P.06-009-Wed
Light control of lipid metabolism in the brown alga *Undaria pinnatifida*: consequences for chloroplast ultrastructure and photosynthetic competence

N. Zhukova[1], I. Yakovleva[2]

[1]*Far Eastern Federal University, Vladivostok, Russia,* [2]*National Scientific Center of Marine Biology, Far East Branch, Russian Academy of Sciences, Vladivostok, Russia*

Light produces a variety of effects on algal lipid metabolism and therefore lipid composition. Glycolipids determine the physicochemical properties of the thylakoid membrane that are essential in supporting the photosynthetic capacity, and, hence, they should be included into the concept of light acclimation of photosynthesis. Long-term exposure to varying light intensity (100, 290 and 400 μmol photons/m^2/s) influenced the lipid and fatty acid composition of *U. pinnatifida*, as well as on growth rate and photosynthetic activity. The changes in total lipid content were accompanied by variations in lipid classes. Each lipid class exhibited a specific fatty acid composition and changed considerably at a different light intensity. Under adaptation to low light, besides the increased synthesis of glycolipids, monogalactosyldiacylglycerol MGDG, sulfoquinovosyldiacylglycerol SQDG, and phosphatidylglycerol PG we observed also active n-3 desaturation with the formation of 18:3n-3, 18:4n-3 and 20:5n-3 acids. These changes were accompanied by the active synthesis of Chl a+c and fucoxanthin pigments as well as a significant increase in the PSII maximum quantum efficiency and the electron transport rate. In contrast, the high–light samples displayed a significant decline in n-3 polyunsaturated fatty acid content, increase in the amounts of storage lipids, triacylglycerols, rich in 16:0 and 18:0 and a decline in photosynthetic activity accompanied with increase in malondialdehyde content. The consequent accumulation of n-3 fatty acids in glycolipids could facilitate the thylakoid membrane fluidity, and, therefore, the velocity of electron flow involved in photosynthesis during light acclimation. Thus, a prolonged exposure to low and high light considerably affects lipid synthesis, suggesting a correlation between the activity of photosystems and the process of synthesis and desaturation of fatty acids. The work was supported by the Russian Science Foundation (14-50-00034).

P.06-010-Mon
What happens with tobacco metabolism if protein casein is the only source of nitrogen?

K. Bělonožníková[1], M. Černý[2], H. Synková[3], H. Gielen[4], R. Valcke[4], V. Hýsková[1], O. Hodek[5], T. Křížek[5], R. Schnablová[3], H. Ryšlavá[1]

[1]*Department of Biochemistry, Faculty of Science, Charles University, Hlavova 2030, Praha, Czech Republic,* [2]*Laboratory of Plant Molecular Biology, Institute of Biophysics AS CR, v.v.i. and CEITEC — Central European Institute of Technology, Mendel University in Brno, Zemedelská 1, Brno, Czech Republic,* [3]*Institute of Experimental Botany, Academy of Sciences of the CR, Rozvojová 313, Praha, Czech Republic,* [4]*Molecular and Physical Plant Physiology, Faculty of Sciences, Hasselt University, Agoralaan building D, Diepenbeek, Belgium,* [5]*Department of Analytical chemistry, Faculty of Science, Charles University, Hlavova 2030, Praha, Czech Republic*

The well-known paradigm that plants must rely on soil fauna for the breakdown of organic matter has been challenged by many scientists now. We took a closer look on what happened with tobacco metabolism if grown *in vitro* in sterile conditions with casein as a sole nitrogen (N) source. Casein promoted the root growth, providing the plant with a robust root system. Also, the protein and total free amino acid content together with the C/N ratio were not significantly reduced in comparison with the other two experimental groups grown with inorganic forms of N. We determined an increased concentration of free branched-chain (Ile, Leu) and basic (Arg, His, Lys) amino acids in the plants supplemented with casein. Their proteomic analysis of the root exudates revealed three classes of proteases as being secreted to the medium, and that some apoplastic proteases in the roots were downregulated, except for aleurain-like protease that was significantly upregulated. However, most of proteins involved in N metabolism remained unchanged. We detected that the plants supplemented with casein showed inducible proteolytic activity at lower pH than neutral. Their high activity of endo-1,3-β-glucanase in the roots was related to the cell wall adjustment resulting in the loosening of the transport pathways for metabolites, including peptides and proteins. Taken together, our findings suggest that tobacco plants accumulate mainly branched-chain and basic amino acids from casein, secrete proteases into the medium and break the peptides in the apoplast. This project was supported by Charles University (UNCE 204025/2012).

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Defining a metabolic core module of stress response in *Arabidopsis thaliana*

L. Fürtauer[1], A. Pschenitschnigg[2], H. Scharkosi[2], W. Weckwerth[2,3], T. Naegele[1]

[1]*LMU München/Dept. Biology I, Munich, Germany,* [2]*University of Vienna, Althanstrasse 14, A-1090 Vienna, Austria,* [3]*Vienna Metabolomics Center ViMe, Althanstrasse 14, A-1090 Vienna, Austria*

Abiotic stress exposure of plants induces metabolic reprogramming which is a tightly regulated and complex process affecting signalling cascades, transcriptional, translational and metabolic regulation. The complexity of resulting interconnected stress-responsive networks impedes the functional understanding of molecular plant stress response compromising the design of breeding strategies and biotechnological processes. Consequently, defining a molecular network enabling the prediction of a plant's stress mode promises to significantly promote the understanding of stress-induced biochemical reprogramming and its technological application. In the presented study, *Arabidopsis* wild type plants and three mutant lines with enzymatic deficiencies in the central carbohydrate metabolism were grown under ambient conditions as well as under low temperature/high light stress conditions. Stress-induced dynamics of metabolome and proteome were quantified in a mass spectrometry-based high-throughput experiment. Together with chlorophyll fluorescence parameters, which indicated a significant stress impact on photosystem reactions, this multidimensional molecular data set was used to train a machine learning algorithm to predict stress behaviour of all genotypes. Based on multivariate statistics and machine learning approaches on wild type data, a core module consisting of 20 proteins was identified enabling the prediction of the stress mode of all mutant lines. Further, among these protein candidates a protein-protein interaction network was identified connecting transcriptional regulation with regulation of primary and secondary plant metabolism. In summary, the identified stress-responsive core module defines a tightly regulated molecular network being preliminary for reprogramming of metabolism during stress and for the predictability of complex biochemical regulation during environmental fluctuation.