

Reporting Summary

Nature Research 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 Research 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 data.

Data analysis Data analyses were conducted in R version 4.0.1

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

Fungal and oomycete cardinal temperature data are available in Dryad <https://doi.org/10.5061/dryad.tjq2bvw6> and from Magarey, R. D., Sutton, T. B., & Thayer, C. L. (2005). A Simple Generic Infection Model for Foliar Fungal Plant Pathogens. *Phytopathology* 95(1), 92–100. <https://doi.org/10.1094/PHYTO-95-0092>.

The annual crop yield projections data used in this study the Inter-Sectoral Model Intercomparison Project (ISIMIP), <https://www.isimip.org>

Fungal and oomycete host plant data and geographical distributions (the Plantwise database) were used under license for the current study, and are available with permission from CABI, Wallingford, UK.

The FAOSTAT commodity list is available from <http://www.fao.org>

Global gridded climate data and climate projections are available from <https://www.worldclim.org>

Global gridded crop distribution data used in this study are available from EarthStat <https://www.earthstat.org> and MIRCA2000 <https://www.uni->

frankfurt.de/45218031/data_download

Fungal and oomycete names and name disambiguation data were obtained from Index Fungorum <http://www.indexfungorum.org/> and associated Species Fungorum <http://www.speciesfungorum.org/> as well as MycoBank <http://www.mycobank.org/>

Annual per capita GDP at purchasing power parity (PPP) data were obtained from the World Bank <https://data.worldbank.org/>

CMIP5 single level monthly near surface relative humidity data were obtained from the Climate Data Store (<https://cds.climate.copernicus.eu>).

Administrative boundaries for maps were obtained from GADM (<https://www.gadm.org>). Coastal outlines were obtained from package rworldmap version 1.3-6 for R version 4.0.1.

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	This study compared changes in global agriculture of 12 major crops and plant pathogenic fungi and oomycete infection risk under climate change. This study utilised available data concerning annual crop yield projections, pathogen cardinal temperature, pathogen host plant interactions and geographical distributions, global gridded climate data and climate projections, global gridded crop distributions, and GDP PPP data.
Research sample	This study was based on available data concerning crop hosts, pathogens, climate change, and GDP. Fungal and oomycete cardinal temperature data are available in Dryad https://doi.org/10.5061/dryad.tqjq2bvw6 and from Magarey, R. D., Sutton, T. B., & Thayer, C. L. (2005). A Simple Generic Infection Model for Foliar Fungal Plant Pathogens. <i>Phytopathology</i> 95(1), 92–100. https://doi.org/10.1094/PHYTO-95-0092. The annual crop yield projections data used in this study the Inter-Sectoral Model Intercomparison Project (ISIMIP), https://www.isimip.org Fungal and oomycete host plant data and geographical distributions (the Plantwise database) were used under license for the current study, and are available with permission from CABI, Wallingford, UK The FAOSTAT commodity list is available from http://www.fao.org Global gridded climate data and climate projections are available from https://www.worldclim.org Global gridded crop distribution data used in this study are available from EarthStat https://www.earthstat.org and MIRCA2000 https://www.uni-frankfurt.de/45218031/data_download Fungal and oomycete names and name disambiguation data were obtained from Index Fungorum http://www.indexfungorum.org/ and associated Species Fungorum http://www.speciesfungorum.org/ as well as MycoBank http://www.mycobank.org/ Annual per capita GDP at purchasing power parity (PPP) data were obtained from the World Bank https://data.worldbank.org/ CMIP5 single level monthly near surface relative humidity data were obtained from the Climate Data Store (https://cds.climate.copernicus.eu). Administrative boundaries for maps were obtained from GADM (https://www.gadm.org). Coastal outlines were obtained from package rworldmap version 1.3-6 for R version 4.0.1.
Sampling strategy	No sample size calculations were performed. Sample sizes were determined by available data in the various data sources utilised in this publication.
Data collection	Fungal and oomycete cardinal temperature data, global gridded climate data and climate projections, global gridded crop distribution data, and fungal and oomycete names and name disambiguation data were collected by TMC. Annual crop yield projections data, GDP PPP data, and the Plantwise database were collected by DPB.
Timing and spatial scale	All relevant time scales relating to when data were collated and processed are provided in the Methods section of this study.
Data exclusions	Global estimates of average fractional proportion grid cell harvested (5 arc minute spatial resolution) were obtained from EarthStat (http://www.earthstat.org) for 150 crops. Crops that could not be clearly identified as species (e.g. “mixed grain”) or contained a large number of different plant genera (e.g. “vegetables”) were excluded. Most crops classified as “not elsewhere specified” (nes) were also excluded. Table S6 details crops used in this analysis. All full list of available crop distributions are available from EarthStat (http://www.earthstat.org). Thirteen pathogens (<i>Alternaria cucumerina</i>, <i>Botrytis cinerea</i>, <i>Cercospora carotae</i>, <i>Didymella arachidicola</i>, <i>Diplocarpon earlianum</i>, <i>Fusarium oxysporum</i> f.sp. <i>conglutinans</i>, <i>Fusarium roseum</i>, <i>Globisporangium ultimum</i>, <i>Nothopassalora personata</i>, <i>Puccinia menthae</i>, <i>Septoria glycines</i>, <i>Stigmia carpophila</i>, and <i>Wilsoniana occidentalis</i>) were excluded from model validation and pathogen sampling bias analyses, due to an apparent lack of observational records.
Reproducibility	The study did not use experiments, but collated and analysed preexisting available data. Therefore, no measures to ensure reproducibility were implemented. However, all data utilised in this study are either provided, freely available from the relevant referenced literature/sources, or available from CABI (upon request), to reproduce results reported here. See Data Availability statement for further details.

Randomization

No randomization was performed.

Blinding

This was not an experimental study, hence blinding was not necessary.

Did the study involve field work?

☐ Yes☒ No

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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