

Supplementary data

Cold-induced changes of protein and phosphoprotein expression patterns from rice roots as revealed by multiplex proteomic analysis

Jinhui Chen^{1,†}, Tian Lin^{2,†}, Huifang Xu^{3,5}, Dagang Tian⁴, Yuming Luo³, Chongmiao Ren³, Liming Yang^{3,*}, Jisen Shi^{1,*}

Table S1. Identification of differentially expressed phosphoproteins in cold-stressed rice roots by MALDI-TOF/TOF MS analysis of the Pro-Q Diamond–stained 2DGE gels.

Table S2. Identification of differentially expressed proteins in cold-stressed rice roots by MALDI-TOF/TOF MS analysis of the silver-stained 2DGE gels.

Table S1. Identification of differentially expressed phosphoproteins in cold-stressed rice roots by MALDI-TOF/TOF MS analysis of the Pro-Q Diamond–stained 2DGE gels.

Spot No	Exp. MW (kDa)/pI	Coverage(%) / Number of peptides matched	Score	NCBI accession	Theor. MW (kDa)/pI	Protein identity	Protein function
1	52.6/5.6	45.5%(15)	125	ABG65935	48.5/6.3	Enolase	Carbohydrate metabolism
2	43.5/5.2	39.6%(10)	103	AAA82047	36.6/7.4	Glyceraldehyde-3-phosphate dehydrogenase	Carbohydrate metabolism
3	17.3/5.3	35.7%(5)	94	AAG60181	16.1/6.2	Nucleoside diphosphate kinase	Signal transduction
4	28.5/5.4	36.3%(7)	98	BAA08264	27.5/5.8	Ascorbate peroxidase	Redox homeostasis
5	52.6/5.5	22.6%(9)	75	ABG65935	48.0/6.2	Enolase	Carbohydrate metabolism
6	40.6/5.3	42.3%(11)	124	EAZ23871	37.2/4.9	Adenosine kinase	Signal transduction
7	45.8/5.3	46.1%(15)	116	EAZ02359	38.4/5.3	CPK1 adapter protein 2	Signal transduction
8	55.1/5.3	28.6%(11)	89	YP_002000594	54.2/6.4	ATP synthase subunit alpha	Energy metabolism
9	75.0/5.3	37.2%(23)	138	ABG22093	79.0/7.2	Methionine synthase 1	Amino acid metabolism
10	30.1/5.4	30.4%(6)	75	BAA08264	27.5/5.5	Ascorbate peroxidase	Redox homeostasis
11	52.6/5.7	38.3%(14)	89	Q42971	48.0/5.4	Enolase	Carbohydrate metabolism
12	48.7/6.2	33.5%(9)	104	AAX96762	49.7/4.8	Tubulin	Cell structure

Table S2. Identification of differentially expressed proteins in cold-stressed rice roots by MALDI-TOF/TOF MS analysis of the silver-stained 2DGE gels.

Spot No	Exp. MW (kDa)/pI	Coverage(%) / Number of peptides matched	Score	NCBI accession	Theor. MW (kDa)/pI	protein identity	protein function
1	29.0/4.5	52%(9)	133	BAB17666	27.1/5.2	ascorbate peroxidase	Redox homeostasis
2	25.5/5.1	64%(10)	86	AAL71856	23.6/5.8	dehydroascorbate reductase	Redox homeostasis
3	39.7/5.8	31%(9)	71	Q0JGZ6	34.7/5.1	fructokinase-1	Carbohydrate metabolism
4	78.5/6.1	26%(8)	66	BAD13711	87.7/6.2	pentatricopeptide (PPR) repeat-containing protein	Defense related
5	48.3/5.8	32%(13)	103	ABF94252.1	52.1/6.4	Adenylosuccinate Synthetase	metabolism
6	78.5/6.2	38%(12)	122	AAO65876	71.4/5.1	heat shock 70 protein	Protein folding and assembly
7	60.0/5.7	51%(16)	84	BAB78494	41.4/5.9	26S proteasome regulatory particle triple-A ATPase subunit3	Protein degradation
8	37.6/5.7	50%(11)	111	P14656	39.2/5.5	Glutamine synthetase cytosolic isozyme 1-1	Amino acid metabolism
9	55.0/5.6	30%(10)	74	ABF98584	55.1/5.6	glutamate decarboxylase	Amino acid metabolism
10	36.2/5.8	34%(7)	86	CAH69301	37.0/5.6	TPA: class III peroxidase 59 precursor	Redox homeostasis
11	58.1/5.9	42%(18)	142	AAT77033	59.0/5.39	putative TCP-1/cpn60 chaperonin family protein	Protein folding and assembly
12	37.2/6.2	44%(10)	72	BAD09896	36.9/5.7	glyceraldehyde-3-phosphate dehydrogenase	Carbohydrate metabolism
13	56.7/6.2	69%(17)	235	BAD45436	42.2/6.2	phosphoglycerate kinase 1, cytosolic	Carbohydrate metabolism

14	47.1/6.5	39%(17)	125	Q9FXT9	47.7/6.0	26S protease regulatory subunit 7	Defense related
15	53.4/6.6	28%(9)	101	AAO84040	55.2/5.7	catalase	Redox homeostasis
16	56.4/5.4	34%(12)	117	BAA77260	52.6/6.2	alanine transaminase	Amino acid metabolism
17	80.1/6.5	19%(12)	90	Q0DZE0	77.0/5.9	Phenylalanine ammonia-lyase	Redox homeostasis
18	57.6/6.6	43%(14)	111	ABA97736	52.9/5.6	UDP-glucose 6-dehydrogenase	Carbohydrate metabolism
19	72.5/6.8	51%(26)	89	EEC70619	66.1/6.9	ferredoxin-nitrite reductase precursor	Redox homeostasis