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The role of hepatocyte growth factor in regulating excitatory synapses

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Activity-dependent modifications of excitatory synapses are hypothesized to underlie neurological processes such as processing and storing information. The neurotrophin hypothesis of neural plasticity proposes that synaptic activity induces secretion of growth factors that then induce functional and structural modifications of synapses. We are investigating the role of hepatocyte growth factor (HGF) and its receptor, the oncogene c-Met, in regulating the structure and function of excitatory synapses. HGF and c-Met are best known for their roles in organ development and cancer, and can regulate aspects of cell biology including protein expression, cell survival, cytoskeletal structure, and structure of intercellular junctions. We demonstrate that HGF and c-Met are located at excitatory synapses, that HGF is secreted in response to synaptic activity, and that they induce structural and functional changes at synapses. Thus HGF and c-Met may play an important role in information processing in the brain.

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Recent Experimental Method for Life Science and Biotechnology
Proteomic pattern-based analysis of physiological responses and genetic variations in *Arabidopsis*

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Light critically affects the physiology of plants. Using two-dimensional gel electrophoresis, we used a proteomics approach to analyze the responses of *Arabidopsis thaliana* to red (660 nm), far-red (730 nm) and blue (450 nm) light, which are utilized by type II and type I phytochromes, and blue light receptors, respectively. Under specific light treatments, the proteomic profiles of 49 protein spots exhibited over 1.8-fold difference in protein abundance, significant at $P< 0.05$. Most of these proteins were metabolic enzymes, indicating metabolic changes induced by light of specific wavelengths. The differentially-expressed proteins formed seven clusters, reflecting co-regulation. We used the 49 differentially-regulated proteins as molecular markers for plant responses to light, and by developing a procedure that calculates the Pearson correlation distance of cluster-to-cluster similarity in expression changes, we assessed the proteome-based relatedness of light responses for wild-type and phytochrome mutant plants. Overall, this assessment was consistent with the known physiological responses of plants to light. However, we also observed a number of novel responses at the proteomic level, which were not predicted from known physiological changes. We also performed a comparative analysis of intra-species proteome variation in *Arabidopsis* ecotypes to investigate differences in proteomic pattern derived from genetic diversity of ecotypes. This topic will be also presented.