Seed hemicelluloses tailor mucilage properties and salt tolerance

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Summary

- While Arabidopsis seed coat epidermal cells have become an excellent genetic system to study the biosynthesis and structural roles of various cell wall polymers, the physiological function of the secreted mucilaginous polysaccharides remains ambiguous. Seed mucilage is shaped by two distinct classes of highly substituted hemicelluloses along with cellulose and structural proteins, but their interplay has not been explored.
- We deciphered the functions of four distinct classes of cell wall polymers by generating a series of double mutants with defects in heteromannan, xylan, cellulose, or the arabinogalactan protein SALT-OVERLY SENSITIVE 5 (SOS5), and evaluating their impact on mucilage architecture and on seed germination during salt stress.
- We discovered that *muci10* seeds, lacking heteromannan branches, had elevated tolerance to salt stress, while heteromannan elongation mutants exhibited reduced germination in $CaCl_2$. In contrast, xylan made by *MUCILAGE-RELATED21* (*MUCI21*) was found to be required for the adherence of mucilage pectin to microfibrils made by CELLULOSE SYNTHASE5 (CESA5) as well as to a SOS5-mediated network.
- Our results indicate that the substitution of xylan and glucomannan in seeds can fine-tune mucilage adherence and salt tolerance, respectively. The study of germinating seeds can thus provide insights into the synthesis, modification and function of complex glycans.

Introduction

Cellulose microfibrils are deposited around plant cells and enmeshed in a complex matrix of hemicelluloses, pectin, and, to a lesser extent, structural proteins. The roles of specific classes of cell wall polymers have been difficult to study even in model organisms. For instance, *Arabidopsis thaliana* has nine *CELLULOSE SYNTHASE-LIKE A* (*CSLA*) genes that are at least putatively involved in the synthesis of heteromannan (HM), a class of hemicellulose mainly built of β-1,4-linked mannosyl units. While HM polymers could store carbon to feed growing seedlings or directly control cell wall structure (Schröder *et al.*, 2009), their physiological roles in Arabidopsis are poorly understood. Genetic disruption of *CSLA7* is embryo-lethal, but *csla2 csla3 csla9* triple mutant stems had no phenotypic changes despite lacking detectable HM (Goubet *et al.*, 2009). Significant insights into the biosynthesis and functions of various cell wall

components, including HM, have been gained using the Arabidopsis seed coat as a genetic model (Šola *et al.*, 2019). The seed coat epidermis secretes large amounts of polysaccharides that rapidly swell upon hydration to release non-adherent mucilage as well as an adherent capsule. Unbranched pectin is the dominant mucilage component, but the adherent capsule also contains hemicellulosic polymers typical of secondary walls (Voiniciuc *et al.*, 2015c), which are deposited after cells expand.

In the past decade, several classes of carbohydrate-active enzymes have been found to influence mucilage content and properties (Griffiths & North, 2017; Šola *et al.*, 2019). At least three genes are required to maintain pectin adherence to the seed surface (Fig. 1a): *CELLULOSE SYNTHASE* (*CESA5*), *SALT-OVERLY SENSITIVE5* (*SOS5*) and *MUCILAGE-RELATED21/MUCILAGE-MODIFIED5* (*MUCI21*/*MUM5*). CESA5 is a member of the cellulose synthesis complex (Sullivan *et al.*, 2011; Mendu *et al.*, 2011; Harpaz-Saad *et al.*, 2011; Griffiths *et al.*, 2015), while the SOS5 arabinogalactan protein could be part of a mucilage proteo-glycan or a kinase signalling pathway (Harpaz-Saad *et al.*, 2011; Griffiths *et al.*, 2014; Basu *et al.*, 2016). Although its predicted xylosyltransferase activity remains to be confirmed *in vitro* (Voiniciuc *et al.*, 2015a; Zhong *et al.*, 2018), MUCI21 is required to substitute xylan with xylose branches (Voiniciuc *et al.*, 2015a) that facilitate pectin-cellulose interactions (Ralet *et al.*, 2016). Galactoglucomannan, another branched hemicellulose in Arabidopsis mucilage, is elongated by CSLA enzymes and substituted by MANNAN α-GALACTOSYLTRANSFERASE1/MUCILAGE-RELATED10 (MAGT1/MUCI10; Yu *et al.*, 2014, 2018; Voiniciuc *et al.*, 2015b). Unlike xylan, branched HM maintains cellulose deposition and pectin density without appearing to influence mucilage adherence (Fig. 1a).

Biochemical and histological analyses of double mutants have clarified how SOS5 and cellulosic ray-like structures provide two distinct mechanisms to anchor pectin to seeds (Griffiths *et al.*, 2014, 2016; Ben□Tov *et al.*, 2018). The contrasting roles of the two hemicelluloses on mucilage properties have yet to be evaluated in detail. The physiological roles of Arabidopsis seed mucilage are still ambiguous, even though angiosperm seed coats have been involved in seed dormancy, dispersal and germination (Western, 2012; North *et al.*, 2014). In contrast to the Columbia wild type, Arabidopsis varieties with impaired mucilage release (Saez-Aguayo *et al.*, 2014) or adherence (Voiniciuc *et al.*, 2015a) have elevated buoyancy and could be dispersed on

water. Seed germination is essential for plant establishment and is highly sensitive to salt stress. In this study, we therefore explored how genes affecting different wall polymers modulate mucilage properties, seed germination and early growth under salt stress (Fig. 1a).

Materials and Methods

Plant materials

Mutations were genotyped using primers listed in Table S1 and Touch-and-Go PCR (Berendzen *et al.*, 2005). The double mutants generated in this study are available from the Nottingham Arabidopsis Stock Center. Plants were grown in climate-controlled chambers as previously described (Voiniciuc *et al.*, 2015b). The germination assays were performed using seeds produced by plants grown individually in 8 cm round pots at 100-120 µE m^{-2} s^{-1} light, 22°C and around 60% relative humidity. Flowering plants were staked and mature, dry seeds (~10 weeks) were harvested, separated from the chaff and stored in separate paper bags (one per plant) in a temperature-controlled laboratory (~23°C, 40 to 50% humidity).

Microscopic analyses

Seeds were stained with 0.01% ruthenium red (RR) in 24-well plates and quantified in Fiji (https://fiji.sc/; Schindelin et al., 2012) using established protocols (Voiniciuc *et al.*, 2015b). For staining without shaking, seeds were imbibed in 300 µL of 0.01% RR solution for 15 min. Images were acquired with two stereomicroscope-camera setups: MZ12 with DFC 295, or M165FC with MC170 HD (all from Leica). Mucilage immunolabeling with CCRC-M139 (Carbosource, Complex Carbohydrate Research Center) and counter-staining with S4B (Direct Red 23; Sigma Aldrich) was performed using a published protocol and Leica TCS SP8 confocal setup (Voiniciuc, 2017). Germinated seeds were stained with calcofluor white and propidium iodide (0.05%, w/v, for both dyes) for 10 min, rinsed well with water, and imaged on a Zeiss Imager.Z2 with a 10x Plan-Fluar (NA 0.30), Axiocam 506, and DAPI/Texas Red filters.

Biochemical analyses

Total mucilage was extracted with a ball mill, hydrolyzed, and quantified via high performance anion exchange chromatography with pulsed amperometric detection (HPAEC-PAD) as previously described (Voiniciuc & Günl, 2016). The quantification of mucilage detachment via HPAEC-PAD has also been described in detail (Voiniciuc, 2016). HPAEC-PAD of mucilage

was conducted on a Dionex system equipped with CarboPac PA20 columns (Voiniciuc & Günl, 2016). For alcohol-insoluble residue (AIR) isolation, all material (72 h post-stratification) from four biological replicates was pooled, finely ground and sequentially washed with 70% ethanol, chloroform:methanol (1:1, v/v) and acetone. Monosaccharide content of germinated seed AIR after 2 M trifluoroacetic acid hydrolysis was analyzed on a Metrohm 940 Professional IC Vario (Voiniciuc *et al.*, 2019), equipped with Metrosep Carb 2-250/4.0 guard and analytical columns.

Seed germination assay

All germination assays were performed in sterile 24-well culture plates (VWR International; 734-2779), using 500 µL of the specified solution and dry seeds (typically 20, but up to ~100 worked) from a single plant per well. The four corners had only water and the plates were sealed with lids and 3M micropore tape to reduce desiccation. Replicates from high-quality seed lots were distributed to avoid positional bias, and at least three biological replicates per genotype showed consistent results. Seeds were hydrated in 500 µL of distilled water, 150 mM $CaCl_2$ or 150 mM NaCl directly in the plate, or first de-mucilaged via ball mill extraction in water (Voiniciuc & Günl, 2016) before rinsing and being transferred in the final solvent (500 µL) to the plates. Floating seeds were counted as the number remaining in the center of each well, atop the solution. Plates were stratified for 66 h (dark, 4°C), transferred to a phytochamber (22°C, 100 µE m^{-2} s^{-1} constant light), and then imaged every 24 h with a Leica M165FC stereomicroscope. Seeds were defined as germinated if radicle length was >70 µm, when quantified in Fiji (line tool).

To compare ionic and osmotic effects, germination assays were performed in 150 mM $CaCl_2$ or $MgCl_2$ salts, 450 mM sorbitol, and 61 mM polyethelene glycol (PEG) 4000, all with an equal osmotic pressure (1.11 MPa) based on the van 't Hoff formula and experimental data (Money, 1989). Radicle protrusion versus elongation effects were tested by switching water and 150 mM $CaCl_2$ at 24 h post-stratification following three sequential 450 µL solvent exchanges.

Figures and statistical analysis

Micrographs were processed uniformly in Fiji. Numerical data were plotted as bar graphs in Microsoft Excel 365 or as box/violin/jitter plots in the Past 4 statistics software package

(https://folk.uio.no/ohammer/past/; Hammer *et al.*, 2001)). Panels were assembled in Inkscape (https://inkscape.org/). ATH1 microarray expression, including GSE20223 dataset (Narsai *et al.*, 2011), was visualized in GENEVESTIGATOR Professional (https://genevestigator.com/). Two-samples and multiple samples statistics were performed in Excel and Past 4, respectively. Carbohydrates were drawn according to the Symbol Nomenclature for Glycans (SNFG).

Results and Discussion

Mucilage adherence requires multiple wall polymers, except HM

To dissect the roles of the four genes listed in Fig. 1a, we generated a series of double mutants with defects in HM, xylan, cellulose or an AGP (SOS5). We crossed the *muci10-1* (Voiniciuc *et al.*, 2015b) and *muci21-1* (Voiniciuc *et al.*, 2015a) hemicellulose mutants to each other, as well as to *cesa5-1* (Mendu *et al.*, 2011) and *sos5-2* (Harpaz-Saad *et al.*, 2011). After shaking and RR staining, the seeds of all single and double mutant combinations had wild-type seed area but were surrounded by smaller mucilage capsules (Fig. 1b,c). *MUCI21*, *CESA5* or *SOS5* were epistatic to *MUCI10* in terms of adherent mucilage size. While all mutants produced wild-type percentages of rhamnose and galacturonic acid in total mucilage extracts (Table S2), significant reductions in minor sugars were associated with *muci10* (galactose and mannose) and *muci21* (xylose) mutations (Fig. 2a). Consistent with previous results (Griffiths *et al.*, 2014), *cesa5* and *sos5* mutations did not alter matrix polysaccharide composition. The *muci10 muci21* double mutant phenocopied the biochemical deficiencies of the respective single mutants, indicating that xylan and HM substitution can be uncoupled in the seed coat.

Sequential mucilage extractions (Fig. 2b and Table S3) as well as direct hydration in RR solution (Fig. 2c) showed that more pectin detached from seeds containing *muci21*, *cesa5*, and/or *sos5* mutations compared to wild-type and *muci10*. Xylan detachment increased proportional to that of pectin in mutants lacking *CESA5* and/or *SOS5* (Fig. 2b; Table S3), consistent with covalent linkages between these polymers (Ralet *et al.*, 2016; Voiniciuc *et al.*, 2018). Unbranched xylan epitopes, labelled by the CCRC-M139 monoclonal antibody (Ruprecht *et al.*, 2017), closely surrounded *muci21* and *cesa5* seeds, but were further from the surface of *sos5* and other genotypes (Fig. S1a,b), proportional to the RR-stained adherent capsule size (Fig. 1b,c).

Each mutation also had distinct effects on S4B staining, which primarily detects cellulose (Anderson *et al.*, 2010), and all the double mutants seeds lacked the ray-like structures that were observed around the wild type (Fig. 2d). Among the single mutants, only *muci21* and *cesa5* displayed clear ray-like structures (Fig. 2d), while *sos5* only had more diffuse cellulose as previously shown (Fig. 2d; Griffiths et al., 2014). The impact of the different mutant combinations on cellulose architecture were also supported by crystalline polymer birefringence (Fig. S1c). In short, *CESA5*, *SOS5*, or *MUCI21* were epistatic to *MUCI10* for pectin adherence (Fig. 2b,c), via partially overlapping mechanisms, and the loss of any two players severely impaired cellulose structure. This double mutant analysis highlights the genetic complexity of cell wall biosynthesis in the seed coat and reveals how extracellular polysaccharide organization can be dramatically reshaped when more than one structural component is modified.

The elongation and substitution of HM modulate salt tolerance

The newly generated mutant collection affecting multiple classes of wall polymers enabled us to investigate the physiological consequences of altering mucilage structure. We established a novel seed germination and salt stress assay using aqueous solutions in 24-well plates. Nearly all wild-type and mutant seeds imbibed in water germinated within 24 h post-stratification (Fig. 3a). However, when placed in 150 mM $CaCl_2$, few wild-type seeds germinated even after 48 h of exposure to constant light. We initially hypothesized that mucilage-defective mutants might be more susceptible to salt stress, but unexpectedly found that *muci10* and *muci10 muci21* seeds had over 5-fold higher germination rate at this stage (Fig. 3a). The other mutant combinations germinated like the wild type at all time points. Only *muci10* and *muci10 muci21* had significantly longer radicles at 72 h in 150 mM $CaCl_2$ (Fig. 3b and Fig. 3d), even though most mutants had around a two-fold higher flotation rate compared to the wild type (Fig. 3c). The enhanced germination rate and radicle growth of *muci10* in 150 mM $CaCl_2$ was replicated in multiple assays, including up to 100 seeds per well and independent growth batches (Fig. 3e-g).

To evaluate the basis of the observed salt tolerance, we assayed the effects of the *muci10* mutation in additional stress conditions. The use of 150 mM NaCl also reduced the rate of seed germination, but radicles that protruded from NaCl-treated seeds failed to further elongate compared to the $CaCl_2$ treatment (Fig. S2). Nevertheless, *muci10* and *muci10 muci21* germinated faster than wild type in both salt treatments (Fig. 3a and Fig. S3a). All seeds sunk in water within the stratification period (Fig. S3b), but a significant proportion of certain seeds (only *muci21* in

NaCl, and most mutants in $CaCl_2$) continued to float in the salt solutions (Fig. S3c). When subjected to ionic (150 mM $CaCl_2$ or $MgCl_2$) or purely osmotic stress (PEG 4000 or sorbitol) of equivalent pressure, the germination rate of *muci10* seeds was significantly higher than wild type only in calcium salt stress (Fig. 4a). Once protruded from the seed coat, *muci10* radicles elongated significantly faster than wild type in both $CaCl_2$ and sorbitol treatments (Fig. 4b; despite 3-fold difference in sample sizes), while the magnesium and PEG solutions showed higher toxicity to both genotypes. Overall, unbranched HM mutant seeds primarily tolerated high amounts of Ca^{2+} cations, which can cross-link unesterified pectin (Voiniciuc *et al.*, 2015c; Šola *et al.*, 2019). Switching water and 150 mM $CaCl_2$ solutions at 24 h post-stratification demonstrated that *muci10* enhances growth in calcium stress during radicle emergence as well as subsequent elongation (Fig. S3d,e).

We then investigated how mucilage removal impacts salt tolerance, by extracting seed coat polysaccharides using a ball mill prior to stratification. With or without mucilage, $CaCl_2$-treated *muci10* seeds germinated faster than wild-type (Fig. 4c). Mucilage β-glucans continue to encapsulate wild-type seeds at 72 h post-stratification (Fig. 4d), but were absent from de-mucilaged wild-type seeds and from HM-deficient *muci10* seeds (regardless of treatment). Despite not altering the germination rates of after-ripened seeds, the mucilage extraction significantly reduced the radicle length of each genotype compared to the intact controls (Fig. 4e). To evaluate the roles of different enzymes involved in HM biosynthesis, we then compared the germination rates of *muci10* and *csla2-3* (Fig. S4), which have similar mucilage defects (Voiniciuc *et al.*, 2015b). $CaCl_2$-treated *csla2* resembled the wild type, but the mannose content of *csla2* germinated seeds was reduced by only 7% (t-test, $P < 0.05$) in either water or $CaCl_2$ (Fig. S4c and Table S4), suggesting that additional CSLAs elongate HM in the same tissues. Using microarray data, we found that the transcription of *CSLA2*, *CSLA3*, *CSLA9* along with *CSLA7* and *CSLA11* (to a lesser extent) increased during germination relative to dry seeds (Fig. S4d). Compared to the wild type, we found that the *csla2-1 csla3-2 csla9-1* triple mutant (abbreviated as *csla239*), reported to have glucomannan-deficient stems (Goubet *et al.*, 2009), had significantly lower germination (Fig. 4f) and smaller radicles (Fig. 4g) in the $CaCl_2$ treatment. The *csla239* triple mutant reduced the mannan content of germinated seeds by one-third (Fig. 4h and Table S5), indicating that even a partial reduction of HM elongation significantly impaired growth under salt stress. Since a *csla7* mutant was defective in

embryogenesis (Goubet *et al.*, 2003, 2009), we expect that the full disruption of HM elongation in seeds would be lethal.

In summary, we found that the biosynthesis of two substituted hemicelluloses in the seed coat epidermis can be uncoupled and that HM and xylan have largely independent functions. HM substituted by MUCI10 is responsible for controlling pectin density, supporting cellulose synthesis and modulating seed tolerance to salt stress. In contrast, *MUCI21*, *CESA5* and *SOS5* are all epistatic to *MUCI10* for pectin adherence to the seed surface, via partially overlapping means (Fig. 1a). Since *muci21*, *cesa5* and *sos5* had additive effects (Fig. 1, Fig. 2, and Fig. S1, *cesa5 sos5* from Griffiths *et al.*, 2014, 2016), Arabidopsis seed mucilage structure must be controlled by a genetic network that is more complex than its carbohydrate composition suggests. For instance, the disruption of HM biosynthesis (Fig. 2; Yu *et al.*, 2014; Voiniciuc *et al.*, 2015b) or of cortical microtubule organization (Yang *et al.*, 2019) reduces the distribution of cellulose but not mucilage adherence. Our analysis of *muci10* and *cesa5* single and double mutants indicates that the cellulosic microfibrils essential for pectin attachment might be closer to the seed surface than previously thought (see remnants of rays in Fig. 2d and Fig. S1c).

In addition to gaining insight into the genetic regulation of mucilage properties, we discovered that HM structure modulates seed germination in $CaCl_2$ solutions, and to a lesser extent in other ionic/osmotic conditions. Ca^{2+} ions can cross-link unesterified mucilage pectin and all the generated double mutants had elevated flotation compared to the wild type. However, only the *muci10* mutation promoted germination in $CaCl_2$, while the *csla239* triple mutant reduced it. Consistent with these effects, *MUCI10* and other HM biosynthetic genes were up-regulated during seed germination (Fig. 1d and Fig. S4d), while *MUCI21* was not. Since *CESA5* was also expressed in germinating seeds (Fig. 1d) and *sos5* roots are overly sensitive to salt (no ATH1 microarray probe; Basu *et al.*, 2016), *muci10 cesa5* and *muci10 sos5* double mutants may offset the benefit of *muci10* (Fig. 3). The presence of unbranched HM could directly alter the ability of cell walls to expand under salt stress. HM deficiencies also modify pectin properties, by lowering the degree of methylesterification (Yu *et al.*, 2014), so *muci10* mucilage might be able to sequester calcium ions that would otherwise inhibit the expansion of inner cell layers.

In addition, unsubstituted HM in *muci10* should be more readily hydrolyzed or transglycosylated by β-1,4-mannanases (MAN; Schröder *et al.*, 2009), which are expressed during Arabidopsis seed imbibition (Fig. 1d,e). Mutations in *MAN5*, *MAN7*, and particularly

MAN6 are known to reduce germination in favorable conditions (Iglesias-Fernández *et al.*, 2011). We hypothesize that MAN enzymes might directly alter cell wall expansion, mobilize energy reserves and/or release an HM-derived molecular signal to enhance salt tolerance. Only water-treated seedlings accumulated large amounts of glucose (Tables S4 and S5), likely derived from starch. Seeds germinating in salt stress might need to mobilize carbon reserves from HM and potentially other mucilage polymers to sustain growth (Fig. 4). HM structure varies extensively in natural Arabidopsis populations (Voiniciuc *et al.*, 2016), so it might already modulate how seeds disperse, germinate and tolerate brackish waters containing hostile levels of Ca^{2+} and/or Na^{+}. Consistent with this hypothesis, the constitutive expression of an enzyme involved in producing GDP-mannose, the sugar donor for HM elongation, elevated the mannose content of Arabidopsis seedlings and their tolerance to 150 mM NaCl (He *et al.*, 2017). Since the world faces rising sea levels and the expansion of saline environments, engineering salt tolerance remains a major challenge in crop production.

In conclusion, we have deciphered the contrasting roles of two classes of hemicelluloses in establishing seed mucilage properties and demonstrated new roles for HM elongation and substitution in radicle emergence as well as elongation during calcium salt stress. The multiwell cultivation system established in this study can be used to explore the physiological consequences of additional cell wall modifications. The overlapping expression profiles of multiple HM-related genes (Fig. 1d and S4d) highlights the need to investigate the specificity of these players on the cellular level in future studies. Future studies using *in vitro* (Liepman *et al.*, 2005; Yu *et al.*, 2018) or synthetic biology (Voiniciuc *et al.*, 2019) approaches are required to elucidate the glycan structures yielded by different enzyme isoforms, or combinations thereof.

Accession Numbers

MUCI10 (At2g22900); MUCI21 (At3g10320); CESA5 (At5g09870); SOS5 (At3g46550); CSLA2 (At5g22740); CSLA3 (At1g23480); CSLA9 (At5g03760)

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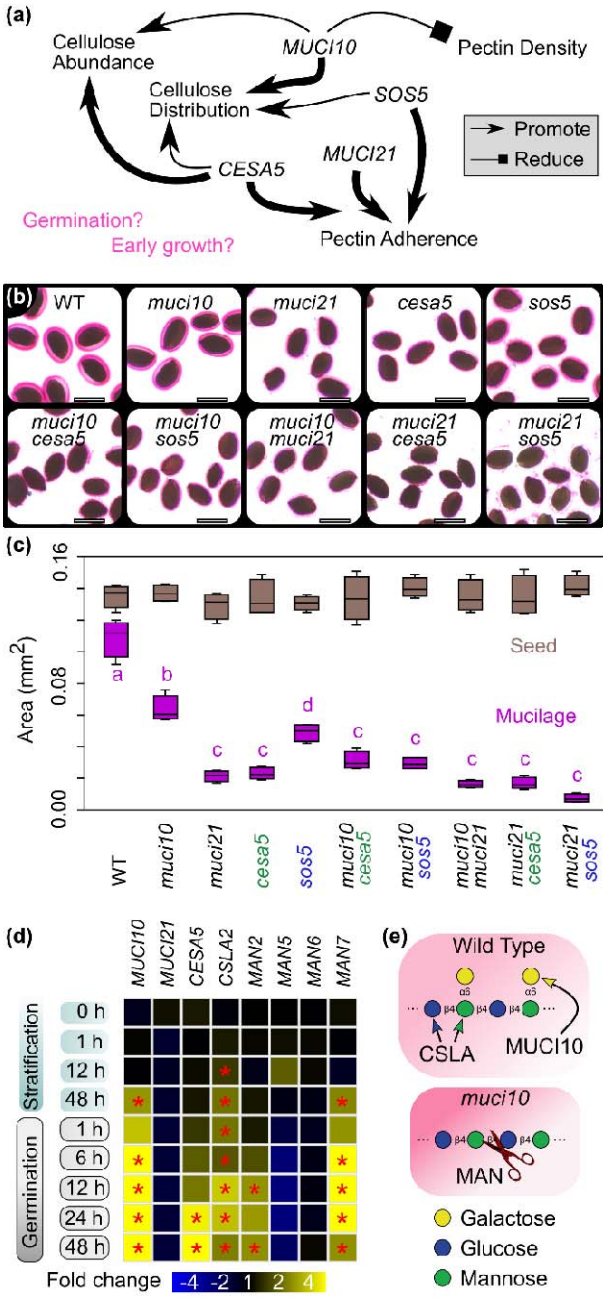
Author Contributions:

B.Y. and C.V. designed the research. B.U. and C.V. supervised the first and second halves of the project, respectively. B.Y., F.H. and C.V. performed experiments and data analysis. C.V. wrote the article using drafts from B.Y. and valuable feedback from B.U.

Figures



318

319 **Fig. 1. Impact of different players on mucilage properties.** (a) Schematic of previously
320 reported functions of four genes on Arabidopsis seed mucilage properties. Genetic interactions
321 between these players and their physiological roles remain unknown. (b) Wild-type (WT) and
322 mutant seeds were gently mixed in water and RR was used to stain adherent pectin (pink). Scale
323 bars = 0.6 mm. (c) Box plots of projected seed and mucilage areas of four biological replicates
324 (each with around 17 seeds) per genotype. Letters denote significant differences (one-way
325 ANOVA with Tukey test, $P < 0.01$). (d) Transcriptional changes (asterisks; $P < 0.001$) during
326 stratification and germination relative to dry seeds (0 h), profiled in GENEVESTIGATOR.
327 (e) Schematic of HM structure in wild-type and *muci10* mutant, which is expected to be more
328 accessible to cleavage or re-modelling by β-1,4-mannanases (MAN).

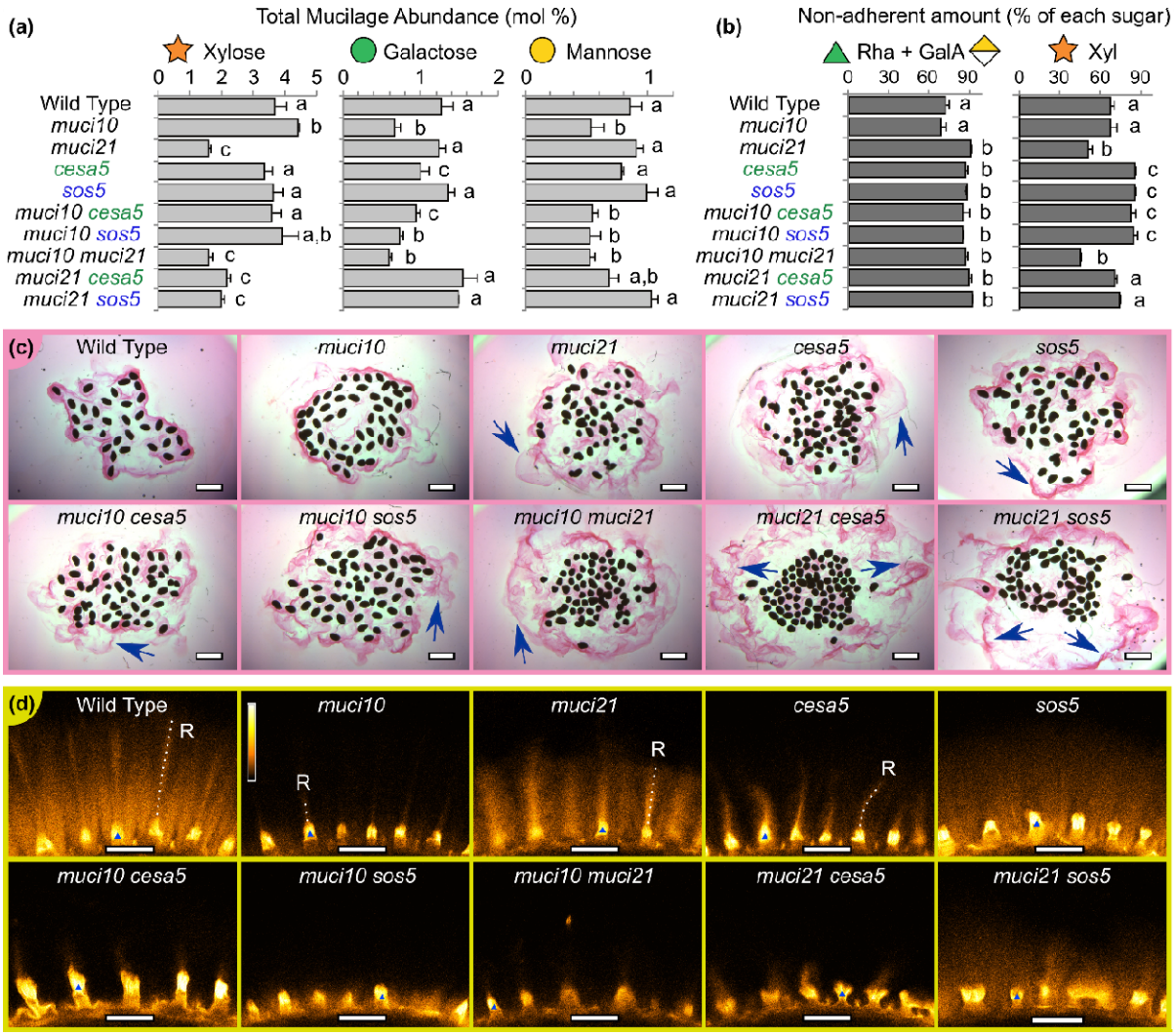


Fig. 2. Mucilage polysaccharide composition and distribution. (a) Relative abundance of hemicellulose-derived monosaccharides in total mucilage. (b) The non-adherent proportion of mucilage pectin (sum of rhamnose and galacturonic acid) and xylan (built of xylose residues). Data show mean + SD of four biological replicates, except only two for *sos5* in (b), and letters denote significant differences (one-way ANOVA with Tukey test, $P < 0.05$). (c) Hydration of seeds in RR solution, without shaking. Blue arrows indicate non-adherent mucilage. (d) S4B staining of cellulose, coloured using Orange Hot LUT in Fiji (see bar in *muci10* subpanel). Blue triangles mark volcano-shaped columellae on the seed surface, and the dashed lines indicate cellulosic rays (labelled R). Scale bars = 1 mm (c), 50 µm (d).

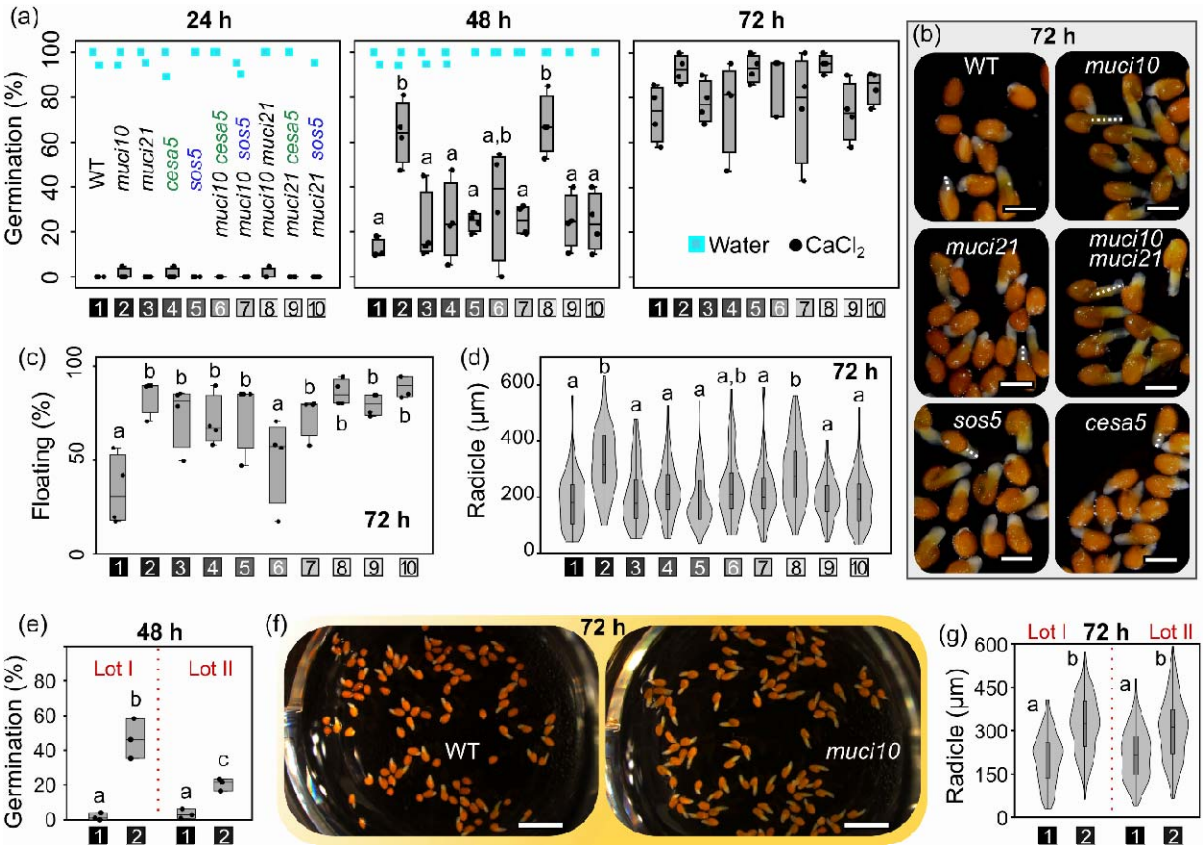


Fig. 3. Germination of seeds in water and $CaCl_2$. (a) Germination of stratified seeds. Box plots show germination of single and double mutants (4 plants, ~20 seeds each, per genotype) treated with 150 mM $CaCl_2$. In water, nearly all seeds germinated within 24 h. (b) to (d) Further analyses of seeds from (a) in the $CaCl_2$ treatment at 72 h. (b) Representative images of germinated seeds, with dashed lines indicating radicle length. (c) Box plots of seed flotation. (d) Violin and box plots of the radicle lengths. (e) to (g) Elevated *muci10* tolerance to 150 mM $CaCl_2$ stress compared to the wild type (WT) was validated using larger quantities of seeds from two independent growth batches. (e) Germination rates at 48 h (3 plants, with ~100 seeds each) per genotype and seed lot. (f) Images of wells from the first seed lot at 72 h. (f) Radicle growth in $CaCl_2$ in two seed lots. All X-axes are labeled using the legend in (a), and letters mark significant changes (one-way ANOVA with Tukey test, $P < 0.05$). Scale bars = 0.5 mm (b) and 2 mm (f).

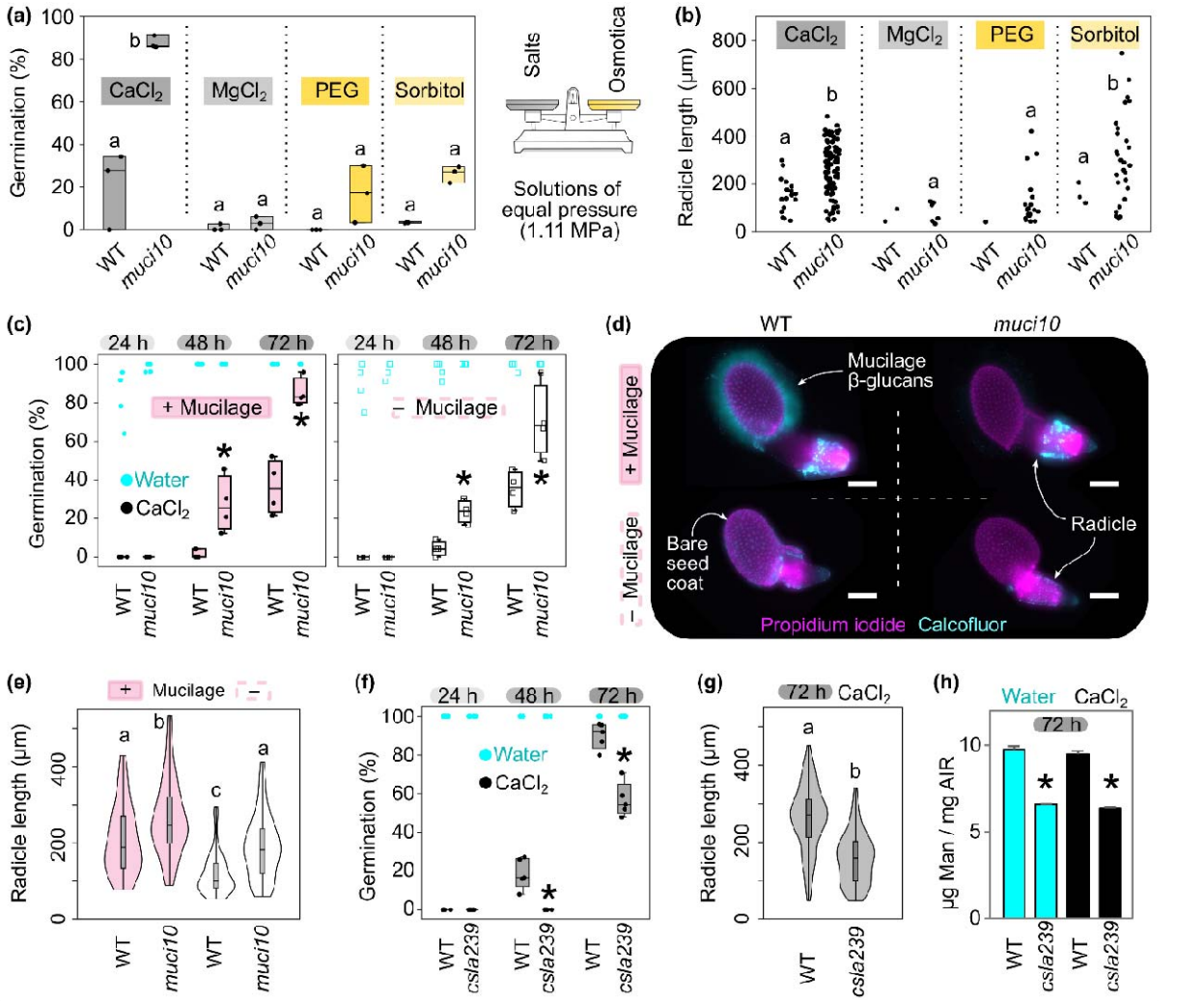


Fig. 4. Dissecting how HM structure impacts germination in adverse conditions. (a) Germination rates at 72 h post-stratification in 150 mM $CaCl_2$, $MgCl_2$ or two osmotica (PEG 4000 and sorbitol), with an equal osmotic pressure. (b) Jitter plots showing radicle lengths at 72 h, from the seeds that germinated in (a). (c) Germination of seeds with (+) or without (–; mill-extracted) mucilage. (d) Dual cell wall staining of seeds germinated at 72 h in $CaCl_2$. All *muci10* seeds as well as mill-extracted wild-type (WT) seeds lack mucilage β-glucans. Scale bars = 200 µm. (e) Radicle lengths of seeds from (c) at 72 h in $CaCl_2$. (f) Germination of WT and *csla239* triple mutant. (g) Radicle length of *csla239* is reduced compared to WT. Data is shown from three biological replicates in (a) and (b), or four biological replicates in (c) to (g). (h) Mannose content in germinated seeds shown as mean + SD of two technical replicates. In all panels, significant changes are marked by different letters (one-way ANOVA with Tukey test, $P < 0.05$) or asterisks (student's t-test, $P < 0.05$; compared to the corresponding WT).

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Supporting Information

Additional Supporting Information is found in the online version of this article

Fig. S1 Xylan and crystalline cellulose distribution around seeds.

Fig. S2 Morphology of seeds in CaCl2 and NaCl treatments.

Fig. S3 Seed germination and flotation rates in water and salt stress.

Fig. S4 Roles of heteromannan-related genes during seed germination.

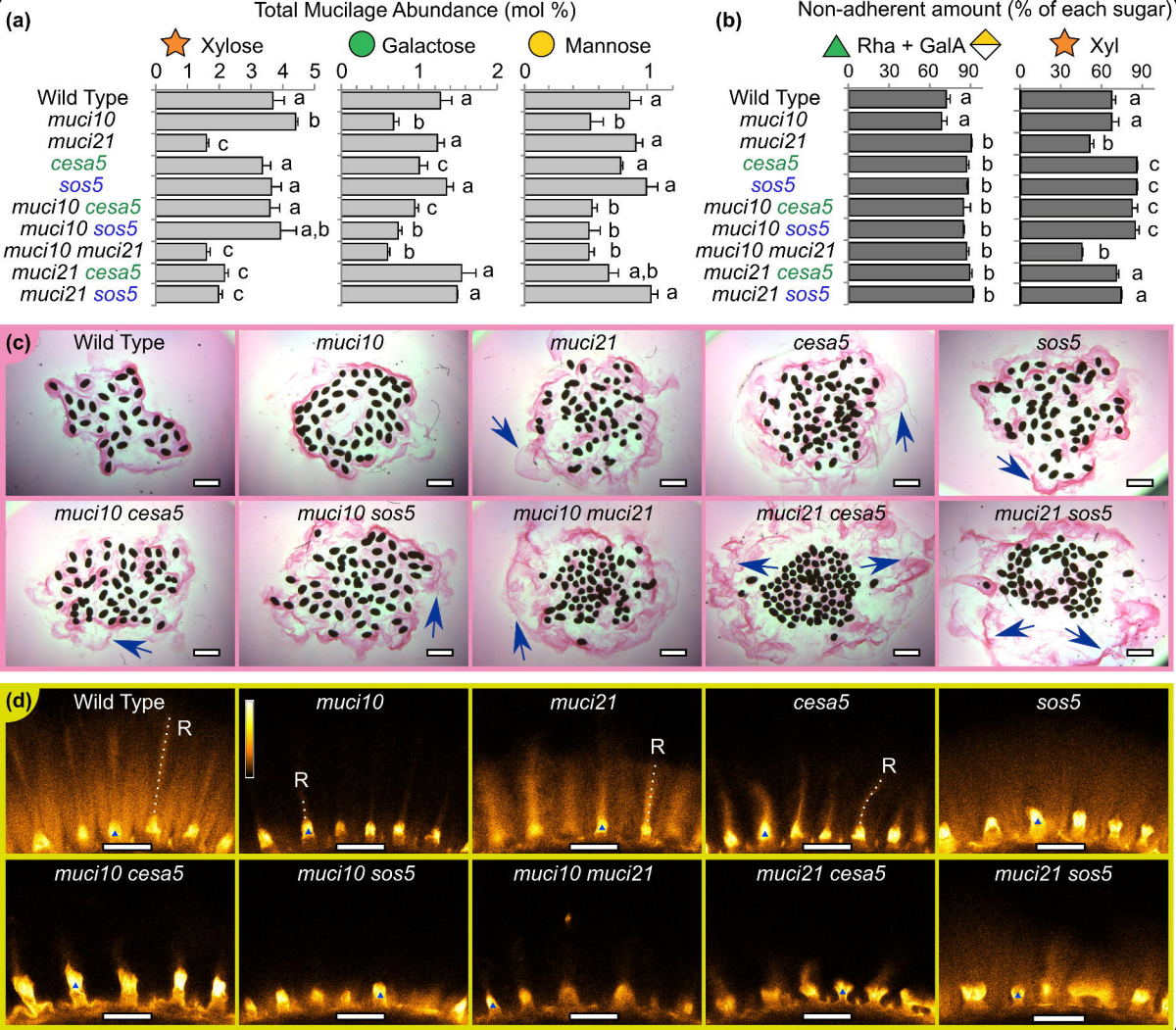
Table S1 Insertional mutants and genotyping primers used in this study.

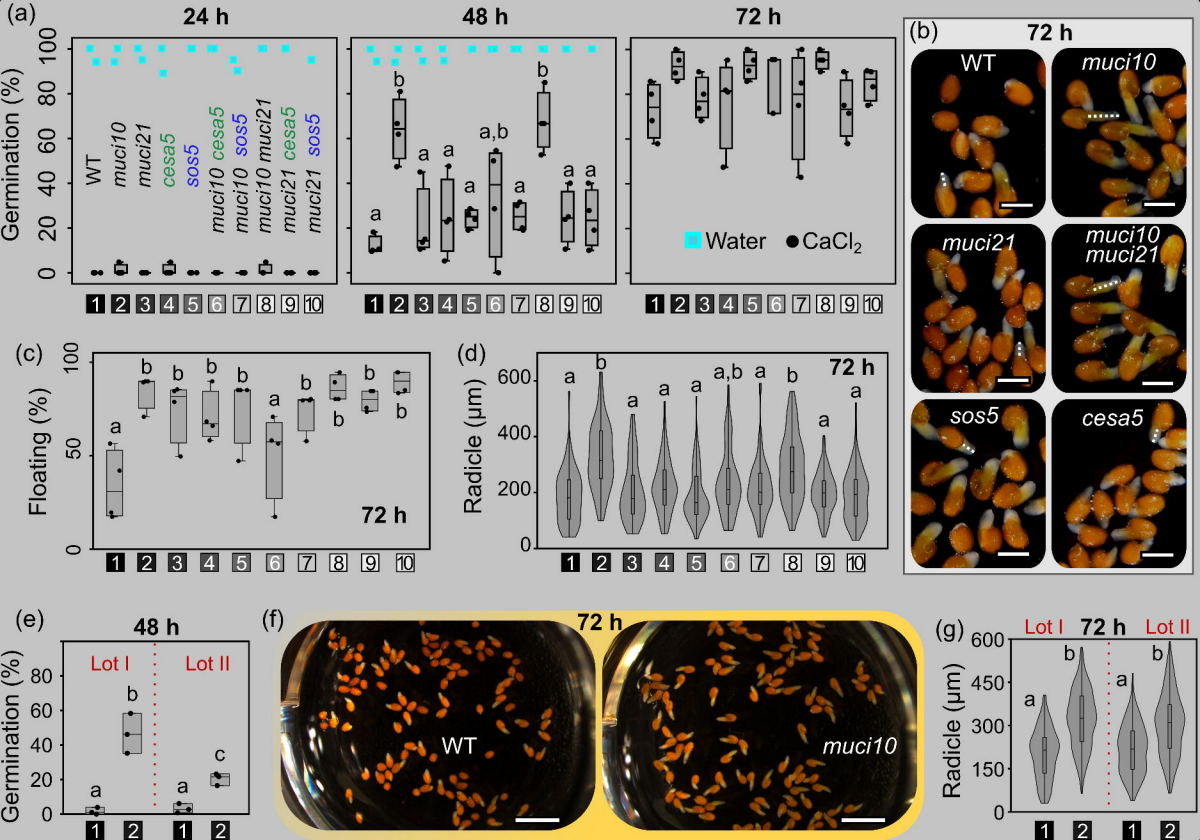
Table S2 Monosaccharide composition of total mucilage extracted from seeds.

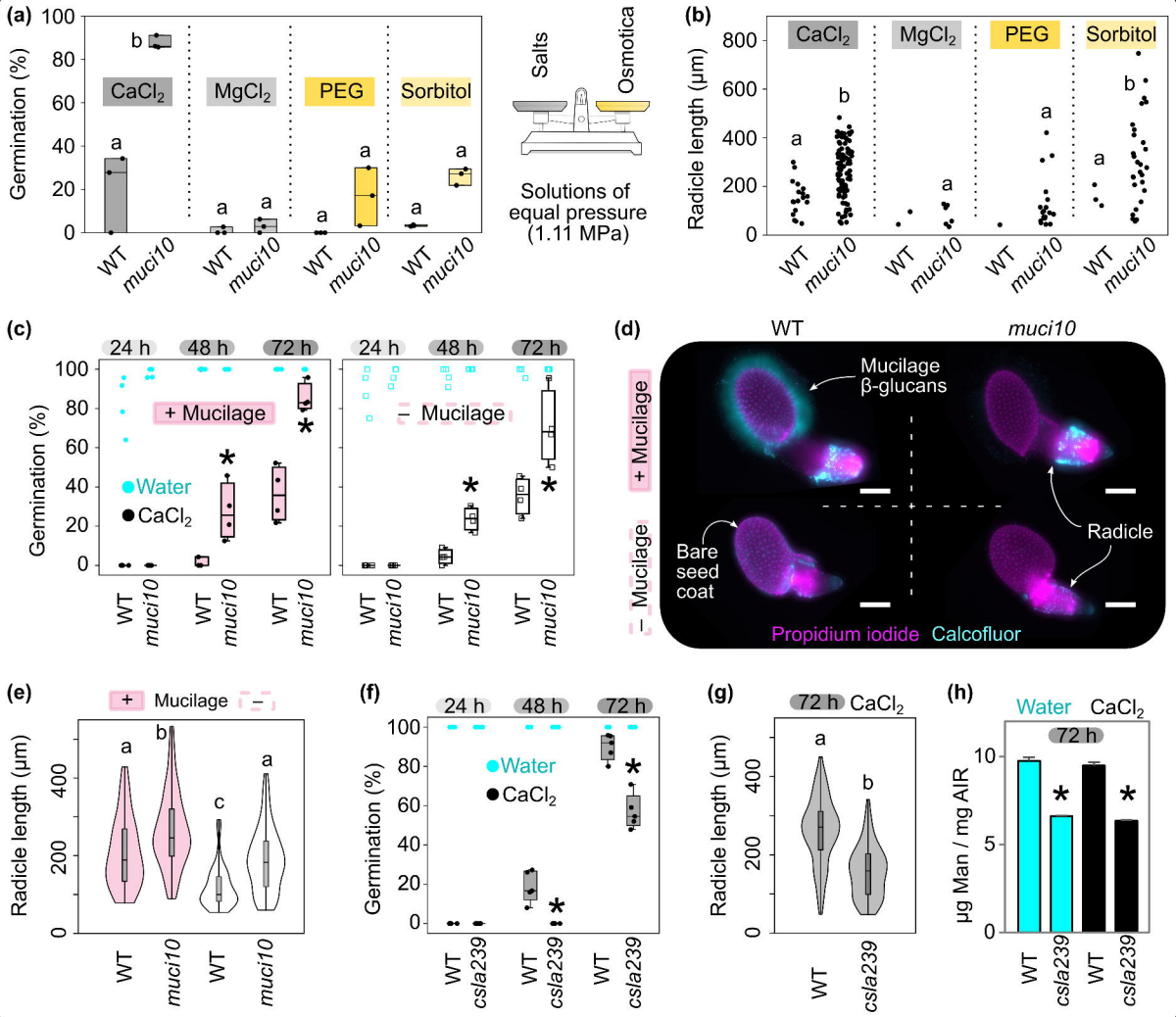
Table S3 Detachment of mucilage components after gentle shaking.

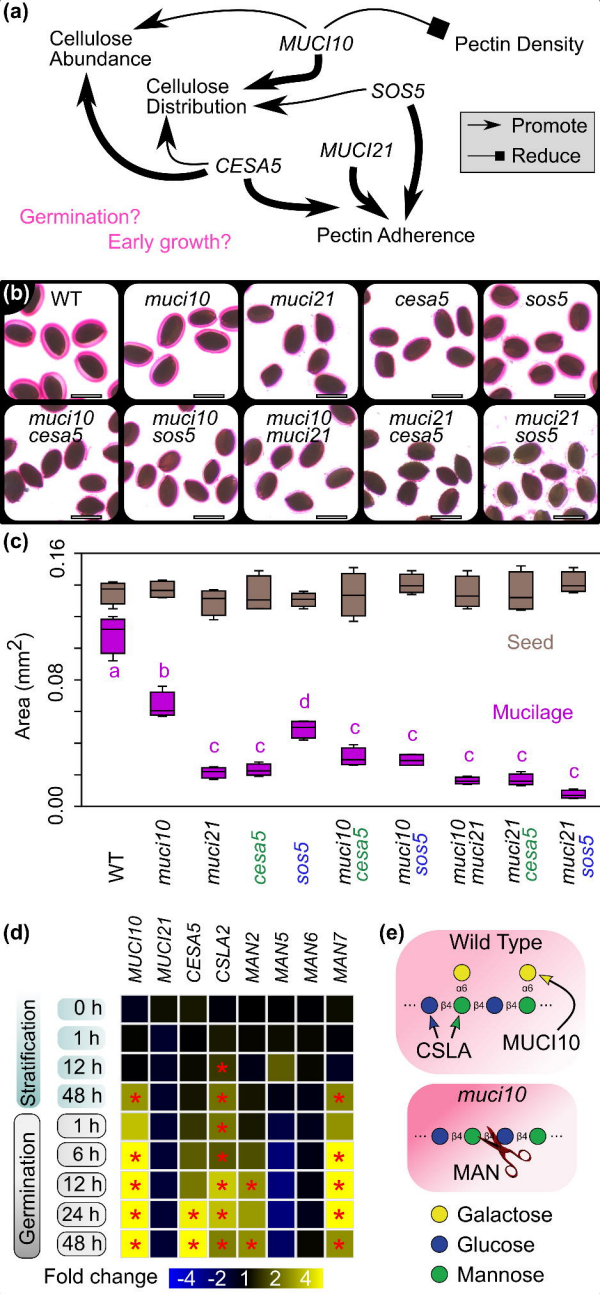
Table S4 Cell wall composition of *csla2* mutant germinated seeds.

Table S5 Cell wall composition of *muci10* and *csla239* germinated seeds.


(a)
Total Mucilage Abundance (mol %)
Xylose
Galactose
Mannose
0 1 2 3 4 5
0 1 2
0 1
Wild Type
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
a b c a a a a,b c b c
a b a c a b b a a,b a
a b a a a b b b b a
(b)
Non-adherent amount (% of each sugar)
Rha + GalA
Xyl
0 30 60 90
0 30 60 90
Wild Type
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
a a b b b b b b b b
a a b c c c c b a a
(c)
Wild Type
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
(d)
Wild Type
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
R


(a)
24 h
48 h
72 h
Germination (%)
WT
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
Water
CaCl2
(b)
72 h
WT
muci10
muci21
muci10 muci21
sos5
cesa5
(c)
Floating (%)
72 h
(d)
Radicle (µm)
72 h
(e)
48 h
Lot I
Lot II
Germination (%)
(f)
72 h
WT
muci10
(g)
Lot I
72 h
Lot II
Radicle (µm)


(a)
Germination (%)
CaCl2
MgCl2
PEG
Sorbitol
WT
muci10
Salts
Osmotica
Solutions of equal pressure (1.11 MPa)
(b)
Radicle length (µm)
(c)
24 h
48 h
72 h
+ Mucilage
– Mucilage
Water
CaCl2
(d)
WT
muci10
+ Mucilage
– Mucilage
Mucilage β-glucans
Radicle
Bare seed coat
Propidium iodide
Calcofluor
(e)
+ Mucilage
– Mucilage
Radicle length (µm)
(f)
Germination (%)
csla239
(g)
72 h CaCl2
(h)
Water
CaCl2
72 h
µg Man / mg AIR


(a)
Cellulose Abundance
MUCI10
Pectin Density
Cellulose Distribution
SOS5
Promote
Reduce
MUCI21
CESA5
Germination?
Early growth?
Pectin Adherence
(b)
WT
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
(c)
Area (mm2)
0.16
0.08
0.00
Seed
Mucilage
a
b
c
c
d
c
c
c
c
c
WT
muci10
muci21
cesa5
sos5
muci10 cesa5
muci10 sos5
muci10 muci21
muci21 cesa5
muci21 sos5
(d)
MUCI10
MUCI21
CESA5
CSLA2
MAN2
MAN5
MAN6
MAN7
Stratification
0 h
1 h
12 h
48 h
Germination
1 h
6 h
12 h
24 h
48 h
Fold change
-4 -2 1 2 4
(e)
Wild Type
α6
β4
CSLA
MUCI10
muci10
MAN
Galactose
Glucose
Mannose