

Supporting Information Table S3. List of isoforms of proteins identified in the leaves of *P. tenuiflora* under salt treatment

Thr. MW(Da)/pI ^(c)	Category and name ^(b)	Plant Species ^(c)	gi Number ^(d)	Spot no. ^(a)	Exp. MW(Da)/pI ^(f)	Cov (%) ^(g)	Sco ^(h)	QM ⁽ⁱ⁾	Vol% ^(j)
80,549/6.12	putative transketolase	<i>O. sativa</i> (japonica cultivar-group)	28190676	8865	89,022/5.68	11	393	9	
				7410	83,690/5.70	13	531	15	
55,318/6.11	ATP synthase CF1 alpha subunit	<i>T. aestivum</i>	14017569	7624	65,370/6.88	21	466	10	
				7632	62,218/6.50	33	746	22	
55,287/5.94	ATP synthase alpha subunit	<i>T. aestivum</i>	552976	8715	15,571/5.55	5	122	3	
				8931	68,118/6.21	6	151	3	
				8320	29,211/6.52	13	377	7	
53,806/5.12	Vacuolar ATP synthase subunit B2	<i>H. vulgare</i>	2493132	7672	62,905/5.39	38	806	19	
				7867	45,850/6.68	9	191	4	
80,654/4.96	cytosolic heat shock protein 90	<i>H. vulgare</i>	32765549	7374	92,383/5.27	31	1211	22	
				7353	95,477/5.27	16	665	12	
25,828/5.39	Os02g0634900, containing cd03750 proteasome_alpha_type_2 domain	<i>O. sativa</i> (japonica cultivar-group)	115447473	8402	27,125/5.55	25	294	16	
				8611	18,839/5.80	14	125	4	

98,550/5.79	OSJNBa0039C07.4, containing O. sativa (japonica cultivar-group)	cd00009 AAA ATPases domain:	38347158	7345	98,000/5.80	38	1800	39	
				7340	98,540 /5.98	40	1951	40	
				8491	24,131/5.43	10	430	7	
				8556	20,978/6.83	10	369	8	
29,361/4.83	14-3-3 protein homolog	H. vulgare	100554	8250	30,886/5.03	58	876	24	
				8532	22,614/4.90	34	453	9	
				8231	31,841/5.02	38	624	11	
28,794/4.8	TaWIN2, containing pfam00244 14-3-3 protein domain	T. aestivum	9798605	7375	91,752/6.10	29	222	5	
				8465	25,181/6.51	17	97	3	
31,807/8.47	Os05g0401100, containing O. sativa (japonica cultivar-group)	pfam04536, domain of unknown function (DUF477)	115463773	8513	23,226/5.55	7	107	4	
				8553	21,484/5.55	7	101	2	

^a Assigned spot number as indicated in Figure 6. ^b The name and functional categories of the proteins identified by ESI-Q-TOF MS.

^c The plant species that the peptides matched from. ^d Database accession numbers from NCBI nr. ^{e, f} Theoretical (e) and experimental (f) mass (kDa) and pI of identified proteins. Experimental values were calculated using Image Master 2D Platinum Software. Theoretical values were retrieved from the protein database. ^g The amino acid sequence coverage for the identified proteins. ^h The Mascot score obtained after searching against the NCBI nr database. ⁱ The number of unique peptides identified for each protein. ^j The mean values of protein spot volumes relative to total volume of all the spots and the standard error (SE).

Supporting Information Table S4. Protein spots with multiple *de novo* sequenced proteins identified in a single spot on 2D gels of *P. tenuiflora* leaves

Spot No. (^a)	<i>de novo</i> sequenced peptide (^b)	Matched/given protein name (^c)	Species(^d)	gi Number(^e)	Thr. MW(Da) /pI(^f)	Exp. MW(Da) /pI(^g)
7450	KELAELNR	hypothetical protein CresD4_00200	<i>Corynebacterium resistens</i> DSM 45100	300932462	48,034/ 5.07	77,073/ 4.61
	YESSLSVSR	PuDnSP11			-/-	
8404	VGGGPLGEGLDK	light-harvesting complex	<i>Selaginella moellendorffii</i>	302810440	28,616/ 5.30	37,394/ 5.01
	KNQVLHSR	PuDnSP12			-/-	
8567	LAANDFR	oxidoreductase molybdopterin binding protein	<i>Intrasporangium calvum</i> DSM 43043	317126495	57,707/ 8.20	20,536/ 4.28
	TNAELEFVKSK	PuDnSP13			-/-	
8626	LELSELNR	oxysterol-binding protein-like protein 7	<i>Salmo salar</i>	158702302	97,773/ 7.33	13,865/ 5.20
	ALEESNYELWK	PuDnSP14			-/-	
8732	QQLAELNR	hypothetical protein BACCAP_01792	<i>Bacteroides capillosus</i> ATCC 29799	154497814	53,740/ 9.63	7,881/ 5.30
	MTLDDFR	CBR-MLK-1 protein	<i>Caenorhabditis briggsae</i> AF16	309362239	121,568/ 8.63	
	LQQELATYR	PuDnSP15			-/-	

^aAssigned spot number as indicated in Figure 6. ^b*de novo* sequenced peptides as indicated in Supporting information Figure S2. ^cThe name of the matched proteins by BLAST and novel peptides. ^dThe plant species that the peptides matched from. ^eDatabase accession numbers from NCBI. ^{f, g}Theoretical (f) and experimental (g) mass (kDa) and pI of identified proteins. Experimental values were calculated using Image Master 2D Platinum Software. Theoretical values were retrieved from the protein database.