

CAR modulates plasma membrane nano-organization and immune signaling downstream of RALF1-FERONIA signaling pathway

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1 CAR modulates plasma membrane nano-organization and

2 immune signaling downstream of RALF1-FERONIA

3 signaling pathway

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- 26 Brief heading: The RALF-FER regulates the nano-organization on the membrane via
- 27 CAR family

Summary

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- The receptor-like kinase (RLK) FERONIA (FER) senses peptide ligands in the plasma membrane (PM), modulates plant growth and development, and integrates biotic and abiotic stress signaling for downstream adaptive response. However, the molecular interplay of these diverse processes is largely unknown.
- Here, we show that FER, the receptor of Rapid Alkalinization Factor 1 (RALF1), physically interacts with C2 domain ABA–related (CAR) proteins to control the nano-organization of the PM in *Arabidopsis*.
- During this process, the RALF1–FER pathway upregulates CAR protein translation, and then more CAR proteins are recruited to the PM. This acts as a rapid feedforward loop that stabilizes the PM liquid-ordered phase. FER interacts with and phosphorylates CARs, thereby reducing their lipid-binding ability, and breaking the feedback regulation at latter time point.
- Similar to FER mutant, pentuple *car14569* mutants inhibit flg22-induced FLS2-BAK1 immune complex formation, which depends on the integrity of nanodomains.
- Together, we propose that the FER-CAR module controls the formation of the PM
 nano-organization during RALF signaling through a self-contained amplifying
 loop including both positive and negative feedbacks.
- 47 **Key words**: FER, C2 domain ABA-related proteins, lipid-binding, nanodomains, immune complex.

Introduction

Catharanthus roseus receptor–like kinase 1–like protein (CrRLK1L) FERONIA (FER) is a receptor-like kinase with versatile and tissue–specific functions in plant cell growth and survival. FER functions with its ligands, rapid alkalinization factors (RALFs, e.g., RALF1 and RALF23), as a regulator of fertilization (Escobar-Restrepo et al., 2007; Li et al., 2015), cell growth (Guo et al., 2009; Duan et al., 2010; Du et al., 2016; Li et al., 2018), hormone signaling (Guo et al., 2009; Duan et al., 2010), stress responses (Chen et al., 2016), immune signaling (Stegmann et al., 2017) and energy and RNA metabolism (Yang et al., 2015; Xu et al., 2019; Wang et al., 2020; Zhu et al., 2020). However, the mechanism through which FER quickly responds to and integrates external signals and transmits them to varied downstream targets remains unknown. Recent report showed that FER acts as a scaffold to regulate the formation of the immune receptor complex (FLS2 and BAK1) to respond to the pathogen-associated molecular pattern (PAMP) flagellin 22 (flg22) in a RALF-dependent manner (Stegmann et al., 2017). Furthermore, the RALF-FER pathway modulates the plasma membrane nanoscale dynamics of immune receptors, via so far elusive mechanisms (Gronnier et al., 2022).

Biological membranes are made of a plethora of co-existing nanodomains, which are characterized by their small size (i.e., below 1 μm) and specific proteolipid composition (Spira *et al.*, 2012; Jarsch *et al.*, 2014; Jaillais & Ott, 2020). Such membrane domains are critical in signaling notably because they can locally concentrate proteins, a process known as nanoclustering (Ott, 2017; Jaillais & Ott, 2020). By increasing the local concentration of proteins, nanoclustering favors the formation of protein complexes or post-translational modifications, which often act as a trigger to initiate signaling (Jaillais & Ott, 2020; Gronnier *et al.*, 2022). The small protein family flotillin (Flot) and plant-specific remorin protein family are localized in nanodomains in a sterol-dependent manner at the plasma membrane. Multiple evidences suggest that Flots and remorins are not only nanodomain resident proteins but are also crucial to stabilize these nanodomains. Furthermore, they recruit signaling

molecules into these structures (Liang *et al.*, 2018; Huang *et al.*, 2019; Jaillais & Ott, 2020; Pan *et al.*, 2020). In addition, protein nanoclustering is regulated through the formation of various protein—lipid and protein—protein interactions (Simons & Gerl, 2010; Garcia-Parajo *et al.*, 2014; Sezgin *et al.*, 2017; Pan *et al.*, 2020). As such, they act as versatile signaling platforms with very diverse composition in term of lipids and proteins (Burkart & Stahl, 2017; Platre *et al.*, 2019; Jaillais & Ott, 2020). However, how plants regulate the nano-organization of the plasma membrane during signaling is just starting to be elucidated.

Accumulating evidence has shown that in plants, nanodomains are important for the cellular response to environmental cues and improving the fitness of plants (Demir et al., 2013; Wang et al., 2015; Bucherl et al., 2017; Huang et al., 2019). Several works have linked the abscisic acid (ABA) response with nanodomain dynamics (Demir et al., 2013; Diaz et al., 2016). For example, a 10-member family of lipid-binding C2 domain ABA-related proteins (CARs, CAR1 to CAR10) was identified and found to interact with pyrabactin resistance 1 (PYR1)/PYR1-like (PYL)/regulatory components of ABA receptors (RCAR) ABA receptors and to positively regulate ABA signaling (Rodriguez et al., 2014). CARs oligomerize at the PM in a calcium-dependent manner and has been identified in detergent-resistant membranes (DRMs). Furthermore, they induce membrane fusion, possibly by promoting membrane curvature (Martens & McMahon, 2008; Demir et al., 2013; Diaz et al., 2016). However, the upstream regulator(s) that link CARs with the modulation of the PM landscape is still unknown. Herein, we propose a working model in which FER works together with lipid-binding CAR proteins to regulate the partitioning of liquid-ordered and liquid-disordered phases of the plasma membrane. In this scenario, activation of FER by RALF1 triggered the accumulation and phosphorylation of downstream CAR proteins, thereby modulating the plasma membrane nano-organization in a dynamic manner.

Materials and Methods

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Plant Material and Growth Conditions.

- 107 Arabidopsis (Col-0) was used as the wild-type (WT). The following transgenic and
- mutant lines were used in this study: CAR1-Myc, CAR4-Myc, CAR5-Myc, CAR6-Myc,
- 109 CAR9-Myc, CAR10-Myc, CAR9-Myc/fer-4, YFP-CAR9, YFP-CAR9/fer-4, CAR9^{3M}-
- 110 YFP, CAR9^{3M}-YFP/fer-4 and car59, car145, car459, car149, car159, car1459,
- 111 $car14569-\Delta 1$, $car14569-\Delta 4$, $car14569-\Delta 10$, $car14569-\Delta 20$.
- 112 Arabidopsis thaliana seeds were first surface sterilized by 75 % (v/v) ethanol. After
- stigmatization at 4 °C for 3 d, seeds were growing on 1/2 MS with 0.8 % sucrose and
- 1.0 % Phytagel (Sigma-Aldrich) at 22 °C in a 16-h light/8-h dark condition for
- subsequent analysis. Details of this information are described in Methods S1.

Yeast Two-Hybrid (Y2H) Assay.

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- Y2H assays were performed as previously described (Du et al., 2016). Briefly, the
- cytoplasm domain of CrRLK1L family members (AT3G51550, FER, 469–896 amino
- acids; AT2G39360, CVY1, 429-815 amino acids; AT5G38990, MDS1, 462-880
- amino acids; AT5G39020, MDS3, 459–813 amino acids; AT1G30570, HERK2, 451–
- 849 amino acids), and two RLKs (AT5G46330, FLS2, 870-1155 amino acids;
- AT4G39400, BRI1, 814–1196 amino acids) were fused in-frame with the GAL4
- DNA-binding domain of the bait vector pGBKT7. The CDS of CARs were fused with
- the GAL4 DNA-activating domain of the prey vector pGADT7 (AD-CAR). Distinct
- plasmid pairs were transformed into yeast AH109 cells. The diluted transformants were
- plated onto synthetic dropout medium lacking tryptophan/leucine (SD/–Trp–Leu+His)
- and synthetic dropout medium lacking tryptophan/leucine/histidine (SD/-Trp-Leu-
- His) but supplemented with 20 mM 3-amino-1,2,4-triazole (3-AT) for 4 days to test
- the interaction.

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Co-Immunoprecipitation (Co-IP) Assay.

- 131 Co–IP was performed as previously described with some modifications (Li et al., 2018).
- Seven–day–old seedlings 35S::CARs–Myc (about 0.5 g) were ground to a fine powder
- in liquid nitrogen and solubilized with 500 µL TBST buffer [50 mM Tris–HCl (pH 7.5),
- 134 150 mM NaCl, 5 mM MgCl₂, 1 mM EDTA, 1 % Triton X–100] containing 1 × protease

- inhibitor cocktail (78430, Thermo Fisher Scientific) and 1 × phosphatase inhibitor
- 136 (78420, Thermo Fisher Scientific) and spun for 1 hour at 4 °C. The extracts were
- centrifuged at 16,000 g at 4 °C for 10 min, and 500 μL supernatant was transferred to
- incubate with prepared 20 μL Anti–Myc magnetic beads (B26301) overnight at 4 °C,
- and 100 µL supernatant was used as input. Then, the beads were washed 3 times with
- the washing buffer [50 mM Tris–HCl (pH 7.5), 150 mM NaCl, 0.1 % Triton X–100]
- containing 1 × protease inhibitor cocktail and eluted with elution buffer (0.2 M Glycine,
- 142 1 % Triton X-100, 1 mM EDTA, pH 2.5). And proteins were run on a 10 % SDS-
- 143 PAGE gel and analyzed by anti-FER (Du et al., 2016; Li et al., 2018) and anti-Myc
- 144 (CST, 2276S) antibody.

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In vitro Phosphorylation Assay.

- 146 The phosphorylation and dephosphorylation assays were described as previously (Du,
- et al., 2016). GST-CAR9, GST-CAR5, FER-CD-His and FER^{K565R}-CD-His (kinase)
- dead form) were purified for phosphorylation assay *in vitro*.
- The ABA-induced phosphorylation co-expression system was described
- previously (Li et al., 2018). Vectors of pACYC-PYL1-FER (S-tag), pACYC-PYL1-
- 151 FERK565R (S-tag), and pRSF-ABI1-CAR9 (His-tag) were constructed and co-
- transformed into one BL21 (DE3) E. coli strain. His-CAR proteins were purified and
- then subjected to liquid chromatography-tandem mass spectrometry (LC-MS/MS).
- Details of this method are described in Methods S1.

In vivo Phosphorylation Assay.

- Phos–tag assay was performed as described previously (Chen et al., 2018). Seven–day–
- old CAR-Myc seedlings were used to analyze phosphorylated band in vivo. For
- phosphorylation sites detecting *in vivo*, *CAR–Myc* was enriched by immunoprecipitate.
- 159 The CAR-Myc bands digested and analyzed by LC-MS/MS as described previously.
- Details of this method are described in Methods S1.

Pan-anti-CARs Antibody Production.

Antibody production was performed as previous study (Li *et al.*, 2018). This antibody is raised by using full–length CAR9 expressed and purified from *E.coli* BL21. A 1–month–old ICR mouse (SLAC laboratory animal) was injected with 50 µg GST–CAR9 protein emulsified with Complete Freund's adjuvant (F5881, Sigma–Aldrich). Two weeks later, 50 µg GST–CAR9 protein emulsified with Incomplete Freund's adjuvant (F5506, Sigma–Aldrich) was injected into the ICR mouse and then once again in the next week. The serum of the immunized mouse was obtained as antibody for immunoblot detection. We tested the antibody in WT, *car9*, *car459* and *car14569* mutant lines by an immunoblot. Because of ten CAR family members share common motif and sequence, we still detected homologs in CAR9 signal mutants using this antibody, but this interacted band will be sharply reduced when using in CARs multiple mutants. Thus, we named this antibody as pan–anti–CARs antibody.

Lipid Binding Assay.

- Phospholipid binding to proteins was assessed as described (Rodriguez *et al.*, 2014). Briefly, phosphatidylserine (PS): phosphatidylcholine (PC) (25:75) was prepared in chloroform and dried to obtain a thin layer under a stream of nitrogen. The dried lipids were resuspended in buffer A (100 mM NaCl, 50 mM HEPES, pH 6.8) and mixed by vortexing for 20 min. Large multilamellar vesicles were obtained by centrifugation at 16,000 g for 20 min. Resuspended the vesicles in 1 mL of buffer A with multiple concentrations of free Ca²⁺ and stored at 4 °C. The vesicles (about 100 μg of phospholipids) were mixed with the different forms of GST–CAR9 (5 μg). The mixture was incubated with or without 1 mM Ca²⁺ via gentle shaking (250 rpm) for 30 min at room temperature. The vesicles and the bound proteins were pelleted by centrifugation at 12,000 g at 4 °C for 10 min and washed twice with 0.5 mL of buffer A. Samples were boiled with 1 × protein loading buffer for 10 min and separated by 10 % SDS–PAGE.
- Variable-Angle Total Internal Reflection Fluorescence Microscopy (VA-TIRFM)

Proteins were revealed by using anti–GST antibody.

Imaging.

VA-TIRFM was performed as previously described (Li et al., 2012). For observation, seedlings were softly transferred onto a glass slide and soaked with liquid 1/2 MS, then covered with a coverslip. A custom-built VA-TIRFM based on an Olympus IX-71 microscope equipped with a total internal reflective fluorescence illuminator and a 100 × oil-immersion objective (numerical aperture of 1.45, Olympus) was used here. The 473 nm laser line from a diode laser was used to excite GFP. The emission fluorescence signals were detected with a back-illuminated EM-CCD camera (ANDOR iXon DV8897D-CS0-VP; And / or Technology, Belfast, UK) after filtering with band-pass filters. The gain of the EMCCD camera was set to 300 throughout all single-molecule imaging experiments; the setting was in the linear dynamic range of the EMCCD camera. Images were acquired with an exposure time and analyzed with Image J.

Polysome Profiling Assay and Real-Time qPCR.

Arabidopsis polysomes profiling assay was performed as described (Missra & Von Arnim, 2014; Zhu *et al.*, 2020). Briefly, 7–day–old seedlings (about 0.5 g) were treated with RALF1 (1 μM) for 10 min and then ground in liquid nitrogen followed by resuspension in polysome extraction buffer. Supernatant was loaded onto a 15 %–60 % sucrose gradient and spun in a Beckman SW 32 Ti rotor at 170,000 g for 4 h at 4 °C. We manually collected 11 fractions. Then, isolated the RNA from the last four fractions by RNAiso plus (Takara) kit. RT–qPCR analysis was used to quantify the total target relative transcript content in the input and the relative content of target transcripts associated with heavier polysomes in the bottom four fractions. Primers for RT–qPCR is shown in Table S1. *ACTIN* as a reference gene to detect the RNA levels of CARs.

Di-4-ANEPPDHQ Lipid Staining.

For di–4–ANEPPDHQ lipid staining, four–day–old seedlings are collected for each genotype. 5 μM (work concentration) di–4–ANEPPDHQ was added in liquid 1/2 MS medium for staining. Quantification of lipid polarity in root cell has been described previously (Huang et al., 2019; Owen et al., 2011). Details of this method are described in Methods S1.

- 218 ROS Burst Assay.
- 219 The flg22-induced ROS burst measurement assay was performed as previously
- described (Stegmann et al., 2017). Four-week-old Arabidopsis rosette leaves were
- 221 used for ROS dynamic determination. ROS fluorescent probe H2DCF-DA staining
- 222 (James et al., 2015) 6-day-old seedlings were treated with the liquid 1/2 MS medium
- 223 containing 10 µM H2DCF-DA. Fluorescence was monitored with a confocal
- 224 microscope using an excitation wavelength of 488 nm. Details of this method are
- described in Methods S1.
- 226 Pto DC3000 infection assay.
- For Pto DC3000 infection assay (Stegmann et al., 2017), Pseudomonas syringae pv.
- 228 Tomato (Pto) DC3000 strains were grown overnight in King's B medium (10 g/L
- proteose peptone, 1.5 g/L anhydrous K₂HPO₄, 5 g/L MgSO₄) with shaking at 28°C.
- 230 Bacteria were collected from centrifuge tube and resuspended in water containing
- 231 0.02% Silwet L77 (Sigma Aldrich) to an $OD_{600} = 0.2$ (108 colony forming units per
- 232 mL). This bacterial suspension was sprayed on 4-week-old plants, which were covered
- with vented lids for 3 days. Three leaf discs per sample from different plants were
- collected in different microfuge tubes and ground with a drill-adapted pestle. Serial
- dilutions were plated on LB agar and colonies were counted 2 days later.
- 236 Statistical Analysis.
- Software SPSS Statistics 17.0 was used. Data are shown as mean \pm s.d.; * p < 0.05, **
- 238 p < 0.01, *** p < 0.001; n.s., not significant. One—way ANOVA with Tukey's test were
- used as mention in figure note.
 - Results

240

- 241 Lipid-binding CAR proteins physically interact with the receptor kinase FER at
- **242 the PM**
- FER is involved in response to multiple extracellular signals (Zhu et al., 2021), and
- 244 controls the dynamics of FLS2 and BAK1 in response to RALF signal (Gronnier et al.,

2022). To understand the functions of FER, we performed a yeast two-hybrid (Y2H) 245 screen using the cytoplasmic domain of FER (FER-CD, 469-896 amino acids, aa) as 246 bait (Du et al., 2016). Among the interacting proteins, we found CAR9, which belongs 247 to a 10-member family of lipid-binding C2 domain ABA-related proteins (Rodriguez 248 et al., 2014; Diaz et al., 2016; Qin et al., 2019). We cloned the full-length genes for the 249 ten CAR family members (CAR1 – CAR10) and found that CAR1, CAR4, CAR5, CAR6, 250 CAR9 and CAR10 were able to directly interact with FER-CD in Y2H assays (Fig. 1a 251 252 and Fig. S1a). Next, glutathione S-transferase (GST) pull-down assays further confirmed the interaction between CARs (GST-tagged CAR1, CAR4, CAR5, CAR6, 253 CAR9 and CAR10) and His-tagged FER-CD (Fig. 1b and Fig. S1b). Furthermore, 254 bimolecular fluorescence complementation (BiFC) assays were used to test the 255 256 interaction between CARs and FER in Arabidopsis protoplasts. The results showed that CAR1, CAR4, CAR5, CAR6, CAR9, and CAR10 interacted with FER at the PM (the 257 protein-protein interaction caused green fluorescence, which overlapped with FM4-64 258 PM red fluorescence) (Fig. 1c). We next performed coimmunoprecipitation (co-IP) 259 260 assays and confirmed the interaction between Myc-tagged CAR proteins (i.e., CAR1, CAR4, CAR5, CAR6, CAR9, CAR10) and FER in vivo (Fig. 1d and Fig. S1c). To 261 further verify the specificity of the interaction between CARs and FER, we cloned the 262 cytoplasmic domains of five CrRLK1L family members (CVY1, AT2G39360; BUPS1, 263 AT4G39110; MDS1, AT5G38990; MDS3, AT5G39020; HERK2, AT1G30570) and 264 two LRR-RLKs (FLS2 and BRI1) and further analyzed their interaction with CAR9. 265 The results of the Y2H assays showed that CAR9 interacted specifically with FER and 266 BUPS1, but not with the other six kinase domains (Fig. S1d). We also performed co-267 IP assays between Y2H noninteracting CARs (e.g., CAR3 and CAR7) and FER (Fig. 268 S1e). The results revealed no interaction of CAR3 and CAR7 with FER in vivo, which 269 indicates that the interaction between certain CARs and FER is specific. Taken 270 together, these data suggest that FER physically interacts with a subset of CAR proteins 271 at the PM. 272

FER phosphorylates CARs, which further regulates the interaction of CARs with 273 lipids 274 275 To evaluate whether CARs could be substrates of FER, we first tested CAR5 and CAR9 by using phosphorylation assays in vitro. The results showed that recombinant FER-276 CD induced a higher phosphorylation level in the CAR5 and CAR9 proteins (Fig. 2a). 277 To further assess whether the phosphorylation levels of these two proteins were 278 enhanced by RALF1 in vivo, Phos-Tag-PAGE analysis (Chen et al., 2018) was used 279 280 to detect phosphorylated forms of CAR5 and CAR9 (thereafter referred to as pCAR5 and pCAR9) in plants expressing Myc-tagged CARs with or without RALF1 treatment 281 (Fig. 2b). Notably, RALF1 treatment altered CAR protein abundance in Arabidopsis 282 (detailed description in Fig. 3); thus, we adjusted the total protein levels (including 283 284 those of phosphorylated and dephosphorylated proteins). We found a slow running form of CAR5 and CAR9, that was strongly reduced by alkaline phosphatase treatment 285 (CIP), suggesting that they corresponded to pCAR5 and pCAR9. RALF1 treatment (1 286 µM, 30 min) increased the phosphorylation levels of both CAR5 and CAR9 in vivo 287 288 (Fig. 2b). Time series analysis indicated that the phosphorylation level of CAR5 and CAR9 increased at 20 min and 40 min post RALF1 treatment (protein abundance was 289 adjusted prior to western blotting) in the WT background, but not in fer-4 (Fig. S2). 290 Together, our results indicate that RALF1-mediated CAR phosphorylation is dependent 291 292 on FER. We further identified the FER-mediated phosphorylation sites of CAR5 and CAR9 293 using a previously developed ABA-induced co-expression system (Li et al., 2018). A 294 kinase-dead mutant of FER-CD (Lys at 565 was mutated into Arg, FER-CD^{K565R}) was 295 used as a negative control (Escobar-Restrepo et al., 2007). Electrospray ionization 296 (ESI) mass spectrometry (ESI-MS) analysis indicated that after ABA induction, FER 297 phosphorylated CAR5 at Ser61, Ser62, and Tyr65 (Fig. S3a-S3c). Of note, in the same 298 assay, Thr26, Ser27, and Tyr30 were phosphorylated in CAR9 (Fig. S3d and S3e), 299 which are the equivalent phosphorylated residues in CAR5 (Fig. S4a), reinforcing the 300 idea that those phosphorylation sites could be physiologically relevant. Moreover, 2 out 301 of 3 sites were further verified *in vivo* by label–free quantitative MS, and we found that 302

RALF1 enhanced the CAR5 phosphorylation level at Ser62 and Tyr65 compared with mock-treated plants (Fig. 2c and Fig. S3f). To confirm that GST–CAR5 and GST–CAR9 were phosphorylated by FER–CD on these three residues, we next mutated the phosphorylated Serine/threonine into alanine (Ala) and tyrosine into phenylalanine (Phe) (GST–CAR5^{3M}/9^{3M},) (Li *et al.*, 2018; Zhou *et al.*, 2018). GST–CAR5^{3M} and GST–CAR9^{3M} remained unphosphorylated by FER in vitro (Fig. 2d). These data suggest that RALF1 promotes the FER-mediated phosphorylation of CAR5 and CAR9 at those specific sites.

We found that after adding ATP into the reaction system to activate the phosphorylation activity of FER, the intensity of the interaction between the FER and CAR9 was significantly attenuated. However, the intensity of CAR9^{3M} interaction with FER was no longer significantly regulated by phosphorylation (Fig. 2e and S4b). We then tested the effect of a CAR9 phosphorylation mimic on this interaction. We mutated three phosphorylation sites of CAR9 (Thr26, Ser27, Tyr30) to Asp (D) (GST–CAR9^{3D}) to test how the mutant residues affected the FER–CAR9 association. Compared with wild-type CAR9, GST–CAR9^{3D} exhibited a lower association with FER–CD (41% ± 5.2% weakened) and FER^{K565R}–CD (42% ± 7.4% weakened) (Fig. 2f). These results indicated that the phosphorylation of CAR9 reduces its affinity toward FER.

CARs have been found located in nanodomains and directly interact with negatively-charged phospholipid to promote membrane fusion (Martens *et al.*, 2007; Demir *et al.*, 2013; Rodriguez *et al.*, 2014). To test whether FER regulates the interaction between CAR and lipids via phosphorylation, we investigated the lipid-binding ability of CAR under phosphorylated and non-phosphorylated states (Rodriguez *et al.*, 2014). Since the Ca ²⁺-dependent anionic phospholipid binding is a hallmark of many C2 domains (Rodriguez *et al.*, 2014), we confirmed that several CAR proteins (CAR5, 6, 9, and 10) directly interact with negatively charged phospholipid vesicles [25:75 (w/w) mixture of phosphatidylserine: phosphatidylcholine] in the presence of free Ca²⁺ (Fig. S5a and S5b). Furthermore, we compared the effect of wild-type FER and kinase-dead FER (FER^{K565R}) on CAR5 and CAR9 in lipid

cosedimentation assays and found that phosphorylated CAR5 and CAR9 (coincubated with FER–CD and ATP) had a weakened capacity to interact with anionic phospholipids (Fig. 2g and 2h). Furthermore, comparison of the lipid binding ability of two mutant forms of CAR9 protein (GST–CAR9^{3M} and GST–CAR9^{3D}) toward negatively-charged phospholipid vesicles revealed that CAR9^{3M} exhibited a similar association with vesicles than the wild-type CAR9, whereas CAR9^{3D} showed weaker binding ability (Fig. 2i).

A previous study used negative stain transmission electron microscopy (TEM) to show that CAR can interact with negatively-charged phospholipid vesicles and further induce membrane curvature (Diaz *et al.*, 2016). To answer whether FER could modulate membrane curvature via regulating the affinity between CARs and anionic phospholipids, we tested the effect of CAR9 phosphorylation on its membrane bending activity (Fig. S5c–S5j). Addition of free Ca²⁺ and CAR9 to negatively-charged phospholipid vesicles induced strong tubulation of the liposomes (Fig. S5g and S5j). GST–CAR9^{3M} induced strong tubulation of liposomes (Fig. S5h and S5j), whereas GST–CAR9^{3D} significantly reduced tubulation (Fig. S5i and S5j). Thus our data indicate that FER phosphorylates CARs at specific sites, which further fine-tunes the association of FER and CARs. Moreover, in vitro, CAR9-induced membrane curvature is finely regulated by the kinase activity of FER.

RALF1-FER regulates CAR nanoclustering via promoting CAR protein

353 translation

From above, several evidences implied that CAR proteins localization in nanodomains may be regulated by FER. To investigate how RALF1-FER affects the CAR nanoclusters on the PM, time-lapse images were collected with a variable–angle total internal reflection fluorescence (VA-TIRF) microscope for 4-day-old *YFP-CAR9* root cells followed by single-particle-tracking method (Pan *et al.*, 2020). Treatment with 1 µM RALF1 resulted in an increase in the density of YFP-CAR9 particles (Fig. 3a and

Fig. 3b), which suggests that more CAR proteins are localized to the membrane and recruited into CAR-associated nanoclusters. Furthermore, similar to the treatment with sterol-depleting agent methyl–β–cyclodextrin (MβCD), density of YFP-CAR9 particles in fer-4 background was significantly decreased (Fig. 3a and Fig. 3b). Evidence shows that many proteins on the PM are not uniformly mixed with membrane lipids via free diffusion-based equilibrium, but laterally segregated into nanodomains with a limited diffusion and specific lipids (Jaillais & Ott, 2020; Pan et al., 2020). Treatment with RALF1 induced a slower diffusion coefficient of YFP-CAR9-containing nanoclusters (Fig. 3c). By contrast, YFP-CAR9 nanodomains showed a higher diffusion coefficient after treatment with MβCD, or in the fer-4 background (Fig. 3c). Next, we tested the dynamic changes in membrane order induced by RALF1 treatment. We found that RALF1 promotes the liquid-ordered phase of the plasma membrane in the first 10 min of the treatment. Intriguingly, with the prolongation of RALF1 treatment, the proportion of lipid ordered phase maintained a dynamic equilibrium (Fig. S6a and S6b), which showed a similar trend with CAR phosphorylation (Fig. S2). Then, we expressed the YFP-CAR9^{3D} and YFP-CAR9^{3M} in WT background. VA-TIRFM analysis showed that YFP-CAR9^{3D} particles resulted in a shorter dwell time at the plasma membrane than YFP-CAR9 and YFP-CAR9^{3M} (Fig. S6c-S6f). These results suggest that RALF1 promotes the formation of CAR9 nanoclusters, possibly by recruiting more CAR proteins into nanodomains. Subsequently, FER negatively regulates the dwell time of CAR proteins in nanodomains via directly interacting with and phosphorylating CAR on the membrane, thus forming a feedback loop.

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A recent study showed that the RALF1–FER promotes protein synthesis through facilitating translation initiation (Zhu *et al.*, 2020); thus, we hypothesized that RALF1–FER facilitates the formation of CAR-containing nanoclusters via promoting their protein synthesis. To test this hypothesis, we investigated the protein accumulation of CARs by using a pan–anti–CARs antibody (see Methods for details) (Fig. S7a). Western blots showed that that RALF1 triggered the rapid accumulation of CAR proteins in WT, but not in the *fer–4* mutant (Fig. 3d). The RALF1–triggered rapid accumulation of CAR1, 4, 5, 6, 9, and 10 proteins was further confirmed in transgenic

lines expressing Myc-tagged CAR proteins (Fig. S7b). We also tested the accumulation of three CAR proteins (i.e., CAR2, CAR3 and CAR7) which have no interaction with FER, and found that RALF1 induced protein accumulation of CAR2, but not CAR3 or CAR7 (Fig. S7c). This may imply that the RALF peptides and FER modulate CAR protein accumulation in a sophisticated way. In addition, treatment with ABA (10 μM) did not induce the accumulation of CAR9 (Fig. S7d). We then tested whether the RALF1-FER complex modulated CAR mRNA translation using polysome profiling analysis (Zhu et al., 2020). RALF1 promoted the mRNA translation of CAR1, 4, 5, 6, 9, and 10 in WT (Fig. 3e). However, the fer-4 mutant blocked RALF1-triggered CAR1, 4, 5, 6, 9, and 10 mRNA translation (Fig. 3f), confirming that RALF1 upregulated the protein synthesis of CAR via FER. Together, these results suggest that RALF1-FER promotes CAR proteins synthesis by facilitating their translation rate. Accumulated CAR proteins are then recruited to the PM, facilitating the formation of nanoclusters.

CAR proteins are required for RALF1-FER-induced lipid ordering

We next investigated whether RALF1-FER affects the nano-organizations of the PM. Lipid membranes lateral segregate into domains that are in a liquid-disordered (Ld) or liquid-ordered (Lo) phase. The Lo phase is enriched in sterols and glycosphingolipids, which are segregated into a more tightly packed phase (Huang *et al.*, 2019; Jaillais & Ott, 2020). To test whether RALF1–FER directly impact the lipid order in biological membranes, we took advantage of the lipid order–sensitive probe di–4–ANEPPDHQ (Owen *et al.*, 2011; Huang *et al.*, 2019; Pan *et al.*, 2020). When di–4–ANEPPDHQ molecules detect lipid phases with different dipole potentials in the cell membrane, there is a large shift in the peak emission wavelength of the dye from 630 nm in the Ld phase to 570 nm in the Lo phase (Fig. S8A). The Lo phase shows a higher generalized polarization (GP) value (increased green fluorescence compared with red) (Huang *et al.*, 2019). Taking advantage of this assay, we found that *fer–4* had a lower GP value than the WT, indicating a general decreased level of ordered lipids in the PM (Fig 4a and 4b). Furthermore, treatment with 1 μM RALF1 promoted the higher GP value in WT, but not in *fer-4* (Fig 4a and 4b). To validate this RALF1 effect, we examined lipid

order in the presence of MβCD, which depletes sterols, reducing the Lo phase (Huang et al., 2019). As expected, the GP value strongly decreased after MβCD treatment in WT (Fig. 4c and 4d), and the effect of RALF1 on Lo phase formation was also suppressed by MβCD treatments (Fig. 4c and 4d).

Next, we used the Di–4–ANEPPDHQ stain assay to analyze lipid order before and

Next, we used the Di-4-ANEPPDHQ stain assay to analyze lipid order before and after RALF1 treatment in high–order CAR mutants. A *car59* double mutant did not show obvious changes in lipid order, and the sensitivity of *car59* to RALF1-triggered higher lipid order formation, was similar to WT using 1 μM RALF1 (Fig. 4e and 4f). We thus generated higher–order CAR mutants, and observed a significant difference in lipid order between *car459* or *car1459* mutants and WT (Fig. 4e and 4f). Notably, lipid order of *car1459* showed lower sensitivity to RALF1 than WT (Fig. 4f). Next, we generated 4 independent *car14569* pentuple mutants by designing a CRISPR-Cas9–mediated CAR6 knockout in *car1459* background, termed as *car14569*–Δ1, *car14569*–Δ4, *car14569*–Δ10, *car14569*–Δ20 (all of them harbor out-of-frame deletions in *CAR6*, details in materials and methods). Di–4–ANEPPDHQ stain revealed that the pentuple mutant *car14569*–Δ20 strongly attenuated the lipid order of the PM, and as expected, *car14569*–Δ20 displayed insensitivity to RALF1–induced lipid order formation (Fig. 4e and 4f). We also analyzed lipid ordering in WT, *fer-4*, and CAR9–Myc/*fer-4* plants. When overexpressed in the *fer-4* background, CAR9–Myc partly rescued the lipid order defects of *fer-4* (Fig. S8b and S8c).

To confirm that RALF1 promotion of Lo formation is dependent on the rapid accumulation of CAR proteins, we tested lipid ordering phase in the *eif4e1 eif(iso)4e* translation initiation factor double mutant (Zhu et al., 2020). This double mutant is impacted in the rapid translation of downstream proteins regulated by FER, including CAR proteins. The results showed that membranes exhibited low lipid ordering and no longer responded to RALF1 regulation in the *eif4e1 eif(iso)4e* background (Fig. S9a, S9b, S9e and S9f). Moreover, pretreatment with the translation inhibitor cycloheximide (CHX) before RALF1 indicated that RALF1 no longer promotes Lo phase formation once the rapid accumulation of CAR proteins was prevented by CHX treatment (Fig. S9c, S9d, S9e and S9f). Taken together, these data indicate that rapid accumulation of

CAR proteins is necessary for RALF1-FER-triggered higher lipid ordering phase

formation, and this process is regulated by multiple CAR family members.

RALF1-FER-CARs regulates plant immunity by regulating FLS2_BAK1

452 association.

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A recent study found RALF-FER regulates the assembly of immune receptor kinases 453 454 complexes via modulating plasma membrane nanoscale landscape (Gronnier et al., 455 2022). Our data described above show that the receptor kinase FER regulates membrane 456 biophysical properties through CAR proteins in response to the RALF1 peptide. Thus, we wondered whether the RALF1-FER-CAR axis, through the promotion of an ordered 457 lipid phase of the PM, is able to modulate the assembly of immune complexes. ROS 458 459 burst results showed that when MBCD pretreatment was used to deplete sterols from membranes, the response of plants to RALF and flg22 peptides was significantly 460 weakened (Fig. S10a-S10d). Next, we examined the flg22-induced association between 461 immune receptor kinases FLS2 and its co-receptor BAK1 in car14569-Δ20 pentuple 462 463 mutant. In agreement with previous results (Stegmann et al., 2017), we confirmed that the association of FLS2 and BAK1 was severely weakened in fer-4 compared to WT 464 after flg22 treatment (85% \pm 4.5% reduction of the Co–IP signal) (Fig. 5a and 5c). The 465 Co–IP assay of FLS2-BAK1 was also weakened in *car14569*–Δ20 after flg22 treatment 466 compared to WT (25% \pm 6.2% reduction). This effect was weaker than in fer-4, 467 possibly because of residual CAR activity remaining in the pentuple car mutant (Fig. 468 5b and 5c). As RALF23 does (Stegmann et al., 2017), the activation of FER by RALF1 469 inhibited FLS2 and BAK1 interaction induced by flg22 in the WT ($48\% \pm 8.2\%$ 470 471 reduction) (Fig. 5a and 5c). In this co-signaling context, in the absence of FER (fer-4), RALF1 had no effect, whereas the residual CAR activity of the *car14569*–Δ20 mutant 472 still mediated the RALF1 inhibitory effect on FLS2-BAK1 interaction, although less 473 efficiently than in WT (compare WT lanes +flg22/+flg22+RALF1 with corresponding 474 car14569–Δ20 lanes) (Fig. 5b and 5c). To answer whether CARs can directly respond 475 to flg22-triggered plant immunity, firstly, we tested the accumulation of CAR proteins 476 after flg22 treatment, and the result showed that CAR proteins abundance was 477

insensitive to flg22 treatment (Fig. S11a). Then, VA-TIRFM analysis of CAR9 nanoclustering on the membrane found that flg22 treatment has no significant effect on CAR9 nanoclustering in WT and *fer-4* background (Fig. S11b and S11c). This suggests that flg22 is not directly involved in the regulation of CAR proteins' nanoclustering.

To further examine the biological relevance of CARs' function in the RALF-FER pathway, we analyzed CARs' role in RALF1-FER-mediated immunity response. Flg22-induced ROS production was attenuated in pentuple CAR mutants (Fig. 5d, 5e, S12a, and S12b). The pentuple CAR mutants were more susceptible to the *Pseudomonas syringae pv.tomato* (*Pto*) DC3000, albeit not to the same extent as *fer-4* (Fig. 5f and 5g). In addition, overexpression of wild-type CAR9 in *fer-4* partially restored the immunodeficient phenotype of *fer-4*, but not CAR9^{3M} (Fig. 5f and 5g). Taken together, the RALF1-FER-CAR module is necessary for the regulation of plant immunity, which depends on the assembly of immune receptor complexes in specific membrane nanodomains.

In addition, FER has also been reported to be involved in cell growth, hormone signaling, stress responses (Zhu *et al.*, 2021). Notably, by comparing the phenotype of *fer-4* and multiple CAR mutants, we observed that *fer-4* and CAR mutants showed a similar defect in root hair and epidermal cell growth and overexpression of CAR9 in *fer-4* background was also able to partly rescue the root hair growth defect (Fig. S13a-S13d). Furthermore, analysis of the effects of temperature stresses on *fer-4* and *car14569*–Δ20, showed hypersensitive phenotypes to temperature stress in both mutants (Fig. S13e-S13h). Together, this set of results shows that RALF1 induces the formation of ordered lipid nanodomains through CAR proteins, and is crucial for FER to regulate multiple signaling pathways.

Discussion

The molecular mechanisms through which eukaryotic cells modulate their PM landscape via activating receptor kinases in response to external signals remain unclear (Jaillais & Ott, 2020). Our study reveals that FER regulates the general lipid order of the membrane in response to RALFs extracellular peptides. Proteins with C2 domains

are involved in protein transport and membrane fusion via interacting with negatively charged phospholipid (Martens *et al.*, 2007; Martens & McMahon, 2008; Rodriguez *et al.*, 2014). A lipid binding protein family with C2 domain, CAR, lipid ordering via their rapid accumulation in response to RALF1 (within 10 min after RALF1 treatment). Multiple CAR proteins interact with FER at the PM and are phosphorylated by the kinase (20 min after RALF1 treatment), weakening the ability of CARs to interact with lipids thus form a negatively feedback. The higher ordered lipids, which are particularly induced by RALF1-FER-CAR axis, might be involved in signaling multiple rapid responses, including immunity (Fig. 6).

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An early and rapid response to the RALF1 peptide is the FER-triggered Ca²⁺ wave (Ngo et al., 2014). Thus, it is reasonable to assume that the RALF1-FER-induced Ca²⁺ wave can further enhance the PM location of CAR proteins (Rodriguez et al., 2014). In agreement with previous studies, we found that Ca²⁺ upregulates the lipid binding and membrane curvature ability of CARs (Rodriguez et al., 2014; Diaz et al., 2016). We envision that RALF1 may promote the rapid accumulation of CAR proteins to induce membrane curvature and the nano-organization of the plasma membrane. Furthermore, we found that FER-dependent phosphorylation of CARs, which occurs in the proximity of conserved Asp residues involved in Ca²⁺ binding (Diaz et al., 2016), seems to impair CAR binding to vesicles. Therefore, in the first minutes following RALF1 perception (<10 min), FER stimulates CAR proteins accumulation by upregulating its translation and might also trigger CAR membrane recruitment in a Ca²⁺-dependent manner. In a second step (>20 min), phosphorylation of specific Ser/Thr/Tyr residues in the C2 domain of CARs might tune CAR binding to membranes. Mechanistically, the addition of negative charges within the lipid-binding pocket of the C2 domain by phosphorylation might repel the interaction with negatively charged phospholipid in the PM (Simon et al., 2016; Platre et al., 2018). Thus, the system appears to be designed for a fast-self-amplified recruitment of CAR in PM, followed by a brake mechanism leading to CAR membrane dissociation. This scenario becomes even more complex when considering that RALF1-FER signaling is a master regulator of cell wall integrity (Zhang et al., 2020), and the cell wall also has profound roles in the diffusion

coefficients and PM compartmentalization of resident proteins (Luu *et al.*, 2012; Martiniere *et al.*, 2012; McKenna *et al.*, 2019; Danek *et al.*, 2020; Jaillais & Ott, 2020).

A recent study unraveled the regulation of FLS2 and BAK1 nanoscale organization by the RALF receptor FER (Gronnier *et al.*, 2022). How FLS2 and BAK1 associate in a ligand-dependent manner within the plasma membrane in response to RALF peptides needs further study. Herein, we found that the receptor kinase FER regulate the lipid order of the PM via CAR proteins, which may offer a strategy to modulate the formation of other receptor kinase complexes (e.g., FLS2 and BAK1). Various studies indicate that FER regulates many aspects of plant biology, including growth, development, environmental adaptability, and immunity, by sensing a variety of external signals (Zhang *et al.*, 2020; Zhu *et al.*, 2021). Similarly, we also found a pleiotropic phenotype in the high–order CAR mutants (Rodriguez *et al.*, 2014), indicating that CAR-mediated regulation of membrane order could be pivotal for additional signaling systems.

Interesting future research topics include whether RALF1–FER regulates various cell type–specific outputs and/or signaling events via the dynamic nanoclustering of proteins and lipids (involving other receptor kinase complexes, ROPs, CARs and phosphatidylserine) of the PM. More studies are also needed to verify whether signal–triggered PM compartmentalization based on kinase receptors and C2 domain–containing proteins is a common mechanism in eukaryotic cells. In addition, previous evidence indicates that CAR proteins are located not only in the PM but also in the cytoplasm and nucleus, where these proteins participate in ABA signaling (Rodriguez *et al.*, 2014) and interact with LOT1 to enhance plant drought tolerance (Qin *et al.*, 2019). It would be interested to address whether the RALF1-mediated regulation of CAR accumulation, its membrane interaction dynamics, and its phosphorylation may also impact ABA signaling.

Data availability

The authors declare that the data supporting the findings of this study are available 564 within the paper and its supplementary information. 565 566 Acknowledgments We thank Liming Xiong, Tao Qin, and Chao Li for providing plant materials and Cyril 567 Zipfel for critical comments and suggestions. This work was supported by grants from 568 National Natural Science Foundation of China (NSFC-31871396, 31571444), China 569 570 Postdoctoral Science Foundation funded project (2020M672475), and the Science and Technology Innovation Program of Hunan Province (2021JJ40060) to F.X. Work in 571 P.L.R. laboratory was supported by grant PID2020-113100RB funded by MCIN/AEI/ 572 573 10.13039/501100011033. 574 **Author contributions** F.Y., and W.C. conceived the project and designed the research; W.C., H.Z., S.Z., F.X., 575 M.Y., G.X., J.C. A.C., L.R., Y.L, Q.X., and Q.F performed the research; D.W., X.L., 576 577 A.C., X.L, and P.L.R. contributed new reagents/analytic tools; F.Y. and W.C. analyzed data and wrote the paper with contribution from P.L.R. and Y. J.; all authors reviewed 578 and approved the manuscript for publication. 579 580 **Conflicts of interest** The authors declare no competing financial interests. 581 References 582 583 Bucherl CA, Jarsch IK, Schudoma C, Segonzac C, Mbengue M, Robatzek S, MacLean D, Ott T, 584 Zipfel C. 2017. Plant immune and growth receptors share common signalling components but 585 localise to distinct plasma membrane nanodomains. Elife 6. 586 Burkart RC, Stahl Y. 2017. Dynamic complexity: plant receptor complexes at the plasma membrane. 587 Curr Opin Plant Biol 40: 15-21. 588 Chen GH, Liu MJ, Xiong Y, Sheen J, Wu SH. 2018. TOR and RPS6 transmit light signals to enhance 589 protein translation in deetiolating Arabidopsis seedlings. Proc Natl Acad Sci U S A 115(50): 590 12823-12828. 591 Chen J, Yu F, Liu Y, Du C, Li X, Zhu S, Wang X, Lan W, Rodriguez PL, Liu X, et al. 2016. FERONIA 592 interacts with ABI2-type phosphatases to facilitate signaling cross-talk between abscisic acid

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721 Figures and legends

- 722 Fig. 1 FER physically interacts with CARs.
- 723 (a) Y2H assays showing the interaction between CARs and FER. SD (–His/–Leu/–Trp)
- selection medium containing 20 mM 3-AT was used to test the interaction. The CAR
- members were cloned into the pGADT7 (AD) vector, and the FER-CD was cloned into
- 726 the pGBKT7 (BD) vector.
- 727 (b) GST pull-down assay. The indicated GST-tag and His-tag were detected by anti-
- 728 GST and anti–His, respectively.
- 729 (c) FER interacts with CARs in BiFC assays in Arabidopsis protoplasts. Negative
- control (cCFP + FER-Venus) are shown, and FM4-64 indicates the PM (red).
- 731 (d) Co–IP assays. The immunoprecipitated CAR9 and coimmunoprecipitated FER were
- 732 indicated using anti–FER and anti–Myc antibodies, respectively.
- At least three biological replicates of (a) (d) were performed with similar results.
- Fig. 2 RALF1-FER phosphorylates CAR proteins and further regulates the
- 735 interaction of CAR proteins and lipid.
- 736 (a) In vitro phosphorylation assays showing that FER-CD can phosphorylate GST-
- 737 CAR5 and GST-CAR9 are detected using anti-pSer/Thr, and anti-GST and anti-His.
- 738 (b) Phostag–PAGE assays *in vivo*. Phosphorylated CAR5–Myc and CAR9–Myc bands
- are indicated as pCAR5–Myc and pCAR9–Myc.
- 740 (c) Examples of phosphopeptides of CAR5 in vivo. The maximum probability shown
- for each phosphorylation site was calculated by the Andromeda algorithm integrated in
- 742 MaxQuant.
- 743 (d) In vitro phosphorylation assays showing that GST-CAR5^{3M} and GST-CAR9^{3M}
- were not phosphorylated by FER-CD.
- 745 (e) GST pull-down assay showing that phosphorylated FER-CD exhibits a higher
- affinity towards GST-CAR9^{3M}. The relative protein intensity of FER-CD-His and
- 747 FER^{K565R}–CD–His in the output was analyzed using ImageJ.
- 748 (f) GST pull-down assay. GST-CAR9^{3D} shows a weaker interaction with FER-CD-
- 749 His and FERK565R-CD-His. The relative protein intensity of FER-CD-His and
- 750 FER^{K565R}–CD–His in the output was analyzed using ImageJ. The red arrow pointing

- 751 the weakened anti-His panel.
- 752 (g-h) Phosphorylated CAR5 and CAR9 (0.1 μM) show weaker lipid binding ability in
- 753 the presence of 1 mM CaCl₂.
- (i) Lipid binding abilities of three forms of CAR9 in the presence or absence of 1 mM
- 755 CaCl₂. Immunoblot assays showing the protein levels by ImageJ.
- At least three biological replicates of (a) (i) were performed with similar results.
- 757 Fig. 3 RALF1-FER promotes the formation of CAR-nanoclustering by enhancing
- 758 their translation rate.
- 759 (a) VA-TIRFM images of YFP-CAR9 at the PM in root cells with or without RALF1
- 760 (1 μM, 10 min) or MβCD (10 mM, 30 min) treatment in WT and fer-4 background.
- (b) Quantitative comparison of YFP-CAR9 particle density in different groups.
- 762 (c) Comparison of diffusion coefficients of YFP-CAR9 particles in different groups.
- 763 (d) RALF1-induced accumulation of CAR proteins in WT and fer-4. CAR proteins
- were detected by pan-anti-CARs antibody (see Methods for details of this antibody).
- 765 The relative accumulation of CAR proteins was analyzed using ImageJ.
- 766 (e-f) Upper panel: ribosome profiles. Fractions (8–11) containing mRNAs associated
- with polysomes are indicated with a black line. Lower panels: RT-qPCR results of
- 768 polysome-associated CAR mRNAs.
- At least three biological replicates were performed with similar results. Data are shown
- as the mean \pm s.d., ***p < 0.001, n.s., not significant. One–way ANOVA with Tukey's
- 771 test.
- Fig. 4 RALF-FER module regulates the formation of ordered lipid nanodomains
- 773 through CAR proteins.
- (a) Di–4–ANEPPDHQ lipid staining assay of WT and fer–4 root cells with or without
- RALF1 treatment. The GP value is indicated with a colored box. The white triangles
- indicate the regions for GP value quantification.
- (b) Statistical analysis of the GP value in (a). The white triangle in (a) indicates the
- regions for GP value quantification. For each treatment, 42 54 cells from 5 roots were
- 779 measured.

- 780 (c) Di-4-ANEPPDHQ lipid staining assay of WT root cells with or without MβCD and
- 781 RALF1 treatments. The GP value is indicated with a colored box. The white triangles
- 782 indicate the regions for GP value quantification.
- 783 (d) Statistical analysis of the GP value in (c). The white triangle in (c) indicates the
- regions for GP value quantification. For each treatment, 42 54 cells from 5 roots were
- 785 measured.
- 786 (e) Di-4-ANEPPDHQ lipid staining assay in root cells of WT, *car59*, *car459*, *car1459*
- and car14569– $\Delta 20$ with or without RALF1 treatment. The GP value is indicated with
- 788 a colored box.
- 789 (f) Statistical analysis of the GP value in (e). The white triangle in (e) indicates the
- regions for GP value quantification. For each treatment, 41 60 cells from 5 roots were
- 791 measured.
- All experiments were replicated three times with similar results. Data are shown as the
- 793 mean \pm s.d.; *p < 0.05, **p < 0.01, ***p < 0.001, n.s., not significant. One-way
- ANOVA with Tukey's test.
- 795 Fig. 5 RALF1-FER-CAR axis as a signaling platform to integrate immunity
- 796 response.
- 797 (a-b) Co–IP assay showing the weaker interaction between FLS2 and BAK1 in fer–4
- 798 and car14569–Δ20 with or without RALF1 and flg22 treatment for 10 min. Western
- 799 blots were probed with anti-FLS2 and anti-BAK1 antibodies. The relative protein
- intensity of FLS2 and BAK1 was analyzed using Image J.
- 801 (c) Quantitative comparison of FLS2 and BAK1 interaction strength in (a) and (b). The
- ratio of BAK1 to FLS2 in (a) and (b) were normalized.
- 803 (d-e) The ROS burst was measured after elicitation of leaf discs from the indicated
- mutant lines with 0.1 µM flg22 and/or 1 µM RALF1 in (d). (e) was showed the ROS
- integration as mean values of total photon counts over 1500 second in (d).
- 806 (f) Colony-forming units (cfu) of *Pto* DC3000 bacteria after infection for 3 days.

- 807 (g) Bacterial populations statistics after infection for 3 days. Bacterial inoculations were
- performed as described in (f). Log₁₀ CFU/cm², log₁₀ colony-forming units per cm² of
- leaf tissue.
- All experiments were replicated three times with similar results. Data are shown as the
- mean \pm s.d.; ***p < 0.001, n.s., not significant. One—way ANOVA with Tukey's test.
- Fig. 6 A working model for RALF1-dependent plant response through the FER-
- 813 CAR axis in the formation of proper lipid ordered nanodomains
- The RALF1–FER signaling first promotes CAR protein synthesis, and then, more CAR
- proteins localize to the PM via binding Ca²⁺ and interacting with negative charge
- 816 phospholipids, which positively regulates formation of lipid ordered nanodomains and
- membrane curvature. Finally, FER interacts with and phosphorylates CARs in a
- 818 RALF1-dependent manner. The enhanced phosphorylation level of CARs reduces their
- binding to negatively charged phospholipids. This maintains the dynamic balance of
- 820 CAR proteins on the membrane, thus, serving for fine-tuning of the system sensitivity.
- Proteins and structures are not to scale.

822 **Supporting Information**

- Fig. S1 FER physically interacts with CARs.
- Fig. S2 Phostag-PAGE analysis dynamics of CAR5 and CAR9 protein phosphorylation.
- Fig. S3 ESI mass spectrometry identification of CARs phosphorylation sites.
- 826 **Fig. S4** Functional analysis of CAR protein phosphorylation sites.
- 827 **Fig. S5** CAR proteins directly interact with anionic lipids and promote lipid tubules.
- Fig. S6 The effect of phosphorylation on the dwell time of CAR9 in nanodomain.
- 829 **Fig. S7** RALF1 induces CARs protein accumulation.
- 830 **Fig. S8** CAR9 partially rescued the lipid order of fer-4.
- Fig. S9 RALF1 induces the formation of lipid ordering through rapid accumulation of CAR proteins.
- Fig. S10 Lipid order nanodomains are crucial for plant immunity.
- Fig. S11 The nanocluster of CAR9 is insensitive to flg22 treatment.
- Fig. S12 FER-CAR module is crucial for immune response.
- Fig. S13 fer-4 and multiple CAR mutants phenotype analysis.

Table S1 Primers used in this study.

Methods S1 Detailed Methods Description

Figures and legends

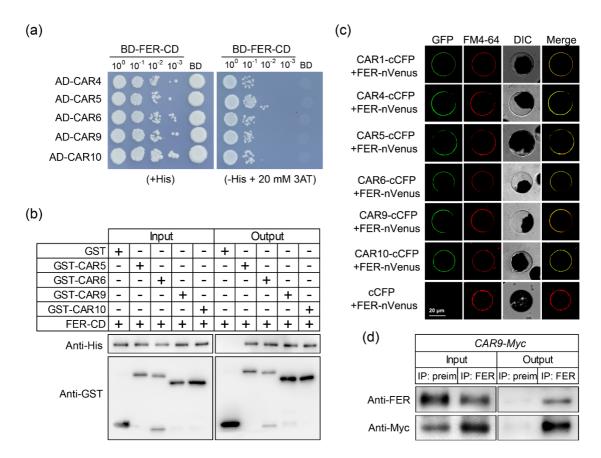


Fig. 1 FER physically interacts with CARs.

- (a) Y2H assays showing the interaction between CARs and FER. SD (–His/–Leu/–Trp) selection medium containing 20 mM 3–AT was used to test the interaction. The CAR members were cloned into the pGADT7 (AD) vector, and the FER-CD was cloned into the pGBKT7 (BD) vector.
- (b) GST pull-down assay. The indicated GST-tag and His-tag were detected by anti-GST and anti-His, respectively.
- (c) FER interacts with CARs in BiFC assays in Arabidopsis protoplasts. Negative control (cCFP + FER-Venus) are shown, and FM4-64 indicates the PM (red).
- (d) Co–IP assays. The immunoprecipitated CAR9 and coimmunoprecipitated FER were indicated using anti–FER and anti–Myc antibodies, respectively.

 At least three biological replicates of (a) (d) were performed with similar results.

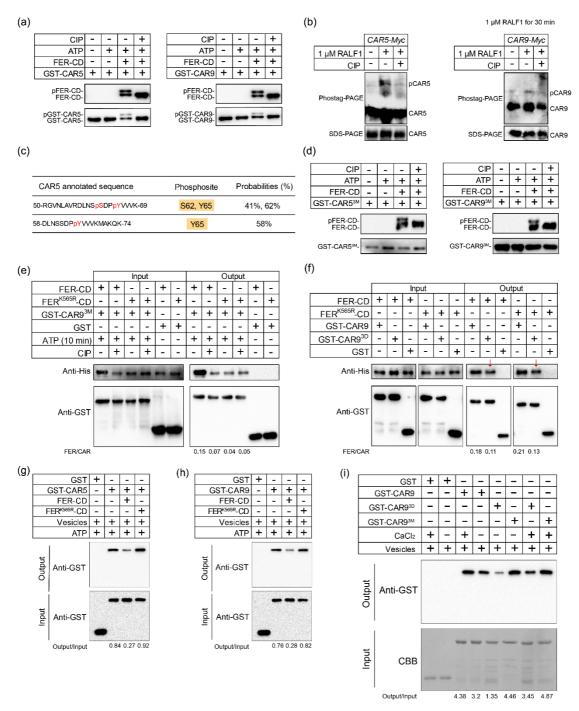


Fig. 2 RALF1-FER phosphorylates CAR proteins and further regulates the interaction of CAR proteins and lipids.

- (a) *In vitro* phosphorylation assays showing that FER–CD can phosphorylate GST–CAR5 and GST–CAR9 are detected using anti–pSer/Thr, and anti–GST and anti–His.
- (b) Phostag-PAGE assays *in vivo*. Phosphorylated CAR5-Myc and CAR9-Myc bands are indicated as pCAR5-Myc and pCAR9-Myc.
- (c) Examples of phosphopeptides of CAR5 *in vivo*. The maximum probability shown for each phosphorylation site was calculated by the Andromeda algorithm integrated in

MaxQuant.

- (d) *In vitro* phosphorylation assays showing that GST-CAR5^{3M} and GST-CAR9^{3M} were not phosphorylated by FER-CD.
- (e) GST pull-down assay showing that phosphorylated FER-CD exhibits a higher affinity towards GST-CAR9^{3M}. The relative protein intensity of FER-CD-His and FER^{K565R}-CD-His in the output was analyzed using ImageJ.
- (f) GST pull-down assay. GST-CAR9^{3D} shows a weaker interaction with FER-CD-His and FER^{K565R}-CD-His. The relative protein intensity of FER-CD-His and FER^{K565R}-CD-His in the output was analyzed using ImageJ. The red arrow pointing the weakened anti-His panel.
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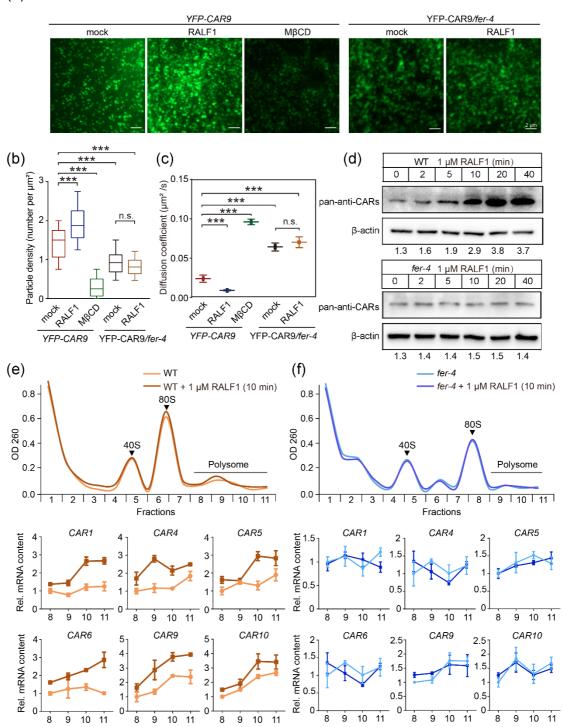


Fig. 3 RALF1-FER promotes the formation of CAR-nanoclustering by enhancing their translation rate.

- (a) VA-TIRFM images of YFP-CAR9 at the PM in root cells with or without RALF1 (1 μ M, 10 min) or M β CD (10 mM, 30 min) treatment in WT and *fer-4* background.
- (b) Quantitative comparison of YFP-CAR9 particle density in different groups.
- (c) Comparison of diffusion coefficients of YFP-CAR9 particles in different groups.

- (d) RALF1-induced accumulation of CAR proteins in WT and *fer-4*. CAR proteins were detected by pan-anti-CARs antibody (see Methods for details of this antibody). The relative accumulation of CAR proteins was analyzed using ImageJ.
- (e-f) Upper panel: ribosome profiles. Fractions (8–11) containing mRNAs associated with polysomes are indicated with a black line. Lower panels: RT–qPCR results of polysome–associated CAR mRNAs.

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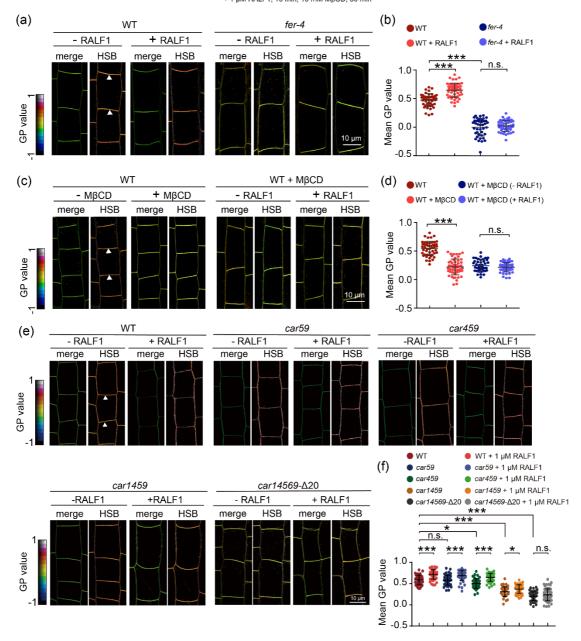


Fig. 4 RALF-FER module regulates the lipid order of the plasma membrane through CAR proteins.

- (a) Di-4-ANEPPDHQ lipid staining assay of WT and *fer-4* root cells with or without RALF1 treatment. The GP value is indicated with a colored box. The white triangles indicate the regions for GP value quantification.
- (b) Statistical analysis of the GP value in (a). The white triangle in (a) indicates the regions for GP value quantification. For each treatment, 42 54 cells from 5 roots were measured.

- (c) Di–4–ANEPPDHQ lipid staining assay of WT root cells with or without M β CD and RALF1 treatments. The GP value is indicated with a colored box. The white triangles indicate the regions for GP value quantification.
- (d) Statistical analysis of the GP value in (c). The white triangle in (c) indicates the regions for GP value quantification. For each treatment, 42 54 cells from 5 roots were measured.
- (e) Di–4–ANEPPDHQ lipid staining assay in root cells of WT, *car59*, *car459*, *car1459* and *car14569*–Δ20 with or without RALF1 treatment. The GP value is indicated with a colored box.
- (f) Statistical analysis of the GP value in (e). The white triangle in (e) indicates the regions for GP value quantification. For each treatment, 41 60 cells from 5 roots were measured.

All experiments were replicated three times with similar results. Data are shown as the mean \pm s.d.; *p < 0.05, **p < 0.01, ***p < 0.001, n.s., not significant. One–way ANOVA with Tukey's test.

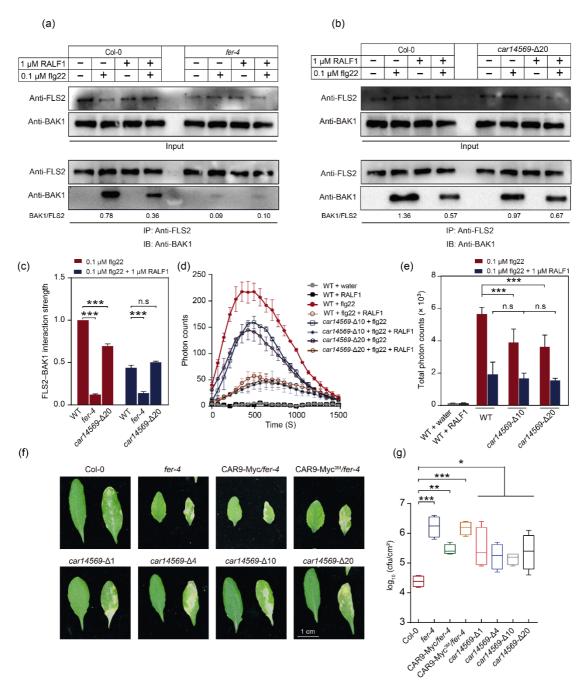


Fig. 5 The RALF1-FER-CAR axis as a signaling platform to integrate immunity response.

- (a-b) Co–IP assay showing the weaker interaction between FLS2 and BAK1 in *fer–4* and *car14569–*Δ20 with or without RALF1 and flg22 treatment for 10 min. Western blots were probed with anti–FLS2 and anti–BAK1 antibodies. The relative protein intensity of FLS2 and BAK1 was analyzed using Image J.
- (c) Quantitative comparison of FLS2 and BAK1 interaction strength in (a) and (b). The ratio of BAK1 to FLS2 in (a) and (b) were normalized.

- (d-e) The ROS burst was measured after elicitation of leaf discs from the indicated mutant lines with 0.1 μ M flg22 and/or 1 μ M RALF1 in (d). (e) was showed the ROS integration as mean values of total photon counts over 1500 second in (d).
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- (g) Bacterial populations statistics after infection for 3 days. Bacterial inoculations were performed as described in (f). Log₁₀ CFU/cm², log₁₀ colony-forming units per cm² of leaf tissue.

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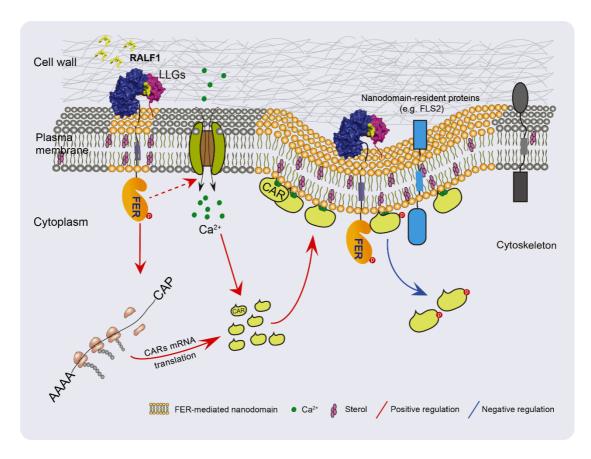


Fig. 6 A working model for RALF1-dependent plant response through the FER-CAR axis in the regulation of plasma membrane nano-organization.

The RALF1–FER signaling first promotes CAR protein synthesis. CAR proteins localize to the PM via binding Ca²⁺ and interacting with negatively charged phospholipids. At the plasma membrane, they induce membrane curvature and promote a liquid-ordered state of the plasma membrane. Finally, FER interacts with and phosphorylates CARs in a RALF1–dependent manner. The enhanced phosphorylation level of CARs reduces their binding to negatively charged phospholipids. This maintains a dynamic balance of CAR proteins on the membrane, and fine-tune the sensitivity of the system. Proteins and structures are not to scale.