The Ca²⁺ Status of the Endoplasmic Reticulum Is Altered by Induction of Calreticulin Expression in Transgenic Plants¹

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To investigate the endoplasmic reticulum (ER) Ca^{2+} stores in plant cells, we generated tobacco (*Nicotiana tabacum*; NT1) suspension cells and Arabidopsis plants with altered levels of calreticulin (CRT), an ER-localized Ca^{2+} -binding protein. NT1 cells and Arabidopsis plants were transformed with a maize (*Zea mays*) *CRT* gene in both sense and antisense orientations under the control of an Arabidopsis heat shock promoter. ER-enriched membrane fractions from NT1 cells were used to examine how altered expression of *CRT* affects Ca^{2+} uptake and release. We found that a 2.5-fold increase in CRT led to a 2-fold increase in ATP-dependent ${}^{45}Ca^{2+}$ accumulation in the ER-enriched fraction compared with heat-shocked wild-type controls. Furthermore, after treatment with the Ca^{2+} ionophore ionomycin, ER microsomes from NT1 cells overproducing CRT showed a 2-fold increase in the amount of ${}^{45}Ca^{2+}$ released, and a 2- to 3-fold increase in the amount of ${}^{45}Ca^{2+}$ retained compared with wild type. These data indicate that altering the production of CRT affects the ER Ca^{2+} pool. In addition, *CRT* transgenic Arabidopsis plants were used to determine if altered CRT levels had any physiological effects. We found that the level of CRT in heat shock-induced *CRT* transgenic plants correlated positively with the retention of chlorophyll when the plants were transferred from Ca^{2+} -containing medium to Ca^{2+} -depleted medium. Together these data are consistent with the hypothesis that increasing CRT in the ER increases the ER Ca^{2+} stores and thereby enhances the survival of plants grown in low Ca^{2+} medium.

Calcium is an essential second messenger that controls a variety of cellular functions (Bush, 1993, 1995; Sanders et al., 1999). The efficacy of calcium as a signaling molecule is dependent on tightly regulated transport and storage. Ca2+ is stored in organelles, e.g. endoplasmic reticulum (ER), vacuole, mitochondria and chloroplasts, and the cell wall. Although the vacuole is the main Ca^{2+} sequestration site in plant cells, the ER has also been suggested to play an important role in regulating Ca²⁺ homeostasis (Klusener et al., 1995). Calcium is also a required micronutrient and lack of calcium can be detrimental to plant growth and development (Marshner, 1986). Plants grown on calcium-deficient media are more susceptible to plant pathogens, and show reduced growth of the apical meristem, chlorotic leaves, softening of tissues, and cell wall breakdown (Simon, 1978). The cell's sensitivity and response to various stresses, such as salinity, cold, and Ca²⁺ deficiency, is dependent on its ability to sequester and use Ca2+ from internal Ca²⁺-signaling stores (Hirschi, 1999, 2001; Miseta et al., 1999; Cessna and Low, 2001). The ability to modulate intracellular Ca²⁺ pools therefore could provide a means for plants to gain resistance to various external stresses.

The ER contains a variety of Ca²⁺-binding proteins such as the molecular chaperone binding protein (BiP), calnexin, and calreticulin (CRT). Of these, CRT is responsible for the main Ca²⁺-retaining pool in plants (Hassan et al., 1995). CRT is an evolutionarily conserved protein containing an HDEL retention sequence for ER lumen localization in plants. It has a globular N domain and two Ca^{2+} -binding regions; a high-affinity, low-capacity P domain, and a low-affinity and high-capacity Ca²⁺-binding C domain. The C domain of the mammalian CRT can sequester at least 25 mol Ca²⁺ per mole protein (for review, see Krause and Michalak, 1997; Michalak et al., 1999; Corbett and Michalak, 2000). Because of its high Ca²⁺-binding capacity, CRT has been suggested to be involved in Ca²⁺ signaling (Camacho and Lechleiter, 1995; Mery et al., 1996; John et al., 1998). Furthermore, CRT has been proposed to be involved in chaperone activity (Denecke et al., 1995; Nauseef et al., 1995; Hebert et al., 1996; Otteken and Moss, 1996; Crofts et al., 1999; Saito et al., 1999), cell adhesion (Coppolino et al., 1997), gene expression (Burns et al., 1994; Dedhar et al., 1994), apoptosis (Nakamura et al., 2000; Taguchi et al., 2000), and in store-operated Ca²⁺ fluxes through the plasma membrane (Mery et al., 1996; Fasolato et al., 1998; Llewelyn et al., 1998; Xu et al., 2000).

The Ca^{2+} -binding properties of CRT are similar in both mammalian and plant homologs (Chen et al., 1994; Mery et al., 1996). Although no reports have

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characterized CRT's Ca²⁺-storing ability or its potential role in Ca²⁺ signaling in plants, several reports in mammalian systems have shown that increased production of CRT increases cellular Ca^{2+} levels and affects the response of cytosolic Ca^{2+} to external stimuli (Bastianutto et al., 1995; Mery et al., 1996; Opas et al., 1996). Using mouse L fibroblast cells, Mery et al. (1996) showed that an increase in CRT leads to an increase in the ER Ca²⁺-signaling pool. Addition of either extracellular ATP, an activator of the P2y purinergic receptors, or ionomycin plus thapsigargin resulted in a 1.5-fold increase in cytosolic Ca^{2+} in *CRT* overexpressing lines compared with wild-type lines (Mery et al., 1996). In addition, it was shown in CRT overexpressing HeLa cells that stimulation by two agonists, ATP and histamine, added in succession resulted in increased cytosolic Ca²⁺ after the second agonist (Bastianutto et al., 1995). The increase in cytosolic Ca²⁺ was observed in both fura-2 loaded CRT-overexpressing cells, and in CRToverexpressing cells cotransfected with aequorin. The magnitude of the response varied with the stimulus used and the physiological status of the cell, consistent with the hypothesis that CRT can function not only as a Ca²⁺-buffering device but also as a regulator of agonist-triggered Ca²⁺ release.

In view of the complexity of the role of CRT in the regulation of cellular Ca²⁺ homeostasis and of the yet unexplored properties of CRT in plants, we decided to investigate whether perturbation of CRT levels could affect ER Ca²⁺ in tobacco (*Nicotiana tabacum*; NT1) suspension cells and Arabidopsis plants. Here, we show that CRT levels can be selectively modulated in plant cells using a heat shock-inducible promoter and a maize (Zea mays) CRT cDNA. 45Ca2+ measurements were carried out in ER-enriched membrane vesicles generated from NT1 cells. Heat shockinduced production of CRT caused a significant increase in ER-accumulated Ca²⁺ in vitro. In a similar manner, decreased CRT levels correlated with a decrease in ER Ca²⁺ accumulation in vitro. Treatment with the Ca²⁺ ionophore ionomycin showed that the ER Ca²⁺-buffering capacity was CRT dependent. We also examined how an altered level of CRT affects plant responses to stress. Heat shock-induced production of CRT in transformed Arabidopsis plants enhanced the survival of plants transferred from Ca²⁺-containing medium to Ca²⁺-depleted medium, compared with wild-type controls. These results suggest that CRT plays a key role in the regulation of the Ca2+ status of the plant ER and that the ER, in addition to the vacuole, is an important Ca^{2+} store in plant cells.

RESULTS

Selection of Transgenic Tobacco Cell Lines

We used a transgenic approach to determine if ER calcium levels could be modulated by altered expres-

sion of the calcium-binding protein CRT. Because calcium is sequestered in various cellular compartments, we used an inducible promoter to control the *CRT* transgene to guard against long-term compensatory mechanisms that might reestablish normal Ca^{2+} levels. By perturbing one component of the Ca^{2+} storage/regulatory network, we hoped to begin to determine how cytoplasmic calcium levels are regulated.

Tobacco suspension culture cells (NT1) are readily transformed (An, 1985), and provide ample material for isolating ER microsomes. NT1 cells were transformed with Agrobacterium tumefaciens binary vectors carrying sense or antisense CRT cDNA sequences, or mgfp5 (encoding ER-targeted green fluorescent protein [GFP]; Haseloff et al., 1997), all under the control of an Arabidopsis heat shock promoter. Twelve independent kanamycin-resistant cell cultures were isolated for each construct. All twelve cell lines showed HS-inducible changes in CRT expression. Three cell lines transformed with sense CRT cDNA were selected and labeled Nt CRT:1, Nt CRT:5, and Nt CRT:7, one cell line transformed with the CRT cDNA in antisense orientation was selected and labeled Nt CRT-A:3, and one cell line transformed with mgfp5 was selected and labeled Nt GFP:4. Levels of gene induction were tested by immunoblots of total protein (Fig. 1C), or by monitoring GFP fluorescence (data not shown) of cells, harvested 16 h after a 2-h heat shock.

To investigate the effects of altered CRT levels on ER Ca²⁺ fluxes in vitro, microsomes were isolated from wild-type, CRT transgenic cell lines, and mgfp5 transgenic cell lines and were fractionated by discontinuous Suc gradients (45%, 38%, and 22% [w/v] Suc) to isolate ER-enriched fractions. One-milliliter fractions were collected from the Suc gradients and equal amounts of protein per fraction were analyzed by SDS-PAGE, blotted, and immunostained with polyclonal antibodies against either CRT or BiP, an ERlocalized chaperone. CRT showed a similar fractionation pattern as BiP (Fig. 1A and B). The highest amounts of both proteins were recovered at approximately 40% (w/v) Suc (fraction 2). This fraction was designated the ER-enriched fraction. The fractionated microsomes from all the above-mentioned cell lines showed a similar distribution of BiP and CRT based on western-blot analysis (data not shown). Our results are consistent with other studies in which the ER was recovered in the range of 30% to 40% (w/v) Suc using similar isolation conditions (Ahmed et al., 1997).

The levels of CRT for both the wild-type and the transgenic cell lines, containing the maize *CRT* gene in sense (*Nt* CRT:7), antisense (*Nt* CRT-A:3), or *mgfp5* gene (*Nt* GFP:4), were investigated by immunoblot analysis of ER-enriched membrane fractions. Typical expression patterns are shown in Figure 2. In three individual experiments, the overexpressing line (*Nt*



Figure 1. CRT and BiP, an ER-localized chaperone, show similar distribution on Suc gradients. Microsomes were isolated from the wild-type cell line and layered onto a discontinuous Suc gradient (45%, 38%, and 22% [w/v] Suc). One-milliliter fractions were collected and equal amounts of protein were analyzed by 10% (w/v) SDS-PAGE (10 μ g protein lane⁻¹). The bottom and top of the gradient are indicated. A, Equal amounts of protein from collected gradient-fractions of a wild-type cell line, visualized with Gelcode staining. B, Immunostaining of gradient fractions from a wild-type cell line with polyclonal antibodies against maize CRT (1:5,000) and polyclonal antibodies against BiP (1:10,000), an ER marker (Denecke et al., 1991). C, Comparison of CRT in ER-enriched fraction 2 from gradient-fraction of wild-type and CRT overproducing cell line 7 (Nt CRT:7). Gelcode-stained gel is on the left and immunostained western blot is on the right. Lane 1, Heat-shocked wild type; Lane 2, heat-shocked CRT sense line 7 (Nt CRT:7). Migrations of standards and CRT are indicated.

CRT:7) showed a 2- to 3-fold increase and the antisense line (Nt CRT-A:3) a 1.5- to 2-fold decrease in CRT expression levels following heat shock. The fold increase of CRT production in the Nt CRT:7 cell line is consistent with the fold increase observed in mammalian CRT-overproducing cells (Bastianutto et al., 1995; Mery et al., 1996). The induced Nt GFP:4 transgenic line and the wild-type line both showed similar levels of CRT (Fig. 2C).

To ensure that the maize *CRT* transgene was being expressed, ER-enriched fractions from wild type and *Nt* CRT:7 were analyzed by a 10% (w/v) SDS-PAGE large-gel (20 cm) system, blotted, and probed with polyclonal antibodies against a castor bean CRT (1: 10,000) (Fig. 2D). As can be seen from Figure 2D, the

maize *CRT* is expressed in the heat-shocked *Nt* CRT:7 line, and the maize CRT and tobacco CRT could be resolved using a 10% (w/v) SDS-PAGE 20-cm gel. One of the two bands detected in the *Nt* CRT:7 line correlated with a purified maize CRT (lane 1), and one band correlated with the band that was recognized by the antibody in the wild-type line (lane 3). Our normal minigel system did not resolve maize and tobacco CRT, and therefore was used to monitor changes in total CRT. For each experiment, CRT production was monitored in one aliquot of the ER-enriched fractions to ensure that expression levels were within ranges indicated above for each transgenic cell line.

Alterations of CRT Levels Affect the Ca²⁺ Uptake Capacity in Vitro

To investigate the effects of altered CRT levels on ATP-dependent Ca^{2+} uptake, ER-enriched vesicles were assayed for ${}^{45}Ca^{2+}$ uptake in the presence and absence of 3 mм ATP (Table I; Fig. 3). After 20 min of ATP-dependent ⁴⁵Ca²⁺ uptake, the ER-enriched membrane fractions from the heat-shocked Nt CRT:7 (sense) line had accumulated 22.2 \pm 2.2 nmol 45 Ca²⁺ mg⁻¹ protein, whereas the heat-shocked wild-type line had accumulated 11.1 \pm 0.7 nmol 45 Ca²⁺ mg⁻ protein (Table I). The ATP-dependent ⁴⁵Ca²⁺ uptake for the non-heat-shocked wild-type line was 10.0 \pm $0.2 \text{ nmol} {}^{45}\text{Ca}^{2+}\text{ mg}^{-1}$ protein. These values are comparable to values obtained when the ER and plasma membrane Ca²⁺-ATPases from carrot suspension culture cells were characterized (Hwang et al., 1997). ER-enriched membrane vesicles from the CRToverproducing line showed a 2.0 \pm 0.3-fold increase (mean \pm sp of duplicate values from three experiments) in ATP-dependent Ca²⁺ uptake after about 20 min of incubation compared with the heat-shocked wild-type line (Fig. 3A). In addition, the ER from the antisense line showed a 40% decrease in Ca²⁺ uptake at 20 min when compared with the heat-shocked wild-type cell line. These values showed a positive correlation in ATP-dependent Ca²⁺ uptake and relative levels of CRT (compare Figs. 2 and 3).

Because stress, e.g. heat shock, can affect the expression levels of chaperones such as CRT and BiP, it was important to compare heat-shocked with non-heat-shocked controls for each of the cell lines (Conway et al., 1995; Nguyen et al., 1996; Leborgne-Castel et al., 1999). As predicted, heat-shocked wild-type cells showed an increase in CRT compared with non-heat-shocked wild type (Fig. 2); however, the CRT increase in the wild-type cells was small relative to that in heat-shocked cells carrying the inducible *CRT* construct. It is important that in all instances, there was a positive correlation between CRT production and ATP-dependent Ca²⁺ uptake (compare Figs. 2 and 3).



Figure 2. Altered *CRT* expression in ER-enriched vesicles from transgenic cell lines. ER-enriched vesicles from *CRT*, *GFP* transgenic, and wild-type cell lines were separated on Suc gradients. Fraction 2, containing ER-enriched membrane vesicles (Fig. 1), was analyzed by 10% (w/v) SDS-PAGE (15 μ g protein lane⁻¹), blotted, and immunostained with polyclonal antibodies against maize CRT (1:5,000). A, Increased production of CRT in *CRT* sense lines. Lane 1, Non-heat-shocked wild type. Lane 2, Heat-shocked wild type. Lane 3, Non-heat-shocked *CRT* sense lines. Lane 1, Non-heat-shocked *CRT* sense line (*Nt* CRT:7). B, Lowered production of CRT in *CRT* antisense lines. Lane 1, Non-heat-shocked wild type. Lane 2, Heat-shocked wild type. Lane 3, Non-heat-shocked antisense *CRT* (*Nt* CRT-A:3). Lane 4, Heat-shocked antisense *CRT* (*Nt* CRT-A:3). C, No significant changes in CRT production in *mgfp5* transgenic cell lines (*Nt* GFP:4). Lane 1, Non-heat-shocked *Nt* GFP:4 transgenic line. D, Expression of a maize *CRT* in the transformed line *Nt* CRT:7. Lane 1, Purified maize CRT. Lane 2, Heat-shocked *Nt* CRT:7. Lane 3, Non-heat-shocked wild type. Lane 4, Standard. E, Protein visualized with silver staining. Lane 1, Purified maize CRT. Lane 2, Heat-shocked *Nt* CRT:7. Lane 4, Standard.

When we compared CRT production in non-heatshocked wild type and *Nt* CRT:7, we observed higher levels of CRT in the uninduced *Nt* CRT:7 cell lines (Fig. 2A) and correlating higher Ca²⁺ uptake (Fig. 3A), suggesting that the heat shock promoter in that cell line was leaky. To determine whether enhanced ER protein accumulation per se would alter Ca²⁺ transport, we analyzed ATP-dependent ⁴⁵Ca²⁺ uptake in transgenics expressing an ER-targeted GFP. Both the heat-shocked and the non-heat-shocked ER-GFP-expressing cell line showed no significant deviations in Ca²⁺ uptake compared with the wild-type line (Fig. 3B). These data indicate that a general increase in a non-Ca²⁺-binding ER protein, such as GFP, does not affect Ca²⁺ uptake.

To determine whether the enhanced Ca²⁺ accumulation in the ER-localized CRT-overproducing line was due to vanadate-sensitive, P-type ATPase activity, Ca²⁺ uptake was measured either in the presence

Table 1. An increase in CRT levels increases ATP-dependent ⁴⁵Ca²⁺ accumulation of ER-enriched membranes in vitro

ER-enriched membranes vesicles (fraction 2, Fig. 1), were obtained from heat-shocked and non-heat-shocked *CRT* transgenic and wild-type cell lines as indicated in "Materials and Methods." ATPdependent ⁴⁵Ca²⁺ uptake was performed on the ER-enriched vesicles and terminated after a 20-min incubation. The ATP-dependent ⁴⁵Ca²⁺ uptake was measured in the presence and absence of 3 mM ATP, and is shown as the amount accumulated of ⁴⁵Ca²⁺ per milligram protein after subtraction of control values (absence of ATP). Data (mean of two values ± range) are shown from one experiment. The experiment has been repeated at least three times with consistent results.

Cell Type	Recovered ⁴⁵ Ca ²⁺
	nmol ⁴⁵ Ca ²⁺ mg protein ⁻¹
Wild type	10.0 ± 0.2
Nt CRT:7	14.1 ± 0.2
Heat-shocked wild type	11.1 ± 0.7
Heat-shocked Nt CRT:7	22.2 ± 2.2



Figure 3. Increased levels of CRT increase Ca^{2+} uptake capacity in vitro. ER-enriched membrane vesicles (fraction 2, Fig. 1), were obtained from *CRT* transgenic, *Nt* GFP:4 transgenic, and wild-type cell lines as indicated in "Materials and Methods." ATP-dependent $^{45}Ca^{2+}$ uptake was performed on the ER-enriched vesicles (see "Materials and Methods"). The ATP-dependent Ca^{2+} uptake was measured in presence and absence of 3 mM ATP, and is shown as Δ ATP. Black symbols denote heat-shocked cells and white symbols denote non-heat-shocked cells. A, ER-enriched membrane vesicles from CRT overproducing (triangles), wild-type (squares), and *CRT* antisense (circle) cell lines were assayed for ATP-dependent $^{45}Ca^{2+}$ uptake (10 μ g protein aliquot⁻¹ see "Materials and Methods"). The $^{45}Ca^{2+}$ recovered was 11.1 \pm 0.7 nmol $^{45}Ca^{2+}$ mg protein⁻¹ at 20 min for heat-shocked wild type. B, ER-enriched membrane vesicles from GFP expressing (triangles) and wild-type (squares) cell lines were assayed for ATP-dependent $^{45}Ca^{2+}$ uptake (10 μ g protein aliquot⁻¹). Data (mean of two values \pm the range) are shown from one experiment. The experiment has been repeated at least three times with consistent results. The increase in $^{45}Ca^{2+}$ uptake in the *CRT* sense lines compared with heat-shocked wild type was 2.0 \pm 0.3-fold (mean \pm sD) for three experiments.

or absence of 200 µM vanadate. Vanadate has been shown to inhibit P-type ATPases and hence would inhibit the P-type ER Ca²⁺-ATPases (Cantley et al., 1977; O'Neal et al., 1979). In the presence of vanadate, there was no increase in ⁴⁵Ca²⁺ uptake over time, indicating that uptake was dependent on a P-type ATPase. In the absence of vanadate, CRT overproducing lines showed a 2-fold increase in ⁴⁵Ca²⁺ accumulation, and CRT antisense lines showed a lowered ⁴⁵Ca²⁺ uptake compared with wild type similar to data shown in Figure 3A. The difference in ⁴⁵Ca²⁺ uptake did not result from a variation in the specific activity of the ATPase because there was no significant difference in the specific activity of the vanadate-sensitive ATPase in wild-type and CRToverproducing lines (data not shown).

Alterations of CRT Levels Facilitate an Increase in Ca²⁺ Storing Ability in Vitro

We investigated whether or not the ERaccumulated Ca²⁺ pool was released by a Ca²⁺ ionophore and, if so, how this release was affected by an alteration in ER-localized CRT. Ionomycin (1.5 μ M), a Ca²⁺/H⁺ ionophore, was added to the ⁴⁵Ca²⁺ uptake assay when equilibrium was reached (after 22 min incubation, see Fig. 3). Addition of the ionophore resulted in a decrease of the ⁴⁵Ca²⁺ in the Ca²⁺loaded vesicles (Fig. 4A). A low, stable steady-state level was attained almost immediately after addition of ionomycin (data not shown). Figure 4C shows that the CRT-overproducing cell line retained approximately 2.5 times more ⁴⁵Ca²⁺ in the ER than the



Figure 4. CRT affects the amount of released and retained ER Ca^{2+} after treatment with ionomycin in vitro. ER-enriched membrane vesicles (fraction 2, Fig. 1), were collected from CRT transgenic, Nt GFP:4 transgenic, and wild-type cell lines. Membranes were incubated with ATP in the presence of ⁴⁵Ca²⁺ for 22 min (see "Materials and Methods"). The Ca²⁺ ionophore ionomycin (1.5 μ M) was added and membrane vesicles were analyzed for ${}^{45}Ca^{2+}$ after 5 min. White bars, vesicles from non-heat-shocked cells; black bars, vesicles from heat-shocked cells. A, ER-enriched vesicles from CRT over- and under-producing cell lines were assayed for ATP-dependent $^{45}Ca^{2+}$ uptake (10 μ g protein aliquot⁻¹), and compared with wild type. Data are shown as amount ${}^{45}Ca^{2+}$ released after addition of ionomycin. The heat-shocked CRT sense lines showed a 2 \pm 0.5-fold higher amount of released ⁴⁵Ca²⁺ than heat-shocked wild type (8.1 \pm 1.8 nmol ⁴⁵Ca²⁺ mg protein⁻¹ for heat-shocked wild type, and 16 \pm 1.6 nmol ⁴⁵Ca²⁺ mg protein⁻¹ for the CRT sense line). B, ER-enriched vesicles from the Nt GFP:4 cell line were assayed for ATP-dependent ${}^{45}Ca^{2+}$ uptake (10 μ g protein aliquot⁻¹), and compared with wild type. Data are shown as amount ⁴⁵Ca²⁺ released after addition of ionomycin. C, ER-enriched vesicles from CRT over- and under-producing cell lines were assayed for ATP- dependent ${}^{45}Ca^{2+}$ uptake (10 μ g protein aliquot⁻¹), and compared with wild type. Data are shown as amount $^{45}Ca^{2+}$ associated with the ER vesicles after ionomycin treatment. The CRT sense lines had a 2.5- \pm 1-fold higher amount of retained ⁴⁵Ca²⁺ after ionomycin treatment, compared with heat-shocked wild type $(2.9 \pm 1.0 \text{ nmol} {}^{45}\text{Ca}^{2+}\text{ mg protein}^{-1}$ for heat-shocked wild type, and $8.2 \pm 1 \text{ nmol} {}^{45}\text{Ca}^{2+}\text{ mg protein}^{-1}$ for the CRT sense line). D, ER-enriched vesicles from Nt GFP:4 cell line were assayed for ATP-dependent $^{45}Ca^{2+}$ uptake (10 μ g protein aliquot⁻¹), and compared with wild type. Data are shown as amount ${}^{45}Ca^{2+}$ associated with the ER vesicles after ionomycin treatment. Data are shown from one experiment. All experiments have been repeated at least three times with similar trends.

heat-shocked wild-type ER after treatment with the ionophore. Furthermore, when the Ca^{2+} contents from wild-type and *CRT* antisense cell lines were compared, the ER-enriched vesicles from wild type con-

tained almost three times more ${}^{45}Ca^{2+}$ than the *CRT* antisense lines (Fig. 4C). No significant difference in the rate of ${}^{45}Ca^{2+}$ released between the induced and noninduced transgenic cell lines and the wild-type

control line could be detected. Overproducing GFP in the ER had no significant effect on ionomycin-induced ${}^{45}Ca^{2+}$ release or retention (Fig. 4B). These data indicate that the remaining ${}^{45}Ca^{2+}$ is sequestered, i.e. bound, and that overproducing CRT increases a potential Ca^{2+} storage pool in the ER.

It has been suggested that $InsP_3$ might trigger a Ca^{2+} release from the ER in plant cells (Muir and Sanders, 1997). Therefore, $InsP_3$ was added to the ER-enriched membrane vesicles and Ca^{2+} release was measured. No significant ${}^{45}Ca^{2+}$ release was observed after $InsP_3$ treatment (data not shown). Either $InsP_3$ is not an agonist for Ca^{2+} release from the isolated ER fraction or essential components involved in an $InsP_3$ -mediated release are absent in this in vitro study (Dasgupta et al., 1997).

Phenotypic Analysis of CRT Transgenic Arabidopsis Lines

To investigate if increased production of CRT had any physiological effects in Arabidopsis plants, we generated 40 transgenic lines of Arabidopsis, 20 with the sense cDNA construct, denoted At CRT:1-20, and 20 with the antisense construct, denoted At CRT-A: 1-20. All 40 T₂ generation lines showed alterations in *CRT* expression after heat shock. Three plant lines, *At* CRT:3, At CRT:7, and At CRT-A:5, were selected for further study based on immunoblot analysis of CRT levels (Fig. 5A) following heat shock. To increase transgene expression and potential physiological effects, At CRT:3 seedlings were given repeated heat shock treatments. As shown in Figure 5, B and C, 2-h heat shock treatments given on each of three consecutive days resulted in the largest increase in CRT. This 2-h, 3-d heat shock regime was used on seedlings for all subsequent physiological studies. Heat shock induction of the CRT transgene throughout development was not tested because of potential secondary effects.

Plants carrying the *CRT* transgene but not exposed to the inductive heat shock displayed no obvious phenotypic differences in appearance, growth rate, time to flower, or seed production when grown to maturity in soil (data not shown). There also were no apparent phenotypic differences when seeds from the CRT transgenic line At CRT:3 were germinated on AT medium, which contains 2 mM calcium, and heat treated to induce transgene expression. However, when heat shock-induced transgenic seedlings were transferred to calcium-depleted medium (AT medium containing 10 mM EGTA), phenotypic variations appeared (Fig. 5D). By d 9 after transfer to calcium-depleted medium, the heat-shocked At CRT:3 plant line showed less chlorosis when compared with the non-heat-shocked At CRT:3. In addition, the heat-shocked At CRT-A:5 showed severe chlorosis on calcium-depleted medium (Fig. 5D). In similarly treated sibling plants, there was an inverse (compare CRT levels and chlorosis in Fig. 5). Greater than 80% of the heat-shocked *At* CRT:3 plants remained green a minimum of 5 and 8 d longer than the noninduced *At* CRT:3 plants and the heatshocked *At* CRT-A:5, respectively. To determine whether the observed phenotype on the calciumdepleted medium was reversible, we transferred plants to calcium-depleted medium containing an additional 12 mM Ca²⁺. Chlorotic tissue did not regreen, but all lines except the heat shock-induced *At* CRT-A:5 recovered and grew new leaves when the medium was supplemented with Ca²⁺ (data not shown).

correlation between CRT levels and the extent of

chlorosis after growth on calcium-depleted medium

We altered the expression levels of CRT and investigated its potential role in ER Ca²⁺ homeostasis. We have shown that a 2.5-fold increase in ER CRT levels led to a 2-fold enhancement of ATP-dependent Ca²⁺ accumulation in isolated ER vesicles. These observations are consistent with earlier studies in mammalian systems where an increase in *CRT* expression resulted in an increased accumulation of cellular Ca²⁺ in vivo (Bastianutto et al., 1995; Mery et al., 1996). In all instances, the altered ER Ca²⁺ accumulation correlated positively with ER-associated CRT levels and was shown to be ATP dependent.

A CRT-mediated alteration of the ER Ca²⁺ pool could potentially make Ca²⁺ more readily accessible for release into the cytosol. CRT has been suggested to be associated with agonist-triggered Ca2+ channels and might be important for regulating ERderived Ca²⁺ signals (Michalak et al., 1998; Corbett and Michalak, 2000). Alterations in CRT levels thus might affect both the Ca²⁺-holding capacity in the ER and be involved in the regulation of Ca^{2+} release. To investigate the buffering capacity in the CRToverproducing lines, ⁴⁵Ca²⁺-loaded ER vesicles were treated with ionomycin, an ionophore that will allow passive transport of free and/or loosely bound Ca²⁺ across membrane vesicles. The amount of Ca²⁺ released by ionomycin from the ER of the CRToverproducing lines was higher than both the wild-type and antisense lines. In addition, CRTover-producing lines showed higher levels of retained Ca²⁺ after ionomycin treatment. Although the Ca²⁺ released when calculated as percentage of the total Ca²⁺ taken up is similar for the wild-type and the CRT-overproducing line, the 2-fold increase in the total amount of ${}^{45}Ca^{2+}$ released and retained in CRT overexpressors indicates that overproduction of CRT would lead to an enhanced Ca²⁺-buffering capacity in the ER and thereby could affect the availability of Ca^{2+} for an ER Ca^{2+} -signaling pool.

In *Xenopus laevis* oocytes, CRT interacts with a SERCA 2b isoform, an ER/SR Ca²⁺-ATPase and de-



Figure 5. Increased transient expression of CRT decreases chlorosis of Arabidopsis plants transferred to calcium-depleted medium. Seeds from At CRT:3 and At CRT-A:5 were germinated on nutrient medium. Sixteen days after germination, plants were incubated at 35°C for 2 h (heat shock) and allowed to recover at 21°C overnight. The heat shock procedure was repeated for 3 consecutive d. Heat-shocked plants were either placed on fresh calcium-depleted medium on d 4 or harvested, homogenized, and analyzed by 10% (w/v) SDS-PAGE (2.5 µL homogenate lane⁻¹). Proteins were blotted and immunostained with polyclonal antibodies against CRT. A, Immunostaining of CRT in homogenized transgenic plant lines with polyclonal antibodies against maize CRT (1:5,000). Lanes 1 through 5, Non-heat-shocked plants; Lanes 6 through 10, heat-shocked plants. Lanes 1 and 6, At CRT:7; lanes 2 and 7, At CRT:3; lanes 3 and 8, At CRT-A:3; lanes 4 and 9, At CRT-A:4; lanes 5 and 10, At CRT-A:5. B, Immunostaining of CRT in homogenized At CRT:3 with polyclonal antibodies against castor bean CRT (1:10,000). Lane 1, Non-heat-shocked At CRT:3. Lane 2, At CRT:3 heat shocked 1 d. Lane 3, At CRT:3 heat-shocked 2 d. Lane 4, At CRT:3 heat-shocked 3 d. Lane 5, Standard. C, Total protein visualized with Gelcode staining. Lanes as indicated in B. D, Upper, photographs show non-heat-shocked and heat-shocked wild type (left), At CRT:3 (center), and At CRT-A:5 (right) plants 16 h after induction; lower, photographs show a non-heat-shocked and heat-shocked wild type (left), At CRT:3 (center), and At CRT-A:5 (right) plants transferred after induction to calcium-depleted medium (Arabidopsis [AT] medium containing 10 mM EGTA) for 9 d. Twelve seedlings for each transgenic line and medium treatment were germinated, one-half were induced for transgene expression, and one-half were maintained as non-induced controls. (Note: the wild-type plants shown were from a separate experiment.) The experiment has been repeated three times with similar results. In subsequent experiments, 20 to 50 seedlings for each line were assessed. In all experiments, a minimum of 80% of the plants showed the phenotypes represented.

creases its activity (Camacho and Lechleiter, 1995; John et al., 1998). Overexpression of both *CRT* and *SERCA 2b* resulted in an inhibition of repetitive $InsP_3$ -induced Ca^{2+} oscillations in the oocytes. The SERCA 2b isoform contains a glycosylation site, which was shown to be essential for an interaction between the ATPase and CRT. Two Ca^{2+} -ATPases have been reported in plant ER, one similar to the classical ER-type pump and one that is activated by calmodulin (Liang et al., 1997; Hwang et al., 2000). Although we cannot rule out a possible regulation of ER Ca^{2+} -ATPases by CRT, no obvious glycosylation sites were present in the sequence for Eca1, an ER Ca^{2+} -ATPase from Arabidopsis (Liang et al., 1997), and no significant decrease in ATPase activity was detected when CRT overproducing lines were compared with wild-type controls.

In addition to CRT, other ER-localized chaperones, such as BiP, have been shown to affect Ca^{2+} homeostasis. Lièvremont et al. (1997) showed that an overexpression of BiP in HeLa cells resulted in an increased InsP₃-sensitive Ca^{2+} pool. Both BiP and CRT are induced by stress, e.g. heat shock. In this study we observed that in wild-type cells both BiP and CRT increased in response to heat shock [1.5-fold (data not shown) and 1.2-fold, respectively (Fig. 2). BiP has been shown to bind 1 to 2 mol Ca²⁺ mol protein⁻¹ and to account for about 25% of the total

ER Ca²⁺ in HeLa cells (Lièvremont et al., 1997). Because CRT binds at least 25 mol Ca²⁺ mol protein⁻¹ and is the primary Ca²⁺-binding protein in ⁴⁵Ca²⁺ ligand overlay studies in peas (Hassan et al., 1995), it is unlikely that BiP would make a major contribution to the total ER Ca²⁺ in this study. Furthermore, the increase in a non-Ca²⁺-binding ER protein, such as GFP, did not affect the ER Ca²⁺ uptake or the ER-buffering capacity (Fig. 3 and 4).

It has been proposed that plants use different Ca^{2+} stores and signaling patterns in response to different signals (Knight et al., 1996, 1997; Sanders et al., 1999; Trewavas, 1999). Variations in location, amplitude, and frequency thereby can cause opposing responses, as in the closure and opening of stomata in response to abscisic acid and auxin-induced Ca^{2+} signals (Irving et al., 1992; Allen et al., 1999, 2000; Staxén et al., 1999; McAinsh et al., 2000). If the ER Ca^{2+} is important in plant signaling, then an increased level of CRT could affect the ER- Ca^{2+} signaling pool and thereby regulate Ca^{2+} homeostasis.

To investigate whether transient overproduction of CRT in the ER has any physiological effect in planta, CRT transformed Arabidopsis plants were grown on Ca²⁺-containing medium, induced for CRT transgene expression and subsequently transferred to Ca2+depleted medium. Inducible overproduction of CRT delayed chlorosis on Ca²⁺-depleted medium, and further strengthening the notion that the increased Ca²⁺-buffering capacity generated by an overproduction of CRT was available for the cell to help maintain its Ca^{2+} homeostasis. In support of these data, we recently showed that expression of a heat shock-inducible ER-targeted CRT C domain in Arabidopsis enhanced survival on calcium-depleted medium (Wyatt et al., 2001). The CRT C-domain plants contained significantly higher levels of total Ca²⁺ (approximately 10%) per gram dry weight. Increasing intracellular Ca²⁺ levels alone, however, is not the key to withstanding lower levels of extracellular Ca²⁺ (Hirschi, 2001). For example, Hirschi (1999) showed that an overexpression of the vacuolar $H^+/$ Ca^{2+} antiporter (CAX1) in tobacco resulted in a 2-fold increase in Ca²⁺ per dry weight as compared with wild-type plants. In spite of the increased total Ca^{2+} , the CAX1-overproducing plants, unlike the CRT-overproducing plants were more sensitive to lowered external Ca^{2+} levels than the wild-type plants.

In summary, the data reported here strongly suggest that ER Ca^{2+} is involved in maintaining Ca^{2+} homeostasis in the plant cell and that CRT has a key role as an ER Ca^{2+} -sequestering protein in plants. The challenge is now to determine the various roles for different Ca^{2+} stores and to understand how the orchestration of intracellular Ca^{2+} signals is affected when levels and activities of Ca^{2+} storage and transporting proteins are altered.

MATERIALS AND METHODS

Plasmid Constructs

A full-length CRT cDNA was isolated from a maize (Zea mays) endosperm library (R.L. Wrobel and R.S. Boston, unpublished data). The cDNA was sequenced (GenBank accession no. AF190454), and was used in all CRT-derived constructs. The constructs used for transformation consist of a binary plasmid vector containing an Arabidopsis heat shock promoter (AtHSP), followed by the CRT gene in either sense (pBIN2101) or antisense (pBIN210A) orientation, or the GFP (pBIN2011). For these plasmids, the AtHSP was inserted into pUCAP (van Engelen et al., 1995) to generate a plasmid containing the AtHSP, a multiple cloning site, and the ocs terminator. The resulting plasmid, labeled pWY2000, was digested with XbaI. A 1,365-bp fragment containing the CRT coding sequence and 40 bp of DNA upstream of the start codon was isolated using XbaI, purified, and ligated into the pWY2000, creating both a sense, pWY2101, and antisense, pWY210A, CRT construct under control of the AtHS promoter. The DNA fragments consisting of the AtHSP-CRT-ocs sequence and the AtHSPantisense CRT-ocs sequence were ligated into the AscI and PacI sites of the binary plasmid vector pBINPLUS (van Engelen et al., 1995), which contains a plant kanamycin resistance cassette. The resulting plasmids were labeled pBIN2101 and pBIN210A, respectively.

To serve as a control, an *At*HSP-*mgfp5* construct was designed. The *mgfp5* gene encodes an ER-localized GFP (Haseloff et al., 1997). The 35S promoter was removed from plasmid pWY1011 (Scott et al., 1999), containing the 35S promoter-driving *mgfp5*, and the *ocs* terminator, by digestion with *Hind*III and *Bam*HI. The promoter was replaced with the *At*HSP that had been similarly removed from plasmid pWY2000. The DNA fragment consisting of the *At*HSP-*mgfp5-ocs* sequence was then ligated into the *Asc*I and *Pac*I sites of the binary plasmid vector to produce pBIN2011.

Tobacco (Nicotiana tabacum) Tissue Cultures

Tobacco cell cultures (NT1 cells, An, 1985) were maintained in 50 mL of liquid culture medium (1× Murashige and Skoog salts; Gibco BRL, Bethesda, MD), 0.18 g L⁻¹ KH₂PO₄, 0.1 g L⁻¹ myo-inositol, 1 mg thiamine HCl, 0.2 mg L⁻¹ 2,4-D, and 30 g L⁻¹ Suc, pH 5.7) at 27°C with gyratory shaking at 125 rpm, in darkness. Cells were subcultured weekly with a 6% (v/v) inoculum. Care was taken to use cell lines with similar growth rates (25–30 g, 50-mL flask were recovered after initial centrifugation of cells).

Culture Transformation and Selection

NT1 cells were transformed using *Agrobacterium tume-faciens*-mediated gene transfer (An, 1985). pBIN2101, pBIN210A, and pBIN2011 were electroporated into *A. tu-mefaciens*, strain LBA-4404, using a Gene Pulser system (Bio-Rad, Hercules, CA). A single transformant *A. tumefa*-

ciens colony for each plasmid was cultured in 5 mL yeast extract broth (0.5% [w/v] beef extract, 0.5% [w/v] peptone, 0.5% [w/v] Suc, 0.1% [w/v] yeast extract, and 0.05% [w/v] MgCl₂) containing 50 mg L⁻¹ kanamycin, at 27°C and 250 rpm for 2 d. Wild-type NT1 were grown to logarithmic growth phase (Allen et al., 1993) in 100 mL NT1 culture medium for 4 d at 125 rpm. Four milliliters of this culture was gently mixed with 200 µL of 2-d A. tumefaciens cultures transformed with pBIN2101, pBIN210A, or pBIN2011. The NT1 cell-A. tumefaciens mix was incubated for 48 h at 27°C and suspended in an equal volume of NT1 culture medium. Approximately 0.5 mL of the resulting cell suspension was plated onto NT1 culture medium-0.8% (w/v) phytagar (Gibco BRL) containing 50 μ g mL⁻¹ kanamycin and 200 μ g mL⁻¹ timetin. Plates were incubated for 14 d at 27°C. For each transformation, at least 40 independent, transgenic microcalli were picked, each microcalli was suspended in 1 mL NT1 medium containing 50 μ g mL⁻¹ kanamycin and 200 μ g mL⁻¹ timetin, and incubated for 7 d at 27°C, at 190 rpm in darkness.

For each transformation, 12 of these cell lines were selected and screened for heat shock-inducible transgene expression. Each of the 12 cell lines showed heat shockinducible transgene expression based on western-blot analysis. Three cell lines transformed with pBIN2101, one cell line from pBIN210-A, and one cell line from pBIN2011 were maintained for subsequent experiments. The selected cell lines were transferred to 4 mL NT1 culture medium containing 50 μ g mL⁻¹ kanamycin and 200 μ g mL⁻¹ timetin, and incubated for 7 d as described above. Three replicate cultures were established for each independent, transgenic NT1 line by subculture of 0.5 mL of cell suspension into 5 mL of NT1 culture medium containing 50 μ g mL⁻¹ kanamycin. One of these replicates was cultured for 7 d and subcultured as described above to maintain the line (Allen et al., 1993). The other two replicates were cultured for 4 d, to logarithmic growth phase. One replicate set was incubated at 35°C for 2 h with shaking at 190 rpm and then returned to 27°C for 12 h. The other replicate set was not heat shocked.

Cells from putative CRT transgenic lines were purified by filtration and frozen in liquid N₂. One-hundred milligrams of frozen cells was ground in 100 μ L 2 \times SDS-PAGE sample buffer, heated to 100°C for 3 min, and centrifuged for 1 min at 13,000 rpm. Proteins in these crude lysates were separated by SDS-PAGE, electroblotted, and probed with antibodies that recognize CRT. Cultures that showed high variation in CRT signal compared with the non-heatshocked control were retained for further analysis. Cell lines from putative *mgfp5* transgenic lines were screened for ER-targeted fluorescence under the microscope, using an excitation wavelength of 488 nm, and emission wavelength recording at 500 to 550 nm. Cells that showed GFP fluorescence were retained. Transgenic cell lines expressing pBIN2101, pBIN210A, and pBIN2011 were labeled Nt CRT, Nt CRT-A, and Nt GFP, respectively. Transgenic cell cultures were transferred to 5 mL NT1 medium containing 50 μ g mL⁻¹ kanamycin and incubated for 7 d at 27°C, at 190 rpm. Stock cultures were maintained in this manner by weekly subculture of 0.3 mL into 5 mL NT1 medium with 50 μ g mL⁻¹ kanamycin.

Plant Transformation and Selection

Arabidopsis plants were also transformed using A. tumefaciens-mediated gene transfer. Binary vectors pBIN2101, pBIN210A, and pBIN2011 were electroporated into A. tumefaciens, strain GV3101, using an electroporator according to the manufacture's instructions (Bio-Rad). Wild-type Arabidopsis var. Columbia plants (generation T0) were then transformed by vacuum infiltration as described (Bechtold and Pelletier, 1998). Seeds from these plants, labeled generation T1, were sterilized for 30 min in 30% (v/v) commercial bleach and plated onto AT medium {4.3 g L⁻¹ Murashige and Skoog salts [Gibco BRL]; 1× B5 vitamins; 2% [w/v] Suc; 0.05% [w/v] MES [2-(Nmorpholino)-ethanesulfonic acid], pH 5.8; 1% [w/v] phytagar [Gibco BRL]} containing 30 mg L⁻¹ kanamycin. Plants were grown for 2 weeks at 21°C in constant light. Kanamycin-resistant plants were transferred to soil and cultivated at 21°C, under an 8-h-light/16-h-dark photoperiod. Plants were then transferred to a 16-h-light/8-hdark photoperiod, allowed to self fertilize, and the resulting seed collected (T₂ generation). T₁ lines whose progeny segregated 3:1 for kanamycin resistance, as would be expected for a single locus event, were selected for further analysis. T₂ plants from these lines were germinated on kanamycin-containing medium at 35°C for 2 h for induction of the HS promoter and then allowed to recover overnight at 21°C. Leaf samples were taken from all plants, weighed, frozen in liquid N_{2} , and stored at $-80^{\circ}C$ for analysis of protein expression.

Preparation of ER-Enriched Microsomal Membrane Fraction

NT1 cells were harvested by centrifugation at 1,000g for 10 min at 4°C. All subsequent operations were performed at 4°C and/or on ice. Four grams of cells were homogenized in 5 mL homogenization buffer {200 mм Suc; 25 mм HEPES [4-(2-hydroxyethyl)]-1-piperazineethanesulfonic acid-КОН, pH 7.0; 3 mм EGTA; 1 mм MgSO₄; 1 mм phenylmethylsulfonyl fluoride [PMSF]; and 1 mM dithiothreitol [DTT]} using a tightly fitting glass/glass tissue grinder. The homogenate was centrifuged at 1,000g for 10 min and the supernatant was centrifuged at 7,000g for 20 min. The 7,000g supernatant was loaded on a discontinuous Suc gradient and centrifuged at 100,000g for 2 h. The Suc gradient consisted of 2 mL each of 22%, 38%, and 45% (w/v) Suc in 25 mм HEPES-KOH (pH 7.0), 1 mм DTT, and 1 mM PMSF. Fractions (1.0 mL) were collected. Equal amounts of protein were analyzed on SDS-PAGE and western blots. The ER-enriched membrane fraction (fraction 2, based on western-blot analysis) was diluted with 5 mL of dilution buffer containing 200 mM Suc, 25 mM HEPES-KOH (pH 7.0), 1 mM DTT, and 1 mM PMSF and centrifuged at 40,000g for 90 min. The pellet was resuspended in dilution buffer to a final concentration of 1 μ g protein μ L⁻¹.

Protein Determination

Protein concentrations was determined by the Bradford method (Bio-Rad protein assay) following the manufacturer's protocol. Bovine serum albumin was used as a standard.

⁴⁵Ca²⁺ Uptake and Release

Ca²⁺ uptake and release were performed at 22°C and measured with ⁴⁵CaCl₂ as described by Hsieh et al. (1991) with some modifications. Transport was measured in an ATPase assay buffer containing 200 mM Suc, 25 mM HEPES-KOH (pH 7.0), 10 mM KCl, 100 μM ⁴⁵CaCl₂ (2 μCi mL⁻¹), 100 μ M EGTA (yielding a final approximate Ca²⁺ concentration of 0.5 µм; Bers et al., 1994), 3 mм MgSO₄, 1 mм DTT, and 3 mм ATP. ATP-dependent ⁴⁵Ca²⁺ transport into the ER microsome lumen was initiated by addition of 100 μ L of the membrane fraction (100 μ g protein) in a final volume of 1 mL. Aliquots (100 μ L) from duplicate reactions were removed, filtered, and washed with 200 mM Suc, 25 тм HEPES-KOH (pH 7.0), 10 тм KCl, and 100 µм CaCl₂ using a single millipore filter set. The ⁴⁵Ca²⁺ retained on the filter was determined by liquid scintillation counting. Net active transport was determined as the difference in activity in presence and absence of ATP. Ca²⁺ release was triggered from ⁴⁵Ca²⁺-loaded (22 min) vesicles by addition of the ionophore ionomycin (final concentration of $1.5 \ \mu M$). Ionomycin was taken from a 660-µM stock solution in dimethyl sulfoxide. The net release was determined as the difference of ⁴⁵Ca²⁺ recovered after the addition of ionomycin versus addition of dimethyl sulfoxide alone. Results shown were obtained from at least two replicate experiments run in parallel with a wild-type control from three individual Nt CRT-Sense lines, one Nt CRT-antisense line and, as a control, one Nt GFP line.

ATPase Assay

ATPase activity was measured at 22°C. Ten microliters of membrane (10 μ g) was assayed in a buffer containing 200 mM Suc, 25 mM HEPES-KOH (pH 7.0), 10 mM KCl, 3 mM MgSO₄, 3 mM ATP, 1 mM DTT, 100 μ M CaCl₂, and 100 μ M EGTA (yielding a final approximate Ca²⁺ concentration of 0.5 μ M; Bers et al., 1994) in a final volume of 200 μ L. The reaction was incubated for 30 min and stopped by the addition of 2 mL NH₄/FeSO₄ reagent containing 1% (w/v) NH₄Mo, 1 N H₂SO₄, and 0.18 M FeSO₄-H₂O. *A*₆₆₀ was read and the generated inorganic phosphate was determined as the difference in activity in the presence or absence of 200 μ M vanadate. KH₂ PO₄ (0–0.1 μ mol) was used as a standard. Inorganic free phosphate was measured according to Taussky and Schorr (1953).

Phenotypic Analysis of Arabidopsis Lines

Seeds of each line T_3 were germinated on normal AT growth medium (4.3 g L⁻¹ Murashige and Skoog salts, Gibco BRL; 1× B5 vitamins, 2% [w/v] Suc, 0.05% [w/v] MES, pH 5.8, and 1% [w/v] phytagar, Gibco BRL). On d 16, 17, and 18 after germination, the plants were incubated at

 35° C for 2 h each day to induce expression of the transgene. On d 19, Parafilm was removed from the plates for 6 h, and the plates opened in a laminar flow hood for 30 min to increase transpiration and calcium uptake. The plants were then transferred to fresh AT growth medium, calciumdepleted medium (AT growth medium with 10 mM EGTA), or calcium-depleted medium with 12 mM CaCl₂. In the initial experiments, 12 seedlings for each transgenic line and medium treatment were germinated, one-half were induced for transgene expression, and half were maintained as noninduced controls. Images of these plants were taken at d 2, 4, 6, 9, and 12 d after transfer. In subsequent experiments, only *At* CRT:3 and *At*CRT-A:5 were used and 20 to 50 seedlings for each line were assessed.

SDS-PAGE and Immunoblotting

Protein was solubilized by addition of an equal volume of sample buffer (125 mM Tris-HCl [pH 6.8], 4% [w/v] SDS, 20% [v/v] glycerol, 10% [w/v] β -mercaptoethanol, and 0.02% [w/v] bromphenol blue). Equal amounts of solubilized proteins were separated on a 10% (w/v) SDSpolyacrylamide gel at pH 8.8. For Arabidopsis plants, 20- to 50-mg samples of young leaves were collected from each plant, weighed, and frozen in liquid nitrogen. Leaves were ground in sample buffer using 1 μ L of buffer to 1 mg of plant material and equal amounts of plant tissue were loaded on a 10% (w/v) SDS-polyacrylamide gel at pH 8.8. Gels were either stained with Gelcode Blue Stain protocol (Pierce, Rockford, IL) or transferred to a hydrophobic polyvinylidene difluoride membrane (Gelman Sciences, Ann Arbor, MI). Proteins were wet blotted for 1 h at 100 V. After transfer, the polyvinylidene difluoride membranes were blocked with 1% (w/v) blocking reagent (Roche Biochemical, Indianapolis) in Tris-buffered saline with 0.2% (v/v) Tween 20 for 1 h at 22°C. The membranes were incubated with either an antiserum against CRT from maize diluted 1:5,000, an antiserum against CRT from castor bean diluted 1:10,000, or an antiserum against BiP from maize diluted 1:10,000. Antibodies were visualized with a chemiluminescent detection of horseradish peroxidase according to the Supersignal West Pico blotting protocol (Pierce), and microdensiometry of bands was analyzed using Imagequant software.

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