

025(F025)

EXAMINATION OF THE CONSERVATIVE MECHANISM FOR CHLOROPLAST DIVISION

Ryuuichi ITOH, Makoto FUJIWARA, Noriko NAGATA, Shigeo YOSHIDA; Plant Functions Lab., RIKEN, Wako 351-0198

Cell division of eubacteria, from which chloroplasts were originally derived, is accomplished by cooperative interaction between cytoskeletal machinery Z ring composed of Fts proteins and division site-selection system composed of Min proteins. In recent years chloroplasts in higher plants have been also found to utilize the division protein FtsZ and the division inhibitor MinD for their division, suggesting the prokaryote-derived conservative mechanism for chloroplast division. MinE is a component of Min system and suppresses the MinCD inhibitory complex at the midcell to specify the cell division plane in eubacteria. *minE* gene was reported to be encoded in chloroplast genomes of some algal species but not in those of higher plants, which implied that in evolutionary lineage of higher plants this gene was transferred from chloroplasts to the nucleus. In this context we identified the nuclear-encoded *minE*, designated as *AtMinE1*, of *Arabidopsis thaliana*. *AtMinE1* contains both N- and C-terminal extensions as compared to eubacterial and algal chloroplast-encoded MinE; the N-terminal extension represents typical features of transit peptides. We generated transgenic plants overexpressing a full-length *AtMinE1* by a CaMV35S promoter and examined the subcellular structures of those plants. In transgenic plants chloroplast morphology and number per cell were aberrant to variable range, while mitochondrial morphology was similar to that of wildtype plants. These observations suggest that MinE is the third conservative component involved in chloroplast division control. Investigations on expression pattern of *AtMinE1* and subcellular localization of *AtMinE1* by use of GFP and/or specific antibody are underway.

026(F026)

SYSTEMATIC ANALYSIS OF PLANT TATA-LESS PROMOTERS

Masayuki NAKAMURA, Tomoaki YOSHITSUGU, Tatsuhiko TSUNODA¹, Gerit WEINZIERL², Irena SHERAMETI², Hiroyuki HIBINO, Ayumi IMURA, Masahiro SUGIURA³, Ralf OELMÜLLER² and Junichi OBOKATA; Ctr. Gene Res., Nagoya Univ., Nagoya 464-8602, ¹SNP Res. Ctr., RIKEN, Yokohama 230-0045, ²Inst. Allgemeine Botanik, Friedrich-Schiller-Universität, D-07743 Jena, Germany, ³Grad. Sch. Natural Sci., Nagoya City Univ., Nagoya 467-8501

TATA box plays a key role in RNA polymerase II-dependent transcription, and locates in the vicinity of -30. Recently, we found that promoters of more than 60% of photosynthesis genes lack TATA box, though the frequency of TATA-less promoters in non-photosynthesis genes is less than 10%. Extremely high frequency of TATA-less promoters appears to be a characteristic of nuclear-encoded photosynthesis genes. To elucidate the biological significance of this phenomenon, we initiated the comparative analyses of core-promoter architecture and gene regulation among thylakoid membrane protein genes.

027(F027)

ISOLATION OF VACUOLAR MEMBRANE FROM *Arabidopsis* AND IDENTIFICATION OF ITS PROTEINS

Sumie KETA¹, Katsuhiko SHIRATAKE¹, Takashi SAZUKA², Daisuke SHIBATA², Masayoshi MAESHIMA¹, Shohei YAMAKI¹ (¹Grad. Sch. Bioagr. Sci. Nagoya Univ., ²Kazusa DNA Res.Inst.)

It is important to make catalogues of organelles by the proteome approach. Our focus is on vacuolar membrane (VM) of higher plants. We isolated VM from *Arabidopsis* plants with less contamination by sucrose density gradient centrifugations.

It has been reported that 2D-PAGE is not suitable for separating hydrophobic proteins. Therefore, instead of 2D-PAGE, VM proteins were separated firstly according to the difference of solubilization with detergents or chaotropic ion and secondly by SDS-PAGE. Hydrophobic and hydrophilic proteins could be effectively separated by the solubilization steps.

These proteins are going to be identified using TOF-MS.

028(F028)

MORPHOLOGY OF ARABIDOPSIS ROOT PLASTIDS VISUALIZED BY GREEN FLUORESCENT PROTEIN

Makoto FUJIWARA, Yasuo NIWA¹, Shigeo YOSHIDA; Plant Functions Lab., RIKEN, Saitama 351-0198, ¹Grad. Sch. Nutri. Environ. Sci., Univ. of Shizuoka, Shizuoka 422-8526

Green fluorescent protein (GFP) is a vital marker protein in plants as well as other organisms. Recent studies on GFP-labelled plastids with confocal laser scanning microscopy have revealed plastid tubules, stromules (stroma filled tubules), emanating from the 'plastid body'. The observation that chloroplast stroma-localized GFP flew into the interconnected plastids through stromules exhibited a role of the tubules in the intercommunication between plastids. In this study, we studied on tissue dependency and plastid type specificity of stromule formation using the transgenic *Arabidopsis* plant that express the GFP fusion with the N-terminal transit peptide sequence of RBCS1A. Stromules appeared frequently from root plastids through the elongation zone to differentiation zone of the root tips, and most proliferated in the mature parts of old roots, while relatively low from the chloroplasts or plastids of leaves, petals and trichomes.