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EXPRESSION OF 11 NITRATE TRANSPORTER (*AtNRT*) GENES IN *ARABIDOPSIS THALIANA*

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Higher plants possess both high- and low-affinity nitrate transporters. Since the first *Arabidopsis thaliana* low-affinity nitrate transporter gene (*AtNRT1.1*) was isolated in 1993, three low-affinity, and seven high-affinity nitrate transporter gene homologues (*AtNRT2*) have been identified in this species. We investigated the transcript abundance of all eleven genes in response to NO_3^- provision, by relative RT-PCR. Each gene showed different levels and/or expression patterns. *AtNRT2.1*, *2.2*, and *AtNRT1.1* were highly induced by 1 mM NO_3^-, peaking at 3 to 12 hours, and declining during 3 subsequent days. *AtNRT2.5* transcript was the least abundant among the *NRT2* family in roots, but the most abundant in shoot tissues. Shoot and root *AtNRT2.7* mRNA levels, which were moderate under non-inducing conditions, were strongly suppressed by nitrate provision. *AtNRT2.3*, *2.4*, and *2.6* showed a constitutive pattern of transcript abundance in roots and shoots. The localization of members of the *AtNRT2* family, by promoter::*uidA* fusions, will be demonstrated.

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FUNCTIONAL ANALYSIS OF LOW-AFFINITY SULFATE TRANSPORTER *Sultr2;2* IN *ARABIDOPSIS*

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Sulfate transporter gene family of *Arabidopsis* is consisted of 11 isoforms classified into 4 distinct groups by their functions. *Sultr2;2* belongs in the group of the low-affinity, vascular tissue-specific isoforms. *Sultr2;2* mRNA was accumulated both in leaves and roots under sulfur-limited growing conditions. Transgenic *Arabidopsis* plants expressing the fusion gene construct of the 5'-region of *Sultr2;2* and green fluorescent protein (GFP) showed accumulation of GFP in the phloem of roots and bundle sheath cells of leaf vascular tissues. Antisense suppression of *Sultr2;2* caused over-accumulation of *Sultr3;3* mRNA in leaves suggesting a possible compensatory role of *Sultr3;3* for the loss of sulfate transport activities driven by *Sultr2;2*. Cell type-specific expression of *Sultr3;3* is studied to identify its function.

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CHARACTRIZATION OF CHROLOPLASTIC SULFATE TRANSPORTERS IN *ARABIDOPSIS*

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Multiple isoforms of sulfate transporters are responsible for distribution of sulfate between different cell compartments in plants. Among the 11 isoforms of the sulfate transporter gene family, *Sultr4;1* encoded an unique transporter localizing in the chloroplast. Recently, we have isolated *Sultr4;2* as a homologue of *Sultr4;1* in *Arabidopsis* genome. *Sultr4;2* cDNA encoded a 677 amino acids polypeptide showing similarities with predicted ORFs for higher plant-type sulfate transporters in cyanobacteria and algae. The N-terminus region of the protein was predicted to have signal peptides for chloroplast localization. *Sultr4;2* mRNA was abundantly accumulated under low sulfate conditions. The increase of mRNA levels of *Sultr4;2* by sulfur limitation was stronger than in the case of *Sultr4;1*. Organelle and tissue specificity of *Sultr4;2* is studied using green fluorescent protein (GFP) as a reporter.

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CHARACTERIZATION OF SODIUM DEPENDENT SULFATE TRANSPORTER HOMOLOGUE FROM *Arabidopsis*

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In higher plants, multiple isoforms of sulfate transporters are responsible for the uptake and distribution of the sulfate anion. We have isolated an *Arabidopsis* cDNA (*ASST11*) encoding a homologue of rat sodium dependent sulfate transporter. *ASST11* encoded a 540 amino acid polypeptide that was predicted to be a membrane-bound transporter with 12 membrane spanning domains. However, *ASST11* was unable to complement the yeast mutant CP154-7A lacking two sulfate transporter genes. *ASST11* mRNA was accumulated both in roots and leaves of *Arabidopsis*, and the expression was slightly induced under sulfur deficient condition. A fusion gene construct carrying the coding sequence of *ASST11* in the antisense direction under CaMV 35S promoter was introduced in *Arabidopsis* plants. Growth was not affected by suppression of *ASST11* both under normal and sulfur deficient conditions. Fluctuation of metabolite levels and mRNA levels of sulfur assimilation genes are characterized in these antisense transgenic plants.