

Supplementary Material

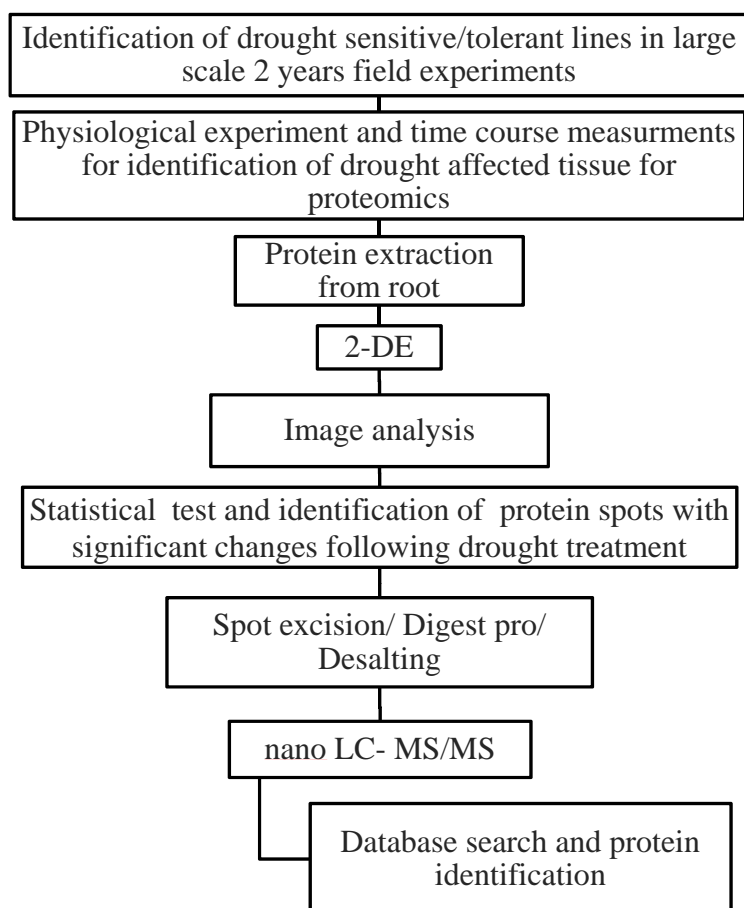
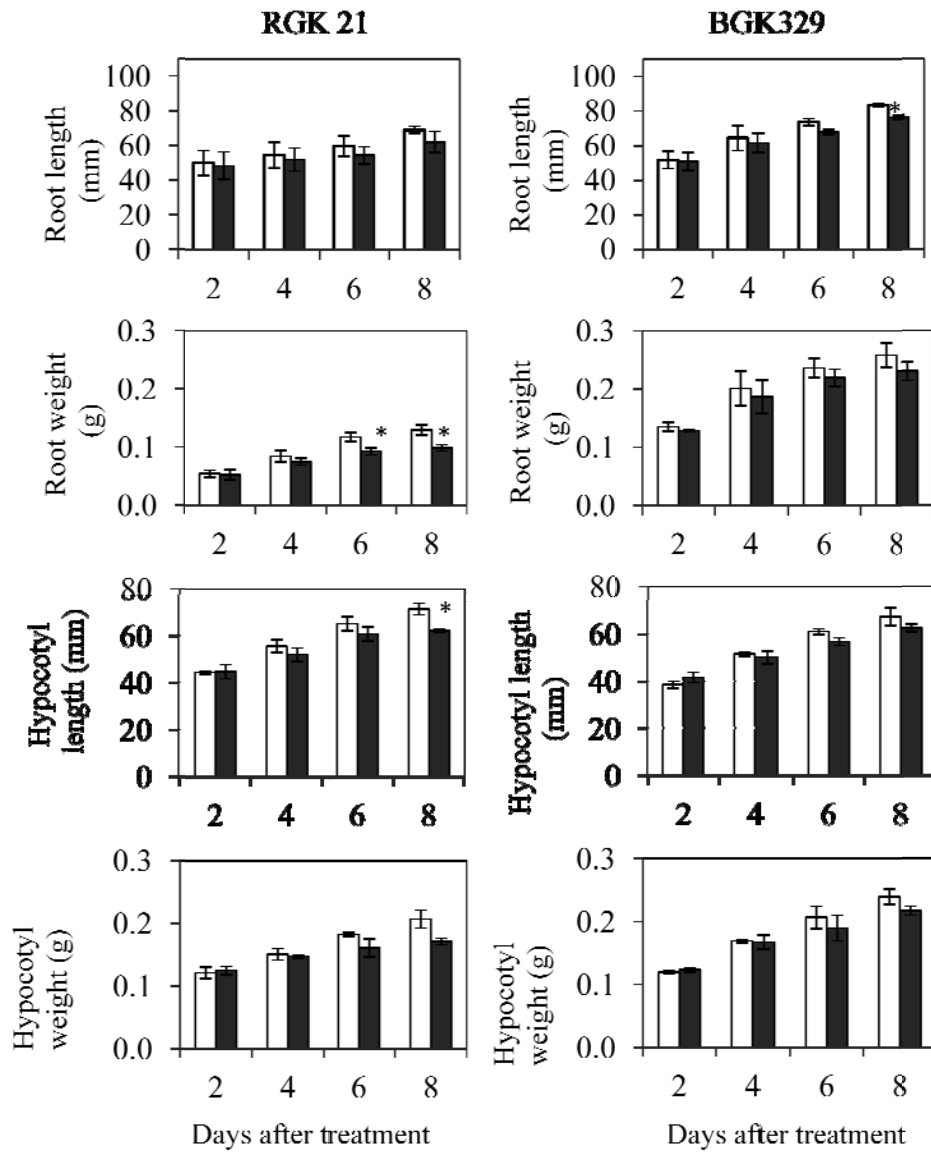


Fig. S1. Flowchart of experimental system.

(a)



(b)

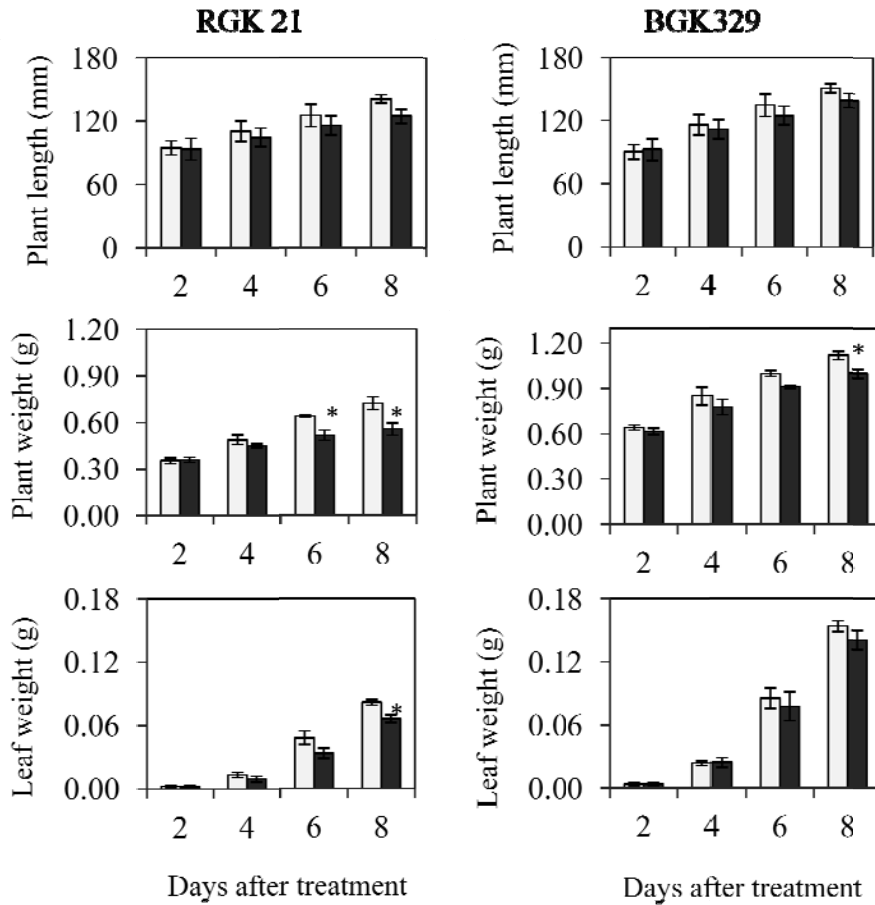


Fig. S2. Effects of drought stress on growth of sunflower seedlings. Sensitive line (RGK 21) and tolerant line (BGK 329) were used. Drought stress was imposed 3 days after sowing. After treatment root and hypocotyl length and weight (a) and plant length, plant weight and leaf weight (b) were measured 2, 4, 6 and 8 days after treatment for control (white bars) and treated (black bars) plants. Values are the mean \pm s.e. from three physiological independent experiments. Asterisks indicate significant difference between control and drought stress treatment (* $P < 0.05$, ** $P < 0.01$).

Table S1. Mean over 2 years field experiments data for physiological characteristics of sunflower lines in control (C) and drought (D) conditions

Each value comes from 18 replications

Lines	Relative water content (%)				Leaf area (cm ²)				Proline content (mg/g fresh weight)				Seed yield (g/ plant)			
	C	s.e.	D	s.e.	C	s.e.	D	s.e.	C	s.e.	D	s.e.	C	s.e.	D	s.e.
BGK 109	77.4	0.8	59.5	0.9	2738	40	1550	23	5.5	0.5	9.4	0.4	8.0	0.1	5.3	0.1
BGK 147	78.1	1.2	59.6	0.8	3229	39	2164	46	5.8	0.6	12.4	1.1	8.9	0.3	6.8	0.3
BGK 195	81.7	0.9	65.3	1.3	3033	30	1858	43	6.7	0.5	10.9	1.3	9.4	0.4	5.2	0.2
BGK 221	81.0	0.9	62.6	1.0	2825	29	1521	56	6.6	0.7	12.2	0.9	9.7	0.2	5.2	0.2
BGK 259	78.5	1.0	60.3	1.2	2512	37	1454	65	6.7	0.7	17.2	0.6	9.2	0.3	5.4	0.2
BGK 309	77.7	1.0	59.5	1.2	3041	30	1940	27	6.3	0.2	14.4	0.6	8.4	0.3	5.2	0.2
BGK 329	82.0	0.5	66.8	0.6	3578	26	2447	83	6.3	0.3	16.4	0.8	12.0	0.4	8.0	0.2
BGK 343	79.2	1.0	60.1	1.0	2649	27	1223	57	5.6	0.2	13.1	1.3	9.6	0.1	5.5	0.1
BGK 345	81.3	0.9	61.0	1.0	2737	30	1475	36	5.5	0.3	12.3	1.1	8.1	0.3	4.7	0.1
BGK 355	78.7	0.5	59.8	0.7	1938	20	1333	29	5.7	0.4	12.4	0.6	7.1	0.4	4.4	0.2
RGK 21	80.6	0.6	58.5	0.8	2750	65	1225	56	5.2	0.1	9.2	0.6	10.6	0.3	4.2	0.2
RGK 23	80.4	0.7	64.3	1.1	2661	34	1617	32	5.9	0.5	11.9	0.7	9.0	0.3	5.1	0.1
RGK 26	79.1	0.7	65.5	1.7	2913	61	1994	54	6.0	0.3	16.5	1.4	10.1	0.3	7.1	0.5
RGK 3	78.6	0.7	63.8	0.8	3246	44	2193	57	6.5	0.4	13.2	1.2	9.9	0.5	6.1	0.3
RGK 46	81.6	0.6	66.8	1.0	3397	37	2434	61	6.2	0.2	15.4	1.5	10.4	0.4	6.6	0.2
RGK 56	79.9	1.3	65.0	1.2	3100	36	2060	32	5.1	0.3	11.1	0.5	9.3	0.3	5.6	0.2

Table S2. Identities of sunflower roots proteins corresponding to the protein spots shown in Fig. 4

Spot	Homologous protein	Accession no ^b	Score ^c	Cov	MP ^e	Blast	Mr ^g (kDa) / pI ^h	FC ^k	P	Local ^m	
Metabolism											
1	Lipin domain- containing protein	AEE00748.1	141	14	4	1714	97.4/4.73	96/4.5	3.37	0.037	Plas
3	ATP:citrate lyase	AAK13318.1	118	12	5	1186	66.38/7.11	62.5/5.2	0.26	0.004	Plas
13	Adenosylhomocysteinase 1	NP_193130.1	135	24	11	953	53.99/5.58	60/5.4	0.62	0.059	Cyto
15	Triosephosphate isomerase, cytosolic	P48493.1	925	43	7	387	20.76/5.28	27/5.2	0.71	0.045	Cyto
19	UDP-L-rhamnose synthase	ACJ11713	289	18	7	613	33.95/5.73	36/5.9	0.74	0.011	Nucl.
30	ATP:citrate lyase	AAK13318.1	118	12	5	1186	66.38/7.11	62.5/5.2	0.61	0.016	Plas
35	Triosephosphate isomerase, cytosolic	P48493.1	925	43	7	387	20.76/5.28	29/5.5	1.31	0.030	Cyto
37	Phosphoglycerate mutase, 2,3-	NP_187471.1	122	14	6	1127	60.99/5.53	58/5.6	0.72	0.022	Cyto
40	UDP-L-rhamnose synthase	ACJ11713	289	18	7	613	33.95/5.73	36/5.9	0.76	0.039	Nucl.
41	Methionine synthase	ABI35986.1	374	23	16	1427	84.86/6.02	66/6.1	0.67	0.019	Cyto
Energy											
4	ATP synthase subunit a, chloroplastic	A0A323	505	15	6	948	26.69/5.23	27/5.1	0.51	0.022	Plas
8	Enolase	NP_001105896.1	149	17	7	884	48.26/5.20	58/5.2	0.56	0.009	Cyto
9	Enolase	P42896.1	120	18	4	879	48.11/5.56	66.5/5.2	0.62	0.005	Cyto
10	ATP synthase subunit beta, mitochondrial	P17614.1	189	24	9	967	59.93/5.59	55/5.3	0.45	0.008	Mito
11	Enolase	P42896.1	102	7	2	879	48.11/5.56	41/5.3	0.78	0.042	Cyto
12	Phosphoglycerate mutase, 2,3-	NP_187471.1	122	14	6	1127	60.99/5.53	64/5.4	0.59	0.006	Cyto
14	Enolase	P42896.1	102	7	2	879	48.11/5.56	41/5.3	0.62	0.018	Cyto
31	ATP synthase subunit a, chloroplastic	A0A323	505	15	6	948	26.69/5.23	29/5.3	1.68	0.020	Plas
33	Enolase 1	NP_001105896.1	149	17	7	884	48.26/5.20	58/5.2	0.55	0.007	Cyto
34	Enolase 1	NP_001105896.1	149	17	7	884	48.26/5.20	41/5.3	0.72	0.001	Cyto
42	ATP synthase f1, gamma subunit, putative	XP_002531492.1	100	13	3	620	35.8/8.95	37/6.2	2.04	0.007	Mito
47	Glyceraldehyde 3-phosphate dehydrogenase	AES72079.1	240	30	7	580	37.1/6.97	38/6.7	1.42	0.028	Cyto
Disease/defense											
5	Ascorbate peroxidase 2-like protein	ADD64890.1	135	42	6	186	13.21/4.61	32/5.2	3.67	0.009	Cyto
7	Ascorbate peroxidase 2-like protein	ADD64890.1	117	26	3	186	13.21/4.61	39/5.2	0.37	0.008	Cyto
16	Cu/Zn superoxide dismutase	CAH06454	108	49	6	315	15.52/5.61	19/5.5	0.78	0.019	Cyto
25	Heat shock protein, putative	XP_002526446.1	112	11	3	1154	75.41/5.24	96/4.8	6.26	0.002	Plas
26	Heat shock protein hsp70	AAV97978.1	157	10	6	1191	71.22/5.11	96/4.9	0.53	0.029	Cyto
27	Chloroplast heat shock protein 70-1	ABZ04080.1	167	24	17	1242	74.48/5.14	66/4.9	1.89	0.022	Plas
28	Catalase	P45739.1	322	19	5	1036	57.00/6.60	43/5	1.77	0.010	Pero
32	Ascorbate peroxidase 2-like protein	ADD64890.1	117	26	3	186	13.21/4.61	39/5.2	2.46	0.004	Cyto
36	Cu/Zn superoxide dismutase	CAH06454	108	49	6	315	15.52/5.61	20/5.5	1.2	0.019	Cyto

Table S2. Continued

Cell Structure											
2	Alpha-tubulin	ABK28851.1	158	33	13	836	50.46/4.94	48/5.1	0.46	0.002	Cyto
17	Indole-3-acetic acid-amido synthetase	O81829	234	23	5	471	69.28/5.72	66/5.7	1.94	0.011	Nucl
29	Alpha-tubulin	ABK28851.1	158	33	13	836	50.46/4.94	48/5.1	0.58	0.014	Cyto
45	Lignin forming anionic peroxidase	Q02200	730	32	9	1023	30.50/6.38	30/6.3	1.29	0.030	Plas
Secondary metabolism											
6	(S)-tetrahydroprotoberberine oxidase	AEK69741.1	183	18	4	466	25.46/6.08	36/5.2	1.66	0.037	Plas
22	Lignin forming anionic peroxidase	Q02200	730	32	9	1023	30.50/6.38	30/6.3	1.81	0.036	Plas
23	Chalcone synthase	Q9ZU06	278	19	4	747	42.48/6.99	41/6.7	1.37	0.023	Cyto
46	Chalcone synthase	Q9ZU06	278	19	4	747	42.48/6.99	41/6.7	0.67	0.015	Cyto
Protein Destination											
18	Proteasome subunit alpha type, putative	XP-002271929.1	294	31	9	469	27.42/5.91	29/5.8	0.55	0.017	Cyto
38	Ubiquitin carboxyl-terminal hydrolase	XP_002524120.1	112	5	5	2181	131.76/5.44	90/5.7	0.68	0.046	Cyto
44	Chaperonin containing t-complex protein 1, eta subunit, tcph, putative	XP_002528805.1	177	19	8	872	61.64/6.03	53/6.4	0.54	0.038	Cyto
Cell growth/Division											
20	Anaphase-promoting complex subunit 6	B3DNN5	364	17	5	921	61.76/5.93	62/5.9	0.62	0.036	Nucl
Signal transduction											
21	Nucleotide binding protein	NP_001147117.1	132	14	7	969	63.59/5.37	48/6	0.80	0.050	Nucl
24	14-3-3-like protein	O65352.1	150	35	8	456	29.04/4.65	33/4.7	1.34	0.041	Plas
48	G protein beta-subunit-like protein	CAA96528.1	115	21	5	618	36.5/7.42	36/6.7	0.68	0.024	Nucl
Transport											
43	Probable aquaporin TIP4-1	Q75GA5	292	25	7	961	25.66/6.21	26/6.2	1.44	0.027	Cyto
Unknown											
39	Auxin-induced protein	AAB84222.1v	107	8	2	685	37.67/6.03	39/5.8	0.73	0.012	Nucl
49	ND	-	-	-	-	-	-	43/5.9	0.55	0.024	-
50	ND	-	-	-	-	-	-	40/6	1.64	0.009	-
51	ND	-	-	-	-	-	-	25/6.1	1.22	0.044	-
52	ND	-	-	-	-	-	-	39/7.7	1.58	0.017	-
53	ND	-	-	-	-	-	-	29/6.2	1.33	0.014	-
54	ND	-	-	-	-	-	-	37/8	1.66	0.047	-

^a Spot no, spot number as given in Fig. 4. ^b Accession no according to the NCBI database, ^c Score, ions score of identified protein using NCBI sequence databases. ^dCov., Sequence coverage. ^eM.P., number of query matched peptides, ^fBlast score, the score of high scoring segment pair from that data base sequence; ^gMr, molecular weight; ^hpI, isoelectric point, ⁱTheo., theoretical; ^jExp., experimental ^kF.C., fold change, The protein spots showed a significant change in abundance compared to the control analyzed by student t-test, ^lp value, indicates the significance of increased/decreased level of protein spots according to the student t-test, ^mLocal., Localization, category using local classification, Mito, mitochondria; Nucl, nuclear; Cyto, cytoplasm; Plas, plastid; Pero, peroxisome.