Supporting Online Material for

Parallel Declines in Pollinators and Insect-Pollinated Plants in Britain and the Netherlands


*To whom correspondence should be addressed. E-mail: j.c.biesmeijer@leeds.ac.uk

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Materials and methods

Pollinator diversity calculations

The analyses were based on databases that consist of records: for the purposes of analysis, a single record represents one or more observations of a given species on a given day at a given site. Next, datasets were split to create a pre-1980 and a post-1980 (including 1980) record set. The main reasons for splitting the datasets at 1980 were: (i) that many changes in land use and agriculture happened before 1980 in both Britain and the Netherlands, whereas since 1980 fewer changes seem to have taken place; and (ii) both pre-1980 and post-1980 subsets contained sufficient data for a broad national analysis for both countries, whereas splitting the data earlier would have rendered few landscapes with sufficient pre cut-off date data.

We carried out analyses in 10×10 km cells with:

(i) at least 50 records per period. For the analysis of British cells with data only available on eusocial bees, (containing up to about 20 species), cells with at least 20 records per period were included.

(ii) a records-to-species ratio of at least 1.5 in each of the two time periods.

(iii) a less than 10-fold difference in numbers of records between periods. For bee analyses, this produced a total of 81 cells in Britain and 99 cells in the Netherlands, whereas for hoverfly analyses 157 and 211 cells were included in the two countries respectively. Note that for large parts of Britain and the Netherlands either pre-1980 or post-1980 data or both were insufficient to be included. Such areas include all of Scotland and much of Wales and
Northern England. Extrapolation of our findings to all of Britain should therefore be done with care. We are currently accumulating additional data (through fieldwork) to fill some of these gaps.

Rarefaction analysis is a commonly-used method to estimate species richness within incompletely surveyed biotic communities (S1-3), allowing a comparison of samples of different size. A number of methods have been developed, most of which rely on randomly subsampling from existing records and plotting the accumulation curve of species with increasing sample size. In this study, rarefaction was performed on both pre-1980 and post-1980 sets using the program EstimateS 7.5 (S1,S4) and species richness was compared following Gotelli and Colwell (S3) and Magurran (S1). Rarefaction analysis was chosen because of unequal size of most of the dataset pairs. We used individual-based rarefaction (S3) to assess whether the number of species found in the smaller sample was larger, similar or smaller than the rarefied number of species in the larger sample at the same sample size, i.e. number of individual records. This can be achieved by using the confidence interval around the rarefaction curve, calculated by the EstimateS program using the method of Colwell and colleagues (S2). We used Chi-square tests for homogeneity to assess whether the numbers of cells decreasing and increasing were significantly different for the pre-1980 and post-1980 periods. Results are given in Table S1.

We need to point out caveats related to any comparison of records collected by many different recorders, over long time-spans, using different collecting techniques, and incorporating literature, collection and field data. The bee and hoverfly data used here have not been collected following a standardized sampling scheme, and the pre-1980 recording period shows high supra-annual variability. In addition, collections and literature records may over-represent rare species, whereas field observations may
over-represent species that are easily observed and identified; e.g. some common hoverflies or bumblebees. We know of no method to correct for possible biases of this nature. To limit these problems we concentrated on well-studied 10×10km cells and restricted our bee analyses to eusocial bees or alternatively to solitary bees for cells with unbalanced data for the other bee group (Fig. S1). Honeybees (*Apis mellifera*) were excluded from all analyses, due to their widespread domestication.

**Pollinator species change**

We analyzed shifts in area of occupancy and recording frequency for all bee and hoverfly species in the above-mentioned selected cells. To assess differences in occupancy, we have examined the number of grid cells recorded as gained and lost by each species, and compared that to the number expected given the overall shift in species × cell observations between the two time periods. To assess differences in frequency, we examined the number of records for each species, and compared that to the number expected given the overall shift in records × cell observations between the two time periods. Note that this produces measures of relative change in occurrence and frequency rather than of absolute change; if some species decline in relative terms then other species must increase, but the number of winners and losers need not be the same. Change could not be assessed for many of the rarer species by this method, because expected values are too low.

**Pollinator trait comparisons**

To assess whether shifts in pollinator species imply a functional shift in pollinator traits we compiled a trait database for European bee species (compiler Stuart Roberts as part of the pollinator loss module of the EU- FP6 ALARM-project), and used a
published trait database for European hoverflies, Syrph the Net (S5). We excluded the eusocial bees, bumblebees and honeybees from the analysis because most previous analyses of pollinator loss in the focal region have focussed exclusively on this group and the bumblebees form a specific guild of bees being all eusocial, polylectic and long-tongued. However, we have added a Table (S2) with trends based on all wild bees. We compared the prevalence of decline and increase among the species with two contrasting states of a number of traits and analyzed 2 × 2 tables using Chi-square test or, if expected values were too low, Fisher exact tests (S6). The following traits were used (see Table 2 in main text):

* Habitat use: narrow or wide. For bees, descriptions of habitat use in the database were recoded into broad habitat types, e.g. grassland, heathland, forest, wetland, anthropogenic. Species were then coded as ‘narrow’ (if they used a single broad habitat type) or ‘wide’ (if they used 2 or more broad habitat types). For hoverflies, we used similar definitions for narrow and wide habitat use based on the broad categories in Syrph the Net (S5).

* Bee tongue length: long or short. This trait refers to the morphological and phylogenetic distinction of bee families (S7) into long-tongued bees (tongues normally longer than 6mm; Apidae and Megachilidae) and short-tongued bees (tongues normally shorter than 5mm; Colletidae, Halictidae, Melittidae, Andrenidae). We did not measure actual sizes of bee tongues.

* Bee flower specificity: oligolectic or polylectic in flower choice. An oligolege uses a single plant species, genus or family for pollen (and nectar) collection, whereas a polylege uses multiple plant families for food.

* Hoverfly larval food: macro-organisms (living plants or animals) or micro-organisms. The Syrph the Net database (S5) provides the following note to the
categorization: “Larval food [is] categorised according to whether it is living animals or plants, or decomposing organic matter. Although the larvae which feed on decomposing organic matter are generally understood to be microphagous, their actual food is uncertain. They are all considered as microphages here, but it is recognised that their status may change following more detailed investigation.”

* Hoverfly adult food: narrow (nectar only) or wider (nectar plus sap or pollen).

* Number of generations per year: univoltine (up to 1 generation per year) or multivoltine (more than 1 generation per year).

* Hoverfly migration: migratory or resident.

**Plant distributional analyses**

We used an index of relative population change recently published for the flora of the British Isles (S8; comparison of the periods 1930-1969 and 1987-1999). For the Netherlands we calculated the difference between frequency classes reported for 1990 and 1940 (S9; for discussion of Dutch plant data see S10).

We compiled a database of reproductive characters (from the Ecological Flora database, ECOFLOR (S11), and from BIOLFLOR (S12)) to investigate whether obligate outcrossing species dependent on insect pollinators have declined more than obligate outcrossing species dependent on abiotic pollination (wind and water) and near-obligate selfers. We limited the analysis to native non-tree species (to exclude range expansion due to recent introduction and tree planting). The databases provided consistent information on breeding system for 70% of the species and on pollen vector for 63% of the species. We classified species as obligate outcrossers if ECOFLOR described a species as obligate outcrossing, or BIOLFLOR classified a species as allogamous for plant species present in just one of the databases; for species present in
both databases, species were regarded as obligate outcrossing if they were defined as such in ECOFLOR and as allogamous, or facultatively allogamous in BIOLFLOR, or if they were defined as normally outcrossing in ECOFLOR and as allogamous in BIOLFLOR. These outcrossers were included as insect-pollinated when either or both databases mentioned insects as the only pollen vector, or when plants were unique to one of the databases and insects alone were mentioned as pollen vectors. All plants mentioned as being wind or water pollinated in at least one of the databases were classified as wind or water pollinated irrespective of whether insect pollen vectors were mentioned as well; the reason being that all these species can be pollinated in the absence of insects. We classified species as predominantly self-pollinating if: (i) they were unique to ECOFLOR and mentioned as “normally self” (the most extreme selfing category mentioned in this database); (ii) they were unique to BIOLFLOR and mentioned as “autogamous”; or (iii) they were mentioned as normally self in ECOFLOR and as autogamous or facultative autogamous in BIOLFLOR. Species with intermediate or conflicting breeding system values in the two datasets were excluded from this analysis, to provide a clearer contrast.

References cited:


11. The Ecological Flora of the British Isles at the University of York (www.york.ac.uk/res/ecoflora/cfm/ecofl/index.cfm).

Table S1. Summary of species richness analysis for bees and hoverflies in the Netherlands and Britain (GB). Given are the numbers of 10x10 km cells that show a significant decline, no change or a significant increase in the rarefaction analysis of pre-1980 versus post-1980 accumulation curves.

<table>
<thead>
<tr>
<th>Species group</th>
<th>Decline</th>
<th>No change</th>
<th>Increase</th>
<th>Chi-square value</th>
<th>P</th>
<th>Mean ± 1 SD</th>
<th>Median</th>
</tr>
</thead>
<tbody>
<tr>
<td>GB hoverflies</td>
<td>52</td>
<td>66</td>
<td>39</td>
<td>1.86</td>
<td>0.17</td>
<td>0.5±21.2</td>
<td>-1.7</td>
</tr>
<tr>
<td>GB bees</td>
<td>42</td>
<td>31</td>
<td>8</td>
<td>23.12</td>
<td>&lt;0.0001</td>
<td>-10.4±21.9</td>
<td>-12.5</td>
</tr>
<tr>
<td>NL hoverflies</td>
<td>37</td>
<td>102</td>
<td>72</td>
<td>11.24</td>
<td>0.0008</td>
<td>9.1±22.7</td>
<td>6.1</td>
</tr>
<tr>
<td>NL bees</td>
<td>66</td>
<td>29</td>
<td>4</td>
<td>&gt;25.6</td>
<td>&lt;0.0001</td>
<td>-18.5±17.4</td>
<td>-20.3</td>
</tr>
</tbody>
</table>
Table S2. Trait-based patterns in bee declines. Similar to Table 1 in main text, but now calculated for all wild bees; i.e. solitary bees plus bumblebees. Proportions are based on species that showed significant change in number of cells in which they were reported during the two time periods. Traits were assigned using (23).

<table>
<thead>
<tr>
<th>Trait</th>
<th>Trait category</th>
<th>All bees</th>
<th>Britain</th>
<th>NL</th>
<th>Trait category</th>
<th>All bees</th>
<th>Britain</th>
<th>NL</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Proportion declining</td>
<td></td>
<td>p</td>
<td>n</td>
<td>Proportion declining</td>
<td></td>
<td>p</td>
<td>n</td>
</tr>
<tr>
<td>Habitat range</td>
<td>Narrow</td>
<td>0.92</td>
<td>0.42</td>
<td>0.0007</td>
<td>Narrow</td>
<td>0.87</td>
<td>0.67</td>
<td>0.164</td>
</tr>
<tr>
<td></td>
<td>Wide</td>
<td>0.42</td>
<td>0.42</td>
<td></td>
<td>Wide</td>
<td>0.67</td>
<td>0.67</td>
<td>0.164</td>
</tr>
<tr>
<td>Flower specificity</td>
<td>Oligolectic</td>
<td>0.86</td>
<td>0.50</td>
<td>0.082</td>
<td>Oligolectic</td>
<td>0.55</td>
<td>0.81</td>
<td>0.091</td>
</tr>
<tr>
<td></td>
<td>Polyleptic</td>
<td>0.50</td>
<td>0.50</td>
<td></td>
<td>Polyleptic</td>
<td>0.81</td>
<td>0.81</td>
<td>0.091</td>
</tr>
<tr>
<td>Tongue length</td>
<td>Long</td>
<td>0.74</td>
<td>0.41</td>
<td>0.011</td>
<td>Long</td>
<td>1.00</td>
<td>0.51</td>
<td>0.003</td>
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<tr>
<td></td>
<td>Short</td>
<td>0.41</td>
<td>0.41</td>
<td></td>
<td>Short</td>
<td>0.51</td>
<td>0.51</td>
<td>0.003</td>
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<tr>
<td>Generations</td>
<td>Univoltine</td>
<td>0.64</td>
<td>0.14</td>
<td>0.013</td>
<td>Univoltine</td>
<td>0.68</td>
<td>0.55</td>
<td>0.433</td>
</tr>
<tr>
<td></td>
<td>Multivoltine</td>
<td>0.14</td>
<td>0.14</td>
<td></td>
<td>Multivoltine</td>
<td>0.55</td>
<td>0.55</td>
<td>0.433</td>
</tr>
</tbody>
</table>
Figure S1. Richness changes in 10x10 km British cells with data for (A) Eusocial + solitary bees, (B) Eusocial bees only, (C) Solitary bees only. Changes in species richness were calculated from rarefaction analyses.
Figure S2. Cumulative frequency distributions for changes in bee and hoverfly richness (i.e. numbers of species) in 10x10 km grid cells in Britain (GB) and the Netherlands (NL).