAEIRDVPKKTRVWLGTFDTAQQA	66
At1g50640	MRRGRGSSAVAGPTVVAAINGSVKEIRFRGVRRKPWGRFAAEIRDVPKKARVWLGTFDSAEAA	63
At1g53170	MPNITMGLKPDVPAPTNPTHHESNAAKEIRYRGVRRKPWGRYAAEIRDVPKKTRVWLGTFDTAQQA	66
PhERF6	MAPKEKGGATIGKVNSSKEVHYRGVRRKPWGRYAAEIRDVPKKSRVWLGTFDTAEAA	58
PhERF7	MRHRKSSELNRPRSDIPKQPES.DPPRYRGVRRKPWGRFAAEIRDVPKKTRVWLGTFDTAEAA	62
PhERF8	MRRGRAAAAAVFAAVNGEMNG...SIRFRGVRRKPWGRFAAEIRDVPKKTRVWLGTFDSAEAA	60
	ERF domain	
At1g28370	ARAYDAAARDFRGVKAKTNEGV.....IVGSSPTQSSTVVDSPPTAARFIT.....	111
At1g50640	ARAYDSAARNLRGPKAKTNEPIDSSSPPPNLRFNQIRNQNQNQVDFPMDHRLFTDHQQQFPVNR	129
At1g53170	ARAYDAAARDFRGVKAKTNEGV.....IVGSSPTQSSTVVDSPPTAARFIT.....	111
PhERF6	AKAYDAAAREFRGAKAKTNEPLD.....DLKINVVEKKYNDKSYSPSSSTVESSR..DGAVN	115
PhERF7	ARAYDDAARALRGSKAKTNEPV.....VPVTTTIQNTTGVSP..GQFELFP.....R	107
PhERF8	ARAYDAAARTLRGPKAKTNEPL.....PHHPYNQSFNNPNNEG..VNSRIYPQDNP..VITQR	115
At1g28370	PPHLELSLGGGGACRRKIPLVHPVYY.....YNMATYPKMT	147
At1g50640	PTSSSMSTVESFSGPRPTMKPATT.....KRYPRTPPVV	165
At1g53170	PPHLELSLGGGGACRRKIPLVHPVYY.....YNMATYPKMT	147
PhERF6	VDSSPLDLSLGGSNIGHNSVMFPLQNHQLRTFGPPTVNHMYYLEALARAGVINLEKNQPKKTVDFL	181
PhERF7	PACSSMSTLESSESGPRGAGSGHHKVVGATRLK.....IPRPVLIP	148
PhERF8	PTSSGMSSTVESFSGPRPPLLRQQTVP.....SRKYPRSPPVV	153
At1g28370	TCGVQSESETSSVVDFEGGAGKISPP.....LDLNLNLPPEAE	185
At1g50640	PEDCHSDCDSSSVIDDDDDIA.....SSRRRNPPFQFDLNFPLDCVDLFGADDLHCTDLRL	225
At1g53170	TCGVQSESETSSVVD..FEGGAGKISPP.....LDLNLNLPPEAE	185
PhERF6	GGTCGSESDSSVIDFNHVKPTIKGLN.....LDLNFPPENMM	220
PhERF7	TQDCRSDCDSSSVVDDRCDDVD....QTSSLMQKQPLPFDLNLPPPLSDDA...AADDLHV TALC	206
PhERF8	PDCRSDCDSSSVVVDGECGDGENDVIVSSFRKPLPFDLNLPPPEMDDVD....SDELRC TELC	215
	CMVIII-2	
	CMVIII-1 (EAR)	

Supplementary Fig. S1c: Amino acid sequence alignment of Group V ERFs that includes PhERF6, PhERF7, PhERF8, At1g28370/AtERF11, At1g50640 /AtERF3 and At1g53170/AtERF8 using DNAMAN program. Conserved residues are shaded in black. Grey shading indicates similar residues in five out of six of the sequences. The filled black bar below the sequences represents the CMVIII-1 (EAR) motif and the gray bar below the sequences represents the CMVIII-2 motif.