

Proteomic Analysis of Expressed Proteins from Increased Illumination Periods in Arabidopsis

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Many developmental processes including flowering time, cotyledon expansion, hypocotyl elongation and circadian clock are influenced by light intensity and duration. These morphological changes are resulted from changes at the protein expression level as well as the transcription level. To better analyze these protein expression changes for the light treatment, proteomics was used.

Five-day dark-grown Arabidopsis seedlings were irradiated in the light condition of $100 \mu\text{molm}^{-2}\text{s}^{-1}$ intensity for 3, 6, and 12h. Cotyledons started to be green with 3h illumination and became completely green with 12h illumination. For each period of time, total proteins were compared with successive silver-stained gels and analyzed accurately in quantity using ImageMaster 2-D software. Over 1,200 protein spots stained on each sample were matched except for newly appeared or disappeared spots. Among differently expressed spots, constantly increased or decreased spots were targeted and 100 spots were picked for MALDI-TOF MS analysis from Coomassie-stained gels.

2-D results indicated that proteins were decreased at pH4-5 range, while increased at pH6-7 range and high-molecular weight region with increased illumination time periods. Among 39 identified proteins, 25 proteins were increased and 14 proteins were decreased. Most proteins were known to be involved in light signal transduction (e.g. protein kinase) and photosynthesis (e.g. oxidoreductase).