

The effects of drought on changes in photosynthesis, hormone levels and grain yield in wheat (*Triticum aestivum* L.)

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Wheat is one of the main crops consumed by humans and it is cultivated in different environments. Under the temperate zone early-summer droughts are increasingly frequent and limit grain yield since they coincide with the grain filling period. There are several physiological traits related to water stress, and scientists make considerable effort to find direct correlations between these parameters and grain yield to facilitate the selection of cultivars for drought tolerance.

Photosynthesis is one of the main metabolic processes determining crop production. Chlorophyll fluorescence is a tool for monitoring the function of the photosynthetic apparatus, changes in response to water stress. The effect of drought on photosynthesis has long been a controversial subject and it is still not clear whether chlorophyll fluorescence parameters are good indicators for drought sensibility (Flexas et al. 2002). The plant hormone abscisic acid (ABA) plays a major role in plant responses to drought stress, facilitating plant survival (Zahng et al. 2006).

A comparison was made between changes of the parameters mentioned above, in seedling stage under osmotic stress and in reproductive growth phase under soil drought in two Hungarian (*Triticum aestivum* L. cv. MV Emese (resistant) and GK Élet (sensitive)) and two internationally known (*Triticum aestivum* L. cv. Plainsman (resistant) and Cappelle Desprez (sensitive)) wheat cultivars.

Our object was to compare the effects of osmotic and drought stress to find correlation between these treatments, and to compare the effects of water deficit on different physiological parameters, hormone levels (ABA and cytokine), grain yield and storage protein content in tolerant and sensitive varieties in the grain filling period. The water status parameters, CO₂ assimilation, chlorophyll *a* (*chl a*) fluorescence, pigment content and hormone levels were determined as a function of the development under osmotic stress in seedling stage (from germination to the 21st day after germination) and under water deficit in the grain filling period (from booting stage to the 24th day after anthesis).

Our results suggest that the photosynthetic parameters measured under osmotic stress are not comparable with those measured in flag leaves in the grain filling period. Different genotypes showed unique diversity in changes of these parameters, but common tendencies between the tolerant or sensitive cultivars were not found.

Pre- and post-anthesis soil drought did not result in characteristic modifications in PS II photochemistry of flag leaves in dark and light-adapted leaves, demonstrating that in this experiment these parameters did not correlate with sensitivity. Plants showed early senescence under water deficit. We found that sensitivity of the generative organs could be responsible for the higher decrease in grain yield. Changes of the ABA levels in the kernels showed a differing tendency: sensitive genotypes maintained high hormone levels, which can be unfavourable for grain growth. The different storage protein fractions of the mature grains were not significantly modified by drought, which confirm earlier results (Panozzo et al. 2001), but the gliadin to glutenin ratio increased significantly in one of the tolerant varieties.

Our results indicate that when the sensitivity of a genotype to drought stress are defined whole plants responses have to be taken into consideration. Responses of the vegetative and generative organs can be different and sensitivity of the generative phase and the fertilization process to water deficit may overwrite the efficient acclimation of vegetative organs.

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Microarray and interaction network based identification of genes involved in germ cell development in *Drosophila melanogaster*

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Embryonic germ cell development of fruit fly (*Drosophila melanogaster*) depends on the germ plasm, the most posterior part of the egg cytoplasm. The germ plasm contains all factors which are necessary to induce germ cell fate. It has a characteristic distribution of proteins and contains a large number of localized RNA species, too (Williamson et al. 1996). Certain gene products being present in germ plasm might play crucial roles in germ cell determination and its subsequent development such as the germ cell migration, the passage through the embryonic midgut, and gonad formation. *Drosophila* is one of the most accepted model organism of germ cell research in the post sequencing era since numerous large *Drosophila* genomic databases are available for researchers.

We have developed and apply a microarray-based method to identify germ plasm enriched RNA-s. We performed a series of experiments on different microarray platforms to compare the RNA content of numerous germ plasm-less, germ plasm overexpressing and wildtype conditions. Collating our datasets with the list of the known germ plasm enriched transcripts, we found that germ plasm overexpressing vs. wildtype comparison is the most appropriate method to identify new germ plasm enriched transcripts. In such comparisons 380 transcripts showed at least four times increase in germ plasm overexpressing condition. These transcripts were chosen for further analysis to confirm their germ plasm localization by making use of fluorescent RNA in situ hybridization (Lecuyer et al. 2007) on early *Drosophila* embryos. To be able to accomplish such a large number of in situ hybridisations we have developed a suitable PCR based single strand DNA labeling method.

Another approach we used, is a network based identification of novel germ plasm factors. We built up and investigated a germ plasm specific gene interaction network. First, we searched RNA localization databases (BDGP, Fly-FISH) and original publication for genes whose transcripts are exclusively or highly enriched in the germ plasm (Szuperák et al. 2005). This way, 136 as we called "original" germ line specific genes were found. Then we identified their primary genetic and yeast two-hybrid interactors by using the BioGRID database. Based on the GEO database, those primary interactors which are not expressed at early embryonic stages were filtered out. Finally, we constructed a gene interaction network which indicates all known interactions (325) among the original germ line specific factors (136) and primary interactors (325). We assume that the number of interactions of a given gene may mirror its importance in the network. Genes with large number of interactions, also called hubs, can refer to a central role of a given gene that have a good chance to show phenotype when it is mutated. We confirm this hypothesis by RNAi induced phenocopy analysis. We are currently analyzing the germ line specific phenocopies of a representative group of hubs as well as of the low connectivity control genes. The phenocopy of the RNA silencing is followed by the time laps video microscopy which allows distinguishing different type phenocopies: the complete absence or decreased number of germ cells, or its migration defects.

BDGP, Patterns of gene expression in *Drosophila* embryogenesis. <http://www.fruitfly.org/cgi-bin/ex/insitu.pl>

BioGRID, General repository for Interaction Datasets. <http://www.thebiogrid.org/>

Fly-FISH, A Database of *Drosophila* embryo mRNA localization patterns. <http://fly-fish.cabr.utoronto.ca/>

GEO: Gene Expression Omnibus. <http://www.ncbi.nlm.nih.gov/geo/>: GEO Accession: GSE3955

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Oxidative stress, intrauterine retardation, modes of delivery

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Oxidative stress arises when the balance between oxidants and antioxidants is disturbed. The source of free radicals is the unpaired electron of molecular oxygen, which makes it unstable and electrically charged. In the lack of antioxidant molecules and enzymes, free radicals target lipids, proteins and DNA. Oxidative damage to DNA is a result of interaction of the nucleic acid with hydroxyl radical that generates strand breaks on the DNA. Oxidative stress is a physiological event in the fetal-to-neonatal transition.

The steadily increasing global rate of cesarean sections (CS) has become one of the most debated topics in maternity care. The mode of delivery may have a considerable effect on the state and health of the newborn. CS is a surgical intervention with potential hazards for both mother and child. The opinions of obstetrician-gynecologists regarding normal vaginal delivery (VD) and CS are highly contradictory. The results of previous studies display great differences. We have approached this question from a consideration of oxidative stress and set out to determine a wide range of parameters relating to the oxidative status of neonates born via VD or undergoing CS.

We conclude that the mode of delivery does not have a serious effect on the level of free radical damage if there is no emergency situation. The elective CS does not have an advantage over VD with respect to oxidative stress (Hracsko et al. 2007).

Intrauterine growth retardation (IUGR) is a complication of pregnancy. A newborn with IUGR weighs less than do 90% of all other newborns of the same gestational age. The reported incidence of IUGR ranges between 7 and 10 per cent. This abnormality is associated with increased level of morbidity and mortality, and deformation of the umbilical cord.

The mechanism of development of IUGR has still not been appropriately described, although it is most probably a consequence of an abnormal fetomaternal blood circulation. Accordingly we have carried out examinations on umbilical cord blood and endothelium in order to establish how the antioxidant status of full-term IUGR infants changes and whether the results indicate significant oxidative stress. We compared the antioxidant status and the level of lipid peroxidation (LP) of the umbilical blood in healthy mature neonates and in IUGR neonates. The level of LP was high in the IUGR group while the antioxidant enzyme activities and the levels of antioxidants were significantly