Herbivory-responsive calmodulin-like protein CML9 does not guide jasmonate-mediated defenses in *Arabidopsis thaliana*

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**Abstract**

Calcium is an important second messenger in plants that is released into the cytosol early after recognition of various environmental stimuli. Decoding of such calcium signals by calcium sensors is the key for the plant to react appropriately to each stimulus. Several members of Calmodulin-like proteins (CMLs) act as calcium sensors and some are known to mediate both abiotic and biotic stress responses. Here, we study the role of the *Arabidopsis thaliana* CML9 in different stress responses. CML9 was reported earlier as defense regulator against *Pseudomonas syringae*. In contrast to salicylic acid-mediated defense against biotrophic pathogens such as *P. syringae*, defenses against herbivores and necrotrophic fungi are mediated by jasmonates. We demonstrate that CML9 is induced upon wounding and feeding of the insect herbivore *Spodoptera littoralis*. However, neither different CML9 loss-of-function mutant lines nor overexpression lines were impaired upon insect feeding. No difference in herbivore-induced phytohormone elevation was detected in cml9 lines. The defense against the spider mite *Tetranychus urticae* was also unaffected. In addition, cml9 mutant lines showed a wild type-like reaction to the necrotrophic fungus *Alternaria brassicicola*. Thus, our data suggest that CML9 might be a regulator involved only in the defense against biotrophic pathogens, independent of jasmonates. In addition, our data challenge the involvement of CML9 in plant drought stress response. Taken together, we suggest that CML9 is a specialized rather than a general regulator of stress responses in *Arabidopsis*.

**Introduction**

The environment of organisms is continuously changing over their lifetime. Whereas most of the organisms are able to escape unfavorable conditions, plants are sessile and need to cope up with these changes. Thus, they developed a plenty of strategies to overcome biotic as well as abiotic stresses throughout evolution [1–3]. Since abiotic and biotic alterations of the
environment often occur simultaneously, a complex signaling network is coordinating all the different plant stress responses. Phytohormones play an essential role in these signaling pathways, such as abscisic acid (ABA) as key regulator of abiotic stress responses and salicylic acid (SA) and jasmonic acid (JA) as main mediators of biotic stress responses [3–5]. Resulting from the multiplicity of environmental changes, these stress-related phytohormone pathways overlap. For instance, defense reactions against the specialist herbivore Pieris rapae L. (Lepidoptera, Pieridae) and the generalist Spodoptera littoralis Boisd. (Lepidoptera, Noctuidae) are co-regulated by ABA and JA [6]. Plant-pathogen interactions are highly influenced by abiotic conditions and thus regulated by ABA as well [7]. Besides, the crosstalk between JA and SA has been largely investigated and several examples in herbivory and pathogen defense are known [3, 6, 8, 9].

Upstream of the phytohormone network, changes in the intracellular calcium (Ca\(^{2+}\)) level are one of the earliest signaling events after treatment with various environmental stimuli [10]. Depending on the stimulus different calcium signatures can be measured that vary in their location in the cell as well as in their dynamics [11]. To react appropriately to each stimulus, decoding of the particular calcium signature is necessary. The first step in translating the calcium code into a stress response is the recognition of the Ca\(^{2+}\) by sensor proteins. Calcium sensors are proteins that are able to bind Ca\(^{2+}\) via a helix-loop-helix structure, called EF-hand [12]. Two classes of calcium binding proteins are distinguished: sensor relays and sensor responders. Calcium sensor responders have an enzymatic function additional to their EF-hands that is activated upon binding calcium and by this initiating further signal transduction. In contrast, sensor relays have no other functional domain besides the EF-hands. By binding Ca\(^{2+}\) their conformation is changed, so that an interaction with the respective targets is possible [11]. In the model plant Arabidopsis thaliana (L.) Heynh., 250 calcium sensing proteins are identified, including sensor relays like calmodulins (CAMs), calmodulin-like proteins (CMLs) and calcineurin B-like proteins (CBLs) and sensor responders like Ca\(^{2+}\)-dependent protein kinases (CPKs) [13].

Among them, the group of CMLs is of particular importance for the plant calcium decoding, since they are unique for plants. Several studies revealed that they play a role in calcium perception in a wide range of plant stress responses. CML24 is known to be regulated upon touch, extreme temperatures, darkness, ABA and \(H_2O_2\) treatment and it is a regulator of salt stress response [14, 15]. CML11, CML12, CML16, CML17 and CML23 are induced by elicitors in insect oral secretions (OS), suggesting their possible role in defense against herbivores [16]. Furthermore, some CMLs are known to regulate abiotic as well as biotic stress responses and by this being of special interest in understanding the complex signaling network of the plant. Recently it was shown that CML37 and CML42 are regulators of plant defense against the herbivore S. littoralis and of drought stress. Whereas CML37 is a positive regulator of both stress responses, CML42 acts antagonistically to CML37 [17–19]. Besides, CML37 is induced upon infection with the (hemi)biotrophic pathogen Pseudomonas syringae (van Hall) as well [20]. Another CML coordinating different stress responses is CML9, also known as CAM9. It was suggested to be a negative regulator of the ABA pathway during seed germination and seedling growth. In addition, knock-out of CML9 was leading to a higher salt and drought stress tolerance of the adult plants [21]. On the other hand, CML9 was shown to be upregulated upon P. syringae infection and treatment with SA [22, 23]. Depending on the bacterial strain, CML9 was acting either as a positive or negative regulator of the plant immune reactions [23]. Additionally CML9 is induced by mechanical stimuli and by S. littoralis OS [14, 16, 21], supposing that it might also play a role in herbivore defense.

In order to verify this hypothesis, we studied the functional relevance of CML9 in the defense against the insect herbivore S. littoralis and the spider mite Tetranychus urticae Koch (Trombidiformes, Tetranychidae). We show here that CML9 is rapidly induced upon feeding
of the insect. The employment and analysis of CML9 knock-out and overexpression mutants revealed that CML9 does not regulate the defense against these herbivores. To gain further insight into the putative role of CML9 in abiotic and biotic stress responses, we also investigated, if CML9 might regulate the defense against the necrotrophic pathogen Alternaria brassicicola (Schwein.) Wiltshire, and reexamined its function in drought stress reactions. Our data indicate that none of which is regulated by CML9. Thus, a role for CML9 as a coordinator of abiotic and biotic stress responses has to be reconsidered.

Material and methods

Plant growth

A. thaliana ecotype Col-0 and knock-out mutant lines cml9-a (SALK_006380C) and cml9-b (SALK_126787C; intronic T-DNA insertion lines, Col-0 background), obtained from Nottingham Arabidopsis Stock Center (NASC, Nottingham, United Kingdom), were used for the experiments. Additionally, feeding assays were repeated using the knock-out lines cml9-1 (intronic T-DNA insertion, Col-8 background) and cml9-2 (exonic T-DNA insertion, Ws-4 background) [21] and the overexpression lines OE-CC-2 and OE-CC-5 (Col-8 background) [23]. A. thaliana ecotypes Col-8 and Ws-4 were used as wild type, respectively. Most of the experiments were performed at MPI CE Jena. Seeds were sown in round pots with 10 cm diameter and kept at 4˚C for 2 d. After stratification, plants were grown under short day conditions (10 h : 14 h, light : dark) in a growth chamber at 21˚C and 50–60% humidity. FLUORA bulbs (OSRAM, Garching, Germany) were used as light source and kept in 30 cm distance to the plants to achieve a light intensity of 100 μmol m⁻² s⁻¹.

T. urticae assays were performed at the TU Dresden. Plants were grown under the described conditions at MPI CE Jena in 7 cm x 7 cm rectangular pots to allow monitoring of spider mite development. At the age of 4 weeks, plants were transferred to Dresden into a growth cabinet with slightly changed conditions. Humidity was 60–70%, temperature was around 19˚C, and a mixture of F32T8/TL741/Alto and F17T8/TL741/Alto bulbs (Philips, Hamburg, Germany) was used as light source with same light intensity as FLUORA bulbs.

Alternaria treatments were performed at the FSU Jena. Plants were cultivated as described in Johnson, Sherameti [24]. After 10 days, plants were transferred to soil and further incubated under the published short day conditions with 9 h photoperiod.

Insect and spider mite rearing

S. littoralis larvae were hatched from eggs (Bayer Cropsience, Monheim, Germany) and reared on an artificial diet consisting of 500 g ground beans, 1.2 L water, 9 g vitamin C, 9 g 4-ethylbenzoic acid, 9 g vitamin E Mazola oil mixture (7.1%), 4 mL formaldehyde, 1 g β-sitosterol, 1 g leucine, 10 g AIN-76 vitamin mixture, 200 mL agar solution (7.5%) (modified after Bergomaz and Boppré [25]). Insects were grown at 23–25˚C with a photoperiod of 14 h.

T. urticae females (Weixdorf population) were provided by D. Voigt, TU Dresden, Germany. They were kept on Phaseolus vulgaris (L.) ‘Valja’ and ‘Saxa’ plants (ISP-International Seeds Processing GmbH, Quedlinburg, Germany) at 22–24˚C, 50–65% humidity and a 16 h : 8 h light : dark cycle.

Growth and maintenance of fungi

A. brassicicola (FSU-218) was obtained from Jena Microbial Resource Centre, Jena, Germany. The fungus was grown on potato dextrose agar (PDA) medium (pH 5.6) at 22 ± 1˚C in a temperature-controlled chamber in the dark and 75% relative humidity for 2 weeks.
Plant treatments

5- to 6-week old plants were used for all herbivory-associated experiments. Insect biomass assays, short term feeding assays with *S. littoralis* larvae and OS treatment were performed according to Scholz, Vadassery [18]. MecWorm [26] was used for continuous mechanical wounding of the plant. Six different shaped areas (rectangular and circular), each lasting 30 min using a speed of 12 punches per minute, were designed to realize the given time points. Areas were arranged over the leaf lamina without wounding the midrib. Tissue samples for later extraction were immediately frozen in liquid nitrogen. For investigation of the possible interaction of ABA and wounding, plants were sprayed with a 100 μM ABA solution, containing 0.02% of ethanol. After 1 h, plants were treated with MecWorm for 30 min. Time points and ABA concentrations were chosen according to Magnan, Ranty [21] and prior results in this study.

For spider mite performance assay each plant was infested with one 3- to 5-day-old adult female. Mites were kept for 2 days on the plants to allow oviposition and were removed afterwards. Plants were monitored daily over development of one generation of spider mites. Number of eggs and immatures were counted and fitness parameters calculated.

For fungi treatment *A. brassicicola* spore suspension was prepared as follows: 5 ml of sterile-filtrated 0.01% Tween-20 were dropped on plates of 2-week old *A. brassicicola* cultures and plates were gently pivoted. Remaining spores were carefully removed with a spatula. The spore suspension was washed 3 times with 0.01% Tween-20 and filtrated through a 75 μm nylon membrane. The spore concentration was determined using a haemocytometer and was adjusted to 1 x 10⁶ colony forming units (cfu) ml⁻¹. Mature leaves of 5- to 6-week-old *Arabidopsis* plants were used for inoculation assay. Single leaves were detached and placed in petri dishes containing sterilized filter paper soaked with 1.5 ml water. 2 μl of *A. brassicicola* spore suspension or solvent control was inoculated to each leaf. Plates were sealed to keep high humidity and incubated under continuous light as described above. To analyze the viability of treated leaves, chlorophyll fluorescence parameters were measured using a FluorCam FC 800-C (PSI, Brno, Czech Republic). Before measurement, the sealed plates were incubated in the dark for 20 min. Afterwards, plates were placed into the FluorCam and analyzed using following settings: Act 1: 50%, Act 2: 50%, Super: 100%. The QY_max (maximum PSII quantum yield) was recorded.

The drought stress assay was done with four week old plants as described in Scholz, Reichelt [19]. First drought period was extended to 11 days according to Magnan, Ranty [21]. After 11 days plants were watered till soil was fully soaked, followed by a second drought period of 1 week. To avoid competition between wild type and mutant plants, each was kept in single pots. Pots were placed randomly on the same tray, to minimize experimental variation.

Quantitative real time (qRT)-PCR

RNA from single leaves was isolated using TRIzol® Reagent (Invitrogen™, Darmstadt, Germany) according to the manufacturers’ instructions with slight modifications. Leaf material was ground using 2010 Geno/Grinder® (SPEX® SamplePrep, Metuchen, USA) with a pre-cooled cryoblock. All centrifugation steps were performed at 4°C and 16000 x g. After adding TRIzol®, samples were incubated for 20 min at room temperature. 300 μL chloroform was added, followed by incubation on ice for 20 min. The samples were centrifuged for 30 min. The aqueous phase was transferred into 600 μL isopropanol and samples precipitate overnight on -20°C. To pellet the RNA, samples were centrifuged for 30 min. Pellet was washed with 80% ethanol and air dried. The dried pellet was dissolved in 80 μl preheated water. RNA was treated with TURBO DNase (TURBO DNA-free™ Kit, Invitrogen™, Darmstadt, Germany) to avoid DNA contamination. RNA concentration was measured with a photospectrometer and 1 μg of RNA was transcribed into cDNA using Omniscript® Reverse Transcription Kit.
(Qiagen, Hilden, Germany) and Oligo(dT)12-18 Primer (Invitrogen™, Darmstadt, Germany). RPS18B was used as housekeeping gene and primers published for RPS18B and CML9 [16] were used for expression analysis of CML9 after herbivore-associated stimuli. RPS18B was used as housekeeping gene and primers published for RPS18B and CML9 [16] were used for expression analysis of CML9 after herbivore-associated stimuli. For quantification of exon1-exon3 fragment of CML9, primers (see S1 Table) producing a product of 168 bp, were designed in NCBI Primer-BLAST (http://www.ncbi.nlm.nih.gov/tools/primer-blast/) and cross checked in Vector NTI Express 1.2.0 software (Thermo Fisher Scientific™, Schwerte, Germany). QRT-PCR was performed in 96 well plates in a CFX96 Touch™ Real-Time PCR System (Bio-Rad, München, Germany). Brilliant II QPCR SYBR green Mix (Agilent, Waldbronn, Germany) was used as master mix. The normalized fold expression was calculated with the ΔΔCT method [27]. Untreated plants or, in case of ABA spray, plants sprayed with 0.02% ethanol were used as controls and their expression level was defined as 1.

**Phytohormone quantification**

Phytohormone analysis was performed according to Jimenez-Aleman, Scholz [28] with modifications. Approximately 250 mg ground plant tissue was extracted with 1.5 mL methanol containing 60 ng D6-abscisic acid (Santa Cruz Biotechnology, Santa Cruz, U.S.A.), 60 ng of D6-jasmonic acid (HPC Standards GmbH, Cunnersdorf, Germany), 60 ng D4-salicylic acid (Sigma-Aldrich) and 12 ng of jasmonic acid-13C6-isoleucine conjugate as internal standard. LC-MS/MS measurements were performed on an Agilent 1200 HPLC system (Agilent, Waldbronn, Germany) coupled to an API 5000 tandem mass spectrometer (Applied Biosystems, Darmstadt, Germany) with a Turbo spray ion source in negative ionization mode. The analyte parent ion → product ion for multiple reaction monitoring (MRM) were the following: m/z 263.0 → 153.2 (collision energy (CE) -22 V; declustering potential (DP) -35 V) for abscisic acid; m/z 269.0 → 159.2 (CE -22 V; DP -35 V) for D6-abscisic acid; m/z 209.1 → 99.0 (CE -24 V; DP -35 V) for jasmonic acid; m/z 215.1 → 99.0 (CE -24 V; DP -35 V) for D6-jasmonic acid; m/z 136.9 → 93.0 (CE -22 V; DP -35 V) for salicylic acid; m/z 140.9 → 97.0 (CE -22 V; DP -35 V) for D4-salicylic acid; m/z 290.9 → 165.1 (CE -24 V; DP -45 V) for cis-(+)-12-oxophytodienoic acid (cis-OPDA), m/z 322.2 → 130.1 (CE -30 V; DP -50 V) for jasmonic acid-isoleucine conjugate; m/z 328.2 → 136.1 (CE -30 V; DP -50 V) for jasmonic acid-13C6-isoleucine conjugate. For ABA quantification after drought stress the elution profile was modified as follows: 0–0.5 min, 10% B; 0.5–4.0 min, 10–90% B; 4.0–4.02 min 90–100% B; 4.02–4.5 min 100% B and 4.51–7.0 min 10% B keeping a flow rate of 1.1 mL/min.

**Genotyping**

For genotyping, DNA of single leaves of 3-week-old plants was isolated according to a modified protocol of Konieczny and Ausubel [29]. Samples were ground as described above. Extraction was performed using half of the given volumes of chemicals and buffer. All centrifugation steps were carried out at 16000 x g. After precipitation, sample was centrifuged for 20 min and pellet was directly washed in 70% ethanol. The dried pellet was dissolved in 30 μL water to achieve a higher concentration. Genotyping primers were designed with SALK T-DNA primer design tool (http://signal.salk.edu/tdnaprimers.2.html). Sequences of the primers are listed in S1 Table. Native Taq DNA polymerase and 10 mM dNTP Mix (both Invitrogen™, Darmstadt, Germany) were used for PCR. Mastermix was prepared according to the manufacturers’ protocol and scaled down to a reaction volume of 10 μL, including 1.5 μL of template.

**Semiquantitative reverse transcription (RT)-PCR**

RNA isolation, DNase treatment and cDNA synthesis were carried out as described above. ACTIN2 was used as housekeeping gene. The same primer sequences for ACTIN2 were used as
described before [17]. CML9 primers were designed with the same tools as qRT-PCR primers (see S1 Table). PCR was performed as described above.

Statistical analysis
Statistical significances were tested using t-test or Wilcoxon-test in RStudio 0.98.1103.0, or by ANOVA using SigmaPlot 12.2.0 (Systat Software GmbH, Erkrath, Germany). False discovery rate (FDR, [30]) was calculated if t-test or Wilcoxon-test was repeated more than 3 times in 1 data set. Statistical tests used for different experiments are indicated in the figure legends.

Results
Expression of CML9 is induced upon herbivory
Several transcript studies in Arabidopsis already indicated that CML9 is induced by herbivore-associated stimuli [14, 17, 21]. Nevertheless, other data showed no change of the expression level after wounding or herbivory and even repression of the gene after application of methyl-JA [31]. In order to test these contradictory results, we treated the plants with various herbivore-associated stimuli and analyzed the CML9 expression level using qRT-PCR. We found that CML9 is significantly induced about 1.5-fold already after 30 min feeding of the chewing insect S. littoralis (Fig 1A)). This induction was transient and reached the base level after 60 min, further reduction of the expression levels at 2 and 3 h was not significant. Since feeding of herbivores can be recognized by the mechanical wounding pattern as well as by elicitors in the OS of herbivores [32], we tested further if both stimuli can induce a change in CML9 transcript level. Therefore, plants were mechanically wounded with a pattern wheel and either water or S. littoralis-derived OS was applied to the wounds. In both cases CML9 was quickly and transiently upregulated (Fig 1(B)), as was found in the real insect treatment. After 30 min, wounding induced CML9 one-fold, compared to the untreated controls. The application of insect OS increased CML9 transcript level even two-fold compared to controls, suggesting that both stimuli cause the induction of CML9 upon feeding of S. littoralis to a similar extend. Additionally, wounding treatment was repeated using MecWorm, a robotic larva mimicking the wounding pattern of a chewing insect [26], to confirm the results of the artificial wounding with a pattern wheel. MecWorm treatment caused the same expression pattern as all the treatments before (Fig 1(C)): CML9 was induced about 1.5-fold shortly after wounding by MecWorm. This regulation was also transient and CML9 transcript level decreased in later time points.

CML9 was shown to be induced by ABA as well [21]. Regarding to the given crosstalk between the ABA pathway and the defense against herbivores [6], we tested if there is an additive or synergistic effect of both treatments together on the CML9 expression level. We compared the expression level of plants treated only with MecWorm or ABA with plants that were treated with both (Fig 1(D)). All three treatments induced CML9 expression to the same extends. These data exclude an additive effect of ABA and wounding by an herbivore on the induction of CML9.

Herbivore performance is not affected by CML9 knock-out or overexpression
Because of the fast induction of CML9 after S. littoralis feeding, the functional relevance of CML9 to the plant defense against this herbivore was further investigated by studying CML9 loss of function mutants. Two homozygous intronic T-DNA insertion lines (cml9-a and cml9-b) were used in a conventional one-week feeding assay. Feeding performance of the larvae was determined by measuring the larval weight (Fig 2). Larvae feeding on cml9-a gained
little but significantly more weight than larvae feeding on corresponding wild type plants, although the measured effect was small. However, this result was not confirmed with the second knock-out line. Larvae feeding on cml9-b gained as much weight as on wild type plants (Col-0) (Fig 2(A)). Since the different response of these two loss-of-function mutants, two more knock-out mutant lines (cml9-1 and cml9-2 [21]) and two overexpression lines (OE-CC-2 and OE-CC-5[23]) were tested in feeding assays. All of the additional mutant lines display a different ecotype background: whereas cml9-1 and both overexpression lines are in Col8 background, cml9-2 is in Ws background. In general, S. littoralis larvae gained more weight on genotypes with the Ws ecotype than on those with the Col background (Fig 2(B)). However, the larvae gained as much weight on the knock-out lines as on the corresponding wild types, confirming the results of the cml9-b lines (Fig 2(B)). Moreover overexpression of CML9 did not influence the larval performance as well (Fig 2(C)).
To further investigate the different susceptibility of \textit{cml9-a} and \textit{cml9-b} to \textit{S. littoralis} feeding, we measured the phytohormone content after feeding of the larvae. Especially the jasmonates are main regulators of this defense response [4]. Thus, we measured the content of JA, its precursor \textit{cis}-12-oxophytodienoic acid (\textit{cis}-OPDA) and the active jasmonate, jasmonic acid-isoleucine (JA-Ile) (Fig 3(A)–3(C)). All three jasmonates increased after feeding of \textit{S. littoralis}, but to the same extend in both \textit{cml9} lines as in Col-0 wild type plants. Besides, SA and ABA have been shown to modulate herbivore defense [6, 8, 9]. Hence, we analyzed the levels of these phytohormones additionally (Fig 3(D) and 3(E)). The ABA content was slightly increased upon insect feeding, whereas the SA level was nearly the same as in control plants. Nevertheless, there were no significant differences in the SA or ABA level obtained between the \textit{cml9} lines and in comparison to the wild type. Both \textit{cml9} lines show similar results for all tested phytohormones, thus slight differences observed in the feeding behavior of \textit{S. littoralis} between the lines are not due to a change in phytohormone elevation.

Regarding the data of the \textit{S. littoralis} feeding performance on the \textit{cml9} lines, we tested the performance of a second herbivore with a different feeding strategy on \textit{cml9-a} and \textit{cml9-b} mutants in comparison to wild type plants. We used the piercing-sucking spider mite \textit{T. urticae}. Different fitness parameters of \textit{T. urticae} were monitored daily over development of one generation (Fig 4). Spider mites established successfully on all plants and dispersed over the leaves. Infested plants showed numerous chlorotic spots. All tested fitness parameters in the early stage of spider mite development that we obtained on the \textit{cml9-a} and \textit{cml9-b} were comparable to those on Col-0 wild type plants, such as fecundity, time of egg development and the egg mortality. Even the time of immature development and the sex ratio were not changed in \textit{cml9-a} and \textit{cml9-b} plants compared to the Col-0 wild type. Only the immature mortality of \textit{T. urticae} reared on \textit{cml9-a} plants was little higher than on wild type plants. Collectively, these results suggest that CML9 is not a regulator of plant defense against the tested herbivores.

\textbf{Arabidopsis thaliana cml9 plants show a wild type-like response to \textit{Alternaria brassicicola}}

CML9 is described to modulate plant defense against different strains of the phytopathogenic bacteria \textit{P. syringae} [23]. To further investigate if CML9 might act as a regulator in defense against other pathogens, we examined the reaction of \textit{cml9-a} and \textit{cml9-b} plants upon fungal infection with \textit{A. brassicicola}. \textit{A. thaliana} wild type Col-0 and \textit{cml9-a} and \textit{cml9-b} leaves were inoculated with a spore solution or mock treated and analyzed 3 and 4 days post-inoculation. Both \textit{cml9} lines showed the same level of susceptibility than the wild type (Col-0) to the pathogen at tested time points (Fig 5(A)). There were no obvious differences in the formation and size of lesions at the macroscopic level observed. Additionally, we evaluated plant susceptibility by measuring chlorophyll fluorescence parameters of the inoculated leaves. In all plants the determined QY-max coefficient (0.75) indicated a decrease in fluorescence upon treatment.
Nevertheless, chlorophyll fluorescence in the treated mutant lines was reduced to the same extent like in infected wild type (Col-0) plants, confirming the phenotypic results. Hence, CML9 does not seem to modulate plant defense against *A. brassicicola*.

**Loss-of-function mutants are as susceptible to drought as wild type plants**

In previous studies it was shown that CML9 is very likely a negative regulator of ABA-related stress responses, e.g. drought [21]. It was hypothesized that the higher drought tolerance of...
Role of CML9 in herbivory

cml9 could be explained by hypersensitivity of the mutants to ABA, since both of the tested mutant lines showed a wild type-like ABA content upon drought [21]. Nevertheless, in that study ABA elevation was just analyzed after some hours of drought stress, but not in long term stress treatment like it was done for other CMLs by Scholz, Reichelt [19]. To elucidate whether a later increase in the ABA level could explain the higher resistance of cml9 against drought, we kept the plants under drought conditions for 11 d or 18 d with watering once after 11 d. In contrast to previous published results, cml9-a and cml9-b mutants were as tolerant to drought

Fig 4. T. urticae performance on cml9-a and cml9-b. Different fitness parameter monitored over development of one generation of spider mites are shown in box plots: fecundity (number of eggs per female per 24 h) (a), egg development (means of all eggs on one plant) (b), egg morality (c), immature development (means of all immatures pooled together on one plant: larva, nymphochrysalis, protonymph, deutochrysalis, deutonymph, teleochrysalis) (d), immature mortality (sum of mortality of all immature stages) (e), sex ratio (males : females) (f). The box indicates the middle 50% of the data points. At least n = 31 plants per genotype were used. Black triangles represent outliers and the black squares the means. Whiskers are defined as 1.5 fold IQR. Statistically significant differences between Col-0 wild type and mutant lines were determined by unpaired two-sample Wilcoxon test. Asterisk indicates significance (" P < 0.05), n.s. means not significant.

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as wild type plants (Fig 6(A)). Parallel to this stress treatment we quantified the ABA level in all genotypes. Without stress, all plants had similar endogenous ABA content (Fig 6(B)). As expected, a significant increase in this ABA content was observed in wild type (Col-0) 11 and 18 days after the beginning of the stress treatment (Fig 6(B)). Although we measured a slightly lower content of ABA at 11 d and 18 d in cml9-a and cml9-b control plants, the ABA elevation after drought showed the same profile and levels as the corresponding wild type line. Taken together, our data suggest that CML9 does not act as a key regulator of drought stress responses in plants.

Fig 5. Response of A. thaliana wild type and cml9 lines to A. brassicicola infection. Macroscopic observation of lesion formation (a) and measurement of chlorophyll fluorescence (b) of wild type and mutant leaves 3 and 4 day post-inoculation (dpi) with A. brassicicola spore suspension (Ab) or 0.01% Tween-20 solution as mock (M). Experiment was repeated three times independently. Plants shown are representative. Statistically significant differences in chlorophyll fluorescence of different genotypes among one treatment were determined by one-way ANOVA. No significant differences were measured, as indicated by the letters.

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In this study two independent intronic T-DNA insertion lines were used as knock-out mutants, both with a T-DNA insertion in the third intron (Fig 7(A)). Prior to all experiments, the insertion of the T-DNA was confirmed by genotyping (Fig 7(B)). Two different primer

![Comparison of drought stress response of wild type and cml9 mutants.](https://doi.org/10.1371/journal.pone.0197633.g006)
Fig 7. Genetic differences between cml9-a and cml9-b. (a) Schematic overview of CML9 with T-DNA insertions and the used primers for RT- and qRT-PCR. Exons are indicated with E, introns with I. Light gray triangles indicate T-DNA insertions. RT primers used are indicated by black arrows, qRT primers by grey arrows (qRT FP1 and qRT RP1 are published as CML9 primers in Vadassery, Scholz [16]). Total length of CML9 gDNA without insertions is 1137 bp. (b) Verification of T-DNA insertions in CML9 by genotyping. The expected product length is indicated on the right sites of the respective pictures. (c) Semi quantitative RT-PCR analysis of CML9 expression in wild type and knock-out mutants. Plants were treated with a pattern wheel and either water (WW) or S. littoralis oral secretion.
pairs were used for PCR: one gene specific primer pair and a second one including the left border of the insertion. In both mutants there was no product for the intact CML9 detectable (upper row, Fig 7(B)). Only a product consisting of truncated CML9 and the T-DNA border was observed (lower row, Fig 7(B)). Both lines were verified as homozygous. The absence of the full length CML9 transcript in MecWorm treated mutants was confirmed by semi quantitative RT-PCR (S1 Fig). Since these two cml9 lines exhibited slightly different responses to herbivore treatments as described above, a more detailed genetic analysis for both lines was performed.

Although T-DNA insertion mutants are usually very stable, the use of intronic insertion lines can be problematic. It was shown that different environmental stimuli can cause alternative splicing of introns leading to a loss of the T-DNA insertion and, thus, to a wild type-like expression of the gene [33, 34]. In order to examine whether herbivory by S. littoralis is able to stimulate such an alternative splicing event in the two cml9 lines, we analyzed the cml9 gene expression by another semi quantitative RT-PCR. Since the first RT-PCR (S1 Fig) revealed that mechanical wounding by the larvae is not leading to any CML9 transcript accumulation in the mutants, we investigated if treatment with the insect-derived OS may stimulate gene expression. The OS treatment was performed as described above. No CML9 transcript was detectable in both mutants upon application of OS ((Fig 7(C)), upper row). Furthermore, the same was observed for the water treatment, confirming the result of the first RT-PCR. Thus, a loss of the entire T-DNA insertion by alternative splicing due to herbivory is unlikely for both cml9 mutant lines.

The expression of fragments upstream or downstream of a T-DNA insertion can lead to the production of a truncated protein [35]. Just recently it has been shown, that two T-DNA alleles of a receptor kinase respond differently, due to the production of a truncated protein in one of these lines [36]. To exclude this possibility, the expression of the fragment upstream of the T-DNA insertion (from the first to the third exon) was investigated by RT-PCR. In all treatments and controls in the mutants, this fragment was expressed ((Fig 7(C)), middle row). In cml9-a plants, two additional unspecific bands were detectable. Sequencing of these fragments revealed that they are artefacts of an incorrect splicing event. The sequences or part of the sequences of the first and second intron are still included in the products. Thus, the T-DNA insertion in cml9-a seems to influence the splicing process of the CML9 RNA, suggesting that it is unlikely that a truncated, but functional protein is produced. In cml9-b only the correctly spliced fragment was found. If a truncated protein was produced, two of the four EF-hands would miss, leading to a lower Ca$^{2+}$ binding capacity and probably to reduced activities.

When comparing the expression of the expected CML9 fragment with the house keeping gene expression ((Fig 7(C)), lower row), the transcript level of the fragment was lower in both mutants than in the wildtype. To refine this observation a qRT-PCR was performed (Fig 7(D)). Data were analyzed by two-way ANOVA, in order to test whether there is a difference among the treatments and the genotypes and if one of those could be explained by the other. The statistical analysis revealed that there is a significant increase in the fragment transcript.
abundance upon OS treatment in all three genotypes (Table 1). Nevertheless, even when a very low threshold of two-fold was used, upon both treatments an induction of the fragment could only be observed in the wild type. In cml9-b the fragment is only induced upon OS treatment, whereas in cml9-a the fragment is not induced at all. Furthermore there is a significant difference between the genotypes. However, this statistical difference between the genotypes was not due to the treatments. This suggests that the two cml9 lines vary genetically and this also might explain some varying results in herbivore treatments.

**Discussion**

In plants, the perception of environmental stimuli is followed by a fast calcium elevation inside the cells [10]. These calcium signals encode information about the stimulus that need to be translated into the appropriate response [11]. However, relatively little is known about the decoding of such calcium signals. CML proteins are important in sensing calcium signals after various external stimuli. Here we focused on the CML9. By using different CML9 mutant lines, we investigated the role of this calcium sensor in biotic and abiotic stress responses.

**CML9 is not a regulator of plant herbivore defense**

CML9 was described as a regulator of the plant defense against phytopathogenic bacteria [23]. The signaling cascade after recognition of a pathogen is also related to the signaling pathway after herbivory [32]. Thus, we examined if CML9 is also involved in the herbivore defense. First, we demonstrated that CML9 is induced upon feeding by the insect herbivore S. littoralis (Fig 1(A)). This enhancement in the transcript level is caused by the mechanical wounding of the larvae as well as by the OS (Fig 1(B) and 1(C)). Unlike the known defense regulators CML37 and CML42 that are mainly regulated by one of the two stimuli [17, 18], CML9 is equally induced by both. The result that CML9 is a wound-inducible gene is of great interest, because the yet published literature was contradictory [21, 31]. Besides, our data indicate that the induction of the CML9 transcript level after wounding is not synergistically regulated by ABA. Although CML9 expression was upregulated by either of the treatments, ABA had no additional effect on the transcript level (Fig 1(D)). This suggests that the regulation of CML9 mRNA levels after herbivory might be independent of ABA. Among all herbivore-associated treatments CML9 displayed a characteristic expression dynamic. Like CML42, CML9 expression was fast and transiently up-regulated and down-regulated at later time points. This result was quite surprising, since it was described that CML9 expression occurred late and remained high after OS treatment [16]. On the other hand, the fast and transient expression profile seems to be typical for CML9. The same dynamics were found after drought and pathogen-associated stress treatments [21, 23]. Compared to the stimulation of CML37 and CML42 mRNA levels after herbivory, the CML9 transcript is only slightly induced [17, 18]. The same holds true for the CML9 mRNA level after pathogen treatments [23]. Moreover, semi quantitative RT-PCR revealed that the basic level of the CML9 transcript in untreated plants is already

<table>
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Role of CML9 in herbivory

quite high (Fig 7(C)), suggesting that CML9 is rather constitutively expressed than strongly induced.

Despite the fast upregulation of CML9 after herbivore treatment, the analysis of different CML9 knock-out lines revealed that CML9 is not a key player in herbivore defense. In three independent lines (cml9-b, cml9-1, cml9-2) the performance of the chewing insect S. littoralis was unaffected by the loss of function of the gene (Fig 2A and 2B). Similar results were obtained for the performance of the piercing-sucking spider mite T. urticae on the knock-out line cml9-b (Fig 4). Only in cml9-a line, slight changes in the herbivore performance were observed. In detail, T. urticae displayed a higher immature mortality (Fig 4), which represents one out of six examined parameters. On the other hand, S. littoralis larvae performed better on the cml9-a line than on the Col-0 wild type (Fig 2(A)), suggesting a positive influence of CML9. However, compared to loss-of-function mutants of the positive defense regulator CML37 [18], cml9-a line was only slightly more susceptible to S. littoralis and more similar to the three additional knock-out lines tested (Fig 2(A) and 2(B)). As treatment with T. urticae showed similar results (Fig 4), all these data strongly suggest that the effects in cml9-a are not due to the loss-of-function of CML9.

Besides, throughout all feeding assays with S. littoralis, larvae gained more weight on plants with the Ws-4 ecotype background than on plants with Col-0 background (Fig 2(B)). This result is in agreement with previous studies showing that different insect species prefer Ws-0 to Col-0 ecotypes [37, 38] and could be correlated with lower glucosinolate content in the Ws-0 ecotype [37], a finding that also explains why the larvae fed better on Ws-4 lines (Fig 2(B)). Nevertheless, when using plants with different ecotype background for insect assays this difference between Col and Ws ecotypes should be taken into account.

Further analysis of cml9-a and cml9-b showed that both lines differ genetically (Fig 7(C) and 7(D)) that might explain the little variances in the herbivore treatment observed. Moreover, knock-out of CML9 does not lead to a change in the phytohormone response to S. littoralis feeding (Fig 3) indicating once more that CML9 is not a key player in herbivore defense regulation.

In Arabidopsis, 50 CMLs are known and among them eight are regulated upon S. littoralis herbivory [16–18, 31]. Thus, it is conceivable that some of these proteins have redundant or overlapping functions. Inactivation of one of them does not necessarily have a great impact on a particular plant stress response. For example, the cml24 but not cml23 mutant shows under certain conditions a phenotype that differs from the wild type; however, in the cml24xcml23 double mutant the cml24 effect is modulated [39]. To exclude this scenario in case of CML9, CML9 overexpression lines were examined. Both tested lines were as susceptible to S. littoralis feeding as their corresponding wild type, supporting the conclusion, that CML9 does not play any role in the defense against this herbivore.

Taken the results of gene expression data and the mutant analysis together, we suggest further to interprete gene regulations more cautiously. Even though CML9 is significantly upregulated after herbivore treatment, it is not relevant for the defense response.

CML9 is not regulating defense against necrotrophs

In Arabidopsis 50% of the upregulated genes upon A. brassicicola infection are also induced upon P. syringae treatment, although the response to both microbes is mediated via different pathways [40]. Because CML9 is described as mediator of the defense against the biotrophic bacterial pathogen P. syringae [23], we also examined its role in the defense against the necrotrophic fungal pathogen A. brassicicola. We found that CML9 has no functional relevance in the plant immune response to A. brassicicola. Both mutant lines, cml9-a and cml9-b, were as
susceptible to the fungus as to Col-0 wild type plants (Fig 5). The defense against this fungus is mainly regulated by jasmonates like the defense against herbivores [3, 41], while the response to \textit{P. syringae} is mediated mainly by SA [3]. Thus, our results are in one line with the results obtained in the herbivore assays and suggest that CML9 is also not regulating the defense against this necrotrophic pathogen. Hence, the different impact of CML9 on both pathogens might be explained by their different lifestyles that trigger different signaling pathways. Another explanation could be that CML9 is only coordinating the response to bacterial but not to fungal pathogens. The fact that CML9 has been shown to contribute to plant defense against bacteria mainly through a flagellin dependent pathway would favor this hypothesis [23]. Additional experiments with other pathogens with different lifestyle or virulence strategies will help to better position CML9 in plant defense pathways.

\section*{CML9 does not mediate drought stress tolerance in general}

In contrast to previous studies, our data suggest that CML9 is not a common regulator of drought stress. It was reported earlier that CML9 negatively regulates the drought response [21], but under our experimental conditions both \textit{cml9a} and \textit{b} mutants displayed the same behavior as the wild type (Col-0) upon drought treatment (Fig 6(A)). Consistent with this observation, no significant difference in the kinetics and level of ABA elevation was observed between drought stress-exposed mutants and the wild type plants (Fig 6(B)). Thus, it is unlikely that CML9 plays a key role in the drought stress response. The divergent results of our and previous studies might be caused by different experimental setups: while our plants were grown in single pots during the drought stress, many plants were cultivated together in one pot in the previous study, a situation that can cause intra- and interspecific competition [21]. Furthermore we did our stress treatment under short day conditions while the other setup was done under long day conditions. It could well be that the role of CML9 in drought stress response is dependent on the length of the photoperiod. However, our data indicate that CML9 seems not to be a general regulator of the plant drought stress response.

\section*{Conclusion}

Here, we investigated in more detail the role of CML9 in plant stress responses. CML9 was described to act as a calcium sensor at the crossroads of different pathways, like pathogen defense and abiotic stress responses [21, 23]. Our study specifies the known functions of CML9. Based on our data, CML9 does not regulate the plant drought stress response in general as otherwise suggested [21], but might have a role under certain conditions. It also does not regulate plant defense against herbivores, neither against chewing lepidopteran larvae nor against piercing-sucking spider mites. We further showed that knock-out of CML9 does not affect the response of the plant to the fungal pathogen \textit{A. brassicicola}. These results suggest that CML9 is not a general regulator of plant pathogen defense, but very likely specialized on defense against pathogenic bacteria or (hemi)biotrophic pathogens like \textit{P. syringae} [23]. Moreover, the results of both the herbivore and pathogen assays further suggest that CML9 does not regulate jasmonate-mediated pathways at all. Therefore, we propose that CML9 should not be included in a group of CMLs that have a general role in plant stress regulation.

\section*{Supporting information}

S1 Table. Primers used for different PCRs.

(DOCX)
S1 Fig. Verification of cml9-a and cml9-b. Semi quantitative RT-PCR analysis of CML9 full transcript expression in wild type and knock-out mutants after 30 min of MecWorm treatment. Expression of ACTIN2 was used as quantitative control. Water was used as negative control. The expected product length is written on the right sites of the respective pictures.

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