

**Proteomic Analysis of Salt-stressed Tomato
(*Lycopersicon esculentum*) Seedlings: Effect of
Genotype and Exogenous Application of
Glycinebetaine**

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Supplementary Material

Supplementary table 1: Identification of tomato protein induced during osmotic stresses. a) The numbering corresponds to the 2-D gel in Figures 3-8; b) Gi number in NCBI databases (2007/10/01); c) All proteins were identified by LC-ESI-MS. For each identified protein, the number of matched peptides was more than 1, and the scope of marched peptides was more than 70.

Spot number ^a	GI Number ^b	Protein Name ^c	Identified peptides			
			Number	Score	Mass	Sequence
1	77554415	Chaperone protein DnaK (<i>Oryza sativa</i> (japonica cultivar-group))	1	96	1472.8	KQDITITGASTLPK
			2	91	1595.7	AKFEELC(+57)SDLIDR
			3	92	1344.7	QDITITGASTLPK
			4	94	1396.6	FEELC(+57)SDLIDR
			5	71	728.4	LVGQIAK
			6	95	1472.8	KQDITITGASTLPK
			7	78	761.4	LTEAAEK
			8	93	1566.8	AVVTVPAYFNDSQR
			9	90	1595.7	AKFEELC(+57)SDLIDR
			10	77	861.4	NTTLPTSK
			11	97	1723.9	IINEPTAASLAYGFEK
			12	76	2437.2	SEVFSTAADGQTSVEINVLQGER
2	3492854	Mitochondrial small heat shock protein (<i>Lycopersicon esculentum</i>)	1	79	1392.6	MDM(+16)PGLDKENVK
			2	98	1665.8	GWDVKEDDNALYIK
			3	90	1117.6	LEIPQNIYK
			4	93	1228.7	VAVEENTLIK
			5	96	1376.6	MDMPGLDKENVK
			6	97	1665.8	GWDVKEDDNALYIK
			7	90	1080.5	EDDNALYIK
			8	72	2532.1	SVSQLLNM(+16)M(+16)DQM(+16)M(+16)DSPFVAAPR
3	15080913	Ferritin (<i>Malus xiaojinensis</i>)	1	94	1078.6	ISEYVAQLR
			2	92	1639.8	GDALYAM(+16)ELALSLEK
4	19317	Photosystem II 23 kDa protein (<i>L. esculentum</i>)	1	87	1296.7	HQLITATVNDGK
			2	96	1306.6	EYYVLSVLTR
			3	80	1384.7	KFVENAATSFSIA
			4	86	2127	TADGDEGGKHLITATVNDGK
			5	91	1572.7	SITDYGSPPEFLSK
			6	87	807.4	VDYLLGK
			7	83	849.3	TADGDEGGK
			8	93	2127	TADGDEGGKHLITATVNDGK
			9	72	1256.6	FVENAATSFSIA
5	3341464	Hsp20.1 protein (<i>L. peruvianum</i>)	1	94	901.5	VLQISGER
			2	94	974.5	FRLPENAK
			3	91	1502.8	KEEVKVEIEDR
			4	76	1071.6	EEVKKPDVK
			5	81	1771.9	VEIEEDRVLQISGER
			6	86	1947	ASM(+16)ENGVLTVTPKEEVK
			7	94	1374.7	EEVKVEIEDR
			8	70	713.4	ADLPLGK
			9	95	1445.7	ASMENGVLTVPK
			10	98	1461.7	ASM(+16)ENGVLTVTPK
			11	89	2257.1	EEVKVEIEDRVLQISGER
			12	89	889.4	VEIEEDR
			13	90	1931	ASMENGVLTVPKKEEVK
			14	89	1057.5	ETPEAHVFK
6	31088230	Glyceraldehyde 3-phosphate dehydrogenase (<i>L. esculentum</i>)	1	76	659.4	AGIALSK
			2	89	1434.7	AASFNIIPSSTGAAK
			3	92	1470.8	VPTADVSVVDLTVR
			4	88	767.4	SSIFDAK
			5	99	2145	GILGYTEDDVVSTDFVGDSSR
7	4836473	17.6 kD class I small heat shock protein (<i>L. esculentum</i>)	1	94	901.5	VLQISGER
			2	94	974.5	FRLPENAK
			3	95	1488.7	KEEVKVEVEEDR
			4	93	1057.5	ETPEAHVFK
			5	99	1085.6	EEVKKPEVK
			6	78	1947	ASM(+16)ENGVLTVTPKKEEVK
			7	98	1360.6	EEVKVEVEEDR

			8	70	713.4	ADLPGLK
			9	95	1445.7	ASMENGLTVTVPK
			10	98	1461.7	ASM(+16)ENGLTVTVPK
			11	87	2243.1	EEVKVEVEDRVLQISGER
			12	96	1757.9	VEVEDRVLQISGER
			13	90	1931	ASMENGLTVTVPKKEEVK
			14	94	1941.9	ELGFPSTNSGESSAFANTR
8	77744859	Temperature induced lipocalin' (<i>L. esculentum</i>)	1	99	925.4	GSIEGTAYK
			2	95	1023.5	YLWILC(+57)R
			3	88	1854.9	QPHLDEEIIYNQLVEK
			4	96	1255.6	WYEIASFPSR
			5	91	2391.1	ATYTLNQDGTVHVLNETWSGGK
			6	76	896.4	EVGYDVSK
			7	90	2391.1	ATYTLNQDGTVHVLNETWSGGK
9	4836471	17.8 kD class I small heat shock protein (<i>L. esculentum</i>)	1	95	901.5	VLQISGER
			2	86	1947	ASM(+16)ENGLTVTVPKKEEVK
			3	97	1445.7	ASMENGLTVTVPK
			4	99	1461.7	ASM(+16)ENGLTVTVPK
			5	94	1931	ASMENGLTVTVPKKEEVK
			6	97	1971.9	ELGFPSTNSGESSAFANTR
			7	99	2009.9	SSSM(+16)FDPFSDVDFPFR
			8	96	1057.5	ETPEAHVFK
			9	91	3962.8	SSSM(+16)FDPFSDVDFPFRFRELGFSTNSGESSAFANTR
10	3676294	Mitochondrial ATPase beta subunit (<i>Nicotiana glauca</i>)	1	82	1869.9	M(+16)LSPHILGEDHYNTAR
			2	99	1393.7	ESINSFQGVLDGK
			3	88	2148	NLQDIIAILGM(+16)DELSEDDK
			4	92	2690.3	NLQDIIAILGMDELSEDDKMTVAR
			5	86	2706.3	NLQDIIAILGM(+16)DELSEDDKMTVAR
			6	94	2722.3	NLQDIIAILGM(+16)DELSEDDKM(+16)TVAR
			7	92	2379.1	YDDLSEQSFYVGGIDEVIAK
			8	90	2395.1	YDDLSEQSFYM(+16)VGGIDEVIAK
11	3790441	Chaperonin 60 alpha subunit (<i>Canavalia lineata</i>)	1	99	898.6	GILNVAAIK
			2	92	1043.6	VVNDGVTIAR
			3	96	1182.7	LADAVGLTLGPR
			4	91	1192.6	DSTTHADAASK
			5	84	802.4	VLVTDQK
			6	96	1636.8	TNDSAGDGTASVLR
			7	97	1754.9	AIELPDAMENAGALIR
			8	96	1770.9	AIELPDAM(+16)ENAGALIR
			9	88	940.6	DIIPLEK
12	11991527	Mitochondrial formate dehydrogenase precursor (<i>Solanum tuberosum</i>)	1	94	955.6	GVLIVNNAR
			2	78	1048.5	DGELAPQYR
			3	95	1591.8	LKM(+16)DSELENQIGAK
			4	91	1157.6	GHQYIVTPDK
			5	99	1334.6	MDSELENQIGAK
			6	96	1350.6	M(+16)DSELENQIGAK
			7	87	1381.6	GEDFFAENYIVK
			8	94	2215	GHQYIVTPDKKEGPDC(+57)ELEK
			9	99	1501.8	C(+57)DIVVINTPLTEK
			10	83	795.4	AYDLEGK
			11	92	2649.3	AAAAAGLTVAEVTGSNTVSVAEDELM(+16)R
			12	89	895.4	FEEDLDK
			13	90	1907	NLQLLLTAGIGSDHVDLK
			14	80	2454.1	ANEYAE MNPNFLGC(+57)AENALGIR
13	53830834	Osmotin-like protein (<i>S. phureja</i>)	1	86	1111.4	TNC(+57)NFDGAGR
			2	96	1726.6	GWC(+57)QTGDC(+57)GGVLEC(+57)K
			3	81	2181.9	C(+57)HPIQC(+57)VANINGEC(+57)PGSLR
			4	81	3134.2	C(+57)PDAYSYPQDDPTSTFTC(+57)QSWTTDYK
14	4836469	17.7 kD class I small heat shock protein (<i>L. esculentum</i>)	1	95	901.5	VLQISGER
			2	93	974.5	FRLPENAK
			3	86	1947	ASM(+16)ENGLTVTVPKKEEVK
			4	89	1360.6	EEVKVEVEDR
			5	97	1445.7	ASMENGLTVTVPK
			6	99	1461.7	ASM(+16)ENGLTVTVPK
			7	94	1931	ASMENGLTVTVPKKEEVK
			8	97	1971.9	ELGFPSTNSGESSAFANTR
			9	99	1993.9	SSSMFDPFSDVDFPFR
			10	99	2009.9	SSSM(+16)FDPFSDVDFPFR
			11	96	1057.5	ETPEAHVFK
			12	91	3962.8	SSSM(+16)FDPFSDVDFPFRFRELGFSTNSGESSAFANTR
15	475734	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>Juanulloa aurantiaca</i>)	1	87	1245.6	FLFC(+57)AEALFK
			2	99	1261.7	DITLGFVDLLR
			3	75	737.4	GGLDFTK
			4	96	1546.7	WSPELAAAC(+57)EVWK
			5	97	1579.8	EIVFNFAAVDVLDK
			6	80	976.5	AQTETGEIK
16	1518139	Chloroplast heat shock	1	94	910.4	FDM(+16)PGLSK

		protein (<i>L. esculentum</i>)	2	98	928.5	KVIDVQIN
			3	93	984.6	LSLPDNVVK
			4	88	1005.4	NYSSYDTR
			5	96	1087.6	NGVLFISIPK
			6	97	1246.7	VSVENDMLVIK
			7	90	1262.7	VSVENDM(+16)LVIK
			8	99	1313.6	LFEDTMTFPGR
			9	97	1329.6	LFEDTM(+16)TFPGR
			10	96	1611.7	TPWDIHDDENEIK
			11	96	1962.9	MALDVSPFGVLDPMSPMR
			12	96	2366.1	DTSVDVHHSSAQGGNNQGTAVER
17	3336892	Hsp20.0 protein (<i>L. peruvianum</i>)	1	95	901.5	VLQISGER
			2	94	974.5	FRLPENAK
			3	74	1057.5	ETPEAHVFK
			4	99	1445.7	ASMENGLTVTVPK
			5	96	1461.7	ASM(+16)ENGLTVTVPK
			6	97	1947.9	STSVDFPFSIDVDFPFK
			7	74	3916.8	STSVDFPFSIDVDFPFKELGFTVSNSETSAFANTR
18	218312	Chloroplast elongation factor TuB (EF-TuB) (<i>N. sylvestris</i>)	1	97	1081.6	FEALVYVLK
			2	92	1307.6	YDEIDAAPEER
			3	91	1354.6	NTTVTGVEMFQK
			4	91	1370.6	NTTVTGVEM(+16)FQK
			5	85	2108	VNM(+16)VVELIMPVAC(+57)EQGM(+16)R
			6	99	1435.7	KYDEIDAAPEER
			7	77	1444.8	QVGVPMVVFLNK
			8	86	721.4	TTDVTGK
			9	89	1460.8	QVGVPM(+16)VVFLNK
			10	87	823.5	EHILLAK
			11	95	1699.9	ILDEAMAGDNVGLLLR
			12	95	1715.9	ILDEAM(+16)AGDNVGLLLR
			13	89	872.5	TVGAGVIQK
			14	97	1810.9	GITINTATVEYETENR
			15	80	2673.3	NMITGAAQMDGAILVVSAGDGPMPQTK
			16	82	2705.3	NM(+16)ITGAAQMDGAILVVSAGDGP(+16)PQTK
21	809113	33kDa precursor protein of oxygen-evolving complex (<i>S. tuberosum</i>)	1	98	964.6	VPFLFTIK
			2	95	1220.6	IQGIWYAQLE
			3	95	1252.6	RLTYDEIQSK
			4	90	1328.6	FC(+57)LEPTSFTVK
			5	92	1417.7	GDEEELQKENVK
			6	91	1456.7	KFC(+57)LEPTSFTVK
			7	85	2294.1	FEEKDGIDYAAVTVQLPgger
			8	82	2298.2	QLVASGKPEFSFGFLVPSYR
			9	99	1562.7	GGSTGYDNAVALPAGGR
			10	90	791.4	NTASLTGK
			11	78	2381.1	GTGTANQC(+57)PTIEGGVGSFAFKPGK
			12	99	1760.9	DGIDYAAVTVQLPgger
			13	91	906.4	NSAPDFQK
			14	91	1096.5	LTYDEIQSK
			15	97	2310.1	LYTYLDEIEGPFVSPDGTVK
22	5257554	Cytosolic ascorbate peroxidase (<i>Fragaria x ananassa</i>)	1	92	1347.7	LAWHSAGTYDVK
			2	91	1403.6	C(+57)YPTVSEYK
			3	81	936.4	LSELGFAEA
23	20018	Ribosomal protein L12-1 (<i>N. tabacum</i>)	1	89	898.5	ELIEGLPK
			2	93	1405.7	EGVSKDEAEDAKK
			3	73	816.5	ALTSLALK
			4	90	1690.8	TEFDVVIDEVPSNAR
			5	73	898.5	ELIEGLPK
			6	96	1914	VVQLGDEISNLTADAQK
			7	91	1007.5	LVEYLQDK
24	1149571	Mitochondrial elongation factor Tu (<i>Arabidopsis thaliana</i>)	1	93	899.5	ELLSFYK
			2	85	1021.5	AIAFDEIDK
			3	83	1114.5	STVTGVEM(+16)FK
			4	77	1460.8	QVGVPSLVC(+57)FLNK
			5	99	1575.8	AIAFDEIDKAPEEK
			6	82	1632.8	LMDAVDEYIPDPVR
			7	87	1648.8	LM(+16)DAVDEYIPDPVR
			8	72	1667.9	ILDNGQAGDNVGLLLR
			9	77	919.5	TTLTAATK
			10	78	927.5	VELPENVK
25	71151986	Nascent polypeptide-associated complex subunit alpha-like protein 3 (<i>A. thaliana</i>)	1	97	1659.9	DIELVM(+16)TQAGVSKPR
			2	99	1484.7	SPASDITYVIFGEAK
			3	95	1643.9	DIELVMTQAGVSKPR
			4	97	1921.9	IEDLSSQLQSQAEEQFK

Supplementary table 2: The type and relation of protein-protein interactions in biological networks generated for salt stress. This table corresponds to the Figure 8A.

Type	Relation	Ref.	Type	Relation	Ref.
Regulation	SOD --+> differentiation	1	Regulation	Antioxidant ---> photosynthesis	10
Regulation	Antioxidant ---> regulation of signal transduction	5	Regulation	APX ---> hypersensitive response	2
Regulation	SOD ---> oxidative stressed	4	Regulation	APX ---> GPX	2
Regulation	APX --+> RPS6K	1	Regulation	APX ---> photophosphorylation	2
Regulation	PSII ---> photosynthesis	75	Regulation	APX1 ---> regulation of signal transduction	3
Regulation	Superoxide dismutase ---> GPX	2	Regulation	Superoxide dismutase ---> oxidative stressed	3
Regulation	Peroxynitrite --- APX	1	Regulation	SOD ---> systemic acquired resistance	2
Regulation	Antioxidant ---> Plant development	2	Regulation	RubisCO ---> photosynthesis	202
Regulation	cAPX ---> hypersensitive response	2	Regulation	SOD ---> photosynthesis	8
Regulation	APX ---> photosynthesis	4	Regulation	antioxidant ---> necrosis	5
Regulation	Antioxidant ---> oxidative stressed	29	Regulation	APX ---> plant defense	2
Regulation	PSII ---> photorespiration	7	Regulation	Antioxidant ---> salinity response	2
Regulation	Superoxide dismutase ---> photosynthesis	6	Regulation	SOD ---> necrosis	1
Regulation	PSII ---> photoinhibition	35	Regulation	cAPX ---> regulation of signal transduction	1
Regulation	oxygen ---> photoinhibition	3	Regulation	Antioxidant ---> fruit ripening	2
Regulation	Superoxide dismutase --+> 3-(imidazol-5-yl)lactate dehydrogenase	1	MolSynthesis	Antioxidant ---> ascorbate	5
Regulation	SOD ---> salinity response	2	MolSynthesis	APX ---> ascorbate	7
Regulation	Antioxidant ---> plant defense	11	MolSynthesis	APX ---> ascorbic acid	4
Regulation	Saline --+> MUJ8.3	1	MolSynthesis	Antioxidant ---> lipids	4
Regulation	APX2 ---> photosynthesis	2	MolSynthesis	APX ---> oxygen	7
Regulation	APX2 --+> APX	1	MolSynthesis	SOD ---> oxygen	6
Regulation	L-ascorbate oxidase ---> plant growth	2	MolSynthesis	Antioxidant ---> H2O2	3
Regulation	SOD ---> GPX	2	MolSynthesis	APX ---> lipid	1
Regulation	Saline --+> APX	1	Regulation	RubisCO ---> oxidative stressed	1
Regulation	APX1 --+> APX	1	Regulation	Copper --+> SOD	1
Regulation	Superoxide dismutase --+> AT4G35090	1	Expression	Saline --+> SOD	1

Supplementary table 3: The type and relation of protein-protein interactions in biological networks generated for salt stress. This table corresponds to the Figure 8B.

Type	Relation	Ref.	Type	Relation	Ref.
Regulation	PSII ---> photosynthesis	75	Regulation	OEC ---> photoinhibition	1
Regulation	PSII ---> photodamage	19	MolTransport	PS II ---> oxygen	1
Regulation	PSII ---> electron transfer	29	Expression	At1g17030 --> PSII	1
Regulation	PSII ---> photoinhibition	35	Regulation	PS II ---> respiration	1
Regulation	PS II ---> photoinhibition	6	MolTransport	PSII ---> DCBQ	1
Regulation	PSII ---> reductive pentose-phosphate cycle	3	Regulation	OEC ---> mutagenesis	1
Regulation	ATP synthase ---> photosynthesis	11	Binding	OEC ---- PSII	1
Regulation	PS II ---> photosynthesis	10	Regulation	PSII ---> absorption of light	1
Regulation	PS II ---> electron transfer	7	Regulation	PS II ---> mutagenesis	2
Regulation	PSII ---> DNA recombination	3	Binding	GTPase activity ---- PSII	1
MolSynthesis	PSII ---> water	35	Expression	OEC23 --> PSII	1
MolSynthesis	PSII ---> oxygen	14	MolSynthesis	OEC ---> chlorophyll	1
Regulation	OEC ---> photosynthesis	1	MolTransport	PS II ---> Mn2+	1
MolSynthesis	OEC ---> water	1			

Supplementary table 4: Fold changes in tomato seedling under salt stress as compared with non-salt treated controls after 2 different staining methods.

Fold changes in tomato seedling under salt stress as compared with non-saline controls		
Spot number	Silver staining (Shown in our paper)	Collodial Coomassie staining
4 (F144 radicles)	(+) 18.3 ± 2.17	(+) 16.2 ± 2.89
6 (F144 radicles)	(+) 7.8 ± 0.37	(+) 7.6 ± 0.24
7 (F144 radicles)	(+) 10.5 ± 0.19	(+) 9.1 ± 0.42
9 (F144 radicles)	(+) 2.0 ± 0.09	(+) 2.3 ± 0.36
13 (Patio hypocotyls)	(-) ∞	(-) ∞
17 (F144 hypocotyls)	(+) 2.6 ± 0.13	(+) 2.3 ± 0.38
18 (Patio hypocotyls)	(-) 2.2 ± 0.26	(-) 1.9 ± 0.15
19 (F144 radicles)	(+) 3.8 ± 0.13	(+) 3.2 ± 0.25
22 (F144 radicles)	(+) ∞	(+) ∞
25 (F144 hypocotyls)	(-) 3.9 ± 0.25	(-) 3.3 ± 0.29