Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network

Plants generate effective responses to infection by recognizing both conserved and variable pathogen-encoded molecules. Pathogens deploy virulence effector proteins into host cells, where they interact physically with host proteins to modulate defense. We generated an interaction network of plant-pathogen effectors from two pathogens spanning the eukaryote-eubacteria divergence, three classes of Arabidopsis immune system proteins, and ~8000 other Arabidopsis proteins. We noted convergence of effectors onto highly interconnected host proteins and indirect, rather than direct, connections between effectors and plant immune receptors. We demonstrated plant immune system convergence of effectors onto highly interconnected host proteins and indirect, rather than direct, connections between effectors and plant immune receptors. Thus, pathogens from different kingdoms deploy independently evolved virulence proteins that interact with a limited set of highly connected cellular hubs to facilitate their diverse life-cycle strategies.

Interactions between disease-causing microbes and their hosts are complex and dynamic. Plants recognize pathogens through two major classes of receptors. Initially, plants sense microbes via perception of conserved microbe-associated molecular patterns (MAMPs) by pattern-recognition receptors (PRRs) located on the cell surface. This first level of recognition results in MAMP-triggered immunity (MTI), which is sufficient to fend off most microbes (1). To counter MTI, evolutionarily diverse plant pathogens independently evolved mechanisms to secrete and deliver effector proteins into host cells (2, 3). Effectors interact with cellular host targets and modulate MTI and/or host metabolism in a manner conducive to pathogen proliferation and dispersal (3–5). Plants deploy a second set of polymorphic intracellular immune receptors to recognize specific effectors. Nearly all are members of the nucleotide-binding site–leucine-rich repeat (NB-LRR) protein family, analogous to animal innate immune NLR proteins (6, 7). NB-LRR proteins can be activated upon direct recognition of an effector or indirectly by the action of an effector protein on a specific host target (3–5). NB-LRR activation causes effector-triggered immunity (ETI), which is essentially a high-amplitude MTI response that results in robust disease-resistance responses that often include localized host cell death and systemic defense signaling (3, 5).

We systematically mapped physical interactions between proteins from the reference plant Arabidopsis thaliana (hereafter, Arabidopsis) and effector proteins from two pathogens: the Gram-negative bacterium Pseudomonas syringae (Psy) and the obligate biotrophic oomycete Hyaloperonospora arabidopsidis (Hpa). These two pathogens last shared a common ancestor over 2 billion years ago and use vastly different mechanisms to colonize plants. Despite independent evolution of virulence mechanisms, we hypothesized that these two pathogens would deploy effectors to manipulate a largely overlapping set of core cellular MTI machinery (4, 5).

Mapping of a plant-pathogen protein–protein interactome network. We used experimentally validated Psy effector proteins (8), candidate effectors from Hpa (9, 10), and immune-related Arabidopsis proteins or “immune proteins” including the following: (i) N-terminal domains of NB-LRR intracellular immune receptors; (ii) cytoplasmic domains of LRR-containing receptor-like kinases (RLKs), a subclass of PRRs; and (iii) known signaling components or targets of pathogen effectors (defense proteins) (fig. S1 and table S1)(10). We mapped binary protein-protein interactions between these 552 immune and pathogen proteins and the ~8000 full-length Arabidopsis proteins (AProteome2.0) used to generate the Arabidopsis interactome, version 1 (AI-1), using the same yeast two-hybrid–based pipeline (10)–(12). This resulted in an experimentally determined plant-pathogen immune network containing 1358 interactions among 926 proteins, including 83 pathogen effectors, 170 immune proteins, and 673 other Arabidopsis proteins (hereafter, immune interactors) (Fig. 1A and table S2) (10). Because our data set was acquired using the same pipeline as that used to define AI-1 (11), we estimate that the two data sets are equivalent in quality with (i) a coverage of ~16% of all possible interactions within the tested space (fig. S1) and (ii) a proportion of true biophysical interactions statistically indistinguishable from that of well-documented high-quality pairs from the literature (11). We combined our data set with interactions from AI-1 and literature-curated interactions (LCI) (11) involving the same 926 proteins. This resulted in a “plant-pathogen immune network, version 1" (PPIN1) containing 3148 interactions (fig. S2 and table S2).

We display in Fig. 1, fig. S2, and an interactive Web interface (http://signal.salk.edu/interactome/PPIN1.html) PPIN1 in four layers. (Fig. 1A shows the experimentally determined network, fig. S2, the derived PPIN-1). The top layer contains effectors from both pathogens; the second layer consists of host proteins directly interacting...
with those effectors (effector targets); the third layer depicts the three previously defined classes of *Arabidopsis* immune proteins: NB-LRR, defense proteins, and RLK proteins; and the fourth layer consists of immune interactors.

Of the 673 immune interactors, only 66 were among the 975 proteins encoded by open reading frames (ORFs) in AtORFeome2.0 with a Gene Ontology (GO) annotation related to immunity (GO-immune proteins) (table S3) (P > 0.05) (table S4). This may be because of the technical limitations of both large- and small-scale experiments (12–15) and limited knowledge about the plant immune system. Although 239 of the 673 immune interactors interacted with a GO-immune protein in the systematically mapped subset of AI-1, termed “AI-1MAIN” [see Glossary (10) and (11)], 368 were neither GO-immune proteins nor previously known to interact with a GO-immune protein (fig. S3).

We identified 165 putative effector targets in PPIN-1, compared with ~20 described previously (16). Although the functions of most of these *Arabidopsis* proteins are unknown, they are enriched in GO annotations for regulation of transcription, metabolism, and nuclear localization (table S5) (10). We noted significant enrichment of the effector targets in immune and hormone-related GO annotations (table S4) (10, 17). Angiosperm-specific proteins are overrepresented among the effector targets, in comparison with all proteins encoded in AtORFeome2.0 (P = 0.0007) (table S4).

To characterize the transcriptional response of genes encoding proteins in PPIN-1, we categorized all corresponding proteins into 10 nonoverlapping groups (table S6); two immune protein groups (the two combined classes of receptors and the defense proteins); one group containing all effector proteins; and seven groups containing subsets of the immune interactors corresponding to their pattern of interactions with the three aforementioned groups (figs. S4 and S5 and table S7) (10). Many receptor genes were differentially regulated under a variety of defense-related conditions (fig. S5); however, genes encoding specific interactors of these receptors were not (figs. S4 and S5 and table S7). This suggests that pathogen detection sensitivity is specifically modulated via transcriptional regulation of receptor genes (18, 19). Receptors might also associate with proteins unrelated to the defense machinery.

**PPIN-1 proteins evolve faster than those of AI-1.** The LRR domains of both plant immune receptor classes exhibit footprints of positive diversifying selection (3, 20). Host-pathogen “arms races” are assumed to drive adaptive evolution of immune system genes, although this is an oversimplification for plant-pathogen interactions (21). We defined a set of 333 *Arabidopsis* genes with one-to-one orthology relations in *Papaya* (10) as a reference and estimated the ratio of nonsynonymous-to-synonymous mutations per site in their coding sequences (dN/dS) (fig. 1B). Nonreceptor immune interactors are evolving very slowly overall, which suggests functional constraint and purifying selection. They nevertheless exhibit a significantly higher evolution rate than proteins in AI-1MAIN (P < 0.01) (fig. 1B) (10). This was not the case for control gene groups encoding hormone-related proteins (fig. S6A) (17) or metabolic enzymes (fig. S6B) (22, 23). Hence, even the nonreceptor proteins from PPIN-1 evolve faster than other protein groups or the proteins in AI-1MAIN in general.

**Pathogen effectors converge onto highly connected proteins in the plant interactome.** Our hypothesis was that many effectors from evolutionarily diverse pathogens would converge onto a limited set of defense-related host targets and molecular machines (4, 5), as opposed to each effector having evolved to target idiosyncratic, pathogen life-style–specific targets. To test this, we compared the number of effector targets identified in PPIN-1 to the number of targets expected with randomly assigned connections between effectors and *Arabidopsis* proteins (“random targets”). PPIN-1 defined 165 direct effector targets; 18 of these were targeted by effectors from both pathogens (fig. 1A, and figs. S7A, left, and S8, right) (10). In contrast, simulations identified an average of 320 random targets, of which less than 1% would be targeted by effectors from both pathogens (P < 0.001, empirical P value) (fig. 2A and figs. S7A and S8) (10). We investigated the connectivity between the 137 observed effector targets that are also present in AI-1MAIN. They are connected by 139 interactions in AI-1MAIN (P < 6.7 × 10–5, empirical P value) (fig. 2B and table S8), whereas we expect an average of only 22 (maximum 59) connections if effector targets were randomly distributed in a network with the same structure as AI-1MAIN (fig. 2B and fig. S7B).

Collectively, these data support our hypothesis that diverse pathogens deploy virulence effectors that converge onto a limited set of host cellular machines.

Scale-free networks are resilient to random perturbations but sensitive and easily destabilized by targeted attack on their most highly connected hubs (24). AI-1MAIN shares this property even though it is not perfectly scale-free (fig. S9). Simulations demonstrate that an attack on experimentally identified effector targets is much more damaging to the network structure than an attack on the same number of randomly selected proteins (fig. S9). Consistent with this, we found that the number of interaction partners (degree) of the effector targets present in AI-1MAIN was significantly higher than that of proteins in AI-1MAIN that are not in PPIN-1 (fig. 2C). Remarkably, 7 of the 15 hubs of degrees greater than 50 (hubS50) in AI-1MAIN were targeted by effectors from both pathogens (P = 6.5 × 10–12) (tables S4 and S8), and 14 of the 15 hubs50 were targeted by effectors from at least one pathogen (P = 6.9 × 10–13) (tables S4 and S8) (10), consistent with observations of human-virus infection systems (25–28).

We evaluated whether this connectivity explains the observed convergence (fig. 2A and fig. S8). We performed simulations where the probability of an *Arabidopsis* protein to randomly interact with an effector was proportional to its degree in AI-1MAIN. We found that 51 of 2661 AI-1MAIN proteins were actually targeted significantly more often by effectors than expected given their respective degrees (e.g., “significant targets”) (table S8). These include 5 of the 14 hubs50 that interact with effectors (P = 5 × 10–6) (fig. 2D and table S4) and 4 of the 7 hubs50 that are targeted by...
effectors from both pathogen species \( (P = 0.006) \) (table S4). Among the 17 proteins interacting with effectors from both pathogens that are also present in AI-MAIN, 12 are significant targets \( (P = 0.003) \) (table S4). These results indicate that the convergence of effectors onto a set of host targets cannot be explained merely by the high connectivity of those targets and, thus, likely reflects additional aspects of the host-pathogen co-evolution history.

In addition to effector targets, other PPIN-1 proteins displayed high connectivity in AI-MAIN (Fig. 2, C and E). Consequently, immune interactors form a highly connected cluster in the plant interactome (figs. S10 and S11A). This is not the case for well-annotated subnetworks involved in hormone-related or metabolic processes (fig. S11, B and C) \( (17, 22, 23) \). Thus, PPIN-1 proteins as a whole, and effector targets in particular, are highly connected nodes within the overall plant network.

The plant response: Guarding high-value targets. We found that only 2 out of 30 NB-LRR immune receptor fragments in PPIN-1 directly interacted with a pathogen effector \( (P = 0.04) \) (table S4). In contrast, nearly half of the NB-LRR interactors (24 out of 52), including 7 of the 15 hubs, were effector targets \( (P = 4.6 \times 10^{-5} \text{ and } P = 8 \times 10^{-12} \text{ respectively}) \) (table S4). N-terminal domains of NB-LRRs can associate with either cellular targets of effector action or with downstream signaling components \( (10) \). Thus, our results are consistent with the proposition that NB-LRR proteins can monitor the integrity of cellular proteins and are activated when pathogen effectors act to generate “modified self” molecules \( (4, 5) \) for the 30 NB-LRR proteins fragments present in PPIN-1. We note that the interactors of full-length NB-LRR proteins in AI-MAIN include two of the hubs that are targeted by both pathogens (TCP14 and CSN5a) \( (11) \). Furthermore, in PPIN-1 only 4 of 90 putative RLK receptors interacted directly with a pathogen effector \( (P = 10^{-5}) \) (table S4), whereas 46 out of 162 interactors of RLKs were effector targets \( (P = 0.02) \) (table S4). This contrasts with the direct perturbation of PRR-RLK kinase function observed for two Ps type III effectors \( (2) \). In sum, our observations are consistent with the view that pathogen effectors are mostly indirectly connected to at least those host immune receptors represented in PPIN-1.

Effector targets and immune receptors participate in diverse potential protein modules. Many effector targets are cellular hubs and, thus, likely to be part of various protein modules across different cellular and developmental contexts. We extracted modules of two, three, or four physically connected PPIN-1 proteins (Fig. 3 and table S9) and found that the 18 proteins targeted by effectors from both pathogens were involved in 303 combinatorial modules of Psy type effector \(-Arabidopsis\) protein \(-Hpa\) effector (Fig. 3, A and B). Similarly, we noted several redundant combinatorial modules involving 192 interacting Arabidopsis protein pairs where both partners are targeted by effectors from one or both pathogens (Fig. 3, A and B, and table S9). Of the 105 effector targets involved in these modules, 91 are present in AI-MAIN, where they have an average degree of 29 (compared with an average degree of 4.8 and 2.6 for PPIN-1 and non-PPIN-1 proteins, respectively, in AI-MAIN). The targeting of an Arabidopsis protein, or a pair of
of interacting proteins, by effectors from both pathogens suggests an important function for these cellular machines. We do not infer that these combinations exist in vivo, because both pathogens rarely infect the same plant. We also found 19 and 41 proteins interacting with only Psy or Hpa effectors, respectively (Fig. 3, A and B); this apparent pathogen specificity may reflect the limited sensitivity of our experimental pipeline (11) or pathogen life-style–specific interactions.

We also assembled a number of combinatorial modules where pathogen effectors indirectly interacted with either an RLK (855) or NB-LRR (249) receptor domain protein via an Arabidopsis protein (Fig. 3C). Furthermore, single Arabidopsis proteins mediated combinatorial modules between a cytoplasmic RLK domain and an NB-LRR N terminus in 119 cases (Fig. 3C).

Experimental validation of host proteins targeted by multiple pathogen effectors. We functionally validated the 18 proteins targeted by effectors from both pathogens (Figs. 1A and 3A). This subset includes 7 of the 15 hubs50 proteins from AI-1MAIN (table S8). We assayed whether these effector targets function to positively regulate host defense (mutation leads to enhanced host susceptibility), negatively regulate host defense (mutation leads to enhanced host resistance), or function to facilitate infection (mutation also leads to enhanced host resistance). We discovered enhanced disease susceptibility to two different Hpa isolates, Emwa1 and Emoy2, for 9 of 17 loci for which insertion mutants were available (29, 30) (Fig. 4A, fig. S12A, and table S10). Mutants in the eight remaining loci did not exhibit enhanced disease susceptibility. However, at least six of these eight exhibited enhanced disease resistance to the virulent Hpa isolate Noco2 (Fig. 4B and table S10). Moreover, this enhanced disease-resistance phenotype was maintained at a later time point in the infection cycle (table S10). Hence, 15 of 17 proteins targeted by effectors from both pathogens, including all 7 of the 15 hubs50 proteins, have mutant phenotypes, consistent with immune system functions.

Preliminary observations also suggest that the mutants for JAZ3 (At3g17860) and LSU2 (At5g24660) expressed an enhanced disease susceptibility phenotype after inoculation with P. syringae DC3000 (avrRpt2) (fig. S12B), in addition to being required for full immune function during Hpa infection (Fig. 4A). This suggests that these genes are required for pathogen growth-suppression mediated by the resistance to P. syringae 2 (RPS2) NB-LRR protein.

In yeast, deletion of genes encoding hubs in a binary protein interaction network tend to cause multiple phenotypes (15). We were therefore surprised that the seven hubs50 among the 17 proteins targeted by effectors from both pathogens did not express pleiotropic morphological mutant phenotypes. CSN5a (At1g22920), a subunit of the COP9 signalosome and a hubs50 in AI-1MAIN, did. CSN5a interacts with 29 distinct effectors from Hpa and Psy in our experiment and is a demonstrated target of a geminiviral virulence protein (31). It also interacts with the N termini of NB-LRR proteins and the cytoplasmic domains of RLKs (table S9). The morphological consequences of csn5a pleiotropy can be suppressed by reducing the expression of either of the two Arabidopsis CUL3 subunits (32). We found that csn5a-2 cul3a

![Fig. 3. Combinatorial modules in PPIN-1. (A) The PPIN-1 subnetwork of pathogen effector proteins and their Arabidopsis targets. Proteins (nodes) are color coded as in Fig. 1A and fig. S1. Gray edges, experimental interactions from Fig. 1A; green edges, added interactions from AI-1 and LCI (fig. S2). From the total of 165 effector targets, 105 interact with at least one other target; 41 and 19 interact only with Hpa or Psy effectors, respectively. (B) Schematic representation of combinatorial modules involving effectors and effector targets in PPIN-1 [data extracted from (A)]. Number of proteins (top) and number of combinatorial modules (bottom) are indicated for each category. (C) Schematic representation of novel combinatorial modules involving immune receptors. The numbers for each category are listed on top. eLRR, extracellular domain of leucine-rich repeat; CC/TIR, coiled-coil or Toll–interleukin 1 receptor homology domain.](image-url)
seedlings displayed enhanced disease resistance compared with controls after infection with virulent Hpa (Fig. 4C). These results correlated with infection-triggered overaccumulation of PRI protein, a common marker for MTI, in Hpa- (fig. S12C) or Psy-infected (fig. S12D) csn5a-2 cul3a plants, compared with Col-0. Hence, our observed enhanced disease-resistance phenotype of csn5a is not due to its pleiotropic morphological phenotypes. Many proteins are substrates for CSN5a-dependent degradation, perhaps including many of its interactors; thus, its elimination or perturbation by effectors could plausibly alter immune function by altering clearance of both host and pathogen proteins.

We also validated prefoldin 6 (PFD6; At1g29990) (Fig. 4D and fig. S13) because of its interaction with the known defense regulator EDS1 (enhanced disease susceptibility 1) and two bacterial effectors (table S9) (10). We tested whether pfd6-1 exhibited signs of modified MTI by assaying flagellin (flg22 peptide)-induced disease resistance. Bacterial growth in flg22 pretreated leaves of Col-0 plants was 1/10th to 1/20th that in mock pretreated leaves, which reflected successful MTI. This flg22-induced MTI was compromised in pfd6-1 plants (Fig. 4D). Transcriptional induction of flg22-pretreated leaves of Col-0 plants was 1/10th to 1/20th that in mock pretreated leaves, which reflected successful MTI. This flg22-induced MTI was compromised in pfd6-1 plants (Fig. 4D). Transcriptional induction of flg22-pretreated leaves of Col-0 plants was 1/10th to 1/20th that in mock pretreated leaves, which reflected successful MTI. This flg22-induced MTI was compromised in pfd6-1 plants (Fig. 4D). Transcriptional induction of flg22-pretreated leaves of Col-0 plants was 1/10th to 1/20th that in mock pretreated leaves, which reflected successful MTI. This flg22-induced MTI was compromised in pfd6-1 plants (Fig. 4D).
Evidence for Network Evolution in an Arabidopsis Interactome Map

Arabidopsis Interactome Mapping Consortium†

Plants have unique features that evolved in response to their environments and ecosystems. A full account of the complex cellular networks that underlie plant-specific functions is still missing. We describe a proteome-wide binary protein-protein interaction map for the interactome network of the plant Arabidopsis thaliana containing about 6200 highly reliable interactions between about 2700 proteins. A global organization of plant biological processes emerges from community analyses of the resulting network, together with large numbers of novel hypothetical functional links between proteins and pathways. We observe a dynamic rewiring of interactions following gene duplication events, providing evidence for a model of evolution acting upon interactome networks. This and future plant interactome maps should facilitate systems approaches to better understand plant biology and improve crops.

Classical genetic and molecular approaches have provided fundamental understanding of processes such as growth control or development and molecular descriptions of genotype-to-phenotype relationships for a varie-

References and Notes

10. Glossary, materials and methods, supporting figures, and supporting tables are available as supporting material online.
17. Z. Y. Peng et al., Nucleic Acids Res. 37, 2286 (Database issue), D975 (2009).
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Supporting Online Material
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Materials and Methods SOM Text Figs. S1 to S18 Tables S1 to S10 References 1 February 2011; accepted 6 June 2011 10.1126/science.1203659