The Sucrose Transporter of Celery. Identification and Expression during Salt Stress

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In celery (Apium graveolens L.), long-distance transport of reduced carbon occurs both in the form of sucrose (Suc) and manni-
tol. The presence of mannitol has been related to the resistance of celery to salt stress. To investigate the transport events occurring
during salt stress, we have cloned the H+/Suc transporter of celery
AgSUT1 (A. graveolens Suc uptake transport 1) from a mature leaf
cDNA library. The function of the encoded protein was confirmed
by expression in yeast. AgSUT1 is a H+/Suc transporter with a high
affinity for Suc (K_m of 139 mM). Another closely related cDNA
(AgSUT2) was also identified. AgSUT1 is mainly expressed in ma-
ture leaves and phloem of petioles, but also in sink organs such as
roots. When celery plants were subjected to salt stress conditions
(30 d watering with 300 mM NaCl) favoring mannitol accumulation
Plant Physiol 106: 281–292), AgSUT1 expression was decreased in
all organs, but markedly in roots. The results are discussed in
relation to the physiology of celery.

Plants are autotrophic organisms using the energy of
light through photosynthesis to reduce ambient CO_2
to carbohydrates and other compounds. Plant organs are spe-
cialized into source (producers and exporters of sugars)
and sink (importers and users of sugars) organs. Sugars are
generally transported in the form of Suc (see below) from
source to sink organs by mass flow into specialized cells of
the phloem called the sieve tubes. This so-called “long-
distance” transport of sugar is therefore an important de-
terminant of plant productivity (Gifford and Evans, 1981).

In many species, the high Suc concentration measured in
the phloem sap (Winter et al., 1994) compared with surround-
ing cells has led to the model of an active transport of
Suc into the sieve element/companion cell complex from
the apoplastic space. This model has received confirma-
tion after the cloning of a cDNA encoding a H^+/Suc carrier
from spinach (SoSUT1: Spinacia oleracea Suc uptake trans-
port 1; Riesmeier et al., 1992), potato (SISUT1: Solanum
ruberosum SUT1; Riesmeier et al., 1993), and then many
species (for review, see Lemoine, 2000). The localization of
the carrier to plasma membranes of sieve elements (Kühn
et al., 1997) and companion cells (Truernit et al., 1995) and
the impairment of Suc export from leaves of plants where
the expression of the Suc carrier was lowered (Riesmeier
et al., 1994; Bürkle et al., 1998) demonstrated the involvement
of SUT carriers in the loading of Suc in the sieve element/com-
panion cell complex.

In a significant number of species, Suc is transported in
parallel with other types of sugars such as oligosaccharides
(e.g. raffinose and trehalose in cucurbits; Turgeon, 1996)
and polyols (mainly mannitol and sorbitol). Polyols (or
sugar alcohols) are the reduced form of α-ketoses and are
found in more than 100 species (Stoop et al., 1996). The
derivatives of Glc (sorbitol or dulcitol) and Man (mannitol)
are the most frequently found polyols. It has been calcu-
lated that up to 30% of the carbon fixed by plants on earth
is in the form of polyols (Bieselski, 1982). The exact function
of the polyols is still unknown, but their presence has been
related to different events. Mannitol has been implicated in
the resistance to stress (mainly salt), because its synthesis is
increased in response to stress in celery (Apium graveolens)
(Everard et al., 1994). Mannitol, like other polyols, is con-
sidered to be a compatible solute, accumulating in stressed
cells to increase their osmotic potential while protecting
cellular structures and activities. Seeds from Arabidopsis
plants engineered to produce mannitol showed an in-
creased resistance to salt stress (Thomas et al., 1995). In
planta, mannitol is synthesized in the cytoplasm of source
leaves from photosynthesis-derived hexose phosphate and
exported to sink organs, presumably in the same way as
Suc. Several lines of evidence indicate that Suc and man-
nitol are transported by different carriers in celery (Daie,
1987; Salmon et al., 1995), but the transport events in
polyol-synthesizing species received little attention except
in Plantago major (Gahrtz et al., 1994), where sorbitol is also
transported.

Salt stress has been studied extensively as salt salinity
represents an increasing problem for agriculture in many
countries. Several species are tolerant to salt and can still
show some growth when cultivated on soils containing
high NaCl levels. For example, celery plants develop new
leaves when grown on a 300 mM NaCl solution, a salinity
equal to one-half that of seawater. Under such conditions,
both in plants (Everard et al., 1994) and cell cultures (Prata
et al., 1997), mannitol accumulation is the result of an
increase in mannitol synthesis at the expense of Suc and a
decrease of mannitol catabolism. However, the flux of
sugar from source and to sink organs has not been consid-
ered in such situations. Generally speaking, regulation of

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Suc transporter expression has been rarely studied and very few reports are available (see Delrot et al., 2000; Lalonde et al., 1999).

In this paper, we report the identification of Suc transporters from celery, AgSUT1 and AgSUT2 (A. graveolens Suc uptake transport 1 and 2) and the regulation of their expression during salt stress. We demonstrate that in response to salt stress, AgSUT1 expression is lowered in all organs but to different extents. Those results are discussed in relation to the physiology of celery.

Materials and Methods

Plant Material

Celery plants (Apium graveolens L. var dulce cv Vert d’Elne) were grown under greenhouse conditions as described by Davis et al. (1988). Mature plants were approximately 4 months old. Prior to salt stress treatment, the open surfaces of 5.4-L pots containing the plants were covered with plastic film to minimize surface evaporation. Salt treatments were stepped up in 50 m\(\text{M}\) increments (25 m\(\text{M}\) in the morning, 25 m\(\text{M}\) in the afternoon) until the desired final concentration (300 m\(\text{M}\)) was achieved. NaCl was dissolved in either Peters 20:20:20 fertilizer (100 ppm nitrogen working strength) or tap water. Plants were watered alternatively with each solution for 4 weeks. At the end of the 300 m\(\text{M}\) NaCl treatment, half of the treated plants were watered for 1 week with tap water without salt (rehydrated plants).

Strains

The following strains were used in this study. Escherichia coli strains DH5\(\alpha\) (supE44, \(\Delta\)lacU169 [proAB, lacZAM15], hsdRI7, recA, endA1, gyrA96, thi-1, and relA1), XL1Blue MRF\(^+\) (Stratagene, La Jolla, CA), and SOLR (Stratagene) were cultured according to standard techniques (Sambrook et al., 1989). The yeast strain SUSY7 (suc2: \(\Delta\)IRA3, mal10, and trp1) expresses a potato Suc synthase gene (Riesmeier et al., 1992).

Screening of cDNA Library and DNA Manipulations

The source leaf cDNA library in AZAP II was a generous gift from Prof. W.H. Loescher (Everard et al., 1997). Recombinant phages (750,000) were screened using SoSUT1 as a radioactive probe according to the manufacturer’s protocols (Stratagene). Hybridization-N nylon filters (Amersham, Les Ulis, France) were hybridized overnight at 42°C according to standard conditions (Sambrook et al., 1989). Filters were washed 15 min at 42°C with 0.1% (w/v) SDS and 2\(\times\) SSC (1\(\times\) SSC = 0.15 m NaCl and 0.015 m sodium citrate), 15 min at 50°C with 0.1% (w/v) SDS and 2\(\times\) SSC, and 30 min at 50°C with 0.1% (w/v) SDS and 1\(\times\) SSC. In vivo excision was performed on the eight clones that gave positive signals during the three rounds of screening.

The cDNAs were sequenced using an automated sequencer (ABI 310, Perkin-Elmer, Foster City, CA). Sequence comparisons with other databases were performed through the National Center for Biotechnology Information via the BLAST site (Altschul et al., 1997). Transmembrane regions and protein orientation were predicted using the TMpred tool (Hofmann and Stoffel, 1993).

Expression of AgSUT1 in Saccharomyces cerevisiae

AgSUT1 cDNA was ligated into the EcoRI-Xhol site of the yeast shuttle vector YEP112A1XE (Riesmeier et al., 1992). This vector allows expression of full-length cDNAs under the control of the S. cerevisiae ADH1 promoter. Competent yeast cells were prepared and transformed according to the method of Dohmen et al. (1991). SUS7 transformed with YEP 112A1XE was used for control experiments.

Uptake of Radiolabeled Sugars

Yeast cells were grown to the early logarithmic phase, washed with distilled water, and resuspended to 1% (w/v) in yeast nitrogen base (YNB) medium containing 25 mm 2-(N-morpholino)-ethanesulfonic acid (MES) buffer, pH 4.5. The pH dependence of Suc uptake was determined in YNB medium buffered at different pH values with 25 mm MES. A 100-\(\mu\)L aliquot of the cell suspension was incubated at 28°C for 0, 60, 120, 180, and 300 s in 100 \(\mu\)L of a solution containing \(\text{[H]}\)Suc (final specific activity: 14.8 MBq mmol\(^{-1}\)). The reaction was stopped by addition of 8 mL of ice-cold water and filtration on glass-fiber filters (13400–25–S, Sartorius, Palaiseau, France). The radioactivity incorporated in the cells was determined in a liquid scintillation counter (Packard Instruments, Meriden, CT). For inhibition and competition studies, reagents were added 30 s prior to Suc.

RNA Isolation and Northern-Blot Analyses

For each organ studied, samples from four independent plants treated under the same conditions were harvested after 4 h of photosynthesis, pooled, and frozen in liquid nitrogen. Total RNA was isolated as described by Kay et al. (1987). Twenty micrograms of total RNA was separated on 1.2% (w/v) agarose gels containing formaldehyde and transferred to nylon filters as described in Sambrook et al. (1989). Hybridization was at 65°C and the EcoRI/Xhol fragment of AgSUT1 was used as a probe. The final wash was 0.1% (w/v) SDS, 0.5\(\times\) SSC at 68°C for 15 min. Radioactivity in the reacting bands was counted with an Instant Imager (Packard Instruments), and the background counts of the membrane were subtracted. The amount of RNA loaded in each lane was calibrated by hybridization with a 250 riboprobe and Instant Imager counting (Packard Instruments) as described above. The values obtained with the riboprobe were used to calculate the relative intensity of the signals for AgSUT1 in each lane.

Results

Isolation of Celery Suc Transporters

Screening of the celery leaf cDNA library with the radiolabeled DNA of the spinach Suc transporter SoSUT1 (Ries-
meier et al., 1992) resulted in eight positive clones (l1–8). In vivo excision was performed with these clones, which were then partially sequenced. One of these clones did not show any similarity to the Suc transporters. The remaining seven clones were homologous to the SoSUT1 sequence. However, some of the clones differed in the length of their 5’ and 3’ non-coding regions. This phenomenon was already observed when the Man-6-P reductase of celery was cloned in the same library (Everard et al., 1997). Three different cDNAs were therefore identified: two (AgSUT2A, accession no. AF167415, and AgSUT2B, accession no. AF167416) had identical coding regions, whereas the third one (AgSUT1, accession no. AF063400) also showed slight differences in the coding region (nine different amino acids residues compared with AgSUT2A/B). Two 5’ noncoding sequences were identified: one starts 109 bp in front of the ATG, the other was 43 nucleotides shorter in the more distal 5’ region (Fig. 1A). All 3’-untranslated ends had a polyadenylation signal (AATAAA) upstream of the poly(A+) tail. These regions were different downstream of this motif (Fig. 1B). In addition, the 5’ and 3’ noncoding sequences share between 73% and 80% identical nucleotides with those of DcSUT2 (Daucus carota SUT2; Shakya and Sturm, 1998) cDNA.

The sequence of the longest cDNA clone l1, AgSUT1, is shown in Figure 2. The longest open reading frame for AgSUT1 is 1536 bp long, encoding a protein of 512 amino acid residues, a calculated molecular mass of 54.5 kD, and a pI of 9.27. The AgSUT1 protein sequence shows 12 hydrophobic regions (underlined in Fig. 2; Kyte and Doolittle, 1982; see Lemoine, 2000 for a detailed predictive model) representing potential transmembrane helices. As shown in Table I, the AgSUT1 protein shares between 63% and 70% identical amino acids with the Suc transporters from spinach (Riesmeier et al., 1992), from Arabidopsis (Sauer and Stolz, 1994) and from Plantago major (Gahrtz et al., 1994). However, a very high identity (92%) was found with DcSUT2, the Suc transporter from carrot, another member of the Apiaceae family. Interestingly, AgSUT1 was identified from a leaf cDNA library, whereas DcSUT2 was found in a root cDNA library (see below for a longer discussion of this point). Two Asn residues that are part of a consensus sequence for N-glycosylation (Asn-3 and Asn-134) are located on the cytoplasmic side and should therefore not be glycosylated. Potential phosphorylation sites are located at residues T136, T175, S252, and S263.

**Characterization of AgSUT1 in S. cerevisiae**

To demonstrate that the identified cDNAs code for Suc carriers, they were heterologously expressed in yeast. AgSUT1, AgSUT2A, and AgSUT2B cDNAs were ligated into the EcoRI-XhoI sites of the S. cerevisiae expression plasmid YEP 112A1XE. Competent YSH SUSY7 cells (Riesmeier et al., 1992) were transformed with those plasmids and YEP 112A1XE was used as a control.

Figure 3 shows that yeast cells expressing AgSUT1 transported 3H-Suc at a much higher rate (4.1 nmol Suc mg⁻¹ protein min⁻¹) than control cells (0.2 nmol Suc mg⁻¹ protein min⁻¹). Although not presented, similar results were obtained with AgSUT2A and AgSUT2B. Due to the very
A high level of sequence identity, only AgSUT1 was used for the rest of the characterization of Suc uptake.

The pH dependence of Suc transport by AgSUT1 was determined in the pH range of 4.5 to 7.5 (Fig. 4). AgSUT1 is much more active at pH 4.5, and the relative activity decreased to 10% when the pH was increased to 5.5 (Fig. 4). Therefore, as far as pH dependence is concerned, AgSUT1 is more closely related to, e.g. SoSUT1 or AtSUC2 than AtSUC1, which displays a broader optimal pH range. These data are in agreement with a Suc/proton cotransport mechanism.

When the uptake of Suc by AgSUT1 in yeast cells was studied for 1 min at concentrations ranging from 25 to 750 μM, a clear saturation was visible (data not shown). The Lineweaver-Burk plot of the data (Fig. 5) gave an apparent affinity (K_m) of 139 μM and a maximum velocity (V_max) of 5.9 nmol mg⁻¹ protein min⁻¹. The K_m value of AgSUT1 for Suc is in the same range as the K_m value determined for this carrier in plasma membrane vesicles from phloem strands (K_m = 280 μM; V_max = 3 nmol mg⁻¹ protein 30 s⁻¹; Salmon et al., 1995).

A protonophore such as carbonyl cyanide m-chlorophenylhydrazone strongly inhibits Suc transport catalyzed by AgSUT1 protein (Table II). These data confirm the assumption that Suc uptake is mediated by a proton cotransport mechanism. Suc transport by AgSUT1 is also sensitive to thiol reagents such as N-ethylmaleimide and 1,10-phenanthroline.

Table I. Percentage of identical amino acid residues between AgSUT1 and Suc transporters from other species

<table>
<thead>
<tr>
<th>Suc Transporter</th>
<th>Accession No. (EMBL)</th>
<th>Identity %</th>
</tr>
</thead>
<tbody>
<tr>
<td>SoSUT1</td>
<td>X67125</td>
<td>70</td>
</tr>
<tr>
<td>AtSUC1</td>
<td>X75365</td>
<td>70</td>
</tr>
<tr>
<td>AtSUC2</td>
<td>X75382</td>
<td>63</td>
</tr>
<tr>
<td>PmSUC2</td>
<td>X75764</td>
<td>70</td>
</tr>
<tr>
<td>DcSUT1A</td>
<td>Y16766</td>
<td>50</td>
</tr>
<tr>
<td>DcSUT2</td>
<td>Y16768</td>
<td>92</td>
</tr>
</tbody>
</table>

Figure 3. Uptake of Suc into transgenic S. cerevisiae cells. The Suc concentration was 250 μM and the external pH 4.5. ■ Uptake into cells transformed with AgSUT1 cDNA; ○ Suc uptake into control cells transformed with the plasmid YEP. The results are the means ± SD of three independent experiments (three replicates per experiment).

Figure 4. pH dependence of Suc transport in transgenic yeast cells expressing AgSUT1. Measurements were performed at 250 μM Suc in YNB medium containing 25 mM MES buffered at the indicated pH. Incubation time was 2 min. The results are the means ± SD of three independent experiments (three replicates per experiment).
-chloro-mercuriphenylsulfonic acid or to diethylpyrocarbonate (an imidazole group reagent). The histidyl residue involved in diethylpyrocarbonate sensitivity identified in AtSUC2 (Lu and Bush, 1998) is also conserved in AgSUT1 at position 66. Thiol groups and imidazole groups may therefore be implicated in substrate recognition or in the uptake reaction itself.

To determine the substrate specificity of AgSUT1, transport of Suc was studied in the presence of various sugars and derivatives that might be potential substrates for a Suc transporter (Table III). Mannitol had no influence on the transport rates, which supports the assumption that Suc and mannitol uptakes are mediated by two independent transport systems in celery (Daie, 1986; Salmon et al., 1995). α-Phenylglucoside strongly inhibits Suc uptake, which agrees with published data on other Suc carrier specificity (AtSUC1/2, SoSUT1, and StSUT1). On the other hand, the inhibition by maltose is weak, in the same range as for StSUT1 (Riesmeier et al., 1993) and RcSCR1 (Weig and Komor, 1996). All other Suc carriers expressed in yeast are inhibited by maltose (see Lemoine, 2000). The addition of raffinose led to a higher inhibition than that noted for other Suc carriers expressed in yeast. This could be related to the fact that small amounts of raffinose are detected among the soluble sugars present in celery (N. Noiraud, L. Maurousset, S. Delrot, and R. Lemoine, unpublished data).

### Table II. Sensitivity of the AgSUT1 activity to inhibitors

<table>
<thead>
<tr>
<th>Inhibitor</th>
<th>Relative Transport Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>100</td>
</tr>
<tr>
<td>50 µM CCCP</td>
<td>9.0 ± 11.2</td>
</tr>
<tr>
<td>100 µM PCMBS</td>
<td>29.1 ± 7.8</td>
</tr>
<tr>
<td>100 µM NEM</td>
<td>24.9 ± 6.7</td>
</tr>
<tr>
<td>0.5 mM DEPC</td>
<td>40.6 ± 5.9</td>
</tr>
</tbody>
</table>

Expression of AgSUT1 in Different Organs and Tissues

The results presented in Figure 6 have been obtained with AgSUT1 as a probe, and the quantity of RNA loaded per lane was calibrated with a riboprobe. The results are expressed as a percentage of expression in mature leaf, where AgSUT1 was found to be maximal. This is therefore

### Table III. Specificity of the AgSUT1 Suc carrier

<table>
<thead>
<tr>
<th>Carrier</th>
<th>Absorption</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>100</td>
</tr>
<tr>
<td>5 mM Suc</td>
<td>65.4 ± 0.4</td>
</tr>
<tr>
<td>5 mM Mannitol</td>
<td>90.0 ± 1.2</td>
</tr>
<tr>
<td>5 mM Maltose</td>
<td>81.6 ± 1.2</td>
</tr>
<tr>
<td>5 mM Raffinose</td>
<td>74.7 ± 1.6</td>
</tr>
<tr>
<td>2 mM α-Phenylglucoside</td>
<td>32.0 ± 1.1</td>
</tr>
</tbody>
</table>

Figure 5. Lineweaver-Burk plot of Suc uptake as a function of concentration in transgenic yeast cells expressing AgSUT1. The results are the means ± so of three independent experiments (three replicates per experiment).

Figure 6. Expression of AgSUT1 in the different organs and tissues of celery. Organs from four different plants were pooled before RNA extraction. A, Film of the northern-blot analysis with AgSUT1 as a probe (20 µg RNA per lane). B, Scan of the image obtained after radioactivity counting with an Instant Imager (Packard Instruments). C, Same as B except that a 25S riboprobe from Arabidopsis was used to calibrate the amount of RNA loaded per lane. D, Quantification of AgSUT1 expression as percent of mature leaves (100%). Results derived from radioactivity counts obtained in B and C.
in agreement with AgSUT1 being the ortholog to SUT1 in other species. AgSUT1 expression was also detected in young leaves, but only at low level in roots. As originally described by Daie (1986), phloem strands are easy to isolate from celery fleshy petioles. Those phloem strands are composed of sieve elements, companion cells, and phloem parenchyma cells, and can be used for plasma membrane isolation (Salmon et al., 1995) and RNA extraction. As can be seen in Figure 6, AgSUT1 expression was also high in phloem from both mature and young petioles, which corresponds to the same developmental stage as mature and young leaves. On the contrary, AgSUT1 expression in the storage parenchyma or total petiole was very weak.

Expression of AgSUT1 during Salt Stress

The expression of the Suc carrier was investigated under salt stress conditions. Plants were watered during 4 weeks with 300 mM NaCl as described by Everard et al. (1994). Under these conditions, growth of young leaves still occurred, but the senescence of older leaves was accelerated and roots were shorter and larger (Everard et al., 1994; N. Noiraud, S. Delrot, and R. Lemoine, unpublished data). Half of the stressed plants were watered with tap water for 1 extra week (rehydrated plants).

The results presented in Figure 7 show that under salt stress conditions, the expression of Suc carriers was lowered in all organs but to a different extent. In source leaves the expression was reduced by 30%. A strong reduction (50%) of AgSUT1 expression was observed in young leaves. In phloem tissues isolated from either young or mature petioles, AgSUT1 was only slightly reduced to 80% of control in both cases. The most striking alteration was noted in the roots: the expression was dramatically reduced in the case of salt stress, representing only 10% of expression in control roots. If AgSUT1 expression pattern in the different organs of control plants is taken into consideration (Fig. 6), the residual expression in young leaves and roots was very low following a 1-month salt stress. In all organs studied, a 1-week rehydration period was not sufficient to restore AgSUT1 expression to control levels (without salt stress). Work by Pardossi et al. (1998) indicated that a significant reduction in the salt content of stressed celery plants was only observed after a 4-month rehydration period. Therefore, the 1-week rehydration period used here was certainly not sufficient for a significant reduction in the salt content.

DISCUSSION

Suc Transporters in Celery

Three different cDNAs encoding Suc transporters were identified by hybridization screening. Two of these (AgSUT2A and AgSUT2B) have identical coding sequences and differ only in their 5’ and 3’ non-coding regions. AgSUT1 and AgSUT2A/AgSUT2B are closely sequence related, because they only differ by nine amino acids. Moreover, all the coding sequences have the same length and are all able to transport Suc when expressed in yeast. This situation is reminiscent of that in carrot, in which two cDNAs encoding Suc carriers also differ only in these regions (DcSUT1A and DcSUT1B; Shakya and Sturm, 1998). However, in that case, the third cDNA identified (DcSUT2) was not closely related to the other two. As expected from species of the same family, a high conservation level was found between AgSUTs and DcSUT2 (more than 90% identity at the amino acid level, and 80% at the nucleotide level). Surprisingly, the conservation extends to 5’ and 3’ flanking regions of cDNAs such as the AgCam (A. graveolens calmodulin, accession no. AF064552) and the DcCam-1 (D. carota calmodulin, accession no. X59751) (data not shown). This indicates that gene sequences are highly conserved between those two members of the Apiaceae family.

According to its kinetic characteristics (pH dependence, sensitivity to protonophores), AgSUT1 works as an H+/Suc transporter functionally related to the other SUT1 transporters identified so far. The K_m value for AgSUT1 (139 μM) represents the highest affinity determined so far for Suc transporters expressed in yeast (Riesmeier et al., 1992, 1993; Gahrzt et al., 1994; Sauer and Stolz, 1994). However, due to different protocols and/or yeast strains used for uptake experiments, the differences in affinity may not be significant. Mannitol had no influence on the activity of AgSUT1, confirming the existence of independent transport systems for both substrates (Daie, 1986; Salmon et al., 1995).

Localization of AgSUT1 Expression

AgSUT1 was used as a probe for northern analysis. However, due to the very high level of sequence identity with AgSUT2A/AgSUT2B, cross-hybridization is more than probable and it was not possible to discriminate the expression of either of these carriers. For the rest of the discus-
sion, we will refer to AgSUT to indicate that the signals observed in northern experiments were either due to AgSUT1 or AgSUT2. All of the transport interpretations are based on results obtained at the mRNA level and, therefore, post-transcriptional regulation has not been considered here. Some recent data indicate that phosphorylation could regulate the Suc carrier activity (Roblin et al., 1998), but transcriptional regulation is also important. This was demonstrated by the rapid turnover of the Suc carrier mRNA and protein measured in potato leaves (Kühn et al., 1997), and by the parallel decrease of Suc transporter mRNA levels and Suc transport activity in transgenic potato leaves (Lemoine et al., 1996) and sugar beet leaves (Chiou and Bush, 1998). Moreover, results showing higher AgSUT expression in phloem than in storage parenchyma in mature petioles (Fig. 6) are in perfect agreement with the higher Suc transport activity reported in plasma membrane vesicles from phloem than from storage parenchyma (Salmon et al., 1995).

AgSUT expression is higher in source leaves than in any other organ, and higher in phloem than in surrounding tissues in mature petioles, in agreement with results obtained with SUT1 carriers in other species. In spite of the direct access to phloem in petioles of celery, AgSUT expression is higher in leaves (all tissues of the leaves) than in phloem strands, which are highly enriched in conducting cells. This indicates that the minor veins network of mature leaves is the site where expression of Suc carriers is the highest.

Expression of AgSUT in mature petioles of celery may indicate a different role for the Suc transporter as, for example, in potato stem. In potato, it was proposed that the Suc carrier retrieved Suc leaking from the phloem (Riesmeier et al., 1993). Daie (1986) suggested that in mature Suc transporter mRNA and protein measured in potato leaves (Kühn et al., 1997), and by the parallel decrease of Suc transporter mRNA levels and Suc transport activity in transgenic potato leaves (Lemoine et al., 1996) and sugar beet leaves (Chiou and Bush, 1998). Moreover, results showing higher AgSUT expression in phloem than in storage parenchyma in mature petioles (Fig. 6) are in perfect agreement with the higher Suc transport activity reported in plasma membrane vesicles from phloem than from storage parenchyma (Salmon et al., 1995).

Changes in AgSUT1 Expression in Response to Salt Stress

There are many situations where plants have to adapt their carbon allocation to sink organs and define new priorities among sinks. It is well known that under limiting nutrient supply, plants can flower and set seeds much faster than under normal conditions. Salt stress can be regarded as a situation in which plants have to cope both with decreased water availability and ion toxicity (Levitt, 1980). Carbon metabolism under stress has been investigated mainly in plants able to synthesize compatible solutes such as Pro, Gly betaine, and, as in celery, polyols. Polyols are unique because, like Suc, they are primary photosynthetic products and are thus different from nitrogen compounds. However, in many cases the source-to-sink transport of these compounds has not been taken into consideration. In celery, mannitol and Suc are synthesized in source leaves and then transported to sink organs. A shift in photosynthetic carbon allocation from Suc towards mannitol has been reported (4-fold increase in the mannitol/Suc ratio compared with controls; Everard et al., 1994) in the same stress conditions as the ones used in this study.

To maintain a high level of mannitol (an osmoprotectant), mannitol dehydrogenase is repressed, and it has been suggested that Suc is then metabolized to meet the need for energy of stressed tissues (Everard et al., 1994), just as in flowering plants and sink tissues (Fellman and Loescher, 1987). A high level of Suc (hexose) was shown to repress mannitol dehydrogenase expression in celery cells
(Prata et al., 1997). This would indicate that Suc transport has to be maintained, which is in agreement with the rather low reduction of AgSUT expression reported here in source-exporting organs (leaves and petioles). The general down-regulation of AgSUT expression could be the result of a decreased demand for energy as growth is reduced. A more dramatic reduction of AgSUT expression is observed in roots. Expression of Suc carriers in roots has been related to Suc unloading (Riesmeier et al., 1993; Truernit and Sauer, 1995). If this is true, this would indicate that, in the case of salt stress, Suc unloading in roots is extremely reduced. As roots are the primary site of contact with the salt solution, mannitol accumulation may be of major importance in increasing the osmotic potential and allowing water uptake. Root growth is dramatically reduced in the case of salt stress (Everard et al., 1994; our own observations). Therefore, the reduced expression of AgSUT in roots could be the result of a decreased metabolic demand. Residual expression of AgSUT might be sufficient to account for the reduced flux of Suc to the roots. However, the possibility of salt-induced expression of a root-specific Suc carrier not related to AgSUT1 or AgSUT2 cannot be ruled out at the present time.

The salt stress results presented here certainly represent a new steady state in celery plants adapted to growth on high-salt conditions. Other studies on sugar carrier regulation have been conducted on much shorter periods of time (Weber et al., 1997; Chiou and Bush, 1998), because they were run on detached organs. The only transporter that has been studied in planta under salt stress conditions is the Pro transporter ProT2 from Arabidopsis (Rentsch et al., 1996), the expression of which is highly increased in response to 200 mM NaCl. In that case, an increase in ProT2 expression was already detected after 4 h. Interestingly, this increase in ProT2 expression is paralleled by a decrease in a general amino acid permease. In celery, this could mean that mannitol transporter expression is increased during salt stress.

Growing plants on high soil salinity represents a challenge for the future and it is therefore important to understand the strategies used by plants to cope with such stress. Up to now, most of the research devoted to polysols concerned their metabolism, both at the fundamental level and in transgenic plants engineered for salt resistance. However, transport events of osmolytes may be of significant importance because they are synthesized only in leaves. Plants such as celery may represent an excellent model for the study of polyol and sugar transport in response to stress because of a variety of responses (Stoop and Pharr, 1994; Pardossi et al., 1998). This work demonstrates down-regulation of a Suc transporter expression in roots in response to an abiotic stress highly relevant to culture conditions. Although mannitol biosynthesis has been considered as a response to salt stress, our results indicate that Suc transport is certainly not suppressed under such conditions. Further work is now under way to relate the changes in Suc metabolism and, more precisely, to describe the transporters involved by identifying their respective promoters.

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