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The control exerted by ABA on lignan biosynthesis in flax (*Linum usitatissimum* L.) is modulated by a Ca²⁺ signal transduction involving the calmodulin-like LuCML15b

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Abstract

The *LuPLR1* gene encodes a pinoresinol lariciresinol reductase responsible for the biosynthesis of (+)-secoisolariciresinol, a cancer chemopreventive lignan, highly accumulated in the seedcoat of flax (*Linum usitatissimum* L.). Absciscic acid (ABA) plays a key role in the regulation of *LuPLR1* gene expression and lignan accumulation in both seeds and cell suspensions, which require two *cis*-acting elements (ABRE and MYB2) for this regulation. Ca^{2+} is a universal secondary messenger involved in a wide range of physiological processes including ABA signaling. Therefore, Ca^{2+} may be involved as a mediator of *LuPLR1* gene expression and lignan biosynthesis regulation exerted by ABA. To test the potential implication of Ca^{2+} signaling, a pharmacological approach was conducted using both flax cell suspensions and maturing seed systems coupled with a β -glucuronidase reporter gene experiment, RT-qPCR analysis, lignan quantification as well as Ca^{2+} fluorescence imaging. Exogenous ABA application results in an increase in the intracellular Ca^{2+} cytosolic concentration, originating mainly from the extracellular medium. Promoter-reporter deletion experiments suggest that the ABRE and MYB2 *cis*-acting elements of the *LuPLR1* gene promoter functioned as Ca^{2+} -sensitive sequences involved in the ABA-mediated regulation. The use of specific inhibitors pointed the crucial roles of the Ca^{2+} sensors calmodulin-like proteins and Ca^{2+} -dependent protein kinases in this regulation. This regulation appeared conserved in the two different studied systems, i.e. cell suspensions and maturing seeds. A calmodulin-like, LuCML15b, identified from gene network analysis is proposed as a key player involved in this signal transduction since RNAi experiments provided direct evidences of this role. Taken together, these results provide new information on the regulation of plant defense and human health-promoting compounds, which could be used to optimize their production.

Keywords: Absciscic acid, Calcium, Calmodulin, Flax, Lignan, Pinoresinol-lariciresinol reductase

1. Introduction

Over the last decades, flax seed coat lignans have been of growing significance, particularly for their numerous benefits on human health (Lainé et al., 2009; Oomah, 2001; Westcott and Muir, 2003). Lignans are an important class of 8-8' linked phenylpropanoid (C₆C₃) dimers widely distributed across the vascular plants. They are supposed to play a role in plant defense (Corbin et al., 2017; Gang et al., 1999). Flaxseeds represent one of the richest source and are considered as an attractive model to study lignan biochemical and/or physiological functions, particularly since its seed coats accumulate (+)-secoisolariciresinol lignan derivatives in high amount. However, flaxseed lignans have been well studied and characterized for their beneficial properties on human health (Hano et al., 2013; Lainé et al., 2009) but their physiological functions and regulation of biosynthesis *in planta* remain elusive. The direct *in vivo* implication of the *LuPLR1* gene and its rate-limiting action on (+)-secoisolariciresinol diglucoside (SDG) biosynthesis has been evidenced by RNAi technology applied to the down-regulation of the *LuPLR1* gene expression in developing flax seeds (Renouard et al., 2014). Its gene expression regulation by abscisic acid (ABA) during seed maturation and in flax cell suspensions have been evidenced (Corbin et al., 2013b, 2013a; Renouard et al., 2012a). On the contrary, a second PLR isoform (i.e., LuPLR2) was functionally characterized in flax, and its involvement in the biosynthesis of (-)-yatein, a lignan deriving from the opposite (-)-secoisolariciresinol enantiomer, in flax leaves evidenced (Corbin et al., 2017). However, the end product of this alternative pathway (-)-yatein is barely detectable in both flax seeds and cell suspensions, whereas (-)-secoisolariciresinol, the LuPLR2 product, is only accumulated in minor amount in seed and not detected in cell suspension (Corbin et al., 2017; Corbin et al., 2018).

In plants, ABA plays a critical role in the regulation of seed development and maturation but is also involved in other physiological and developmental processes such as seedling growth, flowering or environmental adaptation to biotic stress or abiotic stress such as drought, salt and cold (Finkelstein et al., 2002; Frey et al., 2004; Gutierrez et al., 2007). As many as 10% of the genes of *Arabidopsis thaliana* are responsive to ABA (Finkelstein et al., 2002), some of which are associated with seed development, maturation processes or stress responses such as those involved in the phenylpropanoid pathway (Finkelstein et al., 2002).

ABA actions are mediated by changes in the expression of target genes harboring specific *cis*-acting elements in their promoters (Abe et al., 2003; Busk and Pagès, 1998; Finkelstein et al., 2002; Gutierrez et al., 2007). Such *cis*-acting elements have been identified and characterized

in the promoter of the *LuPLR1* gene encoding the pinoresinol lariciresinol reductase involved in the biosynthesis of (+)-secoisolariciresinol, the main lignan under its diglucoside form accumulated in flax seeds (Hano et al., 2006b). Studies with immature flaxseed or cell cultures, have evidenced an ABA-mediated transcriptional activation of the *LuPLR1* gene acting through two important *cis*-acting sequences (ABRE and MYB2) (Corbin et al., 2013a, 2013b, Renouard et al., 2014, 2012b).

Calcium (Ca^{2+}) is known to be an important second messenger in abscisic acid (ABA) signal transduction, through the action of Ca^{2+} sensors including Ca^{2+} -dependent protein kinases (CDPKs), calmodulin (CaM) and CaM-related proteins (Zhao et al., 2011b). Ca^{2+} is a ubiquitous secondary messenger involved in a wide range of signaling cascades (Lecourieux et al., 2006) and a convergence point of many different signaling pathways (Tuteja and Mahajan, 2007) especially in development and stress (Arimura and Maffei, 2010; Hepler, 2005; Reddy et al., 2011). This ion could represent up to 5% of the plant dry weight (White and Broadley, 2003) but could be very toxic at high concentrations so its cytoplasmic concentration should be tightly controlled at both temporal and spatial levels. Consequently, there is a gradient of concentration on both sides of the plasma membrane with a high Ca^{2+} concentration in the extracellular medium, as well as in cellular organelles such as the central vacuole, which represents the largest intracellular Ca^{2+} store (Batistič and Kudla, 2012; Pottosin and Schönknecht, 2007). Upon signal perception, a transient increase occurs in the intracellular Ca^{2+} concentration, triggering a signaling cascade (Batistič and Kudla, 2012; Tuteja, 2009). These cytosolic Ca^{2+} ions could originate from either extracellular or intracellular stores and the use of specific Ca^{2+} channel inhibitors or extracellular chelators enables their origin to be determined.

To date there is only few examples for the role of Ca^{2+} signaling in the regulation of plant secondary metabolism and no one reports on lignan (*sensu stricto*) biosynthesis. The transcriptional regulation of the genes related to lignan biosynthesis has been investigated rarely although such data could yield information about the role of these compounds *in planta*. Here, we explored the possible involvement of Ca^{2+} ion fluxes and Ca^{2+} signaling in this ABA-mediated transcriptional regulation of the lignan biosynthesis in flax cell suspensions and maturing seeds.

2. Materials and Methods

2.1. Plant materials

All flax (*Linum usitatissimum* L.) plant material was generated from the linseed cultivar Barbara supplied by Coopérative Terre de Lin (St Pierre le Viger, France). The wild type LuCY1 and the transgenic promoter *LuPLR1*:GUS (*uidA* β -glucuronidase reporter gene under the control of the complete version of the *LuPLR1* gene promoter) are cell suspension cultures of *Linum usitatissimum* cv Barbara established from hypocotyl-derived calli and cultured in M2 medium derived from the MS medium (Murashige and Skoog, 1962) supplemented with 3% (w/v) sucrose, 8.88 μ M benzylaminopurine and 2.68 μ M α -naphthalene acetic acid but depleted or modified in Ca^{2+} concentration for the requirements of the experiments. All suspension cultures were incubated on a gyratory shaker at 120 rpm in darkness at 25°C and subcultured every 14 days as described in Hano et al. (2006a) (Hano et al., 2006a) with 5 g of cells in 100 ml of medium in 250 ml Erlenmeyer flasks.

2.2. Plasmid constructs

Mutated versions of the *LuPLR1* gene promoter in which the ABRE and/or MYB2 *cis*-acting elements were disrupted (described in (Corbin et al., 2013b)).
RNAi vector targeting CML15b (Lus10027243) was obtained as follow: a 155bp fragment of the CML15b coding was amplified by PCR using the following specific primers: iCML15b-F (5'-CACCGTTCGATAGGGACGGGAAC-3' and iCML15b-R (5'-TCGAGAACTCCGTGAAGCTAA-3'), purified (Gel extraction kit, Thermo) and subcloned into the pENTR/D TOPO cloning vector (Invitrogen) following the manufacturer's recommendations. This target sequence was designed using the pssRNAit server tool dedicated to the design of effective and specific (limiting off-target silencing) and non-toxic siRNAs for plant RNAi (Dai and Zhao, 2011). The resulting constructs was then used for transfer into the pP7FWG2 destination vector (Karimi et al., 2002) by using the Gateway technology (Invitrogen) to obtain the iCML15b vector (T-DNA scheme). The construct was sequenced (MWG Biotech). The plasmids were then transferred into the disarmed *A. tumefaciens* strain GV3101 (pGV2260) with *E. coli* strain HB101 (pRK2013) as helper.

2.3. Transient cell transformation

The protocol for transient expression described by Berger et al. (2007) (Berger et al., 2007) were used. Briefly, a single colony of *A. tumefaciens* strain GV3101 with the binary vector

was inoculated into YEB liquid medium containing 50 mg ml⁻¹ kanamycin and grown at 28°C in a gyratory shaker (180 rpm) to an absorbance of 1.5 at 600 nm. Bacterial cells were harvested by centrifugation at 6,000 g for 5 min and washed twice with 10 ml of fresh M2 culture medium. After 5 min of centrifugation at 6,000 g, the pellet of bacterial cells was resuspended in 1 ml of medium containing 20 µM acetosyringone (Sigma, St Quentin Fallavier, France). Ten-day-old flax cell suspensions were harvested by centrifugation at 3,000 g for 5 min, rinsed three times with buffer medium and resuspended at a 1:4 dilution in 2.5 ml of fresh buffer medium in six-well sterile culture plates. Fifty µl of the resuspended bacterial cells was added to the flax cell suspension. After 24 h of co-culture (dark, 25°C, 120 rpm), each cell suspension was treated with chemicals.

2.4. Chemicals and cell suspension treatments

All chemicals used in the present study were purchased from Sigma (St Quentin Fallavier, France). After the exponential growth phase (day 10), cell suspension cultures were transferred into the incubation medium (0.5 M mannitol, 10 mM PIPES, pH 5.8) and subjected to the different chemical treatments. The same volume (25 µL) of 100X concentrated stock solution of each chemical reagent (dissolved in DMSO and diluted with incubation buffer at the mentioned concentration) was added to 2.5 ml of cell suspension (125 mg) cultured in sterile six-well culture plates. Control cells were inoculated with the same volume of DMSO-containing-buffer medium. Microplates were maintained on a gyratory shaker at 120 rpm in darkness at 25°C. Cells were observed under a microscope or collected 24 h after treatment for RNA extraction and gene expression measurement, 48 h for β-glucuronidase analysis and 96 h for lignan quantification by centrifugation at 3,000 g for 10 min and stored at -80°C until further analysis. The growth of cell suspensions during a cycle was measured by the packed cell volume (PCV) method. Briefly, PCV was determined following centrifugation of 20 mL of cell suspension in a graduated conical centrifuge tube of 50 mL at 200 g for 5 min. The volume of sedimented cells was measured and the PCV was calculated as percentage of sedimented cells vs total volume.

2.5. Immature seed treatments

Capsules containing immature developing flaxseeds (stage 2, (Hano et al., 2006b)) were submitted to exogenous administration of (±) *cis-trans* ABA (50 µM) combined or not with staurosporine (5 µM) or calmidazolium (25 µM) as described by Renouard et al. (2012)

(Renouard et al., 2012b). Briefly, secondary inflorescence stems of wild or transgenic flax plants (stage 2) were harvested and placed directly in deionized water. Capsules with a remaining peduncle (around 1 cm) were pruned from stems and immediately size-sorted. Three fresh capsules for each treatment were placed in one well of a 96-well microplate and maintained at 25°C under a 16-h photoperiod. After uptake, capsules were dissected, and seeds (*ca.* 60 per condition) were stored at –80°C until their use for RT-qPCR and phytochemical analysis ((+)-secoisolariciresinol and ABA contents).

2.6. β -glucuronidase activity

β -glucuronidase (GUS) activity assays were performed by measuring 4-methylumbelliferone (4-MU, Sigma, St Quentin Fallavier, France) produced from the glucuronide precursor 4-methylumbelliferyl- β -D-glucuronide (4-MUG, Sigma, St Quentin Fallavier, France). Fifty mg of cells were ground and homogenized in 500 μ L of extraction buffer containing 50 mM sodium phosphate; pH 7.0, 10 mM EDTA, 0.1% (v/v) Triton X-100, 0.1% sarcosyl, and 10 mM β -mercaptoethanol at 4°C. Following 15 min of centrifugation at 12,000 *g* at 4°C, GUS activity was quantified in the supernatant using a fluorescence spectrophotometer (BioRad, Marnes-la-Coquette, France). Protein concentrations were determined using a fluorometer and the Quant-iT Protein Assay Kit (Invitrogen) adapted for the Qubit fluorometer according to the manufacturer's protocol. β -glucuronidase activity was expressed as RFU (Relative Fluorescence Unit) per mg of soluble proteins.

2.7. RNA extraction and quantitative PCR

Total RNA was extracted from 100 mg of ground frozen tissues using the RNeasy Plant Kit (Qiagen, Courtabeuf, France) and the RNase free DNase set (Qiagen, Courtabeuf, France) in order to eliminate DNA contamination, as described in Hano et al. (2006b) (Hano et al., 2006b). RNAs were quantified using a fluorometer and the Quant-iT RNA Assay Kit (Invitrogen) adapted for the Qubit fluorometer according to the manufacturer's protocol. Reverse transcription was performed using the First-strand cDNA synthesis kit (Thermo, Villebon sur Yvette, France).

Quantitative PCR was performed in 96-well plates with a PikoReal real time PCR system (ThermoFisher) using the DyNAmoColorFlash SYBR Green qPCR Kit (ThermoFisher, Villebon sur Yvette, France). The reaction was carried out in 20 μ L (1 μ L diluted cDNAs, 10 μ L of 2x SYBR Green mix and primer pairs at 1 μ M). All PCR reactions followed the same

protocol: 7 min at 95°C, 40 cycles of 10 s at 95°C, 10 s at 55°C and 30 s at 72°C. The specificity of the amplified product was confirmed for each primer pair using a melting curve. Data analysis was carried out with PikoReal software. Three biological replicates and two technical repetitions were performed for each sample. Relative transcript levels of the *LuPLR1* and CML15b (*Lus10027243*) genes were obtained using the specific primers qLuPLR1-F: 5'-TATGGAGATGGCAACGTCAA-3', qLuPLR1-R: 5'-TTGGTTGCCTGAGAGCTTTT-3', qCML15b-F: 5'-GGCAACGAGATACACGACCT-3' and qCML15bR: 5'-CCCTATCGAACAGCTGGAAG-3', designed with Primer3 software (Koressaar and Remm, 2007), and normalized using the comparative $\Delta\Delta C_q$ method using two validated housekeeping reference genes selected by Huis *et al.*, 2010b (Huis *et al.*, 2010): *LuCYC* encoding cyclophilin (using primers qLuCYC-F: 5'-TGATTGCGGTCAGCTGTAG-3' and qLuCYC-R: 5'-AGGTGAAACGCTAGGCAGAA-3') and *LuETIF5A* encoding an Eukaryotic Translation Initiation Factor 5A (using primers qLuETIF5A-F: 5'-TGCCACATGTGAACCGTACT-3' and qLuETIF5A-R: 5'-CTTTACCCTCAGCAAATCCG-3').

2.8. Gene expression network

Putative coding sequences were searched through BLAST-P against the *L. usitatissimum* proteome available on Phytozome database. Public RNAseq data were downloaded from <http://142.244.185.16/downloads/RNASeq/> and normalized using the geometric mean of cyclophilin *LuCYC* (*Lus10012167*) and the eukaryotic translation initiation factor 3H *LuETIF3H* (*Lus10007054*) gene expressions followed by log₂ transformation. Visualization and data analysis were carried out with MeV 4.9.0 (Saeed *et al.*, 2006). Hierarchical clustering was performed with the Pearson uncentered metric with the average linkage clustering method. The complete list of these genes and their Phytozome numbers is presented in Table S1. A gene expression correlation matrix was then constructed using pair-wise Pearson correlation coefficients (PCC). A co-expression network was visualized using Cytoscape 2.8.3 software representing only significant PCC values at $p < 0.05$ with a cut-off value of 0.95. Colors from yellow to red indicate increasing PCC values where the connection size indicates the strength of the connection.

2.9. *Secoisolariciresinol* extraction and HPLC analysis

The secoisolariciresinol extraction procedure described by Renouard et al. (2010) (Renouard et al., 2010) was adapted for lignan extraction from flax cell suspensions and immature seeds. Briefly, 500 mg of lyophilized cells were incubated with 20 ml of 80% (v/v) aqueous methanol, for 2 h at 60°C under stirring in a water bath. Following centrifugation, the solid residue was discarded and the supernatant was subsequently evaporated to dryness at 40°C and then resuspended in 1 ml of 0.1 M citrate-phosphate pH 4.8 buffer containing 5 units.ml⁻¹ of β-glucosidase from almonds (Sigma, St Quentin Fallavier, France) for secoisolariciresinol release during 4 h at 40°C. It was finally extracted twice with ethyl acetate, evaporated to dryness, resuspended in ethanol and filtered (0.45 μm, Millipore, Molsheim, France) before HPLC injection. The HPLC procedure was described in our previous work (Corbin et al., 2013a).

2.10. ABA extraction and quantification

The ABA extraction from whole seeds was based on the procedure of Agrawal et al. (2001) (Agrawal et al., 2001). Immature seeds (100 mg FW) were weighed, freeze-dried for 3 h, and extracted for 16 h at 4°C in the dark with MilliQ (Millipore, Molsheim, France) water (water/tissue ratio 50:1, v/w). ABA was quantified using a Phytodetek ABA ELISA kit (Agdia, Grigny, France) with (±) *cis-trans* ABA (Sigma, St Quentin Fallavier, France) as a standard.

2.11. Fluorescence imaging and estimation of cytosolic Ca²⁺

The fluorescence imaging of the cells was recorded in the presence of 5 μM of Fluo 3-AM (Sigma), a Ca²⁺-specific probe, according to the protocol described by Li et al. (2015). Cells placed in water on a glass slide with a cover slip were examined under light or fluorescence microscopy using an Olympus CX40 equipped with an Olympus U-RFLT50-200 laser (Olympus, Mannheim, Germany) **using a 488 nm excitation filter and a 515-565 nm wavelength pass filter**. Pictures were taken with an 8 megapixel eyesight camera (MD239 F/A). Image analysis was performed with ImageJ software (Abràmoff et al., 2004). The plot profile tool was used to quantify the fluorescence signal intensity in the cytoplasm.

2.12. Protein Kinase C activity

PKC activity was determined using the PepTag assay (Promega, Charbonnières les Bains, France) according to the manufacturer's instructions. Briefly, a PKC-specific fluorescent

peptide was phosphorylated by the active PKCs of the cell lysate. The reaction mixture was 1 μ l cell lysate, 0.4 mg/ml peptide, 100 mmol HEPES (pH 7.4), 6.5 mmol CaCl_2 , 5 mmol dithiothreitol, 50 mmol MgCl_2 , 5 mmol adenosine triphosphate, 10 μ mol leupeptin and 1 mg/ml phosphatidylserine. Following 30 min of incubation at 37°C, phosphorylated and dephosphorylated peptide molecules were separated by 0.8% (50 mmol Tris-HCl, pH 8.0) agarose gel electrophoresis for 15 min at 100 V. The resulting bands were visualized under UV light.

2.13. Statistical analysis of the data

All data presented in this study are the means and standard deviations of at least three independent replicates (at least three independent biological replicates and two technical replicates, the number of independent biological replicates is indicated in each figure legend). Comparative statistical analyses of groups were performed using Student's t-test or one-way analysis of variance, according to the data.

3. Results

3.1. Cytosolic Ca^{2+} content is enhanced by ABA and displays a synergistic effect with ABA activation of *LuPLR1* gene expression

In previous work (Corbin et al., 2013b, 2013a; Renouard et al., 2012b), we showed the positive role of ABA in *PLR1* gene expression. In order to evaluate whether cytosolic Ca^{2+} was involved in this regulation, increasing concentrations of ABA were applied on flax cell suspensions. The variation in the cytosolic Ca^{2+} level in response to ABA treatment was assessed using the Ca^{2+} -sensitive fluorescent dye, Fluo 3-AM. Cell imaging of intracellular fluorescence clearly indicated an increase in cytosolic Ca^{2+} in response to exogenous ABA (Fig. 1A-C). The ABA-mediated increase in cytosolic Ca^{2+} was dose-dependent, reaching a plateau at 100 μM (Fig. 1C). Interestingly, when cells were treated with elevated concentrations of ABA (i.e. 100 μM), fluorescent granules were clearly observed (Fig. 1A). These Ca^{2+} granules could either act as ion stores or constitute accumulation sites for detoxification as observed in other living organisms (Simkiss and Taylor, 1994).

Next, increasing concentrations of Ca^{2+} and ABA were applied on flax cell suspensions stably transformed with a construct containing the complete *LuPLR1* gene promoter fused to the *uidA* reporter gene. The resulting β -glucuronidase reporter gene activity values are presented in Fig. 2a. For each exogenous ABA concentration applied (ranging from 0 to 100 μM), the *LuPLR1* gene promoter activity was increased by the addition of Ca^{2+} with external exogenous concentrations ranging from 0 to 5 mM (Fig. 2A). Interestingly, while an increase in ABA concentration alone was sufficient to trigger a rise in *LuPLR1* promoter activity, an increase in Ca^{2+} concentration alone did not lead to any significant changes in *LuPLR1* gene expression (Fig. 2A). This effect of Ca^{2+} and ABA was confirmed by RT-qPCR analysis of *LuPLR1* gene expression in cells subjected to ABA treatment with different extracellular Ca^{2+} concentrations (Fig. 2B). Accordingly, the (+)-secoisolariciresinol accumulation, resulting from the *LuPLR1* activity, was largely enhanced after Ca^{2+} addition in ABA-treated cells (Fig. 2C). On the contrary, for cells growing in Ca^{2+} -depleted medium, only a slight induction of lignan production was noted in response to exogenous ABA treatment (Fig. 2C), demonstrating the essential role of Ca^{2+} in this regulation.

3.2. ABA-mediated activation of *LuPLR1* gene expression is impaired by Ca^{2+} influx disruption

In order to test whether the Ca^{2+} effect on *LuPLR1* expression activation was due only to a direct uptake from the extracellular Ca^{2+} or if Ca^{2+} intracellular stores, such as the vacuole, were also involved, the effect of a series of specific inhibitors was assessed. It should be noted that all the specific inhibitors used in the present study have been used in plants to modulate Ca^{2+} signaling (Angeles Sánchez-Sampedro et al., 2005; Dammann et al., 1997; Dubrovina et al., 2009; Hashimoto and Kudla, 2011; Zhao et al., 2011b, 2011a). The concentration of each compound was chosen to ensure that they exerted their maximal effects (inhibition or activation based on *LuPLR1* gene expression) without affecting cell growth (Fig. S1).

First, the modulatory effects of an extracellular Ca^{2+} chelator, EGTA, or a Ca^{2+} competitor, cadmium (Cd^{2+}), on the ABA-mediated transcriptional activation of the *LuPLR1* gene promoter were investigated using 100 μM ABA-treated flax cells cultured in incubation medium supplemented with 5 mM Ca^{2+} (Fig. 3). Following addition of Cd^{2+} or EGTA, *LuPLR1* promoter activity and (+)-secoisolariciresinol level decreased down to the level observed for untreated cells (Fig. 3A), evidencing a crucial role of Ca^{2+} influx in this metabolite pathway through the ABA-mediated transcriptional regulation of *LuPLR1* (Fig. 3B).

As Cd^{2+} could be toxic for cells, even at the concentration used here, more specific inhibitors were then tested to confirm this result. Nifedipine (NIF), an outer membrane channel blocker, was able to abolish the increase in cytosolic Ca^{2+} level in response to ABA addition (Fig. 4A-B), which reduced both the ABA effect on *LuPLR1* gene expression induction (Fig. 4C) and lignan accumulation (Fig. 4D), confirming the requirement of the Ca^{2+} influx for this ABA-related regulation. On the contrary, the use of heparin (HEP), an inhibitor of vacuolar Ca^{2+} release, had less impact on the increase of Ca^{2+} level in response to ABA (Fig. 4A-B), as well as on the activation of the *LuPLR1* promoter (Fig. 4C) and lignan accumulation (Fig. 4D). These results indicate that the Ca^{2+} flux mediating the ABA effect on *LuPLR1* gene expression originates more from the extracellular medium than from intracellular stores.

3.3. Ca^{2+} sensors CaM and CDPK are required for the ABA-mediated transcriptional activation of the *LuPLR1* gene in cell suspension

In order to decipher the Ca^{2+} transduction signaling involved in the *LuPLR1* gene promoter activation in response to an exogenous ABA supply, the respective involvement of the CaM- and/or CDPK-type Ca^{2+} sensors was investigated using their specific inhibitors: staurosporine (STAU), an antagonist of CDPKs, and calmidazolium (CALM), a potent inhibitor of CaMs.

The inhibition of CDPKs resulting from STAU treatment was first assessed by an in-gel kinase assay using a specific CDPK fluorescent substrate and total protein extracts prepared from flax cells (Fig. 5A). In cells treated with ABA, CDPK activity was detected and increased with protein concentration (Fig. 5A). On the contrary, STAU addition resulted in a dramatic decrease in the CDPK activity confirming its inhibitory action on these enzymes (Fig. 5A). As STAU could be toxic for plant cells, two different concentrations classically used in the literature were tested (i.e. 5 μ M (Stau1) and 10 μ M (Stau2), Fig. 5A). The lowest concentration of STAU was effective in inhibiting CDPK activity (Fig. 5A), so this concentration was used in subsequent experiments to limit the potential toxic and pleiotropic effects of this drug.

Application of 5 μ M of STAU led to a significant decrease in the positive action of Ca^{2+} on the activation of *LuPLR1* promoter in response to ABA, supporting the involvement of CDPKs in this regulation (Fig. 5B). This transcriptional regulation resulted in a marked decrease in (+)-secoisolariciresinol accumulation (Fig. 5C).

Likewise, the effect of Ca^{2+} and ABA on the activity of *LuPLR1* promoter and lignan accumulation was abolished by CALM treatment (Fig. 5B-C), evidencing the critical role of CaMs as Ca^{2+} sensors in this ABA-driven regulation.

3.4. CaM and CDPK are also required for ABA control of lignan biosynthesis during flaxseed maturation

To assess the role of Ca^{2+} signaling in ABA-driven *LuPLR1* gene expression and (+)-secoisolariciresinol accumulation during seed maturation, we took advantage of a system previously used to elucidate lignan biosynthetic pathway and ABA regulation of this pathway in flax maturing seeds (Ford et al., 2001; Renouard et al., 2012b). Capsules containing immature flaxseeds (developmental stage 2, Fig. 6A; (Hano et al., 2006b)) were placed in wells of a 96-well microplate with peduncles soaking in solutions containing mock, ABA and/or Ca^{2+} signaling inhibitor (Fig. 6A). This treatment confirmed the up-regulation of *LuPLR1* gene expression (Fig. 6B), concomitantly with the increase in ABA concentration measured in flaxseed leading to a strong increase in the (+)-secoisolariciresinol net synthesis (Fig. 6C). Interestingly, even though a high ABA level remained in the seeds, application of STAU and CALM abolished the effect of high ABA concentration on *LuPLR1* gene expression and (+)-secoisolariciresinol synthesis (Fig. 6B-C), confirming that both CDPKs and CaMs-related are required for the control of ABA on the lignan biosynthesis in flaxseed.

3.5. Promoter cis-acting elements are involved in the Ca^{2+} modulation of the ABA-mediated transcriptional activation of the *LuPLR1* gene

To investigate whether the two characterized ABA-responsive *cis*-acting elements of the *LuPLR1* promoter, ABRE and MYB2 (Corbin et al., 2013b; Renouard et al., 2012a), were involved in the Ca^{2+} modulation of *LuPLR1* expression, the consequences of mutations on single or both elements were analyzed (Fig. 7A). β -glucuronidase activities of transiently transformed flax cell suspensions treated with ABA and Ca^{2+} in the presence of different inhibitors were monitored (Fig. 7B). Both elements are involved in the Ca^{2+} -dependent ABA response of *LuPLR1* gene expression since their single disruption resulted in the complete loss of the additive effect of Ca^{2+} on the ABA regulation of this gene (Fig. 7B). The simultaneous disruption of the ABRE and MYB2 patterns suppressed the positive Ca^{2+} effect on the ABA-mediated transcriptional activation of *LuPLR1* and no further effect was observed for additional inhibitor treatment (Fig. 7B) indicating that these two elements are required and sufficient to confer transcriptional regulation of the *LuPLR1* gene in response to the ABA-mediated cytosolic Ca^{2+} increase. The *LuPLR1* promoter activity resulting from the mutation of the sole ABRE element (Fig. 7A) was greatly affected by HEP and to a lesser extent by CALM (Fig. 7B). On the contrary, stronger inhibition effects resulting from STAU, NIF and HEP treatments were measured (Fig. 7B) with the mutation of the sole MYB2 motif (Fig. 7A).

3.6. Identification and characterization of *CML15b* as a key regulator for the Ca^{2+} -dependent ABA activation of SDG biosynthesis

To gain further insight into the identification of potential regulators, a global search for protein domains of calcium sensors such as CaM, CML or CDPK was carried out within the flax deduced proteome (Wang et al., 2012), available on the Phytozome database (Goodstein et al., 2012), using BLOSUM62 as comparison matrix at the score value of > 300 and e-value $< e^{-100}$. The PFAM, PANTHER and KEGG domains used for this search are mentioned on Table S1, and the retrieved gene encoding for the corresponding proteins from flax were named according to their closest orthologs from *Arabidopsis thaliana*. Then, their relative expression profiles during flax seed development were extracted from RNAseq public datasets for flax (Fenart et al., 2010; Kumar et al., 2013) normalized and presented using the MeV suite (Saeed et al., 2006). Results including the expression profiles of *LuDIR5*, *LuPLR1*

425 and *LuUGT74S1* (Corbin et al., 2018; Dalisay et al., 2015; Fofana et al., 2017; Renouard et
 426 al., 2014), the 3 biochemically and functionally characterized genes involved in SDG
 427 biosynthesis, are depicted in Fig. S2. From these data a co-expression network with
 428 candidates potentially involved in Ca^{2+} signaling and the lignan biosynthetic genes *LuDIR5*,
 429 *LuPLR1* and *LuUGT74S1* was generated using Cytoscape software with a cut-off value of
 430 0.95 at a p -value < 0.05 (Kumar et al., 2013). From this analysis, 18 candidates appeared
 431 significantly correlated with *LuPLR1* (6 CMLs (*CML15b*, *CML15d*, *CML18b*, *CML30f*,
 432 *CML30g* and *CML42b*), 4 CDPKs (*CDPK14c*, *CDPK17a*, *CDPK24a* and *CDPK24b*) as well
 433 as 6 others CBPs (Ca^{2+} -binding proteins: *CBP2*, *CBP11*, *CBP15*, *CBP16*, *CBP17* and *CBP18*)
 434 and 2 IQs (isoleucine glutamine) domain containing proteins (*IQ3a* and *IQ12*) (Figure 8a).
 435 Among them 6 were significantly linked with *LuDIR5* (*CML15b*, *CML30g*, *CBP11*, *CBP15*,
 436 *IQ3a* and *IQ12*) whereas only 3 were linked with *LuUGT74S1* (*CML15b*, *CBP11* and *IQ3a*)
 437 (Fig. 8A, Table S2). Considering its expression profile depicted in Fig. 8B and the key role of
 438 CaM and CML highlighted by the aforementioned results from this study, we decided to focus
 439 on the role of CML15b. To provide direct *in vivo* evidence for the possible involvement of
 440 CML15b in the regulation of the Ca^{2+} -dependent ABA activation of SDG biosynthesis we
 441 generated an RNAi construct (Fig. 8C). For this purpose, the target sequence was designed
 442 using the pssRNAit server tool dedicated to the design of effective and specific (limiting off-
 443 target silencing) and non-toxic siRNAs for plant RNAi (Dai and Zhao, 2011). The T-DNA
 444 was transferred in flax cells using transient *A. tumefaciens*-mediated transformation. The
 445 efficiency of the transformation was asserted by the visualization of the *E-GFP* expression
 446 under fluorescence microscopy observation of the flax cells as shown in Fig. 8D. As expected,
 447 a significant decrease in *CML15b* gene expression was detected by RT-qPCR in transformed
 448 cells (*iCML15b*, Fig. 8E) - both untreated and ABA-treated in presence of 5 mM exogenous
 449 Ca^{2+} , as compared to untransformed cells (WT, Fig. 8E). We also noted that this ABA-
 450 treatment led to an increase in *CML15b* gene expression (Fig. 8E). This RNAi approach also
 451 had a significant impact on *LuPLR1* gene expression by significantly decreasing its activation
 452 by ABA treatment (Fig. 8F). This trend was confirmed at metabolic level by a significant
 453 decrease of (+)-secoisolariciresinol accumulation in response to ABA treatment in the
 454 transgenic cells (Fig. 8G). Taken together, these results revealed a strong and significant
 455 impact of *CML15b* gene expression disruption on the Ca^{2+} -dependent ABA activation of
 456 *LuPLR1* gene expression and SDG biosynthesis, thus providing direct *in vivo* evidence for the
 457 involvement of CML15b.

458

459 **3.7. Proposed model**

460 Overall, these results demonstrate a crucial role for Ca^{2+} as a mediator of the ABA control of
461 lignan biosynthesis through the transcriptional regulation of the *LuPLR1* gene and provide the
462 outline for a gene regulatory mechanism described in Fig. 9. Upon perception, ABA triggers
463 an increase in the cytosolic Ca^{2+} concentration originating mainly from the extracellular
464 compartment, although the intracellular stores also seem to participate in the transcriptional
465 activation specifically through the MYB2 binding element. The Ca^{2+} signal is then relayed by
466 CaM and CDPK, which modulate ABA signaling through activation of transcription factors
467 (TFs) such as MYB, ABF or bZIP either by a phosphorylation cascade or a direct interaction.
468 As a final point, these TF act specifically on the ABRE and MYB2 boxes of the *LuPLR1* gene
469 promoter, activating its gene expression and thereby lignan biosynthesis. The present results
470 support a more likely activation of the ABRE *cis*-acting element through the action of CDPK-
471 dependent TF whereas the MYB2 binding site was found to be more sensitive to the
472 disruption of the CaM action. A key role of LuCML15b is here proposed in this regulation.

473

4. Discussion

Application of Ca^{2+} inhibitors, chelators or competitors, affecting the Ca^{2+} level and/or availability, evidenced a critical role for Ca^{2+} concentration and availability in the ABA-mediated lignan biosynthesis regulation through transcriptional activation of the *LuPLR1* gene. Ca^{2+} is a well-known second messenger of ABA signaling which have been described to trigger Ca^{2+} release into the cytosol from extracellular medium and/or intracellular stores (Lecourieux et al., 2006). This action of ABA on the control of cytosolic Ca^{2+} movements may explain why Ca^{2+} alone was not able to increase *LuPLR1* gene expression nor SDG accumulation. The inhibition observed in our experiments when using EGTA or Cd^{2+} showed the importance of Ca^{2+} as a modulator of the ABA action in the context of lignan biosynthesis in flax and revealed that the rise in cytosolic Ca^{2+} in response to exogenous ABA was due to an increased Ca^{2+} influx. Such a specificity of intra- vs extra-cellular Ca^{2+} origin has been observed in *Silybum marianum* cell suspensions (Angeles Sánchez-Sampedro et al., 2005). Changes in intracellular Ca^{2+} concentration have to be detected in order to produce the correct cascade of events, such as protein phosphorylation or gene expression reprogramming (Hashimoto and Kudla, 2011). For this purpose, plants display an extensive and complex array of specific sensors decoding Ca^{2+} concentration variations. These include CaM and/or CaM-like proteins as well as CDPK and their interacting kinases, which represent specific, robust and flexible information processing sensors for the correct signal transduction as observed for ABA signaling (Zhao et al., 2011a, 2011b). In potato, ABA-inducible wounding genes were inhibited by STAU application resulting in an effective inhibition of CDPKs (Dammann et al., 1997). In our experiments, CALM and STAU inhibitors of Ca^{2+} transduction prevented the induction of *LuPLR1* expression by ABA, thus suggesting a key role for both CaMs and CDPKs as Ca^{2+} sensors modulating ABA signaling.

In the regulation of the biosynthesis of phenylpropanoid-derived products, Ca^{2+} was shown to enhance the production of flavonolignans in an elicited cell culture of *S. marianum* (Angeles Sánchez-Sampedro et al., 2005). More recently, Ca^{2+} and ABA interplay have been evidenced in the accumulation regulation of total phenolics and anthocyanins in grape cell suspension (Martins et al., 2018). In *Vitis amurensis* cultures, CDPKs are essential for the production of resveratrol (Dubrovina et al., 2009). CMLs have been shown to positively regulate the expression of flavonoids biosynthetic genes in grape (Gollop et al., 2002; Vitrac et al., 2000). Foliar application of Ca^{2+} enhanced both the expression of anthocyanin biosynthetic genes as well as anthocyanin accumulation in strawberry fruits (Xu et al., 2014) through CaM/CML

actions (Peng et al., 2016). Here, direct evidences for the role of CML15b in the regulation of lignan biosynthesis in response to ABA in flax were provided by RNAi experiments and confirmed the key role of this gene family in the control of secondary metabolites accumulation.

We have previously demonstrated the roles of the ABRE and MYB2 cis-acting elements in the ABA-mediated regulation of lignan biosynthesis through the transcriptional control of the *LuPLR1* gene (Corbin et al., 2013a). Here, the effects of mutations of these two elements in the *LuPLR1* gene promoter support a function as Ca^{2+} -sensitive sequences involved in this ABA-mediated regulation. ABRE and MYB2 binding sites are very common in the promoters of ABA-regulated genes (Abe et al., 2003; Finkelstein et al., 2002; Gutierrez et al., 2007) and the ABRE-related sequences constitute well known Ca^{2+} -responsive *cis*-acting elements (Kaplan et al., 2006; Whalley et al., 2011). CDPKs have been shown to phosphorylate the ABA-responsive TFs, ABFs (ABRE-Binding Factors), which are important mediators of ABA-mediated signaling (Choi et al., 2005; Zhu et al., 2007).

Furthermore, the MYB2 transcription factor possesses a binding domain for CaM proteins and its DNA binding capacity is regulated in a Ca^{2+} -dependent manner (Yoo et al., 2005). CaMs may control CDPKs phosphorylating target transcription factors, both having consequences on the regulation of transcription (Reddy, 2001). Future works will be conducted to elucidate the complete molecular mechanism of this regulation.

5. Conclusions

To conclude, the results described herein demonstrate a crucial role for Ca^{2+} signaling in the ABA-positive regulation of lignan biosynthesis through the transcriptional control of the *LuPLR1* gene and allow the identification of CML15b as a key mediator of this regulation. This regulation was conserved in both systems studied: cell suspensions and maturing seeds. Taken together, these results provide important new information on the regulation of lignans biosynthesis. These results could help with the design of future biotechnological approaches directed toward *in planta* lignans production for broad ranges of possible applications since these compounds are involved in both plant defense and human health-promotion. **Indeed the present results clearly demonstrate that *L. usitatissimum* cell suspension elicited by both ABA and Ca^{2+} could be an attractive renewable system for the production of SDG.**

Declarations of interest

None

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List of abbreviations:

ABF: ABRE Binding Factor; ABI3: ABA Insensitive 3; ABRE: ABA Response Element; b-ZIP: Leucine Zipper factor; Ca²⁺: Calcium; CALM: Calmidazolium; CAM: Calmodulin; CML: Calmodulin-like; Cd²⁺: Cadmium; CDPK: Calcium-Dependent Protein Kinase; Cq: Quantification cycle; CTL: Control; cv: cultivar; CYC: Cyclophilin; DMSO: Dimethylsulfoxide; EGTA: Ethylene Glycol Tetra-acetic Acid; ER: Endoplasmic Reticulum; ERA1: Enhanced Response to ABA 1; ETIF5A: Eukaryotic Translation Initiation Factor 5A; GUS: β -Glucuronidase; HEP: Heparine; InsP3: Inositol Triphosphate; MS: Murashige and Skoog; MU: 4-methylumbelliferone; MUG: 4-methylumbelliferyl- β -D-glucuronide; MYB: Myeloblastosis-derived transcription factor; NIF: Nifedipine; PCV: Packed Cell Volume; PLR: Pinorexinol Lariciresinol Reductase; RFU: Relative Fluorescence Unit; ROS: Reactive Oxygen Species; RT: Reverse Transcription; STAU: Staurosporine; TF: Transcription Factor; uidA: β -Glucuronidase encoding gene.

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Figure legends

Figure 1. Quantification of cytosolic Ca^{2+} in flax cell after ABA treatment

A. Cell imaging of intracellular fluorescence of the Fluo 3-AM Ca^{2+} probe in response to exogenous ABA supply. Flax cell suspensions were observed 24 h after probe addition and/or ABA supplementation under fluorescent (odd numbers) or visible (even numbers) light. Three controls were used: without probe or ABA supply but only DMSO addition (A1/A2); 50 μM ABA treatment (A3/A4) or probe addition (A5/A6). ABA concentrations: 10 μM in A7 and A8, 25 μM in A9 and A10 and 50 μM in A11 and A12.

B. Cell imaging of intracellular fluorescence of the Ca^{2+} probe Fluo 3-AM after 24 h of 100 μM exogenous ABA supply in flax cell suspensions under fluorescent (B1) or visible (B2) light and merged (B3). Arrows indicate granules.

C. Relative Fluorescence Units (RFUs) of flax cells in response to increasing ABA concentrations corresponding to the relative cytosolic Ca^{2+} concentration determined using a fluorometer after 24 h of treatment.

Data are expressed as the mean of 3 independent experimentations $\pm$ standard deviation of the mean and different letters indicate significant differences between conditions ($P < 0.05$).

(Color online).

Figure 2. Effect of different combined Ca^{2+} and ABA treatments on *LuPLR1* gene expression and (+)-secoisolariciresinol production in flax cells

A. The β -glucuronidase reporter activity of stably transformed flax cell suspensions was determined 48 h after an exogenous supply of ABA (from 0 to 100 μM). Data are expressed as the mean ($n=3$) $\pm$ standard deviation of the mean. Significant differences in comparison to the corresponding control at $p<0.05$: *, $p<0.01$: **, $p<0.001$: *** according to the Student test.

B. Relative *LuPLR1* gene expression determined through RT-qPCR analysis determined 24 h after treatment. **c.** (+)-secoisolariciresinol content quantified by HPLC 96 h after treatment.

Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean and different letters indicate significant differences between conditions ($P < 0.05$).

(Color online).

Figure 3. Effect of EGTA and Cd^{2+} on *LuPLR1* gene expression and lignan accumulation in flax cells

A. Effect of EGTA addition (Ca^{2+} chelator) and Cd^{2+} addition (Ca^{2+} competitor) on the ABA-mediated transcription activation of the *LuPLR1* gene. The β -glucuronidase activity was quantified 48 h after treatment in a stably transformed cell suspension of flax harboring the complete *LuPLR1* gene promoter *GUS* fusion construct. Cells were cultured in incubation medium supplemented with 100 μM ABA and 5 mM Ca^{2+} and subjected to either EGTA addition at 5 mM or Cd^{2+} addition at 2 mM final concentration. CTL corresponds to the control without treatment (DMSO addition).

B. (+)-secoisolariciresinol content quantified by HPLC 96 h after the same treatments described above.

Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean and different letters indicate significant differences between conditions ($P < 0.05$).

(Color online).

Figure 4. Effect of nifedipine (NIF) and heparin (HEP) treatments on cytosolic Ca^{2+} content, *LuPLR1* gene expression and lignan accumulation in flax cells

A. Cell imaging of intracellular fluorescence of the calcium probe Fluo 3-AM in response to an exogenous ABA supply combined with a calcium channel inhibitor. Flax cell suspensions were observed 24 h after probe addition, ABA and inhibitor addition under fluorescent (odd numbers) or visible (even numbers) light. In the negative control, cells were supplemented only with the probe (A1/A2) whereas in the positive control, cells were treated with ABA 100 μM (A3/A4) and the probe. Effect of nifedipine (NIF, a Ca^{2+} influx channel blocker) addition in A5/A6 or heparin (HEP, a Ca^{2+} efflux channel blocker) addition in A7/A8 on ABA-treated flax cells. ABA concentration used was 100 μM .

B. Relative Fluorescence Units of flax cells in response to exogenous ABA supply combined with calcium channel inhibitors (NIF and HEP) determined using a fluorometer after 24 h of treatment corresponding to the relative cytosolic Ca^{2+} concentration.

C. Effect of NIF (25 μM) and HEP (10 μM) addition on the ABA-mediated transcription activation of the *LuPLR1* gene. The β -glucuronidase activity was determined 48 h after treatment in stably transformed cell suspensions of flax harboring the complete *LuPLR1* gene promoter *GUS* fusion construct. Cells were cultured in incubation medium supplemented with 100 μM ABA and 5 mM Ca^{2+} and subjected to NIF or HEP addition. CTL represents the control without treatment (DMSO addition).

D. (+)-secoisolariciresinol content quantified by HPLC 96 h after the same treatments described above.

Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean and different letters indicate significant differences between conditions ($P < 0.05$).

(Color online).

Figure 5. Effect of staurosporine (STAU) and calmidazolium (CALM) treatments on *LuPLR1* gene expression and lignan accumulation in flax cells

A. Detection of in-gel CDPK activity with varying concentrations of total soluble proteins extracted from ABA-treated cells and impact of STAU, a CDPK inhibitor, addition on this activity (Stau1 and Stau2 corresponding to STAU additions at 5 and 10 μ M, respectively).

B. Effect of STAU (5 μ M) and CALM, a CaM inhibitor, (25 μ M) addition on the ABA-mediated transcription activation of the *LuPLR1* gene. The β -glucuronidase activity was determined 48 h after treatment in stably transformed cell suspensions of flax harboring the complete *LuPLR1* gene promoter *GUS* fusion construct. Cells were cultured in incubation medium supplemented with 100 μ M ABA and 5 mM Ca^{2+} and subjected to either STAU or CALM addition. CTL is the control without treatment (DMSO addition).

C. (+)-secoisolariciresinol content quantified by HPLC 96 h after the same treatments described above.

Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean and different letters indicate significant differences between conditions ($P < 0.05$).

(Color online).

Figure 6. Effects of STAU and CALM treatments combined with ABA supplementation on *LuPLR1* gene expression and lignan accumulation in flax maturing seeds

A. Picture of the experimental procedure for the exogenous application of ABA (100 μ M) and 5 mM Ca^{2+} alone or combined with STAU (5 μ M) or CALM (25 μ M) treatment and seed morphology (SM, developmental stage 2).

B. *LuPLR1* gene expression analyzed by RT-qPCR determined 12 h and 24 h after treatment. CTL is the control without treatment. Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean.

C. (+)-Secoisolariciresinol (in mg/g DW) and ABA (ng/g DW) quantification in treated flaxseed (96h after treatment). CTL is the control without treatment.

Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean. Significant differences in comparison to the corresponding control at $p < 0.05$:*, $p < 0.01$: **, $p < 0.001$: *** according to the Student test.
(Color online).

Figure 7. Roles of ABRE and/or MYB2 *cis*-acting elements in the *LuPLR1* gene promoter activity in flax cell suspensions in response to ABA treatments combined with Ca^{2+} concentration modulators

A. Schematic representations of the different *LuPLR1* gene promoter *GUS* fusion constructs. Crosses indicate mutations in ABRE (A) or MYB2 (M) ABA-response *cis*-acting elements. Lines expressing *GUS* under the wild-type *LuPLR1* promoter (WT), the promoter mutated in ABRE (mABRE), in MYB2 (mMYB2) or in both ABRE and MYB2 (mABRE/MYB2) were used.

B. β -glucuronidase activity in transformed cell suspensions, expressing the different *pLuPLR1:GUS* constructs treated with ABA 100 μM , 5 mM Ca^{2+} and subjected to Ca^{2+} concentration modulators (EGTA, nifedipine (NIF), heparin (HEP), calmidazolium (CALM) and staurosporine (STAU)). CTL is the control without treatment (DMSO addition).

Data are expressed as the mean of 3 independent experiments $\pm$ standard deviation of the mean. Significant differences in comparison to the corresponding control at: $p < 0.05$:*, $p < 0.01$: **, $p < 0.001$: *** according to the Student test.

(Color online).

Figure 8. Implication of CML15b in the Ca^{2+} signaling regulating the ABA-activation of lignan biosynthesis in flax.

A. Co-expression network of flax lignan biosynthetic genes *LuDIR5*, *LuPLR1* and *LuUGT74S1* with putative Ca^{2+} sensor genes during flax seed development extracted from public RNAseq data and constructed using Cytoscape software. Only positive correlations with a cut-off value of 0.95 for the Pearson correlation coefficients were visualized. Colors from yellow to red indicate increasing Pearson correlation values and the connection size indicates the strength of the connection.

B. Relative gene expression of *LuDIR5*, *LuPLR1*, *LuUGT74S1* and *CML15b* during flax seed development.

C. Schematic diagram of the T-DNA region from binary vector for RNAi CML15b. The hairpin construct consisted of a 155bp sequence of the CML15b gene in sense and antisense orientation and separated by an intron. P35S, promoter of the Cauliflower Mosaic Virus 35S RNA gene; OCS-ter, 3'end of the octopine synthase gene; E-GFP: enhanced green fluorescence protein; P-nos and 3'nos, nopaline synthase gene promoter and 3'end respectively; nptII: coding sequence of the neomycin phosphotransferase gene; LB, RB: T-DNA left and right borders.

D. Transiently transformed cells expressing CML15b-RNAi construction. Cells were observed under bright field or fluorescence microscopy (using a 488 nm excitation filter and a 540 nm wavelength pass filter).

E. Relative *CML15b* gene expression analyzed by RT-qPCR determined 24 h after treatment with mock (DMSO) or 100μM ABA and 5 mM Ca²⁺ in wild type (WT) and RNAi-CML15b transgenic flax cells.

F. Relative *LuPLR1* gene expression analyzed by RT-qPCR determined 24 h after treatment with mock (DMSO) or 100μM ABA and 5 mM Ca²⁺ in wild type (WT) and RNAi-CML15b transgenic flax cells.

G. (+)-Secoisolariciresinol (in mg/g DW) HPLC quantification in wild type (WT) and RNAi-CML15b transgenic flax cells 96h after treatment.

Data are expressed as the mean of 3 independent experiments ± standard deviation of the mean and different letters indicate significant differences between conditions ($P < 0.05$).

(Color online).

Figure 9. Proposed gene regulatory mechanism model for the role of Ca²⁺ in the ABA-mediated *LuPLR1* gene expression. ABA: Absciscic Acid; ABFs: ABRE Binding Factors; ABRE: ABA-Response Element; CaM: Calmodulin; CML15b: Calmodulin 15b; Cd²⁺: Cadmium; CDPKs: Ca²⁺-dependent protein kinases; InsP3: Inositol Triphosphate; *LuPLR1*: *Pinoresinol Lariciresinol Reductase 1* encoding gene from *Linum usitatissimum*; MYB2: MYB2 TF-binding site; TF: Transcription Factor.

(Color online).

Figure 1

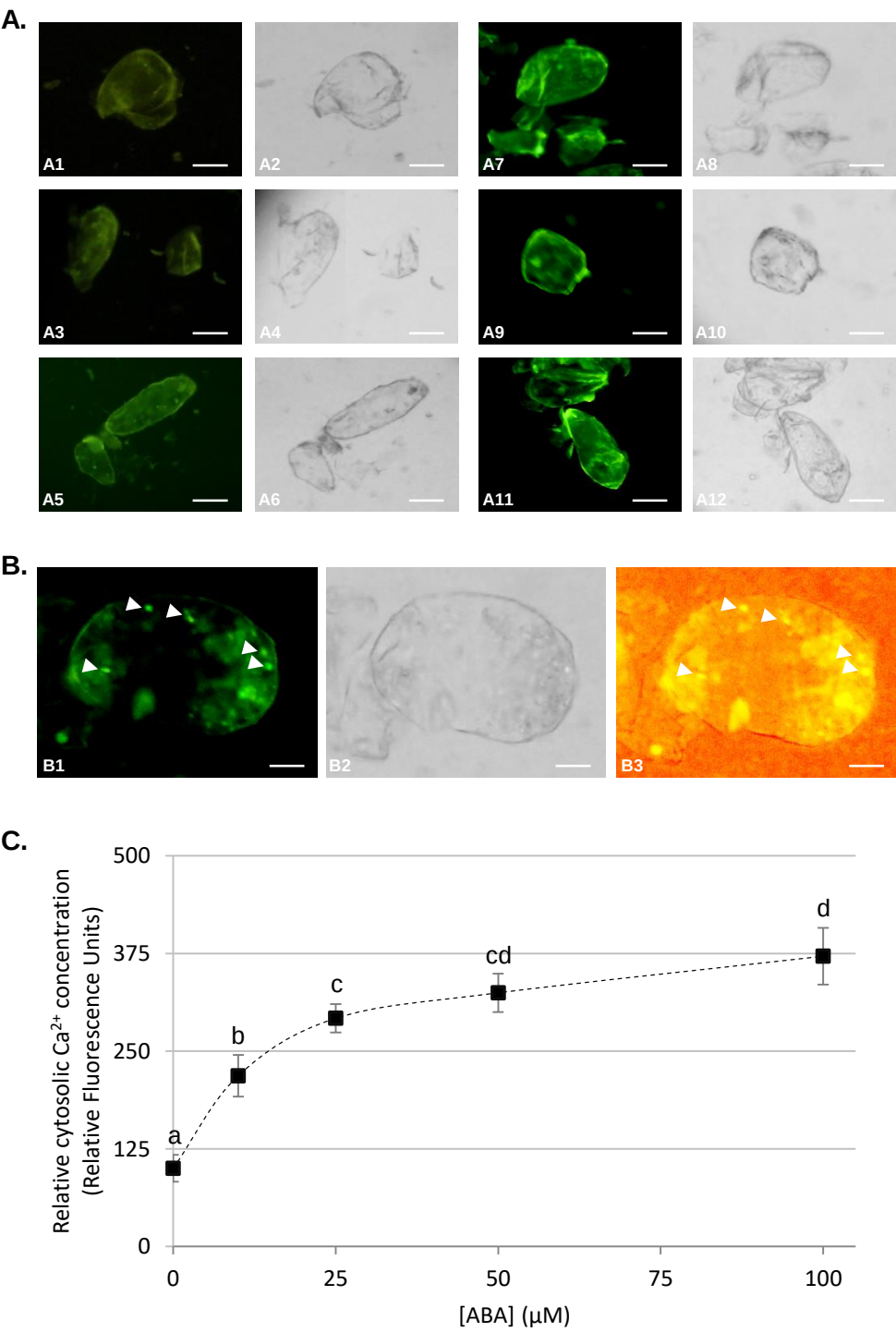


Figure 2

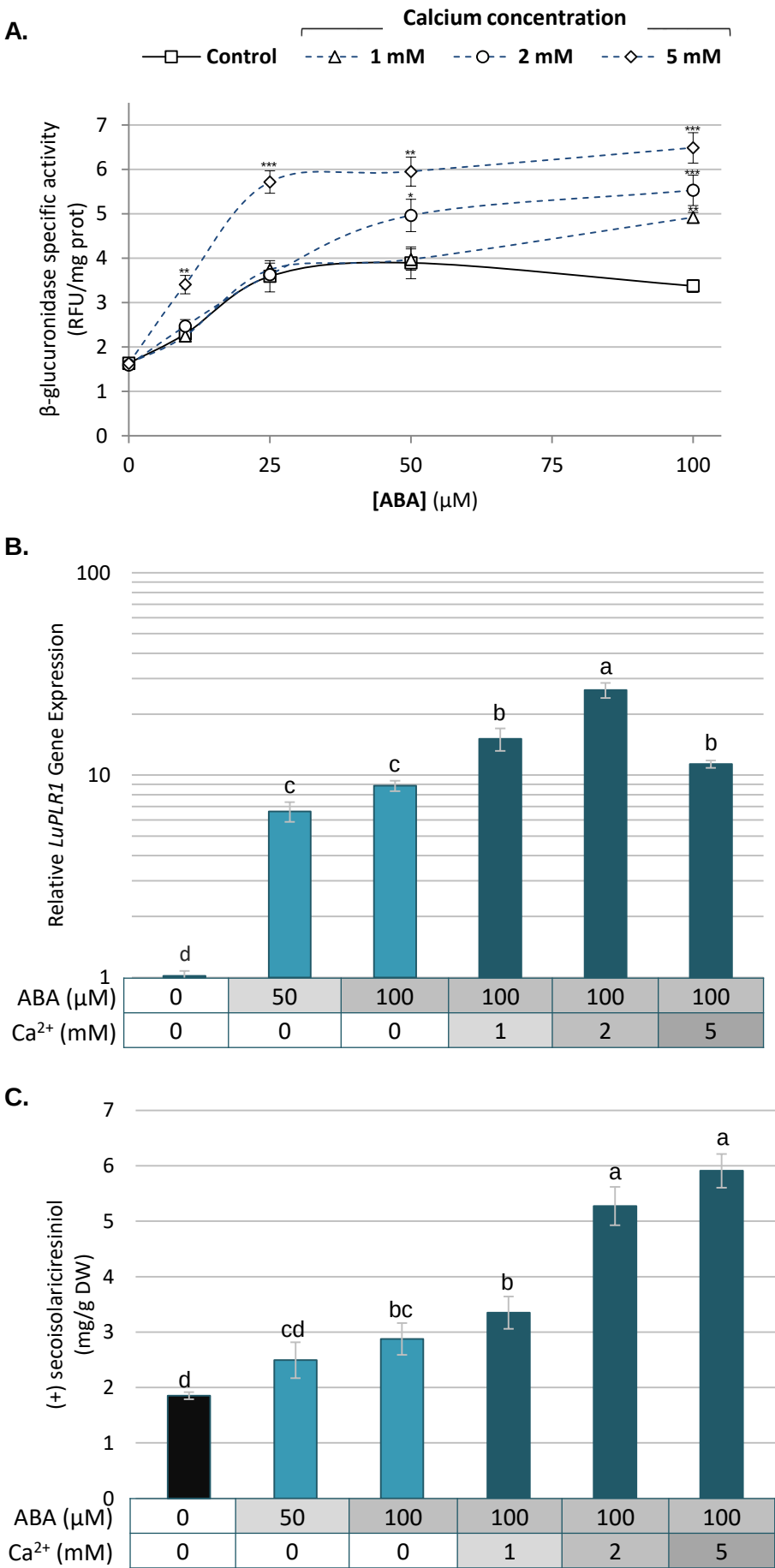
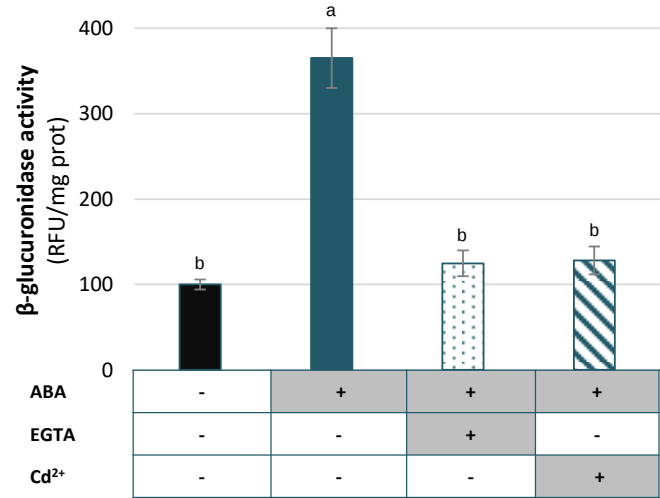


Figure 3

A.



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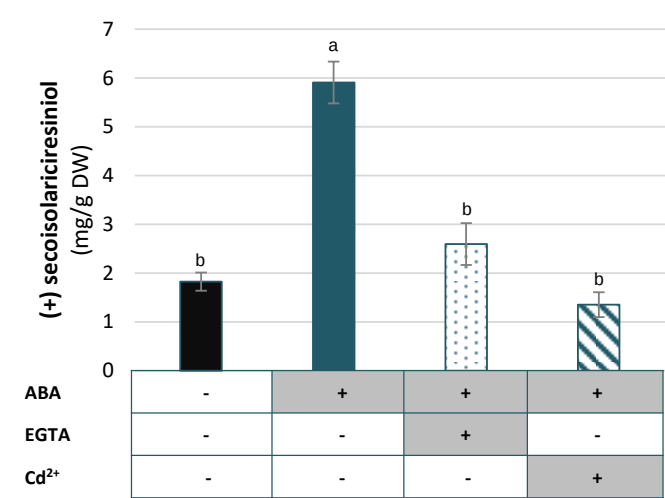
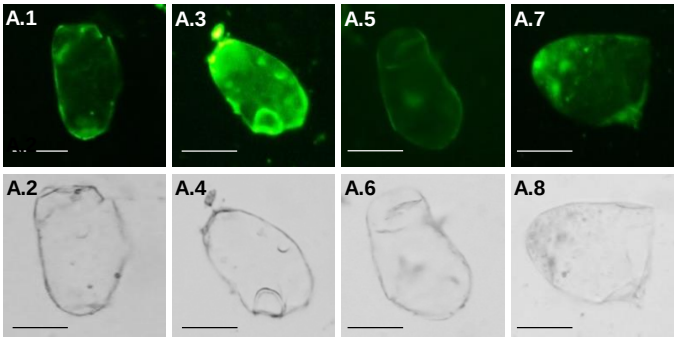
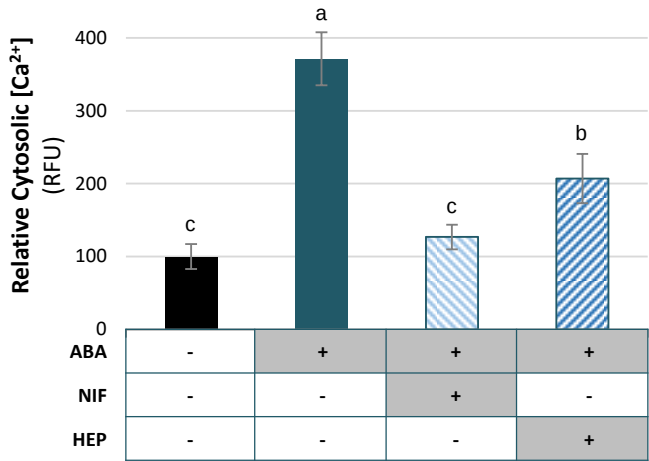


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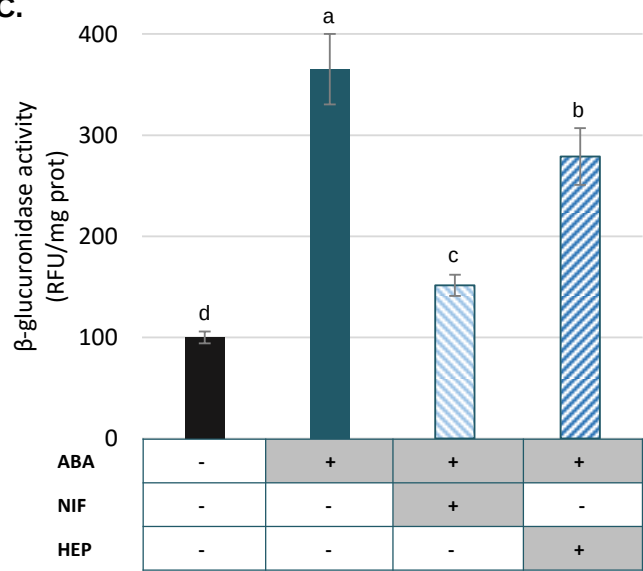
A.



B.



C.



D.

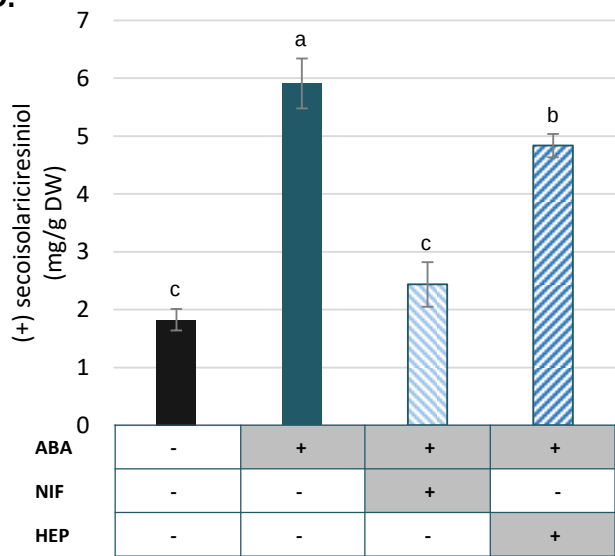


Figure 5

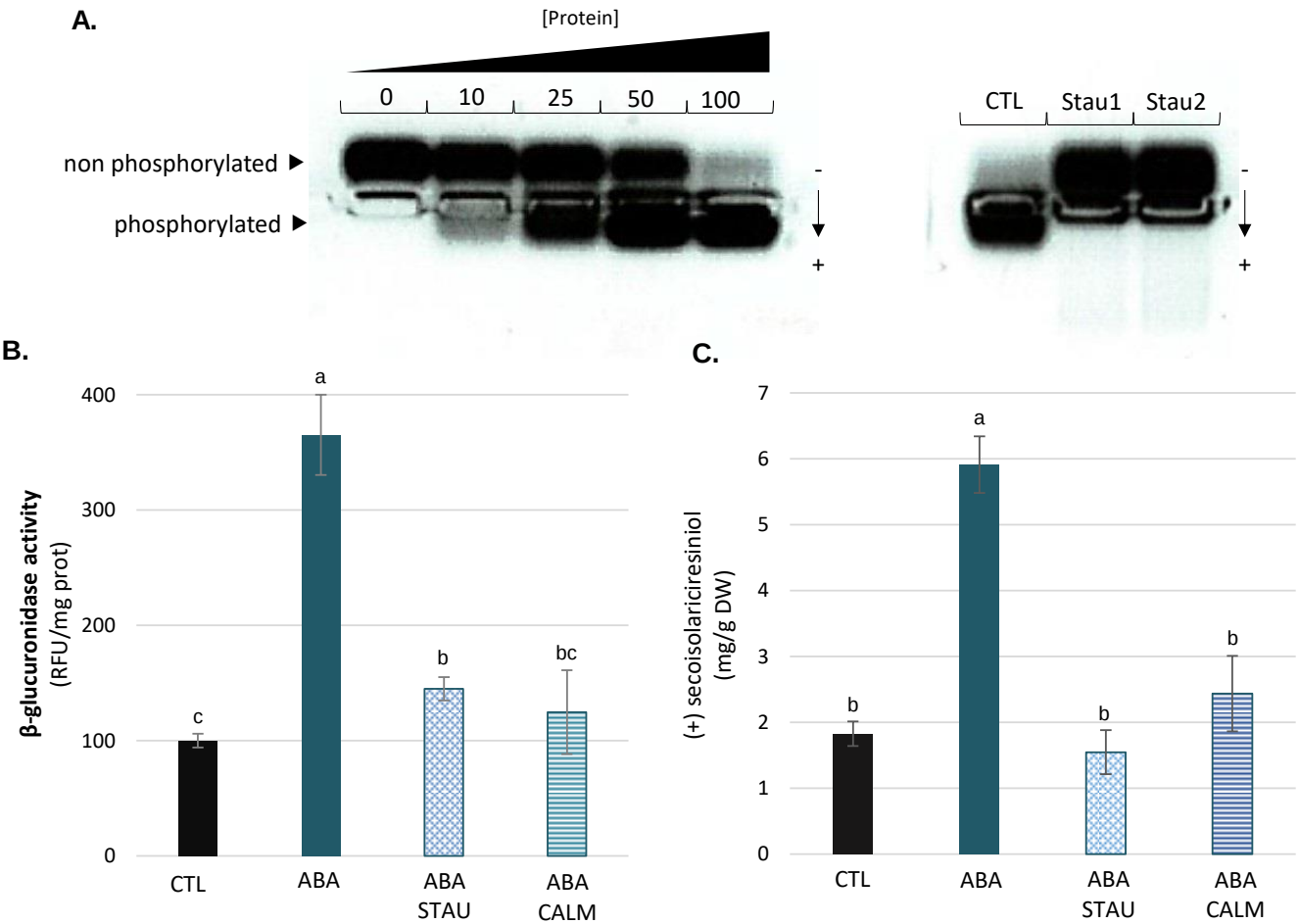


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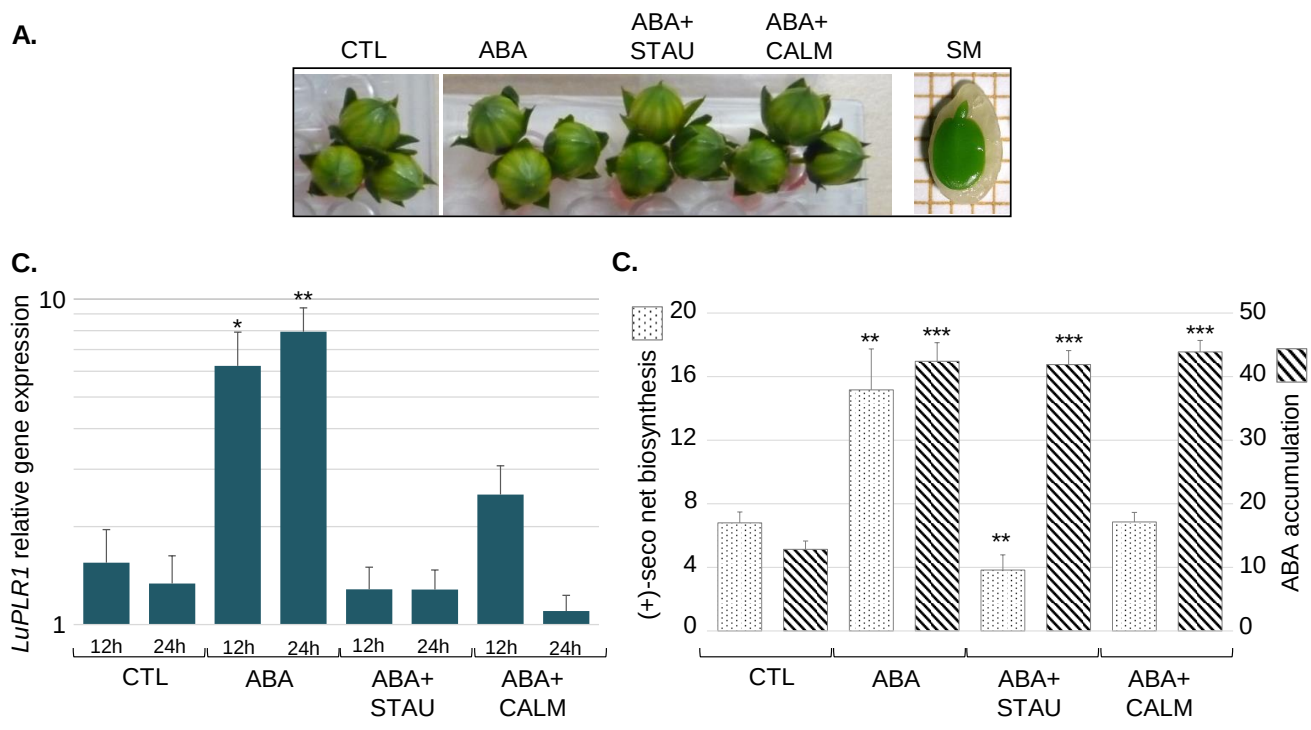
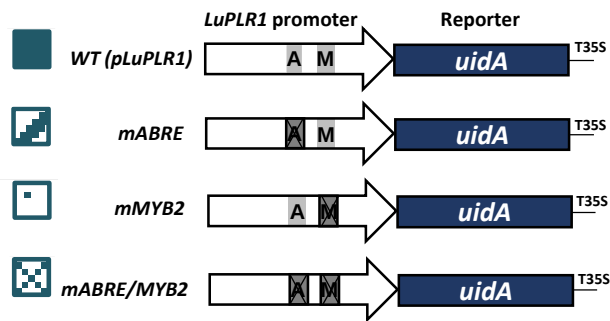


Figure 7

A.



B.

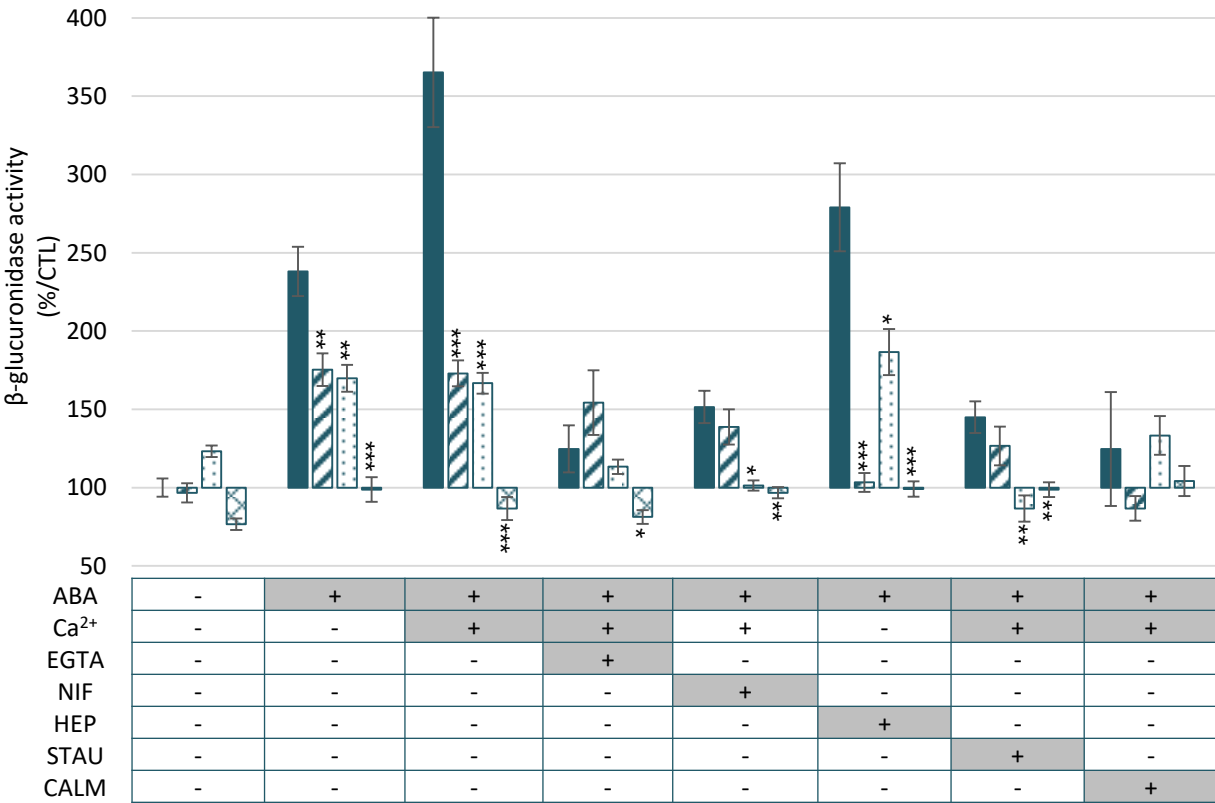


Figure 8

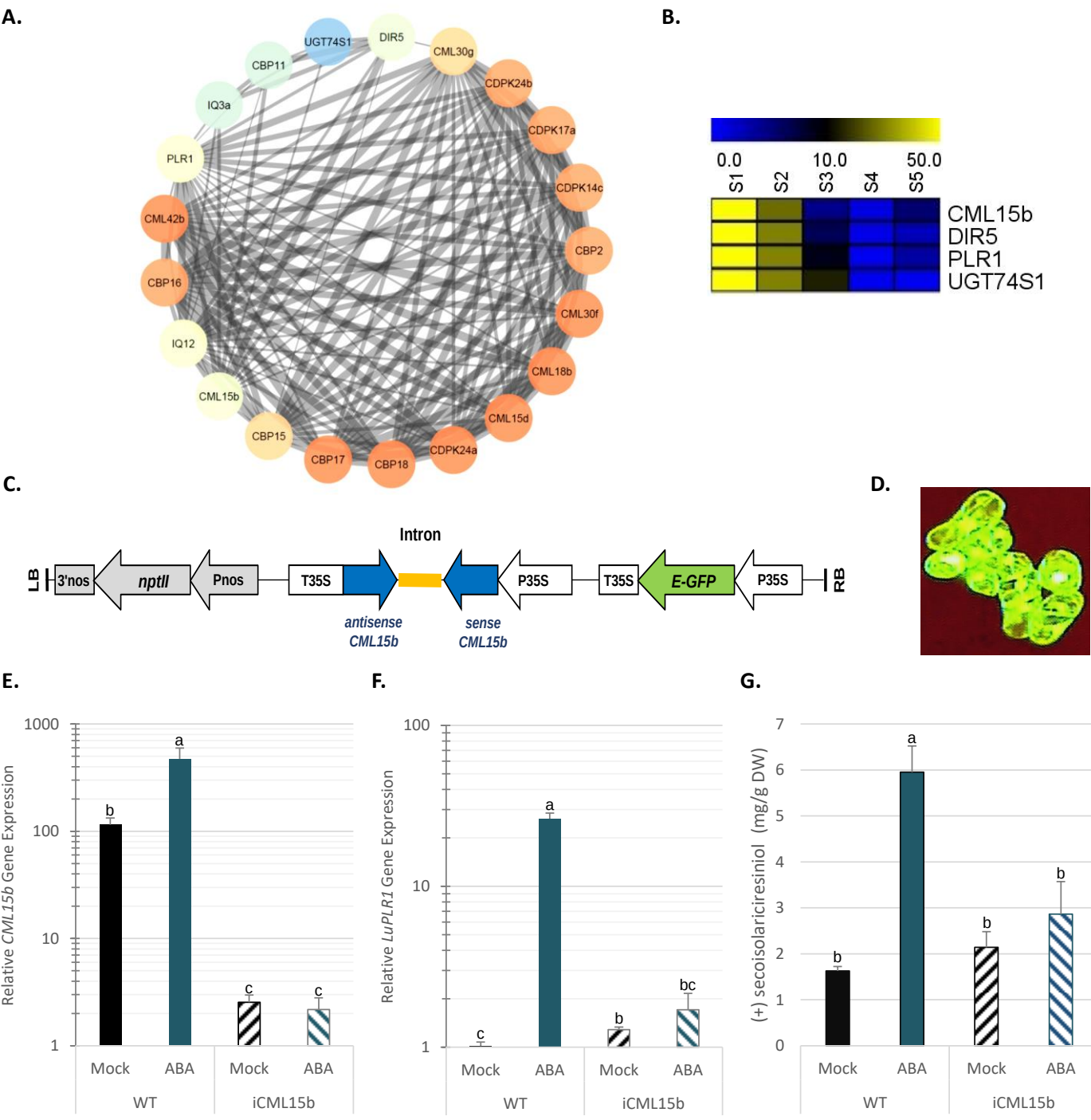


Figure 9

