Using forward genetics in *Nicotiana benthamiana* to uncover the immune signaling pathway mediating recognition of the *Xanthomonas perforans* effector XopJ4

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**Summary**

- The immune pathway responsible for perception of the *Xanthomonas perforans* effector XopJ4 was identified in the plant *Nicotiana benthamiana*. This pathogen causes significant yield loss in commercial tomato cultivation.
- Genetic mapping and viral-induced gene silencing were used to identify immune signaling components of the XopJ4 perception pathway in *N. benthamiana*. Transient complementation assays were performed to determine the functionality of gene variants and co-immunoprecipitation assays were used to gain insight into the molecular mechanism of the pathway.
- Two *N. benthamiana* ethyl methanesulfonate (EMS) mutants deficient for XopJ4 perception were identified as having loss-of-function mutations in the gene encoding the nucleotide binding, leucine-rich repeat (NLR) protein NbZAR1. Silencing of a receptor-like cytoplasmic kinase family XII gene, subsequently named XOPJ4 IMMUNITY 2 (JIM2), blocks perception of XopJ4.
- This study demonstrates the feasibility of conducting mutant screens in *N. benthamiana* to investigate the genetic basis of the plant immune system and other processes. The identification of NbZAR1 and JIM2 as mediating XopJ4 perception in *N. benthamiana* supports the model of ZAR1 being involved in the perception of many different pathogen effector proteins with specificity dictated by associated receptor-like cytoplasmic kinases.

**Introduction**

Bacterial phytopathogens in the genus *Xanthomonas* use a Type III Secretion System to deliver effector proteins into the plant cell. Effector proteins can function to inhibit plant immunity or manipulate the metabolism of the host to favor growth of the bacteria (Guérlebeck *et al.*, 2006). If the plant is able to detect the presence of an effector protein, a strong immune response may be induced which prevents pathogen proliferation and restricts host range (Alfano & Collmer, 2004; Castañeda *et al.*, 2005; Wei *et al.*, 2007; Schwartz *et al.*, 2015). This strong immune response often results in localized cell death known as the hypersensitive response. Identifying the pathways responsible for mediating effector protein recognition can enable efforts to engineer disease resistance in susceptible crop species (Wulff *et al.*, 2011).

The perception of intracellular pathogen effector proteins in plants is frequently mediated by proteins from the nucleotide binding, leucine-rich repeat (NLR) protein family (Jones *et al.*, 2016). NLR recognition of an effector protein can occur through a physical interaction between the NLR and the cognate effector or by an indirect mechanism in which the NLR protein is ‘guarding’ another component which is modified by the effector (Khan *et al.*, 2016). While plants have additional receptor pathways independent from the NLRs, such as receptor-like kinases (Macho & Zipfel, 2014), NLR proteins have been demonstrated to mediate many resistance responses against a broad range of pathogens including bacteria, fungi, oomycetes, viruses and nematodes (Dodds & Rathjen, 2010).

*Tomato* is susceptible to *Xanthomonas perforans*, which causes the disease Bacterial Leaf Spot. This disease can result in significant yield losses in commercial tomato production and there is limited genetic resistance available within commercial cultivars (Stall *et al.*, 2009; Kim *et al.*, 2015). The plant *Nicotiana benthamiana* is resistant to *X. perforans* due to the presence of several pathways capable of perceiving effector proteins found in this pathogen including AvrBsT, XopQ and XopJ4/AvrXv4 (Roden *et al.*, 2004; Schwartz *et al.*, 2015). The XopJ4 effector is widely conserved among strains of *X. perforans* and has therefore been proposed as a good target for identifying genetic mechanisms of disease resistance against this pathogen (Timilsina *et al.*, 2016).

XopJ4 is part of the YopJ family of effector proteins. These effectors are distributed across many species of bacterial...
The YopJ effector protein HopZ1a from *Pseudomonas syringae* is recognized in *Arabidopsis thaliana* and triggers a hypersensitive cell death response that depends on the NLR protein ZAR1 and the Receptor-Like Cytoplasmic Kinase (RLCK) family XII protein ZED1 (Lewis et al., 2015). The NLR protein RPS4 is required for RRS1-mediated perception of PopP2 and is thought to form a complex with RRS1 (Narasaka et al., 2009; Williams et al., 2014). The widespread distribution of YopJ-family effector proteins and the existence of two evolutionarily independent mechanisms for the perception of YopJ effectors highlights the importance of these proteins in pathogenesis.

Four YopJ effector proteins have been identified in various *Xanthomonas* species, although not all *Xanthomonas* have YopJ effectors. These include XopJ/AvrRx4, XopJ, AvrRxv and AvrBsT. AvrRxv, XopJ and AvrBsT have all been associated with avirulence responses in various Solanaceous plant species, although the recognition mechanisms for the perception of these effectors are not well understood (Minsavage et al., 1990; Whalen et al., 1993; Astua-Monge et al., 2000). The AvrBsT effector triggers a strong avirulence response on pepper and *N. benthamiana*. The recognition of AvrBsT in pepper has been reported to be dependent on SGT1 and PIK1 (Kim et al., 2014). AvrRxv triggers an avirulence response on tomato line Hawaii 7998, the basis for which is multigenic based on segregation analysis (Whalen et al., 1993; Yu et al., 1995). XopJ triggers an avirulence response on *Solanum pennellii* accession LA716. While efforts have been made to map the resistance genes for AvrRxv and XopJ4 (Yu et al., 1995; Astua-Monge et al., 2000; Sharlach et al., 2013), the genes involved have not been conclusively identified.

In this work, we used a forward genetic screen to identify components of the XopJ4 perception pathway in the model plant *N. benthamiana*. This resulted in the identification of an NLR protein, NbZAR1, which is a homolog of the *A. thaliana* protein ZAR1 (AtZAR1) and is required for XopJ4 perception. To our knowledge this represents the first reported example of mapping an ethyl methanesulfonate (EMS) mutant in *N. benthamiana*, which is a widely used model plant but is challenging to use for forward genetics due to it being an allotetraploid with a large (c. 3.1 Gb) and incomplete reference genome (Naim et al., 2012). A subsequent reverse genetic screen identified an RLCK XII gene also required for the perception of XopJ4 which was named XOPJ4 IMMUNITY 2 (JIM2). The identification of these components enables future work to engineer resistance against *Xanthomonas* in tomato and other crop species.

**Materials and Methods**

**Generation of *N. benthamiana* mutant population**

Seeds of *N. benthamiana* 16c (line expressing green fluorescent protein) (Ruiz et al., 1998) were chemically mutagenized with EMS (Weigel & Glazebrook, 2006). Briefly, the seeds were pre-soaked at room temperature in potassium phosphate buffer (PPB, 100 mM, pH 7.5) for 2 h, then transferred to 100 mM PPB supplemented with 0.4% EMS and incubated for 15 h at 28°C with gentle shaking at 60 rpm. The treated seeds were washed 20 times with sterile water and dried on filter paper. Approximately 450 mutagenized individual plants were grown and selfed to create the M2 mutant population.

**Genetic mapping in *N. benthamiana* using high-throughput sequencing**

The *N. benthamiana* zar1-1 mutant was backcrossed to the wild-type and the F1 progeny were selfed to create an F2 mapping population. F2 plants were phenotyped by transient expression of XopJ4 using *Agrobacterium* and placed into two separate pools, based on the presence or absence of a cell death response, before genomic DNA extraction. Illumina DNA sequencing was performed using one HiSeqX lane with 150 bp paired-end reads for each pool. The reads were mapped to the *N. benthamiana* reference genome (Naim et al., 2012) and single nucleotide polymorphisms (SNPs) were identified using the GATK toolkit (DePristo et al., 2011). The SNPs were filtered for mapping quality, possibility of being caused by EMS, and having a large difference in frequency between the mutant and wild-type pools (> 0.25).

**Transient expression**

*Agrobacterium tumefaciens* strain GV3101 was used for transient expression. The binary plasmids pE1776 (with OCS promoter and UAS for strong expression) (Ni et al., 2011) and single nucleotide polymorphisms (SNPs) were identified using the GATK toolkit (DePristo et al., 2011). The SNPs were filtered for mapping quality, possibility of being caused by EMS, and having a large difference in frequency between the mutant and wild-type pools (> 0.25).
Xanthomonas gene knockout and complementation

For the knockout of XopJ4 in X. perforans 4B, 1046 bp upstream and 1127 bp downstream of XopJ4 was cloned into the pLVC18 plasmid containing a SacB counter-selectable marker (Lindgren et al., 1986). This plasmid was conjugated into X. perforans already lacking the XopQ and AvrBsT genes (Schwartz et al., 2015) and selected on NYG (0.5% peptone, 0.3% yeast extract, 2% glycerol) plates containing tetracycline (10 μg ml⁻¹). Colonies were screened for a single crossover event at the target locus by PCR. Positive colonies were grown overnight and plated on NYG plates with 5% sucrose to select for a second crossover event. Colonies were again screened by PCR to obtain XopJ4 deletion strains. For complementation, the XopJ4 gene including the promoter and terminator was cloned onto the plasmid pVSP61 (obtained from William Tucker, DNA Plant Technology, Oakland, CA). This plasmid, which can replicate in Xanthomonas, was conjugated into X. perforans and selected for with 25 μg ml⁻¹ kanamycin. The primers used for construction of the knockout and complementation plasmids are listed in Table S1.

Bacterial growth assays and visible immune responses

Xanthomonas liquid cultures were grown in NYG media with selection overnight. Cells were collected by centrifugation, washed once and suspended in 10 mM MgCl₂ to an OD₆₀₀ of 0.0001. Plant leaves were infiltrated by needleless syringe. For the growth assay, punches were collected from infiltrated leaf tissue 0 and 6 d after infiltration, homogenized in 10 mM MgCl₂ and serially diluted before plating on NYG plates with selection.

Viral-induced gene silencing

For VIGS, c. 300 bp of the target gene was cloned into the TRV2 vector (Liu et al., 2002). This vector was transformed into A. tumefaciens GV3101. The resulting Agrobacterium strain was grown overnight and coinfiltrated with another Agrobacterium strain harboring the TRV1 vector at an OD₆₀₀ of 0.2 each by needleless syringe. Plants were infiltrated at c. 4 wk old and used for transient assays 2–4 wk after infiltration.

Com Immunoprecipitation

The desired proteins were coexpressed in N. benthamiana leaf tissue using Agrobacterium-mediated transient expression. The tissue was frozen in liquid nitrogen and ground using a mortar and pestle. The samples were suspended in immunoprecipitation buffer (150 mM NaCl, 50 mM Tris-HCl pH 7.5, 0.3% Igepal, 10 mM 1,4-dithiothreitol, 1× protease inhibitor cocktail) and centrifuged (20 min, 21 000 g, 4°C). The supernatant was incubated with α-Flag beads (10 μl, A2220 Sigma) at 4°C for 3 h. The samples were centrifuged (2 min, 1000 g) and washed three times with immunoprecipitation buffer, before elution by boiling with Laemmlı buffer. The α-Flag western blots were performed using α-Flag antibody (F7425, Sigma) as the primary antibody and α-Rabbit IgG-Peroxidase (A0545, Sigma) as the secondary antibody. A single α-HA-Peroxidase antibody (3F10, Roche) was used for the α-HA western blots.

Results

Identification of two allelic N. benthamiana mutants impaired in XopJ4 recognition

We conducted a forward genetic screen of 2000 M₂ plants from an EMS-mutagenized population of N. benthamiana for individuals lacking a cell death response to transiently expressed XopJ4. Two mutants were identified that failed to respond to XopJ4 (Fig. 1). These mutants were crossed to each other and to wild-type plants and the resulting F₁ progenies were phenotyped by transient expression of XopJ4 (Fig. S1). A cell death response was observed in the backcrossed F₁ progeny but not in the F₁ progeny of the two mutants, indicating that both are recessive and allelic.

Mutations in NbZAR1 are causative for the loss of XopJ4 recognition

An F₂ mapping population generated from one of the backcrossed plants was used for identification of the mutation responsible for the loss of XopJ4 recognition. Forty-three individuals lacking a response to XopJ4 were identified out of 188 F₂ plants. These mutant individuals were pooled for genomic DNA extraction along with a separate pool of F₂ plants from the same population that were capable of responding to XopJ4. These pools were subjected to illumina sequencing yielding c. 30× genome coverage. SNPs were annotated by comparison to a reference genome (Naim et al., 2012) and filtered by mapping quality,
possibly of being induced by EMS, and showing a differing absolute abundance of at least 25% between the mutant pool and wild-type pool. Out of 2994 SNPs passing these filters, 33 were predicted to occur within gene sequences and three were predicted to result in an amino acid change (Table 1). One of these was a mutation introducing a stop codon at position 195 (Q195Stop) in the predicted protein sequence of the gene Nbv5tr6207061, named NbZAR1 after its Arabidopsis homolog. The sequence of NbZAR1 was confirmed by Sanger sequencing and deposited into the NCBI database (accession MH532570). Cosegregation of the mutant phenotype with this mutation was confirmed by Sanger sequencing of this SNP in 43 mutant F2 plants, which were all homozygous for the mutation (Fig. S2). Sequencing of NbZAR1 in the second allelic mutant revealed the presence of a single nucleotide change resulting in the substitution of threonine 191 with an isoleucine in the predicted protein sequence. Together with the allelism test, these data indicate that both mutants, subsequently named zar1-1 and zar1-2, are loss-of-function mutations in NbZAR1 that prevent XopJ4 recognition in *N. benthamiana*. Both mutations are present within the predicted NB-ARC domain of NbZAR1, with T191I occurring of-function mutations in NbZAR1 that prevent XopJ4 recognition of threonine 191 with an isoleucine in the predicted protein sequence. Together with the allelism test, these data indicate that both mutants, subsequently named zar1-1 and zar1-2, are loss-of-function mutations in NbZAR1 that prevent XopJ4 recognition in *N. benthamiana*. Both mutations are present within the predicted NB-ARC domain of NbZAR1, with T191I occurring within the conserved P-loop motif (Fig. S3).

*N. benthamiana* zar1-1 and zar1-2 are deficient for resistance against *X. perforans* expressing XopJ4

To test whether the avirulence activity of XopJ4 was compromised in the zar1 mutants, the XopJ4 gene was knocked out in an *X. perforans* (Xp) strain already deficient for XopQ and AvrBsT, as these two effectors trigger avirulence responses in *N. benthamiana* (Schwartz *et al.*, 2015). This knockout strain, along with parental and complemented strains, was infiltrated into *N. benthamiana* leaves at a low inoculum concentration and bacterial growth was assayed by measuring colony forming units 6 d after infiltration. Growth of Xp ΔAvrBsT ΔXopQ ΔXopJ4 was found to be c. 100-fold greater in wild-type *N. benthamiana* leaf tissue compared to Xp ΔAvrBsT ΔXopQ and the complemented strain Xp ΔAvrBsT ΔXopQ ΔXopJ4 + XopJ4 (Fig. 2). This indicates that XopJ4 triggers an avirulence response on wild-type *N. benthamiana*. No avirulence effect of XopJ4 was observed on the zar1-1 and zar1-2 mutants as a similar high level of bacterial growth was observed regardless of the presence of XopJ4 (Fig. 2). Consistent with the growth phenotypes, a visible immune response was observed in wild-type *N. benthamiana* plants infiltrated with Xp expressing XopJ4 (Fig. 2). This response was not observed in the zar1-1 and zar1-2 mutants.

Identification of JIM2, a kinase required for XopJ4 perception

The ZAR1 protein from *A. thaliana* interacts with several RLCK XII proteins which are required for the recognition of specific bacterial effectors including ZED1 (HopZ1a recognition) (Lewis *et al.*, 2013), RKS1 (AvrAC recognition) (Wang *et al.*, 2015) and ZRK3 (HopF2a recognition) (Seto *et al.*, 2017). We therefore hypothesized that an RLCK XII protein may be involved in the ZAR1-mediated recognition of XopJ4. Four RLCK XII genes were identified in the genome of *N. benthamiana* and targeted for silencing by VIGS (Fig. S5). The silencing of one particular RLCK XII, hereafter named XOPJ4 IMMUNITY 2 (JIM2), compromised the ability of the plant to recognize XopJ4 (Fig. S6). The sequence of JIM2 was deposited in the NCBI database (accession MH532571). A codon-altered version of JIM2, JIM2_VR, was designed to evade silencing by VIGS (Fig. S7). Transient expression of JIM2_VR in JIM2-silenced leaves rescued the cell death response triggered by XopJ4 (Fig. 3), demonstrating that JIM2 is required for recognition of XopJ4 in *N. benthamiana*.

Differential recognition of XopJ4 in *N. benthamiana*

In contrast to the results shown in Fig. 2, Xp ΔAvrBsT ΔXopQ has previously been shown to grow and cause apparent disease symptoms on wild-type *N. benthamiana* (Schwartz *et al.*, 2015). We obtained the *N. benthamiana* used in the Schwartz *et al.* study and compared it with the 16c line used to generate the EMS population used for the screen. Transient expression of XopJ4 in the wild-type from the Schwartz *et al.* study did not result in a visible cell death response (Fig. S8). Additionally, a visible immune response to Xp ΔAvrBsT ΔXopQ was not observed (Fig. S8). This explains why an avirulence effect of XopJ4 in *N. benthamiana* was not reported in the Schwartz *et al.* study and suggests that there may be genetic differences between various wild-type *N. benthamiana* used in different research laboratories. To test whether the lack of XopJ4 recognition in the *N. benthamiana*

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Illumina sequencing of pooled mutant and wild-type (WT) plants revealed three predicted candidate mutations for the phenotype of the zar1-1 *Nicotiana benthamiana* mutant.

1Nucleotide present in the reference genome.

2Alternative nucleotide detected.

3Percentage of sequencing reads supporting the alternative nucleotide.

4The annotated name for the most similar Arabidopsis protein.
from the Schwartz et al. study could be complemented by transient expression of either NbZAR1 or JIM2, these proteins were expressed with and without XopJ4 in leaf tissue (Fig. S9). Expression of JIM2 but not NbZAR1 along with XopJ4 was observed to give a strong cell death response in this N. benthamiana variety (Fig. S9), suggesting that a defect in JIM2 may be responsible for the differential recognition of XopJ4. However, sequencing of the JIM2 gene did not reveal any polymorphisms between these two N. benthamiana lines and the basis for the differential response to XopJ4 therefore remains unknown. With the exception of the indicated images in Figs S8 and S9, all wild-type N. benthamiana plants used in this paper are from the 16c line used to make the mutant population.

AtZAR1 and SlZAR1 fail to complement the N. benthamiana zar1-1 mutant

To gain insight into the evolution history of ZAR1, a phylogenetic tree was reconstructed using homologous protein sequences obtained from NCBI and the One Thousand Plant Genomes project (Matasci et al., 2014) (Fig. S10). This analysis revealed that most plants have a single putative ortholog of ZAR1. To test whether AtZAR1 is functionally equivalent to NbZAR1, AtZAR1 was transiently expressed in the zar1-1 mutant along with JIM2 and XopJ4. Whereas transient expression of NbZAR1 was sufficient to restore XopJ4 recognition in the zar1-1 mutant, expression of AtZAR1 was not (Fig. 4). By contrast, transient expression of AtZAR1 in zar1-1 was able to complement the immune response triggered by coexpression of ZED1 and HopZ1a, which is consistent with previously reported VIGS results (Baudin et al., 2017). The inability of AtZAR1 to complement the XopJ4 perception defect in zar1-1 plants indicates a partial functional divergence between NbZAR1 and AtZAR1.

Tomato (Solanum lycopersicum) contains a putative ZAR1 ortholog but is unable to perceive the XopJ4 effector protein (Astuà-Monge et al., 2000). SlZAR1 (Solyc02g084890) was cloned and transiently expressed in the zar1-1 mutant to test if this gene can functionally complement NbZAR1 for XopJ4 perception. Transient expression of SlZAR1, JIM2 and XopJ4 failed to trigger a visible immune response in the zar1-1 mutant (Fig. 5). A multiple sequence alignment of ZAR1 proteins from various plant species revealed several missense mutations at conserved sites in the SlZAR1 protein which may make the protein nonfunctional (Figs S3, S11).

JIM2 coimmunoprecipitates with NbZAR1 but not XopJ4

AtZAR1 has been shown to physically interact with the RLCK XII family proteins ZED1, RKS1 and ZRK3, and these interactions are believed to be important for effector perception (Lewis et al., 2013; Wang et al., 2015). We therefore hypothesized that there may be physical interactions between NbZAR1 and JIM2 and performed coimmunoprecipitation experiments to test for this. The Arabidopsis NLR protein RPP1 was included along with its cognate effector ATR1 as controls (Krasileva et al., 2010). To avoid triggering a hypersensitive response, the experiments were performed in the zar1-1 N. benthamiana mutant using the T191I variant of NbZAR1 (the nonfunctional variant present in zar1-2). JIM2-6xHA was observed to be pulled down

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**Fig. 2** Bacterial growth and visible immune response to Xanthomonas perforans. Nicotiana benthamiana wild-type and zar1 mutants were infiltrated with the indicated genotype of X. perforans at an OD_{600} of 0.0001. Bacterial growth was assayed at 6 d post-infiltration and the visible immune response was photographed at 7 d post-infiltration. Error bars indicate ± SD from three biological replicates. Bacterial abundance at 0 d post-infiltration is presented in Supporting Information Fig. S4.

**Fig. 3** Immune response to XopJ4 in JIM2 VIGS plants. The GUS gene (as a negative control) and JIM2 were targeted for gene silencing using VIGS in Nicotiana benthamiana. XopJ4 and a VIGS-resistant codon-altered version of JIM2 (JIM2_VR) were transiently expressed separately and together using Agrobacterium. The plants were infiltrated at an OD_{600} of 0.5 total and imaged at 3 d post-infiltration.
with NbZar1-T191I-3xFlag (Fig. 6). JIM2-6xHA was not pulled down by RPP1-3xFlag. Interactions were not observed between XopJ4-6xHA and NbZar1-3xFlag or XopJ4-6xHA and JIM2-3xFlag.

Discussion

Mechanism of XopJ4 perception

Recognition of XopJ4 in *N. benthamiana* is dependent on the putative active site of these proteins (Roden *et al.*, 2004), suggesting that they are modifying a host protein, possibly by acetylation, which then triggers an immune response. The YopJ protein HopZ1a from *Pseudomonas* has been reported to acetylate the RLCK XII protein ZED1 in *Arabidopsis* (Lewis *et al.*, 2013), a paralog of JIM2. In contrast to recognition of HopZ1a, the ZAR1-mediated recognition of AvrAC involves not only an RLCK XII protein (RKS1) but an RLCK VII protein as well (PBL2) (Wang *et al.*, 2015). AvrAC directly interacts with and modifies PBL2 but not RKS1. JIM2 was found to interact with NbZAR1 but not XopJ4 by coimmunoprecipitation (Fig. 6). It remains unclear whether NbZAR1 and JIM2 are sufficient for XopJ4 recognition or if there is an additional component of the perception pathway. Although part of the RLCK superfamily, ZED1 lacks a conserved ‘HRD’ motif believed to be essential for kinase activity and is believed to be a pseudokinase (Lewis *et al.*, 2013). JIM2 is also missing the HRD motif and is therefore likely to also lack kinase activity (Fig. S12).

Evolutionary history of ZAR1

A single putative ortholog of ZAR1 was observed in most plant genomes, indicating that this gene has not undergone extensive duplication or divergence as observed for some other NLR genes (Fig. S10). This may be explained by the model that ZAR1 utilizes other proteins such as the RLCK XII’s for specificity and does not directly interact with effector proteins (Innes, 2015). In this model, the RLCK XII’s and other interacting proteins act as sensors that are under varying evolutionary pressures whereas ZAR1 acts as a conserved switch to activate the immune system. Some NLR proteins believed to be ‘helper’ NLRs, which are required for the activation of immune pathways but not directly perceiving a specific effector protein, have been observed to have a similar pattern of evolution as ZAR1 in which most plant species have one or a few copies of the gene which have limited sequence divergence. The helper NLR proteins NRG1 and ADR1 follow this model (Collier *et al.*, 2011). The ZAR1 phylogenetic tree supports the hypothesis that NbZAR1 and AtZAR1 are orthologs but a long branch to the Brassicales sequences (including AtZAR1) is a consequence of divergence of the ZAR1-
The proteins and may explain the inability of AtZAR1 to complement an altered functionality compared to the rest of the ZAR1-like that AtZAR1 and related proteins from the Brassicales may have.

Forward genetics in *N. benthamiana*

*N. benthamiana* is commonly used in plant biology research due to its amenability to transient expression of heterologous proteins and gene silencing. This plant has been used previously to identify components of the plant immune system using reverse genetics (Pearl et al., 2005; Schultink et al., 2017; Wang et al., 2018) but we are not aware of a previous example of EMS mutagenesis being used for forward genetics in this species. Although *N. benthamiana* has a large genome (c. 3.1 Gb) (Naim et al., 2012) and is an allotetraploid with 19 chromosomes (Chase et al., 2003), we demonstrated that it can be readily used for forward genetics. Despite the currently available reference genome for *N. benthamiana* being fragmented, causative mutations can be identified with only modest (30×) sequencing coverage of pooled mutant genomic DNA from a mapping population. This highlights the feasibility of doing forward genetics in nonmodel plants lacking a contiguous reference genome. The generation time of *N. benthamiana*, c. 3.5 months, is longer than that of the commonly used model Arabidopsis, but the ability to rapidly test candidate genes by transient expression or VIGS is a significant advantage. The potential to use transient expression as an assay in *N. benthamiana* for a desired process, including to test immune perception as demonstrated here, enables screens that are not possible in other model plants and allows for conducting independent screens on the same plant. We anticipate greater use of forward genetic mutant screens in *N. benthamiana* and other plants with complex genomes in the future to investigate processes that are not present in traditional genetic model plants.

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**Author contributions**

T.Q. performed the coimmunoprecipitation experiments. J.B. generated the mutant *N. benthamiana* population. A.S. performed the other experiments, designed the project and wrote the manuscript. B.S. designed and supervised the project.

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**References**


**Supporting Information**

Additional Supporting Information may be found online in the Supporting Information section at the end of the article:

Fig. S1 Allelism test of zar1-1 and zar1-2.

Fig. S2 Segregation of the Nb5tr6207061 candidate mutation.

Fig. S3 Multiple protein align for AtZAR1, SlZAR1 and NbZAR1.

Fig. S4 Day zero growth assay.

Fig. S5 Phylogenetic tree of RLCK XII proteins.

Fig. S6 Silencing of RLCK XII genes.

Fig. S7 Sequence of the codon-altered, VIGS-resistant JIM2 construct.

Fig. S8 Differential XopJ4 response among wild type Nicotiana benthamiana varieties.

Fig. S9 Differential XopJ4 response complemented by expression of JIM2.

Fig. S10 Phylogenetic analysis of ZAR1.

Fig. S11 Multiple protein alignment for SlZAR1.

Fig. S12 Multiple protein alignment for RLCK XII proteins.

Table S1 Primer sequences.

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