nature portfolio

Corresponding author(s): Zhaoshi Xu

Last updated by author(s): Dec 25, 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	Skanlt RE Software 5.0 was employed to detect the absorbance in chemical reactions during the calculation of MDA, Pro and CAT content, as well as to detect the LUC luminescence data. The variation frequency program of the wheat genome variation database was used to obtain the variation data of the target gene. Zen 3.3 Blue Edition was employed for BIFC fluorescence detection and mycelial staining fluorescence detection. Indigo software was used to measure the luciferase activity in LCl assays and Dual-luciferase reporter assays within tobacco.
Data analysis	In transcriptome data analysis, Fastp v 0.19.3 software was used to filter the original data and remove adapters from the reads; Paired-end reads were aligned to reference genome by the HISAT2 procedure; read counts mapped to each gene were quantified using HTSeq v.0.6.1; differentially expressed genes were identified by DESeq2. KEGG enrichment analysis was conducted using the DAVID function annotation tool, and GO enrichment analysis was performed using GOEnrichment program of the Triticeae-Gene Tribe web. The significant difference analysis was conducted using the data analysis programs of Excel software and Graphpad Pism9.5 software. The weighted gene co-expression network analysis was conducted using the Metware Cloud web tool.Two-tailed Student's t tests and one-way or two-way ANOVA test were conducted using graphpad software.

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 raw reads from the RNA-seq of wheat inoculated with Fpg were deposited in the NCBI Database (https://www.ncbi.nlm.nih.gov/sra) under Sequence Read Archive (SRA) BioProject ID: PRJNA1139870, reviewer link: https://dataview.ncbi.nlm.nih.gov/object/PRJNA1139870?reviewer=nqtoo26r1fj5hkkbiqt7ln10hl. The SRA of transcriptome analysis of the TaMPK3-transformed line and WT were submitted in the BioProject PRJNA1276293, reviewer link: https://dataview.ncbi.nlm.nih.gov/object/PRJNA1276293?reviewer=dtdthhda60mklh708uk4g3qm93. The SRA of wheat under drought treatment was saved in BioProject ID: PRJNA1056048, reviewer link: https://dataview.ncbi.nlm.nih.gov/object/PRJNA1056048?reviewer=m4dloscOj2q6gtsa2b5pq7it07. Other raw data are archived in the Figshare database, accessible via the link: https://doi.org/10.6084/m9.figshare.29586923. The SRA of Fpg-infected wheat variety Jimai22 was saved in the BioProject ID: PRJNA1390310, reviewer link: https://dataview.ncbi.nlm.nih.gov/object/PRJNA1390310?reviewer=46q27n44es1jik2buqmh981s1k

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	This article focuses on research regarding plants and fungi and does not incorporate any human data.
Reporting on race, ethnicity, or other socially relevant groupings	The article does not include any content regarding race, ethnicity, or other relevant groupings.
Population characteristics	The article does not include any human data.
Recruitment	The article does not include any human data.
Ethics oversight	The article does not include any human data.

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	No sample size calculation was performed. Sample size of all experimental was considered based on the feasibility of sample collection and was sufficient to result in statistical significance and reproducibility. The relevant figure legends and supplementary information describe the sample size, which enables researchers to conduct confident statistical analysis. Sample size for the Fusarium Crown Rot resistance-related survey refers to prior studies, including Yang et al Nature communication 2025, 16:2549. Sample size for the drought resistance-related survey refers to prior studies, including Mu et al Nature plant 2025, 11:1810-1826.
Data exclusions	In the WGCNA analysis, given the substantial difference between the transcriptome data of the first-leaf-blade-3 and that of the other samples, this transcriptome data was excluded from the subsequent co-expression network analysis. This exclusion criteria is pre-established.
Replication	All verification experiments described in the manuscript were performed in triplicate or more to ensure reproducibility, and every replication attempt was successful.
Randomization	All plant samples involved in this article were randomly chosen as plump seeds from the plants. To guarantee the consistency of environmental variables and the growth state of the samples prior to processing, the soil required for all samples in a single repeated experiment was uniformly treated, weighed, and then placed in the culture pots. The plant materials were all germinated in petri dishes, and samples with consistent germination growth were selected and transferred to the soil. The samples in a single repeated experiment were all cultivated in the same culture box. In the field experiment, the plant samples in a single repeated experiment were planted in adjacent plots to ensure consistent water and soil conditions.
Blinding	During the data collection and analysis phase, the investigators were not blinded to group allocation. The samples exhibited significant differences under various treatment conditions, rendering it extremely straightforward to differentiate between the sample groups.

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
[ ]	[x] Antibodies
[x]	[ ] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[ ]	[x] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[x]	[ ] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

TransGen Biotech Company Anti-MBP Mouse mAb, Code#HT701, Lot#Q21019, Exp 20231018; TransGen Biotech Company Anti-Hisl Mouse mAb, Code#HT501, Lot#L10502, Exp 20180502; TransGen Biotech Company Anti-GST Mouse mAb, Code#HT601, Lot#L11224, Exp 20181224. CST Company p44/42 MAPK(Erk1/2) Rabbit mAb (4695S). YEASEN Company Flag-Tag, Mouse mAb (30503ES20).

Validation

Anti-MBP Mouse mAb, antibody profiles: https://www.transgen.com/download/pdf/1/HT701_301/HT701.pdf, relevant citations: SUMOylation-modified Pelota-Hbs1 RNA surveillance complex restricts the infection of potyvirids in plants[J]. Molecular Plant, 2023. Anti-His Mouse mAb, antibody profiles: https://www.transgen.com/download/pdf/1/HT501_299/HT501.pdf, relevant citations:l Arabidopsis pollen tube integrity and sperm release are regulated by RALF-mediated signaling[J]. Science, 2017. Anti-GST Mouse mAb, antibody profiles: https://www.transgen.com/download/pdf/1/HT601_300/HT601.pdf, relevant citations: The D14-SDEL1-SPX4 cascade integrates the strigolactone and phosphate signalling networks in rice[J]. New Phytologist, 2023. CST Company p44/42 MAPK (Erk1/2) Rabbit mAb (4695S), relevant citations: Mitogen-activated protein kinase TaMPK3 suppresses ABA response by destabilising TaPYL4 receptor in wheat[J]. New Phytologist, 2022. YEASEN Company Flag-Tag, Mouse mAb (30503ES20). profiles: https://stream.ysbuy.com/yshop/650d2fdc993229337fb71ea2.pdf.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals

Fusarium pseudograminearum, Fusarium, isolate CS3096 (Identity and pathogenicity of fusarium spp. isolated from wheat fields in Queensland and northern New South Wales[J]. Australian Journal of Agricultural Research, 2004.)

Wild animals

The study did not involve wild animals.

Reporting on sex

The article solely focuses on fungi and plants.

Field-collected samples

The study did not involve samples collected from the field.

Ethics oversight

The article solely focuses on fungi and plants.

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

Plants

Seed stocks

Pinyu 8012 was obtained from Shanxi Agricultural University; Zhengmai 1860 was obtained from Henan Academy of Agricultural Sciences, Jimai 60 was obtained from Shandong Academy of Agricultural Sciences, Jinhe 991 was obtained from Hebei Academy of Agriculture and Forestry Sciences and Ningmai 58 was obtained from Ningxia Academy of Agriculture and Forestry Sciences. The seeds of Heilei were cultivated and harvested at the Shunyi Experimental Station of the Institute of Crop Sciences, Chinese Academy of Agricultural Sciences.

Novel plant genotypes

OE-TaMPK3 and OE-TaCYP51H37 are transgenic lines. The full-length coding DNA sequences (CDS) of the TaMPK3 and TaCYP51H37 genes were cloned into the plant transformation vector pWMB110, which contains the maize ubiquitin promoter. The recombinant vectors were introduced into the host plants via Agrobacterium (EHA105)-mediated transformation. The target genes were detected up to the third generation to identify stable lines. Tampk3 is a gene-edited plant. The editor was CRISPR Cas9. The endogenous targeted sequence (GGCCCTCAAGTACATCCACT) was cloned into the pBUE411 vector for generation of gene-edited wheat. The recombinant vectors were introduced into the host plants by Agrobacterium-mediated transformation.

Authentication

Vector primer PCR was employed to detect the vector introduction status of the plants obtained through Agrobacterium transformation, aiming to identify positive plants. Self-pollination was then performed to obtain the seeds of the first-generation plants. The first-generation plant lines were cultivated, and vector primers were used to detect positive plants. Subsequently, the seeds of the second-generation plant lines were acquired through self-pollination and propagation. The second-generation lines were planted, with 20 samples randomly selected and planted for each line. Vector primers were utilized to detect positive plants in each sample to determine the homozygous lines, and the seeds of the third-generation lines were obtained via self-pollination. The third-generation lines were planted, and the expression levels of the target genes in the overexpressed transgenic lines were detected to identify the transgenic lines for subsequent experiments.

In the first-generation edited lines, positive lines were identified using vector primers. Specific primers were employed to amplify the edited regions of the target genes, aiming to determine the editing status and homozygosity of the target genes in each genome. This approach enabled the identification of lines with edits in all A, B, and D genomes. A disordered sequencing result indicates that the