

Comparative proteomic analysis reveals that antioxidant system and soluble sugar metabolism contribute to salt tolerance in alfalfa (*Medicago sativa* L.) leaves

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Table of contents

Table S1, Primers used in transcriptional analysis of DEPs

Table S2, Raw data total identified proteins in A17 and ZM1. See “Table S2 excel file”.

Table S3, Differentially expressed proteins (DEPs) were identified in A17 and ZM1. See “Table S3 excel file”.

Table S4, Number of DEPs identified from A17 and ZM1.

Table S5, Gene ontology (GO) analysis of DEPs in A17 and ZM1. See “Table S5 excel file”.

Table S6, KEGG pathway enrichment analysis of the DEPs detected in A17 and ZM1.

Table S7, Selected key DEPs with different functions in leaves of A17 and ZM1. See “Table S7 excel file”.

Fig.S1, Correlate coefficients (CCs) of the three replicates for the four experiments A17 and ZM1.

Fig. S2, Protein interaction network consisting of DEPs in table S7 in salt-stressed A17 and ZM1.

Table S1. Primers used in transcriptional analysis of DEPs

NCBI accession	Description	primer-F	primer-R
XM_013607856.1	DREPP plasma membrane protein	TGCTGCTGAGGTTTCCAAGAC	TGCTTGATCACGTTCTTTGACC
XM_013608168.1	sucrose synthase	TTCACAATGGCAAGGCTGGA	CCTCCTGTCTCCAGCTACGA
XM_003615663.2	asparagine synthetase [glutamine-hydrolyzing] protein	TCTTCCCCCAGAACTCAGCA	GCTCTGAATGGCAACCTCAACT
XM_013599312.1	thylakoid membrane phosphoprotein 14 kDa protein	CCTCCAGGGAGACGGAGTAA	CCGGTCCTCAGGTTTATCCCA
XM_003606007.2	photosystem II CP47 chlorophyll A apoprotein	AGTGTCGAACAAGTCGGTGT	GAGCAAACGAAGCATGTCCA
XM_003602413.2	horseradish peroxidase-like protein	AATCCACACTGCAAACTGCCAT	CACATGATACAACTCCGGGGC
XM_013611853.1	superoxide dismutase	CCATCATCATCCACTCCTTACC	TCTCCTCCTCTTTCTCCCTCTC
XM_013610396.1	gamma-tocopherol methyltransferase	ATCATCGTGCTGCTCAGATCC	GCTTGAACAGGGCTGAGAGT
XM_003630473.2	phospholipid hydroperoxide glutathione peroxidase	GGTGGACTCTTTGGGGATGG	AGTGGAGAAGTCGTTGGTGC
XM_013600648.1	heat shock cognate 70 kDa protein	TGTTGGCGGATCGACTAGGA	CGCCATAAGCAACAGCCTCA
XM_013614701.1	trehalose-6-phosphate synthase domain protein	GTTCTGATGCTCCTTCCTCCATTTC	TTCCCACTTACCATTCTCCTCTTTC
XM_003602497.2	actin2, β -actin	GCTGTGGTTGCTTTTTTGGTGTCTC	TGGGCTGCCACAGAACATTGA

Table S4. Number of DEPs identified from A17 and ZM1

	A17	ZM1	Total	Overlap of A17 and ZM1		
				A17	ZM1	Total
UP	208	81	272	21	20	18(6.6%)
DP	110	75	173	15	16	12(6.9%)
Species	282	120	396	-	-	6
unique						
total	318	156	438	36	36	36(8.2%)

Table S6. KEGG pathway enrichment analysis of the DEPs detected in A17 and ZM1

A17	Database	ID	Input number	P-Value
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	mtr00520	15	2.15E-05
Selenocompound metabolism	KEGG PATHWAY	mtr00450	4	0.0016606
Fatty acid biosynthesis	KEGG PATHWAY	mtr00061	6	0.0022426
Ascorbate and aldarate metabolism	KEGG PATHWAY	mtr00053	5	0.0025674
Fatty acid metabolism	KEGG PATHWAY	mtr01212	7	0.0032551
Photosynthesis - antenna proteins	KEGG PATHWAY	mtr00196	4	0.003408
Sulfur metabolism	KEGG PATHWAY	mtr00920	4	0.0128828
Metabolic pathways	KEGG PATHWAY	mtr01100	69	0.0475496
ZM1				
Ribosome	KEGG PATHWAY	mtr03010	15	1.98E-05
Aminoacyl-tRNA biosynthesis	KEGG PATHWAY	mtr00970	4	0.0072352
Starch and sucrose metabolism	KEGG PATHWAY	mtr00500	8	0.016177
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	mtr00520	5	0.0298335

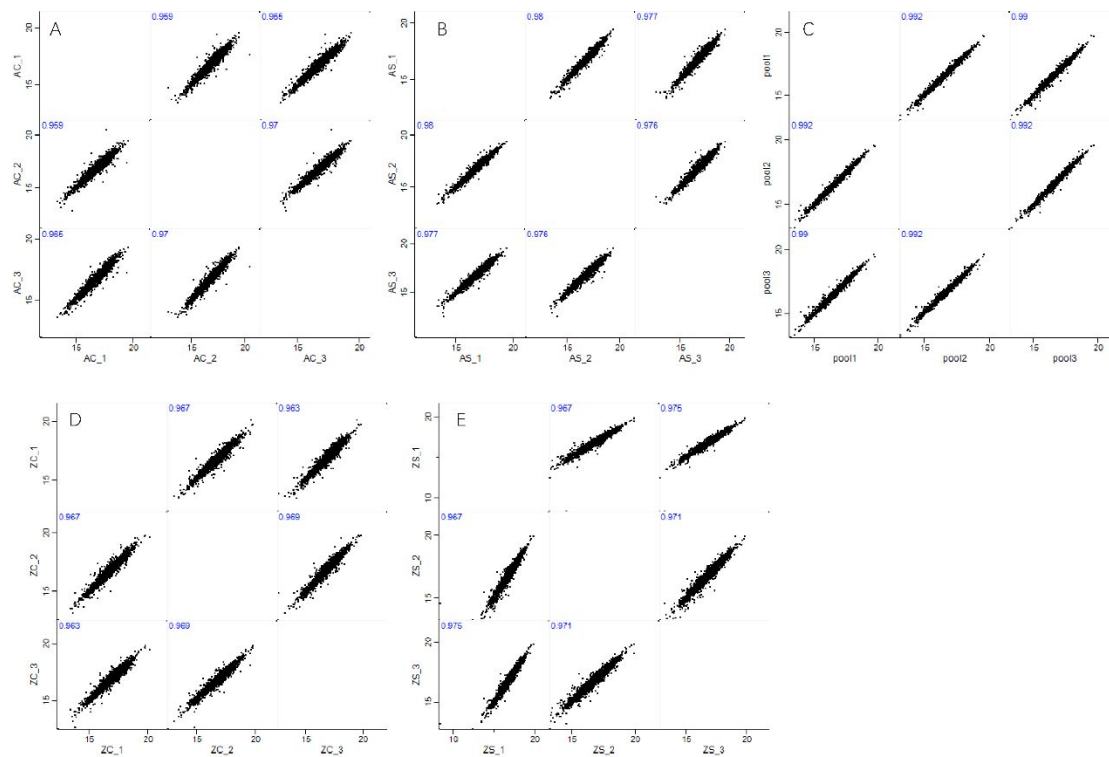


Fig.S1 Correlate coefficients (CCs) of the three replicates for the four experiments A17 and ZM1. AC, A17 plants under normal conditions (113 tag); AS, A17 plants under salt stress (115 tag). Pool, pooled A17-CK, A17-S, ZM1-CK and ZM1-S samples (121 tag); ZC, ZM1 plants under normal conditions (117 tag); ZS, ZM1 plants under salt stress (118 tag).

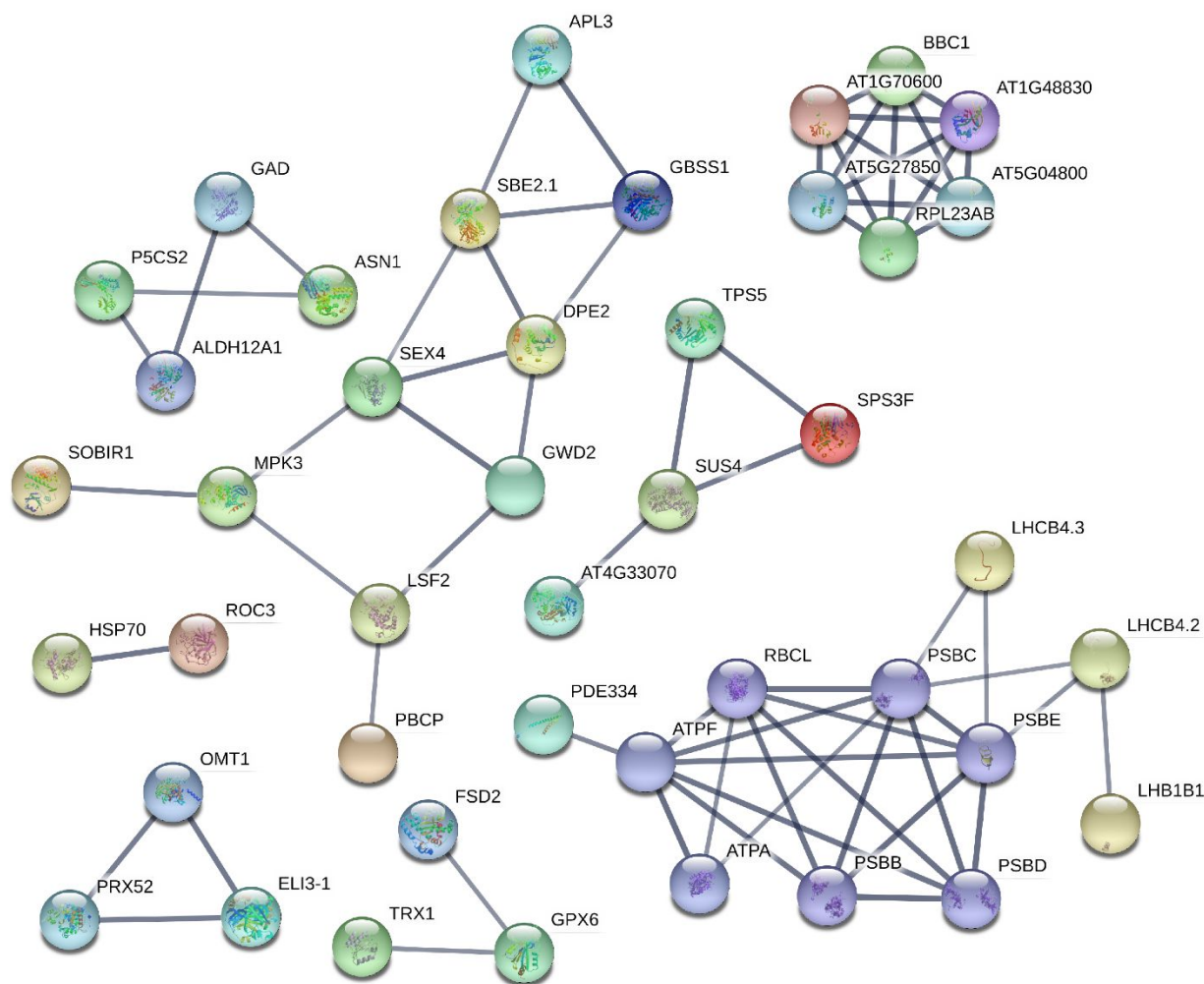


Fig. S2 Protein interaction network consisting of DEPs in table S7 in salt-stressed A17 and ZM1. The network was constructed using the String program (<http://www.string-db.org/>) with a confidence score higher than 0.7. A total of 85 DEPs represented by 43 DEPs are shown in PPI network. Nodes represent proteins, and the thickness of lines between nodes represents the strength of the supporting data.