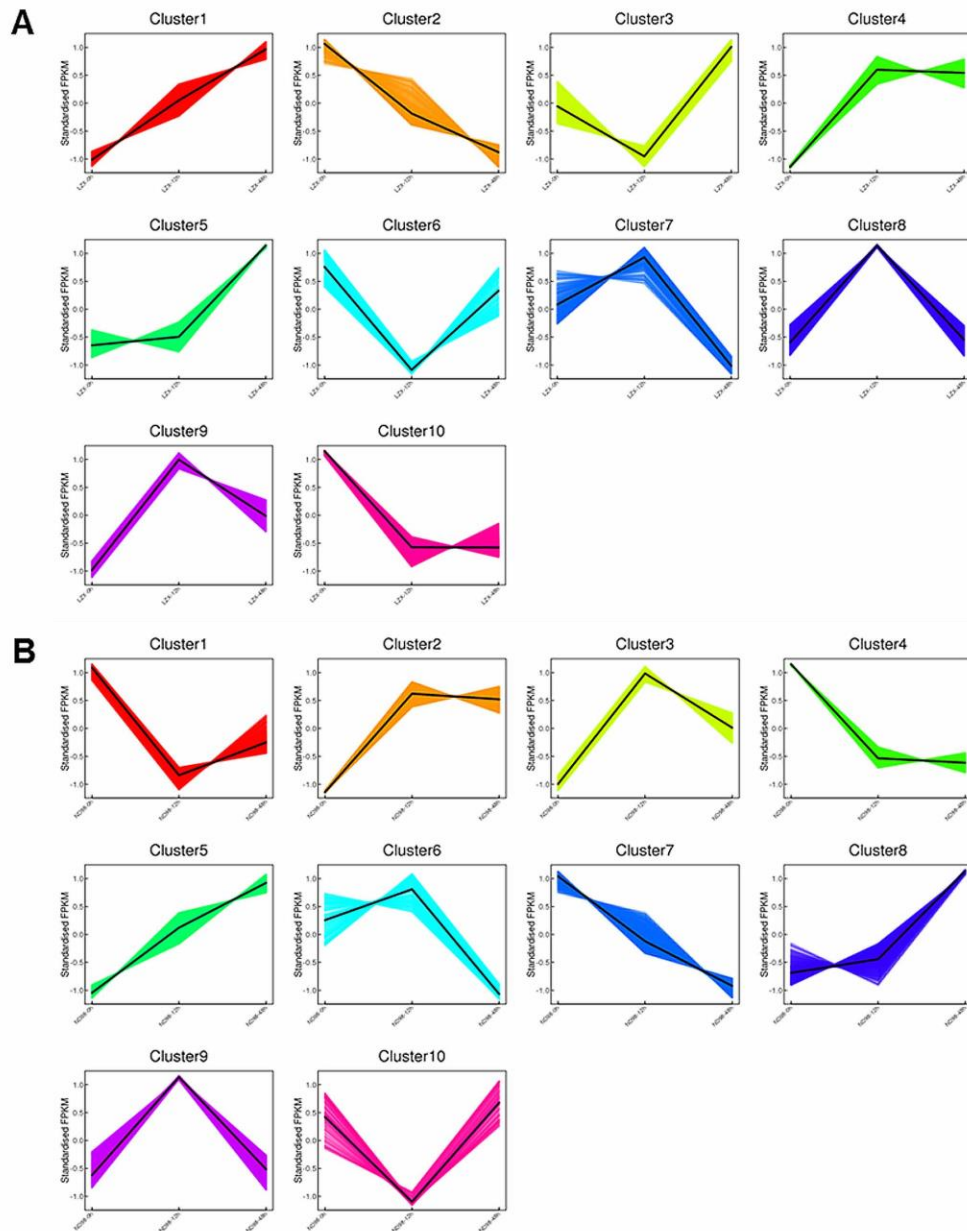


Transcript profile analysis reveals important roles of jasmonic acid signalling pathway in the response of sweet potato to salt stress

Huan Zhang¹, Qian Zhang¹, Hong Zhai¹, Yan Li¹, Xiangfeng Wang¹, Qingchang Liu^{1,*}
& Shaozhen He^{1,*}

¹Beijing Key Laboratory of Crop Genetic Improvement/Laboratory of Crop Heterosis and Utilization, Ministry of Education, China Agricultural University, Beijing 100193, China

*Correspondence and requests for materials should be addressed to S. H. (email: sunnynba@cau.edu.cn) and Q. L. (liuqc@cau.edu.cn)



Supplementary Fig. S1. DEG cluster analysis based on the K-means method. The DEGs were divided into 10 categories in Lizixiang (A) and ND98 (B), respectively, according to their expression patterns.

Supplementary Table S1. Length distribution of the assembled transcripts and unigenes.

Nucleotide length (bp)	Transcript	Unigene
200-300	18,462 (8.01%)	5,871 (9.22%)
300-500	43,511 (18.89%)	22,030 (34.60%)
500-1000	56,596 (24.57%)	17017 (26.73%)
1000-2000	65,110 (25.32%)	11,319 (17.78%)
2000+	46,678 (20.26%)	7,436 (11.68%)
Total number	230,357	63,673
Total length	299,012,560	60,713,683
Mean length	1298.04	953.52

Supplementary Table S2. Statistics of annotated gene information from various databases.

Annotated databases	Unigene	≥ 300 nt	≥ 1000 nt
Annotated in COG	10,351	9,223	6,121
Annotated in GO	18,685	15,883	8,966
Annotated in KEGG	12,240	10,488	6,003
Annotated in KOG	20,059	17,259	10,043
Annotated in Pfam	24,666	22,168	13,946
Annotated in Swiss-Prot	22,764	19,984	11,819
Annotated in TrEMBL	34,086	29,343	16,335
Annotated in Nr	34,689	29,676	16,373
Annotated in Nt	20,746	18,273	12,022
Annotated in at least one database	37,016	31,145	16,623

Supplementary Table S3. The up-regulated, down-regulated and neutral genes in Lizixiang and ND98, respectively. (Supplementary Dataset 1)

Supplementary Table S4. DEGs were higher in ND98 than in Lizixiang for at least one time point during salt treatment. (Supplementary Dataset 2)

Supplementary Table S5. DNA methylation- and demethylation-related genes identified via gene expression profiling. (Supplementary Dataset 3)

Supplementary Table S6. Key genes involved in DNA demethylation and methylation, JA, ABA

and SA biosynthesis and signalling, stomatal opening and closure and ion transport.

Gene	ID	FPKM-LZX.0h	FPKM-LZX.12h	FPKM-LZX.48h	FPKM-ND98.0h	FPKM-ND98.12h	FPKM-ND98.48h
The DNA demethylation-related genes							
<i>IbROS1</i>	c144343.graph_c0	2.925	1.185	1.395	2.860	6.190	1.820
<i>IbDML3</i>	c148603.graph_c0	26.655	16.360	14.315	58.440	45.285	24.545
The DNA methylation-related genes							
<i>IbCMT2</i>	c124784.graph_c0	4.825	4.650	3.805	3.575	5.015	2.050
<i>IbDRM1</i>	c136099.graph_c0	18.515	6.850	11.230	14.860	7.415	10.920
<i>IbDRM2</i>	c156316.graph_c1	49.305	33.700	27.995	42.160	44.825	44.460
<i>IbMET1</i>	c154661.graph_c0	8.433	6.985	6.697	5.720	10.104	11.978
The JA biosynthesis and signalling-related genes							
<i>IbLOX</i>	c154376.graph_c0	75.637	184.720	130.424	148.027	298.626	103.040
<i>IbAOS</i>	c110075.graph_c0	2.476	0.389	0.000	5.853	13.274	2.309
<i>IbAOC</i>	c136730.graph_c0	2.989	4.796	7.071	7.091	8.394	9.872
<i>IbOPR3</i>	c151632.graph_c0	10.287	12.939	10.313	4.943	83.780	18.896
<i>IbCOI1</i>	c148337.graph_c2	28.498	8.007	6.102	16.811	14.038	61.087
<i>IbPDF1.2</i>	c136835.graph_c0	128.199	171.131	116.517	493.801	335.206	122.939
<i>IbMYC2</i>	c143913.graph_c2	51.772	22.515	13.868	12.617	11.600	14.959
The ABA biosynthesis and signalling-related genes							
<i>IbZEP</i>	c158900.graph_c0	12.184	7.554	4.333	26.565	6.384	3.171
<i>IbAO</i>	c150446.graph_c0	2.290	1.811	1.086	5.547	1.617	0.680
<i>IbNCED</i>	c156411.graph_c0	15.977	25.232	43.713	364.130	47.737	40.918
<i>IbSnRK2</i>	c148195.graph_c0	31.011	165.411	173.425	33.339	111.176	143.886
<i>IbABF1</i>	c125138.graph_c1	21.600	13.545	5.685	13.600	8.770	7.155
The SA biosynthesis and signalling-related genes							
<i>IbPAL</i>	c147773.graph_c3	90.323	15.717	13.287	435.560	21.205	16.453
<i>IbNPR1</i>	c151920.graph_c0	8.805	7.100	5.845	14.185	10.470	10.425
<i>IbPRI</i>	c160535.graph_c0	0.313	7.576	5.064	0.163	3.548	7.904
The stomatal opening and closure-related genes							
<i>IbRPT2</i>	c158200.graph_c0	161.200	53.980	92.595	33.455	17.985	42.050
<i>IbbHLH93</i>	c152736.graph_c0	27.455	4.165	2.100	3.945	8.060	4.320
The ion transport-related genes							
<i>IbHKT1</i>	c158185.graph_c0	24.010	3.490	4.395	19.665	36.235	55.295
<i>IbNHX1</i>	c151428.graph_c0	10.765	10.265	9.580	17.940	14.340	15.400
<i>IbNHX18</i>	c158340.graph_c0	1.030	0.000	0.025	17.075	19.380	29.665

Supplementary Table S7. DEGs from different phytohormone signalling pathways.

(Supplementary Dataset 4)

Supplementary Table S8. Primers used in this study.

Primer name	Primer sequence (5'-3')
Primers for MASP	
<i>EcoRI</i> -adaptor1	CTCGTAGA CTGCGTACC
<i>EcoRI</i> -adaptor2	AATTGGTACGCA GTC
<i>HpaII/MspI</i> -adaptor1	GATCATGAGTCCTGCT
<i>HpaII/MspI</i> -adaptor2	CGAGCA GGA CT CAT GA
<i>EcoRI</i> -pre-amplification primer	GACTGCGTACCAATTCA
<i>HpaII/MspI</i> -pre-amplification primer	ATCATGAGTCCTGCTCGG
<i>EcoRI</i> -AAC	GACTGCGTACCAATTCAAC
<i>EcoRI</i> -AAG	GACTGCGTACCAATTCAAG
<i>EcoRI</i> -ACA	GACTGCGTACCAATTCACA
<i>EcoRI</i> -ACT	GACTGCGTACCAATTCACT
<i>EcoRI</i> -ACC	GACTGCGTACCAATTCACC
<i>EcoRI</i> -ACG	GACTGCGTACCAATTCACG
<i>EcoRI</i> -AGC	GACTGCGTACCAATTCAGC
<i>EcoRI</i> -AGG	GACTGCGTACCAATTCAGG
<i>HpaII/MspI</i> -TCT	ATCATGAGTCCTGCTCGGTCT
<i>HpaII/MspI</i> -TCG	ATCATGAGTCCTGCTCGGTCTG
<i>HpaII/MspI</i> -TCC	ATCATGAGTCCTGCTCGGTCTC
<i>HpaII/MspI</i> -TTC	ATCATGAGTCCTGCTCGGTCTC

<i>HpaII/MspI</i> -TTG	ATCATGAGTCCTGCTCGGTTG
<i>HpaII/MspI</i> -TTA	ATCATGAGTCCTGCTCGGTTA
<i>HpaII/MspI</i> -TGA	ATCATGAGTCCTGCTCGGTGA
<i>HpaII/MspI</i> -TGT	ATCATGAGTCCTGCTCGGTGT

Primers for qRT-PCR

β -actin-F	AGCAGCATGAA GATTAAGGTTGTAGCAC
β -actin-R	TGGAAAATTAGAAGCA CTCCTGTGAAC
<i>IbROS1</i> -F	AACACCAGTGGGGAATGTAA GAT
<i>IbROS1</i> -R	ATGATTGCTGTGTTTTGGA GACT
<i>IbDML3</i> -F	CACTCTCCTTCTCCTCCGTCC
<i>IbDML3</i> -R	GAATGGGTTA GTTTCATCGGC
<i>IbLOX</i> -F	GTGCTGAACAACA CGCTTTTAG
<i>IbLOX</i> -R	GTTTTAAGGTAGAACTCATTGGGAT
<i>IbAOS</i> -F	GACGGTTTTTGGACATTCA GG
<i>IbAOS</i> -R	GAACGAATCCTGGAGGCACT
<i>IbAOC</i> -F	GACGAGGATTTTGACGAGCA
<i>IbAOC</i> -R	TGGGATAATACAA GCA GCA GGA
<i>IbOPR3</i> -F	CGCCATCCATTCCAAGTTTAG
<i>IbOPR3</i> -R	GGTCCCCATAATACGCTAAC
<i>IbCOII</i> -F	CGGCA GTTCTGGAATCTCG
<i>IbCOII</i> -R	TATGCGAGGAGATGGGCTG
<i>IbPDF1.2</i> -F	GGCTTCATCTCTTCGTTCA TTT

<i>IbPDF1.2-R</i>	GCAGTTGCTGTCCCGA GAA
<i>IbMYC2-F</i>	TTTGCCAGA GAAACCTTATCCA
<i>IbMYC2-R</i>	GAGGTAAACCCATCGCA GG
<i>IbZEP-F</i>	TCGGTTTGAA GTGTTTTCTGTG
<i>IbZEP-R</i>	CAAACCTTCTCCTCAAACAACGAC
<i>IbAO-F</i>	GTTACTTGCTATTCTCGGGGTG
<i>IbAO-R</i>	GATGAGTCTTGGCTGGGTTG
<i>IbNCED-F</i>	TTTGGCTAAAGTGGACCTCTCA
<i>IbNCED-R</i>	ATTCCTGGGCA GAAAAACG
<i>IbSnRK2-F</i>	GGTGCCA GTGATAACCCTCTAA
<i>IbSnRK2-R</i>	CTTGATAGCCACTTTGTGTCCA G
<i>IbABF1-F</i>	GGAGTTTGGGACA GAAAGGAG
<i>IbABF1-R</i>	AAGCCCCGA CA GTCA CCT
<i>IbPAL-F</i>	TCACTGTGGGTGCTAATGGAG
<i>IbPAL-R</i>	GGCTTGGCGGA GTTCTG
<i>IbNPR1-F</i>	AGTCCGTTCTTCA GGA GCGT
<i>IbNPR1-R</i>	TTCCGCAATAAAGGTAA GCC
<i>IbPR1-F</i>	GCAAGATTACCTAAACCCCCA
<i>IbPR1-R</i>	GGAGTTGGCGTA GTTCTGCG
<i>IbPRT2-F</i>	GGGA GTA GTGCGA GTGTGA GG
<i>IbRPT2-R</i>	AAAGGATTCAACTTCCCCAACT
<i>IbbHLH93-F</i>	GAGAAATGAGTCGTGGGAAGG

IbbHLH93-R

AAAACAAAAGGCGGAGGC
