Research trends and utility of functional proteomics in plants

Sun-Hee Woo[1*] and Jong-Soon Choi[2]
[1]Dept. of Crop Science, Chungbuk National University, Cheongju 361-763, KOREA
[2]Proteomics Team, Korea Basic Science Institute, Daejeon 305-333, KOREA

Since the completion of genome sequences of several model organisms, attention has been focused to determine the function and functional network of proteins by proteomic technologies. These technologies enable the separation and identification of proteins, the determination of their function and functional network, and construction of an appropriate database to be possibile. Many improvements in separation and identification of proteins, such as two-dimensional electrophoresis, nano-scale liquid chromatography and mass spectrometry, have rapidly been achieved. Some new techniques which include top-down mass spectrometry and tandem affinity purification have emerged. During this study, we established high-throughput display proteomics methods for isolation of useful genes from the different developmental stages of grain filling and seed maturation in rice. These techniques have provided the possibility of high-throughput analysis of function and functional network of proteins in plants. However, to cope with the huge information emerging from proteomic techniques, more sophisticated techniques and software are essential for further analysis. The development and adaptation of such techniques will ease analyses of protein profiling, identification of post-translational modifications and protein-protein interaction, which are vital for elucidation of the protein functions. Efficiency of the protein functional analysis in proteomics is strongly ' database-dependent'. Therefore, the improvement of quality and quantity of the proteome database and construction of the software, which can analyze the protein function, are essential for proteome research. Also, the information thus obtained from the plant proteome would be helpful in predicting the function of the unknown proteins and would be useful in the plant molecular breeding and new cultivar.
*** corresponding author: Tel. 043-261-2515, e-mail: shwoo@chungbuk.ac.kr**

<*In vivo* function of an *Oryza sativa* thioredoxin *m*: Its role in photosynthesis and plant development>

Yong Hun Chi, Ho Hee Jang, Jong Cheol Kim, Seung Sik Lee, Soo Kwon Park, Jung Ro Lee, Sang Yeol Lee and Kyun Oh Lee*
Jinju, Gyeongsang National University

Thioredoxins are small, 12-13 kDa proteins found in almost all organisms. Plant cells contain several different thioredoxin isoforms, which are generally characterized according to their sub-cellular location and substrate specificity. Here we describe the cloning and characterization of an *Oryza sativa* cDNA encoding thioredoxin *m* (*Ostrxm*). *Ostrxm* was present as a single copy in the rice genome, and exhibited green-tissue-specific and light-responsive mRNA expression. Recombinant Ostrxm containing a putative signal peptide was present in chloroplasts of rice mesophyll cells, and showed DTT-dependent insulin β -chain reduction activity *in vitro*. *Ostrxm* RNA interference (RNAi) resulted in rice seedlings with severe developmental retardation, a pale green leaf phenotype, increased light sensitivity and impaired chloroplast development. Growth inhibition and sensitivity to light were more marked in *Osxtrm* RNAi plants as they aged. Consistent with the increased light sensitivity phenotype, the photosynthetic efficiency of the *Ostrxm* RNAi transgenic rice was about 50%