

PROTEOME ANALYSIS OF ARABIDOPSIS THALIANA TRANSGENIC PLANTS WITH INCREASED LEVELS OF ENDOGENOUS CYTOKININS

ANALÝZA PROTEOMU TRANSGENNÍCH ROSTLIN ARABIDOPSIS THALIANA SE ZVÝŠENOU HLADINOU ENDOGENNÍCH CYTOKININŮ

Baldrianová J., Dyčka, F., Bobál'ová, J., Brzobohatý B.

Institute of Biophysics, Academy of Sciences of the Czech Republic, Královopolská 135, 612 65, Brno, Czech Republic

Department of Molecular Biology and Radiobiology, Faculty of Agronomy, Mendel University of Agriculture and Forestry in Brno, Zemědělská 1, 613 00, Brno, Czech Republic

Institute of Analytical Chemistry, Academy of Sciences of the Czech Republic, Veveří 97, 602 00, Brno, Czech Republic

E-mail: baldrianova@ibp.cz, brzoboha@ibp.cz

ABSTRACT

Cytokinins are plant hormones that play important roles during plant development and growth. In particular, they influence chloroplast development, nutrient mobilization, delayed senescence, morphogenesis (in association with auxin) and the cell cycle. Light quality and intensity are important factors that affect a range of plant processes. Some effects of cytokinin and light are identical. This fact led us to set up our experiments, whose aim is to identify changes at the protein level in plants grown under different light intensities. In our experiment we used two different light intensities (100 and 200 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and transgenic *A. thaliana* plants with pOp-ipt::35S-LhGR, a construct whose activity is inducible by a suitable activator, generating increases in cytokinin levels. Proteome analysis was performed by 2D gel electrophoresis and subsequent comparison of proteome maps using Decodon Delta 2D software, version 3.6. Total number of resolved spots was 726 and 17 spots showed statistically significant changes indicating presence of differentially regulated proteins. The differentially regulated proteins were identified by MALDI-TOF/TOF. The highest number of changes in protein expression was observed on the fifth day after activation.

Key words: cytokinins, light, proteome, 2D electrophoresis

Acknowledgments: This work was supported by grants 1M06030 and LC06034 (Ministry of Education of the Czech Republic), IAA600040612 and IAA600040701 (Grant Agency of the Academy of Science of the Czech Republic) and AVOZ50040507.