Supporting Online Material for

**Worldwide vulnerability of local pollinator abundance and crop-pollination to land use and climate change**

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**Materials and Methods**

**Pollinator dataset construction**

We used the PREDICTs database, and a set of likely pollinating species identified in PREDICTS (see Millard et al 2021 for a detailed background on the development of this PREDICTS database subset), 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 according to a series of levels (i.e. ‘source’, ‘study’, ‘block’, and ‘site’; see Millard et al 2021 Supplementary Figure 14, and Hudson et al., 2017). Each record in PREDICTS 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 predicted as a function of anthropogenic land-use disturbance (e.g. Newbold et al., 2015; also see Millard et al 2021 ). Land-use type categories in PREDICTS are defined according to the Representative Concentration Pathway land-use estimates (Hurtt et al., 2011), plus plantation and a gradation of stages according to age within secondary vegetation (Hudson et al., 2014). Land-use intensity for each land-use type is defined according to a series of variables, such as fertiliser and pesticide application, mechanisation, and hunting (see Newbold et al., 2015 for more details).

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 (see Millard et al., 2020 for details). 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. Given my set of pollinators identified from Scopus abstracts could only ever be a sample, we then searched for higher-level taxonomic groups, aiming to identify broader groups of animals that we could be confident would pollinate (see Millard et al 2021 for more details). 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 (see Millard et al 2021 for details).

We then built four separate datasets with different subsets of the original set of species in PREDICTS: pollinating vertebrates, non-pollinating vertebrates, 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 pollinators. For each of my four data subsets, we then calculated site-level total abundance (the sum of all species sampled abundances at a site). Sampling effort was accounted for by dividing the abundance values for each measurement by the relative sampling effort among sites within a study, rescaled to a maximum value of 1 in each study, as in (Newbold et al., 2014).

**Climate change data**

We used Climatic Research Unit Time Series (CRU TS) v4.03 (Harris et al., 2020) 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 (Outhwaite et al., 2022). Although extreme temperatures have been shown to predict contemporary changes in biodiversity (Mantyka-Pringle et al., 2011), we used mean temperatures since they provide a measure of the overall 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. Deutsch et al., 2008; Johansson et al., 2020). To calculate our standardised temperature anomaly, we first calculated a 30-year baseline temperature for the years 1901-1930 as the grand mean temperature over all 360 monthly mean daily temperatures for each cell. For each PREDICTS site, we then extracted the sample end date (i.e. the last date at which that measurement was taken) for the measurements at each site, and then for the month of that end date and the 11 months previously we calculated the grand mean temperature over all monthly mean daily temperatures for that sample. We then calculated a climate anomaly for each site as the difference between the 30-year baseline mean and the mean annual temperature at the time of the sample. We then standardised this climate anomaly by dividing the anomaly at each site by the standard deviation of the baseline, calculated as the standard deviation across monthly mean daily temperatures for the same 30-year 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). Again, using CRU TS v4.03, we also calculated a global standardised temperature anomaly independent of PREDICTS sites (for an average of the 36 monthly mean temperatures in the period 2004-2006), which we mapped globally for context (Figure S7). We chose the period 2004-2006 to coincide with the temporal distribution of most records in the PREDICTS database (Hudson et al., 2017).

**Interactive effects of land-use and climate change on pollinator biodiversity**

To model the effects of land-use and 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 (also see Millard et al 2021, showing that log-linear and negative binomial models for land use intensity yielded similar results). We focussed on primary vegetation and cropland given my interest in the interactive effects of land-use and climate change between natural and anthropogenic land. We chose primary vegetation since it best represents natural vegetation, and cropland since it is both an anthropogenic land-use type and most relevant to crop production that depends on animal pollination. Since the interactive effect of land-use and climate change is likely greater between natural and anthropogenic land than among levels of intensity within a land-use type (Outhwaite et al., 2022), 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 (Hudson et al., 2017), we included 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. Random-effects structures were selected to minimise AIC values.

**Potential future risk to crop pollination from land-use and climate change**

Given the importance of insect pollinators to global crop production, we used our model of insect pollinator abundance to predict geographic and temporal patterns of pollination shortfall risk, based on a combination of estimated crop production dependent on animal pollination, and projections of future climate change. 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 that could be at risk of shortfall. 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 pollination dependent production via the international trade. For all measures of risk, we specifically focussed on insect pollinator abundance given that insects make a bigger contribution than vertebrates to global crop pollination (Klein et al., 2007).

Our projections assume that a projected loss in pollinator abundance combined with crop dependence on pollination is a good proxy for risk to crop production. There are three core uncertainties associated with these projections. 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 (Outhwaite et al., 2022; Zaragoza-Trello et al., 2021). Second, we do not account for changes in the distribution of crops from the effects of climate change alone. Third, it remains unclear exactly how local abundance change will impact crop pollination, and in turn how crop pollination will relate to yield change. We attempt to account for this uncertainty by testing multiple pollinator abundance/production relationships, to derive a predictive region within which the ‘true’ risk likely falls. Given these uncertainties however our projections should not be interpreted as absolute projections of yield loss, but rather as a relative measure of crop production risk. Such a measure of global risk does not yet exist, despite its marked importance to policy-makers (IPBES, 2017).

We first used a global dataset of crop production (Monfreda et al., 2008), in combination with the animal pollination dependencies reported in Klein et al (2007), to build a map of global crop production dependent on animal pollination for the year 2000. For each crop in Monfreda et al (2008), we adjusted total production for the pollination dependence ratios reported in Klein et al (2007) (essential, 0.95; great, 0.65; modest/great, 0.45; modest, 0.25; little, 0.05; no increase, 0). Given some Monfreda crops are represented by multiple crops in Klein et al (2007), for each Monfreda et al (2008) crop we first calculated the mean pollination dependence ratio among Klein crops. We then adjusted each crop for its pollination dependence and summed dependence-adjusted production for all crops at each cell as

where *PollinationProd* = animal pollination dependent crop production, *Prod* = crop production, *c* = Monfreda crop category, *d* = average animal pollination dependence ratio, and *i* = a given cell (see Figure S1 for the top 20 crops by total pollination dependent production, and Figure S7 for the global distribution of all pollination dependent production). We also calculated the total production in any given cell (independent of animal pollination dependence) for all crops as

where *TotalProd* = the total crop production of all crops. In any further work, we assumed that the distribution of pollination-dependent production in 2000 will be representative of that in 2050. We also did not exclude pollination-dependent production which relies on either vertebrates or non-insect invertebrates. Although there are some crops recorded in Klein et al (2007) as reliant on either vertebrate or non-insect pollinators, after reconciling these crops with Monfreda et al (2008) there are no crop groups that are exclusively dependent on vertebrates or non-insect invertebrates.

We then used ISIMIP temperature anomalies from Frieler et al (2017) to project potential future change in standardised temperature anomaly under three RCP (Representative Concentration Pathway) scenarios (8.5, 6.0, 2.6; although in the main text we present only RCPs 6.0 and 2.6), using an ensemble mean of the 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 (van Vuuren et al., 2011). ISIMIP temperature anomalies were added onto a historical baseline for the period 1979-2013 (inclusive), calculated as the grand mean over all monthly mean daily CRU temperatures for each cell. For each year, the standardised temperature anomaly was projected across the terrestrial surface of the globe (for the years 2016-2048), using 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 *l* = abundance loss, *t* = each 3-year time window, *aw*= predicted abundance on cropland under projected warming, and *a0*=predicted abundance on cropland under no warming. 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 as

where *ProdRisk* = the total crop production risk (i.e. production risk; Figure 2). 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 (Fig S6). Second, for the average of all climate models at RCP 8.5, we checked the extent to which extrapolating abundance loss beyond the lowest fitted abundance value (i.e. greatest abundance loss) of our PREDICTS models affected my projections (Fig S2). Specifically, we projected change in total pollination-dependent crop production at risk when the greatest loss in predicted abundance is capped at the largest fitted value of standardised temperature anomaly (Fig S2). For our projection in which abundance loss is not capped, we also calculated the percentage of cells where abundance loss was extrapolated beyond the maximum fitted value (Fig S2). Third, we checked the extent to which our projections were susceptible to changes in Monfreda et al (2008) crop production data quality, by iteratively filtering for more reliable data and then rerunning our projections at RCP 8.5 (Fig S4). Fourth, we used two different approaches to test the extent to which different active month thresholds for insect may have changed our projections. The first approach followed the methodology of Outhwaite et al (2022), 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 anomaly incorporating only those months. The second approach defined active months at the baseline as those that have an average temperature of at least 10°C in the 30-year period of 1901-1930, and then calculating the anomaly incorporating only those months. For the first of these approaches we plotted both predicted values for the land-use climate change interaction on primary vegetation and cropland (Figure S11), and for the second 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 each of 16 potential scenarios (i.e. Figure S12). Fifth, we built two additional models to test the extent to which change in relation to the interaction of land-use and standardised temperature anomaly differed across taxonomic groups. In the first approach we built a separate model for each of the main pollinating insect order (Figure S5), and in the second we built a model for the average change on cropland jack-knifed for each pollinating family (again just the pollinating insects) (Figure S10).

Given the uncertainty around the potential relationship between pollinator abundance and crop production, we also incorporated an additional step to account for a set of potential relationships between insect pollinator abundance and crop production. We hypothesised that the relationship between pollinator abundance and crop production could be linear (as we have assumed above), or could follow some form of convex or concave relationship. In other words, it could be that a given area of pollination dependent crop production can afford to lose a large proportion of its pollinators before it experiences any reduction in production (convex). Or it could be that crop production falls rapidly with only minimal reductions in pollinator abundance, and then plateaus at a low level of production (concave). Given prior research it seem likely that some convex relationship best represents the interaction between pollinator abundance and crop production (reference), but the steepness of this relationship is unclear. We therefore used two linear functions to convert local pollinator loss into a production loss, for convex relationships as

and for concave relationships as

where z = a constant describing the convexity or concavity of the relationship between local pollinator abundance loss and crop production loss. For both convex and concave relationships we investigated 4 potential scenarios z (4, 8, 16, and 32). A value of 4 has a shallow slope, whereas 32 is either highly convex or concave.

To identify geographic regions in which a high proportion of crop production could be at risk under an intermediate climate scenario (i.e. RCP 6.0), we projected pollination risk for each cell as above (using the average of all four climate models), and then expressed pollination risk as a proportion of the total crop production within each cell for all crops as

where *PropRisk* = the crop production at risk as a proportion of the total crop production within each cell, under a set of different abundance/production scenarios. A value of 1 therefore indicates a hypothetical region in which all of the crop production in that cell is dependent on pollination, and predicted insect pollinator abundance loss is 100% (i.e. one would expect a very high risk of pollination shortfall). We projected this dependence risk for 2050, and then mapped these projections globally. In the main text we present this projection assuming a linear relationship between production and abundance (Figure 3), and in the Supplementary Material for four concave abundance/production relationships (Figure S8), and the associated uncertainty among all four of these projections (Figure S9).

To investigate which countries and regions of the world might expect the greatest crop pollination risk, we then intersected all spatial cells for each year of our projection with a global basemap, and for each spatial cell pulled out its associated country and continent. For each country we then calculated the median risk among all cells (‘overall risk’) and the total change between the start and the end of the series (‘change in risk’), which we plotted against each other for all countries (Figure 3). We repeated this process for each of the top 20 crops by total pollination dependent production, again plotting the overall risk against the change in risk. For each of the top 20 crops by pollination dependent production, we also calculated the proportion of all pollination dependent production determined to be at risk, here under RCP 8.5 under a linear relationship between pollinator abundance and crop production (Figure S3).

For both crops and countries, we also calculated analogues of associated financial risk which we overlaid onto both plots. For each country, we estimated the total value of pollination dependent crop production per country, which we then adjusted for GDP. We calculated the total value of each pollination dependent crop by multiplying the total pollination dependent production for each crop in each country by the per kg value of each crop, and then taking the sum of the value for all crops in that country. We estimated the per kg value of each crop using data from the FAO (reference). Specifically, we took the FAO estimation of total production of each crop in each country for each of the years 2015-2019, and then divided these values by the total value of production of each crop in each country for the same set of years. This process returned an estimated per kg value of production for each crop in a set of countries for each of the years 2015-2019. We then took the mean of all years within each country crop combination, giving us an estimated per kg value of each crop in each country over the period 2015-2019. For each crop, we then took the median value of each crop among countries, giving us a global estimate of the per kg value of each crop. It’s important to note that these values represent estimations of the price paid to producers at the point of initial sale (reference). We retrieved estimates of each country’s GDP from the package ‘rworldmap’ (variable name ‘GDP\_MD\_EST’). For each crop, our measure of financial risk was the per kg value of each crop, calculated as above.

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, both of which we present in the main text (Figure 4). We used the pollination trade flow data released by Da Silva et al (2021) as a measure of the quantity of pollination dependent production imported by each country. Da Silva et al (2021) contains estimates of the quantity of pollination dependent trade imported by each country (in metric tonnes), broken down by the quantity imported from each individual country, for each year between 2001 and 2015. In the first instance we used Da Silva et al (2021) to calculate the total pollination dependent trade imported across all years for each importer-exporter combination. For each importer (‘reporter country’ in Da Silva et al 2021), we then calculated the total pollination dependent trade flowing into that country from all exporters, again for all years. We then divided the total for each individual importer-exporter combination by the total imported for that country across all exporters, and then multiplied this value by 100, giving us the percentage imported for each country from each of its exporters.

To convert our measure of import flow into a measure of import risk, we reasoned that each unit of pollination dependent production produced in a given country can be attributed to an importer according to the proportion it imports from that country. For example, if an importer is dependent on 3 countries for imports, at a proportion of 30%, 50%, and 20%, then any change in import risk should scale as a function of the local production risk aggregated at those same proportions. To calculate this value, at each time step in our model we multiplied the percentage flow for each importer-exporter combination by the local production at risk in that exporter at that time step, and then for each importer summed this value across all its exporters. We defined this value as the overall import risk, which we then adjusted for population size to give a per capita estimate and then converted to a percentile (Figure 4). We calculated our measure of change in import risk by converting the overall import risk at each timestep into a percentage change, converting this into an index starting at a baseline of 1, and then calculating the difference in this value between the start and end of this series (Figure 4). All analyses were carried out in R v4.0.5. All core analyses can be visualised interactively in a Shiny app currently hosted online ([joemillard.shinyapps.io/pollinator\_dependence\_visualisation/](https://joemillard.shinyapps.io/pollinator_dependence_visualisation/)).

**Supplementary FiguresChart, bar chart, histogram

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Fig S1. Total pollination dependent production for the 20 crops with the highest pollination dependent production. Total production values are for the year 2000, taken from Monfreda et al (2008). Pollination dependent production is calculated by multiplying total crop production for each crop by the pollination dependence ratios for that crop, as reported in Klein et al (2007). For any Monfreda crop represented by multiple dependence ratios, I took the pollination dependence to be the mean of the ratios for that crop.

**Chart, histogram

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**Fig S2**. Projected change in total production risk under three RCP scenarios (8.5, 6.0, and 2.6), for the average of four climate models (GFDL, HadHEM2, IPSL, and MIROC5). Here circles represent a projection in which abundance loss is extrapolated beyond the maximum standardised temperature anomaly (STA) (as in Figure 4.3), whereas triangles represent a projection in which abundance loss is capped at an STA of 1.58 (2dp). Colour refers to the percentage of cells at each time step that have been extrapolated beyond the maximum STA in Figure 4.3, which in the projection in which abundance loss is capped (triangles) will always be 0.

Diagram

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**Fig S3.** Change in proportional production risk for each crop, projected under RCP scenario 8.5 from the average of four climate models (GFDL, HadGEM2, IPSL, and MIROC5), for the top 20 crops by total pollination dependent production (ordered by rate of change). For each crop global standardised temperature anomaly was projected for all areas of pollination-dependent cropland to 2050, using the 3-year average approach as described in Figure 4.3. For each value of standardised temperature anomaly, insect pollinator abundance was predicted according to the model in Figure 1. Insect pollinator abundance at each cell at each time step was then expressed as proportional loss compared to cropland that has experienced no warming (i.e. standardised temperature anomaly of 0). Animal pollination-dependent production at each cell for each crop was then adjusted for the predicted proportional loss of insect pollinator abundance, and then summed for all cells at each time step. The sum at each time step was then divided by the total production for that crop and multiplied by 100, giving a percentage of total production at risk.

**Chart, line chart

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**Fig S4**. Change in production risk for the average of four climate models (GFDL, HadHEM2, IPSL, and MIROC5) under RCP 8.5, here adjusted to an index for each of 4 data quality subsets. For each coloured line crop production was subsetted according to four levels of data quality reported in Monfreda et al (2008), before the projection was then rerun: 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. For each simulation here I converted total production risk to an index by calculating the percentage change between each time point, and then calculating the cumulative product of these percentage changes (starting at an initial index of 1).

Chart, diagram

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**Fig S5**. Response of pollinating insect total abundance to standardised temperature anomaly on primary vegetation and cropland (note that abundance is plotted on a loge scale). Each panel represents a linear mixed-effects model for a pollinating insect order (Coleoptera, Diptera, Hymenoptera, and Lepidoptera). Coloured lines represent mean fitted estimates for each interaction, and shading 95% confidence intervals around that prediction: green, primary vegetation; orange, cropland.

Graphical user interface

Description automatically generated**Fig S6.** Projected change in total production risk (ProdRiskt) under three RCP scenarios (8.5, 6.0, and 2.6), either as the average across all climate models, or dropping each climate model in turn. For each year into the future, the standardised temperature anomaly was projected globally for all cells of pollination-dependent production, using a 3-year rolling average. I used data on crop production from the year 2000 (the latest year when such data are available for all crops), therefore assuming that the distribution of the production of these crops does not change. For each annual projection of standardised temperature anomaly, insect pollinator abundance on cropland was predicted according to the model in Figure 4.1 (top left panel), and then expressed as proportional abundance loss compared to cropland that has experienced no warming (i.e. standardised temperature anomaly of 0). In each cell, animal pollination-dependent production was then adjusted for the percentage reduction in abundance at that cell, before summing animal-pollination-dependent production for all cells at each time step. Colours refer to the climate model excluded in that jack-knife projection with the projection for all models shown in black.

A picture containing timeline

Description automatically generated**Fig S7**. Crop production that depends on animal pollination (A), and standardised temperature anomaly (in regions of animal pollination-dependent production; B) for the years 2000 and an average of 2004-2006, respectively. For the temperature anomaly, I show an average for the years 2004-2006 to coincide with the temporal distribution of most records in the PREDICTS database, and therefore the results in Figure 4.1. A) Animal pollination-dependent production is calculated as total crop production, adjusted for the degree of dependence on animal pollination according to Klein et al (2007). B) Standardised temperature anomaly is the change in the grand 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, for the same 30-year baseline period.

Graphical user interface, application, PowerPoint

Description automatically generated**Fig S8**. Cell-level proportional production risk (i.e. PropRisk*ti*) projected under RCP 6.0 to 2050, from the ensemble-average of four climate models (GFDL, HadGEM2, IPSL, and MIROC5) under 5 different pollinator abundance/crop production scenarios (1st linear and the following 4 convex). Global standardised temperature anomaly was projected to 2050 for all areas of animal-pollination-dependent crop production, using the 3-year average approach as described previously. We used crop production data from the year 2000 (the latest year for which such data are available for all crops), therefore assuming that the distribution of the production of these crops does not change. For each value of standardised temperature anomaly, insect pollinator abundance was predicted according to the model in Figure 1, expressed as proportional loss compared to cropland that has experienced no warming (i.e. standardised temperature anomaly of 0). Animal-pollination-dependent production at each cell was then adjusted for the predicted loss of insect pollinator abundance, and then converted to a proportion of the total production at that cell. A slope parameter of 2 refers to a linear relationship between local pollinator abundance and crop production (top left panel), whilst a slope parameter greater than 2 refers to a convex relationship. Increasing the slope parameter between 4 and 32 increases the convexity of the relationship.

A map of the world

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**Fig S9**. Variation in cell-level proportional production risk (i.e. PropRisk*ti*) projected under RCP 6.0 to 2050, from the ensemble-average of four climate models (GFDL, HadGEM2, IPSL, and MIROC5) among 5 different pollinator abundance/crop production scenarios (1 linear and 4 convex; see Figure S8 for each individual risk projection). The colour of each cell in the map refers to the standard deviation of risk among abundance/production scenarios, highlighting regions of high and low uncertainty for our projections. The inset top right panel refers to the distribution of cell-level standard deviation across all cells in the main map, showing that most cells have a standard deviation of less than ~0.1 among abundance/production scenarios.

Chart, line chart

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**Fig S10**. Average response of pollinating insect total abundance to standardised temperature anomaly on cropland (note that abundance is plotted on a loge scale), jack-knifed for each pollinating family. Predictions were derived from a linear mixed-effects model, with each line the mean fitted estimate for that jack-knife. The dark orange line represents the trend for all insect families included, and each faded line represent the average trend with one family excluded.

Chart, surface chart

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**Fig S11**. Response of pollinating and non-pollinating total abundance to standardised temperature anomaly on primary vegetation and cropland (note that abundance is plotted on a loge scale), when the active season threshold is set at each PREDICTS site at a minimum temperature of 10 °C (as in Outhwaite et al., 2022). Each panel represents a linear mixed-effects model for pollinating or non-pollinating insects and vertebrates. Coloured lines represent mean fitted estimates for each interaction, and shading 95% confidence intervals around that prediction: green, primary vegetation; orange, cropland.

Chart, scatter chart

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**Fig S12**. Response of pollinating total abundance to standardised temperature anomaly on cropland, converted to a percentage change from cropland sites that have not warmed, for a set of active season thresholds calculated from the baseline (as opposed the each PREDICTS site as in Outhwaite et al (2022).

Chart

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**Fig S13**. Projected crop pollination risk as both an index and total production risk, for three RCP scenarios under 9 different potential relationships between pollinator abundance reduction and crop production loss. The top left panel represents the shape of each of the 9 potential abundance/production relationships. Dotted lines represent any concave relationship whereas dashed lines represent any convex relationship. The colour of each line represents the steepness of the slope of the relationship, from linear in dark purple to yellow at the highest levels of either convexity or concavity.

**Tables**

**References**