Short title: Simultaneous ER and cytosol Ca^{2+} imaging

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Simultaneous imaging of ER and cytosolic Ca^{2+} dynamics reveals long-distance ER Ca^{2+} waves in plants

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One-sentence summary: Dual color imaging allows the simultaneous analysis of calcium dynamics in the endoplasmic reticulum and cytosol from single cells to adult entire plants.

FOOTNOTES

Author Contributions

AC and MCB conceived the project with specific input from FR, MG, and AB. MG and AC designed the experiments. FR, MC, and MF generated the constructs. FR, MG, and MF performed and analyzed the experiments. FR and LL generated the transgenic lines. DA and AB performed cross-correlation analyses of Fig. 2 and temporal evolution of signals in Fig. 4. AC and MG prepared the Figures and Videos. AC and MCB wrote the manuscript with input from all co-authors. AC agrees to serve as the author responsible for contact and ensures communication.

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ABSTRACT

Calcium ions (Ca^{2+}) play a key role in cell signaling across organisms. In plants, a plethora of environmental and developmental stimuli induce specific Ca^{2+} increases in the cytosol as well as in different cellular compartments including the endoplasmic reticulum (ER). The ER represents an intracellular Ca^{2+} store that actively accumulates Ca^{2+} taken up from the cytosol. By exploiting state-of-the-art genetically encoded Ca^{2+} indicators (GECIs), specifically the ER-GCaMP6-210 and R-GECO1, we report the generation and characterization of an Arabidopsis (*Arabidopsis thaliana*) line that allows for simultaneous imaging of Ca^{2+} dynamics in both the ER and cytosol at different spatial scales. By performing analyses in single cells, we precisely quantified i) the time required by the ER to import Ca^{2+} from the cytosol into the lumen; and ii) the time required to observe a cytosolic Ca^{2+} increase upon the pharmacological inhibition of the ER-localized type IIA Ca^{2+}-ATPases. Furthermore, live imaging of mature, soil-grown plants revealed the existence of a wounding-induced, long-distance ER Ca^{2+} wave propagating in injured and systemic rosette leaves. This technology enhances high-resolution analyses of intracellular Ca^{2+} dynamics at the cellular level and in adult organisms and paves the way to develop new methodologies aimed at defining the contribution of subcellular compartments in Ca^{2+} homeostasis and signaling.

INTRODUCTION

In animals, besides its role in protein secretion, the endoplasmic reticulum (ER) is a calcium (Ca^{2+}) store participating in the generation and shaping of stimulus-induced cytosolic Ca^{2+} increases (Soboloff et al., 2012). Moreover, in animals, Ryanodine (RyR) and Inositol trisphosphate ($InsP_3R$) receptors are ER-localized, ligand-gated Ca^{2+} permeable channels that release Ca^{2+} into the cytosol (Foskett et al., 2007), whereas the ER Ca^{2+} refilling is dependent on the activity of sarco/endoplasmic reticulum Ca^{2+}-ATPases (SERCA) and the Stromal Interaction Molecule (STIM)-Orai protein complex (Soboloff et al., 2012). In plants, RyR, $InsP_3R$, and the STIM-Orai complex are not present (Edel et al., 2017). However, a battery of P-Type IIA (ER-type Ca^{2+}-ATPases, ECAs) and IIB (Autoinhibited Ca^{2+} ATPases, ACAs) Ca^{2+}-ATPases are localized in the ER membranes and their primary function is to import Ca^{2+} into the ER lumen (Bonza and De Michelis, 2011, Bonza et al., 2013; Shkolnik et al., 2018). In addition, Ca^{2+}-permeable channels (e.g. Cyclic Nucleotide Gated Channels, CNGC) localized in the nuclear envelope (NE, which is in continuity with the ER) (Charpentier et al., 2016; Leitao et al., 2019) and Ca^{2+}/Cation transporters (e.g. CCXs) have been shown to participate in the regulation of Ca^{2+} transport across the ER membranes (Corso et al., 2018).

Ca^{2+} transport over the ER membrane was observed using purified microsomal vesicles loaded with the $^{45}Ca^{2+}$ isotope (Navazio et al., 2000). Later, by using Förster resonance energy transfer (FRET)-based genetically encoded Ca^{2+} indicator (GECI) (SP-YC4.6 and CRT-D4ER Cameleon) localized to the ER lumen, the ER resting Ca^{2+} concentration ($[Ca^{2+}]$) was measured *in vivo* in Arabidopsis (*Arabidopsis thaliana*) pollen tubes and in leaf and root cells (Iwano et al., 2009; Bonza et al., 2013; Tian et al., 2014). By using the ratiometric CRT-D4ER Cameleon, we previously reported, in root-tip cells, the ER Ca^{2+} dynamics in response to different stimuli, such as external adenosine triphosphate (ATP), L-Glutamate, salt stress, and water potential gradient (Bonza et al., 2013, Corso et al., 2018; Shkolnik et al., 2018). Some of these data were later confirmed by Luo and colleagues (2020), who generated a new Arabidopsis line expressing the intensiometric ER-localized sensor R-CEPIA1er (Luo et al., 2020).

Overall, in plants, *in vivo* analyses of ER Ca^{2+} dynamics revealed that it primarily acts as a Ca^{2+} sink, thus contributing to the dampening of the Ca^{2+} transient (Bonza et al., 2013; Corso et al., 2018). However, ER can also work as a Ca^{2+} source, being responsible for the generation of a cytosolic Ca^{2+} transient (Shkolnik et al., 2018; Luo et al., 2020).

Here we report the successful use of spectral variants of the new generation of intensiometric single fluorescent protein GECIs (e.g. ER-GCaMP6-210 and R-GECO1) to perform simultaneous imaging of Ca^{2+} dynamics in the ER and cytosol. We demonstrate this method in single plant cells as well as in adult plants.

RESULTS AND DISCUSSION

Over the years, we have exploited the use of the ratiometric FRET-based CRT-D4ER Cameleon to study Ca^{2+} dynamics in the ER lumen of wild-type and mutant Arabidopsis plants (Bonza et al., 2013; Corso et al., 2018; Shkolnik et al., 2018). This ratiometric sensor proved to be highly reliable to highlight different ER [Ca^{2+}] at resting and in reporting ER Ca^{2+} dynamics in response to various stimuli in different mutants (Corso et al., 2018; Shkolnik et al., 2018). However, in Arabidopsis, the use of the CRT-D4ER sensor showed some limitations. Firstly, for reasons not yet investigated, the CRT-D4ER sensor showed a varying degree of silencing. Despite the use of different promoters and vector backbones, we failed to detect the expression of the sensor in adult Arabidopsis plants (A. Costa. and L. Luoni, unpublished data). Only when we expressed the sensor in the *rdr6-11* Arabidopsis background, which is impaired in gene silencing (Peragine et al., 2004), we detected the sensor expression in leaves of adult plants (A. Costa and L. Luoni, unpublished data). Due to these limitations, we could only study the ER Ca^{2+} dynamics in young seedlings (Bonza et al., 2013; Corso et al., 2018; Shkolnik et al., 2018). Secondly, in some cases, we were unable to obtain knockout mutants expressing the sensor (Corso et al., 2018).

In order to choose a highly sensitive sensor to perform the analysis of ER Ca^{2+} in different cell types, which is also usable in a simple fluorescence microscopy setup, we searched the literature to find a suitable ER single fluorophore-based GECI. This class of GECIs are intensiometric Ca^{2+} sensors, based on a circularly permuted fluorescent protein (e.g. GFP, YFP, or mApple) (Baird et al., 1999; Nakai et al., 2001; Zhao et al., 2011) fused at its C- and N-termini with the components of a Ca^{2+} sensing module (i.e. CaM domain and the M13 peptide). In the presence of Ca^{2+}, this causes tightening of the interaction between C- and N-termini of the fluorophore, leading to increased brightness. *De facto*, this interaction induces an alteration of the spectral properties of the fluorescent protein with a strong increase in the fluorescence emitted (Nakai et al., 2001). Recently, de Juan-Sanz and colleagues (2017), generated two ER-localized, low-affinity Ca^{2+} variants of the intensiometric single fluorophore-based GECI GCaMP6 (Chen et al., 2013), dubbed ER-GCaMP6-150 and ER-GCaMP6-210 (where numbers indicate the *in vitro* Kd for Ca^{2+} of the two sensors expressed in µM) (de Juan-Sanz et al., 2017). Both sensors were found to be efficiently targeted to the ER lumen of animal cells and their sensitivity allowed the observation of a rapid Ca^{2+} accumulation in the axonal ER during an action potential firing (de Juan-Sanz et al., 2017). Remarkably, the two intensiometric GECIs, the ER-GCaMP3 variant and G-CEPIA1er, failed to reveal any signal in nerve terminals during activity, thus demonstrating a superior sensitivity of the ER-GCaMP6 sensors (de Juan-Sanz et al., 2017). Based on the fact that the CRT-D4ER, having an *in vitro* Kd for Ca^{2+} of 195 µM (Palmer et al., 2006; Greotti et al., 2016), efficiently reports ER Ca^{2+} dynamics in plant cells (Bonza et al., 2013), we decided to test the ER-GCaMP6-210 variant to overcome the previous failures of other Ca^{2+} ER sensors in plants.

To express the ER-GCaMP6-210 sensor in plants, we generated different constructs (see Materials and Methods) by placing its coding sequence under the control of two different constitutive promoters (i.e. CaMV35S and pUBQ10) (Grefen et al., 2010; Amack and Antunes, 2020). The original ER-GCaMP6-210 harbours the signal peptide of calreticulin (CRT) at the N-terminus and the KDEL retention motif at the C-terminus which efficiently targeted the sensor to the ER of neuronal cells (de

Juan-Sanz et al., 2017). To verify that the N- and C-terminal sequences were also sufficient to localize the sensor to the ER of plant cells, we transiently co-expressed the two constructs in *Nicotiana benthamiana* leaf epidermal cells with the ER marker nWAK2-mCherry-HDEL (Nelson et al., 2007; Bonza et al., 2013) (**Supplemental Fig. S1**) The fluorescence emissions of ER-GCaMP6-210 and of the ER marker showed a clear merge in the cellular endomembrane system as well as in the NE (**Supplemental Fig. S1D, H, K**). The perfect merge of the two signals was particularly clear at higher magnifications (**Supplemental Fig. 1I-K**). This experiment showed that the sensor was efficiently expressed under both promoters and that was properly localized to the ER (**Supplemental Fig. S1A, E**). When the ER-GCaMP6-210 was stably introduced in Arabidopsis Col-0 plants, the cellular fluorescence distribution was still clearly localized to the ER (Brandizzi et al., 2002; Bonza et al., 2013) and detected in both root and leaf cells **(Supplemental Fig. S2A-D**). Of note, the ER-GCaMP6-210 was efficiently expressed in guard cells where a neat signal in the NE was recognized (**Supplemental Fig. S2G, I**). We tested the functionality of the new sensor in both pCaMV35S- and pUBQ10-ER-GCaMP6-210 Arabidopsis lines, challenging seedlings with external ATP (0.1 mM) as an efficient and reliable stimulus known to trigger a cytosolic Ca^{2+} concentration increase ($[Ca^{2+}]_{cyt}$) in root-tip cells (Tanaka et al., 2010; Bonza et al., 2013; Behera et al., 2018). We performed parallel experiments using Arabidopsis seedlings expressing the cytosolic and nuclear-localized R-GECO1 sensor (Keinath et al., 2015). The first set of experiments were carried out following the same experimental design as that reported in Behera et al. (2018), where we made use of a custom perfusion setup for *in vivo* wide-field fluorescence microscopy imaging in Arabidopsis roots (Behera and Kudla, 2013). A 3-min pulsed ATP administration to the seedlings expressing ER-GCaMP6-210 and R-GECO1 triggered clear fluorescence increases which reflected a transient rise of $[Ca^{2+}]_{ER}$ and $[Ca^{2+}]_{cyt}$ (**Supplemental Fig. S3A**). The $[Ca^{2+}]_{ER}$ peak (**Supplemental Fig. S3B**) temporally followed the $[Ca^{2+}]_{cyt}$ rise (**Supplemental Fig. S3C**) and the ER showed a slower recovery to the prestimulus $[Ca^{2+}]_{ER}$ compared to the $[Ca^{2+}]_{cyt}$ (**Supplemental Fig. S3D**). Importantly, performing a comparison between seedlings expressing the ER-GCaMP6-210 with those expressing the Cameleon CRT-D4ER (Bonza et al.,

2013) revealed that the two sensors reported similar $[Ca^{2+}]_{ER}$ dynamics in response to ATP, with no difference both in the times at which the $[Ca^{2+}]_{ER}$ peak was reached (**Supplemental Fig. S3E, G)** and the times of recovery (**Supplemental Fig. S3H**). Instead, the ER-GCaMP6-210 exhibited a significantly increased signal change compared with the CRT-D4ER (**Supplemental Fig. S3F)**. It has been reported that most of the single fluorescent protein GECIs show pH sensitivity (Zhao et al., 2011; Keinath et al., 2015). On the other hand, pH has a minor effect on the readout of ratiometric FRET-based sensors like Cameleon (Nagai et al., 2004; Behera et al., 2018; Grenzi et al., submitted). The high similarity of Ca^{2+} dynamics monitored by using the ER-GCaMP6-210 and CRT-D4ER suggests that in the ER lumen, the probable pH change, possibly dependent on a coupled Ca^{2+}/H^{+} transport occurring across the ER membrane (e.g. ECAs and ACAs exchange Ca^{2+} with H^{+} (Bonza and De Michelis, 2011; Resentini et al., 2021)), does not seem to affect the ER-GCaMP6-210 sensor readout. To further test the functionality of the ER-GCaMP6-210 sensor, we treated the seedlings (in both pCaMV35S- and pUBQ10 lines) with 0.01 mM naphthalene-1-acetic acid (NAA) (Behera et al., 2018). A 3-min pulsed NAA treatment was also efficient to induce a transient accumulation of Ca^{2+} in both compartments (**Supplemental Fig. S3I, J**), with the ER Ca^{2+} accumulation showing slower dynamics compared to the cytosol concerning both the maximum peak (**Supplemental Fig. S3K**) and the recovery of the prestimulus $[Ca^{2+}]$ (**Supplemental Fig. S3L)**.

Overall, whereas different ATP- and NAA-induced Ca^{2+} dynamics in the cytosol were well documented (Waadt et al., 2017; Behera et al., 2018), these new data showed that different dynamics were also detectable in the ER (**Supplemental Fig. S3A, I**). Specifically, in response to NAA the Ca^{2+} (expressed as $\Delta F_{max}/F_0$) in the ER peak and the time when it was reached was smaller (e.g. 0.37 ± 0.11 for NAA vs 1.47 ± 0.45 for ATP with the pUBQ10-ER-GCaMP6-210 line) and delayed (e.g. 157 ± 32 for NAA vs 129.2 ± 44 for ATP with the pUBQ10-ER-GCaMP6-210 line), respectively, compared to the one measured with the ATP treatment (**Supplemental Fig. S3B, C, J, K**). Noticeably, this new set of results confirmed previously published data showing that the Ca^{2+} accumulation in the ER follows

188 the cytosolic Ca^{2+} transient, again supporting a role of ER as a Ca^{2+} sink in response to stimuli that
189 induce a $[Ca^{2+}]_{cyt}$ increase (Bonza et al., 2013, Corso et al., 2018).

190 Based on this first series of results, we felt confident that the ER-GCaMP6-210 sensor, despite the
191 oxidative environment of the plant ER lumen (Aller et al., 2013) and the lower pH (Martinière et al.,
192 2013), efficiently reports $[Ca^{2+}]_{ER}$ dynamics in accordance with what was reported in animal neurons
193 (de Juan-Sanz et al., 2017). Therefore, having demonstrated the functionality of the new sensor in
194 monitoring ER Ca^{2+} dynamics, we explored the possibility of performing simultaneous imaging of Ca^{2+}
195 in ER and cytosol. To this end, we crossed both the pCaMV35S-ER-GCaMP6-210 and pUBQ10-ER-
196 GCaMP6-210 Arabidopsis lines with the pUBQ10-R-GECO1 line (Zhao et al., 2011; Keinath et al.,
197 2015) and selected seedlings showing both types of fluorescence (**Fig. 1A-D; Supplemental Fig. S4**).
198 Since the stable expression of GECIs might affect plant growth and development (De Col et al., 2017;
199 Waadt et al., 2017), before proceeding with further analyses we phenotypically characterized the
200 Arabidopsis lines expressing the ER-GCaMP6-210 alone alongside those co-expressing the R-
201 GECO1. We measured seedling root length, rosette size, silique length, and the number of seeds per
202 silique of independent pCaMV35S-ER-GCaMP6-210, pUBQ10-ER-GCaMP6-210, and the R-GECO1
203 crossed lines. By comparing these parameters with the Col-0 wild type, we did not observe any gross
204 phenotypic differences in all sensor lines tested (**Supplemental Fig. S5A-D**), with only the
205 pCaMV35S-ER-GCaMP6-210 line showing slightly reduced silique length and seed number
206 (**Supplemental Fig. S5C, D**).

207 The proper expression of the ER-GCaMP6-210 under the control of the pUBQ10 promoter both alone
208 (**Supplemental Fig. S2**) and co-expressed with the R-GECO1 (**Fig. 1A-D; Supplemental Fig. S4**),
209 together with the lack of negative effects on plant growth and development (**Supplemental Fig. S5**),
210 prompted us to choose the pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 line to carry out the
211 simultaneous imaging of Ca^{2+} dynamics in the two cellular compartments.

To prove the validity, usability, and advantages of this new dual biosensor line, we pursued two different approaches: i) high spatio-temporal resolution Ca^{2+} imaging analyses in single cells, and ii) low-magnification Ca^{2+} imaging analyses in adult mature plants.

Initially, we demonstrated the reliability of ATP and NAA to induce a transient Ca^{2+} accumulation in the cytosol and ER (**Supplemental Fig. S3)**. Those experiments were carried out by means of a wide-field microscope which, given its poor optical sectioning, provides averaged responses on several root-tip cells (Costa et al., 2013; Vigani and Costa, 2019). To perform single-cell analyses in seedling root tips, we made use of a Spinning Disk confocal. We independently acquired the ER-GCaMP6-210 and R-GECO1 fluorescence switching between GFP and RFP filters: the delay between the emissions was less than 600 ms and the images were acquired every 2 s (see Materials and Methods). For every experiment, we treated Arabidopsis root tips with 0.1 mM ATP or 0.01 mM NAA pulsed for 3 min using the same perfusion set up described above and we analyzed two different independent cell types (cell 1, C1, and cell 2, C2 in **Fig. 1**) (**Fig. 1E, L; Supplemental Movie S1**). Even at the single-cell level, the ER Ca^{2+} accumulation temporally followed the cytosolic increase (**Fig. 1F, G, M, N**), showing a delayed maximum peak and a slower recovery time (**Fig. 1H, J, K, O, Q, R**). It is noteworthy that the simultaneous imaging of the two compartments allowed us to precisely and directly determine the time delay between the beginning of the $[Ca^{2+}]_{cyt}$ increase and the following $[Ca^{2+}]_{ER}$ accumulation. This delay turned out to be, for both treatments, around 4–5 s (4.8 ± 2.2 s for ATP and 3.7 ± 2.6 for NAA) (**Fig. 1H, O**). Aside from the ability to report different ER Ca^{2+} dynamics in response to different stimuli, this approach allowed us to measure the time required by the ER to import Ca^{2+} in response to a cytosolic Ca^{2+} increase; thus, it represents an *in vivo* measurement of the activity of ER-localized Ca^{2+}-transporters (e.g. ER-localized ACAs and ECAs) (Bonza and De Michelis, 2011). To assess *in vivo* the contribution of ECAs in the active import of Ca^{2+} into the ER lumen, and their impact on the cytosolic Ca^{2+} homeostasis, we used cyclopiazonic acid (CPA). CPA is a non-fluorescent inhibitor of SERCA-like Ca^{2+}-ATPases including plant P-Type IIA ECAs (Liang and Sze, 1998). We treated Arabidopsis root tips of the dual sensor line with 25 µM CPA pulsed for 3 min and

analyzed simultaneously in the same cell (**Fig. 2A, B**) both the $[Ca^{2+}]_{ER}$ and $[Ca^{2+}]_{cyt}$ dynamics (**Fig. 2C**). Since we expected to have a CPA-dependent decrease in the ER-GCaMP6-210 fluorescence, to avoid bleaching of the sensor which might affect the measurement, we acquired images every 5 s instead of 2 s as for the experiments reported in Fig. 1. The CPA administration determined a quick and sustained decrease of ER-GCaMP6-210 fluorescence, indicative of an $[Ca^{2+}]_{ER}$ depletion. The ER Ca^{2+} depletion was followed by a transient increase of $[Ca^{2+}]_{cyt}$ (**Fig. 2C**). The treatment with DMSO alone (used as a solvent for CPA) did not have any effect (dashed lines in **Fig. 2C'**), demonstrating that the observed response was specific to CPA treatment. Based on these data, we measured the time between the initial decrease of $[Ca^{2+}]_{ER}$ and the increase in $[Ca^{2+}]_{cyt}$ that was quantified in 14 ± 9 s (**Fig. 2D, E**). Interestingly, the CPA washout did not allow the recovery of $[Ca^{2+}]_{ER}$ indicating that once the inhibitor has entered the cell it cannot be quickly removed and that the ER-localized pumps are probably kept in an inactive state. Based on this latter result, we can claim that a decreased activity of the ECAs is sufficient to trigger a cytosolic Ca^{2+} increase (**Fig. 2F**), and thus that the ER can potentially work as a cytosolic Ca^{2+} source in signaling processes. At the same time, this experiment underlines the key role played by CPA-sensitive Ca^{2+} transporters for the maintenance of ER Ca^{2+} homeostasis, confirming the data previously obtained with the CRT-D4ER line (Bonza et al., 2013). Nonetheless, this result demonstrates that other Ca^{2+} transporters such as the ACAs and Ca^{2+} exchangers localized to the ER, tonoplast, and PM could be responsible for the observed recovery of the resting $[Ca^{2+}]_{cyt}$ (Resentini et al., 2021).

We can, therefore, foresee that this new dual sensor line will constitute a useful tool to study *in planta*, and in different tissues or cell types at high spatio-temporal resolution, the ER/cytosolic Ca^{2+} handling in response to different stimuli, in different genetic backgrounds, or following pharmacological treatments.

Whereas the experiments carried out in root cells reported ER and cytosolic Ca^{2+} transients in response to the perception of an exogenously applied stimulus or following a pharmacological treatment, we also wanted to investigate the ER/cytosolic Ca^{2+} dynamics with single-cell resolution

during a developmental process, such as the pollen tube growth (Feijo et al., 2004), where a role of ER in the regulation of Ca^{2+} signaling has been suggested (Iwano et al., 2009, Barberini et al., 2018; Ishka et al., 2021). We collected pollen grains from flowers of the pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 mature plants and let them germinate *in vitro* as previously described (Schoenaers et al., 2017). We visually inspected the germinated pollen grains and selected those showing both fluorescence signals. We then followed their *in vitro* growth, acquiring images every 2 s and measuring the fluorescence intensities of both sensors in a Region of Interest (ROI) “a” drawn in the tip region just underneath the clear zone (**Fig. 3A, B, G; Supplemental Movie S2A**). In ROI “a”, the R-GECO1 revealed the typical tip cytosolic Ca^{2+} oscillations (**Fig. 3G, G’**; **Supplemental Movie S2A**) observed when pollens from different species germinate and grow *in vitro* (Damineli et al., 2017; Schoenaers et al., 2017; Barberini et al., 2018; Li et al., 2021). Pollen tubes showed a tip growth with an average speed of 0.033 ± 0.015 µm/s with cytosolic Ca^{2+} oscillations having an averaged frequency of 0.03 ± 0.01 Hz (**Fig. 3G, G’**). These data are consistent with previous reports (Iwano et al., 2009, Damineli et al., 2017; Schoenaers et al., 2017) and confirm that, *in vitro,* the pollens did not have growth defects. This holds also true *in vivo* since no alterations were observed in silique length and seed number (**Supplemental Fig. S5C, D**). The ER-GCaMP6-210 fluorescence in the ROI “a" also showed an oscillating behaviour (**Fig. 3G, G’**), revealing the possible existence of $[Ca^{2+}]_{ER}$ oscillations which might, therefore, correspond with the tip cytosolic Ca^{2+}, which is known to be dependent on an influx of extracellular Ca^{2+} (Holdaway-Clarke et al., 1997). To investigate this possibility, we performed a normalized cross-correlation analysis between the R-GECO1 and the ER-GCaMP6-210 fluorescence signals. This analysis revealed a peak value of 0.28 ± 0.11 (**Fig. 3H**) with a global temporal lag of 6 ± 2 s (**Fig. 3I**) and an average oscillation time of 30 ± 11 s (**Fig. 3J**), thus supporting a correlation between the two parameters. However, the combined effects of the continuous movement of the ER membranes, observed in the apex of the pollen tube (see the analyzed ROI “a" and the kymograph in **Fig. 3D**) (Lovy-Wheeler et al., 2007), and the intensiometric nature of the sensors do not make us confident to ascribe both the increase and decrease of the ER-GCaMP6-210

fluorescence uniquely to the sole change in the $[Ca^{2+}]_{ER}$. In this case, the use of a ratiometric sensor, such as the Cameleon CRT-D4ER, would probably help, but at present, we do not have a line expressing simultaneously the CRT-D4ER and the R-GECO1 in pollen. Nevertheless, the kymographs extracted for both fluorescence emissions of the representative pollen tube (**Fig. 3D-F**) revealed that an increase in the R-GECO1 and ER-GCaMP6-210 signals spread within the shank towards the grain (**Fig. 3D, K; Supplemental Movie S2B**), allowing us to quantify the R-GECO1 and ER-GCaMP6-210 fluorescence emissions in a second ROI "b" drawn in a region of the pollen shank where the movement of the ER membranes was limited (**Fig. 3A, B, D, E)**. Only a subpopulation of growing pollen tubes showed such cytosolic Ca^{2+} transients in the shank (ROI "b"), but when a change of R-GECO1 fluorescence was observed (**Fig. 3K, K'**), a clear increase of ER-GCaMP6-210 fluorescence was present, which followed the cytosolic signal with an average delay of 3.2 ± 1.1 s (**Fig 3L**). Moreover, similar to what was observed in root-tip cells, the ER-GCaMP6-210 fluorescence showed a more sustained increase compared to the cytosolic one (**Fig. 3M**). Based on these observations, we suggest that the variation of ER-GCaMP6-210 fluorescence in the shank faithfully reported a change in the ER Ca^{2+} concentration and was not affected by heterogeneity in volume and concentration of the sensor.

In conclusion, although the ER-GCaMP6-210 allows efficient measurement of ER Ca^{2+} dynamics in pollen tubes, the data obtained by the analyses of the tip region should be taken with care. Nevertheless, we believe that this dual sensor line will be instrumental to re-evaluate, besides CPA, the action of a series of inhibitors, known to affect the ER Ca^{2+} release in animal cells (e.g. 2-aminoethoxydiphenyl borate, heparin, and caffeine), that have also been shown to impact the cytosolic tip Ca^{2+} gradient and growth of pollen tubes in different species (e.g. *Solanum lycopersicum*, *Papaver rhoeas, Nicotiana tabacum*) (Franklin-Tong et al., 1996; Barberini et al., 2018; Li et al., 2021).

The successful detection of single FP GECIs fluorescence (Vincent et al., 2017; Nguyen et al., 2018; Toyota et al., 2018) achieved with simple fluorescence microscopes (e.g. fluorescent stereomicroscopes) made us confident that this dual sensor line could also allow imaging of ER and

316 cytosolic Ca^{2+} dynamics in adult mature plants. Therefore, we imaged three-week-old Col-0 pUBQ10-
317 ER-GCaMP6-210 x pUBQ10-R-GECO1 plants grown in soil, using a fluorescent stereomicroscope
318 equipped with GFP and RFP filters (**Fig. 4A-C**). A rosette leaf was wounded by a tweezer according to
319 Nguyen et al. (2018) and sensors' fluorescence emissions were monitored and quantified both in the
320 wounded (local, l) and in a distal (d) leaf (**Fig. 4A-D**). The wounding induced both a cytosolic and ER
321 Ca^{2+} increase in the local leaf, occurring primarily in the vasculatures and spreading within the leaf
322 lamina and the petiole, eventually reaching a distal leaf (**Fig. 4D-G; Supplemental Movie S3**). Note
323 that the drop of the initial fluorescence signals for both sensors, detectable in the local and distal
324 leaves, was due to the movement of the entire plant when touched with the tweezer (red arrow in **Fig.**
325 **4F; Supplemental Movie S3**)**.** Whereas the cytosolic Ca^{2+} increase was expected to occur both in the
326 wounded leaf and in the distal one (Mousavi et al., 2013; Nguyen et al., 2018), the wounding-induced
327 ER Ca^{2+} accumulation in both sites was a novel observation, demonstrating that the magnitude of the
328 cytosolic Ca^{2+} increase (**Fig. 4H**) was sufficient to trigger the $[Ca^{2+}]_{ER}$ accumulation. Similar to what
329 was observed in the previous experiments, the $[Ca^{2+}]_{ER}$ increase temporally followed the cytosolic one
330 (**Fig. 4I**), being also more sustained (**Fig. 4F, G**). To further analyze the representative experiment, we
331 visually represented the temporal progression of the cytosolic and ER Ca^{2+} accumulation (**Fig. 4L, M**)
332 by using false colors, representing by each color the time at which the maximum intensity in
333 fluorescence occurred. Pixel by pixel, the color was weighted by the absolute value achieved: the
334 brighter the color, the higher the signal. Early signal peaks are labelled with blue color, fading to red
335 and green for middle to late responses, respectively, thus presenting an overall idea about the signal
336 propagation throughout the whole plant (**Fig. 4L, M**).

337 In conclusion, this latter result reports the existence of a long-distance ER Ca^{2+} wave induced by
338 wounding that travels from leaf to leaf and temporally follows the cytosolic Ca^{2+} wave.

339

340 **CONCLUSIONS**

In this article, we report the generation of a new Arabidopsis line expressing both ER-GCaMP6-210 and R-GECO1 GECIs for the simultaneous *in vivo* imaging of Ca^{2+} dynamics in the ER and cytosol of plant cells. Our data confirm the critical role of the ER as a Ca^{2+} buffering system and provide an unprecedented spatial and temporal resolution of the dynamics of $[Ca^{2+}]_{ER}$ accumulation in different cell types in response to independent external stimuli and during a developmental program. This new technology allows us to demonstrate that, in response to leaf wounding, a long-distance ER Ca^{2+} wave is established, which temporally follows the cytosolic one. This introduces an additional layer of complexity in the rapid long-range signaling in plants (Johns et al., 2021) and opens interesting new scenarios. The generation of this dual sensor line provides the basis for future experiments, feasible at any developmental stage, aimed at identifying critical components involved in the Ca^{2+} transport across ER membranes of plant cells that are essential to shed more light on a still underappreciated role of this compartment in the regulation of local and systemic Ca^{2+} signaling in plants.

MATERIALS AND METHODS

Plant material and growth conditions. All Arabidopsis (*Arabidopsis thaliana*) plants were of the ecotype Columbia 0 (Col-0). Seeds were surface-sterilized by vapor-phase sterilization (Clough and Bent, 1998) and plated on half-strength MS medium (Murashige and Skoog, 1962) (Duchefa, http://www.duchefa-biochemie.com/) supplemented with 0.1% (w/v) sucrose, 0.05% (w/v) MES, pH 5.8, and 0.8% (w/v) plant agar (Duchefa, http://www.duchefa-biochemie.com/). After stratification at 4°C in the dark for 2 days, plates were transferred to the growth chamber under long-day conditions (16 h light/8 h dark, 100 µE m^{-2} s^{-1} of Cool White Neon lamps) at 22°C. The plates were kept vertically, and seedlings were used for imaging 6–7 days after germination (DAG). For imaging in adult plants, 3–4-week-old mature plants grown in soil under long-day conditions (16 h light /8 h dark, 100 µE m^{-2} s^{-1} of Cool White Neon lamps) at 22°C and 75% relative humidity were used. *Nicotiana benthamiana* plants were cultivated for 5–6 weeks in a greenhouse under a 16-h light/8-h dark cycle with 60% atmospheric humidity and at 22/18°C.

Plant phenotyping and root growth analyses. For whole-plant phenotyping, plants were grown on soil under long-day conditions in individual pots randomly distributed among standard greenhouse flats. Rosettes and siliques were documented photographically. Seeds were harvested from individual siliques and counted. For phenotypic analysis on roots, surface-sterilized seeds were grown vertically on half-strength MS medium supplemented with 0.1% (w/v) sucrose, 0.8% (w/v) plant agar (Duchefa, http://www.duchefa-biochemie.com/), and root length was measured from 3 to 7 DAG. Lengths and sizes were quantified by Fiji (https://imagej.net/Fiji).

Molecular cloning and plasmid constructs. The original plasmid harboring the sequence coding for the ER-GCaMP6-210 (de Juan-Sanz et al., 2017) was obtained from Addgene (https://www.addgene.org/86919/). The *ER-GCaMP6-210* coding sequence was PCR amplified with

379 the Q5® High-Fidelity DNA Polymerase (New England Biolabs, https://www.neb.com/) using the
380 following forward and reverse primers:

381 AC614 5'-CATGGAATTCATGGGACTGCTGTCTGTGCCT-3' and

382 AC615 5'-CATGGGATCCTCACAGCTCATCCTTGCCTCC-3'

383 harboring the EcoRI and BamHI restrictions sites, respectively (underlined). The amplicon was ligated
384 into the empty EcoRI/BamHI-digested *pGree0029-Ter* binary vector (Ter corresponds to the 19S
385 CaMV terminator sequence) (Hellens et al., 2000; Bonza et al., 2013) to generate the *pGree0029-ER-*
386 *GCaMP6-210-Ter.* pUBQ10 (Grefen et al., 2010) and pCaMV35S (Amack and Antunes, 2020)
387 promoter sequences were amplified using the following primers:

388 AC280 5'-CATGGGTACCGTCGACGAGTCAGTAATAAACG-3';

389 AC281 5'-CATGGGTACCCTGTTAATCAGAAAAACTCAG-3';

390 AC314 5'-CATGGGTACCGATATCGTACCCCTACTCCA-3' and

391 AC315 5'-CATGGGTACCGGGCTGTCCTCTCCAAATGAA-3'.

392 All forward and reverse primers harbor a KpnI restriction site (underlined). The amplicons of both
393 promoters were digested with KpnI and ligated into the KpnI-linearized and dephosphorylated
394 *pGreen0029-ER-GCaMP6-210-Ter* plasmid. The obtained *pGreen0029-pUBQ10-ER-GCaMP6-210-*
395 *Ter* and *pGreen0029-pCaMV35S-ER-GCaMP6-210-Ter* vectors were sequenced to verify the proper
396 directionality of the inserted promoters and the absence of mistakes. The pGreen0029 vector
397 backbone harbors the *nptI* gene, which confers the resistance to kanamycin in bacteria and the *nptII*
398 gene which confers the resistance to kanamycin in plants (Hellens et al., 2000).

399

400 **Generation of transgenic plants**. The *pGreen0029-pUBQ10-ER-GCaMP6-210* and *pGreen0029-*
401 *pCaMV35S-ER-GCaMP6-210* constructs were introduced in *Agrobacterium tumefaciens*
402 *GV3101/pMP90* strain. *Arabidopsis thaliana* Col-0 was transformed by floral-dip (Clough and Bent,

1998). Transgenic lines were selected by the presence of fluorescence for each construct. To obtain the double-sensor lines, the Col-0 pUBQ10-ER-GCaMP6-210 #1 and pCaMV35S-ER-GCaMP6-210 #1 lines were crossed with the Col-0 pUBQ10-R-GECO1 line (Keinath et al., 2015).

Transient expression in *Nicotiana benthamiana* leaves. Leaf infiltration was performed using *Agrobacterium tumefaciens GV3101/pMP90* strain carrying the specified constructs (pUBQ10-ER-GCaMP6-210-Ter; pCaMV35S-ER-GCaMP6-210-Ter, nWAK2-mCherry-HDEL) together with the p19-enhanced expression system according to the method described by Waadt and Kudla (2008). For the confocal imaging analysis after the infiltration, the plants were kept for 3–5 days under incubation conditions described above.

Pollen tube growth dynamics. To perform Ca^{2+} imaging analyses during pollen tube growth, pollen grains from 13–15 flowers-stage plants were germinated in accordance with Rodriguez-Enriquez et al. (2012) and Schoenaers et al. (2017) (292 mM sucrose, 0.16 mM H_3BO_3, 0.1 mM $CaCl_2$; 0.14 mM $Ca(NO_3)_2$; 0.1 mM KCl, 0.003% (w/v) N-Z-Amine A; 0.055 mM myo-inositol, 0.038 mM ferric ammonium citrate; 0.01 mM spermidine; 10 mM gamma-Aminobutyric acid, pH 8.0 adjusted with KOH and 0.5% (w/v) agarose). The solution was heated in a microwave for the agarose to dissolve and cooled down to 50–60°C for the pH to be readjusted to pH 8.0. A 0.5 cm × 0.5 cm cellophane membrane (325P cellulose; AA Packaging Limited, Preston, United Kingdom) was placed on top of the medium, and pollen grains were placed directly onto the membrane, and the cover glass was flipped on another cover glass that was attached to an opening at the bottom of a small Petri dish. Water was applied on the inner sides of the Petri dish to maintain high humidity and the Petri dish was closed using parafilm. The pollen grains were germinated in a climate-controlled room at 23°C in the dark, and visualized approximately 2 h after pollination.

Confocal laser scanning microscopy. Confocal microscopy analyses of stable transgenic Arabidopsis seedling root and shoot cells and transiently transformed *N. benthamiana* leaf cells were performed using a Nikon Eclipse Ti2 inverted microscope, equipped with a Nikon A1R+ laser scanning device (http://www.nikon.com/). For localization studies, images were acquired by a CFI Apo Lambda 40XC LWD WI (N.A. 1.15) and CFI Plan Apo Lambda 60X Oil (N.A. 1.4). ER-GCaMP6-210 was excited with the 488-nm laser and the emission was collected at 505–550 nm. R-GECO1 and mCherry were excited with the 561-nm laser and the emission was collected at 570–620 nm. Chlorophyll was excited with the 488-nm laser and the emission was collected at 663–738 nm. The confocal pinhole was set to 20.43 µm and the images were acquired at 2048 x 2048 pixels resolution (**Fig. 1**). NIS-Elements (Nikon; http://www.nis-elements.com/) was used as a platform to control the microscope. Images in Figure 1 and Supplemental Figure 2A-C and G-I, were denoised by using the NIS-Element Denoise.ai plugin (https://www.microscope.healthcare.nikon.com/en_EU/products/confocal-microscopes/a1hd25-a1rhd25/nis-elements-ai). Non denoised images were analyzed using NIS-Elements and Fiji.

Wide-field fluorescence microscopy. For wide-field Ca^{2+} imaging analyses in seedling roots of pUBQ10-ER-GCaMP6-210, pCaMV35S-ER-GCaMP6-210, pUBQ10-R-GECO1, and pCaMV35S-CRT-D4ER lines, an inverted fluorescence Nikon microscope (Ti-E; http://www.nikon.com/) with a CFI Plan Apo VC 20X (N.A 0.75) was used. Excitation light was produced by a fluorescent lamp (Prior Lumen 200 PRO; Prior Scientific; http://www.prior.com) set to 20% with 488 nm (470/40 nm) for the ER-GCaMP6-210 sensor, 561 nm (540/25 nm) for the R-GECO1, and 440 nm (436/20 nm) for CRT-D4ER. ER-GCaMP6-210 and R-GECO1 fluorescence emissions were collected at 505–530 nm and at 576–626 nm respectively. For the analysis of the CRT-D4ER line, the FRET CFP/YFP optical block A11400-03 (emission 1, 483/32 nm for ECFP; emission 2, 542/27 nm for FRET/Citrine) with a dichroic 510 nm mirror (Hamamatsu) was used. Images were collected with a Hamamatsu Dual CCD camera (ORCA-D2; http://www.hamamatsu.com/). Camera binning was set to 2 x 2 for the ER-GCaMP6-210

and R-GECO1, and to 4 x 4 for the CRT-D4ER. Exposure times (from 100 to 400 ms) were adjusted depending on the line analyzed. Images were acquired every 5 s. Filters and the dichroic mirrors were purchased from Chroma Technology (http://www.chroma.com/). NIS-Elements (Nikon; http://www.nis-elements.com/) was used as a platform to control the microscope, illuminator, and camera. Images were analyzed using Fiji.

Spinning Disk Confocal Microscopy. Confocal spinning disk microscopy analyses of root-tip cells and pollen tubes were performed using a Nikon Eclipse Ti2 inverted microscope, equipped with a Yokogawa Spinning Disk Confocal System (https://www.microscope.healthcare.nikon.com/en_EU/products/confocal-microscopes/csu-series/specifications). The oil immersion CFI Plan Apo Lambda 60X Oil (N.A. 1.4) and the CFI Plan Apo VC 20X (N.A. 0.75) were used as objectives. ER-GCaMP6-210 was excited by a 488-nm single-mode optical fiber laser and the emission was collected at 525–550 nm. R-GECO1 was excited by a 561-nm single-mode optical fiber laser and the emission was collected at 576–626 nm. Images were collected with a Photometrics Prime BSI CMOS camera (https://www.photometrics.com/products/prime-family/primebsi/) with an exposure time of 200–300 ms with a 2 x 2 binning (1024 x 1024 pixels) for each emission.

For dynamic Ca^{2+} imaging analyses, images were acquired every 2 s. The NIS-Element AR (Nikon, Japan, http://www.nis-elements.com/) was used as a platform to control the microscope, laser, camera, and post-acquisition analyses. Images in Figure 2 and 3 were denoised by using the NIS-Element Denoise.ai plugin (https://www.microscope.healthcare.nikon.com/en_EU/products/confocal-microscopes/a1hd25-a1rhd25/nis-elements-ai). Raw, non-denoised images were analysed using Fiji.

Wound-induced calcium imaging in adult plants. Adult plants of pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 were imaged with a Nikon stereomicroscope (SMZ18, http://www.nikon.com/)

equipped with a 5.9 megapixel CMOS DS-Fi3 Microscope Camera. Excitation light was produced by a mercury light source (Intensilight; http://www.nikon.com/) with GFP and RFP filter Cubes. A Plan Apo 0.5X objective was used without zoom for the imaging of the entire plant and images were collected with an exposure time of 1 s with a 2 x 2 camera binning (1440 x 1024 pixels) for each emission. R-GECO1 and ER-GCaMP6-210 images were acquired every 10 s by manually switching between the GFP and RFP configuration. During the entire experiment, plants were continuously illuminated.

Seedling imaging. Seven-day-old seedlings were used for root imaging. For root experiments, seedlings were kept in the growth chamber until the experiment and gently removed from the plate according to Behera and Kudla (2013), placed in the dedicated chambers and overlaid with cotton wool soaked in imaging solution (5 mM KCl, 10 mM MES, 10 mM $CaCl_2$ pH 5.8 adjusted with Tris-base). The root was continuously perfused with imaging solution using a perfusion pump (Behera et al., 2018) while the shoot was not submerged. Treatments were carried out by supplementing the imaging solution with 0.1 mM Na_2ATP (sodium adenosine triphosphate) (from a 200 mM stock solution buffered at pH 7.4 with NaOH), 0.01 mM NAA (from a 10.74 mM stock solution) or 25 µM of CPA (from a 10 mM stock solution dissolved in 100 % (v/v) DMSO) administered for 3 min under continuous perfusion.

Quantitative imaging analysis. Fluorescence intensity was determined over regions of interest (ROIs), which corresponded to: i) cells of the meristematic and transition zone of seedling root tips (wide-field microscope); ii) single meristematic root-tip cells (spinning disk microscope); iii) pollen tube tip or shank (spinning disk microscope), and iv) wounded and unwounded leaves of adult plants (stereo microscope). ER-GCaMP6-210 and R-GECO1 emissions of the analyzed ROIs were used for single fluorescence emissions analyses. Citrine and ECFP emissions of CRT-D4ER of the analyzed ROIs were used for the ratio (R) calculation (Citrine/ECFP). Background subtraction was performed in

all experiments, except in those performed with adult plants imaged with the stereomicroscope. Fluorescence (F) and ratio (R) values at different time points were normalized to the initial fluorescence (F_0) ($\Delta F/F_0$) or ratio (R_0) ($\Delta R/R_0$) and plotted versus time. For pollen experiments, the fluorescence emissions were normalized as (X - mean)/SD. Where X is the fluorescence value at a given time point, mean and SD are respectively the average fluorescence value of all the time points and the associated standard deviation. The analysis of fluorescent intensities was in all cases performed on raw non-denoised images.

Pollen tubes registration and growth analysis. To quantify the tip Ca^{2+} oscillations in pollen tubes, we applied a semi-automatic routine to register the image stacks taken at different times. The registration of each ROI was performed by computing the cross-correlation between each couple of consecutive images. In this way, the pollen tube apex was maintained at the same position. This computation was performed with the Fiji plugin 'Template Matching' (https://sites.google.com/site/qingzongtseng/template-matching-ij-plugin) after selecting the pollen tube apex as a landmark and using a subpixel cross-correlation method. The horizontal and vertical displacements were stored, and the process was iterated for all time points. The average speed of the pollen tube growth was obtained by dividing the total elongation by the time.

Kymograph. To evaluate the pollen tube elongation, we used a graphical method for a space-time representation of the pollen tube tip evolution. We draw a spatial path that follows the tip of the tube during its growth, as observed in the entire image sequence (x,y,t). By using the Fiji "Dynamic Reslice" function we create a new image, which depicts the temporal evolution of the pollen elongation through the spatial path previously defined.

Cross-correlation analyses of fast fluctuations. To evaluate the temporal delay between the two fluorescent channels, we performed a signal analysis based on cross-correlation. To understand the correlation between the fast oscillations occurring in both the R-GECO1 and ER-GCaMP6-210, we used a statistical approach based on the data acquired in the set of 9 independent measurements. First, we removed the slow dynamics in each signal, estimated by subtracting a low-pass version of the temporal signature. Such a low-pass version was obtained by filtering the signal with a gaussian kernel of sigma σ = 80 s. Consecutively, each curve obtained was examined by running cross-correlation analysis in sliding windows of 80 s, with a stride of 2 s. Within each temporal window, we normalized the signal by its standard deviation and subtracted the mean. In this way, we could calculate the normalized version of the cross-correlation. This analysis was repeated by striding the window through the entire signal duration for all the measurements and let us estimate the average cross-correlation and its associated error. The temporal location of the peaks indicates an average temporal delay between the two signals.

Temporal representation of Ca^{2+} waves in mature plants. To produce a visual representation of the overall temporal propagation of the Ca^{2+} signals in the whole plant, we first removed a common background in the images, segmenting the plant (by thresholding) and setting to zero the values outside of the plant. We then realigned each time point of the same leaf by selecting a region that enclosed it. In the successive frames, we compensated for the movement by evaluating the cross-correlation displacement. In this way, the intensity in each pixel described the temporal evolution of the signal in a given position within the leaf. Once each leaf was spatially realigned for the entire duration of the acquisition, it was possible to compute the $\Delta F/F_0$ on the full image sequence. To obtain a visual image that describes the temporal propagation by using a false-color representation, we mapped the temporal location of the maximum intensity in each pixel with a color in the look-up table. The color intensity was chosen to be proportional to the peak intensity found in the temporal evolution

of the pixel. In this representation, the blue color indicates that the peak intensity was achieved at early timings, fading to red and green for middle and late timings.

Statistical analysis. All the data are representative of n ≥ 4 experiments. Reported traces are averages of traces from all single experiments used for the statistical analyses. Results are reported as averages ± standard deviations (SD). p values were calculated with an unpaired Student's *t*-test. Data from experiments with at least n = 5 were plotted as box-and-whisker plots using GraphPad, in which all the experimental points are plotted, and their distribution represented as a box that extends from the 25^{th} to 75^{th} percentiles. The line in the middle of the box is plotted at the median.

SUPPLEMENTAL DATA

Supplemental Figure S1. Subcellular distribution of ER-GCAMP6-210 in *N. benthamiana* leaf epidermal cells.

Supplemental Figure S2. Confocal microscopy analyses revealed efficient ER-GCaMP6-210 expression in different organs of Arabidopsis stable transgenic pUBQ10-ER-GCaMP6-210.

Supplemental Figure S3. Cytosolic and ER Ca^{2+} transients in root-tip cells of Arabidopsis seedlings expressing the R-GECO1 (cytosolic and nuclear localized) and ER-GCaMP6-210 (ER localized) sensors in response to external ATP (0.1 mM) and NAA (0.01 mM), and Cameleon CRT-D4ER (ER localized) in response to external ATP (0.1 mM).

Supplemental Figure S4. Co-expression of ER-GCaMP6-210 and R-GECO1 in guard cells.

Supplemental Figure S5. Plant development is unchanged in the generated calcium indicators lines.

Supplemental Movie S1. Movie from a representative time series of a wt Arabidopsis seedling root tip expressing the ER-GCaMP6-210 (green) and R-GECO1 (magenta) sensors in response to external ATP. Scale bar 15 µm.

Supplemental Movie S2. Movie from two representative time series of wt Arabidopsis pollen tubes expressing the ER-GCaMP6-210 (green) and R-GECO1 (magenta) sensors. Scale bar 20 µm.

Supplemental Movie S3. Movie from a representative time series of a wt Arabidopsis mature plant expressing the ER-GCaMP6-210 (green) and R-GECO1 (magenta) sensors in response to leaf wounding. Scale bar 1 mm.

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COMPETING INTERESTS

The authors have declared that no competing interests exist.

599 **FIGURE LEGENDS:**

600 **Figure 1.** Simultaneous cytosolic and ER Ca^{2+} analyses in root tip at the single-cell level. **(A-D)**
601 Images of root-tip cells of a representative pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 seedling.
602 **(A)** Green: ER-GCaMP6-210 fluorescence. **(B)** Magenta: R-GECO1 fluorescence. **(C)** Overlay of (A)
603 and (B). Scale bar 25 μm. **(D)** Lower magnification image of (C). Scale bar 50 μm. **(E)** Exemplary
604 false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of cell 1 (C1) and cell
605 2 (C1) in root tips of seedlings expressing simultaneously the two Ca^{2+} sensors at steady-state and
606 during the Ca^{2+} transient induced by the treatment with 0.1 mM ATP for 3 min. **(F)** R-GECO1 and ER-
607 GCaMP6-210 normalized fluorescence changes of C1 over the time acquired under continuous
608 perfusion and treated with 0.1 mM ATP for 3 min, as indicated by the black box on the x-axis. **(F')**
609 same as panel (F) but x-axis, y-axis scales, and ranges adjusted. **(G)** R-GECO1 and ER-GCaMP6-
610 210 normalized fluorescence changes of C2 over the time acquired under continuous perfusion and
611 treated with 0.1 mM ATP for 3 min, as indicated by the black box on the x-axis. **(G')** same as panel (G)
612 but x-axis, y-axis scales, and ranges adjusted. The double arrow in (F') and (G') indicates the delay
613 time quantified in (H). **(H)** Mean delay of the fluorescence increase of the ER-GCaMP6-210 compared
614 to the fluorescence change of the R-GECO1 for C1 and C2 following 0.1 mM ATP administration. **(I)**
615 Maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals for C1 and C2 after 0.1 mM
616 ATP administration. **(J)** Time required to reach maximal peaks of ER-GCaMP6-210 and R-GECO1
617 fluorescence emissions for C1 and C2 after stimulus administration. **(K)** Time required to pass half-
618 maximal ER-GCaMP6-210 and R-GECO1 fluorescence signals during recovery after the stimulus. n =
619 7. **(L)** Exemplary false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of
620 C1 and C2 in root tips of seedlings expressing simultaneously the two Ca^{2+} sensors, at steady-state
621 and during the Ca^{2+} increase induced by the treatment with 0.01 mM NAA for 3 min. **(M)** R-GECO1
622 and ER-GCaMP6-210 normalized fluorescence changes of C1 over the time acquired under
623 continuous perfusion and treated with 0.01 mM NAA for 3 min, as indicated by the black box on the x-
624 axis. **(M')** same as panel (M) but x-axis, y-axis scales, and ranges adjusted. **(N)** R-GECO1 and ER-

GCaMP6-210 normalized fluorescence changes of C2 over the time acquired under continuous perfusion and treated with 0.01 mM NAA for 3 min, as indicated by the black box on the x-axis. **(N')** same as panel (N) but x-axis, y-axis scales, and ranges adjusted. The double arrow in (M') and (N') indicates the delay time quantified in (O). **(O)** Mean delay of the fluorescence increase of the ER-GCaMP6-210 compared to the fluorescence change of the R-GECO1 for C1 and C2 following 0.01 mM NAA administration. **(P)** Maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals for C1 and C2 after 0.01 mM NAA administration. **(Q)** Time required to reach maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals for C1 and C2 after stimulus administration. **(R)** Time required to pass half-maximal ER-GCaMP6-210 and R-GECO1 fluorescence emissions during recovery after the stimulus. n = 6. Error bars = SD, ns = not significant, *p ≤ 0.05, **p ≤ 0.005, ***p ≤ 0.0005 (Student's *t*-test).

Figure 2. Simultaneous cytosolic and ER Ca^{2+} analyses in root-tip cells treated with the P-Type IIA inhibitor cyclopiazonic acid (CPA). **(A)** Green: ER-GCaMP6-210 fluorescence, Magenta: R-GECO1 fluorescence, and overlay. Scale bar 50 µm. **(B)** Examples of false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of the selected cell (dashed rectangle in (A)) in root tips of seedlings expressing simultaneously the two Ca^{2+} sensors at steady-state and during the Ca^{2} treatment with 25 µM CPA for 3 min. **(C)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of the selected cell over the time acquired under continuous perfusion and treated with 25 µM CPA for 3 min, as indicated by the black box on the x-axis. **(C')** R-GECO1 and ER-GCaMP6-210 normalized fluorescence of the selected cell over the time acquired under continuous perfusion and treated with DMSO (the CPA solvent) as a control for 3 min, as indicated by the black box on the x-axis. **(D)** same as panel (C) but x-axis, y-axis scales, and ranges adjusted. The double arrow in (D) indicates the delay time quantified in (E). **(E)** Mean delay of the fluorescence increase of the R-GECO1 following the ER-GCaMP6-210 fluorescence decrease. **(F)** The maximal peak of R-GECO1

650 and the minimal level of ER-GCaMP6-210 fluorescence signals for the selected cells after CPA
651 administration. n = 5. Error bars = SD.

652

653 **Figure 3.** Simultaneous ER-GCaMP6-210 and R-GECO1 fluorescence signals in growing pollen
654 tubes. **(A-C)** Images of a representative pollen tube. **(A)** Green: ER-GCaMP6-210 fluorescence. **(B)**
655 Magenta: R-GECO1 fluorescence. **(C)** Overlay of (A) and (B). Scale bar 20 µm. **(D-F)** Kymograph
656 extracted from both fluorescence signals frames by observing the temporal evolution of the pixel line
657 highlighted in yellow. **(D)** Kymograph of 1200 s acquisitions extracted for the R-GECO1 images. **(E)**
658 Kymograph of 1200 s acquisitions extracted for the ER-GCaMP6-210 images. **(F)** Overlay of (D) and
659 (E). (a) = selected ROI for analyses of pollen tube tip fluorescence signals. (b) selected ROI for
660 analyses of pollen tube shank fluorescence signals. **(G)** Representative oscillations of ER-GCaMP6-
661 210 and R-GECO1 fluorescences in the tip (ROI "a"). **(G')** same as panel (G) but x-axis, y-axis scales,
662 and ranges adjusted. **(H)** Normalized cross-correlation analysis between R-GECO1 and ER-GCaMP6-
663 210 averaged in temporal sliding windows of 80 s over n = 9 measurements. The peak-value is 0.28 ±
664 0.11, and it is reached at positive delays, implying that the fast oscillations in the cytosol (R-GECO1)
665 are anticipated by the ones in the ER (ER-GCaMP6-210). **(I)** Distribution of the average delays by
666 locating in time the maximum of the cross-correlations, for each experiment considered. The global
667 temporal lag is 6 ± 2 s. **(J)** Distribution of the period of the fast oscillations in the ER/Cytosol. It is
668 defined by doubling the temporal distance at which the signals correlate (maximum in G) and anti-
669 correlates (minimum). The average is 30 ± 11 s. **(K)** Representative ER-GCaMP6-210 and R-GECO1
670 fluorescences in the shank (ROI "b"). **(K')** same as panel (K) but x-axis, y-axis scales and ranges
671 adjusted. The double arrow in (K') indicates the delay time quantified in (L). **(L)** Mean delay of the
672 fluorescence increase of the ER-GCaMP6-210 compared to the fluorescence change of the R-
673 GECO1. **(M)** Time required to pass half-maximal ER-GCaMP6-210 and R-GECO1 fluorescence
674 emissions during recovery after the spike. n = 5. Error bars = SD, *p ≤ 0.05 (Student's *t*-test).

675

676 **Figure 4.** Simultaneous cytosolic and ER Ca^{2+} analyses in leaves of adult plants challenged with leaf
677 wounding. **(A-C)** Images of a representative pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 mature
678 plant. **(A)** Green: ER-GCaMP6-210 fluorescence. **(B)** Magenta: R-GECO1 fluorescence. **(C)** Overlay
679 of (A) and (B). Scale bar 1 mm. **(D)** Examples of false-color images illustrate R-GECO1 (magenta) and
680 ER-GCaMP6-210 (green) in a local wounded leaf ("l"). **(F)** R-GECO1 and ER-GCaMP6-210
681 normalized fluorescence changes of the local leaf ("l") over the time after its wounding (red arrow). **(E)**
682 Examples of false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of a
683 distal leaf of the same wounded plant of (D). **(G)** R-GECO1 and ER-GCaMP6-210 normalized
684 fluorescence changes of a distal leaf ("d") over the time after wounding of "l". **(H)** Maximal peaks of
685 ER-GCaMP6-210 and R-GECO1 fluorescence signals in the local and distal leaves after wounding. **(I)**
686 Time required to reach maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals in the
687 local and distal leaves after wounding. n = 5. **(L-M)** Digitally extracted images of a representative
688 pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 plant for comparative analyses of the temporal
689 evolution of Ca^{2+} dynamics in the cytosol and ER compartments in response to leaf wounding. **(L)**
690 Temporal analysis of the $\Delta F/F_0$ signal peak in the leaves for the R-GECO1. The temporal window
691 analyzed is of 750 s. The color-bar encodes the time at which the maximum signal is recorded in each
692 pixel. The wounded leaf is colored with blue, since it peaks at around 30 s. The distal leaf is reddish
693 because the maximum signal happens at 500 s. The other two leaves showed a delayed response, at
694 750 s. **(M)** Same analysis for the ER-GCaMP6-210 as in (L). The wounded leaf responded earlier (200
695 s, violet) than the distal one (750 s, green). Error bars = SD, *p ≤ 0.05, **p ≤ 0.005 (Student's *t*-test).

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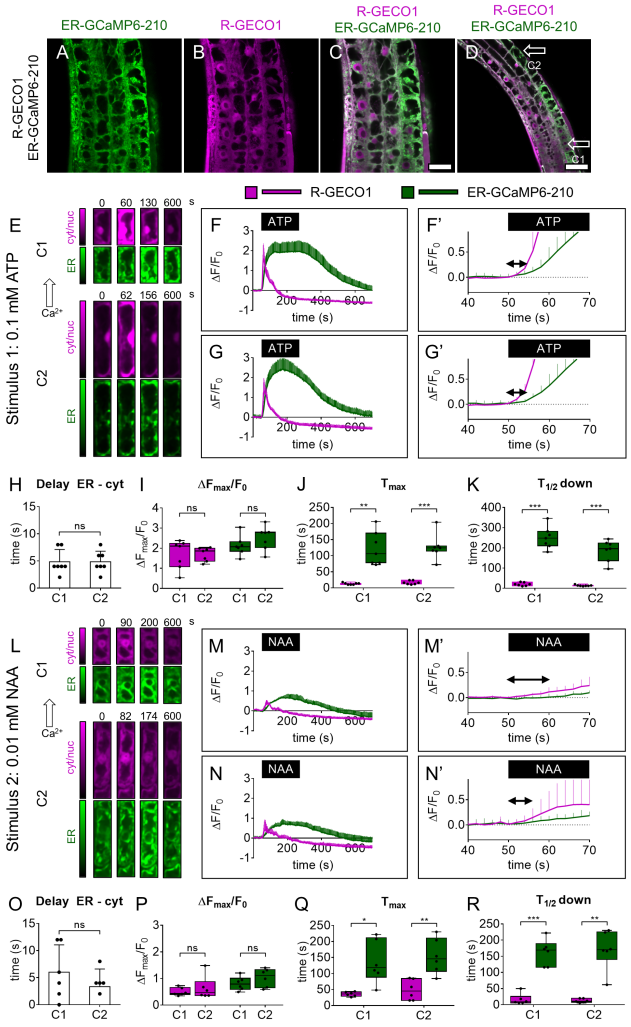

Figure 1. Simultaneous cytosolic and ER Ca^{2+} analyses in root tip at the single-cell level. **(A-D)** Images of root-tip cells of a representative pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 seedling. **(A)** Green: ER-GCaMP6-210 fluorescence. **(B)** Magenta: R-GECO1 fluorescence. **(C)** Overlay of (A) and (B). Scale bar 25 μm. **(D)** Lower magnification image of (C). Scale bar 50 μm. **(E)** Exemplary false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of cell 1 (C1) and cell 2 (C1) in root tips of seedlings expressing simultaneously the two Ca^{2+} sensors at steady-state and during the Ca^{2+} transient induced by the treatment with 0.1 mM ATP for 3 min. **(F)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of C1 over the time acquired under continuous perfusion and treated with 0.1 mM ATP for 3 min, as indicated by the black box on the x-axis. **(F')** same as panel (F) but x-axis, y-axis scales, and ranges adjusted. **(G)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of C2 over the time acquired under continuous perfusion and treated with 0.1 mM ATP for 3 min, as indicated by the black box on the x-axis. **(G')** same as panel (G) but x-axis, y-axis scales, and ranges adjusted. The double arrow in (F') and (G') indicates the delay time quantified in (H). **(H)** Mean delay of the fluorescence increase of the ER-GCaMP6-210 compared to the fluorescence change of the R-GECO1 for C1 and C2 following 0.1 mM ATP administration. **(I)** Maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals for C1 and C2 after 0.1 mM ATP administration. **(J)** Time required to reach maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence emissions for C1 and C2 after stimulus administration. **(K)** Time required to pass half-maximal ER-GCaMP6-210 and R-GECO1 fluorescence signals during recovery after the stimulus. n = 7. **(L)** Exemplary false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of C1 and C2 in root tips of seedlings expressing simultaneously the two Ca^{2+} sensors, at steady-state and during the Ca^{2+} increase induced by the treatment with 0.01 mM NAA for 3 min. **(M)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of C1 over the time acquired under continuous perfusion and treated with 0.01 mM NAA for 3 min, as indicated by the black box on the x-axis. **(M')** same as panel (M) but x-axis, y-axis scales, and ranges adjusted. **(N)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of C2 over the time acquired under continuous perfusion and treated with 0.01 mM NAA for 3 min, as indicated by the black box on the x-axis. **(N')** same as panel (N) but x-axis, y-axis scales, and ranges adjusted. The double arrow in (M') and (N') indicates the delay time quantified in (O). **(O)** Mean delay of the fluorescence increase of the ER-GCaMP6-210 compared to the fluorescence change of the R-GECO1 for C1 and C2 following 0.01 mM NAA administration. **(P)** Maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals for C1 and C2 after 0.01 mM NAA administration. **(Q)** Time required to reach maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals for C1 and C2 after stimulus administration. **(R)** Time required to pass half-maximal ER-GCaMP6-210 and R-GECO1 fluorescence emissions during recovery after the stimulus. n = 6. Error bars = SD, ns = not significant, *p ≤ 0.05, **p ≤ 0.005, ***p ≤ 0.0005 (Student's *t*-test).

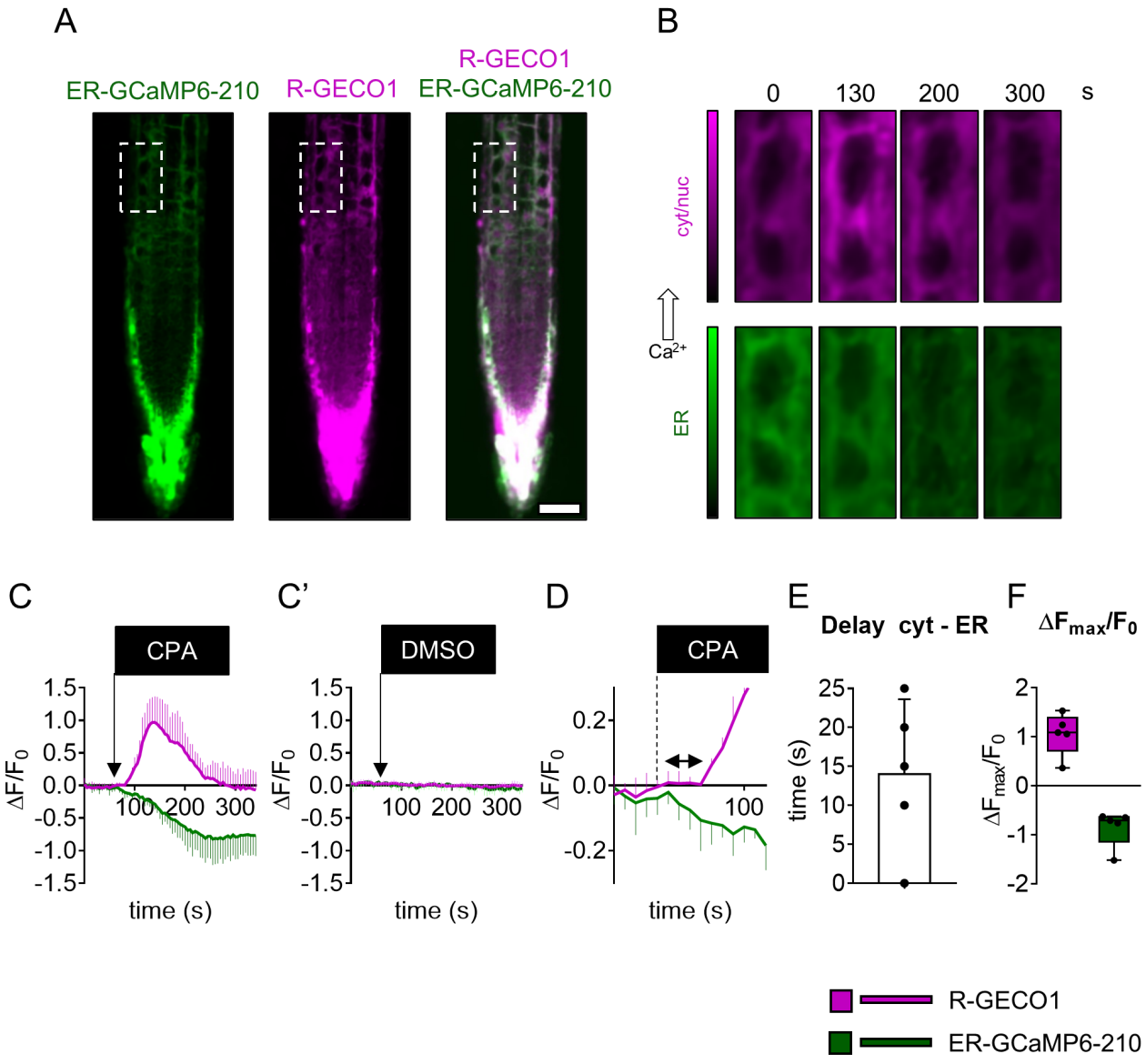

Figure 2. Simultaneous cytosolic and ER Ca^{2+} analyses in root-tip cells treated with the P-Type IIA inhibitor cyclopiazonic acid (CPA). **(A)** Green: ER-GCaMP6-210 fluorescence, Magenta: R-GECO1 fluorescence, and overlay. Scale bar 50 µm. **(B)** Examples of false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of the selected cell (dashed rectangle in (A)) in root tips of seedlings expressing simultaneously the two Ca^{2+} sensors at steady-state and during the Ca^2 treatment with 25 µM CPA for 3 min. **(C)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of the selected cell over the time acquired under continuous perfusion and treated with 25 µM CPA for 3 min, as indicated by the black box on the x-axis. **(C')** R-GECO1 and ER-GCaMP6-210 normalized fluorescence of the selected cell over the time acquired under continuous perfusion and treated with DMSO (the CPA solvent) as a control for 3 min, as indicated by the black box on the x-axis. **(D)** same as panel (C) but x-axis, y-axis scales, and ranges adjusted. The double arrow in (D) indicates the delay time quantified in (E). **(E)** Mean delay of the fluorescence increase of the R-GECO1 following the ER-GCaMP6-210 fluorescence decrease. **(F)** The maximal peak of R-GECO1 and the minimal level of ER-GCaMP6-210 fluorescence signals for the selected cells after CPA administration. n = 5. Error bars = SD.

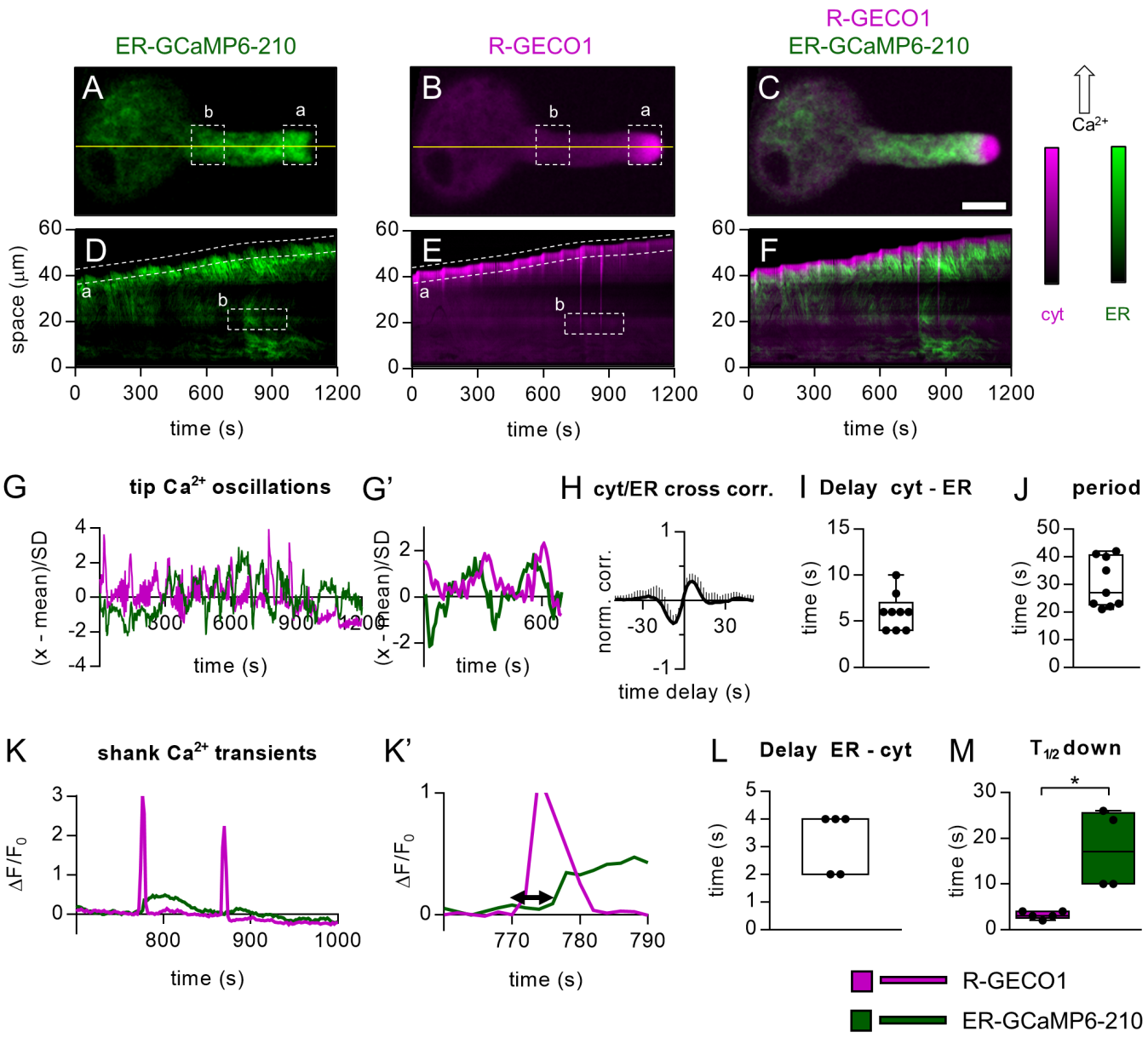

Figure 3. Simultaneous ER-GCaMP6-210 and R-GECO1 fluorescence signals in growing pollen tubes. **(A-C)** Images of a representative pollen tube. **(A)** Green: ER-GCaMP6-210 fluorescence. **(B)** Magenta: R-GECO1 fluorescence. **(C)** Overlay of (A) and (B). Scale bar 20 µm. **(D-F)** Kymograph extracted from both fluorescence signals frames by observing the temporal evolution of the pixel line highlighted in yellow. **(D)** Kymograph of 1200 s acquisitions extracted for the R-GECO1 images. **(E)** Kymograph of 1200 s acquisitions extracted for the ER-GCaMP6-210 images. **(F)** Overlay of (D) and (E). (a) = selected ROI for analyses of pollen tube tip fluorescence signals. (b) selected ROI for analyses of pollen tube shank fluorescence signals. **(G)** Representative oscillations of ER-GCaMP6-210 and R-GECO1 fluorescences in the tip (ROI "a"). **(G')** same as panel (G) but x-axis, y-axis scales, and ranges adjusted. **(H)** Normalized cross-correlation analysis between R-GECO1 and ER-GCaMP6-210 averaged in temporal sliding windows of 80 s over n = 9 measurements. The peak-value is 0.28 ± 0.11, and it is reached at positive delays, implying that the fast oscillations in the cytosol (R-GECO1) are anticipated by the ones in the ER (ER-GCaMP6-210). **(I)** Distribution of the average delays by locating in time the maximum of the cross-correlations, for each experiment considered. The global temporal lag is 6 ± 2 s. **(J)** Distribution of the period of the fast oscillations in the ER/Cytosol. It is defined by doubling the temporal distance at which the signals correlate (maximum in G) and anti-correlates (minimum). The average is 30 ± 11 s. **(K)** Representative ER-GCaMP6-210 and R-GECO1 fluorescences in the shank (ROI "b"). **(K')** same as panel (K) but x-axis, y-axis scales and ranges adjusted. The double arrow in (K') indicates the delay time quantified in (L). **(L)** Mean delay of the fluorescence increase of the ER-GCaMP6-210 compared to the fluorescence change of the R-GECO1. **(M)** Time required to pass half-maximal ER-GCaMP6-210 and R-GECO1 fluorescence emissions during recovery after the spike. n = 5. Error bars = SD, *p ≤ 0.05 (Student's *t*-test).

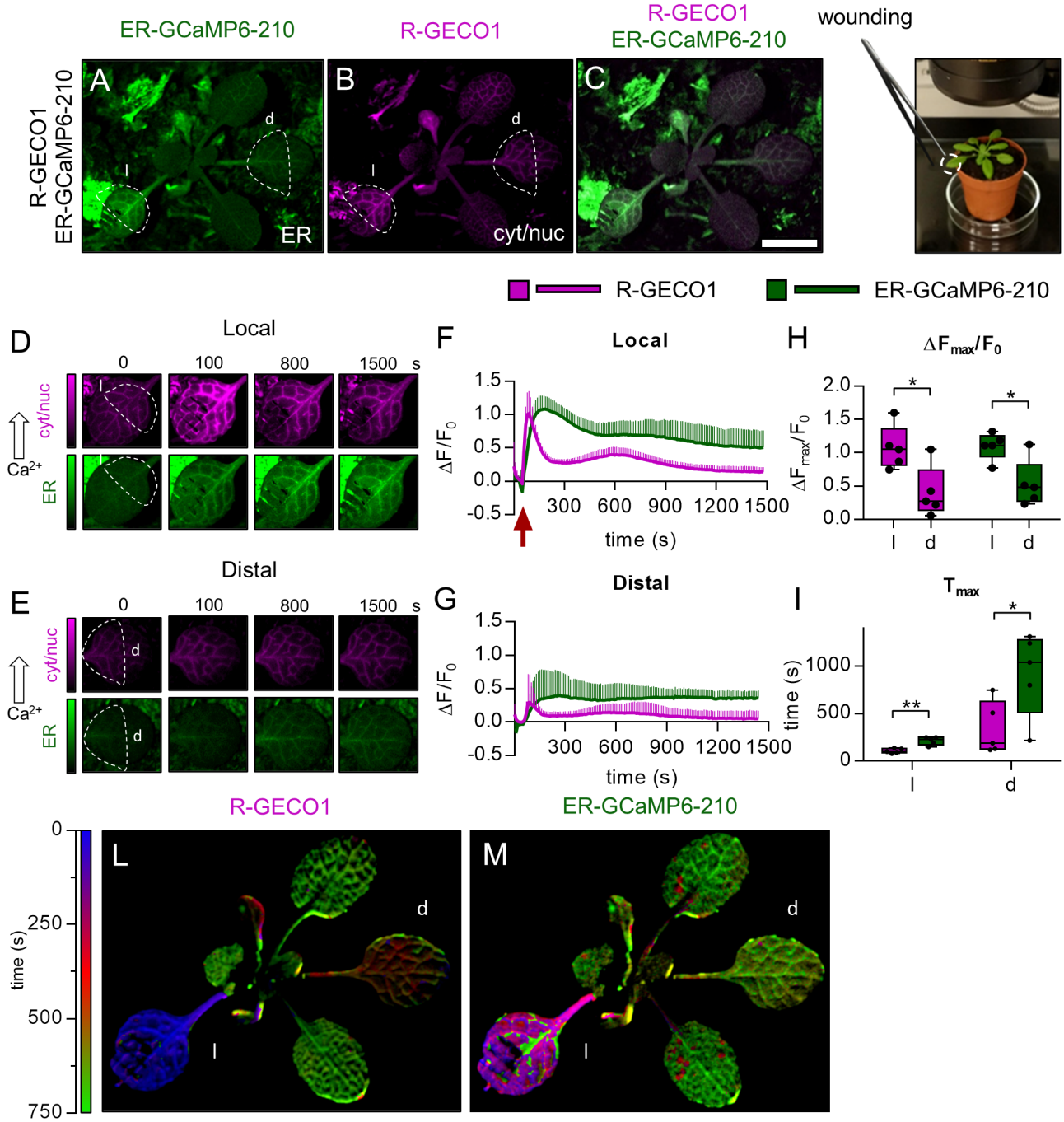

Figure 4. Simultaneous cytosolic and ER Ca^{2+} analyses in leaves of adult plants challenged with leaf wounding. **(A-C)** Images of a representative pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 mature plant. **(A)** Green: ER-GCaMP6-210 fluorescence. **(B)** Magenta: R-GECO1 fluorescence. **(C)** Overlay of (A) and (B). Scale bar 1 mm. **(D)** Examples of false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) in a local wounded leaf ("l"). **(F)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of the local leaf ("l") over the time after its wounding (red arrow). **(E)** Examples of false-color images illustrate R-GECO1 (magenta) and ER-GCaMP6-210 (green) of a distal leaf of the same wounded plant of (D). **(G)** R-GECO1 and ER-GCaMP6-210 normalized fluorescence changes of a distal leaf ("d") over the time after wounding of "l". **(H)** Maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals in the local and distal leaves after wounding. **(I)** Time required to reach maximal peaks of ER-GCaMP6-210 and R-GECO1 fluorescence signals in the local and distal leaves after wounding. n = 5. **(L-M)** Digitally extracted images of a representative pUBQ10-ER-GCaMP6-210 x pUBQ10-R-GECO1 plant for comparative analyses of the temporal evolution of Ca^{2+} dynamics in the cytosol and ER compartments in response to leaf wounding. **(L)** Temporal a nalysis of the $\Delta F/F_0$ signal peak in the leaves for the R-GECO1. The temporal window analyzed is of 750 s. The color-bar encodes the time at which the maximum signal is recorded in each pixel. The wounded leaf is colored with blue, since it peaks at around 30 s. The distal leaf is reddish because the maximum signal happens at 500 s. The other two leaves showed a delayed response, at 750 s. **(M)** Same analysis for the ER-GCaMP6-210 as in (L). The wounded leaf responded earlier (200 s, violet) than the distal one (750 s, green). Error bars = SD, *p ≤ 0.05, **p ≤ 0.005 (Student's *t*-test).

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