

## 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

- |                                     |                                     |  |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of all covariates tested   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | 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 not applicable

Data analysis All scripts and command lines used to prepare and analyse the data (including R packages for data wrangling and visualization) can be found in a public github repository: [https://github.com/afeurtey/WW\\_PopGen](https://github.com/afeurtey/WW_PopGen). We used the R packages tidygraph, ggraphs, stats, LEA and SNPRelate and the scikit-allel python package. Public software used were SPADES v.3.14.1, Trimmomatic v.0.39, bowtie2 v.2.4.1, GATK v4.1.4.1, plink v1.9, vcftools v0.1.17 with a haploid modification (<https://github.com/jydu/vcftools>), bedtools v.2.29.2, GEMMA 0.98.3. SplitsTree v5

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 sequencing data is available from the NCBI Sequence Read Archive (<https://www.ncbi.nlm.nih.gov/sra>). Individual accession numbers can be retrieved from Table S1 and from the Methods section. Climatic data was obtained from the publicly available WorldClim database version 2 (<https://worldclim.org>).

## Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	<input type="text" value="not applicable"/>
Population characteristics	<input type="text" value="not applicable"/>
Recruitment	<input type="text" value="not applicable"/>
Ethics oversight	<input type="text" value="not applicable"/>

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)

## Ecological, evolutionary & environmental sciences study design

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

Study description	<input type="text" value="Genomic characterization of a global set of fungal pathogen strains from infected wheat fields."/>
Research sample	<input type="text" value="We collected a global collection of genomes of the fungal wheat pathogen Zymoseptoria tritici from field-collected isolates with the aim to cover most of the currently known area where this pathogen is found. This included the use of publicly available genomic data, as well as resequencing of isolates to complete the geographical coverage of our samples. The collection contains isolates from all the Americas, North Africa, the Middle-East, Oceania and Europe. They were collected over the last 30 years (earliest recorded sampling in 1989). All resequencing is available online from the NCBI SRA database."/>
Sampling strategy	<input type="text" value="Most samples were collected in a hierarchical manner with multiple isolations made for individual wheat fields. Different samples per wheat field were defined as originating from different wheat leaves to reduce the likelihood of including clonal genotypes. We aimed to cover the global geographical range of this pathogen and sequenced as many genomes as isolates could be made available, while limiting the sequencing of a single field to below 30 for the new sequencing efforts. We used all publicly available genomic sequence data of the pathogen where appropriate."/>
Data collection	<input type="text" value="Information on the date/year and site of collection was recorded in the field by the collaborators (coauthors of this paper). No specific instruments were used for this recoding (aside from paper, pen, and computers)."/>
Timing and spatial scale	<input type="text" value="Sampling was performed on a world-wide scale. Sampling during wheat-growing seasons spanned multiple decades (1980-2010s), depending on the available collections from all coauthors. Detailed location and sampling years are available as a supplementary material, however the month of collection was not always recorded. Individual fields were only sampled once per growing season and only a small set of samples originate from the same field collected in different years. Table S1 identifies sampling year and location."/>
Data exclusions	<input type="text" value="Genomic datasets failing minimum quality criteria (above 20% of missing data) were excluded regardless of their provenance."/>
Reproducibility	<input type="text" value="Not applicable as no experiments were conducted. Association mapping studies were performed using environmental data at the time of collection using all retained samples."/>

Randomization	No randomization was performed as no experiments were conducted. Genetic substructure in the dataset was controlled for using mixed linear models with a kinship matrix to avoid inflated G-E associations.
Blinding	No blinding was performed as no experiments were conducted to assess trait values. Association mapping was performed using environmental data from WorldClim
Did the study involve field work?	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

## Field work, collection and transport

Field conditions	Wheat fields were sampled for infected leaf material. No specific information about the field, location or current climatic conditions was collected.
Location	Locations covered 42 countries: Algeria, Argentina, Australia, Belarus, Belgium, Bolivia, Canada, Chile, Czech, Republic, Denmark, Ecuador, Ethiopia, France, Germany, Hungary, Iran, Ireland, Israel, Italy, Kazakhstan, Kenya, Latvia, Mexico, Morocco, NA, Netherlands, New, Zealand, Peru, Poland, Portugal, Romania, Russia, Spain, Sweden, Switzerland, Syria, Tunisia, Turkey, UK, Ukraine, Uruguay, USA and Yemen. No GPS coordinates or long/lat information were recorded beyond regional information. The detailed list of sampling sites is documented in the supplementary material.
Access & import/export	Samples were collected by co-authors from experimental wheat field plots or agricultural field sites with consent from owners. No permits were required in any sampling location for access and export.
Disturbance	Sampling of the pathogen does not harm the plants or fields, and no wild habitat was disturbed as all sampling was done in agricultural fields with consent of the owners.

## 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	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" 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

### Methods

n/a	Involvement 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

## 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	n/a
Wild animals	n/a
Reporting on sex	n/a
Field-collected samples	Fungal samples were collected from agricultural wheat fields, grown as single-spore isolates and prepared for long-term storage. Method details are provided.
Ethics oversight	n/a

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