(O5-01)

Functional Analysis of Nodulation-Related Gene, MDH (Malate dehydrogenase) in Soybean

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MDH, a sole carbon source for nodule, was shown to be dramatically up-regulated in supernodulating mutant, SS2-2, compared with wild type soybean. Soybean malate dehydrogenase (MDH1, AF180335), one of the *Glycine max* MDH family (AF068689, AF068688, AF068687, AF068686, AY496910), is the nodule protein expressed exclusively in supernodulating mutant and grafting indicated the unique expression of the MDH1 is determined by root not by shoot as expected from supernodulating.

To elucidate the function of MDH1 in supernodulation, loss of function mutants were generated by RNA interference (MDHi) and *Agrobacterium rhizogenes*-mediated hairy root transformation. Since MDH1 have 94% nucleotide and 93% amino acid homology compared with MDH-2, MDH-2 is also expected to be influenced by the MDHi.

The root and nodule transformed with *A. rhizogenes* without any of RNAi genes showed the same genetic traits as those of the parent in either wild type or supernodulation.

The length of the transgenic hairy roots of the SS2-2 transformed with MDHi was longer than that of the empty vector controls and the nodule numbers were increased with a depression of MDH1 gene expression in SS2-2. It appears that MDH1 play a role in determining root length and nodule number, specifically decreasing both root length and nodule number.

Subsequently, nodule proteome analysis from the transgenic hairy root with MDHi was performed and showed some indication of alteration in expression of MDH.

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(O5-02)

Isolation and molecular analysis of Geminivirus from *Lonicera japonica* in Korea

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Honeysuckle yellow vein virus(HYVV) was identified and characterized from *Lonicera japonica* with honeysuckles in leaves. Complete genome of HYVV was amplified by PCR using Uni2/UniB primers specifically designed for begomoviruses in tomatoes. HYVV has a 2.7kb in size as a monopartite genome and is belong to begomoviruses of geminivirus group. HYVV had two virion sence ORFs(AV1 and AV2)and four complementary sense ORFs(AC1, AC2, AC3 and AC4). Phylogenetic analysis with other tomato infecting geminiviruses such as HYVV-[UK1], HYVV-[UK2], Honeysuckle yellow vein virus(HYVMV), HYVMV-[Kagoshima], TbLCJV-[Jp2], TbLCJV-[Jp3], Eupatorium yellow vein virus-[MNS2] and Eupatorium yellow vein virus-[Yamaguchi] shows that HYVV has the highest nucleotide sequence homology with those of HYVV-[UK2]. Each ORFs of HYVV shared 95% to 100% sequence homology to

HYVV-[UK2]. Grafting studies with a HYVV infected plant with a healthy L. japonica showed that virus was transmitted to virus infected L. japonica to healthy L. japonica and produced typical disease symptoms. Electron microscopy of thin sections of infected L. japonica leaves revealed the presence of crystalline inclusion showing a granular structure in some of the nuclei in phloem cells. Based on sequence comparisons and phylogenetic analysis, this virus studied was identified as Korean strain of HYVV and named HYVV-K

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(O5-03)

Evolution of genes encoding non-specific lipid transfer proteins in the *Poaceae* family

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The genes encoding non-specific lipid transfer proteins (nsLTPs), which are members of a small multigene family, show a complex pattern of expression regulation suggesting some diversification caused by the partitioning of their expression after duplication. In this study, the evolution of nsLTP genes in the *Poaceae* family was examined by surveying the pseudogenes and unigenes encoding the nsLTP from rice pseudomoleclues and the NCBI unigene database, respectively. Interestingly, there were nsLTP-rich regions on the distal parts of rice chromosomes 11 and 12, which resulted from the most recent large duplication in the rice genome. Two independent tandem duplications are expected to occur in the nsLTP-rich regions of rice. However, both groups of duplicate genes might have undergone different patterns: one is subfunctionalization and the other is mainly silencing (pseudogenization). Compared with the genomic distribution of wheat nsLTP genes, the nsLTP-rich regions do not appear to exist in other cereals, which is probably due to chromosome rearrangements or gene amplifications followed by differential gene losses after the divergence of the major cereals. The pattern of the genomic distribution of nsLTP genes in the *Poaceae* family show some differences between the cereal nsLTP genes that diverged from an ancient gene. In particular, thelong-term conservation of certain features, e.g. expression frequency and partition, tends to be continued throughout their evolution. There are somewhat fewer nsLTP unigenes in *Androponeae* than those of other tribes, such as *Oryzeae* and *Triticea*, which suggest that the differential loss of nsLTP genes occurred in the *Poaceae* family. These results might provide some clue as to the evolution process of nsLTP genes after the divergence of the *Poaceae* family approximately50 million years ago (Mya).

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Sequence based genetic mapping of *Brassica rapa* BAC clones which compose comparatively tiled path on the *Arabidopsis* chromosomes

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