**E205** Isolation and characterization Late Embryogenesis Abundant cDNA Clone from Green Pepper Leaves under Water Deficit

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Environmental stresses, such as water deficit, increased salinity of soil and extreme temperature are major factors limiting plant growth and productivity. Especially, water stress is one of the most common environmental stress. To study water stress responsive genes, a cDNA library from 4-week old green pepper leaves that were subjected to PEG treated up to 24 hours was constructed. Several water stress responsive cDNA clones have been isolated by differential screening of cDNA library. We report here the isolation and characterization of Late Embryogenesis Abundant(LEA) gene(AF 168168). LEA protein is a broad family of plant proteins that are stored in the dry seed. LEA protein can protect specific cellular structure or ameliorate the effect of drought stress by maintaining a minimum cellular water requirement. However, clear experimental evidences to show the exact functions of LEA protein is yet lacking. The cDNA sequence of LEA from pepper is 709 b.p long with an open reading frame of 495 b.p encoding a protein of 164 amino acids. Southern blot analysis suggests that LEA gene in green pepper are encoded by a small gene family. Northern and western blot analysis show that LEA transcript and translate were increased of the leaves were subjected to water stress. Indicating LEA protein plays a role in probability tolerance against water stress.

**E206** The Significancy of *S*-adenosylmethionine Decarboxylase Gene Expression in Root Development of Seedlings.

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For investigation of the role of *S*-adenosylmethionine Decarboxylase (SAMDC) in plant development, we produced transgenic tobacco plants, in which SAMDC gene were overexpressed or underexpressed using 35S promoter. Even polyamine contents and SAMDC activity significantly increased in sense transgenic plants at T1 generation, their phenotype was almost normal. But, the seedlings of antisense transgenic tobacco, in which SAMDC activity per fresh weight decreased, showed abnormality in root development loosing gravitropism. Also. we produced transgenic plants, in which GUS gene was under the control of 1,824 bp SAMDC promoter. In transgenic seedlings, GUS activity detected extremely high in root, compared with other plant organs. Also, this result was in accord with that of GUS staining in cytohistochemistry assay. Therefore, these results polyamines are required for root development. We will characterize the responsible element in SAMDC promoter for root development using deletion mutants of SAMDC promoter.