

## Supplementary Materials

### Identification and expression characterisation of *SbERECTA* family genes in *Sorghum bicolor*

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**Table S1. The URLs list of biological database**

No.	Website	URLs of database
1	Phytozome v12.1	<a href="https://phytozome.jgi.doe.gov/pz/portal.html">https://phytozome.jgi.doe.gov/pz/portal.html</a>
2	NCBI	<a href="https://www.ncbi.nlm.nih.gov">https://www.ncbi.nlm.nih.gov</a>
3	PROSITE	<a href="https://prosite.expasy.org">https://prosite.expasy.org</a>
4	GSDS	<a href="http://gsds.cbi.pku.edu.cn">http://gsds.cbi.pku.edu.cn</a>
5	Plant-mPLoc	<a href="http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/">http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/</a>
6	PlantCARE	<a href="http://bioinformatics.psb.ugent.be/webtools/plantcare/html/">http://bioinformatics.psb.ugent.be/webtools/plantcare/html/</a>
7	SMART	<a href="http://smart.embl-heidelberg.de">http://smart.embl-heidelberg.de</a>

**Table S2. The sequence of primers related to PCR amplification**

Name	Pair of forward and reverse primers (5'-3')	Tm	Size	Restriction Enzyme	Note
<i>SbER10_X1-2F</i>	GCGAGAACCCACGAAACC AACC	64°C	3376 bp	—	<i>SbER10_X1</i> gene isolation
<i>SbER10_X1-2R</i>	CCCATG ATTCCAACACGGCAAA				
<i>GFP-SbER10_X1-F1</i>	<u>GGGGACGAGCTC</u> <b>GGTACC</b> ATGCCTGTCCGCAGCTCA	62°C	2982 bp	<i>Kpn</i> I <i>Xba</i> I	Subcellular localization
<i>GFP-SbER10-X1-R1</i>	CATGGTGTG <b>CGACTCTAGACT</b> CCATGTTCTGCGAGATGGC				
<i>SbER10-KF</i>	<u>CGGGATCC</u> CCTTCATATGAACATGGCCC	61°C	965 bp	<i>Bam</i> HI <i>Hind</i> III	Prokaryotic expression
<i>SbER10-KR</i>	<u>CCCAAGCTT</u> TTTGATGTAGCTTGGCACGGC				
<i>SbER10-2QF</i>	GCCAGCCGTGCCAAGCTACATC	62°C	179 bp	—	qRT-PCR
<i>SbER10-2QR</i>	CTCCCTGCATCCTTCAACTCCC				
<i>SbActin-F</i>	ACGGCCTGGAT GCGACGTACATG	62°C	185 bp	—	
<i>SbActin-R</i>	GCAGAAGGACGCCTACGTTGGTGAC				

**Table S3. Name and sources of 32 sweet sorghum collection**

Code	No. of national genebank	Origin (province)
<u>1</u>	357	Hei long jiang
<u>2</u>	360	Hei long jiang
<u>3</u>	2349	Shan xi
<u>4</u>	2350	Shan xi
<u>5</u>	7322	Nei meng gu
<u>6</u>	7323	Nei meng gu
<u>7</u>	7324	Liao ning
<u>8</u>	7325	Liao ning
<u>9</u>	7329	Hei long jiang
<u>10</u>	7342	An hui
<u>11</u>	7343	An hui
<u>12</u>	7357	Hu bei
<u>13</u>	7358	Hu bei
<u>14</u>	10246	Ji lin
<u>15</u>	10264	Shaan xi
<u>16</u>	10265	Shaan xi
17	10288	Yun nan
18	10289	Yun nan
19	12484	Bei jing
20	12520	Bei jing
21	12630	Bei jing
22	13241	Si chuan
23	13242	Si chuan
24	13361	Gui zhou

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Code	No. of national genebank	Origin (province)
25	13428	Hu bei
26	13443	Hu bei
27	13543	Hai nan
28	13812	Guangxi
29	13854	Gui zhou
30	14181	He nan
31	M81	American
32	Yuexitian	An hui

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**Table S4. NCBI accession numbers of proteins in phylogenetic tree**

Code	ER family proteins	Plant Species	NCBI accession number	Classification
Group I				
1	SbER10_X1	<i>Sorghum bicolor</i> L.	XP_002438023.1	monocots
2	SbER10_X2	<i>Sorghum bicolor</i> L.	XP_021304405.1	monocots
3	SbER10_X3	<i>Sorghum bicolor</i> L.	XP_021304406.1	monocots
4	SbER4_X1	<i>Sorghum bicolor</i> L.	XP_021314268.1	monocots
5	SbER4_X2	<i>Sorghum bicolor</i> L.	XP_021314269.1	monocots
6	ZmERECTA_1	<i>Zea mays</i> L.	AQK83004.1	monocots
7	ZmERECTA_2	<i>Zea mays</i> L.	AQK83013.1	monocots
8	ZmERECTA_3	<i>Zea mays</i> L.	AQK83012.1	monocots
9	<i>PamERECTA_X2</i>	<i>Panicum miliaceum</i> L.	RLN13615.1	monocots
10	SiERECTA_X2	<i>Setaria italica</i> L.	XP_004964942.1	monocots
11	SiERECTA_X1	<i>Setaria italica</i> L.	XP_004964941.1	monocots
12	OtERECTA	<i>Oropetium thomaeum</i> L.	AYU56584.1	monocots
13	BdERECTA_X1	<i>Brachypodium distachyon</i> L.	XP_003564133.1	monocots
14	BdERECTA_X2	<i>Brachypodium distachyon</i> L.	XP_010227884.1	monocots
15	HvERECTA	<i>Hordeum vulgare subsp. vulgare</i> L.	AKU38976.1	monocots
20	HvERL_1	<i>Hordeum vulgare</i> L.	KAE8808234.1	monocots
17	AetERECTA_X1	<i>Aegilops tauschii subsp. t.tauschii</i> L.	XP_020193416.1	monocots
19	AetERECTA_X2	<i>Aegilops tauschii subsp. tauschii</i> L.	XP_020193417.1	monocots
16	TaERECTA_2	<i>Triticum aestivum</i> L.	AFJ38187.2	monocots
18	TaERECTA_1	<i>Triticum aestivum</i> L.	AFJ38186.2	monocots
21	ObERECTA_X1	<i>Oryza brachyantha</i> L.	XP_006649092.1	monocots
22	ObERECTA_X2	<i>Oryza brachyantha</i> L.	XP_015689543.1	monocots
23	OsERECTA_X1	<i>Oryza sativa Japonica Group</i> L.	XP_015623966.1	monocots

Code	ER family proteins	Plant Species	NCBI accession number	Classification
24	<i>OsERL</i>	<i>Oryza sativa Japonica Group</i> L.	AFJ14786.1	monocots
25	OsERECTA_X2	<i>Oryza sativa Japonica Group</i>	XP_015623967.1	monocots
Group II				
26	AcERECTA_X2	<i>Ananas comosus</i> L.	XP_020081626.1	monocots
27	AcERECTA_X1	<i>Ananas comosus</i> L.	XP_020081619.1	monocots
28	PeERECTA	<i>Phalaenopsis equestris</i> L.	XP_020588182.1	monocots
29	EgERECTA	<i>Elaeis guineensis</i> L.	XP_010917192.1	monocots
30	MaERECTA_X2	<i>Musa acuminata subsp. malaccensis</i> L.	XP_018684789.1	monocots
31	MaERECTA_X4	<i>Musa acuminata subsp. malaccensis</i> L.	XP_009408412.1	monocots
32	MaERECTA_X3	<i>Musa acuminata subsp. malaccensis</i> L.	XP_018684790.1	monocots
33	MaERECTA_X1	<i>Musa acuminata subsp. malaccensis</i> L.	XP_018684788.1	monocots
Group III				
34	SeiERECTA	<i>Sesamum indicum</i> L.	XP_011069519.1	dicots
35	PoERECTA1	<i>Populus trichocarpa</i> L.	XP_024458576.1	dicots
36	PoERECTA2	<i>Populus euphratica</i> L.	XP_011019342.1	dicots
38	GmERECTA2	<i>Glycine max</i> L.	XP_014632764.1	dicots
39	GmERECTA_X1	<i>Glycine max</i> L.	XP_006578096	dicots
40	GmERECTA1	<i>Glycine max</i> L.	XP_003544548.1	dicots
41	PaERECTA_X2	<i>Prunus avium</i> L.	XP_021805236.1	dicots
42	PaERECTA_X1	<i>Prunus avium</i> L.	XP_021805235.1	dicots
43	PmERECTA	<i>Prunus mume</i> L.	XP_008220576.1	dicots
44	VvERECTA1	<i>Vitis vinifera</i> L.	XP_002280069.2	dicots
45	VvERECTA2	<i>Vitis vinifera</i> L.	RVX17310.1	dicots
46	TcERECTA1	<i>Theobroma cacao</i> L.	XP_017983493.1	dicots
47	TcERECTA2	<i>Theobroma cacao</i> L.	EOY30050.1	dicots
48	DzERECTA	<i>Durio zibethinus</i> L.	XP_022754146.1	dicots

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Code	ER family proteins	Plant Species	NCBI accession number	Classification
49	CsERECTA	<i>Citrus sinensis</i> L.	XP_006474503.1	dicots
50	JcERECTA	<i>Jatropha curcas</i> L.	XP_012077188.1	dicots
51	MeERECTA	<i>Manihot esculenta</i> L.	XP_021598132.1	dicots
52	HbERECTA	<i>Hevea brasiliensis</i> L.	XP_021676852.1	dicots
37	AtERECTA	<i>Arabidopsis thaliana</i> L.	NP_180201.1	dicots
Group IV				
53	AtERL_1	<i>Arabidopsis thaliana</i> L.	NP_001190595.1	dicots
54	AtERL_2	<i>Arabidopsis thaliana</i> L.	NP_001331523.1	dicots

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**Table S5. NCBI accession numbers of *ER* genes in phylogenetic tree**

No.	ER family genes	Plant species	NCBI accession number	Classification
Group I				
1	<i>AetERECTA</i>	<i>Aegilops tauschii subsp. tauschii</i> L.	XM_020337827.1	monocots
2	<i>TaERECTA</i>	<i>Triticum aestivum</i> L.	JQ599261.2	monocots
3	<i>HvERECTA</i>	<i>Hordeum vulgare subsp. vulgare</i> L.	KP284445.1	monocots
4	<i>BdERECTA</i>	<i>Brachypodium distachyon</i> L.	XM_003564085.4	monocots
5	<i>SiERECTA</i>	<i>Setaria italica</i> L.	XM_004964885.3	monocots
6	<i>SbERI_XI</i>	<i>Sorghum bicolor</i> L.	XM_002437978.2	monocots
7	<i>ZmERECTA</i>	<i>Zea mays</i> L.	NM_001358834.1	monocots
8	<i>OsERECTA</i>	<i>Oryza sativa Japonica Group</i> L.	XM_015768480.2	monocots
Group II				
9	<i>NtERECTA</i>	<i>Nicotiana tabacum</i> L.	XM_016632277.1	dicots
10	<i>AtERECTA</i>	<i>Arabidopsis thaliana</i> L.	NM_128190.3	dicots
11	<i>GmERECTA</i>	<i>Glycine max</i> L.	XM_003544500.4	dicots
12	<i>PoERECTA</i>	<i>Populus trichocarpa</i> L.	XM_024602808.1	dicots
13	<i>VvERECTA</i>	<i>Vitis vinifera</i> L.	XM_002280033.3	dicots
Group III				
14	<i>AtERL_1</i>	<i>Arabidopsis thaliana</i> L.	NM_001203666.1	dicots
15	<i>AtERL_2</i>	<i>Arabidopsis thaliana</i> L.	NM_001342930.1	dicots

**Fig. S1.** The putative protein transcripts of SbER10\_X1 subcellular localization.

*DNAMAN File: DNAMAN1\_Translation*

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**SbER10\_X1** (subcellular localization)

Total amino acid number: 981, MW=107187  
Max ORF starts at AA pos 1(may be DNA pos 1) for 981 AA(2943 bases), MW=107187

1	ATGCCTGTCCGCGAGCTCAGTGGCCATGACGACGACGGCCCGCCGCTCTCGTCGCCCTC	10	20	30	40	50	60
1	M P V R S S V A M T T T A A R A L V A L						
61	CTCCTCGTCGCGCTCGCCGTCGCCGACGATGGGGCGACGCTGGTGGAGATCAAGAAAGTCC	70	80	90	100	110	120
21	L L V A V A V A D D G A T L V E I K K S						
121	TTCCGCAACGTCGGCAACGTACTGTACGATTGGGCCGGCGACACTACTGCTCCTGGCGC	130	140	150	160	170	180
41	F R N V G N V L Y D W A G D D Y C S W R						
181	GGCGTCTGTGCGACAACGTACATTCGCGTCGCTGGCGCTCAACCTCTCTGGCCTCAAC	190	200	210	220	230	240
61	G V L C D N V T F A V A A L N L S G L N						
241	CTTGAGGGCGAGATCTCTCCAGCCGTCGGCAGCCTCAAGAGCCTCGTCTCCATCGATCTG	250	260	270	280	290	300
81	L E G E I S P A V G S L K S L V S I D L						
301	AAGTCAAATGGGCTATCCGGCAGATCCCTGATGAGATTGGTGATTGTTCACTACTTAGG	310	320	330	340	350	360
101	K S N G L S G Q I P D E I G D C S S L R						
361	ACGCTGGACTTTTCTTCAACAACCTGGATGGCGACATACCATTTTCTATATCAAAGCTG	370	380	390	400	410	420
121	T L D F S F N N L D G D I P F S I S K L						
421	AAGCACCTGGAGAACCTGATATTGAAGAACAACCAGCTGATGGTGGATCCCATCAACA	430	440	450	460	470	480
141	K H L E N L I L K N N Q L I G A I P S T						
481	TTGTCAGAGTCCCAAATTTGAAGATTTGGATTTGGCACAAAACAACTGACTGGGGAG	490	500	510	520	530	540
161	L S Q L P N L K I L D L A Q N K L T G E						
541	ATACCAAGGCTTATCTACTGGAATGAGGTTCTTCAATATCTGGGCTTACGGGGCAATCAT	550	560	570	580	590	600
181	I P R L I Y W N E V L Q Y L G L R G N H						
601	TTAGAAGGAAGCCTCTCTCTGATATGTGCCAGCTGACTGGCCTTGGTACTTTGATGTG	610	620	630	640	650	660
201	L E G S L S P D M C Q L T G L W Y F D V						
661	AAGAACAATAGCTTGACCGGGGTGATACCAGACACCATTGGGAACGTACAAGTTTCAA	670	680	690	700	710	720
221	K N N S L T G V I P D T I G N C T S F Q						
721	GTCTTGGATTGTCTTACAACCGCTTACTGGACCAATCCCATCAACATTGGTTTCCTA	730	740	750	760	770	780
241	V L D L S Y N R F T G P I P F N I G F L						
781	CAAGTGGCTACACTATCCTTGCAAGGGAACAAGTTCACCGGTCCAATTCCTTCAAGTAA	790	800	810	820	830	840
261	Q V A T L S L Q G N K F T G P I P S V I						
841	GGTCTTATGCAGGCTCTCGCTGTTCTAGATCTGAGTTACAACCAATTATCTGGTCCTATA	850	860	870	880	890	900
281	G L M Q A L A V L D L S Y N Q L S G P I						
901	CCATCAATACTAGGCAACTTGACATACACTGAGAAGCTGTACATCCAAGGCAATAAGTTA	910	920	930	940	950	960
301	P S I L G N L T Y T E K L Y I Q G N K L						
961	ACTGGTTCGATACCACCAGAGTTAGGAAATATGTCAACACTTCATTACCTAGAACTGAAC	970	980	990	1000	1010	1020
321	T G S I P P E L G N M S T L H Y L E L N						
1021	GATAATCAACTTACTGGGTCAATTCACCAGAGCTTGAAGGCTAACAGGCTTGTGTTGAC	1030	1040	1050	1060	1070	1080

DNAMAN File: DNAMAN1\_Translation

341 D N Q L T G S I P P E L G R L T G L F D

1090 1100 1110 1120 1130 1140  
1081 CTGAACCTTGC GAATAAACCACCTGGAAGGACCAATTCCTGACAACCTAAGTTCATGTGTG  
361 L N L A N N H L E G P I P D N L S S C V

1150 1160 1170 1180 1190 1200  
1141 AATCTCAATAGCTTCAATGCTTATGGCAACAAGTTAAATGGGACCATTCCCTCGTTTCGTTG  
381 N L N S F N A Y G N K L N G T I P R S L

1210 1220 1230 1240 1250 1260  
1201 CGGAAACTTGAAAGCATGACCTATTTAAATCTGTGCATCAAACCTCATAAGTGGCTCTATT  
401 R K L E S M T Y L N L S S N F I S G S I

1270 1280 1290 1300 1310 1320  
1261 CCTATTGAGTTATCAAGGATCAACAATTTGGACACGCTGGATTATCCTGTAACATGATG  
421 P I E L S R I N N L D T L D L S C N M M

1330 1340 1350 1360 1370 1380  
1321 ACTGGTCCAATTCATCATCAATGGCAGCCTAGAGCATCTATTGAGACTTAACTTGAGC  
441 T G P I P S S I G S L E H L L R L N L S

1390 1400 1410 1420 1430 1440  
1381 AAGAATGGTCTAGTTGGATTTCATCCCGCGGAGTTTGGTAATTTGAGGAGTGTGATGGAG  
461 K N G L V G F I P A E F G N L R S V M E

1450 1460 1470 1480 1490 1500  
1441 ATTGATTTATCCTATAATCACCTTGGTGGCCTGATTCCTCAAGAACTTGAATGCTGCAA  
481 I D L S Y N H L G G L I P Q E L E M L Q

1510 1520 1530 1540 1550 1560  
1501 AACCTGATGTTGCTAAAACCTGAAAAATAACAATATAACTGGTGATCTGTCGCTCTGATG  
501 N L M L L K L E N N N I T G D L S S L M

1570 1580 1590 1600 1610 1620  
1561 AACTGCTTCAGCCTCAATATCTTAAATGTGTCGTACAATAATTTGGTGGTGTGTCCTC  
521 N C F S L N I L N V S Y N N L A G V V P

1630 1640 1650 1660 1670 1680  
1621 GCTGACAACAACCTCACAGGTTTTACCTGACAGCTTTTTAGGTAATCCTGGACTCTGT  
541 A D N N F T R F S P D S F L G N P G L C

1690 1700 1710 1720 1730 1740  
1681 GGATACTGGCTTGGTTCGTGTCGTTCCACTGGCCACCAGAGAACCAGCCTATCTCA  
561 G Y W L G S S C R S T G H H E K P P I S

1750 1760 1770 1780 1790 1800  
1741 AAGGCTGCCATAATGGTGTGCTGTGGTGGACTTGTATCCTCTGATGATCTTAGTA  
581 K A A I I G V A V G G L V I L L M I L V

1810 1820 1830 1840 1850 1860  
1801 GCTGTTTGCAGGCCACATCGTCCACCTGCTTTTAAAGATGTCACTGTAAGCAAGCCAGTG  
601 A V C R P H R P P A F K D V T V S K P V

1870 1880 1890 1900 1910 1920  
1861 AGAAATGCTCCCCCAAGCTGGTGATCCTTCATATGAACATGGCCCTTCATGTATACGAT  
621 R N A P P K L V I L H M N M A L H V Y D

1930 1940 1950 1960 1970 1980  
1921 GACATAATGAGGATGACTGAGAAGTTGAGTGAGAAATACATCATTGGATACGGGGCGTCA  
641 D I M R M T E N L S E K Y I I G Y G A S

1990 2000 2010 2020 2030 2040  
1981 AGTACAGTTTATAAATGTCTCCTAAAGAATTGCAAACCGGTGGCAATAAAAAAGCTGTAT  
661 S T V Y K C V L K N C K P V A I K K L Y

2050 2060 2070 2080 2090 2100  
2041 GCCCACTACCCACAGAGCCTTAAGGAATTTGAAACTGAGCTTGAGACTGTTGGTAGCATC  
681 A H Y P Q S L K E F E T E L E T V G S I

2110 2120 2130 2140 2150 2160  
2101 AAGCACCAGGAACTAGTCAGCCTTCAAGGTAAGTACTATTATCACCTGTTGGGAACCTCCTC  
701 K H R N L V S L Q G Y S L S P V G N L L

DNAMAN File: DNAMAN1\_Translation

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2161      2170      2180      2190      2200      2210      2220
721      TTTTATGATTATATGGAATGTGGCAGCTTATGGGATGTTTTACATGAAGGTTTCATCCAAG
      F Y D Y M E C G S L W D V L H E G S S K

2221      2230      2240      2250      2260      2270      2280
741      AAGAAAAAAGTTGACTGGGAGACTCGCCTACGGATTGCTCTTGGTGCAGCTCAAGGCCTT
      K K K L D W E T R L R I A L G A A Q G L

2281      2290      2300      2310      2320      2330      2340
761      GCTTACCTTACCATGACTGCAGTCCACGGATAATTCATCGGGATGTAAAATCAAAGAAT
      A Y L H H D C S P R I I H R D V K S K N

2341      2350      2360      2370      2380      2390      2400
781      ATACTCCTTGACAAAAGATTATGAGGCCATCTTACAGACTTTGGAATTGCTAAGAGCTTA
      I L L D K D Y E A H L T D F G I A K S L

2401      2410      2420      2430      2440      2450      2460
801      TGTGTCTCAAAAAGTCAACATCAACCTATGTCATGGGAAGTATTGGCTACATTGATCCT
      C V S K T H T S T Y V M G T I G Y I D P

2461      2470      2480      2490      2500      2510      2520
821      GAGTAGCCCGCACTTCCCGTCTCAACGAAAAGTCTGATGTCTACAGCTATGGCATTGTT
      E Y A R T S R L N E K S D V Y S Y G I V

2521      2530      2540      2550      2560      2570      2580
841      CTGCTGGAGCTGCTGACTGGCAAGAAGCCAGTGGCAACGAGTGCATCTCCATCACTTG
      L L E L L T G K K P V D N E C N L H H L

2581      2590      2600      2610      2620      2630      2640
861      ATCCTATCGAAGACGGCAAGCAACGAGGTCATGGATACCGTGGACCTGACATCGGGGAC
      I L S K T A S N E V M D T V D P D I G D

2641      2650      2660      2670      2680      2690      2700
881      ACCTGCAAGGACCTCGGCGAGGTGAAGAAGCTGTTCCAGCTGGCGCTCCTTTGCACCAAG
      T C K D L G E V K K L F Q L A L L C T K

2701      2710      2720      2730      2740      2750      2760
901      CGGCAACCCCTCGGACCGACCGACGATGCACGAGGTGGTGC GCGCTCCTGGACTGCCTGGT
      R Q P S D R P T M H E V V R V L D C L V

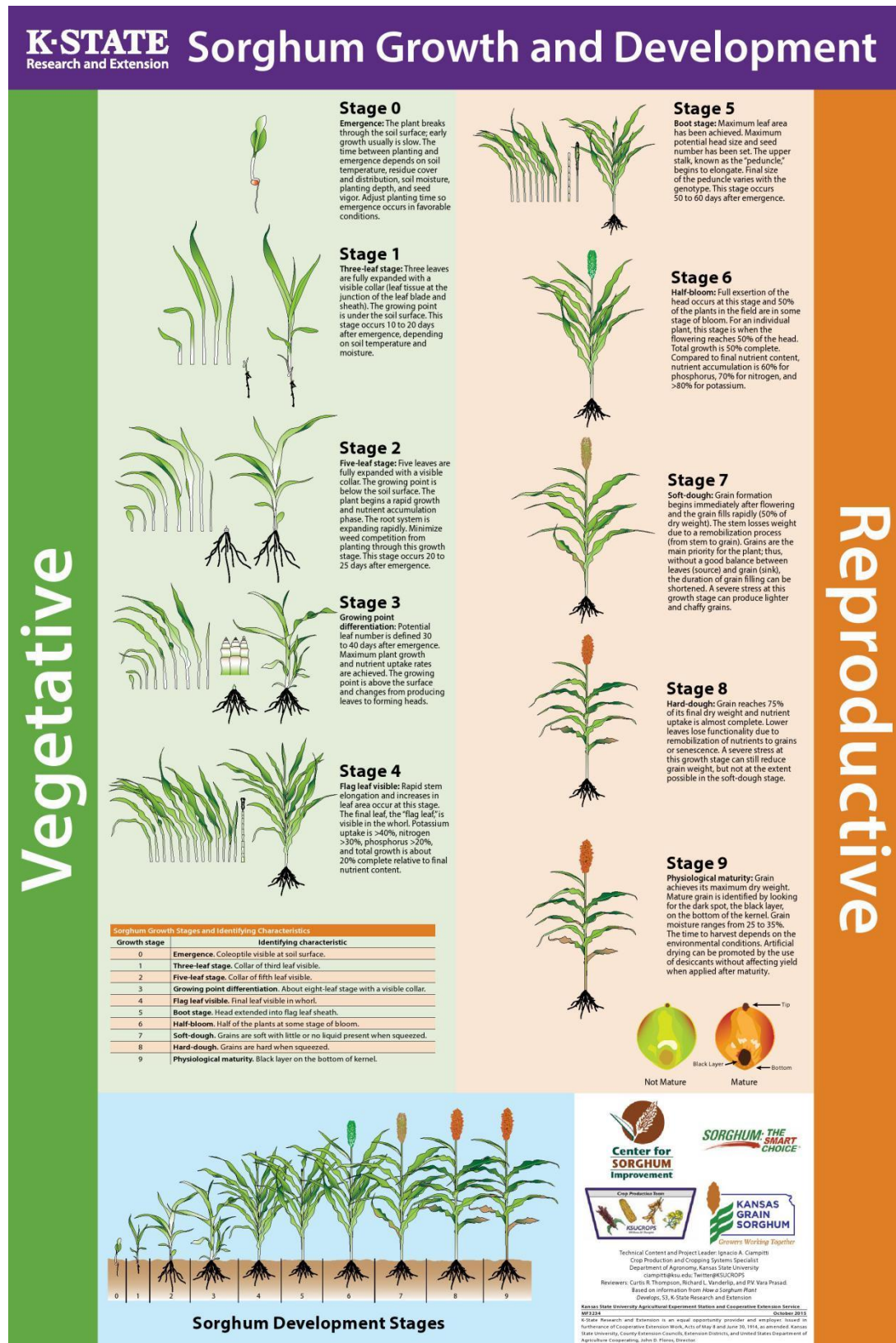
2761      2770      2780      2790      2800      2810      2820
921      AACCCGGACCCCGCCAAAGCCGTCGGCGCACCAAGCTGCGCGAGCCGTCGCCAGCCGTC
      N P D P P P K P S A H Q L P Q P S P A V

2821      2830      2840      2850      2860      2870      2880
941      CCAAGCTACATCAACGAGTACGTCAGCCTGCGGGGCACCGCGCTCTCTCCTGCGCCAAC
      P S Y I N E Y V S L R G T G A L S C A N

2881      2890      2900      2910      2920      2930      2940
961      TCGACCAGCACCTCGGACGCCGAGCTGTTCCCTCAAGTTCGGCGAGGCCATCTCGCAGAAC
      S T S T S D A E L F L K F G E A I S Q N

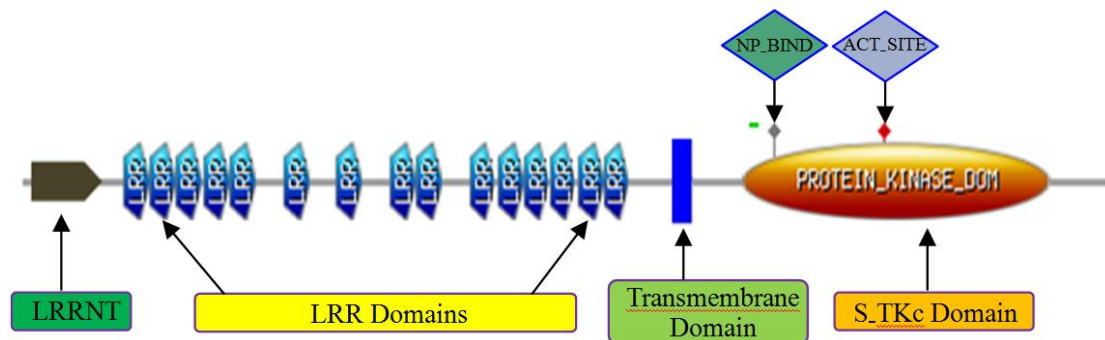
2941      ATGGAG
981      M E
```

Fig. S2. The growth and development stages of sorghum.



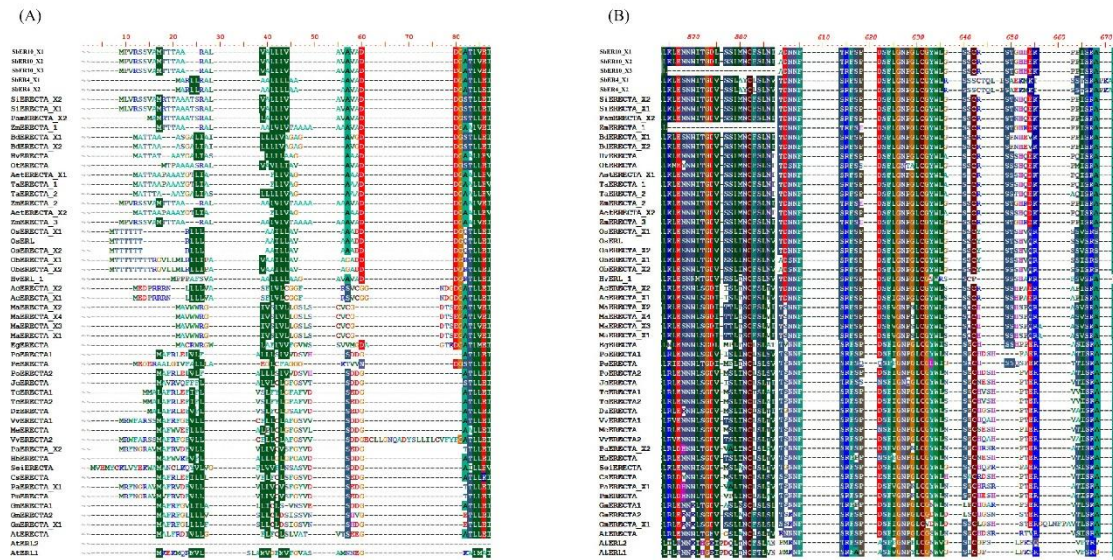


**Fig. S3.** Analysis of conserved domains of SbER family.



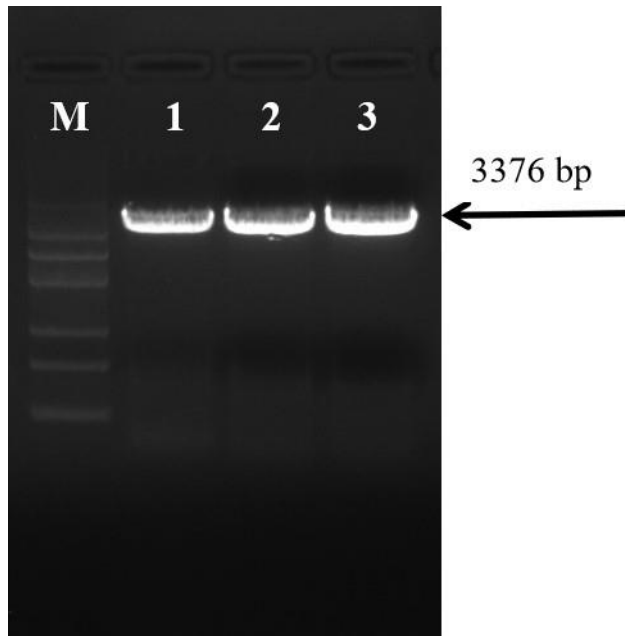
LRRNT was the N-terminal signal peptide region, LRR Domain was the leucine repeat region, S\_TKc was the Serine/threonine protein kinase region, catalytic region, NP\_BIND was the ATP binding site (rich in lysine residues), ACT\_SITE was the proton accepting site (rich in aspartic acid residues).

**Fig. S4.** Amino acid sequence alignment of ER family members in monocotyledonous and dicotyledonous plants.



(A) was the N-terminal signal peptide region; (B) was the transmembrane region.

Fig. S5. *SbER10\_XI* gene isolation.



M was the Maker III (Tian gen, China), lane 1, 2 and 3 were the fragment of *SbER10\_XI* gene