

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection 12 oomycete genomes were downloaded from the NCBI GenBank database and the oomycete Gene Order Browser (OGOB, <https://ogob.ie/v1/gob/data.html>), and the known functional RXLR effectors in *P. infestans* were collected from a literature survey and UniProtKB/Swiss-Prot database. Detailed information is described in supplementary table and methods.

Data analysis Detailed usage and parameter settings are described in methods and supplementary figure legends. We used following programs and open source codes for the data analysis: GraphPad Prism 10, OrthoFinder v2.5.4, SignalP v4.1, HMMer v3.1b, MAFFT v7.407, trimAl, IQ-TREE v1.6.12, ModelFinder, Colabfold_batch v1.5.2, US-align v20230609, networkx v3.1, Cytoscape v3.9.1, NCBI blastp 2.15.0+, Jalview v2.11.3.2, jFATCAT, PyMol v2.5.5, and https://github.com/slt666666/Phylogenetic_distance_plot2.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All the described data in the manuscript is provided in supplementary table and figure or referenced. The datasets generated in this study are available by contacting the corresponding author. We also submitted raw data used for making figures in this study as file.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

Data exclusions

Replication

Randomization

Blinding

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

Methods

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input type="checkbox"/>	<input checked="" type="checkbox"/> Plants

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	All the described plant pathogenic microorganisms described in this study are provided from KACC: Korean Agricultural Culture Collection, https://genebank.rda.go.kr/eng/uat/uia/actionMain.do .
Authentication	All the information and isolating procedure of materials is described in https://genebank.rda.go.kr/eng/uat/uia/actionMain.do .
Mycoplasma contamination	No related result.
Commonly misidentified lines (See ICLAC register)	No related result.

Plants

Seed stocks	Seeds of all the transgenic <i>Nicotiana benthamiana</i> lines described in manuscript and figures are deposited in laboratory. All the materials are available by contacting the corresponding author.
Novel plant genotypes	Transgenic plant expressing R1, R8, or Rpi-amr1 were generated through the agrobacterium-mediated transformation. All T0 plants were tested with transient expression of Avr1, Avr8, and Avramr1, respectively and we selected plant exhibited cell death. Plant expressing R1 (resistance against <i>P. palmivora</i> , <i>P. capsici</i>), R8 (resistance against <i>P. cactorum</i> , <i>P. capsici</i>), and Rpi-amr1 (resistance against <i>P. parasitica</i> , <i>P. cactorum</i> , <i>P. palmivora</i>) exhibited novel resistance phenotypes against multiple Phytophthora pathogens in addition to <i>P. infestans</i> .
Authentication	All the transgenic plants expressin R1, R8, and Rpi-amr1 were tested with HR-inducing ability against corresponding effector. Detailed information is described in supplementary figure 13.