Supporting Online Material for

**Key tropical crops at risk from pollinator biodiversity loss due to climate change and land use**

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**Materials and Methods**

**Biodiversity data for pollinators and non-pollinators**

We used the PREDICTS database (*1*, *2*), and a dataset that identifies species from within PREDICTS likely to pollinate plants (see (*3*) for details), to model the response of local pollinator abundance to the interactive effect of climate change and agricultural land use. PREDICTS is a global database of local biodiversity records, with a hierarchical structure such that each record is nested into a series of levels (‘Source’, ‘Study’, ‘Block’, and ‘Site’ (*2*)). ‘Sources’ represent the individual publications (mostly scientific papers) from which the data were sources. Sources are divided into separate ‘Studies’ if different sampling methods were used or if the data spanned a very large geographical area (e.g., multiple countries). The locations sampled in each Study are divided into ‘Blocks’ if they form distinct spatial clusters. Finally, ‘Sites’ are the locations at which biodiversity was sampled, with the records consisting of a list of named taxa, along with some measurement (most often abundance, sometimes presence or absence, and occasionally an aggregate measure of biodiversity such as species richness). Each record in the PREDICTS database is associated with a land-use type (primary vegetation, mature secondary vegetation, intermediate secondary vegetation, young secondary vegetation, plantation, pasture, cropland, and urban) and land-use intensity (high, low and minimal), meaning change in biodiversity can be modelled as a function of anthropogenic land-use disturbance (e.g. (*3*, *4*)). ‘Primary vegetation’ describes natural habitat with no record of having been destroyed in the past. ‘Secondary vegetation’ is natural habitat that is known to have been destroyed but is now recovering towards its natural state, divided into a ‘young’, ‘intermediate’ or ‘mature’ stage of recovery depending how much the natural structure of the vegetation has been regained. Three agricultural type are recognised within the PREDICTS database: ‘plantation forest’ for areas of woody crops, ‘cropland’ for herbaceous crops, and ‘pasture’ for areas of livestock grazing. Finally, ‘urban’ areas are those occupied by human settlements or areas of civic amenity. Each land-use type can be categorised according to the land-use intensity, with criteria based on, for example, selective logging and bushmeat hunting in natural (primary or secondary) habitats, and crop diversity, livestock density, chemical inputs and degree of mechanization in agricultural areas. Full details of the scheme for classifying land use and land-use intensity can be found in (*1*). We focus in this study on the PREDICTS data for insect species.

We identified pollinating species in PREDICTS through a semi-automatic approach combining text-mining, manual inspection, and expert consultation. We first used the stemmed term ‘pollinat\*’ on Scopus to return all abstracts for English language primary research papers. From this set of abstracts, we then used a set of name-entity recognition algorithms to extract all animal species Latin binomial names (*5*). For each animal genus returned by the name-entity recognition algorithm, we then read the corresponding abstracts searching for evidence confirming that genus as pollinating. We considered a pollinator to be an animal for which there is experimental evidence confirming pollination, evidence of pollen carrying, evidence of nectar/pollen feeding, or evidence of non-destructive/non-predatory flower visitation. Given that the set of pollinators identified from Scopus abstracts could only ever be a sample, we then additionally searched for evidence of pollination across higher-level taxonomic groups (*3*). Specifically, from the confirmed pollinators in our original list of genera, we identified all unique families with at least one pollinator. For each family, we assessed the breadth of evidence for pollination through consulting the abstracts and taxonomic group reference books. For any family with evidence of pollination across multiple branches of that family, and no evidence of any species definitely not pollinating, we assumed that the whole family is pollinating. After compiling our list of pollinators from automated text-analysis and manual searching, we then consulted a group of 7 expert pollination ecologists, and removed or added any groups at their suggestion (*3*).

Our data-preparation process resulted in two datasets with different subsets of the original set of species in PREDICTS: pollinating insects, and non-pollinating insects. Our set of non-pollinating species are not strictly a set of confirmed non-pollinators, rather a set of species not confirmed as being pollinators. For each of the two data subsets, we calculated site-level total abundance (the sum of sampled abundances for all species recorded at a site). Where sampling effort varied among the sites within a single study (8.9% of records in our pollinating insects dataset, and 9.6% 1dp in the non-pollinating insects dataset), we divided the abundance values for each measurement by the relative sampling effort at each site, rescaled to a maximum value of 1 within each study, as in (*6*).

**Climate change estimates**

We used the Climatic Research Unit Time Series (CRU TS) Version 4.03 (*7*) mean daily temperature estimates per month, at a spatial resolution of 0.5°, to calculate a global standardised temperature anomaly (STA) for the year of each PREDICTS sample, using an approach developed previously (*8*). Although extreme temperatures have been shown to predict contemporary changes in biodiversity better than mean temperatures (*9*), we used the latter here since they provide a measure of the central tendency of change in temperature per month. Mean temperatures have been used in a similar manner for a number of other studies on insect thermal tolerance (e.g. (*10*, *11*)), in which they have been shown to be informative of insect biodiversity change. To calculate our standardised temperature anomaly, we first calculated a 30-year baseline temperature for the years 1901-1930 as the mean temperature across all 360 monthly mean daily temperatures for each cell. For each PREDICTS site, we then calculated contemporary temperature as the mean temperature across the 12 months up until the last month of species sampling at the site. We then calculated a climate anomaly for each site as the difference between the baseline and contemporary average temperatures. We then standardised this climate anomaly by dividing the anomaly at each site by the standard deviation across the 360 monthly mean daily temperatures in the baseline period. A standardised temperature anomaly of less than 0 indicates a region that has cooled since the baseline. A value between 0 and 1 indicates a region that has warmed, but current average temperature remains within 1 standard deviation of the variability in baseline temperatures. A value greater than 1 indicates a region in which average warming is 1 standard deviation greater than the variability in the baseline (i.e., it is now experiencing high novel temperatures). We also calculated a global map of the standardised temperature anomaly for the period 2004-2006, also using the CRU TS Version 4.03 (Figure S8). The period 2004-2006 coincides with the midpoint of sampling in the PREDICTS database (*2*).

**Biodiversity responses**

To model the interactive effects of land use and recent climate change on pollinator abundance, we built linear mixed-effects models predicting total abundance as a function of land-use type (primary vegetation and cropland), standardised temperature anomaly, and their interaction. We did not use a generalised linear model with Poisson errors because most recorded measurements are non-integer values. A previous study of land-use impacts using the same biodiversity data showed that very similar results are obtained regardless of the error structure in the models (*3*). We focussed on primary vegetation and cropland given our interest in assessing how pollinator biodiversity change may impact crop production that depends on animal pollination. We didn’t divide cropland sites by their intensity of use, because there are relatively few data for pollinator species compared to insects as a whole, and because a previous study showed that the distinction between land-use types is more important than between levels of agricultural intensity for understanding the impact of land-use-climate interactions (*8*), for both cropland and primary vegetation we grouped together all levels of intensity. We loge-transformed all total abundance values (adding one because of zero values) to normalise the model residuals. Due to the nested nature of the database (*2*), we considered a random intercept of study identity to account for variation in sampling methods, sampling effort, and broad geographical differences among studies, and a random intercept of spatial block within study to account for the spatial structuring of sites. Models that included this random-effects structure had a lower AIC value than models with a simpler combination of the same random effects (i.e. study identity only).

**Potential future risk to crop pollination**

We used our model of insect pollinator abundance, combined with information on crop dependence on animal pollination and projections of future climatic changes, to predict geographic and temporal patterns of potential risk to crop pollination. We focus on three forms of risk: total production risk, proportional production risk, and import risk. Production risk is a measure of the total crop production potentially at risk of pollination shortfalls. Proportional production risk is a measure of the crop production at risk as a proportion of the total production for a given cell, crop, or country. Import risk is a measure of risk to imports of crops dependent on animal pollination via international trade. We focus in this study on insects, which make a particularly large contribution to crop pollination (*12*).

Our projections are based on the assumption that a projected loss in pollinator abundance will be associated with an increased risk to crop production from loss of pollination services. There is strong evidence linking insect abundance with crop pollination (*13*, *14*). Furthermore, even if pollinator losses don’t impact crop yields directly, they may reduce the resilience of crop production in the face of other environmental changes (*15*). Nevertheless, there are three core areas of uncertainty. First, we do not know if there is a mechanistic link between the interactive effects of land-use and climate change on pollinator abundance. We reason that a significant interactive effect is at least likely, however, given prior localised studies demonstrating a synergistic effect of climate change and anthropogenic land use in insects (*16*, *17*). Second, we do not account for changes in the distribution of crops over time, which may occur because of direct effects of climate change, indirect feedbacks caused by pollinator losses, or other environmental or socio-economic factors. Therefore, our projections should be seen as estimates of the risk posed to crops where they are currently grown, which is still an important consideration for food security and livelihoods. Third, it remains unclear exactly how local abundance change will impact crop pollination, how abundance change will interact with richness change, and in turn how crop pollination will relate to yield change. We account for this uncertainty as much as possible, by testing alternative possible relationships between pollinator abundance and production risk (see below for details). Given the uncertainties, our projections should be interpreted as a measure of relative risk to crop production, rather than projections of absolute yield loss.

We first used the Earthstat global maps of the production of individual crops (*18*), in combination with the animal pollination dependencies reported in (*12*), to build a map of global crop production dependent on animal pollination for the year 2000. For each crop represented in Earthstat, we adjusted total production according to the proportional dependence on animal pollination as reported in (*12*) (essential = 0.95; great = 0.65; modest/great = 0.45; modest = 0.25; little = 0.05; no increase = 0). Some crop groups in Earthstat are represented by multiple individual crops in (*12*). For these groups, we calculated the mean dependence on animal pollination. We then summed the dependence-adjusted production values for all crops (*Nc*) grown in each cell as:

where *PollinationProdi* is the total crop production in metric tonnes that is dependent on animal pollination in cell *i*, *Prodci* is production the total production of crop group *c* in cell *i*,and *dc* is the proportional dependence of crop *c* on animal pollination (see Figure S11 for the total production dependent on animal pollination for the top 20 crops, and Figure S8 for the global distribution of all animal-pollination-dependent production). We also calculated the total production of all crops in any given cell (regardless of dependence on animal pollination) as:

where *TotalProdi* is the total production of all crops in cell *i*. Although our study was focused on insects, we considered all crop groups with maps in Earthstat, since none of these crop groups relies exclusively on pollination by vertebrates of non-insect invertebrates.

To project future risk to crop production, we used the ISIMIP (Inter-Sectoral Impact Model Intercomparison Project) predicted temperature anomalies from (*19*) to calculate the standardised temperature anomaly for each year between 2016 and 2050, under three RCP (Representative Concentration Pathway) scenarios (2.6, 6.0 and 8.5; in the main text, we present results only for RCPs 2.6 and 6.0), using an ensemble mean of the general circulation climate models GFDL, HadGEM2, IPSL, and MIROC5. RCP 8.5 represents a worst-case high-emissions scenario, 6.0 a pathway with some degree of mitigation, and 2.6 a pathway with significant reductions in emissions (*20*). RCP 2.6 has a multi-model-median predicted increase of 1.5°C in global average temperatures by 2100 compared to the pre-industrial climate, RCP 6.0 has a predicted increase of 3°C, and RCP 8.5 has a predicted increase of 4.9°C (*21*). ISIMIP temperature anomalies were added to average monthly temperatures across a historical baseline period of 1979-2013. We used the annual standardised temperature anomaly estimates to calculate a 3-year rolling average to smooth change in risk over time. For each 3-year projection window, insect pollinator abundance on cropland was predicted according to the model in Figure 1 (left panel) for all cells containing crop production dependent on animal pollination. These abundance values were then expressed as the proportional loss of abundance compared to the abundance expected on croplands that have experienced no warming (i.e. standardised temperature anomaly of 0) as:

where *lti* is projected abundance loss for (3-year) time period *t* and cell *i*, *ati*is model-estimated abundance on cropland in cell *i* under projected warming for time-period *t*, and *a0*ismodel-estimated abundance on cropland in cell *i* under no warming (standardised temperature anomaly = 0). In each cell, animal-pollination-dependent crop production was then adjusted for the percentage reduction in abundance at that time step, before summing production at risk for all cells (*Ni*) as:

where *ProdRiskt* is the total crop production at risk in time-period *t*.

We carried out a set of robustness checks for our total production risk projections. First, we checked for the influence of single climate models on our projections. Specifically, we calculated one projection as the average of all models for that RCP scenario, and a set of additional jack-knifed projections, dropping each climate model in turn (Figure S4). Second, for the ensemble average of all climate models, and for each of RCPs 2.6, 6.0, and 8.5, we checked the extent to which extrapolating abundance loss beyond the lowest fitted abundance value in the models of land use and climate change impacts (i.e., the greatest model-estimated abundance loss) affected our projections (Figure S5). Third, we checked the extent to which our projections were robust to differences in the data quality in the EarthStat crop production maps, by iteratively filtering the production estimates to include only higher-quality estimates (Figure S6). EarthStat crop production data are broken down into 5 quality levels (1, 0.75, 0.5, 0.25, and 0), from highest to lowest data quality: 1, County level census data; 0.75 state level census data; 0.5, census interpolated data, from within 2 degrees latitude/longitude; 0.25, country level census data; and 0, missing census data. Fourth, we used two different approaches to test whether our projections are influenced by considering the fact that insects are only active in some months of each year (in our main projections, we included all months of the year in the calculation of the standardised temperature anomaly). The first approach followed the methodology of (*8*), defining active months as those that have an average temperature of at least 10°C in the 5 years prior to each PREDICTS sample, and then calculating the standardised temperature anomaly using only those months. The second approach defined active months based on temperatures in the baseline period, i.e., calculating the standardised temperature anomaly based only on months for which the average temperature between 1901 and 1930 was at least 10°C. For both of these approaches we plotted the mean total abundance change (for just the pollinating insects) on cropland relative to sites that have not changed, for a set of potential scenarios (i.e. Figure S3). Fifth, we built additional models to test whether abundance responses to the interactive effects of climate change and land use differed among taxonomic groups. In the first approach we built a separate model for each of the main pollinating insect orders (Figure S1), and in the second we built a series of models dropping each pollinating insect family in turn (Figure S2).

Given the uncertainty in the relationship between pollinator abundance and crop production, we tested a series of potential relationships, including linear, or with some form of convex or concave relationship. In other words, it could be that crop production declines slowly until a large proportion of pollinators have been lost (convex relationships). Alternatively, crop production may decrease rapidly with even small reductions in pollinator abundance (concave relationships). We used two functions describing convex relationships as:

and concave relationships as:

where z = a constant describing the convexity or concavity of the relationship between local pollinator abundance loss and risk of crop production loss. For both convex and concave relationships, we considered 4 values of *z* (4, 8, 16, and 32), describing increasingly steep convex or concave relationships. We assumed that all lines meet at the extreme values of pollinator abundance loss (i.e., no risk to crop production where pollinator abundance is equal to or higher than in the natural baseline condition, and a proportional risk of 1 where all pollinator abundance is lost). In the main text we present only the linear and convex relationships, since these seem more likely to describe the true relationships (*22*).

To identify geographic regions in which a high proportion of crop production could be at risk, we expressed pollination risk as a proportion of the total production of all crops within each cell as:

where *PropRiskti* is the fraction of all crop production in cell *i* and time period *t* at risk from pollinator biodiversity losses. A value of 1 therefore indicates a hypothetical situation in which all of the crop production in that cell is dependent on animal pollination, and predicted insect pollinator abundance loss is 100% (i.e., one would expect a very high risk of crop production loss from pollination shortfalls).

To investigate which countries and regions of the world might expect the greatest crop pollination risk, we intersected our mapped estimates of production risk with a global map of country borders (*23*). For each country, we calculated the median risk in the year 2050 across grid cells (‘overall risk’), and the total change between the start (2016) and end (2050) of the series (‘change in risk’).

To estimate the potential financial risk associated with pollinator biodiversity loss, we estimated, for each country, the total value of pollination-dependent crop production per country. In the main text we present this total value, which we divided by GDP in Figure S12. We calculated the total value of crop production dependent on animal pollination by multiplying the total animal-pollination-dependent production for each crop in each country by the estimated per-tonne value of each crop (*24*), and then summing these values across all crops grown in a given country. Per-tonne values for each crop were estimated by calculating the mean producer price of each crop in each country for the years 2015-2019 (US$ in 2015-2019 values) using FAO estimates (*24*). For each crop, we then took the median value across countries as a global estimate of the per-tonne value of each crop. These values represent estimations of the price paid to producers at the point of initial sale (*24*). We retrieved estimates of each country’s GDP in millions of US$, from the package ‘rworldmap’ (variable name ‘GDP\_MD\_EST’) (*23*).

As a last step, we used our measure of local production risk to calculate a measure of overall import risk and change in import risk. We used estimates of the quantity of production (in metric tonnes) dependent on animal pollination (accounting for the fractional dependence of each crop on animal pollination) imported by each country between 2001 and 2015, broken down by country of origin (*25*). The data used here differs from that of (*25*) in that it does not include a measure of average cropland isolation.

To convert the estimates of import flow into a measure of import risk, we reasoned that each unit of production dependent on animal pollination produced in a given country can be attributed to an importer according to the proportion it imports from that country. To calculate this import risk for 2050, we multiplied the import flow of crops dependent on animal pollination from each producing country (as a proportion of the total imported from all producers) by the total production at risk across all cells in the exporting country in 2050. For each importer, we summed this value across all exporters. Import risk for a given importer country (*I*) at a given time (*ImportRisktI)* is therefore calculated as

where *PE* is the proportional flow between country *E* and *I* and *NE* is the total number of exporters to country *I.* So for example, if one importer receives 20% of one countries exports, 20% of another, and 10% of a third, and each of those countries has a local production risk at time *t* of 100 tonnes, 200 tonnes, and 500 tonnes, *ImportRisktI* will be

We defined this value as the overall import risk, which we then divided by total population size of each country to give a per-capita estimate. All analyses were carried out in R Version 4.0.5.

**Supplementary Figures**

Chart, line chart

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**Figure S1**. Response of the total abundance of individual orders of pollinating insects to standardised temperature anomaly on primary vegetation and cropland. Each panel represents a linear mixed-effects model for one order (Coleoptera, Diptera, Hymenoptera, and Lepidoptera). Coloured lines represent mean fitted estimates for each interaction, and shading 95% confidence intervals around the mean: green = primary vegetation; orange = cropland. Note that abundance is plotted on a loge scale.

Chart, line chart

Description automatically generated

**Figure S2**. Response of pollinating insect total abundance to the standardised temperature anomaly on cropland, jack-knifed by dropping each taxonomic family in turn. Predictions were derived from a linear mixed-effects model of total abundance as a function of land use in interaction with the standardised temperature anomaly. The dark orange line represents the trend for all insect families combined, and each translucent line shows the modelled relationship with one family excluded. Note that abundance is plotted on a loge scale

Chart, scatter chart

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**Figure S3**. Response of pollinating insect total abundance to standardised temperature anomaly on cropland for a set of active season thresholds, calculated using two approaches: 1) Defining active months as any months in the baseline that have a temperature of at least 10°C, and then calculating the STA for only these months in the period 5 years previous to each PREDICTS site (i.e. ‘Baseline’ calculation, orange dots); and 2) defining active months as any months 5 years previous to each PREDICTS site that have a temperature of at least 10°C, and then calculating the STA for only this set of months in the baseline, as in the approach used in (*8*)) (i.e. ‘PREDICTS site’ calculation, black dots). Each point represents the percentage change in insect pollinator total abundance on cropland sites, between a standardised temperature anomaly of 0 and 1. The red dashed line represents change predicted on cropland with no active season adjustment, as in all main text figures.

Graphical user interface

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**Figure S4.** Sensitivity of projected changes in total production risk to dropping temperature projections from individual climate models. Shown are projections for three different RCP climate scenarios (8.5, 6.0, and 2.6), assuming a linear relationship between abundance loss and production risk, either as the average across all general circulation climate models, or dropping each climate model in turn (GFDL, HadGEM2, IPSL, and MIROC5).

Chart

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**Figure S5**. Sensitivity of projections of risk to crop production from extrapolating the underlying models beyond the range of sampled values of recent climate change. Shown are projected changes in total production risk under three RCP scenarios (8.5, 6.0, and 2.6), using average projected temperature changes from four climate models (GFDL, HadHEM2, IPSL, and MIROC5), assuming a linear relationship between abundance loss and production risk. Circles represent a projection in which abundance loss is extrapolated beyond the maximum standardised temperature anomaly (STA) (as in Figure 2 in the main text), whereas triangles represent a projection in which abundance loss is capped at the maximum sampled STA value of 1.61. Colours indicate the percentage of cells at each time step that have been extrapolated beyond the maximum STA in the non-capped projections.

Chart, line chart

Description automatically generated

**Figure S6**. Sensitivity of the projected index of relative risk to variation in the quality of mapped estimates of crop production. Projections are shown for the RCP 6.0 climate scenario, with temperature projections based on the average of four climate models (GFDL, HadHEM2, IPSL, and MIROC5), assuming a linear relationship between abundance loss and production risk. Colours represent projections based on crop-production estimates filtered according to different levels of reported data quality (*18*): 1: county-level census data; 0.75: state-level census data; 0.5: regional interpolation from census data; 0.25: country-level census data; 0: no census data.

A picture containing calendar

Description automatically generated

**Figure S7**. Sensitivity of projected crop production risk to the assumed relationship between pollinator abundance and production risk. Assumed relationships (shown in A) were linear (slope parameter = 2), as well as convex (dashed lines) and concave (dotted lines) relationships of increasing steepness (slope parameters between 4 and 32). Shown are projections of both the relative index of risk (B-D) and total production risk (E-G), for three RCP climate scenarios (2.6: B, E; 6.0: C, F; and 8.5: D, G).

A picture containing chart

Description automatically generated**Figure S8**. Spatial estimates of crop production that depends on animal pollination for the year 2000 (A), and the standardised temperature anomaly averaged for the years 2004 to 2006 (B). Both maps show only grid cells in which there is some crop production dependent on animal pollination. Animal-pollination-dependent production (A) is calculated as estimated total crop production (*18*), adjusted for the proportional dependence on animal pollination (*12*). The standardised temperature anomaly is the change in mean of monthly mean daily temperatures between a baseline period (1901-1930) and 2004-2006, divided by the standard deviation across monthly mean daily temperatures across the 30-year baseline period.

Graphical user interface, diagram, application

Description automatically generated

**Figure S9**. Sensitivity of the spatial distribution of proportional production risk to variation in the assumed relationship between pollinator abundance and production risk. Projections are shown for the RCP 6.0 climate scenario in 2050, based on temperature projections from four climate models (GFDL, HadGEM2, IPSL, and MIROC5), and for four possible relationships between pollinator abundance and production risk: linear (slope parameter = 2), and increasingly steep convex relationships (slope parameters of 4 to 32).

A map of the world

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**Figure S10**. Variation in proportional production risk according to the assumed relationship between pollinator abundance and production risk. Projections are for the RCP 6.0 climate scenario in 2050, using temperature estimates averaged across four climate models (GFDL, HadGEM2, IPSL, and MIROC5). Variation is shown as the standard deviation among proportional risk estimates from 5 possible relationships between pollinator abundance and crop production risk: linear, and increasingly steep convex relationships (as shown in Figure S9). The inset shows the distribution of cell-level standard deviation across all cells in the map.

**Chart, bar chart, histogram

Description automatically generated**Figure S11. Total production dependent on animal pollination for the 20 crops with the highest values. Total production values are for the year 2000, taken from EarthStat (*18*). Animal-pollination-dependent production is estimated by multiplying total estimated production volume (in tonnes) for each crop by the proportional dependence on animal pollination (*12*). For any crop group in EarthStat represented by multiple estimated pollination dependencies, we took the dependence to be the mean across the individual crops.

Graphical user interface

Description automatically generated with medium confidence

**Figure S12.** Proportional production risk at the level of each country in 2050 under the RCP 6.0 climate scenario, assuming a linear relationship between insect pollinator abundance loss and production loss for crops dependent on animal pollination. Here overall risk is the median of proportional production risk for all cells of that country, whilst change in risk is the difference in overall risk between the start and the end of the series. Point size here represents the total value of the pollination dependent production in that country as a proportion of GDP, calculated from the product of total pollination dependent production per annum according to (*18*) and (*12*) and the per tonne value of each crop (*24*). Colour represents the geographic region of each country, distinguishing between regions within a panel: Light blue, Africa; orange, Asia; black, Australia; green, Europe; dark blue, North America; yellow, Latin America; grey, the Caribbean.

A picture containing diagram

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**Figure S13.** Proportional production risk for the 20 crops with the highest total pollination dependent production globally (see Figure S11 for the top 20 crops). Overall risk here is the median of proportional production risk for all spatial cells in which that crop appears, whilst change in risk is the difference in overall risk between the start and the end of the series. Point size represents an estimation of the per tonne value of each crop for the years 2015-2019, calculated from (*24*).

**Map

Description automatically generatedFigure S14.** Spatial distribution of the sites in the PREDICTS database for both pollinating (A and C) and non-pollinating insects (B and D). Panel (A) and (B) are for the distribution of sites among primary vegetation and cropland sites in PREDICTS, whereas (C) and (D) are for the standardised temperature anomaly for each site.

**Tables**

**Table S1.** The total number of ‘cropland’ and primary vegetation sites for pollinating and likely non-pollinating insects in the PREDICTS database.

|  |  |  |
| --- | --- | --- |
| **Land-use type** | **Pollinator status** | **N (sites)** |
| Primary vegetation | Pollinators | 1166 |
| Cropland | Pollinators | 1507 |
| Primary vegetation | Likely non-pollinators | 1747 |
| Cropland | Likely non-pollinators | 922 |

**Table S2.** The total number of species in the PREDICTS database for pollinating and likely non-pollinating insects, on the land-use types ‘cropland’ and ‘primary vegetation’.

|  |  |  |
| --- | --- | --- |
| **Order** | **Pollinator status** | **N (species)** |
| Lepidoptera | Pollinators | 2018 |
| Hymenoptera | Pollinators | 815 |
| Coleoptera | Pollinators | 152 |
| Diptera | Pollinators | 94 |
| Thysanoptera | Pollinators | 1 |
| Lepidoptera | Likely non-pollinators | 310 |
| Hymenoptera | Likely non-pollinators | 475 |
| Coleoptera | Likely non-pollinators | 1674 |
| Diptera | Likely non-pollinators | 317 |
| Thysanoptera | Likely non-pollinators | 4 |
| Hemiptera | Likely non-pollinators | 120 |
| Odonata | Likely non-pollinators | 80 |
| Orthoptera | Likely non-pollinators | 71 |
| Isoptera | Likely non-pollinators | 33 |
| Psocodea | Likely non-pollinators | 12 |
| Archaeognatha | Likely non-pollinators | 2 |
| Blattodea | Likely non-pollinators | 2 |
| Dermaptera | Likely non-pollinators | 2 |
| Neuroptera | Likely non-pollinators | 1 |
| Trichoptera | Likely non-pollinators | 1 |

**Table S3.** AIC and R2 values for linear mixed-effects models with different random-effects structures fitting loge total abundance as a function of land-use type (cropland and primary vegetation), standardised climate anomaly, and their interaction, for both a pollinating and likely non-pollinating insect species. Random-effects structures considered were either study identity, or study identity and spatial block nested within study.

|  |  |  |  |
| --- | --- | --- | --- |
| **Model** | **Pollinator status** | **AIC** | **R2** |
| log(Total\_abundance) ~ standard\_anom \* land\_use + (1|SS) | Pollinators | 7171.79 | 0.017 |
| log(Total\_abundance) ~ standard\_anom \* land\_use + (1|SS) + (1|SSB) | Pollinators | 7042.814 | 0.023 |
| log(Total\_abundance) ~ standard\_anom \* land\_use + (1|SS) | Likely non-pollinators | 6379.434 | 0.017 |
| log(Total\_abundance) ~ standard\_anom \* land\_use + (1|SS) + (1|SSB) | Likely non- pollinators | 6300.413 | 0.018 |

**Table S4.** Proportional dependence on animal pollination for the crops/crop groups mapped in EarthStat (*18*). For each crop group, we show the average and standard error of proportional pollination dependence estimates (*12*) among individual crops. Standard errors are shown as ‘NA’ where there was a one-to-one match between crops in EarthStat and crops with estimated dependence on animal pollination. ‘Monfreda crop group’ is the exact string used in (*18*) for each crop raster layer.

|  |  |  |
| --- | --- | --- |
| **Monfreda crop group** | **Mean pollination dependence** | **Standard error** |
| brazil | 0.95 | NA |
| cocoa | 0.95 | NA |
| kiwi | 0.95 | NA |
| melonetc | 0.95 | NA |
| nutnes | 0.95 | NA |
| pumpkinetc | 0.95 | NA |
| vanilla | 0.95 | NA |
| watermelon | 0.95 | NA |
| almond | 0.65 | NA |
| aniseetc | 0.65 | 0 |
| apple | 0.65 | NA |
| apricot | 0.65 | NA |
| avocado | 0.65 | NA |
| blueberry | 0.65 | NA |
| buckwheat | 0.65 | NA |
| cashew | 0.65 | NA |
| cashewapple | 0.65 | NA |
| cherry | 0.65 | 0 |
| cranberry | 0.65 | NA |
| cucumberetc | 0.65 | NA |
| mango | 0.65 | NA |
| nutmeg | 0.65 | NA |
| peachetc | 0.65 | NA |
| pear | 0.65 | NA |
| plum | 0.65 | NA |
| rasberry | 0.65 | NA |
| berrynes | 0.616667 | 0.202759 |
| tropicalnes | 0.531818 | 0.111043 |
| fruitnes | 0.51 | 0.16 |
| coffee | 0.45 | NA |
| spicenes | 0.45 | 0.2 |
| oilseednes | 0.316667 | 0.176383 |
| broadbean | 0.25 | 0 |
| chestnut | 0.25 | NA |
| coconut | 0.25 | NA |
| currant | 0.25 | NA |
| eggplant | 0.25 | NA |
| fig | 0.25 | NA |
| mustard | 0.25 | NA |
| oilseedfor | 0.25 | NA |
| okra | 0.25 | NA |
| rapeseed | 0.25 | NA |
| sesame | 0.25 | NA |
| soybean | 0.25 | NA |
| stonefruitnes | 0.25 | NA |
| strawberry | 0.25 | NA |
| sunflower | 0.25 | NA |
| bean | 0.15 | 0.1 |
| chilleetc | 0.05 | NA |
| citrusnes | 0.05 | NA |
| greenbroadbean | 0.05 | NA |
| groundnut | 0.05 | NA |
| lemonlime | 0.05 | NA |
| oilpalm | 0.05 | NA |
| papaya | 0.05 | NA |
| pea | 0.05 | 0 |
| persimmon | 0.05 | NA |
| pigeonpea | 0.05 | NA |
| safflower | 0.05 | NA |
| tomato | 0.05 | NA |
| chickpea | 0 | NA |
| grape | 0 | NA |
| greenpea | 0 | NA |
| lentil | 0 | NA |
| olive | 0 | NA |
| pepper | 0 | NA |
| quinoa | 0 | NA |

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