

核定位 SiHSP20 协调细胞器保护增强谷子耐盐性

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Nuclear-localized *SiHSP20* Coordinates Organelle Protection to Enhance Salt Tolerance in Foxtail Millet

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Table S1 Raw data statistics table						
Sample_ID	Total_Reads	Total_Bases	Error%	Q20%	Q30%	GC%
CK-1	59498592	8924788800	0.0256	98.03	93.24	54.58
CK-2	56374526	8456178900	0.0257	97.99	93.23	54.96
CK-3	60914390	9137158500	0.0254	98.12	93.5	54.19
N100-1	54564962	8184744300	0.0254	98.1	93.51	55.11
N100-2	56190328	8428549200	0.0256	97.98	93.38	56.48
N100-3	56355264	8453289600	0.0255	98.03	93.41	55.79
N200-1	66410834	9961625100	0.0254	98.12	93.46	54.47
N200-2	55951382	8392707300	0.0254	98.09	93.48	54.57
N200-3	63074526	9461178900	0.0248	98.42	93.98	57.87

Table S2 Clean data statistical table						
Sample_ID	Total_Reads	Total_Bases	Error%	Q20%	Q30%	GC%
CK-1	59455874	8785997909	0.0253	98.18	93.47	54.64
CK-2	56328864	8307118841	0.0253	98.16	93.48	55.04
CK-3	60877522	8874628085	0.025	98.28	93.81	54.31
N100-1	54522672	7979692566	0.025	98.29	93.81	55.21
N100-2	56129966	8297897955	0.0252	98.17	93.64	56.58
N100-3	56304982	8375330734	0.0252	98.18	93.61	55.84
N200-1	66352716	9825993797	0.0251	98.28	93.67	54.53
N200-2	55896380	8211057221	0.0251	98.27	93.76	54.64
N200-3	63052308	9375279125	0.0247	98.5	94.1	57.94

Table S3 Sequencing data statistics

sample	Raw reads	Raw bases	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)	rRNA Ratio(%)
CK-1	5949859 2	892478880 0	5945587 4	878599790 9	0.0253	98.18	93.47	54.64	7.31
CK2	5637452 6	845617890 0	5632886 4	830711884 1	0.0253	98.16	93.48	55.04	12.96
CK-3	6091439 0	913715850 0	6087752 2	887462808 5	0.025	98.28	93.81	54.31	22.47
N100-1	5456496 2	818474430 0	5452267 2	797969256 6	0.025	98.29	93.81	55.21	6.72
N100-2	5619032 8	842854920 0	5612996 6	829789795 5	0.0252	98.17	93.64	56.58	31.41
N100-3	5635526 4	845328960 0	5630498 2	837533073 4	0.0252	98.18	93.61	55.84	12.62
N200-1	6641083 4	996162510 0	6635271 6	982599379 7	0.0251	98.28	93.67	54.53	23.79
N200-2	5595138 2	839270730 0	5589638 0	821105722 1	0.0251	98.27	93.76	54.64	12.35
N200-3	6307452 6	946117890 0	6305230 8	937527912 5	0.0247	98.5	94.1	57.94	4.66

Table S4 Percentage distribution information of different samples in various regions of the genome

sample_id	Coding	UTR	Intron	Intergenic
CK-1	71.6449	18.2067	2.2063	7.9421
CK2	67.7841	20.3064	2.1124	9.7971
CK-3	65.793	18.8019	3.395	12.0101
N100-1	69.1748	21.0018	1.689	8.1343
N100-2	58.4874	27.5102	1.6945	12.3078
N100-3	68.3371	20.4715	1.7851	9.4063
N200-1	62.4383	22.9305	2.1325	12.4988
N200-2	64.4564	23.3621	1.9264	10.2551
N200-3	68.7709	20.9475	1.7171	8.5645

Table S5 Overview of database annotations

Type	Gene	Transcript
GO	19146	22956
KEGG	10134	12592
NR	31852	36967
PFAM	23586	27810
STRING	187	271
SWISSPROT	19496	23376

Table S6 Significantly different gene GO features in N100_vs_CK comparisons.

GO term	Num of up gene	Num of down gene
biological regulation	197	89
cell killing	3	0
cell population proliferation	2	0
cellular component organization	53	68
or biogenesis		
cellular process	372	297
detoxification	11	1
developmental process	76	40
growth	15	5
immune system process	19	1
localization	86	58
locomotion	1	0
metabolic process	385	266
multi-organism process	74	11
multicellular organismal process	69	37
reproduction	36	27
reproductive process	35	27
response to stimulus	274	96
rhythmic process	2	7
signaling	83	16
carbon utilization	0	1
cell	499	378
cell junction	24	10
cell part	492	378
extracellular region	81	13
extracellular region part	14	3
membrane	288	171
membrane part	246	132
membrane-enclosed lumen	19	20
organelle	295	339
organelle part	101	231
protein-containing complex	20	105
supramolecular complex	1	9
symplast	24	10
nucleoid	0	6
antioxidant activity	16	6
binding	438	252
catalytic activity	423	234
molecular carrier activity	1	0
molecular function regulator	8	3
molecular transducer activity	14	2
nutrient reservoir activity	15	1
protein folding chaperone	1	3
protein tag	2	0
small molecule sensor activity	1	0
structural molecule activity	6	15
transcription regulator activity	72	17

translation regulator activity	4	7
transporter activity	61	36

Table S7 Significantly different gene GO features in N200_vs_CK comparisons.

GO term	Num of up gene	Num of down gene
behavior	1	0
biological regulation	333	619
carbon utilization	1	1
cell killing	5	1
cell population proliferation	2	4
cellular component organization or biogenesis	118	415
cellular process	742	1682
detoxification	15	4
developmental process	131	285
growth	25	46
immune system process	21	36
localization	179	248
locomotion	2	1
metabolic process	741	1501
multi-organism process	114	142
multicellular organismal process	132	252
reproduction	71	143
reproductive process	71	142
response to stimulus	466	679
rhythmic process	7	28
signaling	115	178
biological adhesion	0	3
cell	1005	1990
cell junction	34	102
cell part	1002	1983
extracellular region	109	242
extracellular region part	20	16
membrane	527	860
membrane part	434	635
membrane-enclosed lumen	55	109
organelle	664	1565
organelle part	289	815
protein-containing complex	74	386
supramolecular complex	4	80
symplast	34	102
nucleoid	0	17
antioxidant activity	25	49
binding	794	1443
catalytic activity	783	1387
molecular carrier activity	4	3
molecular function regulator	22	32

molecular transducer activity	23	41
nutrient reservoir activity	20	6
protein folding chaperone	3	5
protein tag	3	0
small molecule sensor activity	1	1
structural molecule activity	10	103
transcription regulator activity	83	136
translation regulator activity	10	14
transporter activity	142	161
toxin activity	0	3

Table S8 Mitochondrial-related of upregulated differentially expressed genes

Gene ID	Homologue in <i>Arabidopsis</i>	Molecular weight /Da	Description
Seita.5G015100	AT1G79900	34,259	mitochondrial substrate carrier family protein;encodes a mitochondrial ornithine transporter that exports ornithine from the mitochondria to the cytosol
Seita.4G262700	AT4G20930	24,616	6-phosphogluconate dehydrogenase family protein
Seita.4G089700	AT5G51440	29,376	HSP20-like chaperones superfamily protein
Seita.3G167200	AT5G11770	22,236	NADH-ubiquinone oxidoreductase 20 kDa subunit
Seita.5G253800	AT4G22220	17,381	SufE/NifU family protein;Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster,which is subsequently transferred to a target apoprotein.
Seita.8G140500	AT3G26690	23,867	nudix hydrolase homolog 13;Encodes AtNUDT13, a mitochondrial Nudix hydrolase specific for long-chain diadenosine polyphosphates.
Seita.2G066900	AT2G14170	54,781	aldehyde dehydrogenase 6B2; Arabidopsis thaliana methylmalonate-semialdehyde dehydrogenase
Seita.9G358900	AT5G40010	57,588	AAA-ATPase 1; Encodes a mitochondrial ATPase involved in seed and silique development.
Seita.9G157700	AT5G46180	40,837	ornithine-delta-aminotransferase; Encodes an ornithine delta-aminotransferase that is transcriptionally up-regulated in young seedlings and in response to salt stress. It is unlikely to play a role in salt-stress-induced proline accumulation, however, it appears to participate in arginine and ornithine catabolism.
Seita.9G443300	AT1G07900	25,223	LOB domain-containing protein 1
Seita.1G210300	AT5G40770	30,424	prohibitin 3
Seita.1G326600	AT5G51440	21,740	HSP20-like chaperones superfamily protein
Seita.3G216900	AT3G12580	71,012	heat shock protein 70
Seita.3G407300	AT3G28580	59,552	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Seita.3G124600	AT3G50940	53,062	P-loop containing nucleoside triphosphate hydrolases superfamily protein

Table S9 Chloroplast-related of upregulated differentially expressed genes

Gene ID	Homologue in <i>Arabidopsis</i>	Molecular weight /Da	Description
Seita.9G341300	AT1G42550	86,803	encodes a plant-specific protein of unknown function that appears to be conserved among angiosperms.
Seita.9G108100	AT1G17870	63,160	ethylene-dependent gravitropism-deficient and yellow-green-like 3, EGY3; EGY3 mediates chloroplastic ROS homeostasis and promotes retrograde signaling in response to salt stress in <i>Arabidopsis</i>
Seita.5G258400	AT3G25690	84,158	actin binding protein required for normal chloroplast positioning
Seita.5G132200	AT1G06800	62,965	encodes a lipase that hydrolyzes phosphatidylcholine
Seita.5G010700	AT4G13250	54,470	encodes a chlorophyll b reductase involved in the degradation of chlorophyll b and LHCII (light harvesting complex II)
Seita.5G241800	AT3G25690	42,247	actin binding protein required for normal chloroplast positioning
Seita.5G356000	AT3G08640	34,996	alphavirus core family protein (DUF3411)
Seita.5G383100	AT2G37970	23,840	SOUL heme-binding family protein
Seita.5G390200	AT2G27510	15,156	ferredoxin 3
Seita.4G168200	AT3G57430	81,538	encodes a chloroplast RNA editing factor.
Seita.4G099200	AT5G15250	74,424	encodes an FtsH protease that is localized to the chloroplast
Seita.7G212200	AT5G13770	78,221	pentatricopeptide repeat (PPR-like) superfamily protein
Seita.6G122600	AT4G27670	28,215	encodes Hsp21, a chloroplast located small heat shock protein
Seita.1G082600	AT1G17240	75,117	encodes a CLAVATA2 (CLV2)-related gene
Seita.1G110500	AT4G38470	60,125	ACT-like protein tyrosine kinase family protein
Seita.1G265600	AT5G03555	56,637	encodes PLUTO (plastidic nucleobase transporter)
Seita.1G002700	AT5G45140	99,535	encodes a subunit of RNA polymerase III (aka RNA polymerase C).
Seita.3G158000	AT1G66840	61,900	encodes a coiled-coil protein WEB2
Seita.3G352700	AT4G24460	36,335	encodes one of the CRT-Like transporters
Seita.8G019400	AT2G40300	28,002	encodes FERRITIN 4
Seita.8G251300	AT2G39730	28,339	a nuclear-encoded chloroplast protein
Seita.2G269000	AT5G41120	60,602	esterase/lipase/thioesterase family protein
Seita.2G263500	AT4G13010	48,412	oxidoreductase, zinc-binding dehydrogenase family protein
Seita.2G381900	AT3G29770	40,408	encodes a protein predicted to act as a carboxylesterase
Seita.2G128600	AT5G58770	32,736	undecaprenyl pyrophosphate synthetase family protein
Seita.2G090000	AT5G01750	22,084	LURP-one-like protein (DUF567)

Seita.2G053300	AT3G22840	18,220	chlorophyll A-B binding family protein;Encodes an early light-inducible protein.
Seita.9G544600	AT3G23920	61,043	beta-amylase 1;Encodes a chloroplast beta-amylase
Seita.9G481900	AT3G49680	43,066	encodes a chloroplast branched-chain amino acid aminotransferase
Seita.9G344200	AT5G52810	34,676	NAD(P)-binding Rossmann-fold superfamily protein
