

Supplementary

Dehydration-Induced WRKY Transcriptional Factor *MfWRKY70* of *Myrothamnus flabellifolia* Enhanced Drought and Salinity Tolerance in *Arabidopsis*

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Table S1. List of primers used in this study

Usage	Primer names	Primer sequences (5' 3')
Clone	pGSA1403-WRKY70-F	CATG <u>CCATGG</u> AGTCACCTTGGTCGGA
	pGSA1403-WRKY70-R	<u>GACTAGTT</u> CAGAAAGTCGAAAATGACATCG
Subcellular location	pHB-WRKY70-YFP-F	<i>ACCAGTCTCTCTCTC</i> <u>CAAGCT</u> TATGGAGTCACCTTGGTCGGA
	pHB-WRKY70-YFP-R	<i>GCTCACCATACTAGT</i> <u>TGGATCC</u> GAAAGTCGAAAATGACATCG
qRT-PCR	AtActin2-F	GGAAGGATCTGTACGGTAAC
	AtActin2-R	TGTGAACGATTCCTGGACCT
	MfWRKY70-F	TCTCTTGAAAGCCCCTCAGA
	MfWRKY70-R	CGGTGTGATGAACGAATGAC
	AtNCED3-F	CGAGCCGTGGCCTAAAGTCT
	AtNCED3-R	GCTCCGATGAATGTACCGTGAA
	AtP5CS-F	GGTGGACCAAGGGCAAGTAAGATA
	AtP5CS-R	TCGGAAACCATCTGAGAATCTTGT
	AtRD29A-F	GATAACGTTGGAGGAAGAGTCGG
	AtRD29A-R	TCCTGATTCACCTGGAAATTTCG

¹ The restriction sites are under-lined and the homologous arm sequences are italicized. F and R represent the forward and reverse primers from 5' end to 3' end.

Table S2. The GenBank accession numbers and corresponding species of some highly humongous WRKYs used to construct phylogenetic tree in **Figure 1**

Genes	Accession numbers	species
PuWRKY70	QLB38140.1	<i>Populus ussuriensis</i>
PaWRKY7	XP_034913577.1	<i>Populus alba</i>
PtWRKY70	XP_002309186.3	<i>Populus trichocarpa</i>
HbWRKY70	XP_021684239.1	<i>Hevea brasiliensis</i>
MeWRKY70	XP_021619295.1	<i>Manihot esculenta</i>
JrWRKY70	XP_018814414.1	<i>Juglans regia</i>
HuWRKY70	XP_021290890.1	<i>Herania umbratica</i>
DzWRKY70	XP_022722727.1	<i>Durio zibethinus</i>
CmWRKY	ANA95961.1:20-328	<i>Citrus maxima</i>
CcWRKY70	XP_006429596.2	<i>Citrus clementina</i>
PIWRKY70	AMW90776.1	<i>Paeonia lactiflora</i>
PsWRKY	ALI57163.1	<i>Paeonia suffruticosa</i>
AcWRKY70	PSS34769.1	<i>Actinidia chinensis</i>
CsWRKY70	XP_006481203.1	<i>Citrus sinensis</i>
AtWRKY70	OAP01603.1	<i>Arabidopsis thaliana</i>

AtWRKY70	MDTNKAKKLVNMQLVEGHDLTTCLQCQLLSQFGS.....GLEDIVARIIVCFNNNTISVLDTFEPISSSSSLAPAVEGSQNASC	77
MfWRKY70	MESPWSENLSADRERATELVRGCEFTKQLRTLLDKEKGDHKAFSAGDLITRILRSFNESISILTYQSDEVSQIPADKDGQ.....	83
OsWRKY45	MTSSMSPAPAPAYACVMDMEKGELEAACLGGLLRDSPE.....AGRFVDCILHTFSRAMRALDKAAVSAPGGEGSEVCSSEVTCG.	80
AtWRKY70	DNDGRFEDSGDSRKRIGFVKGKRGCYHRRKRSETCT.IESTILEDAFSWRKYGQKEILNAKSPRSYFRCTHKYITGGCRATHQVQKVEL	164
MfWRKY70	KSEDSGESRKSSG.LKDRRGCYHRRRTTETWTFTVDTIIVDDGHAWRKYGQKVIINATHPRNYYRCTHKITDGGCCATHQVQRTDE	166
OsWRKY45	GGASAGGKRKAPAADRKANCRRPTQCSSGNSVVKNLDDGCQAWRKYGQKEIQNSKHFKAYFRCTHKYDQICLTAQRQVQRDD	162
AtWRKY70	EPK.MESITYIGNHTCNTNAETPKSKTCDDHDEIEMSEL.....HKSPSLSTSMKEEDNPHRHGSSSTENDISLVWPEMVFEEDYHH	246
MfWRKY70	IDKPTVYRTTYIGHHTCRTLKAP.QIILGAAAPNEANHSP.....SSSASIIINFGSNDRHNNHR.....ESFITPEVIKCED..S	240
OsWRKY45	DPA.SYRVVYIIGEHTCEDPATAPIIAAHVIFCVAAAGNDIGCGGLQAGSPLISFVAAPAEVDAAAAPTITSTITTVTAPGPLLQPLKV	249
AtWRKY70	QASVNGKTSTSIIVTGSQDLMVFGGGG.....FFHSENEHFSIFSSCSNLS.....	294
MfWRKY70	SSDYLFSPDLRPFGEHGDLDEVISGAHS.....SAESSRSFEMDMTCSDVEDD..VIFDF.....	294
OsWRKY45	EGGVGSSDQEEVLSSITPGSSAARGGGGGGVAGPFGPDQGVITSSILHWSYDAVAGMEFEKNDENVFDLDDINGLS	325

Figure S1. Sequence alignment of AtWRKY70, MfWRKY70, and OsWRKY45. Two key residues about salt bridges forming of OsWRKY45 are marked by squares, two serine residues conserved in the MfWRKY70 and OsWRKY45 marked by dots.