

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 [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- An indication of 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 statistics 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
- Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

Survey data was collected using the online survey builder provided by www.123formbuilder.com (commercial). Survey data were collated in a Google Sheet that was only accessible to the author team.

Data analysis

Data cleaning was done in Microsoft Excel 2013 (commercial). Analysis was done in R v3.4 and SYSTAT 13 (commercial). All maps were made in ArcGIS 10.5 (commercial). All graphs were made in R v3.4.

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/reviewers upon request. 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

The anonymised data that support the findings of this study are available from the corresponding author.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Behavioural & social sciences study design

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

Study description	We designed an online survey for crop health experts in order to obtain expert assessments of crop losses for five major crops across the world. We cleaned and standardized the survey responses, associated the responses with additional variables based on their geographic location and characterized each reported pathogen or pest. We used contingency tables and chi-squared tests to examine and interpret patterns of association, for example, to assess the association between loss magnitude and climate. Correspondence analyses provided graphical summaries of these associations. Crop losses were estimated globally and for eight food security hotspots, first by individual P&P and then combined.
Research sample	989 expert reports on where a pest and pathogen was reported to occur, based on information from 219 crop health experts in 67 countries.
Sampling strategy	<p>Our data come from an online, worldwide survey of crop health experts carried out between Nov 1 2016 and Jan 31 2017 and hosted at http://globalcrophealth.org. The participants were crop health experts</p> <p>The survey was launched by the International Society for Plant Pathology (ISPP). The invitation to participate in the survey was first sent to the ISPP mailing list (over 2,500 members registered on the ISPP mailing list were thus emailed directly). There are 63 national scientific societies affiliated to the ISPP, which allowed a large coverage over countries producing the five crops addressed in the survey.</p> <p>The survey was announced in the ISPP November 2016 Newsletter which was circulated to the ISPP mailing list and was further circulated to the 63 national or regional ISPP societies (over 26,000 members). This allowed a large coverage over countries producing the five crops addressed in the survey. The survey was also promoted through a number of crop health mailing lists and Nature.</p> <p>We took several steps to reach a large coverage of experts and generate a large number of response rate. We kept track of the total number of responses per crop × country/region combination on a weekly basis and used this to identify combinations where the response rate was lower than we would expect. We used this information to provide monthly updates in the ISPP newsletters in December 2016 and January 2017 that documented the responses so far and encouraged further responses, both in general and by specific crop × country/region combinations where further responses were desirable (based on our weekly tracking of responses). Thus all recipients of the ISPP newsletter received the survey three times over the duration of the survey.</p> <p>We further emailed 87 specific crop health experts in countries where at least one of the five crops was grown extensively and in countries that hosted CGIAR institutes with mandates for the five crops. 30% of the experts emailed individually provided responses to the survey.</p>
Data collection	An online questionnaire was targeted to crop health experts. The survey (http://globalcrophealth.org) was conducted for three months between Nov 1 2016 and Jan 31 2017. Data were collated by Andy Nelson in a set of Google Spreadsheets, one per crop.
Timing	Nov 1 2016 and Jan 31 2017, global scope, though responses were obtained from 67 countries.
Data exclusions	The survey form sometimes duplicated expert submissions. These duplicates were removed from the dataset prior to any analysis. 1142 responses were recorded. When duplicates were removed, the final dataset was 989 records. No further data were excluded.
Non-participation	<p>We cannot assess how many recipients of the ISPP newsletter declined to respond since we have no way of tracking how many of the email addresses in the mailing list are active and how many recipients would be suitable experts for the survey.</p> <p>Of the 87 crop health experts that we specifically targeted by email, 70% did not respond.</p>
Randomization	No experiments were conducted in this research and thus needed no randomisation was required.

Reporting for specific materials, systems and methods

Materials & experimental systems

- | n/a | Included in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Unique biological materials |
| <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 |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |

Methods

- | n/a | Included 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 |