

Supplementary Material

Overexpression of forage millet (*Setaria italica*) *SiER* genes enhances drought resistance of *Arabidopsis thaliana*

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Supplementary Table S1 The URLs list of biological database

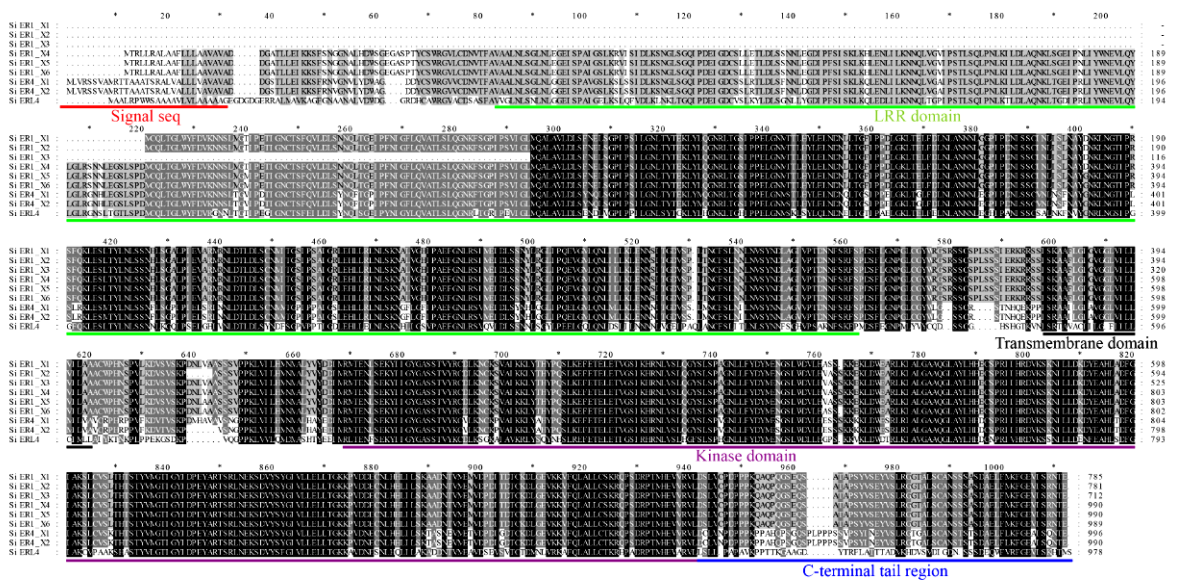
No.	Website	URLs of database
1	Phytozome v12.1	https://phytozome.jgi.doe.gov/pz/portal.html
2	NCBI	https://www.ncbi.nlm.nih.gov
3	SMART	http://smart.embl-heidelberg.de
4	GSDS2.0	http://gsds.gao-lab.org/

Supplementary Table S2 Primers sequence used in PCR reaction

Name	Sequences	Function	Annealing temperature (°C)	Restriction site
<i>SiER1_X4-F2</i>	CCTCCTCGCGAATGCCACTGCTGCC	Target gene cloning	60	—
<i>SiER1_X4-R2</i>	TCGCAGGCTGAACTCTTGAGACGATCG			—
<i>SiER4_X1-F3</i>	GGCAGGCTTGCTGCAGCACGCTTCG		64	—
<i>SiER4_X1-R3</i>	TTCACTATCTGCACCCTCCACCGCCGC			—
<i>SiER4_X1-1302F2</i>	<u>GGGACTCTTGA CCATGG</u> ATGCTTGTCCGCAGCTCAGTG	Vector construction	62	<i>Nco</i> I
<i>SiER4_X1-1302R2</i>	<u>TCAGATCTAC CCATGG</u> CTCCGTGTTCTGCGAGATGG			<i>Nco</i> I
<i>SiER1_X4-1302F2</i>	<u>GGGACTCTTGA CCATGG</u> ATGACCCGCCTCCTCCGGGC		64	<i>Nco</i> I
<i>SiER1-X4-1302R2</i>	<u>TCAGATCTAC CCATGG</u> TTCTGTGTTCCGTGATATCACCTCG			<i>Nco</i> I
<i>SiER1_X4-qRTF3</i>	CTATTGGCGTGTTCTCGTTCT	Target genes	58	—
<i>SiER1_X4-qRTR3</i>	CTTGGGAGGAACACTGCTTGAT			—
<i>SiER4_X1-qRTF3</i>	GGCTGCGATACTTGGCATTG		58	—
<i>SiER4_X1-qRTR3</i>	CCATTGCTCACTGGTTTGCTT			—
<i>SiActin-qRTF1</i>	TGGTATGGAGTCGCCTGGAATC	Reference gene	58	—
<i>SiActin-qRTR1</i>	GCCACCGCTGAGCACAATGTTA			—

Supplementary Table S3 NCBI accession numbers of proteins in phylogenetic tree

No.	ER family proteins	Plant Species	NCBI accession number
Class I			
1	<i>SiER4_X1</i>	<i>Setaria italica</i> L.	XP_004964941.1
2	<i>SiER4_X2</i>	<i>Setaria italica</i> L.	XP_004964942.1
3	<i>SbER10_X1</i>	<i>Sorghum bicolor</i> L.	XP_002438023.1
4	<i>ZmERECTA</i>	<i>Zea mays</i> L.	NP_001345763.1
5	<i>AetERECTA</i>	<i>Aegilops tauschii</i> subsp. <i>t.tauschii</i> L.	XP_020193416.1
6	<i>TaERECTA</i>	<i>Triticum aestivum</i> L.	AFJ38187.2
7	<i>HvERECTA</i>	<i>Hordeum vulgare</i> subsp. <i>vulgare</i> L.	AKU38976.1
8	<i>BdERECTA</i>	<i>Brachypodium distachyon</i> L.	XP_003564133.1
Class II			
9	<i>SiER1_X1</i>	<i>Setaria italica</i> L.	XP_014660111.1
10	<i>SiER1_X2</i>	<i>Setaria italica</i> L.	XP_014660109.1
11	<i>SiER1_X3</i>	<i>Setaria italica</i> L.	XP_014660108.1
12	<i>SiER1_X4</i>	<i>Setaria italica</i> L.	OP492075 (GenBank)
13	<i>SiER1_X5</i>	<i>Setaria italica</i> L.	XP_034576484.1
14	<i>SiER1_X6</i>	<i>Setaria italica</i> L.	XP_034576491.1
15	<i>OsERECTA</i>	<i>Oryza sativa Japonica Group</i> L.	XP_015623966.1
Group III			
	<i>GmERECTA</i>	<i>Glycine max</i> L.	XP_003544548.1
	<i>VvERECTA</i>	<i>Vitis vinifera</i> L.	XP_002280069.2
	<i>AtERECTA</i>	<i>Arabidopsis thaliana</i> L.	NP_180201.1
Group IV			
	<i>SiERL4</i>	<i>Setaria italica</i> L.	XP_004964421.1
	<i>AtERL_1</i>	<i>Arabidopsis thaliana</i> L.	NP_001190595.1
	<i>AtERL_2</i>	<i>Arabidopsis thaliana</i> L.	NP_001331523.1



Supplementary Fig. S1. Amino acid sequence alignment of millet SiER family

Different colored backgrounds were used to highlight identical amino acid sequences and similar amino acid sequences, and colored underscores were used to represent different domains: N-terminal signal sequence was red, LRR domain was green, transmembrane domain was black, kinase domain was purple, and C-terminal tail sequence was blue.