Drought tolerance of potato (*Solanum tuberosum* L.) related to avoidance and tolerance mechanism

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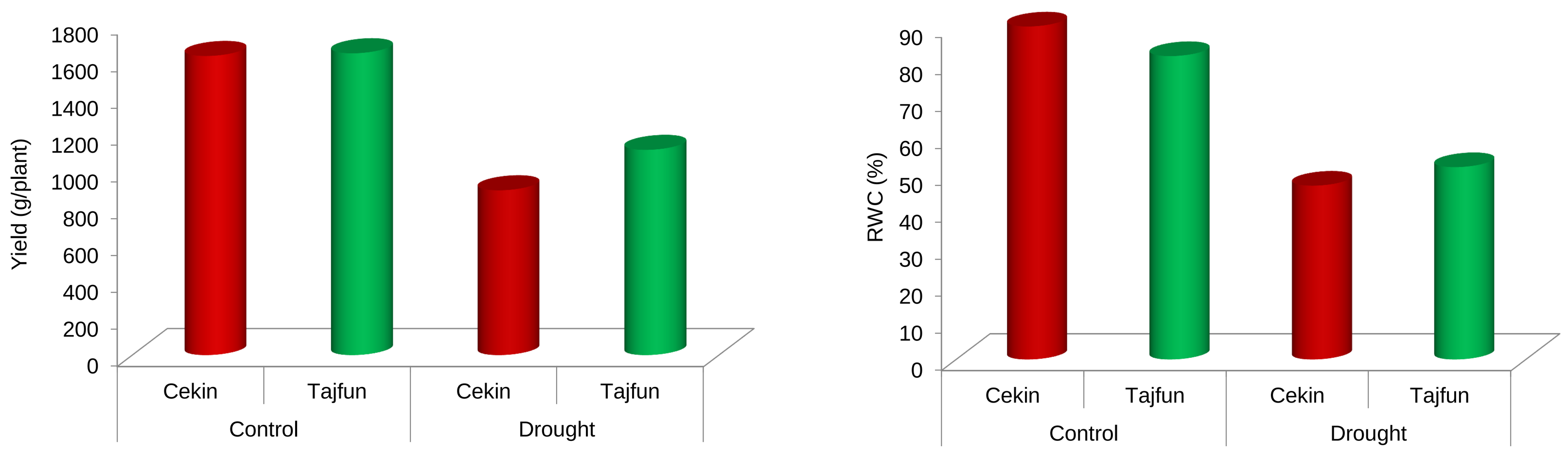
Introduction: Drought is one of the major abiotic stresses affecting plant growth, development and productivity. Potato (Solanum tuberosum L.) is moderately drought sensitive crop (Schafleitner et al., 2007) whose yield is drastically restricted by dehydration. Transcriptome analysis of potato exposed to extreme temperatures or salinity showed changes in expression of at least 3,314 genes in response to any of the applied adverse environmental factor (Rensik et al. 2005). Recent evidence indicates that some of the molecular changes that occur under suboptimal temperatures and/or salinity are also important for dehydration tolerance. The reprogramming of gene expression results in the reorganization of plant metabolism under unfavourable environmental conditions. In the drought tolerant potato a set of drought-tolerant genes has been found to be up-regulated during a drought. Since variations in drought resistance have been observed among different potato cultivars in the present experiments the up- and down-regulated proteins in drought-sensitive Cekin cultivar were assayed in order to establish the molecular markers of the drought. Therefore, three weeks after tuberisation, potato plants were subjected to soil drought by water shortage for 20 days. The proteome of leaves in control condition and subjected to drought were compered.

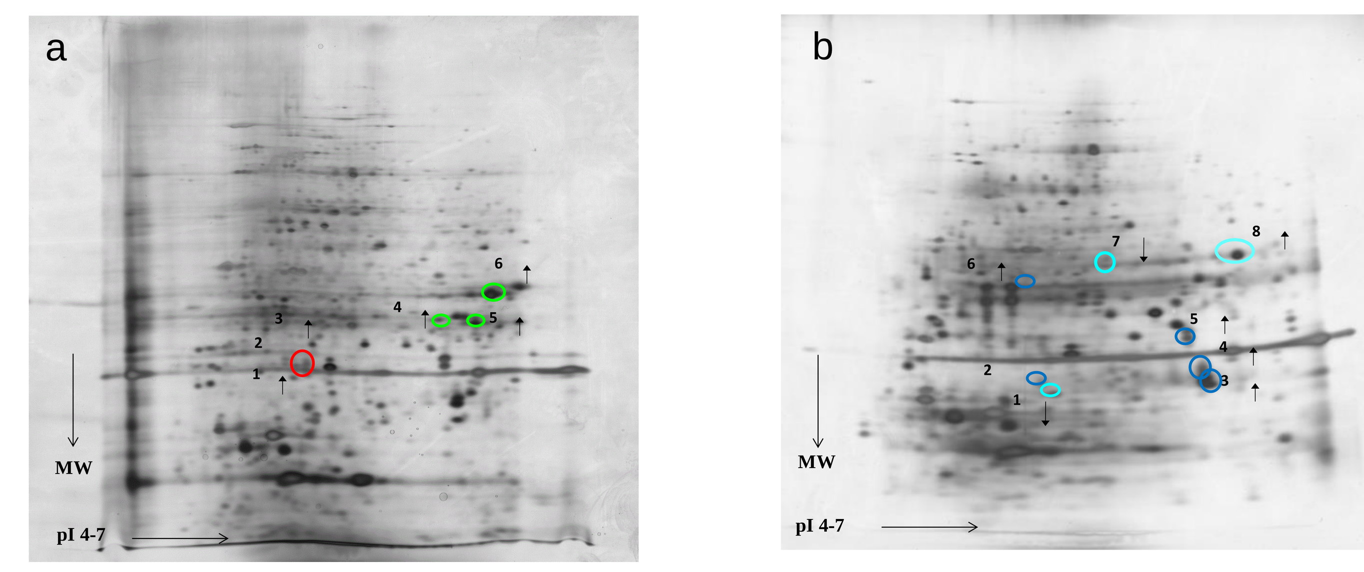
Material and methods: Potato plants, three weeks after initiation of tuberisation, were subjected to soil drought by water shortage for 20days. After a dry period, watering conditions were restored and maintained until the end of the experiment (the full maturity of the plants). During experiment potato yield, gas exchange parameters, trichome and stomata density were evaluated. Analysis of stomatal density was performed on the fully developed apical leaf from the 3rd leaves level. The cleared epidermal peels from the potato abaxial and adaxial were prepared according to Pei et al. (1997) and examined on the microscope Olympus Provis AX70. Trichome density was examined on the leaf surfaces using a binocular microscope SZH10 Olympus.

Proteins were extracted from middle slices of potato tubers and leaves according to standard protocol using a 2-D Clean-Up Kit (GE Healthcare). Samples equal to 30 µg proteins were applied to each gel. Proteins were separated in the first dimension using the isoelectric focusing (IEF) tube gels and in the second dimension using SDS-PAGE. IEF tube gels 11 cm long with pH ranging from 3 to 7 were used. Electrophoresis was carried out at 250 V for 20 min, followed by 8000 V for 2.5 h and at 8000 V to achieve 20,000 V-h. SDS-PAGE was performed using 12% polyacrylamide gels with 4% stacking gels at 25 mA for about 5 h. Finally, the gels were silver-stained. Gels were scanned using ImageScanner III GE Healthcare. During gel image processing up- and down-regulated proteins were assayed due to choose molecular markers of the drought tolerance using non-parametric MANOVA for the analysis of data variation (Zerzucha et al. 2012). Proteins were detected using mass spectrometry (Institute of Biochemistry and Biophysics, Polish Academy of Sciences).

Results:



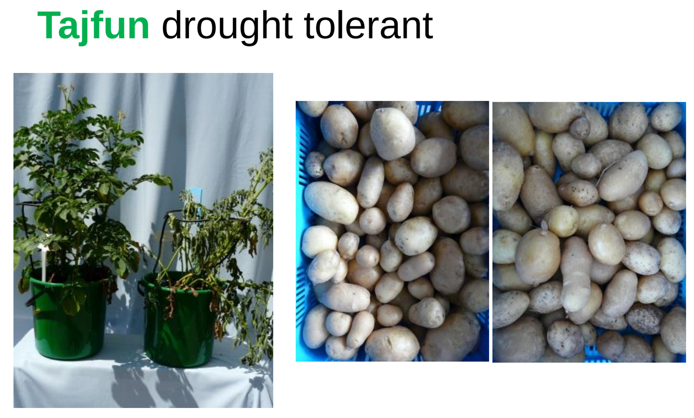
Ryc.1. Potato tuber yield (g/plant) and relative water content in leaves under soil drought condition.



Ryc. 3. Gels of leaves subjected to drought of (a) Cekin and (b) Tajfun cultivar

Cekin drought susceptible

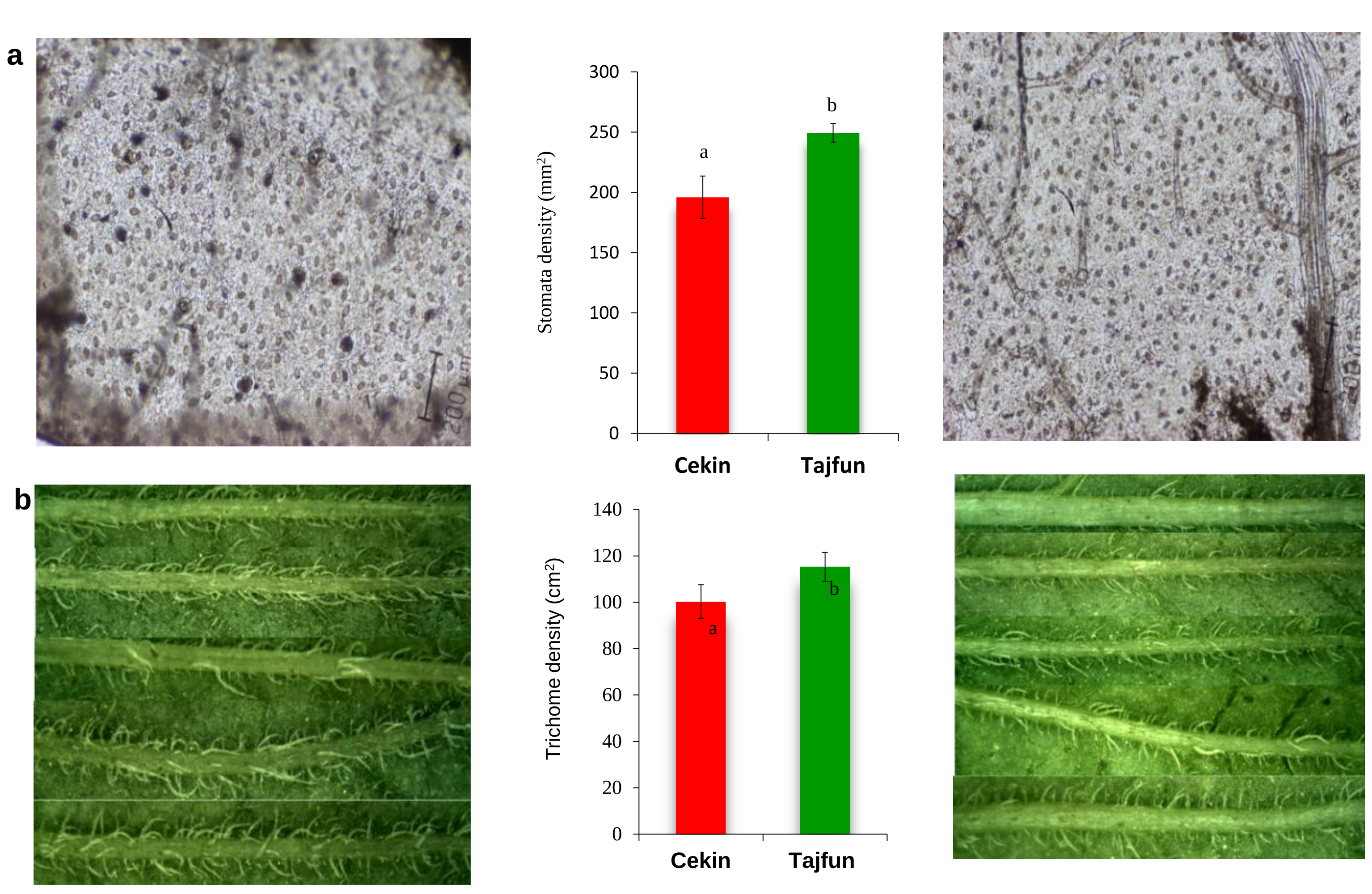
Tajfun drought tolerant



Spot no.	Protein name	Species	% protein coverage	No. peptides mached	score	Protein accesion number	Protein expression
1	Glyoxalase I (GLX I)	*Solanum lycopersicum*	5	2	49	Q42891	↑
2	Methionine sulfoxide reductase	*Arabidopsis thaliana*	10	2	61	Q9LY14	↑
3	Superoxide dismutase Fe (Fe-SOD)	*Nicotiana plumbaginifolia*	4	9	153	P22302	↑
4	Triosephosphate isomerase	*Petunia hybrida*	14	20	839	P48495	↑
5	Chlorophyll a-b binding protein CP24 10A	*Solanum lycopersicum*	2	7	102	P27524	↑
6	Carbonic anhydrase	*Nicotiana tabacum*	3	2	84	P27141	↑

Tab.1. Potato leaves proteins identified from cultivar Cekin.

Abaxial leaf surfaces



Ryc.2. (a) Stomata and (b) trichoma density of abaxial leaf surface.

Spot no	Protein name	Species	% protein coverage	No. peptides mached	score	Protein accesion number	Protein expression
1	ATP synthase CF1 epsilon chain	*Solanum tuberosum*	12	2	70	gi|82754633	↓
2	Eukaryotic translation initiation factor 5A-2	*Nicotiana plumbaginifolia*	7	2	36	gi|124226	↑
3	RNA-binding glycine-rich protein-1a	*Nicotiana sylvestris*	6	2	55	gi|469070	↑
4	putative glycine-rich RNA binding protein-like	*Solanum tuberosum*	27	3	115	gi|82623423	↑
5	chaperonin 21 precursor	*Solanum lycopersicum*	4	2	61	gi|350534934	↑
6	S-adenosylmethionine synthetase	*Arabidopsis thaliana*	5	2	68	gi|166872	↑
7	homologous to plastidic aldolases	*Solanum tuberosum*	5	2	87	gi|1781348	↓
8	glyceraldehyde-3-phosphate dehydrogenase	*Arabidopsis thaliana*	14	3	255	gi|166706	↑

Tab.2. Potato leaves proteins identified from cultivar Tajfun.

Summary:

1. The observed changes in leaf proteome of drought sensitive cultivar were mainly due to the up-regulation of photosynthesis-related proteins, proteins involved in energy metabolism and in antioxidant defense system.
2. The obtained results supported our earlier findings that photosynthetic activity was reduced in susceptible genotypes (Cekin) while tolerant genotypes could continue photosynthesis under soil drought.
3. Stomata and trichoma density on the abaxial leaf surface were significantly higher at drought tolerant cultivar. It seems to be related to maintaince of gas exchange intensity and more effective use of water (WUE).

References:

- Boguszewska D., M. Grudkowska, B. Zagdańska; 2010 Drought responsive antioxidant enzymes in potato (*Solanum tuberosum* L.) Potato Research , 53 (2010) 373-382
- P. Zerzucha, D. Boguszewska, B. Zagdanska, B. Walczak, Non-parametric multivariate analysis of variance in proteomic response of potato to the drought stress, Analytica Chimica Acta, 719 (2012) 1-7