nature portfolio

Corresponding author(s): Shimin Zuo, Zefeng Yang

Last updated by author(s): April 1, 2025

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	For nucleotide diversity and evolutionary analyses, the map layer of precipitation from 1970 to 2000 A.D. was obtained from WorldClim. For RNA-seq analysis, the sequencing data for RNA-seq of 3 independent rice samples were generated from the Illumina NovaSeq 6000 system. The ImageJ 1.53c (https://imagej.net/ij/ij/download.html) was used to evaluate the gray value of western blotting. LC-MS/MS analysis was performed using a Q-Exactive mass spectrometer (Thermo Fisher Scientific, Waltham, MA, USA) with a nanoflow HPLC instrument (EASY-nLC1200 system, Thermo Fisher Scientific).
Data analysis	1. For GWAS analysis: Two kinds of univariate GWAS models, CMLM and BLINK, were employed to evaluate ShB resistance-SNP associations using the Genomic Association and Prediction Integrated Tool (GAPIT). The Manhattan and QQ plots for GWAS were generated using the R package “CMplot”. LD blocks were defined with the Solid Spine method and LD heatmap was constructed using the R package “LDBlockShow”. 2. For nucleotide diversity and evolutionary analyses: The second-generation sequencing data of all 430 varieties with Illumina sequencing depth >20x from the 3K rice population were aligned to Sequence1 using the Bowtie2 software. The results were analyzed using Samtools, and a Perl script was used to count the number of reads successfully covering the 256bp endpoints in the sequencing data of the 430 varieties. The Bowtie2 sequence alignment, Samtools, and Perl script analysis method were used to determine the SNP type of the SNPG/A site in the 430 varieties. The geographical information of cultivated varieties was obtained from RFGB, and marked on map using Cartopy package v0.20.0 in the Python v3.6.0 software to observe geographic distribution of the types of SBRR1-R and SBRR1-S. The average FST values in each 400-kb window were estimated at chromosome 11 between indica and japonica subspecies using VCFtools

v0.1.16.
The nucleotide diversity (π) and Neutral test (Tajima's D) of each population were calculated in 400-kb window using VCFtools v0.1.16.
The phylogenetic tree for SBRR1 was inferred using the UPGMA method in MEGA v11.
The haplotype network was calculated using pegas package v1.252 in the R v4.1.2 software.
The haplotypes that contained more than 3 rice accessions were displayed using plotting module matplotlib v3.6.053 in the Python v3.6.0 software.
3. For RNA-seq analysis:
The screening criteria for DEGs were "FC=2" and "p-value < 0.05." Gene ontology (GO) analysis was performed using the DAVID Resources 6.7 (http://david.abcc.ncifcrf.gov/).
4. Phosphorylated peptides were identified and quantified based on the extracted ion chromatogram peak area using MaxQuant software (1.6.2.10).

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

The data supporting the findings of this study are available in the article and its Supplementary Information files. The data of 109,444 high-quality SNPs covering the whole rice genome of 178 commercial rice cultivars used in this study and GWAS statistics are publicly available from Figshare repository (https://doi.org/10.6084/m9.figshare.25265239.v2). Genomic DNA sequences for SBRR1 from the cultivars XWX7, DJ, YSBR1 and ZD88 can be found in the National Center for Biotechnology Information (NCBI) GenBank under accessions PV423243, PV423242, PV423244 and PV423245, respectively. The phosphorylation MS data has been submitted to Figshare repository (https://doi.org/10.6084/m9.figshare.27939462.v1). The RNA-seq data have been deposited in the National Center for Biotechnology Information Sequence Read Archive under accession code PRJNA953858. Source data for all Figures, Extended data and Supplementary Figures have been provided with this paper.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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

Life sciences study design

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

Sample size	Sample size are indicated in individual figures and figure legends. For evaluation of sheath blight resistance in the field, at least 30 samples were investigated. For evaluation of sheath blight resistance in greenhouse, at least 5 samples were investigated. For evaluation of agronomic traits, at least 10 samples were investigated. For evaluation of grain yield in field, five or six replications, each comprised by 48 plants from 1.32 square meter in each plot with size of 0.95m*1.5m, were investigated. For luciferase reporter assay, 6 biological replicates were performed. For subcellular localization analysis, at least 3 biological replicates were observed and calculated.

For the expression level quantification of genes, 3 biological replicates were performed for each sample.
For RNA-seq analysis and determination of chitinase activity, about 250 mg of leaf sheath samples were collected from the transgenic lines and wild-type plant, and 3 independent repeats of each sample.
For LC-MS/MS analysis, 3 biological repeats were performed.
For the students't two-side t-test and Duncan's multiple range test, at least 3 independent samples were required, so the number of samples were selected more than 3.
No statistical methods were used to predetermine sample sizes.
The sample size was determined according to the reports in the related research subjects, e.g., PMID: 39838095, 34597584, 23423653, 34582620, 35189026, 22353606, 20227662, 35189026, 36307423, 2426394, etc.

Data exclusions: No data were excluded from the analysis.

Replication: At least 3 replicates were used for each experiment. All replicates are true biological (rather than technical) replicates. All replication were successful.

Randomization: ALL samples were randomly allocated to control or treatment groups.

Blinding: The investigators were blinded to group allocation during data collection and analysis.

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

n/a	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Antibody (suppliar name, catalog number, clone name, lot number)
1. Horseradish peroxidase (HRP)-conjugated Mouse anti GST-tag mAb (ABclonal, AE027, AMC0513, 1:3000);
2. HRP-conjugated Mouse anti His-tag mAb (ABclonal, AE028, AMC0484, 1:3000);
3. HRP-conjugated Mouse anti MBP-Tag mAb (ABclonal, AE075, AMC0522, 1:3000);
4. HRP-conjugated Mouse anti Myc-Tag mAb (ABclonal, AE026, AMC0048, 1:3000);
5. HRP-conjugated Mouse anti HA-Tag mAb (ABclonal, AE025, AMC0557, 1:3000);
6. Monoclonal Anti-FLAG M2 antibody (Sigma-Aldrich, F3165, M2 monoclonal, 1:5000);
7. Anti-SIP1 antibody (Beijing Protein Innovation, NA, NA, 1:500);
8. Anti-HSP82 antibody (Beijing Protein Innovation, AbM51099-31-PU, NA, 1:3000);
9. Anti-PIP1;1 antibody (Beijing Protein Innovation, AbP80089-A-SE, NA, 1:3000);
10. Anti-pSer/Thr rabbit polyclonal antibody (ECM Biosciences, PP2551, NA, 1:1000);
11. Goat Anti-Rabbit IgG(H&L)-HRP Conjugated (EASYBIO, BE0101, NA, 80780926, 1:3000);
12. Goat Anti-Mouse IgG(H&L)-HRP Conjugated (EASYBIO, BE0102, NA, 80781014, 1:3000);
13. Anti-plant-Actin Mouse Monoclonal antibody (EASYBIO, BE0028, Q30, 80870207, 1:3000);
14. HRP-conjugated Mouse anti GFP-Tag mAb(ABclonal, AE030, AMC0483R-HRP, 1:3000).

Validation

1. Anti-GST antibody validation could be found in the website: https://abclonal.com.cn/catalog/AE027.
2. Anti-His antibody validation could be found in the website: https://abclonal.com.cn/catalog/AE028.
3. Anti-MBP antibody validation could be found in the website: https://abclonal.com.cn/catalog/AE075.
4. Anti-Myc antibody validation could be found in the website: https://abclonal.com.cn/catalog/AE026.
5. Anti-HA antibody validation could be found in the website: https://abclonal.com.cn/catalog/AE025.
6. Anti-FLAG antibody validation could be found in the website: https://www.sigmaaldrich.cn/CN/zh/product/sigma/f3165.
7. Anti-SIP1 antibody were designed and prepared by Beijing Protein Innovation Company on commission.
8. Anti-HSP82 antibody validation could be found in the website: http://www.proteomics.org.cn/product/202.html.
9. Anti-PIP1;1 antibody validation could be found in the website: http://www.proteomics.org.cn/product/665.html.
10. Anti-pSer/Thr rabbit polyclonal antibody validation could be found in the website: https://ecmbio.com/products/pp2551?_pos=1&_sid=8c1886917&_ss=r.
11.Goat Anti-Rabbit IgG(H&L)-HRP Conjugated antibody validation could be found in the website: https://www. bioeasytech.com/

product/2901.html?goods_id=5786.
12. Goat Anti-Mouse IgG(H&L)-HRP Conjugated antibody validation could be found in the website: https://www. bioeasytech.com/product/2907.html?goods_id=5794.
13. Anti-Actin antibody validation could be found in the website: https://www. bioeasytech.com/product/2363.html?goods_id=4251.
14. Anti-GFP antibody validation could be found in the website: https://abclonal.com.cn/catalog/AE030.

Plants

Seed stocks

The 178 rice cultivars used for GWAS were collevted from different regions of China (148), South Korea (15) and Japan (15). The sbrr1 mutant (3D-50196L) was isolated from a collection of T-DNA insertion lines (http://orygenesdb.cirad.fr/). Two temperate japonica cultivars Taigeng 394 (TG394) and Xudao 3 (XD3) were collected from Jiangsu Province in China.

Novel plant genotypes

For CRISPR/Cas9 knockout construction, oligonucleotides containing an 18-bp gene-specific sequence of SBRR1/SIP1/Chit3/Chit4/bHLH57 were synthesized and annealed to form the oligo adaptors. The oligo adaptors were firstly cloned into the entry vector pOs-sgRNA, then subcloned into the Gateway destination vector pOs-Cas9. To prepare the overexpression constructs, the SBRR1, SIP1, Chit3 and bHLH57 coding regions of DJ were individually inserted into the pCubi1390-3FLAG vector under control of the maize ubiquitin promoter. For genetic complementation, a 2,463 bp coding region of SBRR1 from DJ and its native 2,954 bp promoter fragment from DJ were cloned and inserted into the pCAMBIA2300 binary vector to generate the pSBRR1DJ:SBRR1DJ complement construct. Similarly, constructs pSBRR1DJ:SBRR1K553E (kinase mutant version of SBRR1 protein, the SBRR1 coding region is from DJ) and pSBRR1XWX7:SBRR1DJ (SBRR1 coding region from DJ was driven by a 3,341 bp promoter of elite SBRR1 allele from XWX7) were also generated. Subsequently, these constructs were introduced into Agrobacterium tumefaciens strain EHA105 and used to infect calli of rice varieties by Agrobacterium-mediated transformation method (PMID: 7920717). All primer sequences for the constructs are listed in Supplementary Table 13.

Authentication

The authentication procedures for generating CRISPR/Cas9 knockout, overexpression and complementation lines could be found in the related Reference PMID: 23999856, 31444468 and 33408412, respectively.