

Ectopic Expression of Kenaf (*Hibiscus cannabinus* L.) *HcWRKY50* improves plants tolerance to drought stress and regulates ABA signaling in *Arabidopsis*

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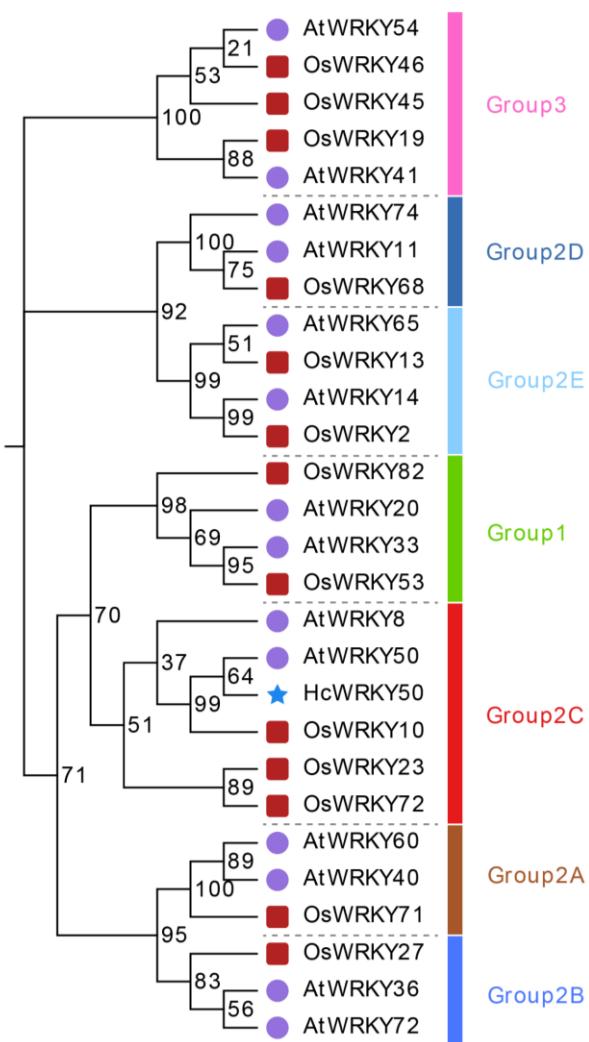
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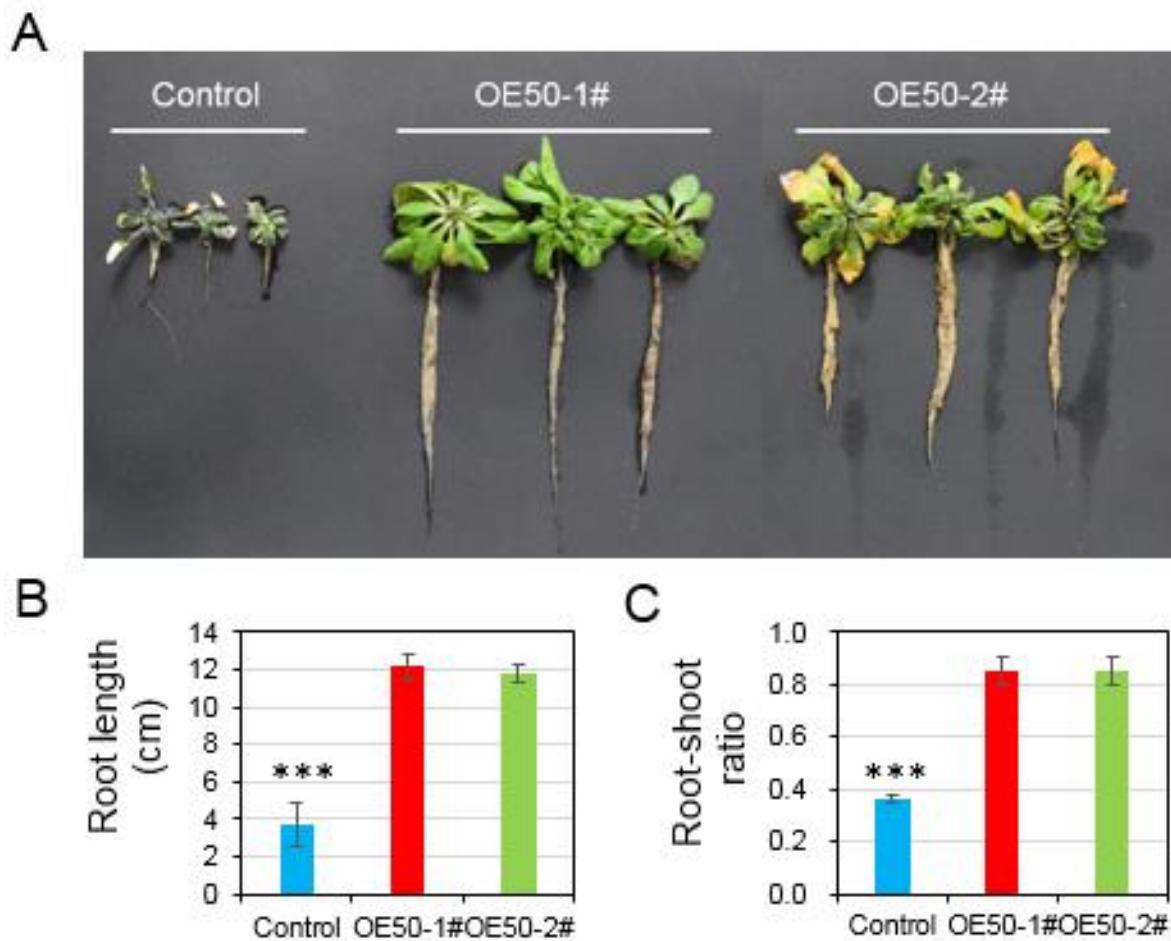
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Supplementary Figure S1. Phylogenetic analysis of different groups of WRKY proteins from different plants. The phylogenetic tree was generated by MEGA7.0. The amino acid sequences of WRKY proteins used for construction of the phylogenetic tree were following: AtWRKY54 (AEC09872), AtWRKY41 (NP_192845), AtWRKY74 (NP_198217), AtWRKY11 (NP_849559), AtWRKY65 (NP_174222), AtWRKY14 (NP_564359), AtWRKY20 (NP_567752), AtWRKY33 (NP_181381), AtWRKY8 (NP_199447), AtWRKY50 (NP_197989), AtWRKY60 (NP_180072), AtWRKY40 (NP_178199), AtWRKY36 (NP_564976), AtWRKY72 (NP_197017) from *Arabidopsis thaliana*; OsWRKY46 (DAA05111), OsWRKY45 (ACX37130), OsWRKY19 (DAA05084), OsWRKY68 (DAA05133), OsWRKY13 (DAA05078), OsWRKY2 (DAA05067), OsWRKY82 (ABC02814), OsWRKY53 (BAF75367), OsWRKY10 (DAA05075), OsWRKY23 (DAA05088), OsWRKY72 (DAA05137), OsWRKY71 (XP_015627417), OsWRKY27 (DAA05092) from *Oryza sativa*.



Supplementary Figure S2. Overexpression of *HcWRKY50* in *Arabidopsis* facilitated the root development and improved root-shoot ratio. (A) The roots and shoots phenotype of the 3-week-old WT and transgenic lines (OE50-1# and OE50-2#) grown without water for 2 weeks and re-watered for 5 days. (B and C) The root lengths and root-shoot ratio of the control line and OE50-1# and OE50-2# lines were measured after being re-watered for 5 days. All the values represent the means of three independent biological replicates; error bars indicate the SD. Significant differences represented by *** $P < 0.01$.



Supplementary Table S1. The primers used in this study.

Primer Name	Sequence (5'-3')	Description
HcWRKY50-F	CTCCACCGGTATCCATCATC	cDNA cloning
HcWRKY50-R	CATCTCAGGGCCAATTCACT	
W50sub-F	catgccccatggCTCCACCGGTATCCATCATC	subcellular localization
W50sub-R	cttcttagaCATCTCAGGGCCAATTCACT	
W50OE-F	gctctagaCTCCACCGGTATCCATCATC	overexpression vector construction
W50OE-R	gctcgagCATCTCAGGGCCAATTCACT	
RD29A-F	GGCGTAACAGGTAAACCTAGAG	qRT-PCR analysis
RD29A-R	TCCGATGTAAACGTCGTCC	
COR47A-F	GGAGTACAAGAACACGTTCCCGA	qRT-PCR analysis
COR47A-R	TGTCGTCGCTGGTGATTCTCT	
COR15A-F	GGCCACAAAGAAAGCTTCAG	qRT-PCR analysis
COR15A-R	CTTGTGTCGGCTTCTTTTC	
NCED3-F	CAGCTTAGCTTTGGGCTGTA	qRT-PCR analysis
NCED3-R	TAACAGAAACCAGCTGAGCTCGA	
KIN1-F	AACAAGAACGCCTCCAAGC	qRT-PCR analysis
KIN1-R	CGCATCCGATAACTCTTCC	
P5CS-F	GCGCATAGTTCTGATGCAA	qRT-PCR analysis
P5CS-R	TGCAACTTCGTGATCCTCTG	
ABI1-F	AGAGTGTGCCTTGTATGGTTTA	qRT-PCR analysis
ABI1-R	CATCCTCTCTACAATAGTCGCT	
ABI2-F	GATGGAAGATTCTGTCTAACGATT	qRT-PCR analysis
ABI2-R	GTTTCTCCTTCACTATCTCCCG	
ABF4-F	AACAACCTAGGAGGTGGGGTC	qRT-PCR analysis
ABF4-R	CTTCAGGAGTTCATCCATGTT	
RD29B-F	ACGCATAAAGGTGGAGAAC	qRT-PCR analysis
RD29B-R	TCTTGCCGGAGAATTCTTGT	
DREB2A-F	AAGGGTCGAAGAAGGGTTGT	qRT-PCR analysis
DREB2A-R	CGAGCCAAAGGACCACAT	
STZ-F	CTAGTAGCGTGTCCAACCTCG	qRT-PCR analysis
STZ-R	TTTGACCGGAAAGTCAAACCG	
ACTIN2-F	TCAGATGCCAGAAGTGTGTT	RT-PCR and qRT-PCR analysis
ACTIN2-R	CCGTACAGATCCTCCTGATAT	
TUB α -F	AATGCTTGCTGGGAGCTTA	qRT-PCR analysis
TUB α -R	GTGGAATAACTGGCGGTACG	