Signaling from the plasma-membrane localized plant immune receptor RPM1 requires self-association of the full-length protein

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Plants evolved intracellular immune receptors that belong to the NOD-like receptor (NLR) family to recognize the presence of pathogen-derived effector proteins. NLRs possess an N-terminal Toll-like/IL-1 receptor (TIR) or a non-TIR domain [some of which contain coiled coils (CCs)], a central nucleotide-binding (NB-ARC) domain, and a C-terminal leucine-rich repeat (LRR). Activation of NLR proteins results in a rapid and high-amplitude immune response, eventually leading to host cell death at the infection site, the so-called hypersensitive response. Despite their important contribution to immunity, the exact mechanisms of NLR activation and signaling remain unknown and are likely heterogenous. We undertook a detailed structure-function analysis of the plasma membrane (PM)-localized CC NLR Resistance to *Pseudomonas syringae pv. maculicola* 1 (RPM1) using both stable transgenic *Arabidopsis* and transient expression in *Nicotiana benthamiana*. We report that immune signaling is induced only by activated full-length PM-localized RPM1. Our interaction analyses demonstrate the importance of a functional P-loop for *in planta* interaction of RPM1 with the small host protein RPM1-interacting protein 4 (RIN4), for constitutive preactivation and postactivation self-association of RPM1 and for proper PM localization. Our results reveal an additive effect of hydrophobic conserved residues in the CC domain for RPM1 function and RPM1 self-association and their necessity for RPM1–RIN4 interaction. Thus, our findings considerably extend our understanding of the mechanisms regulating NLR activation at, and signaling from, the PM.

plant immunity | effector-triggered immunity | NLR receptor | oligomerization | *Arabidopsis thaliana*

During their life cycle, plants and animals encounter a variety of pathogens, such as viruses, bacteria, oomycetes, and fungi. Plant pathogens that breach the waxy cuticular layer atop the epidermis face an efficient plant immune system comprising two layers (1, 2). The first layer consists of plasma membrane (PM)-spanning pattern-recognition receptors (PRRs) that typically recognize and bind pathogen/microbe-associated molecular patterns (PAMPs/MAMPs) and initiate PAMP/MAMP-triggered immunity (PTI/MTI) (3, 4). PRR activation induces downstream signaling, including protein phosphorylation, changes in ion flux, production of reactive oxygen species, transcriptional reprogramming, vesicle transport for polarized delivery of newly synthesized antimicrobial compounds and pathogenesis-related proteins, as well as cell wall reinforcement (5). PTI/MTI is sufficient to prevent microbial colonization and growth in most cases; however, evolutionarily adapted pathogens have independently evolved large arsenals of effectors (virulence proteins), such as the type III secretion system (TTSS) effectors from bacterial pathogens or the RxLR family of effectors from oomycetes (6–8). Effectors are delivered by various means into the apoplast and/or the host cytoplasm, where they target and manipulate key pathways of the host cellular machinery to suppress PTI/MTI, thus leading to effector-triggered susceptibility (1, 9, 10).

To defend themselves against adapted pathogens, plants evolved a second layer of defense, referred to as effector-triggered immunity (ETI) (2). This branch of the plant innate immune system relies on the products of plant disease resistance (R) genes. Most R genes encode proteins of the NOD-like receptor (NLR) family (1). NLRs belong to a subclade of the AAA-ATPase superfamily and are molecular switches regulated via nucleotide binding and hydrolysis (11, 12). NLRs have a central nucleotide-binding site (NB-ARC) with homology to the animal immune receptors Apaf-1 and CED-4, C-terminal leucine-rich repeats (LRRs), and either a Toll-like/IL-1 receptor (TIR) domain or a non-TIR domain at their N termini. The latter contains a subclass containing N-terminal coiled-coil (CC) domains, subdividing NLRs into TNLs, CNLs, and others, respectively (13, 14). The conserved nucleotide-binding site is critical for NLR activation, and negative regulation of this domain, likely via intramolecular interactions, is required to limit ectopic activation, which can result in hyperimmune signaling and ectopic cell death (15, 16). The N-terminal CC or TIR domains

Significance

Pathogen recognition first occurs at the plasma membrane, where receptor-like kinases perceive pathogen-derived molecules and initiate immune responses. To abrogate this immune response, pathogens evolved effector proteins that act as virulence factors, often following delivery to the host cell. Plants evolved intracellular receptors, known as NOD-like receptors (NLRs), to detect effectors, thereby ensuring activation of effector-triggered immunity. However, despite their importance in immunity, the molecular mechanisms underlying effector recognition and subsequent immune activation by membrane-localized NLRs remain to be fully elucidated. Our analyses reveal the importance of and need for self-association and the coordinated interplay of specific domains and conserved residues for NLR activity. This could provide strategies for crop improvement, contributing to effective, environmentally friendly, and sustainable solutions for future agriculture.

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are necessary, and in some cases sufficient, for cell death signaling (17–21).

The current model is that NLRs exist in an equilibrium between a "resting/off" ADP-bound state and an "active/on" ATP-bound state in which the "off" state is strongly favored (22, 23). NLRs can be activated either directly by binding an effector protein or indirectly by monitoring an effector-specific modification of a host target (or a host decoy of a true target) (24, 25). Effector recognition/binding presumably leads to the release of negative intramolecular regulation and conformational changes allowing the exchange of ADP for ATP, thereby tipping the balance toward the ATP-bound "on" state. Recent work on the flax TNLs L6 and L7 suggests that, at least in cases where NLRs directly bind effectors, the effector preferably binds to the ATP-bound "on" state of the receptor, stabilizing this state and preventing recycling to the "off" state (22). In this model, ATP hydrolysis drives a return to the "off" state, thus regulating the switch. The importance of nucleotide binding for NLR activity is reflected by loss-of-function and autoactivation phenotypes caused by mutations in the highly conserved Walker-A (or P-loop) motif (GxxxxGK[T/S]), the Walker-B motif (hhhDD/E), or the MHD motif (with a conserved histidine residue that can also be found in animal NLRs), important for nucleotide binding, ATP hydrolysis, and ADP binding, respectively (26–28). Effector-mediated activation of NLR proteins results in ETI, a rapid and high-amplitude activation of signaling pathways that largely overlaps with PTI/MTI (29, 30). ETI is usually associated with a rapid localized cell death at the infection site, the hypersensitive response (HR), which can inhibit further pathogen proliferation in some cases.

Recent studies of plant and animal NLR proteins support models in which self- and hetero-association of NLRs are key mechanisms of activation and signaling (13, 14, 31, 32) (*SI Appendix*, Table S1). The tobacco TIR-NLR (TNL) N self-associates only in the presence of its cognate effector, and this self-association is P-loop dependent (33). Many plant CC-NLRs (CNLs), i.e., Prf (tomato), RPS5 (*Arabidopsis*), and Rp-1D (maize), self-associate (15, 27, 34); however, data on the role of self-association or oligomerization for plant NLR proteins at both preactivation and postactivation steps are limited and sometimes conflicting. In the case of MLA10, Sr33, and Rx, self-association has been shown for the full-length receptors and for CC fragments (amino acids 1–160) that include a structurally important full fourth helix, but not for shorter CC fragments lacking the C-terminal end of this helix (18, 35, 36). These nondimerizing shorter CC fragments are monomeric in solution, as determined by size-exclusion chromatography-coupled multiangle light-scattering experiments and are biologically inactive, whereas the longer CC fragments (at least spanning amino acids 1–142) also form dimers and cause HR in transient expression in *Nicotiana benthamiana*. This suggests that at least the dimerization of the CC domains in these NLRs is required for activation.

In addition, the sites of NLR activation are heterogeneous. Some plant NLRs require coordinated nucleo-cytoplasmic trafficking to establish a full and adequate immune response, suggesting that NLRs can activate distinct signaling pathways in the cytoplasm and nucleus (35). In contrast, other NLRs require PM or endomembrane localization, and disruption of their proper localization severely affects or blocks function (26, 36, 37). Thus, various mechanisms of NLR activation may have evolved shaped by the constraints of coevolution among effectors, their host targets, and corresponding NLRs (24).

Resistance to *Pseudomonas syringae pv. maculicola* 1 (RPM1) is a well-characterized PM-localized CNL from *Arabidopsis*. RPM1 perceives the *P. syringae* TTSS effectors AvrRpm1 and AvrB (26, 38–40). Once injected into the plant cell, these effectors are acylated and localized to the host PM, where they interact with the small host protein RPM1-interacting protein 4 (RIN4) and induce its phosphorylation, mediated by the receptor-like cytoplasmic kinase RIPK and closely related paralogs (41, 42). The phosphorylation of RIN4 at threonine residue 166 is necessary and sufficient for the activation of RIN4-associated RPM1 (42). RPM1 activation on the PM is necessary and sufficient for its function (26). Activated RPM1 leads to the HR and to growth restriction of *Pseudomonas* strains expressing AvrRpm1 or AvrB; however, the molecular mechanisms leading to RPM1 activation and downstream signaling are unknown, as are whether RPM1 self-associates before or after its activation, and whether this potential oligomerization is necessary for RPM1-mediated immune responses.

Therefore, we undertook a detailed structure-function analysis of RPM1 using both stable transgenic *Arabidopsis* and the heterologous *N. benthamiana* transient expression system. We found that immune signaling is induced only by the activated full-length PM-localized RPM1 protein. Furthermore, our results reveal that RPM1–RIN4 interaction, as well as RPM1 PM localization, is P-loop dependent. We also found an additive effect of conserved hydrophobic residues in the RPM1 CC domain for RPM1 function and self-association and their necessity for RPM1–RIN4 interaction. We characterized the self-association of RPM1 in both preactivation and postactivation states and found that self-association is P-loop dependent. Thus, our analyses considerably extend the sparse knowledge of the mechanisms regulating NLR activation at, and signaling from, the PM (15, 43).

Results

Immune Signaling Requires Full-Length RPM1. Expression of just the N-terminal CC, CC-NB-ARC, or TIR domain of several NLRs is sufficient to initiate immune signaling, eventually leading to HR (19, 44–46). RPM1 activation and HR signaling can be reconstituted in *N. benthamiana* by coexpression of RPM1, RIN4, and AvrRpm1 (or AvrB), by coexpression of RPM1 and phosphomimetic RIN4^{T166D}, or by expression of the autoactive MHD mutant RPM1^{D505V} (26, 42).To analyze whether the CC or any other RPM1 domain can initiate a pathogen-independent HR in *N. benthamiana*, we generated nine RPM1 fragments including single domains, based on secondary structure predictions: CC-1, CC-2, CC-3, CC-4, CC-5, NB-ARC, LRR, CC-NB-ARC, and NB-ARC-LRR (*SI Appendix*, Figs. S1 and S2*A*). When transiently overexpressed in *N. benthamiana*, none of the individual domains or fragments of RPM1 induced HR-like cell death (*SI Appendix*, Fig. S2*B*). Coexpression of either epitope-tagged phosphomimetic RIN4^{T166D} or wild-type RIN4 together with AvrRpm1 did not result in the activation of any RPM1 fragment (*SI Appendix*, Fig. S2*C*).

In addition, we were unable to reconstitute RPM1-induced cell death by co-overexpressing complementary domains in *trans*, i.e., CC, NB-ARC, and LRR (*SI Appendix*, Fig. S2*C*). This is different from the potato CNL RX or the tomato CNL Mi-1.2, in which in *trans* complementation of cell death induction by coexpression of individual domains has been demonstrated (16, 47). Introduction of the autoactivating MHD mutation D505V (26) into NB-ARC, CC-NB-ARC, or NB-ARC-LRR did not render any of these fragments autoactive. As a control for the negative effects of epitope tags on domains, we demonstrated that overexpression of identical but non–epitope-tagged RPM1 domains also did not lead to an HR (*SI Appendix*, Fig. S2*D*). All fragments accumulated to high levels, or to levels comparable to those of full-length RPM1 (*SI Appendix*, Fig. S2*E*).

RPM1 functions at the PM, where it interacts with RIN4. To analyze whether the loss of function of the different RPM1 domains tested could be due to loss of membrane localization, we conducted cell fractionation experiments with transiently expressed RPM1 domains. We found that all analyzed fragments localized to the membrane fraction, the CC, NB-ARC and CC-NB-ARC fragments more prominently than the LRR or NB-ARC-LRR fragments (*SI Appendix*, Fig. S3). These results

suggest that the loss of HR induction is not explained simply by mislocalization of the fragments.

To test whether the absence of HR induction by the membrane-localized CC or CC-NB-ARC fragments in *N. benthamiana* is due to the heterologous expression system, we generated stable transgenic *Arabidopsis* plants expressing either of two C-terminal epitope-tagged RPM1 CCs (CC-2 and CC-4) or the CC-NB-ARC fragments under the control of either estradiol-inducible or the tobacco mosaic viral 35S promoters in *rpm1-3* and *rpm1-3 rps2-101c rin4 pRIN4::T7-RIN4* (*T7-RIN4 r1r2r4*) plants, respectively. We did not observe any morphological differences in the transgenic plants compared with the *rpm1-3* mutant or *T7-RIN4 r1r2r4* plants despite high expression levels from the 35S or the estradiol-inducible promoter after estradiol induction (*SI Appendix*, Fig. S2 *F* and *G*). This could be due to the presence of wild-type RIN4 suppressing any (auto) activity, as we previously demonstrated for $RPM1^{D505V}$ autoactivity (42). Therefore, we used two independent transgenic lines for each construct to determine whether the CC-2, CC-4, or CC-NB-ARC fragment could be activated by bacteria-delivered AvrRpm1. We found no HR in any of the infected transgenic plants, confirming the transient *N. benthamiana* results indicating that RPM1 fragments are insufficient to trigger the HR (*SI Appendix*, Fig. S2 *F* and *G*). Taken together, these data suggest that RPM1 function cannot be recapitulated by these fragments, supporting our contention that it is dependent on the integrity and cooperation of all domains.

***In Planta* RPM1–RIN4 Interaction Is Mediated by All RPM1 Domains.** RPM1 interaction with RIN4 at the PM is necessary to perceive effector-mediated phosphorylation on RIN4 Thr166 and is required to activate RPM1 (41, 42). Initial yeast two-hybrid experiments indicated that the first 176 amino acids of RPM1 (including the CC domain plus the linker region and a small part of the NB-ARC domain; *SI Appendix*, Fig. S1*A*) could interact weakly with RIN4 (40). To extend these observations, we measured the interaction of RPM1 domains with wild-type RIN4 and the phosphomimetic mutant $RIN4^{T166D}$ *in planta*. We performed coimmunoprecipitation (co-IP) analysis of transiently expressed RPM1 fragments and either RIN4 or $RIN4^{T166D}$. We observed a strong interaction of wild-type RIN4 with the CC-1, NB-ARC, and NB-ARC-LRR fragments and only a very weak interaction with the other CC fragments, CC-NB-ARC, and LRR (*SI Appendix*, Fig. S4*A*). Interestingly, the CC fragments lost the ability to interact with $RIN4^{T166D}$, whereas interactions of the NB-ARC, NB-ARC-LRR, and LRR with $RIN4^{T166D}$ were still observed (*SI Appendix*, Fig. S4*B*).

We next addressed whether RIN4 mutations that either abolish RIN4 Thr166 phosphorylation (T166A) or block RIN4–RPM1 interaction (F169A) (42) affect the association with the CC-1, NB-ARC, or LRR domain. We included the longer CC-2 fragment in our analysis, because this CC fragment ends exactly where the NB-ARC fragment starts (*SI Appendix*, Figs. S1 and S2*A*). This experiment confirmed the loss of interaction of $RIN4^{T166D}$ with CC-1 (*SI Appendix*, Fig. S4*C*) and the lack of interaction of any RIN4 allelic variant with the CC-2 fragment (*SI Appendix*, Fig. S4*D*). The NB-ARC and LRR fragments both interacted with RIN4 regardless of the phosphomimetic or phospho-dead status of Thr166 (*SI Appendix*, Fig. S4 *E* and *F*). As has been reported for full-length RPM1 (42), the interaction of NB-ARC and the LRR with RIN4 was lost with the $RIN4^{F169A}$ allele (*SI Appendix*, Fig. S4 *E* and *F*). These results indicate that off-state RPM1–RIN4 interaction is mediated by all RPM1 domains, and that the associations of the NB-ARC and LRR domains with RIN4 are not affected by the phosphomimetic or phospho-dead mutations T166D and T166A, respectively. In addition, phosphorylation of RIN4 Thr166 alters interactions with RPM1, leading to the loss of RIN4–CC interaction, potentially stimulating or stabilizing the activated state of RPM1.

RPM1 Self-Association Is Constitutive and P-Loop Dependent. Self-association and/or dimerization of NLR proteins or their N-terminal domains has been demonstrated to be necessary for immune signaling in animals and plants (31, 32, 45, 48, 49) (*SI Appendix*, Table S1). Therefore, we asked whether RPM1 also self-associates, and whether such self-association is necessary for RPM1 function. Coexpression of differentially epitope-tagged RPM1 proteins in *N. benthamiana* followed by co-IP revealed self-association of the resting-state RPM1 protein *in planta* (Fig. 1*A*). To exclude the possibility that this self-association is due merely to transient overexpression in the heterologous system, we generated stable double-transgenic *Arabidopsis* lines by crossing a well-characterized C-terminally myc epitope-tagged RPM1 line (50) with a newly generated GFP epitope-tagged RPM1 line that fully complements the *rpm1-3* mutant (*SI Appendix*, Fig. S5*A*). Both differentially epitope-tagged RPM1 proteins were expressed from the native RPM1 promoter. Co-IP experiments demonstrated self-association of resting-state RPM1 in *Arabidopsis* (Fig. 1*B* and *SI Appendix*, Fig. S5*B*), suggesting that RPM1 exists as at least a dimer in the preactivation state.

We next analyzed whether this self-association is dependent on a functional P-loop, as has been demonstrated for the TNLs N and RPP1 (33, 45) (*SI Appendix*, Table S1). We transiently coexpressed differentially epitope-tagged P-loop loss-of-function mutant $RPM1^{G205E}$ (26) for co-IP analysis. Our results showed that a functional P-loop, and thus nucleotide binding, is required for resting-state RPM1 self-association (Fig. 1*C*).

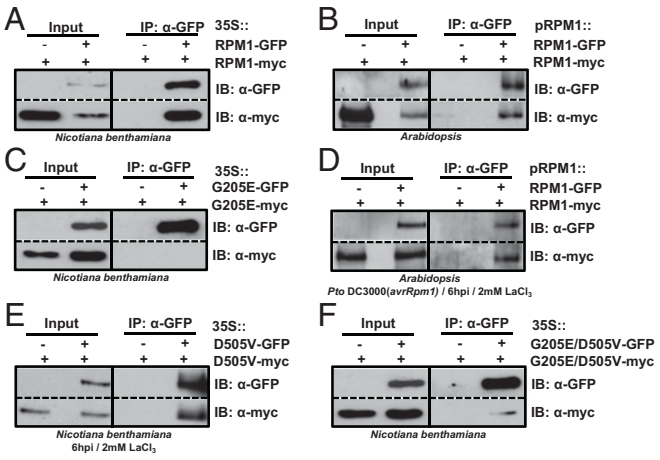

Fig. 1. RPM1 constitutively self-associates preactivation and postactivation. (*A*) Self-association of 35S::RPM1-myc and 35S::RPM1-GFP. *RPM1* constructs were transiently expressed in *N. benthamiana*, immunoprecipitated with anti-GFP magnetic beads, and then immunoblotted for both anti-myc and anti-GFP to assess input, immunoprecipitation, and co-IP. (*B*) Co-IP of native promoter-driven RPM1-myc and RPM1-GFP in transgenic *Arabidopsis*. Protein interaction was tested as described in *A*. (*C*) P-loop mutant $RPM1^{G205E}$ does not self-associate. Myc- and GFP-tagged 35S::$RPM1^{G205E}$ were transiently expressed in *N. benthamiana* and immunoprecipitated with anti-GFP magnetic beads. (*D* and *E*) Self-association of (*D*) effector-activated RPM1 in transgenic *Arabidopsis* (*D*) and of autoactive $RPM1^{D505V}$ in *N. benthamiana* (*E*). (*D*) Transgenic *Arabidopsis*, expressing both myc- and GFP-tagged RPM1 from the native RPM1 promoter, were hand-infiltrated with *Pto* DC3000 expressing *avrRpm1* in 10 mM $MgCl_2$ plus 2 mM $LaCl_3$. Microsomal lysates were extracted at 6 h postinfection (hpi) and immunoprecipitated with anti-GFP beads. (*E*) Expression of C-terminally myc- and GFP-tagged $RPM1^{D505V}$ was induced with 20 μM estradiol plus 2 mM $LaCl_3$ at 24 h postinfiltration in *N. benthamiana* leaves. Lysates were extracted at 6 h after estradiol induction (6 hpi) and immunoprecipitated with anti-GFP beads. (*F*) Self-association of $RPM1^{G205E/D505V}$ in *N. benthamiana*. Protein interaction was tested as described in *A*. IB, immunoblot.

We then tested whether effector-activated RPM1 or the autoactive MHD mutant RPM1^{D505V} also self-associate. To prevent rapid degradation of active RPM1 (26, 50) and thus ensure sufficient protein for co-IP analysis, we blocked RPM1 degradation with lanthanum ($LaCl_3$) treatment in these experiments. $LaCl_3$ blocks the activity of divalent cation channels, mainly calcium channels, and also blocks RPM1-induced HR in *Arabidopsis* (51). We found that $LaCl_3$ prevented the disappearance of activated RPM1 without altering effector (AvrRpm1)-induced posttranslational modification of RIN4 in our experiments, strongly suggesting that most, if not all, RPM1 precipitated in the presence of $LaCl_3$ is in the activated state (*SI Appendix*, Fig. S6*A*). We also found that $LaCl_3$ treatment in *Arabidopsis* did not affect bacterial growth of *Pto* DC3000 or growth restriction of *Pto* DC3000 (*avrRpm1*) (*SI Appendix*, Fig. S6*B*), and thus that loss of HR is not due to a loss of bacterial fitness. $LaCl_3$ also did not affect bacterial growth in rich medium (*SI Appendix*, Fig. S6*C*). Co-IP analysis of effector-activated myc- and GFP-tagged RPM1 in stable transgenic *Arabidopsis* and transiently coexpressed myc- and GFP-tagged autoactive RPM1^{D505V} in *N. benthamiana* demonstrated self-association of active RPM1 *in planta* (Fig. 1 *D* and *E*). Taken together, these results suggest that RPM1 self-associates before and after activation, and that nucleotide binding (P-loop function) is important for resting-state RPM1 self-association.

We previously reported that the autoactivity of RPM1^{D505V} is blocked by P-loop mutations in *cis* (RPM1$^{G205E/D505V}$) (26). This prompted us to analyze whether RPM1$^{G205E/D505V}$ lost the ability to self-associate. To do so, we transiently coexpressed differentially epitope-tagged RPM1$^{G205E/D505V}$ in *N. benthamiana* and performed co-IP analysis. Similar to the P-loop mutant RPM1^{G205E}, RPM1$^{G205E/D505V}$ lost self-association almost completely (Fig. 1*F* and *SI Appendix*, *SI Materials and Methods*). The loss-of-function phenotype of the *cis* double mutant (26) is likely due to a continual requirement for the P-loop in ATP binding and turnover (22, 23). Thus, we interpret our results as follows: RPM1 self-association depends on nucleotide binding, and a P-loop mutation alters NB-ARC domain structure or intramolecular domain interactions in such a way that both resting-state and active-state RPM1 self-association is inhibited or blocked.

RPM1 Plasma Membrane Localization Is P-Loop Dependent. We previously reported that a functional P-loop is necessary for the proper localization of RPM1 to the microsomal fraction in cellular fractionation experiments (26) (*SI Appendix*, Fig. S5*C*). Thus, we examined the subcellular localization of RPM1, RPM1^{G205E}, and the *cis* double-mutant RPM1$^{G205E/D505V}$ by confocal microscopy of C-terminally eYFP-tagged proteins transiently expressed in *N. benthamiana*. All three RPM1 proteins colocalized with tRFP-T7-tagged RIN4 at the PM (Fig. 2 *A*–*C*); however, we also observed a strong cytosolic fluorescence for RPM1^{G205E}-eYFP and RPM1$^{G205E/D505V}$-eYFP that almost disappeared at 72 h postinfiltration, likely due to degradation of the cytosolic (mis)localized proteins (Fig. 2 *B* and *C*). Cellular fractionation experiments in the presence or absence of coexpressed RIN4 confirmed the cytosolic localization of C-terminally myc- and eYFP-epitope tagged RPM1^{G205E} and RPM1$^{G205E/D505V}$ in these experiments (26) (Fig. 2 *D* and *E*). Therefore, P-loop function is necessary for proper RPM1 PM localization, and the presence of *Arabidopsis* RIN4 is not sufficient to rescue the mislocalization of P-loop mutant RPM1^{G205E} in *N. benthamiana* transient expression.

RPM1 Function Is Affected by Mutations in Hydrophobic and Conserved Residues of the CC Domain. It was recently demonstrated that the solution structure of the wheat CNL Sr33 CC fragment differs significantly from that of the published crystal structure of a barley paralog, MLA10, and, rather surprisingly, resembles the structure of the CC fragment from the distantly related potato CNL Rx (52) solved in complex with its interacting protein RanGAP2 (53).

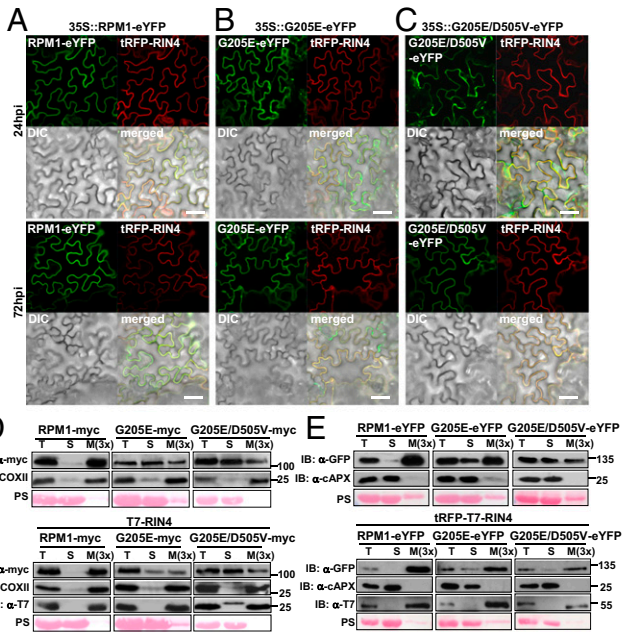

Fig. 2. RPM1 PM localization requires a functional P-loop. (*A* –*C*) Live-cell imaging of RPM1-eYFP (*A*), RPM1^{G205E}-eYFP (*B*), and RPM1$^{G205E/D505V}$-eYFP (*C*) together with tRFP-T7-RIN4 illustrating PM localization of wild-type RPM1 and additional cytosolic localization of RPM1^{G205E} and double-mutant RPM1$^{G205E/D505V}$ on transient expression in *N. benthamiana*. Leaves were imaged at 24 and 72 hpi. Note the reduced cytosolic fluorescence of RPM1^{G205E}-eYFP and RPM1$^{G205E/D505V}$-eYFP at 72 hpi. (Scale bar: 50 μM.) (*D* and *E*) Cell fractionation confirming cytosolic localization of RPM1^{G205E} and RPM1$^{G205E/D505V}$. (*D*) Agrobacteria containing either myc-tagged (*D*) or eYFP-tagged (*E*), 35S-driven RPM1 constructs were infiltrated either alone (*Upper*) or with pRIN4::T7-RIN4 (*D*) or pRIN4::tRFP-T7-RIN4 (*E*) (*Lower*) into *N. benthamiana* leaves. Tissue was harvested at 48 hpi for cell fractionation and immunoblotting with anti-myc (RPM1), anti-COXII (membrane marker), anti-APX (cytosol), and anti-T7 (RIN4) antibodies. Note that the band present in the anti-T7 blot in the soluble (S) fraction of the RPM1$^{G205E/D505V}$-myc plus T7-RIN4 sample is nonspecific. Ponceau S (PS) staining served as loading control and marker for the cytosolic fraction. M(3×) indicates three times enrichment relative to T or S. IB, immunoblot; M, microsomal fraction; S, soluble; T, total extract.

Secondary structure prediction of an RPM1 CC fragment (amino acids 1–120) and homology modeling of this fragment onto the Sr33 CC domain NMR structure suggested that the RPM1 $CC_{1–120}$ fragment also might adopt a four-helix bundle conformation (52) (*SI Appendix*, Figs. S7*A* and S8 *A*–*D*). Functional analyses demonstrated the importance of hydrophobic residues, located in the second helix of the four-helix bundle, in the CC domain for MLA10 function and CC dimerization (18). The hydrophobicity of these residues is conserved in RPM1, Sr33, and Rx (Fig. 3*A*), suggesting that these residues can be involved either in dimer formation or in holding together the monomeric four-helix bundle (52, 54). We wanted to know whether these conserved hydrophobic residues also play a role in RPM1 function. Our analyses also included two loss-of-function mutations in the CC domain that were isolated in a forward genetic screen to identify RPM1 mutations affecting the recognition of AvrRpm1 in Col-0 (55) (*SI Appendix*, Fig. S7*A*). These two mutations, S43F and P105S, map to the second helix and fourth helix, respectively, of the RPM1 CC domain defined by modeling onto the Sr33 CC solution structure with S43 and P105 likely surface-exposed (*SI Appendix*, Figs. S7*A* and S8 *B* and *D*).

We generated stable *Arabidopsis* transgenic plants for all five single mutants and infiltrated herbicide-resistant T2 plants with either *Pto* DC3000(EV) or *Pto* DC3000(*avrRpm1*) to measure

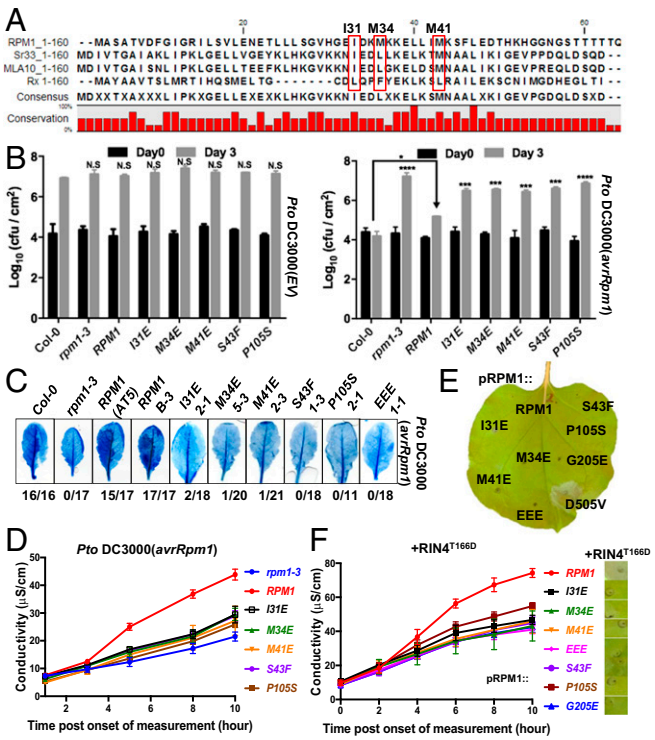

Fig. 3. Mutations in hydrophobic and conserved residues of the CC domain affect RPM1 function. (*A*) Alignment of amino acids 1–160 (only 1–62 shown) of RPM1, Sr33, MLA10, and Rx showing conservation of hydrophobic residues (highlighted; I31, M34, and M41) important for RPM1 function. (*B*) Loss of RPM1-induced bacterial growth restriction. Transgenic plants expressing the indicated RPM1 proteins were hand-infiltrated with *Pto* DC3000(*EV*) (*Left*) or *Pto* DC3000(*avrRpm1*) (*Right*). Error bars represent the SD among three samples. Asterisks indicate statistical significance calculated by one-way ANOVA. (*C*) Trypan blue staining of *Arabidopsis* leaves of indicated genotypes hand-infiltrated with *Pto* DC3000(*avrRpm1*) indicating loss of HR induction by RPM1 single mutants. The numbers below represent the ratio of total leaves infiltrated to leaves with clear HR and strong staining. (*D*) Quantitative measurement of cell death (conductivity) induced by wild-type RPM1 and RPM1 mutants on infiltration with *Pto* DC3000(*avrRpm1*) in transgenic *Arabidopsis*. (*E*) Cell death phenotype of eYFP-tagged RPM1 and indicated RPM1 alleles transiently expressed from the RPM1 promoter in *N. benthamiana*. (*F*) Mutations in the CC domain and the P-loop block the ability of RPM1 to induce HR when coexpressed with $RIN4^{T166D}$. eYFP-tagged RPM1 proteins were expressed from the RPM1 promoter, T7-tagged $RIN4^{T166D}$ from the RIN4 promoter. Conductivity measurements and visual cell death in leaves expressing the indicated proteins are shown. EEE, $RPM1^{I31/M34/M41E}$ triple mutant; N.S, not significant. **P* <0.05, ****P* <0.001, *****P* <0.0001.

bacterial growth restriction (Fig. 3*B*). None of the RPM1 alleles tested significantly restricted the growth of *Pto* DC3000(*avrRpm1*), and none affected *Pto* DC3000(EV) growth. Moreover, they all failed to induce HR on infiltration with a high inoculum of *Pto* DC3000(*avrRpm1*) (Fig. 3 *C* and *D*). Thus, all are loss-of-function alleles.

We also tested these mutant RPM1 proteins, as well as an $RPM1^{I31/M34/M41E}$ *cis* triple mutant, in our transient *N. benthamiana* reconstruction assays for their ability to induce cell death in response to coexpression of $RIN4^{T166D}$. When transiently expressed from the weak RPM1 promoter, all accumulated, albeit to lower levels for the three hydrophobic residue alleles (*SI Appendix*, Fig. S7 *I* and *J*). None of the alleles was autoactive or able to be activated by $RIN4^{T166D}$ coexpression; all were loss of function (Fig. 3 *E* and *F*). However, transient overexpression from the 35S promoter allowed weak $RIN4^{T166D}$-dependent RPM1 activation for the single mutations in the three hydrophobic residues (I31E, M34E, and M41E) and the conserved P105 (P105S) (*SI Appendix*, Fig. S7*D*). The $RPM1^{S43F}$ single mutant and the $RPM1^{I31/M34/M41E}$ triple mutant were not rescued by transient overexpression (*SI Appendix*, Fig. S7 *D* and *F*). Consistent with these findings, the single mutations I31E, M34E, M41E, and P105S altered effector-mediated activation of RPM1 only weakly following expression from the 35S promoter in transient overexpression conditions (*SI Appendix*, Fig. S7*E*), whereas neither the overexpressed $RPM1^{I31/M34/M41E}$ triple mutant nor $RPM1^{S34F}$ was activated by AvrRpm1 coexpression (*SI Appendix*, Fig. S7 *E* and *F*). This is also consistent with only the $RPM1^{I31/M34/M41E}$ triple mutant and $RPM1^{S34F}$ having a significant negative effect on the autoactivity of $RPM1^{D505V}$ in *cis* when transiently overexpressed (*SI Appendix*, Fig. S7 *G* and *H*). None of the tested mutants was autoactive when expressed from the 35S promoter (*SI Appendix*, Fig. S7 *B* and *C*). These results suggest weak effects of P105 and additive effects of the three hydrophobic residues I31, M34, and M41, as well as a strong effect for S43 on RPM1 activation in transient overexpression in *N. benthamiana*. We conclude that mutations in these hydrophobic and conserved residues represent at least partial loss-of-function

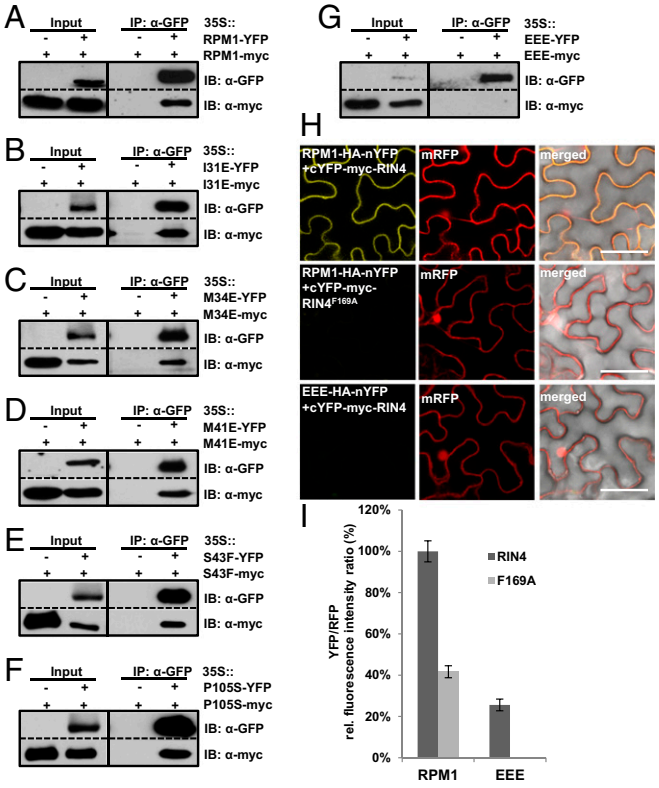

Fig. 4. CC domain mutations affect full-length RPM1 self-association in an additive manner. (*A*–*G*) Co-IP of transiently expressed RPM1 indicating single and $RPM1^{I31/M34/M41E}$ triple mutants in *N. benthamiana*. RPM1 proteins were expressed from the 35S promoter. Total protein extract was immunoprecipitated with anti-GFP magnetic beads, and membranes were immunoblotted for anti-GFP or anti-myc to assess input, immunoprecipitation, and co-IP. (*H*) $RPM1^{I31/M34/M41E}$ loses the interaction with RIN4. In BiFC analyses of RPM1–RIN4 and $RPM1^{I31/M34/M34E}$–RIN4 interactions in *N. benthamiana*, both RPM1 alleles and RIN4 were expressed from the 35S promoter from a single expression vector. $RIN4^{F169A}$ served as a control for loss of RPM1 interaction (42). (Scale bar: 50 mm.) (*I*) Quantification of the ratio of mean YFP fluorescence to RFP indicating the interaction of RPM1 with RIN4, but not with $RIN4^{F169A}$, and the loss of interaction of $RPM1^{I31/M34/M41E}$ with RIN4. Data are mean ± SEM of 8–12 images selected at random over the surface of two leaf samples in each case. EEE, $RPM1^{I31/M34/M41E}$ triple mutant; IB, immunoblot; N.S, not significant.

alleles and putatively alter the structural requirements for RPM1 function or interdomain and intradomain interactions.

Loss-of-Function Mutations in Hydrophobic and Conserved Residues of the CC Domain Affect RPM1 Self-Association. The loss-of-function phenotype of the RPM1 mutants that we tested prompted us to analyze whether these mutations also affect RPM1 self-association. We transiently coexpressed each single mutant and tested for self-association by co-IP. Each of these RPM1 alleles retained the ability to self-associate (Fig. 4 *A*–*F*). The proposed surface-exposed positions of S43 and P105 in the putative CC domain monomer model (*SI Appendix*, Fig. S8 *B* and *D*) suggests that these two residues could function in self-association; however, we did not observe any effect on self-association when these positions were mutated in the full-length RPM1 protein. Thus, they likely are involved in signaling or association with downstream interactors.

Loss of RPM1 activity due to single mutations in any of the hydrophobic residues also is not caused by a mislocalization, given that all properly localized to the membrane in cell fractionation analysis (*SI Appendix*, Fig. S9*A*). To determine whether a combination of mutations of all three hydrophobic residues in *cis* might be necessary to completely block RPM1 self-association, we tested the strong loss-of-function RPM1$^{I31/M34/M41E}$ triple mutant in our co-IP analysis, and noted that it indeed lost self-association *in planta* (Fig. 4*G*). Interestingly, and in contrast to the loss of self-association mutants RPM1^{G205E} and RPM1$^{G205E/D505V}$, the PM localization of the RPM1$^{I31/M34/M41E}$ triple mutant was not affected (*SI Appendix*, Fig. S9 *B* and *C*). Thus, we anticipate that self-association per se is not sufficient for PM localization or function, but is required for signaling, potentially via interactions with RIN4, phosphorylated RIN4, or other signaling partners.

RPM1–RIN4 Interaction Is P-Loop Dependent and Affected by Loss-of-Function Mutations in the CC Domain. To investigate whether these mutants express altered interactions with wild-type RIN4 or phosphomimetic RIN4^{T166D}, we coexpressed each RPM1 single mutant or the RPM1$^{I31/M34/M41E}$ triple mutant together with wild-type RIN4 or with RIN4^{T166D} in *N. benthamiana* and tested for interactions by co-IP. We also included the nonfunctional, mislocalized, and loss of self-association mutant RPM1^{G205E}. All CC domain-localized single mutants retained the *in planta* interaction with both wild-type RIN4 and the phosphomimetic RIN4^{T166D} (*SI Appendix*, Fig. S9 *D* and *E*). However, we consistently observed much weaker interactions of RIN4 and RIN4^{T166D} with RPM1 alleles with mutations in any of the three hydrophobic residues I31, M34, and M41. This observation was supported by our finding that interaction of the triple-mutant RPM1$^{I31/M34/M41E}$ with wild-type RIN4 was lost compared with the single mutants (*SI Appendix*, Fig. S9*D*). We confirmed the loss of RPM1$^{I31/M34/M41E}$–RIN4 interaction by bimolecular fluorescence complementation (BiFC) analysis in *N. benthamiana* (Fig. 4 *H* and *I*). The interaction of RPM1$^{I31/M34/M41E}$ with phosphomimetic RIN4^{T166D} was also abolished (*SI Appendix*, Fig. S9*E*), suggesting that the integrity of the hydrophobic core of the RPM1 CC domain formed by residues I31, M34, and M41 is important not only for RPM1 self-association, but also for RPM1–RIN4 interaction both before and after activation.

We demonstrated that the P-loop mutant RPM1^{G205E} lost interaction with both RIN4 and RIN4^{T166D} (*SI Appendix*, Fig. S9 *D* and *E*), indicating that P-loop function is important for RIN4 interaction and supporting the notion that RPM1 self-association is crucial for RPM1–RIN4 interaction. To test whether restoration of strong PM localization of RPM1^{G205E} could rescue the loss of RIN4 interaction, we tethered this mutant to the PM by adding the first 12 amino acids of calcineurin B-like protein 1 (CBL1) to the N terminus. This N-terminal fusion can target proteins to the PM due to myristoylation and palmitoylation of residues Glycine 2 and Cysteine 3, respectively (56). We previously demonstrated that CBL-tagged wild-type RPM1 is functional, but that functionality of RPM1^{G205E} and RPM1$^{G205E/D505V}$ cannot be restored by forcing these mutants to the PM (26). We included the RPM1$^{G205E/D505V}$ *cis* double mutant in our experiment to also test whether the addition of the MHD mutation has any effect on RPM1–RIN4 interaction. As expected, we observed an interaction of the functional CBL-RPM1 wild-type protein with RIN4 (*SI Appendix*, Fig. S9*G*); however, the interaction of CBL-RPM1^{G205E} and CBL-RPM1$^{G205E/D505V}$ with RIN4 was not restored, consistent with their loss of function, even when tethered to the PM (26) (*SI Appendix*, Fig. S9*G*).

All RPM1 Domains Contribute to Self-Association. CC domain dimerization has been shown to be important for function of the barley CNL MLA10 (18). Recently, it was shown that only relatively longer, functional fragments of the MLA10, Sr33, and Sr50 CC domains dimerize *in planta*, whereas shorter, nonfunctional CC domain fragments that are disrupted in one alpha-helix presumed to be important for CC function do not (44, 52). Thus, we wanted to know whether the RPM1 CC domain also self-associates *in planta*. We coexpressed each of the five CC domain fragments with differential epitope tags in *N. benthamiana* and analyzed self-association by co-IP. In contrast to MLA10, Sr33, and Sr50, all tested RPM1 CC-domain fragments self-associated regardless of their length (Fig. 5*A*). The length of the self-associating RPM1 CC-1 fragment (amino acids 1–135) corresponds to the length of the short, nonfunctional, and non–self-associating Sr33 fragment (amino acids 1–130) (alignment in *SI Appendix*, Fig. S7*A*). However, the RPM1 CC-1 fragment (amino acids 1–135) includes the full predicted alpha-helical region possibly important for CC function (*SI Appendix*, Fig. S7*A*), as is the case for the larger and functional Sr33 CC fragment (amino acids 1–142) (44, 52). Therefore, all of our CC fragments should include the last alpha-helix, a structural characteristic important for MLA10 and Sr33 CC function. Thus, it seems likely that a complete four-helix bundle conformation, rather than a certain length, is important for CC self-association and function. We also confirmed self-association of the CC-2 fragment in BiFC analysis (*SI Appendix*, Fig. S10*A*), and demonstrated that the NB-ARC and LRR domains of RPM1 self-associate (Fig. 5 *C* and *D*). Thus, all domains of RPM1 can self-associate *in planta* and therefore might all contribute to self-association of full-length RPM1.

CC Dimerization Is Affected by Mutations in the Hydrophobic Residues of the CC Domain. We next tested whether the CC domain mutations that render RPM1 inactive alter or inhibit the RPM1–RIN4 interaction and, at least as a triple mutant, abrogate full-length RPM1 self-association also affect self-association as isolated CC-1 fragments. We found that mutations in the hydrophobic residues M34 and M41 dramatically weakened CC-1 self-association, and, as for the full-length RPM1^{I13,M34,M41E}, a combination of all three mutations completely disrupted CC-1 self-association (Fig. 5*B*). We also found a loss of self-association on BiFC analysis of the longer CC-2 fragment when all three residues were mutated (*SI Appendix*, Fig. S10 *A* and *B*). This finding indicates that alteration of these residues disrupts the intramolecular and intermolecular interactions of RPM1 important for function and thus could also affect possible interactions with downstream signaling components.

The RPM1 CC–NB-ARC Interaction Is Affected by Mutations in Residues Required for Nucleotide Binding. Regulated intramolecular CC–NB-ARC interactions have been shown to be important for the function of some NLRs (27, 47). It is assumed that on activation, the intramolecular CC–NB-ARC interaction is altered in such a way that the signal-competent N-terminal domain is released from

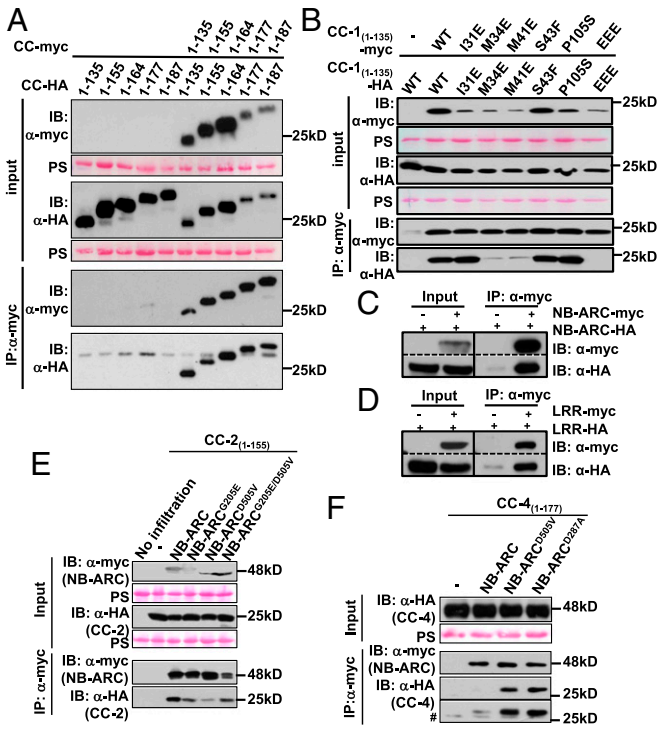

Fig. 5. Intradomain and interdomain interactions contribute to RPM1 self-association. (*A*) *In planta* self-association of CC fragments of different lengths. All five CC fragments were transiently expressed in *N. benthamiana* leaves, and total protein extract was immunoprecipitated with anti-HA magnetic beads. Membranes were immunoblotted for anti-myc and anti-HA to assess input, immunoprecipitation, and co-IP. (*B*) CC domain mutations affect CC self-association in co-IP analysis of transiently expressed CC-1 fragments in *N. benthamiana*. Samples were processed as described in *A*. (*C* and *D*) Self-association of NB-ARC (*C*) and LRR (*D*) domains transiently expressed in *N. benthamiana*. Protein self-association was tested as described in *A*. (*E*) Mutations affecting nucleotide binding in the NB-ARC domain influence CC–NB-ARC interactions. CC-2 was transiently coexpressed with NB-ARC, NB-ARC^{G205E}, NB-ARC^{D505V}, and NB-ARC$^{G205E/D505V}$ to assess interaction by co-IP. Proteins were sampled as described in *A*. (*F*) NB-ARC alleles with mutations affecting ATP binding (D505V) and hydrolysis (D287) enhance CC-4–NB-ARC interactions. Proteins were transiently coexpressed in *N. benthamiana* to assess interaction by co-IP. The second immunoprecipitation panel, labeled with #, denotes longer exposure of the-HA (CC-4) blot. Proteins were sampled as described in *A*. Ponceau staining (PS) of the RuBisCO large subunit is shown as a protein-loading control for the input. EEE, RPM1I31/M34/M41E triple mutant; IB, immunoblot.

intramolecular repression, concomitant with, or as a result, of nucleotide exchange. We wanted to analyze whether the RPM1 CC domain interacts with the NB-ARC domain, and whether this interaction is altered on activation. Because none of the tested RPM1 fragments or domains was (auto)active in our *in planta* expression systems, we mimicked the activated state by introducing NB-ARC mutations generally known to affect nucleotide binding and hydrolysis in NLR proteins into our NB-ARC domain (28). We analyzed interactions of the CC-2 fragment (amino acids 1–155) with wild-type or mutated NB-ARC domains (amino acids 156–535) by co-IP of transiently overexpressed proteins in *N. benthamiana*. We observed a weakened interaction of CC-2 with either loss-of-function mimic NB-ARC^{G205E} or autoactive mimic NB-ARC^{D505V} mutant alleles (Fig. 5*E*). This was also the case in the interaction of the CC-2 with the P-loop MHD *cis* double-mutant NB-ARC$^{G205E/D505V}$ domain (Fig. 5*E*). Interestingly, when using the longer CC-4 fragment (amino acids 1–177), we observed an enhanced interaction with the NB-ARC domain harboring either of two autoactivating mutations in the MHD (D505V) or the Walker B (D287A) motifs (Fig. 5*F*). This suggests that the N-terminal amino acids (155–177) of the NB-ARC domain are responsible for a tighter CC-4–NB-ARC interaction on ATP binding (or the mimicking of ATP binding by MHD mutation).

Discussion

To successfully defend themselves against pathogens, animals and plants evolved efficient innate immune systems. In both kingdoms, proteins of the NLR family are responsible for the detection of effectors (and in animals MAMPs as well) and the subsequent induction of an appropriate immune response (1, 13, 14). In plants, the activation of NLR proteins is often accomplished by at least self-association of either the N-terminal (TIR or CC) domain or the full-length receptor (17, 18, 44, 46, 49, 52, 57, 58). Here we report that constitutive self-association of the PM-localized *Arabidopsis* CNL RPM1 is required for its function, and that all domains—the N-terminal CC, the central NB-ARC, and the C-terminal LRR domain—contribute to intermolecular interactions. Furthermore, our data support a model in which resting- and active-state RPM1 self-association and proper PM localization are P-loop dependent, and that conserved hydrophobic residues in the CC domain play important roles in RPM1 self-association, activation, and RIN4 interaction (Fig. 6).

NLR-mediated immune signaling in animals and plants has been proposed to be dependent on their N-terminal domains, and in many cases (over)expression of this domain by itself is able to induce cell death signaling (18, 19, 45, 59). We were not

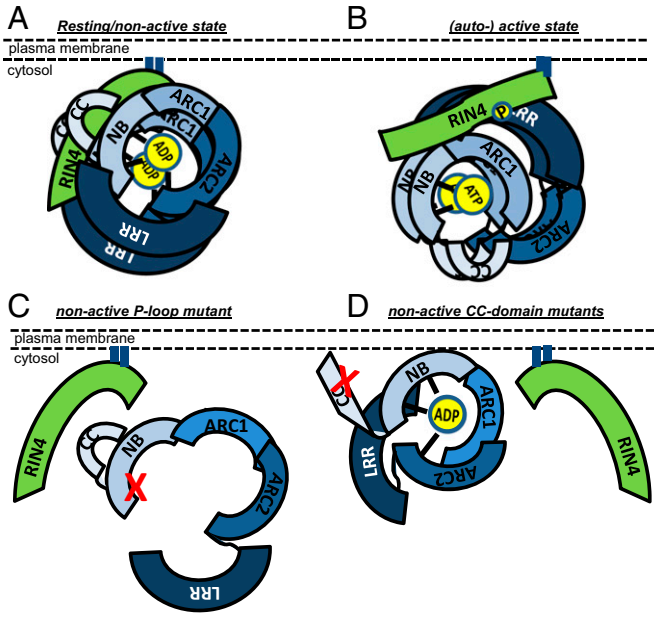

Fig. 6. Model of RPM1 self-association and conformational switch on activation. (*A*) Resting/nonactive state: RPM1 interacts with RIN4 at the PM at least as a dimer in a closed conformation mediated by the NB-ARC, LRR, and CC domains. Intramolecular interactions between the CC and NB-ARC domains and intermolecular interactions mediated by all three domains contribute to RPM1 self-association. (*B*) Activated (and autoactive) RPM1 remains self-associated and in complex with RIN4. Intramolecular interactions between the CC and NB-ARC domains and interaction of the CC domain with phosphorylated RIN4 are altered and thus might allow for the recruitment of downstream signaling partners. (*C*) RPM1 resting-state self-association, full PM localization, and RIN4 interaction are dependent on a functional P-loop motif. P-loop mutation is indicated by the red "X" in the NB part of the NB-ARC domain. (*D*) Mutations in conserved and/or hydrophobic residues of the CC domain affect RPM1–RIN4 interaction, but not PM localization, presumably by altering intramolecular and intermolecular interactions important for activation and/or signaling. Mutations are indicated by a red "X" in the CC domain.

able to induce cell death in either of our expression systems, transient in *N. benthamiana* or stable in transgenic *Arabidopsis*, regardless of the RPM1 domain, fragment, or combinations of domains or whether we used the phosphomimetic RIN4^{T166D} to activate RPM1 (*SI Appendix*, Fig. S2). This suggests that tightly regulated cooperation of all of its domains is required for immune signaling initiated by RPM1. We previously demonstrated that RPM1 signals from the PM (26), and here we have extended this concept by showing that RPM1 membrane localization can be mediated by either the CC or the NB-ARC domain (*SI Appendix*, Fig. S3). Therefore, it is plausible to assume that the CC-NB-ARC domain drives RPM1 to the membrane, where RPM1 interacts with RIN4, which has a carboxyl-terminal acylation/prenylation site required for its localization and function (60), and potentially other components important for signaling. Interactions with putative signaling partners are very likely mediated by more than one or all RPM1 domains, and thus their integrity is necessary for signal induction. This idea is further supported by our finding that all RPM1 domains are involved in interaction with its guardee RIN4 *in planta* (*SI Appendix*, Fig. S4). This is unlike observations reported for other plant NLRs. In those cases, the N-terminal domains of the NLR mediate the interaction with their guardee, whereas the LRR domain is proposed to negatively regulate the NB-ARC and CC or TIR domains, thus keeping the NLR inactive (15, 47, 61–64). Alternatively, all domains of RPM1 are required for the CC domain to adopt the signal-competent state required for function. This model is consistent with the oligomerization observed on activation of animal NLRC4, where the N-terminal signaling domains appear to form a functional signaling platform only when the activated protein oligomerizes via its central NB-ARC, helical domain 1, and winged helix domain to form a functional inflammasome (31, 32). In this context, the functional capacity of any isolated N-terminal signaling domain would depend on its propensity to adopt and maintain a particular functional structure without contributions from any other domain of the full-length NLR. Once at the PM, RPM1 is in a stable association with RIN4, and this association together with intramolecular interactions keeps RPM1 in its "off" state. This "off"-state RPM1–RIN4 interaction depends on an intact P-loop and conserved hydrophobic residues in the RPM1 CC domain, which presumably are important for proper structural conformation of the CC domain and the intermolecular interactions necessary for RIN4 association. Upon effector-induced, host kinase-mediated phosphorylation of RIN4 Thr166, the intrinsically disordered RIN4 (65) might adopt a slightly different structure and contribute to RPM1 activation. This could drive RPM1 intramolecular rearrangements resulting in the loss of CC–RIN4 interaction, a weakened and/or changed interaction between the CC and NB-ARC domains, and eventually the exchange of ADP with ATP required for activation (Fig. 6*B*).

Complex intermolecular and intramolecular domain interactions have been hypothesized to be necessary for proper NLR activation, ADP-to-ATP exchange, and hydrolysis (11). It is widely accepted that the NB-ARC domain of plant NLRs adopts a more open conformation to allow for nucleotide exchange and to release the negative regulatory interactions with the N- or C-terminal domains on recognition of the appropriate pathogen signal (13). We noted a reduced, but not eliminated, interaction of the CC-2 fragment (amino acids 1–155) with RPM1 NB-ARC domains harboring mutations affecting nucleotide binding (Fig. 5*E*). Interestingly, when we used a slightly longer fragment of the CC domain (CC-4; amino acids 1–177) that overlapped with our NB-ARC domain by 22 amino acids, we observed a tighter interaction with the NB-ARC domain mutated in the MHD (ATP-binding) or Walker B (ATP hydrolysis) motif (Fig. 5*F*). Taken together, these findings indicate involvement of the linker region between CC and NB-ARC and of the N-terminal region of the NB-ARC domain—namely, the first part of the NB subdomain—in the intramolecular and also likely the intermolecular interactions (oligomerization) that accompany RPM1 activation. This is consistent with recovery of a loss-of-function RPM1 allele at residue G174 (55), which is extremely conserved in RPM1 orthologs as well as in most *Arabidopsis* CNLs (*SI Appendix*, Figs. S7*A* and S11).

Self-association/oligomerization of NLR proteins can occur either preactivation or postactivation, or can remain constant in both states (*SI Appendix*, Table S1). RPM1 self-association does not depend on activation status (Fig. 1); however, self-association is P-loop dependent. P-loop–dependent self-association on activation has been reported for the tobacco TNL N, *Arabidopsis* TNL RPP1$_{Nd}$, and human NLRC4 proteins (31–33, 45, 46, 66). P-loop–dependent self-association is consistent with ATP binding being necessary for activation. Mutations in the MHD motif are thought to promote a conformational change, opening up the NB-ARC domain to allow for faster or easier exchange of ADP to ATP (67, 68). In addition, a mutation in the MHD motif of the flax TNL M exhibits higher affinity for ATP than for ADP, suggestive of a conformational change on ATP binding and/or activation (28). The RPM1$^{G205E/D505V}$ double mutant is not active and thus presumably does not bind ATP, as has been demonstrated for an equivalent *cis* double-mutant M$^{K286L/D555V}$ of the flax M NLR (23, 28) and thus also loses self-association. However, we speculate that activation of RPM1 leads to a conformational change that either restores or does not affect self-association, likely through the formation of a second, stable intramolecular interaction/oligomerization surface. Consistent with this hypothesis, the generation of an activation-dependent oligomerization surface also has been shown to be necessary for formation of the mammalian Prgj-NAIP2-NLRC4 inflammasome (31). It will be interesting to see whether a similar in *cis* double mutation in other NLRs also affects self-association and, in the case of inflammasome- or apoptosome-forming animal NLRs, function.

The recently published structural analysis of the CC fragments (amino acids 1–120) of wheat Sr33, rye Sr50, barley MLA10, and potato Rx NLRs suggests a shared and conserved monomeric four-helix bundle conformation of this domain (52). However, secondary structure predictions and functional analysis of a longer CC fragment (amino acids 1–160) of these CNLs indicated that the shorter CC fragment used to solve the respective structures lacks a C-terminal alpha-helix and is not functional; only longer CC fragments (consisting of at least amino acids 1–142) are autoactive (for cell death signaling in transient expression in *N. benthamiana*) and can self-associate *in planta* (44). Secondary structure predictions of the RPM1 CC domain indicate that all CC constructs used in this study should include the full C-terminal alpha-helix, likely explaining their observed self-association, yet none was autoactive (Fig. 5 and *SI Appendix*, Fig. S2). Hydrophobic residues, shown to be important for MLA10 function and dimerization, are highly conserved in RPM1 (18) (Fig. 3*A*). We have shown that these residues are also necessary for full activity of RPM1 and, in an additive manner, also for self-association of either the full-length protein or the CC domain. Loss of function of the single mutants RPM1^{I31E}, RPM1^{M34E}, and RPM1^{M41E} is likely due to a weakened interaction of these mutants with RIN4 or RIN4^{T166D} (*SI Appendix*, Fig. S9 *D* and *E*), resulting from loss of or altered CC folding (Fig. 5*B*). Their combination into the RPM1$^{I31/M34/M41E}$ *cis* triple mutant had an additive effect on RPM1 function. Taken together, these findings suggest that these residues are important for the structural conformation of the CC domain necessary for self-association, and thus affect intramolecular interactions important for RIN4 interaction and consequent RPM1 activation/signaling. We favor a model in which the CC and LRR domains interact with the "off"-state ADP-bound NB-ARC domain and both the CC and NB-ARC domains are necessary and sufficient for RPM1–RIN4 interaction at the PM. On effector-induced

phosphorylation of RIN4 Thr166, the RIN4–CC domain association is released, and the CC–NB-ARC interaction eventually changes to allow the exchange of ADP by ATP, thus activating RPM1. Activated RPM1–RIN4 interactions would then be mediated by the NB-ARC and LRR domains (*SI Appendix*, Fig. S4). Phosphorylated RIN4 could stabilize such an activated RPM1 confirmation, as reflected by enhanced interaction of RPM1 with $RIN4^{T166D}$ (42).

We also analyzed the effect of two loss-of-function mutations, S43F and P105S, in the CC domain (55). Self-association of either the isolated CC domain or full-length RPM1 was not affected by either of these mutations. Thus, although S43 and P105 are required for RPM1 function, they are dispensable for resting-state self-association. However, our results show that transient co-overexpression of $RIN4^{T166D}$ does not activate $RPM1^{S43F}$, but does activate $RPM1^{P105S}$. The inability of $RPM1^{S43F}$ to be activated by $RIN4^{T166D}$ is not due to a loss of interaction, but could be explained by the structural requirements of S43 for RPM1 function or interdomain interactions that must occur subsequent to $RIN4^{T166D}$ binding. However, the finding that the S43F mutation also completely blocks D505V autoactivity in *cis* suggests an important function of S43 for RPM1 signaling as well as a structural role. Although $RPM1^{P105S}$ blocks effector-mediated RPM1 activation in *Arabidopsis* and activation by $RIN4^{T166D}$ in coexpression experiments in *N. benthamiana* when expressed from the RPM1 promoter, it does not do so in transient overexpression from the 35S promoter (*SI Appendix*, Fig. S7). In addition, this allele does not block autoactivity of $RPM1^{D505V}$ (26). A proline-to-serine substitution at P105 should have only a very minor effect on RPM1 structure, because serine residues may be relatively common within tight turns on protein surfaces and the serine side chain hydroxyl oxygen could form a hydrogen bond with the protein backbone, effectively mimicking a proline (www.russelllab.org/aas/Ser.html). Therefore, RPM1 function is not (or only very weakly) affected by P105S in transient overexpression in *N. benthamiana*, but this P-to-S substitution is sufficient to effectively interfere with RPM1 function in response to pathogen-delivered AvrRpm1 or AvrB in *Arabidopsis*. This is consistent with the fact that $RPM1^{P105S}$ expressed from the RPM1 promoter cannot complement the *rpm1-3* mutant (Fig. 3).

Recent detailed biochemical and genetic analyses of different plant NLRs have elucidated NLR regulation, activation, and function. It is now generally accepted that plant NLRs, like their counterparts in animals, at least dimerize to initiate an appropriate immune response (14); however, we still lack evidence for plant NLR oligomerization upon activation into high-molecular signaling complexes that are functionally similar to animal apoptosomes or inflammasomes. Furthermore, as yet there is no published structure of a full-length NLR (neither plant nor animal NLR), and thus the exact molecular mechanism of activation via N-terminal domain function remains obscure. It will be interesting to explore whether RPM1 self-association after activation leads to the formation of high-molecular weight complexes and to determine the effect of release of the CC–RIN4 interaction on activation. Does the CC domain recruit downstream signaling components to the RPM1-RIN4 complex, or is it responsible for RPM1 oligomerization and the formation of a signaling hub? Or does the CC itself provide the necessary functions for disease resistance?

Materials and Methods

Plant Material and Growth Conditions. *Arabidopsis thaliana* was grown in walk-in growth rooms maintained at 21 °C/18 °C (day/night) with a 9-h/15-h (day/night) cycle. Transgenic *Arabidopsis* lines were generated using a standard floral dip technique (69). *N. benthamiana* was grown in a walk-in growth room maintained at 26 °C/22 °C with a 12-h/12-h day/night cycle and a LGM550 professional LED grow light system (www.led-grow-master.com/). The following *Arabidopsis* genotypes were used: *Col-0*, *rpm1-3* (39), *pRIN4::T7-RIN4 rpm1-3 rps2-102c rin4* (42), *pRPM1::RPM1-myc rpm1-3* (50), and *pRPM1::RPM1-myc rpm1-3 Dex::AvrRpm1-HA* (70). The *RPM1-myc* and *RPM1-GFP* double-transgenic *Arabidopsis* line was generated by crossing the *pRPM1::RPM1-myc rpm1-3* line with a homozygous *pRPM1::RPM1-GFP rpm1-3* line (this study).

Coimmunoprecipitation and Western Blot Analysis. Frozen *N. benthamiana* leaf tissue (~100–200 mg) was collected and ground in a mortar and pestle with liquid nitrogen and then resuspended in 2 mL of extraction buffer (50 mM Hepes-KOH pH 7.5, 50 mM NaCl, 10 mM EDTA pH 8.0, 0.5% Triton X-100, and 5 mM DTT with 1× plant protease inhibitor mixture; Sigma-Aldrich). Soluble supernatants were cleared by centrifugation at 10,600 × *g* for 5 min and at 20,800 × *g* for 15 min at 4 °C and then incubated for 2 h with end-over-end turning at 4 °C with 35 μL of α-myc–, α-GFP–, or α-HA–conjugated magnetic beads (Miltenyi Biotec). Samples were captured with MACS separation columns (Miltenyi Biotec), and washed three times with washing buffer (extraction buffer with 0.2% Triton X-100 and 150 mM NaCl). Bound proteins were eluted in 120 μL of elution buffer (50 mM Tris·HCl pH 6.8, 50 mM DTT, 1% SDS, 1 mM EDTA pH 8.0, 0.005% bromophenol blue, and 10% glycerol). Samples were resolved by electrophoresis on 8% (for RPM1), 12.5% or 15% (for RPM1 fragments), and 12.5% (for RIN4) SDS/PAGE gels, transferred to nitrocellulose membranes, and blotted with primary antibodies overnight at 4 °C in 5% nonfat dry milk diluted in TBS with 1% Tween. Primary and secondary antibody dilutions were as follows: α-Myc, 1:1,000 (Santa Cruz Biotechnology); α-HA, 1:1,000 (Roche); α-T7 HRP-conjugated, 1:10,000 (Novagen); α-GFP, 1:1,000 (Roche); and α-mouse HRP conjugated, 1:7,500 (R&D Systems). In two out of three experiments, a very weak self-association of $RPM1^{G205E/D505V}$ was observed, which in light of the overexpression in these co-IP experiments might not be biologically relevant.

$LaCl_3$ Treatment. $LaCl_3$ was applied to *N. benthamiana* or *Arabidopsis* as described previously (51.). For this, 2 mM $LaCl_3$ was injected into *N. benthamiana* leaves at 1 h before infiltration of *Agrobacterium* cell suspension expressing $RPM1^{D505V}$-GFP or $RPM1^{D505V}$-myc. To monitor the effects of $LaCl_3$ on RPM1-mediated disease resistance, 2 mM $LaCl_3$ was applied to *Arabidopsis* transgenic plants conditionally expressing AvrRpm1 by dexamethasone (Dex) treatment. AvrRpm1 was induced with 20 μM Dex at 1 h after $LaCl_3$ application. A bacterial growth assay with *Pto* DC3000(EV) and *Pto* DC3000(*avrRpm1*) was performed by infiltrating 1×10^5 cfu/mL of bacterial inoculum in 10 mM $MgCl_2$ with or without 2 mM $LaCl_3$ into rosette leaves of 4- to 6-wk-old Col-0 plants. The same number of bacterial cells (1×10^5 cfu/mL) was grown for 3 h, equivalent to day 0 growth in the bacterial growth assay, at 28 °C in King's B medium in the presence and absence of 2 mM $LaCl_3$ to monitor the effects of $LaCl_3$ on bacterial growth in medium. The effect of $LaCl_3$ on RPM1 intracellular localization was also monitored by confocal microscopy of transiently expressed 35S::RPM1-eYFP and 35S::$RPM1^{D505V}$-eYFP in *N. benthamiana* leaves, and no change was observed compared with mock treatment (data not shown).

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