nature portfolio

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	No software was used to collect the powdery mildew phenotype data.
Data analysis	Raw reads of BSR-Seq were trimmed to remove adapters and low-quality sequences using Trimmomatic v0.38, and high-quality reads were aligned to the durum wheat cv. Svevo reference genome via STAR v2.5.1b on the WheatOmics platform (https://202.194.139.32). PCR duplicates were removed, and split reads spanning introns were retained for variant calling with GATK v4.2.3.0. Variants were filtered using BCFtools v1.9. To identify candidate genomic intervals, single nucleotide polymorphisms (SNPs) and small InDels were analyzed using the varBScore algorithm. Additional association statistics, including the ΔSNP index, G′, and ED⁴, were performed using the WheatGmap online platform (https://www.wheatmap.org). SSR and InDel primers were designed using the software WEKits (v1.0.2) (https://github.com/GP-sir/wekits/releases) and Primer 5. Linkage relationship between the molecular markers and the PmCWI16926 was determined by Mapmaker 3.0b. Gene annotations on the database EnsemblPlants (http://plants.ensembl.org/index.html) and UniProt (https://www.uniprot.org) were used to explore potential disease resistance genes. All the software has been reported previously in published research paper.

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

> Detailed sequence data of PmCWI16926 can be found in National Center for Biotechnology Information (NCBI) under the accession number.

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	None
Reporting on race, ethnicity, or other socially relevant groupings	None
Population characteristics	None
Recruitment	None
Ethics oversight	None

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	Ten resistant parent CWI16926-4Y, ten susceptible parent Langdon (LDN) were crossed to generate ten F_1 progeny, and 207 F_2 individuals, to dissect the genetic basis of this resistance. Altogether, 2000 F2:3 families were used for fine mapping of PmCWI16926.
Data exclusions	Not applicable
Replication	Three biological replicates were performed for qRT-PCR experiments to determine the gene expression levels.
Randomization	Not applicable
Blinding	Not applicable

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

Plants

Seed stocks	The cultivated emmer wheat accession CWI16926-4Y (CIMMYT, accession CWI16926-4Y) was kindly provided by Dr. Hongxing Xu (Henan University).
Novel plant genotypes	None
Authentication	None