Table 1 Suppl. The parameters of Chl *a* fluorescence of dark adapted leaves of wheat seedlings subjected to a gradual drought stress as compared with those grown in control conditions: Ethos - drought tolerant cultivar and Zebra - drought sensitive cultivar. WSD - water saturation deficit. Means of 10 measurements. The Duncan honesty test and the Least Significant Difference (LSD) test (Student t-test) based on one way *ANOVA* were used for detailed comparison of fluorescence parameters ($P \leq 0.05$). The Duncan test was used for comparison of drought influence on particular parameter within cultivar (the same letter mean no statistically important differences between mean values). The LSD test was used for means comparison between cultivars (n.d. = non detected difference).

Parameters	WSD [%]	Ethos	Zebra	LSD
F_0 Initial fluorescence	control	4.397 a	4.378 a	n.d.
	15	4.068 b	3.831 b	n.d.
	30	3.783 bc	3.623 bc	n.d.
	50	3.749 c	3.488 c	n.d.
F_M Maximal fluorescence	control	23.354 a	23.523 a	n.d.
	15	21.590 b	19.662 b	**
	30	19.847 c	17.342 c	**
	50	16.443 d	14.813 d	n.d.
F_V Variable fluorescence $F_V = F_M - F_0$	control	18.957 a	19.145 a	n.d
	15	17.522 b	15.831 b	**
	30	16.063 c	13.719 c	**
	50	12.695 d	11.325 d	n.d.
F_1 Fluorescence at time 0.05 ms	control	5.079 a	4.964 a	n.d.
	15	4.640 b	4.332 b	n.d
	30	4.384 b	4.204 b	n.d.
	50	4.521 b	3.995 b	**
F_2 Fluorescence at time 0.1 ms	control	5.699 a	5.489 a	n.d.
	15	5.161 b	4.779 b	**
	30	4.928 b	4.735 b	n.d.
	50	5.233 b	4.458 b	**
F_3 Fluorescence at time 0.3 ms	control	8.471 a	7.932 a	**
	15	7.481 bc	6.867 b	**
	30	7.291 c	7.040 b	n.d.
	50	8.049 ab	6.514 b	**
F_4 Fluorescence at time 2.0 ms	control	13.777 a	12.967 a	**
	15	12.261 b	11.191 b	**
	30	11.640 b	10.901 bc	n.d.
	50	11.627 b	10.119 c	**
F_5 Fluorescence at time 30 ms	control	19.850 a	20.576 a	n.d.
	15	18.609 b	17.260 b	**
	30	17.422 c	15.675 c	**
	50	14.874 d	13.531 d	n.d.
T_{fm} Time needed to reach F_M [ms]	control	166 b	197 c	**
	15	153 b	226 b	**
	30	244 a	240 b	n.d.
	50	247 a	268 a	n.d.
Area A total complementary area between the x-axis and F_M of the OJIP curve	control	267 a	254 a	n.d.
	15	243 a	222 a	n.d.
	30	245 a	179 b	**
	50	174 b	159 b	n.d.
F_V/F_M Maximum photochemical efficiency of PSII	control	0.812 a	0.814 a	n.d
	15	0.812 a	0.805 a	n.d.
	30	0.810 a	0.791 a	n.d.
	50	0.772 b	0.762 b	n.d.
F_V/F_0 Parameter reflecting the structural alterations on the donor side of the PSII	control	4.309 a	4.382 a	n.d.
	15	4.330 a	4.136 b	n.d.
	30	4.259 a	3.791 c	**
	50	3.393 b	3.233 d	n.d.
RC/ABS The amount of active reaction centers per absorption	control	0.952 a	1.102 a	**
	15	1.047 a	1.056 a	n.d.
	30	0.943 a	0.824 b	n.d.
	50	0.593 b	0.749 b	n.d.
(1-Vj)/Vj	control	0.503 a	0.552 a	**

A measure of forward electron transport	15	0.533 a	0.534 a	n.d.
	30	0.510 a	0.464 b	**
	50	0.376 b	0.406 c	n.d.
PI The performance index of PS II based on absorption	control	2.084 a	2.343 a	**
	15	2.405 a	2.323 a	n.d.
	30	2.078 a	1.508 b	**
	50	0.806 b	1.270 c	n.d.

Table 2 Suppl. Drought-responsive proteins identified by mass spectrometry from leaves of wheat cv. Ethos seedlings subjected to a gradual dehydration inducing 15, 30 and 50 % water saturation deficit (WSD) in comparison with control plants. Proteins differing at least twofold in abundance with P ≤ 0.001 were designated using the *Delta 2* program.

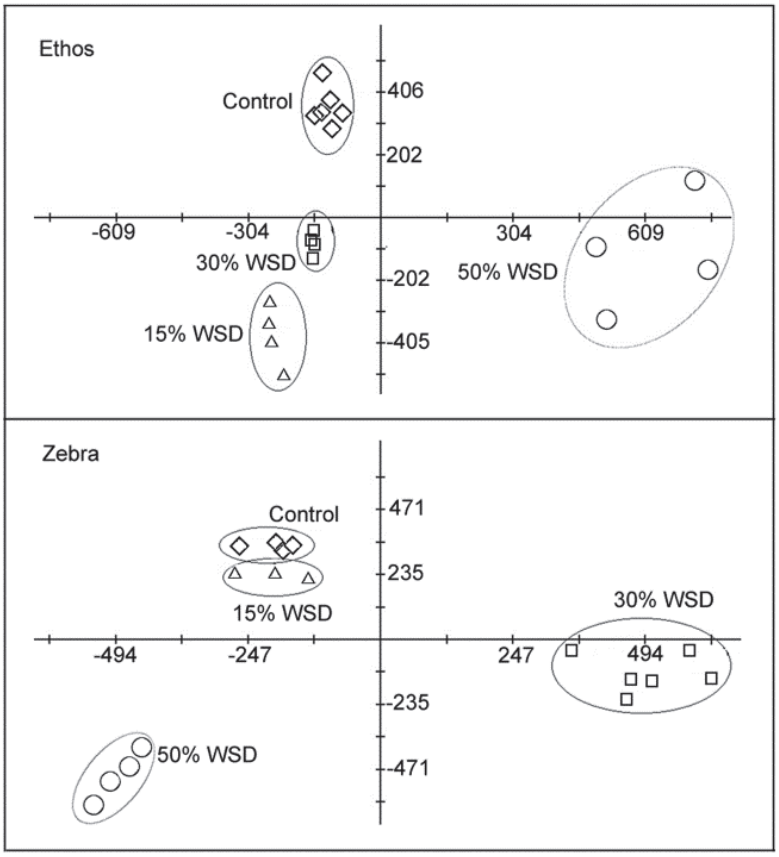
Protein number	Accession	Mascot score	Mass	pI	Pept.. N°	Protein name preceded by /String/ and /Mascot/ classifiers	WSD [%]/ regulation
Photosynthesis/energy metabolism							
5887	gi|302566696	64	28196	4.963	3	/MLOC_945.1/ADL41158.1/ chloroplast light-harvesting chlorophyll a/b binding protein [*T. aestivum*]	15 ↓
6773	gi|4090293	427	19492	8.166	13	/MLOC_64679.1/CAA10497.1/ hypothetical protein [*S. cereale*]/ blasted by gi number from NCBInr as Rubisco small subunit	30 ↓
7634	gi|4038657	239	18600	8.457	11	/MLOC_64679.1/BAA35145.1/ ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [*A. speltoides*]	50 ↓
5750	gi|474311276	821	44825	5.491	17	/MLOC_16226.1/EMS61907.1/ ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic [*T. urartu*]	15 ↑
6027	gi|290875537	1317	28058	7.666	21	/MLOC_43331.1/ADD65763.1/ putative carbonic anhydrase [*S. cereale* x *T. durum*]	15 ↑
5604	gi|326533372	1238	74032	5.347	5	/MLOC_20190.3/BAJ93658.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI nr as transketolase C-terminal domain	15 ↑
5598	gi|326533372	5474	74032	5.347	16	/MLOC_20190.3/BAJ93658.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI nr as transketolase C-terminal domain	15 ↑
5569	gi|326533372	10357	74032	5.347	29	/MLOC_20190.3/BAJ93658.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI nr as transketolase C-terminal domain	15 ↑
6480	gi|357110873	7459	80095	5.938	18	/MLOC_20190.3/XP_003557240.1/ predicted: transketolase, chloroplastic-like [*B. distachyon*] C-terminal domain	30 ↑
6503	gi|357110873	4046	80095	5.938	8	/MLOC_20190.3/XP_003557240.1/ predicted: transketolase, chloroplastic-like [*B. distachyon*] C-terminal domain	30 ↑
6513	gi|357110873	976	80095	5.938	5	/MLOC_20190.3/XP_003557240.1/ predicted: transketolase, chloroplastic-like [*B. distachyon*] C-terminal domain	30 ↑
6486	gi|474352176	1258	68469	5.225	28	/MLOC_20190.3/ E MS63024.1/ transketolase, chloroplastic [*T. urartu*] C-terminal domain C-terminal domain	30 ↑
5762	gi|326502358	459	28671	6.02	8	/MLOC_17604.2/BAJ95242.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI nr as ribose-5-phosphate isomerase	15 ↑
5911	gi|326502358	441	28671	6.02	8	/MLOC_17604.2/BAJ95242.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI nr as ribose-5-phosphate isomerase	15 ↑
5907	gi|326502358	739	28671	6.02	8	/MLOC_17604.2/BAJ95242.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI nr as ribose-5-phosphate isomerase	15 ↑
7604	gi|223018643	106	41988	5.834	7	/MLOC_58958.2/ACM78035.1/ chloroplast fructose-bisphosphate aldolase [*T. aestivum*]	50 ↑
6419	gi|473793124	1850	85864	6.022	40	/MLOC_36667.1/EMS46370.1/ glycine dehydrogenase [decarboxylating] B, mitochondrial [*T. urartu*]	30 ↑
7568	gi|473912215	3706	46903	6.043	24	/MLOC_15296.1/EMS49604.1/ glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic [*T. urartu*]	50 ↑
7536	gi|474416303	1262	45185	6.516	31	/MLOC_58024.1/EMS67204.1/ succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial [*T. urartu*]	50 ↑
Protein metabolism							
7606/5917	gi|71362640	1439	46673	5.69	16	/MLOC_11890.1/AAZ30062.1/ plastid glutamine synthetase isoform GS2c [*T. aestivum*]	15, 50 ↑
7604	gi|121340	844	47064	4.923	15	/MLOC_11890.1/P13564.2/Glutamine synthetase leaf isozyme, chloroplastic	50 ↑
6010	gi|473742116	551	22041	8.773	11	/MLOC_16249.1/EMS45427.1/ 50S ribosomal protein L21, chloroplastic [*T. urartu*],	15 ↑
6923	gi|356463684	214	43929	5.026	5	/MLOC_38604.1/AET08880.1/ metacaspase 1 [*A. speltoides*]	30 ↑
6906	gi|132270	101	14713	4.836	6	/MLOC_65295.2/P15252.2/ Rubber elongation factor protein	30 ↑

Stress-related proteins							
5784	gi|357147646	1935	46482	4.645	13	/MLOC_15227.2/XP_003574425.1/ predicted: peptidyl-prolyl cis-trans isomerase, chloroplastic-like [*B. distachyon*]	15 ↑
6705	gi|357147646	934	46140	4.645	16	/MLOC_15227.2/XP_003574425.1/ predicted: peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic-like [*B. distachyon*]	30 ↑
7559	gi|357147646	642	46140	4.645	15	/MLOC_15227.2/XP_003574425.1/ predicted: peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic-like [*B. distachyon*]	50 ↑
6923	gi|326527909	659	24633	7.105	7	/MLOC_15227.2/BAJ89006.1/ predicted protein [*H. vulgare*]/ blasted as CYP38	30 ↑
5907	gi|108711184	48	20678	5.22	5	/MLOC_80410.1/ABF98979.1/ 26S proteasome non-ATPase regulatory subunit 10, putative, expressed [*O. sativa* Japonica Group]	15 ↑
5532	gi|357149201	6432	97690	5.93	43	/MLOC_73713.1/XP_003575034.1/ predicted: chaperone protein ClpC1, chloroplastic-like [*B. distachyon*]	15 ↑
6534	gi|13925726	527	56406	4.841	30	/MLOC_351.5/AAK49424.1/ protein disulfide isomerase 2 precursor [*T. aestivum*]	30 ↑
5576	gi|2827002	746	70986	4.952	30	/MLOC_72334.1/AAB99745.1/ HSP70 [*T. aestivum*]	15 ↑
6485	gi|326499406	1126	71230	4.908	38	/MLOC_45046.1/BAJ86014.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBInr as HSP70	30 ↑
ROS detoxifying enzymes							
7704	gi|15808779	1165	27622	4.919	10	/COG0376/AAL08496.1/ ascorbate peroxidase [*H. vulgare*]	50 ↑
7689	gi|15808779	1596	27622	4.919	9	/COG0376/AAL08496.1/ ascorbate peroxidase [*H. vulgare*]	50 ↑
7727	gi|28192421	1083	23343	5.898	19	/MLOC_71781.1/AAL71854.1/ dehydroascorbate reductase [*T. aestivum*]	50 ↑
7691	gi|326513514	742	37422	7.334	16	/NOG07211 /BAJ87776.1/ predicted protein peroxidase like, [*H. vulgare*]	50 ↑
Cytoskeleton							
5762	gi|168472715	1019	40933	5.35	20	/MLOC_78511.1/ACA24133.1/ actin [*L. temulentum*]	15 ↑
6679	gi|357135037	626	41701	5.062	22	/COG5277 /XP_003569118.1/ predicted: actin-97-like [*B. distachyon*]	30 ↑

Table 3 Suppl. Drought-responsive proteins identified by mass spectrometry from leaves of wheat cv. Zebra seedlings subjected to a gradual dehydration inducing 15, 30, and 50 % water saturation deficit (WSD) in comparison with control plants. Proteins differing at least twofold in abundance with $P \leq 0.001$ were designated using the *Delta 2* program.

Protein number	Accession	Mascot score	Mass	pI	Peptide number	Protein name preceded by /String/ and /Mascot/ classifiers	WSD [%]/ regulation
Photosynthesis/energy metabolism							
2860	gi|544700	410	24211	7.457	10	/MLOC_65066.2 /AAB29485.1/ chlorophyll a-b binding protein 8 [*H. vulgare*]	50 ↑
1627/ 2758	gi|326499830	1062	26582	4.601	8	/MLOC_74679.1 /BAJ90750.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBInr as ATP synthase delta (OSCP) subunit	30, 50 ↑
267/ 3005	gi|473882355	444	18527	8.06	9	/MLOC_64679.1 /EMS48023.1/ ribulose bisphosphate carboxylase small chain, chloroplastic [*T. urartu*]	15, 30 ↓
2670	gi|473882355	1568	18527	8.06	19	/MLOC_64679.1 /EMS48023.1/ ribulose bisphosphate carboxylase small chain, chloroplastic [*T. urartu*]	50 ↓
2677	gi|61378600	737	52768	6.137	30	/rbcL/AAX44936.1/ ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*A. cristatum*]	50 ↓
1480/ 411/2581	gi|37783283	2181	22322	4.776	20	/MLOC_16226.1/AAP72270.1/ ribulose-1,5-bisphosphate carboxylase activase [*T. aestivum*]	15, 30, 50 ↓
1716/ 2838	gi|290875537	762	28058	7.666	16	/MLOC_43331.1/ADD65763.1/ putative carbonic anhydrase [*S. cereale* x *T. durum*]	30, 50 ↓
2832	gi|290875537	1593	28058	7.666	23	/MLOC_43331.1/ADD65763.1/ putative carbonic anhydrase [*S. cereale* x *T. durum*]	50 ↓
2349	gi|326533372	2256	73519	5.347	40	/MLOC_20190.3/BAJ93658.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI as transketolase	50 ↓
2350	gi|326533372	2059	73519	5.347	39	/MLOC_20190.3/BAJ93658.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBI as transketolase	50 ↓
2349	gi|357110873	1450	79525	5.938	23	/MLOC_20190.3/XP_003557240.1/ predicted: transketolase, chloroplastic-like [*B. distachyon*]	50 ↓
252	gi|357125604	1103	60416	5.412	19	/MLOC_52687.1/XP_003564482.1/ predicted: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like [*B. distachyon*]	15 ↓
1338	gi|32400802	1037	29558	5.266	24	/MLOC_52687.1/AAP80633.1/ phosphoglycerate mutase, partial [*T. aestivum*]	30 ↓
2716	gi|32251039	130	25673	7.274	7	/MLOC_64140.1/AAP74365.1/ glyoxysomal malate dehydrogenase [*T. aestivum*]	50 ↓
607	gi|357145720	325	25398	4.981	4	XP_003573742.1 NAD(P)H-quinone oxidoreductase subunit S	15 ↓
Protein metabolism							
2641	gi|71362640	1835	46673	5.69	19	/MLOC_11890.1/AAZ30062.1/ plastid glutamine synthetase isoform GS2c [*T. aestivum*]	50 ↓
802	gi|326495080	481	18142	5.478	8	/MLOC_52160.1/BAJ85636.1/ predicted protein [*H. vulgare* subsp. *vulgare*]/ blasted by gi number from NCBInr as Ribosomal 50S protein L7/L12	15 ↓
250	gi|133872360	666	25716	5.763	21	/MLOC_52687.1/ABO40247.1/ Bp2A protein, partial [*T. turgidum* subsp. *dicoccon*]/ blasted by gi number from NCBInr as alkaline phosphatase	15 ↓
141	gi|473923422	161	45720	9.134	5	/MLOC_67137.1/EMS49772.1/ elongation factor 1-alpha [*T. urartu*]	15 ↓
1467/ 2568	gi|357148595	760	49546	6.207	16	/MLOC_54897.1/XP_003574826.1/ predicted: glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic-like [*B. distachyon*]	30, 50 ↓
2969	gi|974605	674	16245	4.942	8	/MLOC_17819.1/AAA75104.1/ single-stranded nucleic acid binding protein [*T. aestivum*]	50 ↓
Stress-related proteins							
2908	gi|26017213	1046	17733	4.661	12	/MLOC_32958.1/BAC41494.1/ cold regulated protein [*T. aestivum*]/ blasted by gi number from NCBInr as LEA/Cor protein	50 ↓
2746	gi|17887465	228	56822	5.023	10	/MLOC_62434.1/AAL40895.1/ phosphoethanolamine methyltransferase [*T. aestivum*]	50 ↓

1731	gi|326496957	1665	28213	6.339	17	/MLOC_65694.1/BAJ98505.1/ predicted protein [*H. vulgare* subsp. *vulgare*]/ blasted by gi number from NCBInr as thioredoxine like superfamily	30 ↓
1750	gi|326496957	1307	28213	6.339	16	/MLOC_65694.1/BAJ98505.1/ predicted protein [*H. vulgare* subsp. *vulgare*]/ blasted by gi number from NCBInr as thioredoxine	30 ↓
2438	gi|357149204	224	100000	6.139	13	/MLOC_73713.1/XP_003575035.1/ predicted: chaperone protein ClpC1, chloroplastic-like [*B. distachyon*]	50 ↓
227/ 2400	gi|357141239	295	48938	4.826	10	/MLOC_60122.1/XP_003572147.1/ protein thylakoid rhodenase (RHOD)-like, chloroplastic [*B. distachyon*]	15, 50 ↓
ROS detoxifying enzymes							
2625	gi|121551197	1240	46668	6.654	25	/MLOC_55199.2/ABM55781.1/ thylakoid bound ascorbate peroxidase [*T. aestivum*]	50 ↑
2631	gi|121551197	1129	46668	6.654	25	/MLOC_55199.2/ABM55781.1/ thylakoid bound ascorbate peroxidase [*T. aestivum*]	50 ↑
2743	gi|15808779	1651	27622	4.919	11	/MLOC_69302.1/AAL08496.1/ ascorbate peroxidase [*H. vulgare* subsp. *vulgare*]	50 ↑
2727	gi|473781575	403	29000	7.453	9	/MLOC_74910.1/EMS46089.1/ thylakoid lumenal 29 kDa protein, chloroplastic [*T. urartu*]/ blasted by gi number from NCBInr as peroxidase_like	50 ↑
2881	gi|58221595	532	28080	5.624	10	/MLOC_52444.1/AAW68440.1/ ferritin [*T. aestivum*]	50 ↑
2438	gi|326488597	1968	52405	5.791	29	/MLOC_49486.1/BAJ93967.1/ predicted protein [*H. vulgare*]/ blasted by gi number from NCBInr as dehydrogenese/reductase short chiain	50 ↓



OX axis = PCA1, OY axis = PCA 2

Fig. 1 Suppl. The distribution of tested cultivars in a principal component analysis (PCA) plot created on the basis of digital data from gel images. *Above* - PCA diagram for Ethos - a drought tolerant cultivar: a fully rigid control and samples of 15, 30, and 50 % water saturation deficit (WSD); *Below* - PCA diagram for Zebra - a drought sensitive cultivar: a fully rigid control and samples of 15, 30, and 50 % WSD.

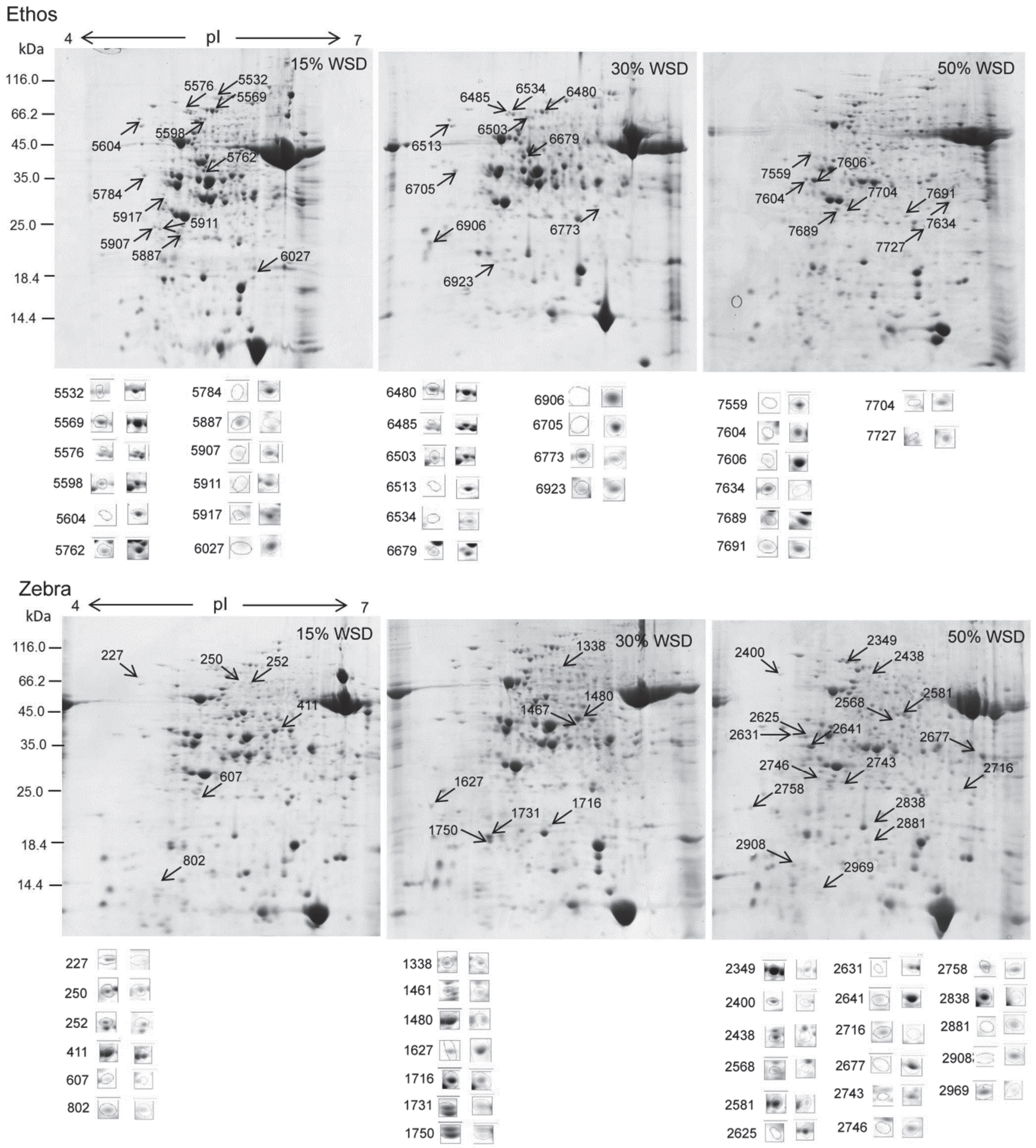


Fig 2 Suppl. Representative gel images obtained as a result of 2D separation of proteins extracted from leaves of 11-d-old wheat seedlings subjected to a gradual dehydration inducing 15, 30, and 50 % water saturation deficit (WSD) in comparison with control plants. For isoelectrofocusing, 250 µg of protein was loaded on a 11-cm *IPG* strip with a nonlinear gradient of pI 4 - 7; 11 % (m/v) SDS-PAGE gels were used for the 2nd dimension. Selection of protein spots differing in amount at least 2-fold was based on the t-test ($P \leq 0.001$).