Localization of sucrose synthase in developing seed and siliques of *Arabidopsis thaliana* reveals diverse roles for SUS during development

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**Abstract**

This study investigated the roles of sucrose synthase (SUS) in developing seeds and siliques of *Arabidopsis thaliana*. Enzyme activity assays showed that SUS activity was highest in developing whole siliques and young rosette leaves compared with other tissues including mature leaves, stems, and flowers. Surprisingly, quantitative PCR analyses revealed little correlation between SUS activity and transcript expression, which indicated the importance of examining the role of SUS at the protein level. Therefore, immunolocalization was performed over a developmental time course to determine the previously unreported cellular localization of SUS in *Arabidopsis* seed and silique tissues. At 3 d and 10 d after flowering (daf), SUS protein localized to the silique wall, seed coat, funiculus, and endosperm. By 13 daf, SUS protein was detected in the embryo and aleurone layer, but was absent from the seed coat and funiculus. Starch grains were also present in the seed coat at 3 and 10 daf, but were absent at 13 daf. Co-localization of SUS protein and starch grains in the seed coat at 3 and 10 daf indicates that SUS may be involved in temporary starch deposition during the early stages of seed development, whilst in the later stages SUS metabolizes sucrose in the embryo and cotyledon. Within the silique wall, SUS localized specifically to the companion cells, indicating that SUS activity may be required to provide energy for phloem transport activities in the silique wall. The results highlight the diverse roles that SUS may play during the development of silique and seed in *Arabidopsis*.

Key words: *Arabidopsis*, companion cells, immunolocalization, nectary, seed development, silique wall, sucrose synthase.

**Introduction**

Sucrose, produced in photosynthetic source tissues, is transported to various vegetative and/or reproductive sink tissues where it is used for active growth processes or may be utilized for biosynthesis of cellulose and of storage carbohydrate such as starch, fructans, or lipids. Cleavage of the glycosidic bond is a prerequisite step for sucrose metabolism (Fu *et al.*, 1995). Two enzymes, sucrose synthase (SUS; EC 2.4.1.13) and invertase (EC 3.2.1.26), catalyse this cleavage reaction *in vivo*. The regulation of these reactions and its consequences has therefore become a central issue in plant carbon metabolism (Koch, 2004). In several plants, SUS activity is the main route for entry of sucrose into cellular metabolism. Previous studies have shown that a reduction in SUS activity reduced the availability of assimilate for storage and normal growth (Craig *et al.*, 1999). For example, inhibition of SUS activity in tomato decreased the fruit setting and sucrose unloading capacity (D'Aoust *et al.*, 1999), and in transgenic potato tubers reduction in the level of SUS activity decreased starch biosynthesis (Zrenner *et al.*, 1995). SUS
has also been localized in the companion cells (CCs) in maize leaves and citrus fruits (Nolte and Koch, 1993), where it has been proposed to play a role in providing energy for loading and unloading in the phloem (Lerchl et al., 1995). In addition, SUS is believed to be involved in cell wall biosynthesis by providing UDP-glucose directly to cellulose synthase (King et al., 1997; Ruan and Chourey, 1998; Haigler et al., 2001). Ruan et al. (2003) reported that a 70% reduction in SUS activity suppressed cell initiation in cotton fibre, probably through inhibition of cell wall biosynthesis.

A small multigene family has been found to encode several SUS isoforms in many plant species examined to date, including maize (Carlson et al., 2002), pea (Barratt et al., 2001), rice (Wang et al., 1992; Huang et al., 1996; Harada et al., 2005; Hirose et al., 2008), Lotus (Horst et al., 2007), and Arabidopsis (Barratt et al., 2001). Studies of the predicted amino acid sequences and gene structure have shown that the AtSUS family consists of six SUS genes, distributed in three separate groups. AtSUS1 and AtSUS4 can be classified into the dicot SUS1 group; AtSUS2 and AtSUS3 belong to the SUSA group; while AtSUS5 and AtSUS6 make a separate group on their own (Baud et al., 2004). Each of these isoforms may have a specific role in planta as revealed through mutant and transgenic plant analysis (Bieniawska et al., 2007). In order to examine the role of the six SUS isoforms in Arabidopsis, comparative analysis was carried out with the SUS gene families of other species (Barratt et al., 2001; Baud et al., 2004; Harada et al., 2005; Bieniawska et al., 2007). Measurement of the changes in the transcript level of the SUS isoforms in response to different treatments (including anoxia, dehydration, cold treatment, and sugar feeding) revealed that some isoforms respond to biotic and non-biotic stresses. For example, under anaerobic conditions, the transcript levels of AtSUS1 and AtSUS4 were found to increase in rosette leaves. This finding was further confirmed by abnormal growth of a sus1/sus4 double mutant under hypoxia (Bieniawska et al., 2007). The roles of AtSUS5 and AtSUS6 remain unclear as their expression levels exhibited no response to treatment conditions (Baud et al., 2004), and a sus5/sus6 double mutant exhibited normal growth when compared with the wild type (Bieniawska et al., 2007). However, it has been shown that the promoter sequences of both of these isoforms are active in the vascular system of the flower and cotyledon (Bieniawska et al., 2007). It is not known, however, whether changes in the expression level of the transcript of SUS isoforms would result in similar changes in the level of SUS activity.

The involvement of SUS in seed development has been investigated in several studies (Doehlert et al., 1988; Xu et al., 1989; Counce and Gravois, 2006). A shrunked seed phenotype in maize was found to be related to a mutation in one of the SUS genes, Sh1 (Chourey et al., 1998). SUS transcript has been shown to be induced during seed development in the legume plant Vicia faba L. (Heim et al., 1993). King et al. (1997) reported that SUS activity increased during development of canola seeds. Further evidence is provided by localization of SUS in developing seeds of cotton (Ruan and Chourey, 1998) and maize kernels (Wittich and Vreugdenhil, 1998). In addition, microarray analysis performed on developing Arabidopsis seeds also showed an increase in SUS expression level during seed development (Ruuska et al., 2002). These results were confirmed by reverse transcription-PCR (RT-PCR) which clearly showed that during the early stages of seed development there is an increase in AtSUS2 transcript level, whilst the amount of AtSUS3 transcript increased during the late stages of seed maturation (Bieniawska et al., 2007). Since the transcript level of AtSUS2 was low in vegetative tissues, AtSUS2 was considered to be a 'seed maturation marker' (Baud et al., 2004). However, in the dicot model plant Arabidopsis thaliana, knowledge of SUS expression during seed development is limited to transcript level measurements, and there is no direct information on changes in temporal and/or spatial expression patterns of SUS protein during seed and silique development. As a model for oilseed plants, which accumulate reserves in the form of carbohydrate during early stages of seed development and convert it to lipids during the later stages (Focks and Benning, 1998), it is important to know where and how SUS protein expression changes in the developing siliques and seed of Arabidopsis.

In this study, a combination of SUS activity assays, transcript expression analysis, and immunolocalization techniques was used to investigate the potential roles of SUS during the early, mid, and late stages of seed development in Arabidopsis. The presence of SUS protein in various tissue and cellular locations at these stages of seed development is discussed in the context of phloem loading and unloading, starch remobilization, and endosperm and embryo development.

Materials and methods

Plants growth and conditions

Arabidopsis thaliana seeds, ecotype Columbia (Col-0), were surface sterilized by incubation in 0.1% (w/v) mercuric chloride followed by several washes in sterile distilled water. The seeds were germinated on a half-strength MS medium, containing 1% sucrose, in a growth room at 23 °C with a 12 h photoperiod. Seedlings were transferred to soil 1 week after germination and were grown at 23 °C under a 14 h light regime. Seedling samples were harvested at the fourth true leaf stage. Samples of stem, cauline leaves, and mature rosette leaves after flowering were harvested at 5 weeks after germination. Individual flowers were tagged at the day of flowering, and developing siliques were collected at 3, 10, and 13 daf.
Protein extraction and SUS activity measurement

Solu ble protein samples were extracted by grinding the tissues (250 mg) in liquid nitrogen, before adding 1 ml of a cold extraction buffer containing 25 mM HEPES-KOH (pH 7.3), 5 mM EDTA, 1 mM dithiothreitol (DTT), 0.1% polyvinyl pyrrolidone (PVP, M, 40 000), 1 mM phenylmethylsulfonyl fluoride (PMSF), and 0.01 mM leupeptin. The supernatants were collected by centrifugation at 13 000 g for 5 min at 4 °C. A 500 μl aliquot of the supernatant was passed through a Sephadex G-25 column (Amersham Biosciences) and collected in 1 ml of elution buffer (50 mM HEPES pH 7.3, 5 mM EDTA). Protein concentrations were determined using the Coomassie Plus™ protein assay kit (Pierce) using bovine serum albumin (BSA; fraction V Sigma) as the standard. SUS activity assays, in the direction of sucrose breakdown, were carried out as described by Ruan et al. (2003), and the resultant UDP-glucose was measured using the method of Lunn and Ap Rees (1990).

RNA extraction and cDNA synthesis

Total RNA samples were extracted using the RNeasy Plant Kit (Qiagen). Briefly, 200 mg of plant tissue was ground to a fine powder in liquid nitrogen. An 850 μl aliquot of RLT buffer containing 0.143 M β-mercaptoethanol was added to the sample. All other steps were performed following the manufacturer’s protocol. After treatment of RNA samples with Turbo DNA-free™ (Ambion), 1 μg of RNA was subjected to first-strand cDNA synthesis using a Thermoscript™ RT-PCR system (Invitrogen) in a total volume of 10 μl.

Quantitative RT-PCR

Specific primers, as used by Bieniawska et al. (2007), were synthesized for all six isoforms of the AtSUS gene family (Table 1). Real-time PCR was performed in order to determine the transcript expression level of each gene. The reactions were carried out on a RotorGene (Corbett research) using SYBR® Green Jumpstart™ (Sigma) following the manufacturer’s protocol. For an internal control, a cyclophilin primer set was used for calibration of the data (Millar et al., 2006). To verify the specificity of the PCR amplification, a heat dissociation protocol at 55–99 °C was performed. Rotor-Gene software was used to estimate relative gene expression level of each gene. The reactions were carried out on an Mx3005P (Cepheid) by western blotting. The membranes were blocked with 5% skimmed milk protein in TTBS buffer (100 mM TRIS-HCl, pH 7.5, 0.5 M NaCl, 0.1% Tween-20). The membranes were probed with an antibody raised against a rice SUS2 peptide (T. Hirose, NARC Japan) used at a dilution of 1:10 000 in TTBS buffer for 16 h at 4 °C. Following washing, the membranes were incubated in secondary antibody, anti-rabbit IgG (FC)—alkaline phosphatase conjugate (Promega) at a 1:10 000 dilution in TTBS buffer. The membranes were subsequently washed, and labelled proteins detected by development with FAST™ BCIP/NBT (Sigma).

Fixation and sectioning of tissues

Samples of flowers harvested at the day of flowering and siliques harvested at 3, 10, and 13 daf were fixed in formaldehyde solution in phosphate-buffered saline (PBS) as described in Scofield et al. (2007). Dehydration was carried out by passing the samples through a graded ethanol series, which was followed by an ethanol:HistoClear series. The samples were infiltrated and embedded in paraffin wax (Paraplast plus, TYCO Healthcare). Longitudinal sections of 12.5 μm thickness were cut using a microtome (Microm HM350) and collected onto drops of distilled water on polysine-coated glass slides. The slides were incubated on a hot plate at 42 °C for 24 h and stored at 4 °C.

Immunolocalization and starch localization

Sections were de-waxed using Histoclear and were re-hydrated through a graded ethanol series and incubated in DIG buffer I (100 mM TRIS-HCl, pH 7.5, 150 mM NaCl). Immunolocalization was carried out as previously described (Scofield et al., 2007). The sections were probed with the anti-rice SUS2 antibody at a dilution of 1 in 200 in blocking solution for 20 h at 4 °C. For the control slides, a pre-immune serum at the same dilution was used. An anti-rabbit IgG (FC)—alkaline phosphatase conjugate antibody (Promega) was carried out as previously described (Scofield et al., 2007). The signal was developed by incubating the slides in a substrate solution containing 0.25 mM nitroterazolium blue chloride (NBT, Sigma) and 0.25 mM 5-bromo-4-chloro-3-indolyl phosphate (BCIP, Sigma). The reaction was stopped by washing the slides in several changes of distilled water.

Starch localization was performed by incubating de-waxed sections in a solution of 0.5% (w/v) iodine in 5% aqueous potassium iodide for 15 min. To identify nuclei, de-waxed sections were incubated in 200 μl of a solution of 0.25 μg ml⁻¹ of 4’,6-diamidino-2-phenylindole (DAPI, Sigma) in distilled water. After

| Table 1. Sequence of primers used in quantitative PCR experiments to measure the transcript level of the Arabidopsis sucrose synthase isoforms |
|-------------|-------------|
| Isoforms    | Primers     |
| AtSUS1 (At5g20830) | 5’-GAACGTCTCGAGAGATTTATGATTCTG-3’ |
| AtSUS2 (At5g49190) | 5’-GTATCAGCGCCTGATCATGGTGAAG-3’ |
| AtSUS3 (At4g02280) | 5’-TAGTGGTCACGCCCAATGACACATTCTT-3’ |
| AtSUS4 (At3g43190) | 5’-TGTCACAAAGAACTGCAAAGATGCTG-3’ |
| AtSUS5 (At5g37180) | 5’-CAGGGACAGAGCATCTACTATAATTCTC-3’ |
| AtSUS6 (At1g73370) | 5’-ATACGCCATTTATGTAACCCGCTTCT-3’ |
| Cyclophilin (At2g29960) | 5’-GGACCAACGATGGAAAGACTTATTTTCCC-3’ |
|             |             |

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45 min incubation at room temperature in the dark, the slides were washed in water for 5 min. Sections were examined using a Leica DMR microscope with brightfield and fluorescence illumination, respectively. Digital images were recorded using a Leica DC500 digital camera.

Sugar extraction and measurement

Water-soluble hexose sugars were extracted from developing siliques (20 mg) harvested at various time points. The samples were ground in liquid nitrogen, and 500 μl of 80% (v/v) ethanol added to each tube and incubated at 80 °C for 60 min. The pellets were collected following centrifugation at 13 000 g for 5 min, and were extracted twice more with 500 μl of 80% ethanol in the same conditions. The supernatants of all three extractions were pooled together and dried to completeness under vacuum. The residue was dissolved in 300 μl of distilled water. The glucose content of the samples was quantified by adding 25 μl of the extracts to a 175 μl volume of hexose determination buffer (0.1 M TRIS-HCl pH 8, 5 mM MgCl2) containing freshly prepared 0.5 mM NADP and 1 mM ATP. The production of NADPH was monitored at 340 nm with a molar extinction coefficient of 6.22 mM⁻¹ cm⁻¹. The fructose content of the samples was determined by adding 1.5 U of phosphoglucoisomerase (Roche) and measurement of subsequent NADPH production. Sucrose was converted to glucose and fructose using sucrose phosphorylase (Roche), and the resultant content of hexoses was determined enzymatically as described above.

Results

Expression of the SUS gene family in Arabidopsis

Due to some noted discrepancies in transcript expression data for the six AtSUS isoforms in previously published work (Baud et al., 2004; Bieniawska et al., 2007), it was decided to repeat transcript expression analysis in a range of tissues from plants cultured in the growth conditions used here. In addition, measurement of SUS activity was performed in the same range of tissues.

To investigate the expression patterns of all six isoforms of SUS in Arabidopsis, transcript levels of each gene were determined in a range of tissues. cDNA samples prepared from seedling, young immature rosette and mature rosette leaves, cauline leaves, stem, flower, and developing siliques at 3 and 10 daf were subjected to quantitative PCR, using gene-specific primers. The cyclophilin transcript level was used for calibration of data, as cyclophilin was found to be expressed at a similar level in all tissues examined (data not shown). The AtSUS1 transcript was present in all tissues examined (Fig. 1A). Cauline leaves and stem contained the lowest amounts of AtSUS1 mRNA compared with other tissues, while flowers contained the highest level of AtSUS1 expression. The transcript levels of AtSUS2 and AtSUS3 were most highly expressed in developing siliques at 10 daf, with lower levels observed at 3 daf, and were expressed at low levels in the other tissues examined (Fig. 1B, C). Young immature rosette leaves contained the highest amount of AtSUS4 transcript in comparison with its level in the other tissues examined (Fig. 1D). At 3 and 10 daf, developing siliques showed slightly higher expression of AtSUS5 compared with other tissues, which is in agreement with the result of Bieniawska et al. (2007). However, these findings were not confirmed by comprehensive microarray analysis using Genevestigator (Laule et al., 2006) (data not shown). AtSUS5 transcript was also found to be expressed in cauline leaves and young rosette leaves (Fig. 1E). The AtSUS6 transcript was found to be expressed at relatively low levels in all the tissues examined (Fig. 1F).

SUS activity in Arabidopsis tissues

SUS activity was subsequently measured in the same tissue samples used for the quantitative PCR analysis (Fig. 2). The highest level of SUS activity was present in developing siliques compared with the vegetative tissues including mature leaves harvested after flowering, stem, flower, cauline leaves, and seedlings; however, SUS activity was also high in young immature rosette leaves.

Immunolocalization of SUS protein in developing seeds and siliques

To determine the cellular localization and temporal expression pattern of SUS protein in developing Arabidopsis seed, immunolocalization was performed on longitudinal sections of siliques at 3, 10, and 13 daf. The three time points selected represent early, mid, and late stages of seed development in Arabidopsis (see Discussion). An antibody raised against a rice SUS2 peptide was used to detect SUS proteins in the Arabidopsis samples. Table 2 shows a comparison between the predicted peptide sequences for the six Arabidopsis SUS proteins and that of rice SUS2. Arabidopsis AtSUS1, AtSUS2, AtSUS3, and AtSUS4 showed high homology with the rice SUS2 protein, with 79, 73, 76, and 82% identity, respectively, while AtSUS5 and AtSUS6 had lower levels of identity, 61% and 66%, respectively. The antibody detected a band at the expected size of 92–95 kDa for SUS on a protein blot of the same range of Arabidopsis tissues as used for SUS activity measurements (Fig. 3A). However, it is not possible to determine which and how many of the SUS isoform(s) were recognized by the antibody, and, as a consequence, the distribution and hence potential roles of SUS may be underestimated. Figures 3B–G illustrate the results of immunolocalization in longitudinal sections of siliques. At 3 daf, SUS labelling was present in the funiculus, seed coat, endosperm, and in the vascular bundle of the silique wall (Fig. 3B). SUS protein was present in the same tissues at 10 daf (Fig. 3D). However, at 13 daf, SUS protein was detected in the embryo, the aleurone layer, and cotyledons (Fig. 3F), but was absent from the funiculus and the seed coat. Labelling was absent in the sections probed with the pre-immune serum (Fig. 3C, E, G).
Starch localization during Arabidopsis seed development

Starch grain localization was carried out on sections of developing seed to examine a possible role for SUS in starch biosynthesis (Fig. 4). Starch grains were present in the seed coat and funiculus of the seed at 3 daf (Fig. 4A). At 10 daf, starch grains localized in the seed coat (Fig. 4B). Interestingly, at 13 daf, starch grains were absent in these tissues (Fig. 4C). Repeatable results were obtained in serial sections on three slides from each of three biological replicate samples. Carbohydrate content was determined in whole silique tissue at similar time points used for starch staining (Fig. 5). In all three developmental stages, the amount of hexose was higher than that of sucrose; however, the ratio of hexose to sucrose declined toward maturation. Glucose and fructose levels in siliques at 3 daf were almost 10 times higher than those at 10 and 13 daf. The sucrose content of the samples remained relatively unchanged during silique development. Whole silique tissues were used for the sugar measurement, and in considering these data it should be pointed out that the silique tissue at 3 daf is somewhat different from those at 10 and 13 daf, as by the later time points seed development is at advanced stages.

Immunolocalization of SUS protein in the companion cells

The vascular bundle of the silique walls (arrow in Fig. 3B), in which SUS protein was localized, is composed of phloem, xylem, and vascular parenchyma cells. Further experiments were therefore conducted to determine the cellular location of the SUS protein within the vascular bundle. Figure 6A shows labelling of SUS protein in the CCs of the phloem but not in the sieve elements or xylem. Labelling was absent in sections probed with the pre-immune serum (Fig. 6B). Since CCs contain nuclei, which are absent from sieve elements, DAPI staining was used to verify the identity of the cells in the phloem (data not shown).

SUS protein is present in the nectaries of Arabidopsis flowers

To determine whether SUS protein is expressed in Arabidopsis carpels prior to the development of siliques, longitudinal sections of whole flowers, harvested at the day of flowering, were probed with the anti-SUS antibody (Fig. 7). SUS labelling was found to be absent from carpels at this stage. However, strong labelling of SUS

Fig. 1. Relative expression levels of the six AtSUS transcripts in a range of Arabidopsis tissues. (A–F) The normalized transcript levels of the AtSUS isoforms 1–6 against cyclophilin, respectively. Relative expres-

sion of AtSUS2 and AtSUS3 was higher in the developing siliques compared with other tissues. SD, seedling; RBF, young rosette leaves before flowering; RAF, mature rosette leaves after flowering; CL, cauline leaves; ST, stem; FW, flower at the day of flowering; SQ3, siliques 3 daf; SQ10, siliques 10 daf. Error bars indicate the SE (n=3).
epitopes was present in the lateral nectaries located at the base of the flower (Fig. 7A). Labelling was absent from sections probed with the pre-immune serum (Fig. 7B). SUS labelling was also found in the phloem of sepals and petals, where it localized to the CCs (data not shown).

**Discussion**

The importance of SUS for sucrose metabolism in starch-storing reproductive structures of legumes such as *Vicia* (Heim *et al.*, 1993) and *Pisum* sp. (Barratt *et al.*, 2001), and in cellulose synthesis in cotton fibre (Ruan *et al.*, 2003) and seeds (Ruan *et al.*, 1997), has been clearly established by enzyme activity, transcript measurements, and protein localization, and through mutant (Chourey and Nelson, 1976) and transgenic plant analysis (Zrenner *et al.*, 1995; D’Aoust *et al.*, 1999). Recently, the surprising absence of a phenotype in reproductive tissues of multiple knockout lines of *AtSUS1*, *AtSUS2*, *AtSUS3*, and *AtSUS4* isoforms in *Arabidopsis* (Bieniawska *et al.*, 2007) has cast doubt on the view that this enzyme is indispensable in starch and cellulose biosynthesis, in contrast to the above evidence. While reverse genetics would be expected to provide definitive evidence of the importance of SUS in *Arabidopsis*, lack of a phenotype could also be due to plasticity in plant metabolism and utilization of alternative pathways of sucrose breakdown (such as invertase, the transcript of which is very high in *Arabidopsis* sink tissues (Tymowska-Lalanne and Kreis, 1998). Why such plasticity in sucrose metabolism is not apparent in the crop species mentioned above is unknown.

Studies on SUS in *Arabidopsis* have focused mainly on measurements of transcript abundance (due to a focus on the complexity of the gene family in *Arabidopsis* and the availability of the genome sequence) (Baud *et al.*, 2004) and, less commonly, by immunological quantification of individual SUS isoforms (Bieniawska *et al.*, 2007). Both these techniques are extremely challenging to quantify when comparing different tissues over development. This is in part due to the difficulty of determining a suitable normalization control transcript. In addition to this technical problem, transcript levels often do not reflect absolute protein level or enzyme activity due to post-transcriptional/translational Regulation. Estimating flux through SUS and determination of its physiological role in *Arabidopsis* tissues would be substantially furthered by bulk enzyme activity measurement and protein localization in the appropriate tissues. In the present study, these tools were used to investigate the potential role(s) of SUS in developing siliques and seeds of *Arabidopsis*.

To calibrate the protein measurements against transcript levels in the same tissue samples, expression levels of all six AtSUS isoforms and SUS activity in a range of tissues were measured, revealing that SUS was predominantly present in sink tissues. Importantly, there was little direct correlation between transcript level of the six genes and SUS activity. This lack of correlation with SUS activity was evident in all tissues examined, except for siliques, where high expression levels of *AtSUS2*, *AtSUS3*, and *AtSUS5* could account for the higher SUS activity, and in young rosette leaves. As discussed above, this inconsistency between gene expression and enzyme activity indicates that SUS protein measurements are crucial in extrapolating transcriptional data to physiological function. High SUS activity was found in vegetative and reproductive sink tissues, including young rosette leaves and developing siliques where the high levels of *AtSUS2* and *AtSUS3* transcripts were found. Interestingly, SUS activity slightly declined towards siliques maturity, while the expression of both isoforms increased. Baud and Graham (2006) also observed a decline in enzyme activity staining towards the maturity stages of *Arabidopsis* embryo development. These results are in agreement with those reported by Hill *et al.* (2003) in oilseed rape. High SUS activity has been reported in reproductive sink
tissues of several other plant species including wheat grain (Dale and Housley, 1986), rice (Chan et al., 1990), tomato fruit (Sun et al., 1992), cotton fibre and seed (Ruan et al., 1997), and canola seed and silique (King et al., 1997). High SUS activity in these tissues indicates a potential role for SUS as a major enzyme of sucrolysis in these tissues in determining sink strength. During early stages of seed development, high SUS activity establishes a strong sink for sucrose by cleavage of imported sucrose to fructose and UDP-glucose. The preference of SUS over invertase in sucrose cleavage in these tissues might be partly due to a decreased inhibitory effect of fructose on SUS in comparison with invertase (Isla et al., 1991). In addition, UDP-glucose produced by the SUS reaction could be channelled to other important pathways such as starch (Munoz et al., 2005) and cellulose biosynthesis (Amor et al., 1995) during cellularization of endosperm, where the demand for cell wall components including UDP-glucose is increasing (Ruan et al., 2008). The resultant fructose from SUS activity may also be used in provision of energy for cell division and expansion of the filial tissues. A significant increase in fructokinase activity and not glucokinase activity has been reported during early to mid stages of seed development (Hill et al., 2003), indicating a possible increase in fructose utilization at these stages.

The Arabidopsis SUS gene family consists of six isoforms as previously reported through genome analysis.

Fig. 3. Immunolocalization of SUS protein in Arabidopsis tissues. (A) A western blot containing protein samples from a range of Arabidopsis tissues was probed with an antibody raised against a rice SUS2 peptide. A single band at ~92–95 kDa was detected in all samples. SD, whole seedlings at the four true leaves stage; RBF, rosette leaves before flowering; RAF, rosette leaves after flowering; CL, cauline leaves; ST, stem; FW, flowers at the day of flowering; SQ3, siliques at 3 daf; SQ10, siliques at 10 daf. Longitudinal sections of siliques at 3 (B, C), 10 (D, E), and 13 (F, G) daf were probed with either the same anti-rice SUS2 antibody (B, D, F) or a pre-immune serum (C, E, G). Antibody labelling of SUS protein, indicated by purple colour development, was present in the funiculus, endosperm, seed coat, and silique wall at 3 and 10 daf, but it was localized in the embryo and aleurone layer at 13 daf. sw, silique wall; en, endosperm; al, aleurone layer; f, funiculus; c, cotyledon; sc, seed coat; em, embryo; vb, vascular bundle. Bar = 100 μm.
Baud et al. (2004) found distinct but partially redundant expression profiles for the six AtSUS genes. Bieniawska et al. (2007) used T-DNA insertion mutants to elucidate the role of each of these isoforms, and measured the transcript levels using quantitative and semi-quantitative RT-PCR. The results of transcript level measurements obtained in these two studies were slightly different. In the current study, the transcript level of all six AtSUS isoforms was measured in several tissues using the same primer sets used by Bieniawska et al. (2007). Except for AtSUS2 and AtSUS3, the isoforms did not show strong tissue-specific expression patterns, which is in agreement with Bieniawska et al. (2007). The presence of the AtSUS1 transcript at similar levels in most of the tissues indicates a possible housekeeping role for this isoform. The transcript levels of AtSUS2 and AtSUS3 increased in developing siliques during seed development. Semi-quantitative RT-PCR in a previous study showed a similar pattern for these two isoforms (Bieniawska et al., 2007). Data analysis obtained from multiple microarrays, accessed via http://www.genevestigator.ethz.ch/mm/ (Laule et al., 2006), also revealed an increase in the transcript level of AtSUS2 and AtSUS3 during mid and late stages of silique and seed development, respectively. These findings indicate a role for AtSUS2 and AtSUS3 during seed development. The AtSUS4 transcript was most highly expressed in young rosette leaves in comparison with its expression level in the other tissues examined. Studies by Baud et al. (2004) and Bieniawska et al. (2007) have reported relatively high AtSUS4 transcript expression in root samples compared with other tissues. These results suggested a role for AtSUS4 in the vegetative rather than reproductive sink tissues. The expression of AtSUS5 was found to be high during silique development; however, young immature rosette and cauline leaves also contained high levels of AtSUS5 transcript. As the kinetics of these enzymes have not been established, it is not known whether higher activity in siliques at 3 daf compared with that in siliques at 10 daf is correlated to the presence of more AtSUS5 transcript at this stage. AtSUS6 expression was found to be relatively low in all the tissues examined. Based on these expression patterns, it is not possible to conclude a specific role for each of these latter two isoforms.
To extend the present study beyond enzyme activity and transcript determinations in bulk tissue samples, immunolocalization of SUS in Arabidopsis tissue sections was performed, using an antibody raised against rice SUS2, to localize SUS protein. The aim was not to separate individual SUS isoforms in these experiments but to compare total SUS protein location with tissue enzyme measurements. Comparison of the predicted peptide sequences of the six AtSUS isoforms with that of rice SUS2 revealed high levels of identity for AtSUS1, AtSUS2, AtSUS3, and AtSUS4, and lower levels of identity for AtSUS5 and AtSUS6. Analysis at four different stages of silique development revealed both spatial and temporal differences in SUS protein localization. The results indicated the involvement of SUS in a range of metabolic processes in reproductive tissues.

In carpels, labelling of SUS protein was found to be absent on the day of flowering. However, SUS protein was found to be present in the lateral nectaries of flowers. The role of SUS in this tissue is not known. It has been shown that the carbohydrate content and composition of nectaries vary greatly between different Arabidopsis ecotypes (Davis et al., 1998). In Columbia, the sucrose to hexose ratio is low, whereas in Landsberg and Wassilewskija the ratio is significantly higher. High SUS activity may reduce the accumulation of sucrose in the nectaries of Columbia, resulting in a higher hexose concentration. Ren et al. (2007) have also reported elevated expression of SUS transcript and protein in developing nectaries of ornamental tobacco. Their results suggested a role for SUS in starch biosynthesis during early stages of nectary development. This starch later remobilized to provide precursors for other pathways in this tissue through hexose production (Ren et al., 2007).

In the silique wall, SUS protein was shown to be present in the CCs of phloem at 10 daf, when the silique is mature and fully expanded. This result is consistent with previous localization studies in citrus fruit, maize leaves (Nolte and Koch, 1993), and radish hypocotyl (Rouhier and Usuda, 2001), where it has been suggested that SUS protein is involved in providing energy for phloem loading/unloading processes (Van Bell et al., 2000). It has previously been shown that photosynthesis occurs in the mature silique walls of Arabidopsis (Robinson and Hill, 1999) and canola (King et al., 1997). Assimilates derived from this source tissue may then be transported to the developing seed sink tissues via the silique wall phloem. SUS protein may therefore be involved in providing energy for uploading of assimilates.
into the phloem. SUS protein was also observed in CCs of the phloem in flower sepals and petals, which are sink tissues. In these tissues, SUS may have a similar role in the provision of energy for active unloading of assimilate, evidence for the possibility of which was provided by Zhang et al. (2004).

In the developing seed, at 3 daf the embryo is at the torpedo developmental stage and the endosperm is undergoing rapid cell division. By 10 daf, the embryo is at the stick-like developmental stage and the cellularized endosperm is rapidly used by the expanding embryo. Accumulation of storage protein and lipids commences at this stage. By 13 daf, cell division declines, the embryo is at the end of the bent cotyledon stage, the endosperm disappears and is replaced by a single cell aleurone layer, and the seed reaches its maximum size (Raz et al., 2001). Therefore, in the current work these three stages were selected as early, mid, and late stages of seed development, respectively. SUS protein was found to be present in the endosperm, seed coat, funiculus, and silique walls during early to mid stages of silique development. Later, at 13 daf, SUS protein was found in the embryo and aleurone layer. These temporal changes in cellular localization of SUS protein during Arabidopsis seed development are comparable with those reported in cotton seed (Nolte et al., 1995), and are consistent with the intracellular localization of SUS in developing kernels of maize (Duncan et al., 2006). SUS protein was also localized in the endosperm, but not in young embryos, during early stages of cotton seed development (Ruan et al., 2008). Previously, in situ staining of SUS activity during maize kernel development (Wittich and Vreugdenhil, 1998) indicated the presence of active SUS protein in a similar pattern to the subsequent protein immunolocalization study. Results from sugar measurements in the current work indicated that a decrease in the hexose to sucrose ratio is a result of a decline in hexose concentration rather than an increase in sucrose accumulation. Starch grains were co-localized with SUS proteins during early to mid stages of seed development. These findings are in agreement with the results of starch measurement in Arabidopsis seeds reported by Focks and Benning (1998). It is known that during the early stages of seed development in oilseed plants, starch accumulates temporarily in the seed coat, which is later remobilized for use in lipid and storage protein biosynthesis (Norton and Harris, 1975; Da Silva et al., 1997; King et al., 1997; Vigeolas et al., 2003; Lin et al., 2006).

Based on the results presented here and those from previous studies, a model is proposed for sucrose partitioning in developing Arabidopsis seed, which might be applicable to other oilseed plants (Fig. 8). During the early to mid stages, sucrose delivered to the seed coat and endosperm, via the funiculus, is utilized by SUS for starch deposition in the seed coat and for cell wall biosynthesis in the endosperm (Fig. 8A). There is evidence to indicate that a sucrose transporter is expressed specifically in the micropylar region of the endosperm up to 8 daf (Baud et al., 2005). However, some of the sucrose may be cleaved by invertase activity in the seed coat, and the resultant hexoses are delivered to the developing embryo and endosperm. Previous studies indicated that acid invertase activity was higher in the seed coat during early stages of seed development compared with that of later stages (Sturm and Tang, 1999; Hill et al., 2003). Temporary storage of assimilates during early stages in the form of starch will maintain constant and strong sink strength by preventing accumulation of sucrose and hexoses in the seed coat and embryo. It may also prevent
negative feedback regulation of photosynthesis in the source tissues due to accumulation of unused sugars in the sink tissue. Later during seed development, sucrose may be delivered to the embryo by maternal tissues (Fig. 8B). The sucrose may be cleaved by SUS in embryo for lipid and protein biosynthesis. At this stage, the starch reserves in the seed coat may be remobilized and utilized by the embryo and aleurone layer. An increase in the transcript expression of amylase genes has been reported during mid to late stages of seed development (Kim et al., 2005). In addition, a centripetal transport of assimilates from outer integument towards filial tissues has been demonstrated in developing Arabidopsis seed from expression of β-glucuronidase protein under different promoters (Stadler et al., 2005).

In summary, from expression analysis at the transcript, protein, and enzyme activity level, SUS is likely to be involved in several separate cellular processes in flower and developing seeds of Arabidopsis. Co-localization of SUS protein and starch grains indicates a possible role in carbon partitioning during early to mid stages of seed development, as a process to maintain sink strength. In later stages, SUS protein might have a role within the embryo, cotyledon, and aleurone layer in sucrose utilization. The current work also provided further evidence for SUS involvement in the provision of energy for phloem loading and unloading, as indicated by localization of the protein in CCs. SUS protein was also localized to the floral nectary, which is previously unreported, indicating a potential role in carbon partitioning within this tissue.

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