Salt stress-induced alterations in the root proteome of barley genotypes with contrasting response towards salinity

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Supplementary material

Supplementary Table 1: Effect of salinity stress on the dry weight of root and leaves in barley cultivars Morex and Steptoe. Plants were harvested after 13 days of stress treatment at NaCl levels ranging from 0 – 250 mM and the dry weight was determined. Values represent the mean ± standard error of 20 plants. Statistical differences between treatments were analyzed following the Duncan multiple range tests. Asterisks indicate significant differences at $p < 0.05$ as compared to the control.

NaCl concentration [mM]	Second leaf [mg]	Third leaf [mg]	Root [mg]
Morex			
0	42,00 ± 2,38	40,80 ± 2,50	37,00 ± 2,40
50	36,90 ± 1,23	33,95 ± 2,78*	34,00 ± 1,93
100	36,75 ± 1,50	17,55 ± 1,51*	26,05 ± 1,42*
150	40,65 ± 1,97	16,70 ± 1,72*	24,60 ± 1,51*
200	36,89 ± 2,11	7,53 ± 1,21*	18,26 ± 1,02*
250	40,39 ± 2,49	5,89 ± 1,45*	18,17 ± 1,39*
Steptoe			
0	54,50 ± 1,97	30,45 ± 2,21	49,25 ± 2,71
50	51,75 ± 1,29	26,65 ± 2,37	49,00 ± 1,99
100	49,40 ± 2,19	4,10 ± 0,66*	33,40 ± 1,82*
150	54,25 ± 2,83	1,33 ± 0,28*	36,80 ± 2,48*
200	40,75 ± 2,85*	0,50 ± 0,17*	23,95 ± 1,44*
250	42,65 ± 2,51*	0,45 ± 0,06*	24,40 ± 1,44*

Supplementary Table 2: The identification of protein spots by MALDI-TOF MS and LC-ESI-Q-TOF MS/MS. For proteins identified by MALDI-TOF MS, the MASCOT score, peptide tolerance in parts per million (ppm) and the number of matching peptides are provided. For MS/MS identifications, the ProteinLynx GlobalServer score, peptide tolerance in ppm, number of *de novo* sequenced peptides and the respective *de novo* peptide sequences are given.

Spot ID	**TIGR**	**Description**	**MALDI-TOF MS**			**LC-ESI-Q-TOF MS/MS**			
			Score	**ppm**	**Matching peptides**	**Score**	**ppm**	**Sequenced peptides**	***De novo* sequences**
895	TC139604	Late embryogenesis abundant protein, *Oryza sativa*				10.83	10	2	(G)LVAGLIPDAGTVR(C) (C)VPITLDFDDIR(T)
900	TC139604	Late embryogenesis abundant protein, *Oryza sativa*				10.83	10	3	(G)LVAGLIPDAGTVR(C) (C)VPITLDFDDIR(T) (G)LPIDHVGGTTR(G)
968	TC130772	Lactoylglutathione lyase, *Oryza sativa*				10.69	10	6	(A)SAEAVLEWPK(G) (A)SAEAVLEWPKQDK(C) (A)GNAYAQVAIGTDDVYK(A) (G)SAEAVELVTK(C) (T)ITSFLDPDGWK(T) (A)VVLVDYADFLK(C)
777	TC131046	S-adenosylmethionine synthetase 1, *Hordeum*	117	100	12				

		vulgare							
1161	TC139656	Carboxymethylenebutenolidase-like protein, *Oryza sativa*				10.83	10	1	(C)EDTTFDAYVVGK(C)
955	TC140370	Peroxidase, *Hordeum vulgare*	140	100	12				
355	TC146955	Lipoxygenase 1, *Hordeum vulgare*				10.83	10	1	(T)EVLAGVNPVMITR(G)
997	TC149802	(1-3)-β-glucanase GV, *Hordeum vulgare*				10.83	10	4	(T)DPSYAAGWVR(T) (A)SNVQAYYPDVLIR(T) (G)FDVITNSFPPSSGVFR(T) (G)NYNQGLIDHIR(G)
703	TC133105	Cytosolic 6-phosphogluconate dehydrogenase, *Oryza sativa*	77	100	10				
939	NP315772	Probable nicotianamine synthase 7, *Hordeum vulgare*				10.83	10	6	(G)ITGLHAAIAK(G) (C)LAPEAQAMR(T) (T)LEYELLAR(A) (G)YVPGGIAPAR(C) (C)GFLYPIVDPQDIGR(T) (A)FGEMVADVTQK(A)
1747	TC137024	Not found				10.83	10	2	(C)VTEEQAATAFR(C) (T)EGAAQAVYVAR(A)
499	TC139384	F23N19.10 stress-inducible protein, *Arabidopsis thaliana*				10.83	10	2	(G)GDISQEDLQEK(C) (C)LINAGIVQTR(A)
759	TC132873	Putative monodehydroascorbate reductase,	85	100	12				

		Oryza sativa							
760	35_16328	Putative nuclear RNA binding protein A, *Oryza sativa*	65	100	9				
931	TC130772	Lactoylglutathione lyase, *Oryza sativa*				10.54	10	4	(G)SAEAVELVTK(C) (T)QPGPLPGLNTK(G) (T)ITSFLDPDGWK(T) (A)VVLVDYADFLK(C)
507	TC139323	Poly(A)-binding protein, *Triticum aestivum*	102	100	12				
689	TC139229	Catalase 1, *Hordeum vulgare*				10.83	10	6	(A)APGVQTPVIVR(A) (C)FSTVVHER(G) (G)DLTDSIAAGNYPEWK(C) (G)TWPEDIIPLQPVGR(G) (T)LGPNYLMLPVNAPK(G) (T)DEEVNYFPSR(T)
871	TC137786	Iron-deficiency specific protein IDS2, *Hordeum vulgare*	78	100	11				
929	TC142112	Iron-deficiency specific protein IDS3, *Hordeum vulgare*	113	100	11				
942	TC147014	Fructokinase 2, *Oryza sativa*				10.08	10	5	(C)LPLWPSAQAAR(C) (C)VSDDEVAFLTQGDANDEK(A) (C)LLIVTDGEK(A) (G)DDSIFYNEAK(C)

						(G)GAIPALPTTATALELISK(G)
943	TC147167	Iron-deficiency induced protein IDI2, *Hordeum vulgare*	123	100	13	
1167	TC145151	Iron-deficiency induced protein IDI1, *Hordeum vulgare*	197	100	19	
1213	TC146774	Glutathione S-transferase F5, *Triticum aestivum*	73	100	9	
1228	TC138639	23 kDa jasmonate-induced protein, *Hordeum vulgare*	82	100	7	
1069	TC131931	Probable L-ascorbate peroxidase 7, *Oryza sativa*	84	100	12	
1216	TC131931	Probable L-ascorbate peroxidase 7, *Oryza sativa*	102	100	15	