

1 Identification of the *Phytophthora* PAMP Pep-13 Receptor

2 Using Diploid Potato Inbred Lines

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ABSTRACT

Plants employ cell surface receptors to recognize pathogen-associated molecular patterns (PAMPs) and activate pattern-triggered immunity, a crucial defense mechanism against invading pathogens. Pep-13 is a PAMP derived from a class of conserved cell wall transglutaminases present in *Phytophthora* species, and its receptor PERU was reported recently. In our parallel study, we observed distinct responses to Pep-13 between two diploid potato inbred lines: E454 recognizes Pep-13, whereas A018 does not. Genetic analysis demonstrated that Pep-13 recognition in E454 is controlled by a single genetic locus, tentatively designated *TGER* (*Transglutaminase elicitor response*). Through bulked segregant analysis sequencing, followed by complementation assays, we found that the *TGERa* gene in E454 is essential for Pep-13 recognition. Sequence alignment revealed that *TGERa* shares 99.91% amino acid sequence identity with PERU, indicating that *TGERa* and PERU are allelic variants of the same gene (*PERU/TGERa*). *TGERb*, a highly homologous gene of *TGERa*, was identified in the E454 genome; notably, *TGERa*, but not *TGERb*, can recognize Pep-13. We further demonstrated that *TGERb* exhibits defects in both ligand binding and association with the co-receptor StSERK3A. Additionally, we found that the *TGERa* allele in A018 is a weak allele with reduced expression levels, presumably resulting from a 3 kb DNA fragment insertion in its first intron. Heterologous introduction of *TGERa* into *Nicotiana benthamiana* and tomato significantly enhanced their resistance to *Phytophthora infestans*. Collectively, our findings confirm that PERU/*TGERa* functions as the Pep-13 receptor in potato and provide a valuable molecular target for improving *Phytophthora* resistance in plants.

Keywords: Potato; *Phytophthora infestans*; Pep-13; Pattern Recognition Receptor (PRR); PERU/*TGERa*.

INTRODUCTION

Potato (*Solanum tuberosum* L.), the most important tuber crop, is a staple food for approximately 1.3 billion people globally (Stokstad, 2019). Cultivated potatoes are primarily propagated asexually via tubers, and the complexity of their tetraploid genome results in a prolonged breeding cycle. To address this challenge, a diploid potato hybrid breeding project was launched based on diploid potato inbred lines (Zhang et al., 2021; Cheng et al., 2025), which not only accelerates the potato breeding process but also provides materials and genomic data resources for researches on potato functional genomics.

Late blight, caused by *Phytophthora infestans*, is a devastating disease affecting potato yield (Nowicki et al., 2012), and harnessing the plant's own immune receptors provides a sustainable and eco-friendly solution for late blight control. Specifically, pattern recognition receptors (PRRs) localized on the plant cell surface recognize pathogen-associated molecular patterns (PAMPs), thereby initiating pattern-triggered immunity that restricts pathogen invasion (Jones and Dangl, 2006; Zhou and Zhang, 2020). A few well-studied PAMPs have been reported in the genus *Phytophthora*, such as INF1, nlp20, and XEG1, which are specifically recognized by ELR (Du et al., 2015) and NbREL (Chen et al., 2023a), *Arabidopsis* RLP23 (Albert et al., 2015), and NbRXEG1 (Wang et al., 2018), respectively. Notably, heterologous expression of such PRRs confers enhanced disease resistance in plants (Albert et al., 2015; Chen et al., 2023a).

Pep-13 is a 13-amino-acid peptide derived from a class of cell wall transglutaminases (TGase) in the genus *Phytophthora*, and Pep-25 is a 25-amino-acid peptide that contains the Pep-13 sequence (Nürnberg et al., 1994). Both peptides share similar activity: certain potato cultivars can recognize Pep-13/25, initiating immune responses including MAPK activation, ROS burst, upregulation of defence genes, and the induction of hypersensitive cell death (Nürnberg et al., 1994; Brunner et al., 2002). However, the receptor for Pep-13 remained unknown for a long time until recently. PERU

(Pep-13 receptor unit), a typical leucine-rich repeat receptor kinase (LRR-RK), was identified as the receptor of Pep-13 from potato cv. DM (Torres Ascurra et al., 2023). Interestingly, PERU from accession LPH680-5 (PERU^{LPH}) was shown to have a broad recognition ability that perceives Pep-13/25 and Pep-25 variants, such as Pep-25W2A (Torres Ascurra et al., 2023).

In our parallel study, we explored the Pep-13-triggered response in the inbred lines A6-10 (also known as A018), A6-26 (also known as A157) and E4-63 (also known as E454), which are the parent lines for hybrid potatoes (Zhang et al., 2021). We found that Pep-13 triggered hypersensitive cell death in A157, E454 and Hybrid 2 (a F₁ progeny of a cross between A018 and E454), but not in A018 (Supplemental Figure 1A). Meanwhile, the F₂ population derived from self-pollinated Hybrid 2 showed phenotypic segregation in response to Pep-13, with the ratio of Pep-13-responsive (HR) plants to non-responsive (non-HR) plants being approximately 3:1 (Supplemental Figure 1B); this result indicates that Pep-13 recognition in E454 is controlled by a single genetic locus, which we tentatively designated *TGER* (*Transglutaminase elicitor response*). However, conflicting with this finding, the research on PERU indicated that there are no PERU homologs in A6-26 and E4-63 (See Supplemental data_s4 of Torres Ascurra et al., 2023), creating a critical knowledge gap that this study aimed to address.

In this study, we identified that *TGERa* in E454 is essential for Pep-13 recognition. Sequence alignment revealed that *TGERa* shares 99.91% amino acid identity with PERU, indicating that *TGERa* and *PERU* are the same gene (designated as *PERU/TGERa*; for simplicity, *TGERa* is used hereafter). We further identified *TGERb*, a highly homologous gene of *TGERa* in the E454 genome, which cannot recognize Pep-13. Additionally, we found that the *TGERa* allele in A018 is a weak allele with reduced expression. Lastly, we showed that introduction of *TGERa* into plants significantly enhanced their resistance to *Phytophthora* pathogens, highlighting the potential of *TGERa* as a valuable molecular target for improving *Phytophthora* resistance in crops.

RESULTS AND DISCUSSION

Differential responses of potato inbred lines A018, A157 and E454 to Pep-13

To identify the receptor responsible for Pep-13 perception using potato inbred lines generated by the Upotato project (Zhang et al., 2021), we first evaluated their responses to Pep-13. As shown in Figure 1A, A157 and E454 exhibited hypersensitive response (HR) cell death to Pep-13 but not to the nearly inactive Pep-13W2A variant (Brunner et al., 2002). Unexpectedly, Pep-13 failed to trigger cell death in A018, although A018 and A157 are homozygous inbred lines derived from the same ancestral parent, PG6359 (Zhang et al., 2021). Additionally, Désirée, but not the Atlantic, exhibited cell necrosis upon Pep-13 treatment (Figure 1A). Consistent with the HR phenotypes, Pep-13 treatment activated MAPK signaling in A157 but not in A018 (Figure 1B and 1C). Notably, four Pep-13-responsive genes (Nietzschmann et al., 2019), namely *StTHT*, *StPALs*, *StFAD*, and *St4-CL*, were strongly induced in A157, but showed little or no induction in A018 (Figure 1D). Collectively, these results demonstrate distinct responses of potato lines to Pep-13, with A018 showing a unique pattern of no cell death but weak induction of some Pep-13-responsive genes.

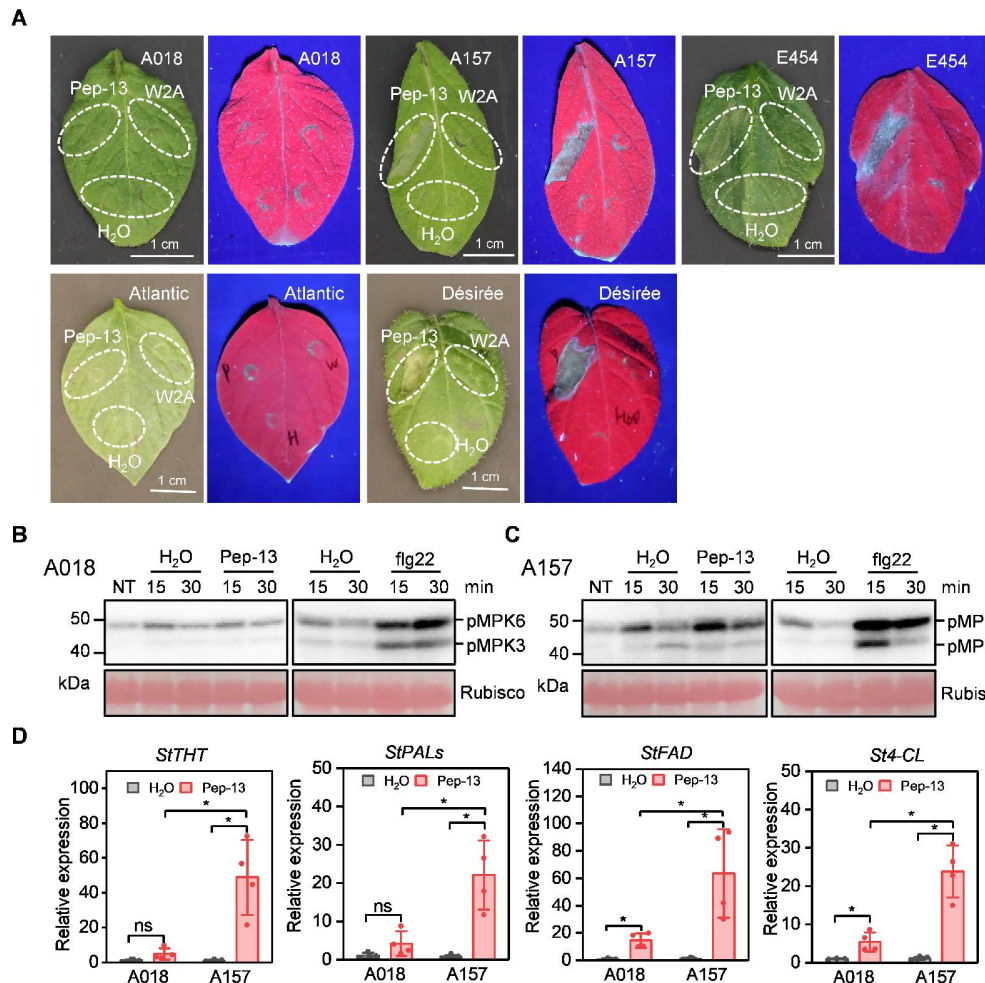


Figure 1. Differential responses of potato inbred lines A018, A157, E454 and cultivars Atlantic and Désirée to Pep-13.

(A) Differential responses of potato cultivars to Pep-13. Leaves were infiltrated with 100 μ M Pep-13, Pep-13W2A (a Pep-13 variant) and H₂O. Photos were taken under natural light (green leaf) and UV light (red fluorescence) at 24 h post-infiltration. Bar = 1 cm.

(B-C) Pep-13-induces MAPK activation in A157 but not in A018. Leaves of A018 **(B)** and A157 **(C)** were sprayed with 100 μ M Pep-13 or H₂O. Samples were collected at 15 and 30 min post-treatment, and MAPK activation was detected by western blot using an anti-p44/42-ERK antibody. flg22 (5 μ M) served as a positive control, and non-treated (NT) leaves served as a negative control.

(D) Pep-13-responsive genes are strongly induced in A157 but show little or no induction in A018. Transcript levels of *StTHT*, *StPALs*, *StFAD*, and *St4-CL* were analyzed by RT-qPCR in leaves of A018 and A157 at 4 h after infiltration with 100 μ M Pep-13 or H₂O. *NbEF1 α* used as reference gene. Data represent mean $\pm$ s.d. n = 4. Asterisks indicate statistically significant differences (**p* < 0.05, Student's t-test); ns, no significant difference.

Genetic mapping of *TGERa* and validation

Using bulked segregant sequencing, we identified that the *TGER* locus is located within the chr 0-3 Mb region of the E454 genome, which was further

narrowed down to 24 candidate genes (see details in Supplemental Note 1). We successfully cloned 21 of these candidate genes and screened their responsiveness to Pep-13 via *Agrobacterium*-mediated transient expression in *N. benthamiana* (*Nb*) leaves. The gene expressed by construct #9 was found to respond to Pep-13 (Supplemental Figure 2), which was designated as *TGERa*. Next, we generated transgenic *Nb* lines expressing *TGERa* under its native promoter (*np-TGERa Nb* lines); these transgenic lines exhibited cell death in response to Pep-25 but showed no or weak cell death to Pep-13 treatment (Supplemental Figure 3A). However, both Pep-13 and Pep-25 were able to induce MAPK activation in *np-TGERa Nb* lines; furthermore, Pep-13 treatment of these transgenic plants significantly activated the expression of *NbACRE31* and *NbCYP71D20* (Supplemental Figure 3B and 3C). These results indicate that *TGERa* is responsive to both Pep-13 and Pep-25, with Pep-25 exhibiting stronger activity in inducing cell death than Pep-13 under conditions of low *TGERa* protein levels. Stable expression of *TGERa* in cv. MicroTOM and potato Atlantic conferred the ability to recognize Pep-13 and Pep-25, leading to the induction of cell death (Supplemental Figure 3D-3G). Collectively, these findings demonstrated that *TGERa* is responsive to Pep-13/25.

Immune-related SERKs are required for Pep-13 perception

TGERa is a typical leucine-rich repeat receptor kinase (LRR-RK). To identify its interacting proteins, immunoprecipitation-mass spectrometry (IP-MS) was performed in *N.benthamiana* (*Nb*) leaves, revealing six *Nb*SERK proteins, including *Nb*SERK3A, *Nb*SERK3B, *Nb*BAK1a, *Nb*BAK1b, *Nb*SERK2a, and *Nb*SERK2b, as Pep-13-induced interacting partners of *TGERa* (Supplemental Figure 4A). Phylogenetic analysis showed that these six *Nb*SERK proteins, together with their potato homologs (*St*SERK2, *St*SERK3A, and *St*SERK3B) and *Arabidopsis* SERKs (Ma et al., 2016; Li et al., 2025), form a single clade (Supplemental Figure 4B). Given the evolutionary conservation of these SERK proteins and their known roles in plant immunity, we further confirmed that

Pep-13 induces the interaction between TGERa and three StSERKs (Supplemental Figure 5A-5C). Additionally, silencing of these six *NbSERK* genes in *Nb* leaves blocked Pep-25/TGERa-induced cell death (Supplemental Figure 5D-5J). Notably, we showed that TGERa can bind to biotin-labeled Pep-13 (Supplemental Figure 5L). Collectively, these results demonstrate that TGERa forms a receptor complex with immune-related SERKs to mediate the perception of Pep-13.

Comparison of coding sequences between TGERa and PERU

Sequence analysis revealed that the coding sequence (CDS) of TGERa^{E454} is 78 bp longer than that of PERU^{DM}, which corresponds to an in-frame upstream open reading frame (uORF) (Supplemental Figure 6A). This observation indicates that the predicted TGERa^{E454} contains an additional 26 amino acids at the N-terminus compared to PERU^{DM}; whereas the remaining protein sequence is nearly identical between the two, with only a single amino acid substitution (A317 in PERU vs. G317 in TGERa-dN26), confirming that TGERa^{E454} and PERU^{DM} are allelic variants of the same gene.

To determine the translational start site of TGERa^{E454}, we individually mutated the ATG codons of uORF1 and the main ORF. Mutation of the main ORF ATG, which restricts protein translation to uORF1, significantly reduced TGERa^{E454} protein accumulation irrespective of being driven by 35S or its native promoters (Supplemental Figure 6B-6E). These findings indicate that TGERa^{E454} protein translation primarily initiates from the main ATG. Given that TGERa is a single-pass transmembrane protein, the additional 26-amino-acid sequence at the N-terminus may impair its signal peptide function and disrupt normal translation processes, thereby reducing TGERa^{E454} protein levels.

In contrast, the annotated PERU protein from LPH60-5 (PERU^{LPH}) contains an extra 24-amino-acid sequence between residues T372 and G373 compared to TGERa/PERU, which is encoded by an in-frame intron 2 (Supplemental Figure 7A and 7B). Further analysis demonstrated that this intron 2 retention occurs in a subset of *TGERa* transcripts extracted from A157 leaves, both under normal

conditions and following *Phytophthora* inoculation (Supplemental Figure 7C and 7D). To characterize the function of the protein translated from transcripts with intron 2 retention, we introduced synonymous mutations into this intron 2 to generate *TGERa-In2R*, which abolishes intron 2 splicing while preserving the encoded sequence as the extra 24 amino acids in PERU^{LPH} (Supplemental Figure 7E and 7F). Functional assays showed that, in contrast to TGERa, TGERa-In2R failed to activate MAPK or induce cell death following Pep-13 treatment (Supplemental Figure 8A and 8B) and was unable to bind Pep-13 or Pep-25 (Supplemental Figure 8C and 8D). These results demonstrate that the protein translated from transcripts with the intron 2 retention is non-functional. Therefore, the additional sequence in PERU^{LPH} is likely attributable to annotation errors and is unrelated to its broad ligand recognition ability.

TGERa/PERU, but not its close homolog TGERb, recognizes Pep-13

Sequence alignment between the gene present in construct #9 and the target gene *E454_03G001350.1* revealed multiple single nucleotide polymorphisms (SNPs) and one insertion/deletion (indel) (Supplemental Table 3). A sequence identical to *E454_03G001350.1* was subsequently re-isolated from the amplification products using the same primers for *E454_03G001350.1* and designated as *TGERb*. Transient expression of *TGERa*, but not *TGERb*, in *N.benthamiana* (*Nb*) leaves triggered MAPK activation and cell death following Pep-13 treatment (Supplemental Figure 9A and 9B). Consistently, Pep-25 treatment induced cell death in transgenic *Nb* lines expressing *TGERa* but not in lines expressing *TGERb* (Figure 2A). In addition, *np-TGERb Nb* lines failed to elicit reactive oxygen species (ROS) burst or MAPK activation following Pep-13 treatment (Figure 2B, 2C, and Supplemental Figure 9C). Further biochemical analyses showed that Pep-13 treatment did not promote the interaction between *TGERb* and StSERK3A (Figure 2D). In contrast to TGERa, TGERb was unable to bind either Pep-13 or Pep-25 (Figure 2E and 2F). Collectively, these results demonstrated that TGERb can not recognize Pep-13 or Pep-25, highlighting a functional divergence between the two highly

242 homologous proteins.

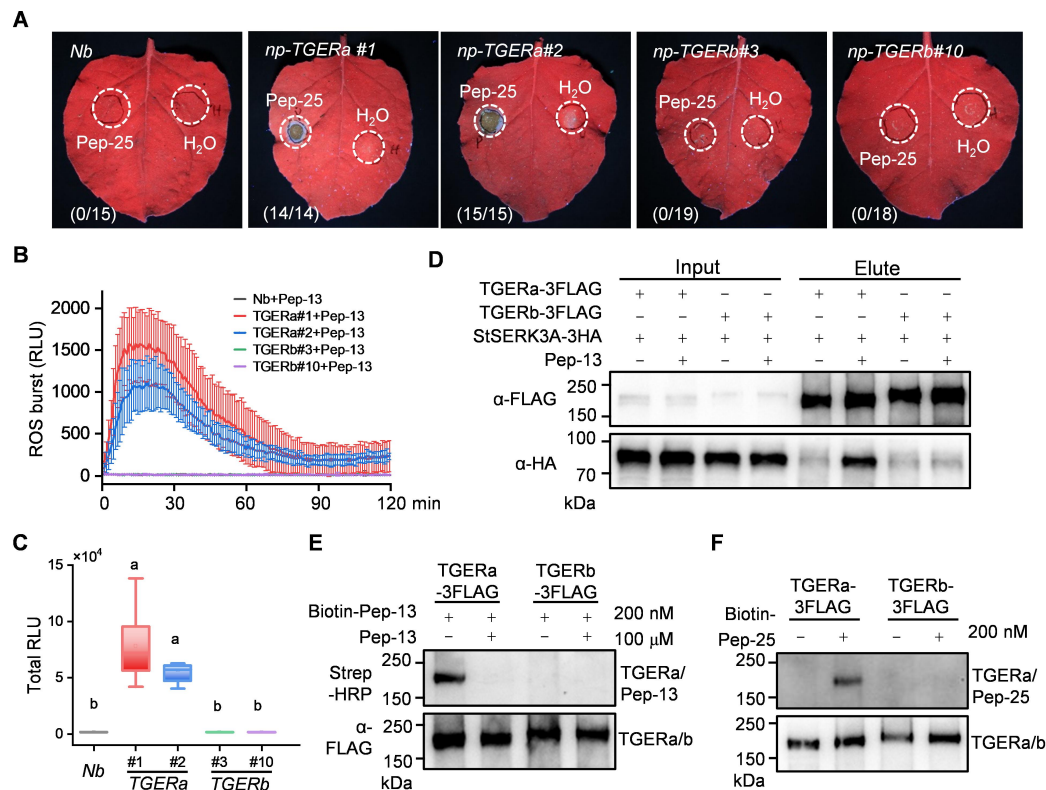


Figure 2. TGERa/PERU, but not its close homolog TGERb, recognizes Pep-13.

(A) Pep-25-induced cell death in transgenic *N. benthamiana* (*Nb*) lines expressing *TGERa* but not *TGERb*. Leaves of transgenic lines *np-TGERa* #1, *np-TGERa* #2, *np-TGERb* #3, and *np-TGERb* #10 (driven by their native promoters) were infiltrated with 100 μM Pep-25. *Nb* plants served as a negative control. Photographs were taken under UV light 5 days after infiltration.

(B-C) Pep-13-induced ROS burst in transgenic lines *np-TGERa* #1 and #2, but not in transgenic lines *np-TGERb* #3 and #10, as shown by the ROS burst curves (B) and total ROS production (C) induced by 100 nM Pep-13. Data was analyzed by two-way ANOVA followed by Tukey's multiple comparison test. Different letters indicate significant differences ($p < 0.05$, $n = 8$).

(D) TGERa, but not TGERb, associates with the co-receptor StSERK3A upon Pep-13 treatment. *TGERa*-3Flag or *TGERb*-3Flag was transiently co-expressed with *StSERK3A*-3HA in *Nb* leaves mediated by *Agrobacterium*. After 24 h, leaves were infiltrated with 100 μM Pep-13 or H₂O. Samples were collected 15 min post-infiltration, and TGERa/b-3Flag proteins were enriched using M2 beads. IP eluates were analyzed by western blot using anti-Flag and anti-HA antibodies.

(E-F) TGERa, but not TGERb, binds biotin-labeled Pep-13 (E) and Pep-25 (F). *TGERa*-3Flag and *TGERb*-3Flag were transiently expressed in *Nb* leaves for 24 h. Leaves were co-infiltrated with 200 nM biotin-Pep-13/25 and 3 mM EGS, then incubated for 30 min at room temperature. Excess unlabeled Pep-13 (100 μM) was included as a competitor. TGERa/b-3Flag proteins were enriched using M2 beads, and IP eluates were detected by western blot using an anti-Flag antibody and Strep-HRP.

TGERb exhibits defects in both ligand binding and association with StSERK3A

Protein sequence analysis revealed that the differences between TGERa and TGERb are primarily inside their ectodomains, which share 85.3% sequence identity (Supplemental Figure 9D). Domain swapping experiments further confirmed that divergence in the ectodomain is responsible for the inability of TGERb to perceive Pep-13 (Supplemental Figure 9E and 9F).

The ectodomain of TGERa contains 27 leucine-rich repeats (LRRs), whereas TGERb harbors an additional 24-amino acid insertion in the region corresponding to LRR24 of TGERa, resulting in a total of 28 LRRs. A TGERa variant carrying this additional sequence (TGERa^{b24aa}) retained the ability to recognize Pep-13 (Supplemental Figure 9G and 9H), indicating that this extra peptide does not affect TGERa function.

To elucidate the mechanism underlying TGERb's inability to recognize pep-13, we first performed in silico LRR substitution and predicted the interface predicted TM-score (ipTM) values between chimeric TGERa variants and Pep-13 using AlphaFold3 (Supplemental Table 4). Based on these predictions, six LRRs from TGERb (LRR5/7/9/10/17/21) were selected for function analysis. Among them, LRR5, LRR7, LRR9, and LRR10 were predicted to contribute to Pep-13 binding, whereas LRR17 and LRR21 were hypothesized to modulate interactions with SERKs. Each of these LRRs was individually substituted into TGERa (Figure 3A). Functional assays revealed that TGERa^{LRR5b} and TGERa^{LRR7b} exhibited impairment in Pep-13-induced cell death and ROS burst, whereas TGERa^{LRR9b}, TGERa^{LRR10b}, and TGERa^{LRR17b} completely lost responsiveness to Pep-13. In contrast, TGERa^{LRR21b} retained normal Pep-13 responsiveness (Figure 3B and 3C). Ligand-binding assays further showed that TGERa^{LRR5b} and TGERa^{LRR7b} had reduced Pep-13 binding capacity, while TGERa^{LRR9b} and TGERa^{LRR10b} failed to bind Pep-13. Surprisingly, TGERa^{LRR17b}, similar to TGERa^{LRR21b}, retained the ability to bind Pep-13 (Figure 3D).

Given that TGERa^{LRR17b} retained Pep-13 binding but failed to trigger immune responses, we next examined its interaction with StSERK3A. TGERa^{LRR9b} and TGERa^{LRR10b} - both unable to bind Pep-13 - exhibited impaired interaction with StSERK3A, consistent with the observation that Pep-13 enhances the interaction between TGERa and StSERK3A. In contrast, Pep-13 failed to induce the interaction between TGERa^{LRR17b} and StSERK3A (Figure 3E). These results demonstrate that TGERb fails to perceive Pep-13 due to defects in both ligand binding and ligand-induced association with StSERK3A.

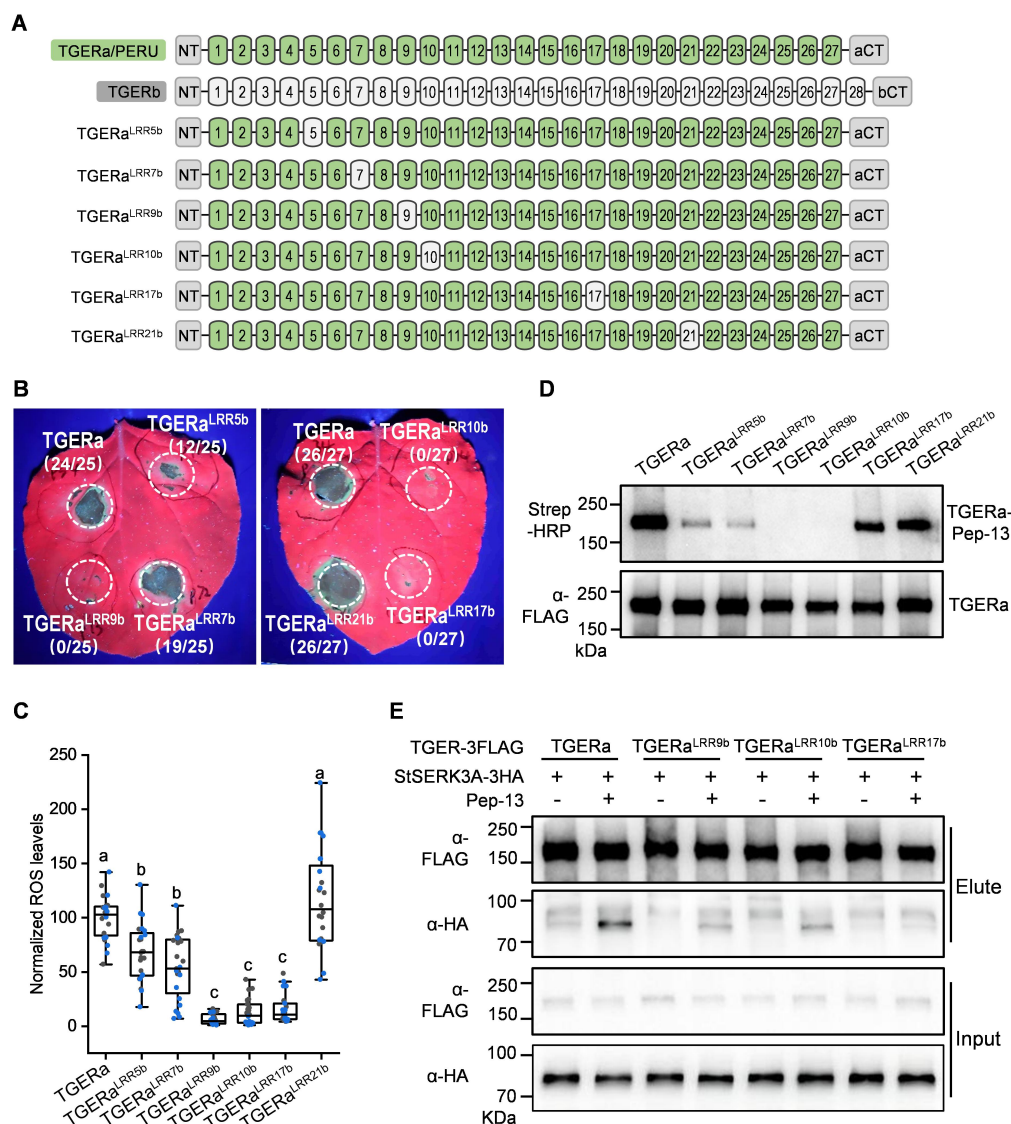


Figure 3. Identification of TGERb's defects in Pep-13 perception.

(A) Schematic representation of leucine-rich repeat (LRR) domain swapping between TGERa and TGERb. The ectodomain of TGERa contains 27 LRRs, whereas TGERb has an additional

24-amino acid peptide in the region corresponding to LRR24 of TGERa, resulting in 28 LRRs. Indicated LRR regions of TGERb were swapped into the TGERa backbone.

(B-C) Pep-13-triggered cell death **(B)** and ROS burst **(C)** in *N. benthamiana* (*Nb*) leaves expressing wild-type *TGERa* and chimeric variants carrying the indicated TGERb LRR regions (*TGERa^{LRRxb}*). *TGERa-3Flag* and *TGERa^{LRRxb}-3Flag* were transiently expressed in *Nb* leaves for 24 h. For cell death assays, leaves were infiltrated with 100 μ M Pep-13, and photos were taken under UV light at 48 h post-infiltration. Numbers in parentheses show the count of necrotic spots versus total spots. For ROS assays, 50 nM Pep-13 was used. The peak value of each ROS curve was normalized to that of TGERa, and analyzed by two-way ANOVA followed by Tukey's multiple comparison test. Different letters indicate significant differences ($p < 0.05$, $n = 24$ from two independent replicates).

(D) Differential binding of TGERa and chimeric *TGERa^{LRRxb}* proteins to biotin-Pep-13. *TGERa-3Flag* and *TGERa^{LRRxb}-3Flag* were transiently expressed in *Nb* leaves for 24 h. Leaves were co-infiltrated with 200 nM biotin-Pep-13 and 3 mM EGS, then incubated for 30 min at room temperature. Proteins were enriched using M2 beads, and eluates were detected by western blot using anti-Flag antibody and Strep-HRP.

(E) TGERa, but not *TGERa^{LRR17b}*, associates with the co-receptor StSERK3A upon Pep-13 treatment. *TGERa-3Flag* and *TGERa^{LRRxb}-3Flag* was transiently co-expressed with *StSERK3A-3HA* in *Nb* leaves. After 24 h, leaves were infiltrated with 100 μ M Pep-13 or H₂O. Samples were collected 15 min post-infiltration, and proteins were enriched using M2 beads. IP eluates were analyzed by western blot using anti-Flag and anti-HA antibodies.

TGERa^{A018} represents a weak allele with reduced expression levels

To investigate the genetic basis underlying the lack of Pep-13 responsiveness in A018, we first examined the genomic organization of TGER loci in diploid potato lines. Using the ePCR function in TBtools-II (Chen et al., 2023b) with TGERa-specific primers, we found that the A157 genome contains duplicated TGERa and TGERb loci arranged in a TGERb-TGERa -TGERb-TGERa pattern, which was inherited from its founder line PG6359 (Supplemental Table 4). Notably, the CDS of *TGERa^{A157}* and *TGERb^{A157}* are identical to those of *TGERa^{E454}* and *TGERb^{E454}*, respectively.

To identify the corresponding locus in A018, we sequenced, assembled, and annotated the A018 genome (Supplemental Figure 10; see Supplemental Note 2 for details). The predicted TGERa^{A018} protein shares 98.9% amino acid identity with TGERa^{E454}. We cloned the CDS of *TGERa^{A018}* and transiently expressed in *Nb* leaves. Similar to TGERa^{E454}, TGERa^{A018} induced MAPK activation and cell death upon Pep-13 treatment (Supplemental Figure 11A

and 11B), indicating that the *TGERa*^{A018} protein is functionally intact. Using TBtools-II ePCR, we further identified the *TGERa* genomic sequence in A018 genome and detected a ~3-kb insertion within the first intron of *TGERa*^{A018} (Supplemental Figure 11C) and this insertion was also present in the founder line PG6359 (Supplemental Table 4), leading us to hypothesize that it might compromise *TGERa* expression in A018. Consistent with this hypothesis, transcript analysis revealed that *TGERa* was strongly induced in A157 following Pep-13 treatment, whereas only weak induction was observed in A018 (Supplemental Figure 11D). Considering that Pep-25 displays stronger cell-death-inducing activity than Pep-13 (Supplemental Figure 3A), we further compared the response of A157, A018, and Atlantic to both Pep-13 and Pep-25. As shown in Supplemental Figure 11E and 11F, A157 exhibited robust cell death as early as 1 day after infiltration with either Pep-25 or Pep-13. In contrast, Pep-25 triggered delayed cell death in A018 at 2-3 days post-treatment, whereas Pep-13 failed to induce visible cell death. Neither peptide elicited cell death in Atlantic. Collectively, these results demonstrate that *TGERa*^{A018} represents a weak allele characterized by diminished expression, most likely caused by the ~3-kb insertion in its first intron.

***TGERa* improves plant resistance to *Phytophthora* pathogens**

To assess the role of *TGERa* in resistance to *Phytophthora* pathogens, detached leaves of *N. benthamiana* transiently expressing empty vector (EV), 35S:*TGERa*, or 35S:*TGERb* were inoculated with *P. capsici* BYA5 and incubated in the dark at 28 °C for 2 days; disease progression was then imaged under UV light (Figure 4A). Quantification of diseased leaf areas revealed that *TGERa* significantly enhanced resistance to *P. capsici* BYA5 compared with EV, whereas *TGERb* did not confer any detectable improvement in disease resistance (Figure 4B).

To further confirm *TGERa* conferred enhanced *Phytophthora* resistance, we

challenged transgenic *np-TGERa* *N. benthamiana* lines with *P. infestans* 1306. Detached leaves from *np-TGERa* *Nb* lines (#1, #2, #3) and wild-type *Nb* plants were inoculated with *P. infestans* and incubated in the dark at 18 °C. Quantification of diseased areas showed significantly smaller lesions in *np-TGERa* lines than in WT (Figures 4C and 4D). Similarly, transgenic *np-TGERa* MicroTom plants exhibited significantly reduced disease symptoms relative to wild-type MicroTom at 2 days post-inoculation (Figures 4E and 4F). Collectively, these results demonstrated that introduction of *TGERa* into heterologous plant species significantly enhances resistance to *Phytophthora* pathogens.

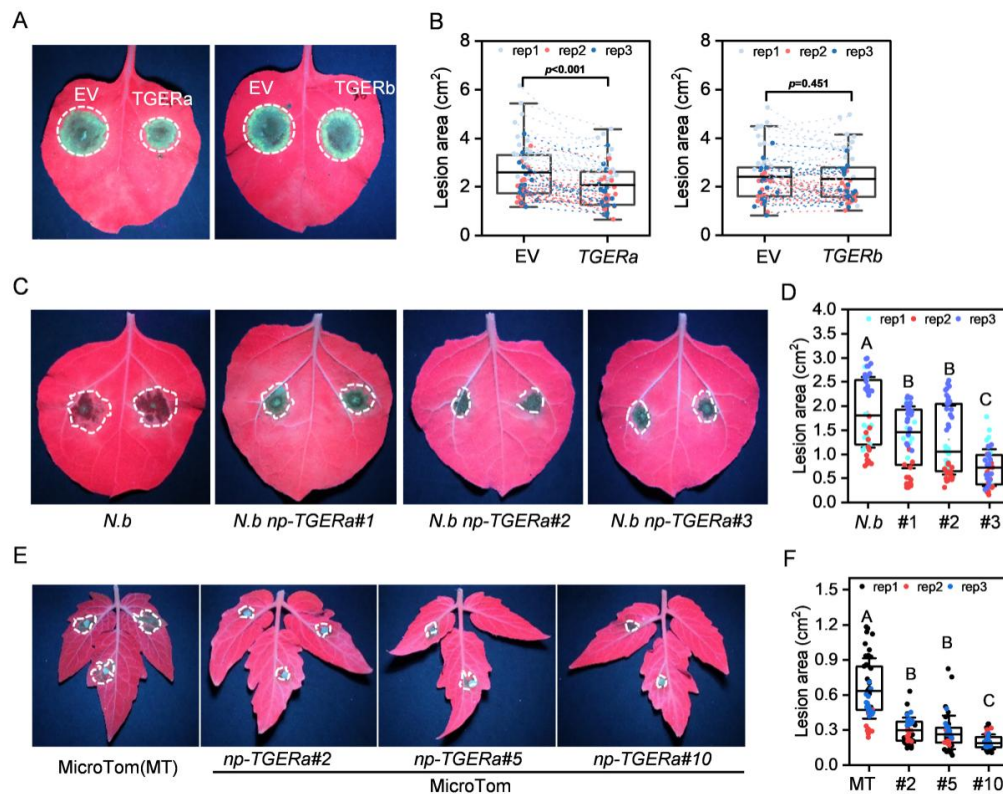


Figure 4. *TGERa* improves plant resistance to *Phytophthora*.

(A-B) *TGERa* enhances resistance to *Phytophthora capsici* when transiently expressed in *N. benthamiana* (*Nb*) leaves. **(A)** Empty vector (EV), 35S-*TGERa* and 35S-*TGERb* were transiently expressed in *Nb* leaves for 24 h, followed by inoculation with an agar plug (5 mm diameter) from colony margins of *P. capsici* strain BYA5. Detached leaves were incubated in the dark at 28°C for 2 days, and lesions were photographed under UV light. **(B)** Quantification of lesion areas using ImageJ. Data were analysed using paired t-test (*TGERa*, $p < 0.05$, $n=55$ from three independent experiments; *TGERb*, $p = 0.451$, $n = 56$ from three independent experiments).

(C-D) Transgenic *Nb* lines expressing *TGERa* exhibit enhanced resistance to *P. infestans*. **(C)** Detached leaves of transgenic *Nb* lines (*np-TGERa* #1, *np-TGERa* #2, *np-TGERa* #3) and wild-type *Nb* plants were inoculated with a spore suspension of *P. infestans* strain 1306 and incubated in the dark at 18°C for 5 days and photographed under UV light. **(D)** Quantification of lesion areas using ImageJ. Data were analyzed using one-way ANOVA followed by Tukey's test. Different letters indicate significant differences ($p < 0.05$, $n = 46$ from three independent experiments).

(E-F) Transgenic tomato (MicroTom) lines expressing *TGERa* display enhanced resistance to *P. infestans*. **(E)** Detached leaves were inoculated with a spore suspension of *P. infestans* strain 1306, and lesion sizes were visualized 2 days post-inoculation under UV light. **(F)** Quantification of lesion areas using ImageJ. Data were analyzed using one-way ANOVA followed by Tukey's test. Different letters indicate significant differences ($p < 0.05$, $n = 45$ from three independent experiments).

METHODS

Plant materials and growth conditions

Tetraploid potato cultivar Atlantic and diploid inbred lines A018, E454, and A157 (Zhang et al., 2021) are maintained in the lab. Potato plants and transgenic lines were propagated on Murashige and Skoog (MS) medium in growth chambers under long-day conditions (16 h light at 23°C and 8 h dark at 22°C).

For genetic analysis, the Pep-13-insensitive line A018 (female parent) was artificially cross-pollinated with E454 (male parent) at anthesis to generate F_1 hybrid progeny. The F_1 plants were subsequently self-pollinated to produce the F_2 population. For soil-grown seedlings, *in vitro*-cultured potato plants were grown on MS medium for 1 week then transferred to sterile soil and further cultivated for 14 days. *N. benthamiana* and *S. lycopersicum* MicroTom were directly seed-sown in soil composed of nutrient soil, vermiculite, and perlite (3:2:1, v/v/v). Plants were grown in a growth chamber under long-day conditions (16 h light at 23°C and 8 h dark at 22°C).

Peptide treatments

Peptides Pep-13 (VWNQPVRGFKVYE), Pep-13W2A (VANQPVRGFKVYE), and Pep-25 (DVTAGAEVWNQPVRGFKVYEQTMS) (Brunner et al., 2002), Biotin-Pep-13, Biotin-Pep-25 and flg22 (QRLSTGSRINSAKDDAAGLQIA)

were synthesized by Sangon Biotech (Shanghai, China) Peptides were dissolved in sterile double-distilled water (ddH₂O) to generate 2 mM stock solutions and stored at -20°C. Working solutions were prepared by diluting stock solutions with sterile water to indicated concentrations.

Vector construction

Primers used in this study are listed in Supplemental Table 6. Full-length coding sequences of *TGERa*, *TGERb*, *StSERK1a*, *StSERK1b*, *StSERK2a*, *StSERK2b*, *StSERK3a*, *StSERK3b* were cloned from cDNA library derived from of E454 leaf. Domain swapping constructs between *TGERa* and *TGERb* LRR regions were generated using gene-specific primers. PCR fragments were inserted into pTF101-35S-3Flag vector (Bu et al., 2021) digested with *Xba*I and *Mlu*I using homologous recombination. *StSERK1a*, *StSERK1b*, *StSERK2a*, *StSERK2b*, *StSERK3a*, *StSERK3b* were inserted into pCambia1300-35S-3HA vector digested with *Hind*III and *Kpn*I using homologous recombination.

For virus-induced gene silencing constructs, TRV2-NbSERK conserved regions (300-500 bp) within *SERK* coding sequences were identified by BLAST analysis against the tobacco genome. Targeted fragments were amplified and inserted into the TRV2 vector via homologous recombination. All constructs were verified by Sanger sequencing.

***Agrobacterium*-mediated transient expression**

Recombinant *Agrobacterium tumefaciens* strains GV3101 harboring the indicated constructs were cultured overnight in LB medium supplemented with kanamycin (50 µg/mL), rifampicin (25 µg/mL), and gentamycin (50 µg/mL) at 28 °C with shaking at 200 rpm. Bacterial cells were harvested by centrifuged at 5000 rpm for 5 min and washed twice with infiltration buffer containing 10 mM MgCl₂, 10 mM MES (pH 5.6), and 200 µM acetosyringone. Cells were resuspended in infiltration buffer to a final OD₆₀₀ of 0.6 and incubated at room temperature in the dark for 3 h. Fully expanded leaves of 4–5-week-old *N. benthamiana* plants were infiltrated on the abaxial side using a needleless

syringe. Plants were maintained under low light conditions for 24 h and then returned to normal growth conditions. Protein expression was verified by immunoblot analysis 24-48 h after infiltration. For elicitor assays, infiltration sites were treated with 100 μ M Pep-13 at 24 h post infiltration. Hypersensitive cell death was evaluated 48 h later under 365 nm UV light.

RNA isolation and RT-qPCR

RNA isolation and RT-qPCR was performed as described (Chen et al., 2024). *NbEF1 α* was used as the reference gene for *N. benthamiana* samples, and *StTUB* was used as the reference gene for potato (*S. tuberosum*). Relative expression levels were calculated using the $2^{-\Delta\Delta CT}$ method. Primer sequences are listed in Supplemental Table 6.

MAPK activation assays

Leaves of potato lines A018 and A157 were sprayed with 100 μ M Pep-13, 5 μ M flg22 or H₂O. Samples were collected at 15 and 30 min after treatment. *N. benthamiana* leaves infiltrated with recombinant *Agrobacterium tumefaciens* GV3101 as described previously for 24 hours, then infiltrated with 50 μ M peptides (Pep-13, Pep-25, W2A) for 15 min. Proteins were separated on 10% SDS-PAGE and detected using anti-p44/42-ERK antibody (Cell Signaling #9101).

Virus-induced gene silencing (VIGS)

Cotyledons of 2-week-old *N. benthamiana* plants or transgenic *np-TGERa* lines were infiltrated with a 1:1 mixture of *Agrobacterium* cultures containing pTRV1 and pTRV2 derivatives, *pTRV2-NbPDS*, *TRV2-GFP*, and *pTRV2-NbSERKs* (Wang et al., 2018) adjusted to OD₆₀₀ = 0.5. Two weeks post-infiltration, plants showing photobleaching in *pTRV2-NbPDS*. Gene silencing efficiency was confirmed by RT-qPCR. Leaves were then treated with 100 μ M Pep-25 or H₂O and cell death responses were documented under 365 nm UV light 48 h later.

Electrolyte leakage assay

Electrolyte leakage assay was performed as reported (Fan et al., 2026). Briefly,

leaf discs (8 mm) were punched from peptide- or water-infiltrated leaves. Six discs per replicate immersed in 2 mL deionized water. After 3 h incubation at 25 °C, initial conductivity (R1) was measured. Samples were boiled for 30 min, cooled to 25 °C, and final conductivity (R2) recorded. Relative electrolyte leakage (REL) was calculated as: $REL (\%) = (R1/R2) \times 100\%$.

Stable transformation of *N. benthamiana*, *Solanum tuberosum* (cv. Atlantic) and *S. lycopersicum* (cv. MicroTom)

Stable transformation of *N. benthamiana*, MicroTom and Atlantic plants was carried out by the BioRun company via *Agrobacterium*-mediated transformation, using the construct *np-TGERa-3Flag* for *N. benthamiana* and MicroTom, and the construct *35S-TGERa-3HA* for Atlantic. Transgenic plants were screened by PCR using gene-specific primer to confirm the presence of the *TGERa* transgene. TGERa protein levels in positive lines were further verified by Western blot analysis.

***In vivo* ligand binding assays**

Agrobacterium tumefaciens GV3101 carrying *TGERa-3flag* or *TGERb-3flag* constructs was transiently expressed in *N. benthamiana* leaves for 24 h. Leaves were then infiltrated with solutions containing 100 nM biotin–Pep-13/25 alone or together with 100 µM unlabeled Pep13/25 as a competition. The infiltration buffer contained 3 mM ethylene glycol bis (succinimidyl succinate) (EGS, Thermo Scientific, #21565) in 25 mM HEPES (pH 7.5). After 30 minutes, approximately 1 g of leaf tissue was harvested and frozen in liquid nitrogen. Proteins were immunoprecipitated using anti-Flag M2 affinity resin (Sigma-Aldrich, A2220-5ML). Bound proteins were analyzed by immunoblotting using anti-Flag antibody (Sigma-Aldrich, F1804-200UG) and streptavidin-HRP (Abcam, Ab7403) to detect receptor-bound biotinylated peptides.

Co-immunoprecipitation assay

Frozen leaf tissue was ground into a fine powder in liquid nitrogen and

homogenized in membrane extract buffer containing 25 mM Tris HCl (pH 7.5), 10% Glycerol, 1 mM EDTA, 150 mM NaCl, 1.5% NP-40, 0.5% sodium deoxycholate, 1 mM NaF, 4 mM DTT, 2% (w/v) PVPP, 1 mM PMSF, and protease cocktail. Protein extracts were incubated on ice for 30 min and centrifuged at 13,000 × g for 15 min at 4 °C. The supernatants were clarified by a second centrifugation under the same conditions. For immunoprecipitation, the supernatants were incubated with 15 µL anti-FLAG M2 affinity resin (Sigma-Aldrich, A2220-5ML) for 2 h at 4 °C with gentle rotation. Input samples were retained for immunoblot analysis. The resin was washed three times with binding buffer containing 25 mM Tris HCl (pH 7.5), 10% Glycerol, 1 mM EDTA, 150 mM NaCl, 1.5% NP-40, 0.5% sodium deoxycholate, 1 mM NaF, 0.2 mM DTT. Bound proteins were eluted by boiling in 2× SDS loading buffer at 95 °C for 5 min. Proteins were separated by SDS-PAGE and detected by immunoblotting using anti-Flag and anti-HA antibodies.

Interacting proteins identified by Immunoprecipitation-Mass Spectrometry (IP-MS)

TGERa-3Flag or empty vector (EV) constructs were transiently expressed in *N. benthamiana* leaves. At 48 h after agroinfiltration, leaves were treated with 100 µM Pep-13 or H₂O and harvested 15 min after treatment. Total proteins were extracted and subjected to immunoprecipitation using anti-FLAG M2 affinity resin as described above. Immunoprecipitated proteins were separated by SDS-PAGE and visualized by Coomassie Brilliant Blue staining. Gel regions containing TGERa protein complex were excised and subjected to in-gel digestion with tryptic.

The resulting peptides were analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) using an EASY-nLC 1200 system coupled to an Orbitrap Exploris 480 mass spectrometer (Thermo Fisher Scientific). Peptides were separated on a C18 analytical column using a linear acetonitrile gradient. Raw MS data were processed using Proteome Discoverer software and

searched against the NbHZ1 protein database (Wang et al., 2024). Carbamidomethylation of cysteine residues was set as a fixed modification, whereas methionine oxidation was considered a variable modification. Up to two missed trypsin cleavage sites were allowed. Peptide spectrum matches were filtered using a false discovery rate (FDR) threshold of <1%. Functional annotation of identified proteins was performed using Gene Ontology (GO), InterPro, COG, and KEGG databases. Only proteins identified in at least two biological replicates were considered for further analysis.

Luminol-based ROS burst assay

Leaf discs (4 mm diameter) were excised from 5-week-old *N. benthamiana* plants were equilibrated overnight in 200 μ L ddH₂O in 96-well white plates. The next day, water was replaced with 100 μ L reaction buffer containing 10 μ g/mL horseradish peroxidase (HRP; Sigma #P6782), 50 μ M luminol (Sigma #A8511), and 50 nM Pep-13. Real-time luminescence was recorded at 1 min intervals for 120 min using a Cytation5 microplate reader (BioTek, Winooski, VT, USA) with the following parameters: gain 130, 5 mm read height, no optical filter, and maintaining a constant temperature of 22 °C.

Pathogen infection assay

Infection assays were performed as described previously (Chen et al., 2024). *P. infestans* strain 1306 was cultured on rye agar medium at 18 °C in darkness for 14 days. Zoospores were released by incubating sporangia in cold water at 4 °C for 2 h and filtered to remove mycelium. Detached leaves were inoculated with 5 μ L zoospore suspension (1×10^5 spores/mL) on the abaxial surface. For *P. capsica* strain BYA5 (Gao et al., 2023), clones were cultured on V8 juice agar medium at 25 °C in darkness for 3 days. Agar plugs (5 mm diameter) from colony margins were placed onto leaf surface and covered with 10 μ L sterile water. Infected leaves were incubated under 100% relative humidity at optimal temperatures (18 °C for *P. infestans*, 25 °C for *P. capsica*) for 4 or 3 days, respectively. Lesion areas were visualized under UV light and quantified using ImageJ (v1.51j8, National Institutes of Health, Maryland, USA) software.

Statistical Analysis

All experiments were performed with at least three independent biological replicates unless otherwise stated. Data are presented as mean $\pm$ standard deviation (SD). Statistical analyses were performed using OriginPro2025 (OriginLab). Statistical significance between two groups was determined using a two-tailed Student's t-test, while comparisons among multiple groups were analyzed using one-way analysis of variance (ANOVA) followed by Tukey's multiple comparison test. Differences were considered statistically significant at $p < 0.05$.

DATA AVAILABILITY

The authors hereby declare that all relevant data supporting the findings of this study are accessible within the research article and its supplemental information. The A018 genome data has been deposited at <http://solomics.agis.org.cn/potato/species>, under Accession A6-10 (A018). Materials generated during the current study are available from the corresponding author upon reasonable request.

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helpful suggestions. The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

T.S., X.F., D.L., and L.C. conceived and designed this study; C.Z., and S.H. provided advice and initial materials; X.F., D.L., Y.Z., and Y.H. performed the experiments; L. C. analyzed BSA-seq data and performed assemble and annotation of A018 genome. T.S., X.F., and L.C. wrote the manuscript from the input from all other authors. All authors reviewed the manuscript.

SUPPLEMENTAL INFORMATION

Supplemental information is available online.

Supplemental Note 1. Mapping the TGER locus by BSA-seq analysis.

Supplemental Note 2. A018 genome assembly and annotation.

Supplemental Figure 1. Mapping of *TGER* locus using bulked segregant analysis sequencing

Supplemental Figure 2. Transient expression of selected candidate genes in *N. benthamiana* leaves by *Agrobacterium* and tested for responding to Pep-13.

Supplemental Figure 3. Functional confirmation of TGERa by transgenic complementation.

Supplemental Figure 4. Identification of six NbSERK proteins as Pep-13 induced interacting proteins of TGERa by IP-MS and phylogenetic analysis of SERK proteins.

Supplemental Figure 5. TGERa relies on SERKs for Pep-13 perception.

Supplemental Figure 6. Translation initiation from uORF1 of TGERa mRNA leads to decreased TGERa protein levels.

Supplemental Figure 7. Intron 2 retention is observed in a subset of TGERa/PERU transcripts.

Supplemental Figure 8. The TGERa protein (TGERa-In2R) translated from TGERa mRNA with intron 2 retention cannot recognize Pep-13/25.

Supplemental Figure 9. Functional characterization of TGERb in Pep-13 perception and signaling.

Supplemental Figure 10. Genome assembly and annotation of potato inbred line A018.

Supplemental Figure 11. TGERa in A018 is a weak allele with reduced expression.

Supplemental Table 1. 1,981 candidate variants on Chr03 of E454 genome identified by BSA-seq analysis.

Supplemental Table 2. SNPs identified in selected 24 candidate genes.

Supplemental Table 3. Selected candidate genes and cloning primers used.

Supplemental Table 4. ipTM between Pep-13 and ectodomains of TGERa, TGERb and TGERa variants predicted using AlphaFold3.
Supplemental Table 5. ePCR results for TGER primers in genomes of A018, A157, E454, E86-69, PG6359, DM and Atlantic.
Supplemental Table 6. Primers used in this study.

REFERENCES

- Albert, I., Böhm, H., Albert, M., Feiler, C. E., Imkampe, J., Wallmeroth, N., Brancato, C., Raaymakers, T. M., Oome, S., Zhang, H., et al. (2015). An RLP23-SOBIR1-BAK1 complex mediates NLP-triggered immunity. *Nat. Plants* 1:1–9.
- Brunner, Â., Rosahl, S., Lee, J., Rudd, J. J., Geiler, C., Scheel, D., and Nu, T. (2002). Pep-13, a plant defense-inducing pathogen-associated pattern from phytophthora transglutaminases. *EMBO J.* 21:6681–6688.
- Bu, T., Lu, S., Wang, K., Dong, L., Li, S., Xie, Q., Xu, X., Cheng, Q., Chen, L., Fang, C., et al. (2021). A critical role of the soybean evening complex in the control of photoperiod sensitivity and adaptation. *Proc. Natl. Acad. Sci. U. S. A.* 118:1–10.
- Chen, Z., Liu, F., Zeng, M., Wang, L., Liu, H., Sun, Y., Wang, L., Zhang, Z., Chen, Z., Xu, Y., et al. (2023a). Convergent evolution of immune receptors underpins distinct elicitor recognition in closely related Solanaceous plants. *Plant Cell* Advance Access published 2023, doi:10.1093/plcell/koad002.
- Chen, C., Wu, Y., Li, J., Wang, X., Zeng, Z., Xu, J., Liu, Y., Feng, J., Chen, H., He, Y., et al. (2023b). TBtools-II: A “one for all, all for one” bioinformatics platform for biological big-data mining. *Mol. Plant* Advance Access published 2023, doi:10.1016/j.molp.2023.09.010.
- Chen, Y., Han, Y., Huang, W., Zhang, Y., Chen, X., Li, D., Hong, Y., Gao, H., Zhang, K., Zhang, Y., et al. (2024). LAZARUS 1 functions as a positive regulator of plant immunity and systemic acquired resistance. *Front. Plant Sci.* 15:1–11.
- Cheng, L., Wang, N., Bao, Z., Zhou, Q., Guarracino, A., Yang, Y., Wang, P., Zhang, Z., Tang, D., Zhang, P., et al. (2025). Leveraging a phased pangenome for haplotype design of hybrid potato. *Nature* 640:408–417.
- Du, J., Verzaux, E., Chaparro-Garcia, A., Bijsterbosch, G., Keizer, L. C. P., Zhou, J., Liebrand, T. W. H., Xie, C., Govers, F., Robatzek, S., et al. (2015). Elicitor recognition

- confers enhanced resistance to *Phytophthora infestans* in potato. *Nat. Plants* **1**:15034.
- Fan, X., Han, Y., Sun, X., and Sun, T.** (2026). Identification and Functional Analysis of Potato Receptor Kinase RDA2 Proteins. *Plants* **15**: 1-14.
- Gao, H., Guo, Y., Ren, M., Tang, L., Gao, W., Tian, S., Shao, G., Peng, Q., Gu, B., Miao, J., et al.** (2023). *Phytophthora* RxLR effector PcSnel4B promotes degradation of resistance protein AtRPS2. *Plant Physiol.* **193**:1547–1560.
- Jones, J. D., and Dangl, J. L.** (2006). The plant immune system. *Nature* **444**:323–329.
- Li, Y., Tao, Y., Yao, X., Cao, R., Xiong, X., Gong, B.-Q., and Li, J.-F.** (2025). SERK5 genetically compensates for the loss of BAK1 and BKK1 in regulating elf18-triggered immune signaling in *Arabidopsis*. *Proc. Natl. Acad. Sci.* **122**:e2513517122.
- Ma, X., Xu, G., He, P., and Shan, L.** (2016). SERKing Coreceptors for Receptors. *Trends Plant Sci.* **21**:1017–1033.
- Nietzschmann, L., Gorzolka, K., Smolka, U., Matern, A., Eschen-Lippold, L., Scheel, D., and Rosahl, S.** (2019). Early Pep-13-induced immune responses are SERK3A/B-dependent in potato. *Sci. Rep.* **9**:1–12.
- Nowicki, M., Foolad, M. R., Nowakowska, M., and Kozik, E. U.** (2012). Potato and Tomato Late Blight Caused by *Phytophthora infestans*: An Overview of Pathology and Resistance Breeding. *Plant Dis.* **96**:4–17.
- Nürnberg, T., Nennstiel, D., Jabs, T., Sacks, W. R., Hahlbrock, K., and Scheel, D.** (1994). High affinity binding of a fungal oligopeptide elicitor to parsley plasma membranes triggers multiple defense responses. *Cell* **78**:449–460.
- Stokstad, E.** (2019). The new potato. *Science* (80-.). **363**:574–577.
- Torres Ascurra, Y. C., Zhang, L., Toghiani, A., Hua, C., Rangegowda, N. J., Posbeyikian, A., Pai, H., Lin, X., Wolters, P. J., Wouters, D., et al.** (2023). Functional diversification of a wild potato immune receptor at its center of origin. *Science* (80-.). **381**:891–897.
- Wang, Y., Xu, Y., Sun, Y., Wang, H., Qi, J., Wan, B., Ye, W., Lin, Y., Shao, Y., Dong, S., et al.** (2018). Leucine-rich repeat receptor-like gene screen reveals that *Nicotiana* RXEG1 regulates glycoside hydrolase 12 MAMP detection. *Nat. Commun.* **9**.
- Wang, J., Zhang, Q., Tung, J., Zhang, X., Liu, D., Deng, Y., Tian, Z., Chen, H., Wang, T., Yin, W., et al.** (2024). High-quality assembled and annotated genomes of *Nicotiana*

709 tabacum and Nicotiana benthamiana reveal chromosome evolution and changes in
 710 defense arsenals. *Mol. Plant* **17**:423–437.

711 **Zhang, C., Yang, Z., Tang, D., Zhu, Y., Wang, P., Li, D., Zhu, G., Xiong, X., Shang, Y., Li,**
 712 **C., et al.** (2021). Genome design of hybrid potato. *Cell* **184**:3873-3883.e12.

713 **Zhou, J., and Zhang, Y.** (2020). Plant Immunity: Danger Perception and Signaling. *Cell*
 714 **181**:978–989.

715