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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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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 sense 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