Global Bee Decline

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One Sentence Summary

Analysis of multi-decadal GBIF occurrence records shows a steep decrease in the diversity of bees being collected worldwide.

Abstract

Wild and managed bees are key pollinators, providing ecosystem services to a large fraction of the world's flowering plants, including ~85% of all cultivated crops. Recent reports of wild bee decline and its potential consequences are thus worrisome. However, evidence is mostly based on local or regional studies; global status of bee decline has not been assessed yet. To fill this gap, we analyzed publicly available worldwide occurrence records from the Global Biodiversity Information Facility spanning more than a century of specimen collection. We found a steep decreasing trend in the number of collected bee species occurring since the 1990's, which today is half from that found in the 1950's. These trends are alarming and encourage swift action to avoid further decline of these key pollinators.

Introduction

Insects are the most specious group of animals and are estimated to encompass a large fraction of the Earth's living biomass. Given their historical abundance and ubiquity, along with the many familiar examples of extreme resilience to natural or intentional extermination, some insects have been traditionally viewed as the ultimate survivors of most apocalyptic scenarios. However, in the last two decades, a series of high-profile reports based mostly on local or regional evidence have repeatedly warned of a significant decline in insect diversity and biomass and raised the alarm about the potential consequence of this decline for the delivery of many ecosystem services. Among affected ecosystem services is plant pollination: insects are the main vectors for pollen transfer of most wild and crop flowering plant species (1–4). Bees (Hymenoptera: Apoidea: Anthophila), a lineage that includes about 20,000 described species, are the most important group of insect pollinators (5, 6). Wild bee species are not only key to sexual reproduction of hundreds of thousands of wild plant species (7), but also to the yield of about 85% of all cultivated crops (4, 8). There is mounting evidence that a decline in wild bee populations might follow or even be more pronounced than overall trends of insect decline (6, 9, 10). Such differential vulnerability might result from a high dependence of bees on flowers for food and a diversity of substrates for nesting, resources that are greatly affected by land conversion to large-scale agriculture, massive urbanization, and other intensive land uses (11–13). However, most studies on "bee decline" to date are based on local-, regional- or country-level datasets, and have a strong bias towards the Northern Hemisphere, particularly North America and Europe, where most long-term research projects capable of generating multidecadal datasets have been conducted (3, 6, 14).

To find an alternative approach to assess whether bee decline is a global phenomenon, we resorted to the data publicly available at the Global Biodiversity Information Facility (GBIF)(15). The GBIF collects and provides "data about all types of life on Earth" from "sources including everything from museum specimens collected in the 18th and 19th century to geotagged smartphone photos shared by amateur naturalists in recent days and weeks"(15). Even though these sources are highly heterogeneous in time and space, we reasoned that if bees are experiencing a global decline in the last few decades, then a generalized decrease in population size and range would result in increased rarity, diminished chance of observation and collection and consequently, a diminished number of total species being observed and recorded worldwide each year.

Results and Discussion

To test our hypothesis of global bee decline, we queried GBIF for all occurrence records of Hymenoptera with a "Preserved specimen" basis of record (16) (see Methods section below). Records of preserved specimens originate in vouchered collections such as those from museums and universities, or associated with biodiversity surveys and molecular barcoding initiatives, among others. These records are likely to represent the most taxonomically trustable source of information within the GBIF dataset. We initially filtered the dataset to six families of the superfamily Apoidea that conform the Anthophila or "true bees": Melittidae, Andrenidae, Halictidae, Colletidae, Megachilidae and Apidae (we excluded the small family Stenotritidae from our analysis, since it has only about 21 species and is restricted to Australia) (5).

A plot of the total number of records and the total number of species reported worldwide each year since 1920 to the present depicts an increasing trend in the number of collected specimens, but a drastic decline in the number of recorded species starting near the end of the 20th century (Fig. 1A). To remove potential biases introduced by year-to-year heterogeneity of data sources, we grouped the data by decade (starting from the 1950's, when the number of species seems to reach a plateau) and used rarefaction based interpolation/extrapolation curves (iNEXT) and asymptotic richness estimators (17, 18) to compare decadal changes in richness of species records. In this analysis, accumulation curves are very similar from the 1950's to the 1990's but flatten considerably to reach lower asymptotes for the 2000's and 2010's (Fig. 1B), implying that the number of species among bee specimens collected worldwide is showing a sharp decline. More specifically, asymptotic richness estimators show that on average global species richness of bee records has halved since the 1950s (Fig. 1C).

While the number of records shows an overall upward trend, we noticed a drop in the last half of the 2010's (Fig. 1A), perhaps due to publication and data incorporation lags, that could potentially cause a downward bias in our estimates. We thus complemented our working dataset with GBIF records with a "human observation" basis (19). These records have shown an exponential increase since the 1980's, in large part due to implementation of citizen science programs (Fig. S1). Consequently, adding these records to our initial dataset greatly boosted the number of total records during the more recent decades. Despite the increased sample size and the tendency of citizen-science programs to over-report rare species relative to common ones (20, 21), we still recovered the same declining trend in richness of species records (Fig. S2). Thus, we conclude that the observed decline in number of recorded bee species is not an artifact of varying sample sizes.

To rule out the possibility that the method we used to estimate richness does not correlate with actual bee diversity, we compared the asymptotic estimators of total richness for each family based on GBIF records with the total known number of species and found a consistent linear correlation between both pairs of values (Fig. S3). Another potential artifact causing a decline in recorded bee diversity could be an increasing loss in taxonomic expertise (22–24). However, under a scenario of increasing taxonomic uncertainty, the fraction of records unidentified to the species level (a reasonable proxy for lack of expertise) should have stayed approximately constant but increased noticeably in the last two decades. While the fraction of records missing species identification shows an overall increase in the last 120 years, this trend has actually reversed since the 2000's (Fig. S4). Therefore, potential loss of taxonomic expertise cannot explain the strong decline in bee record diversity seen at the last two decades.

Bee families in our dataset are heterogeneous in term of richness and abundance, and the observed trends might be driven by just a few bee clades. To make a more phylogenetically-explicit analysis exploring whether bees show a differential temporal trend compared to their closest relatives, and whether particular bee families are more endangered than others, we re-analyzed the initial dataset, this time retaining also records for two families of carnivorous apoid wasps, Crabronidae and Sphecidae, that are sister to Anthophila, and for another highly diverse, non-apoid hymenopteran family, the Formicidae (ants) (25). However, decline was consistent across Anthophila families, as most of them showed a steepening decline starting at the late 1990s/ early 2000's (Fig. 2, lower six rows). These declines in richness of recorded species ranged from 47% for Halictidae to over 77% for Melittidae. Comparisons between Antophila families and two families of apoid wasps sister to bees, and to a more distantly related family, the true ants (Formicidae) revealed contrasting trends (Fig. 2). While both wasp families also show declining trends, they present different patterns than bees: record richness of sphecid and crabronid wasps both show a smoother decrease initiating earlier than the 2000's. In contrast, ants show very little evidence of global record richness decline, but rather a trend towards an increase in the number of recorded species that at most decreased during the last decade. Although the limited number of bee families precludes a formal analysis of phylogenetic patterning, closely related families (e.g., Apidae and Megachilidae, or Colletidae and Halictidae) seem to share more similar patterns of record richness in terms of timing and magnitude than less related families. This hint of phylogenetic patterning becomes even more apparent when considering the two apoid wasp families, Crabronidae and Sphecidae (Fig. 2). Altogether, family-specific trends and asymptotic richness estimates show that the overall decline in global bee record richness is not driven by any particular family. Instead, a generalized decline seems to be a pervasive feature within the bee lineage.

Next, we explored the geographic distribution of the dataset, and repeated the analyses at a continental level. As expected, we find an uneven contribution of each continent to decadal number of records, most coming from North America and Europe (Fig. S5). North America (including Central America and the Caribbean) has the largest and most even representation of records across decades (between 46 and 75% of global records) and shows its steepest decline in species record richness between the 1990's and the 2000's (Fig. S6). In contrast, Europe shows two separate periods of decline, one between the 1970's and the 1980's and a more recent one between the 2000's and 2010's (Fig. S6). Africa shows a sustained fall in species record richness since the 1990's, whereas in Asia the decline seems to have started two or three decades earlier (Fig. S6). The trend in South America is less clear, although it also decreases in the last two decades (Fig. S6). Overall, analyses of the dataset at a continental scale show heterogeneity in both the proportional and absolute contributions to the records, and in the timing and magnitude of the decline in record species richness. However, despite large differences in data availability and, perhaps, except for Oceania, decline in recorded bee diversity seems to be common to all continents.

Global decline in bee record diversity could relate to a proportional decrease in bee abundance, so that rare species become rarer or even extinct, and abundant species less abundant. Alternatively, the less abundant species could be declining strongly, whereas abundant species might be declining at a lower rate or even thriving. These different scenarios are expected to leave a distinctive signature in the temporal pattern of relative abundances. Under the first scenario, the sharp decrease in species richness estimates should not be accompanied by a decrease in evenness, a measure of how equally total record abundance is partitioned among species, whereas under the second scenario there should be a parallel decrease in record evenness. As expected from the hypothesis of an abundance-related differential species decline, decadal estimates of Pielou's index, a common measure of evenness (26), based on bee records decrease strongly since the 1990's (Fig. 3). Therefore, the decline in richness of species records can relate to a process of thousands of species becoming too rare to be sampled while fewer species are becoming dominant and perhaps even increasing in abundance.

Our results support the hypothesis of a massive global decline in bee diversity. If trends in species richness of GBIF records are reflecting an actual trend in bee diversity, then this decline seems to be occurring with distinctive characteristics in every bee family and in most continents. Interestingly, such global bee decline appears to be a relatively recent phenomenon which started in the nineties, at the beginning of the globalization era, and continues to the present. The globalization era has not only been a period of major economic, political and social change, but also of accelerated land-use transformation (27). Bees thrive in heterogeneous habitats, even those driven by man (11, 28), where they find a diversity of floral and nesting resources. However, land devoted to agriculture, particularly to monoculture, has expanded in several regions of the world since the 1990s (27). This has led not only to higher habitat homogeneity, which can relate by itself to more impoverished and spatially homogeneous bee assemblages (11, 29), but also to higher use of pesticides and other agriculture chemical inputs that have direct and indirect lethal and sub-lethal effects on bee health (30). Effects of climate change on shrinking bee geographical ranges have been also documented in Europe and North America (3). Lastly, a booming international bee trade has involved the co-introduction of bee pathogens, that may cause bee decline, like the emblematic case of the giant Patagonian bumble bee, *Bombus dahlbomii* (31). A visual indication of phylogenetic patterning in the trend of recorded species diversity among the different bee families (Fig. 2) suggests that different lineages can be differentially affected by different drivers, likely based both on their common geographical distribution and shared clade-specific biological and ecological traits (32). Two or more of these drivers can act synergistically, which can have accelerated the process of bee decline we are documenting here.

Associated with the declining trend of richness of species records is a trend of increasing dominance of records by a few species. Increasing dominance by one or a few species can be observed at the regional scale, like the case of invasive *Bombus terrestris* in southern South America (33), or globally, as seen for the western honeybee, *Apis mellifera* (Fig. S7). The western honeybee has been introduced in every single continent from its original geographical range in Europe and Africa. Although both domesticated and wild populations of the western honeybee seem to be declining in several countries, this species is still thriving globally (34). A consequence of increasingly less diverse and uneven bee assemblages could be an increase in pollination deficits, causing a reduction in the quantity and quality of the fruits and seeds produced by both wild and cultivated plants. Less diverse bee assemblages at both local and regional scales have been associated with lower and less stable yields of most pollinator-dependent crops (8).

GBIF is certainly not a source of systematically collected data, and this might be cause of concern when interpreting the results of our analyses (35, 36). However, several of its potential biases would be expected to deflate, rather than inflate our results. For example, collectors targeting rare species would be expected to enrich the number of species (unless many species are becoming so scarce that they just cannot be found). Spatial and temporal biases in collection intensity (e.g., targeted programs might enrich the abundance of specific species/groups at specific spans and regions) could also generate spurious trends.

Nonetheless, our continent-level analysis showed that those regions with the best temporal and spatial coverage (i.e., Europe and North America) are the ones showing the clearest signal for decline (Fig. S6). Furthermore, none of those biases can explain the noticeable phylogenetic contagion seen in the trends (Fig. 2) better than the fact that the hymenopteran groups we analyzed have a considerable phylogenetic signal in their ecology and life history traits and would be expected to show phylogenetic clustering in their response to drivers of decline. Thus, while the inherent heterogeneity and biases of aggregated datasets as GBIF's make them unreliable as a direct data source of predictive models, they can still be used within a hypothesis-driven framework to test whether bees as a group are declining worldwide. In this context, our results are largely confirmatory of the hypothesis that bee diversity is declining globally.

Conclusions

One of the most important pieces of missing information of the global report on Pollinators, Pollination and Food Production of IPBES (37) was the lack of data and analysis on global bee decline, despite the many local and a few regional reports pointing out that this decline could add to a global phenomenon. Despite all its shortcomings, GBIF is probably the best global data source available on long-term species occurrence and has the potential to contribute in filling this critical knowledge gap. Its analysis supports the hypothesis that we are undergoing a major global collapse in bee diversity that needs the immediate attention of governments and international institutions. Under the best scenario, this collapse can indicate that thousands of bee species have become too rare; under the worst scenario, they may have already gone extinct. In any case, a decline in bee diversity driven by either increasing rarity or irreversible extinction will have consequences for the pollination of wild plants and crops and knock on ecological and economic consequences. Slowing down and even reversing habitat destruction and land-conversion to intensive uses, implementation of environmentally friendly schemes in agricultural and urban settings, and programs to re-flower our world are urgently required. Bees cannot wait.

Methods

Datasets

An initial query at the database of occurrence records at the Global Biodiversity Information Facility (www.gbif.org) using the filters [Scientific Name = "Hymenoptera" AND Basis of Record = "Preserved Specimen"] resulted on 7,766,219 total records involving 1,026 datasets, which we call the "base dataset" (16). Data were downloaded as a text file and filtered for records identified to species levels and belonging to either Anthophila (defined as the families Melittidae, Andrenidae, Halictidae, Colletidae, Megachilidae and Apidae), two closely related families of apoid wasps (Crabronidae and Sphecidae), or the true ants (Formicidae), retaining 3,248,988 records (2,195,968 records belonging to Antophila). Phylogenetic relations between all these nine families (six bee, two apoid wasp families, and one ant family) follow recent phylogenomic results (25).

To test potential biasing due to recent decreases in record numbers, we re-queried GBIF using the filters [Scientific Name = "Hymenoptera" AND Basis of Record = ("Preserved Specimen" OR "Human observation")]. This query resulted in 9,508,391 records from 1,977 datasets (19), from which we filtered the families of Anthophila as above, resulting in an "expanded bee" dataset (2,883,419 records).

Analyses

All datasets were analyzed using a customized script written and executed within the R computing environment (38). The complete annotated script is available as Supplementary

Materials, and can be used to fully reproduce all results, or adapted to re-run the analyses on other datasets.

After removing records without "year" data, yearly counts of records and species for all three datasets were plotted directly using the `plot` function in the base R package. Trend curves were generated using the `loess` (39) function (`stats` package) with a smoothing α parameter of 0.2. A "decade" field was calculated from "year", and records by species and decade were counted and stored in a matrix of m species × 7 decades (1950's to 2010's). This matrix was used as abundance data input for the `iNEXT` function of the iNEXT package (18) to estimate rarefaction-based interpolation/extrapolation (iNEXT) curves and Chao1 asymptotic estimators of species richness (17). We also compared the asymptotic estimator for species richness for each family with the total number of species listed for each family in the taxonomic framework of the Integrated Taxonomic Information System (www.itis.gov).

To estimate potential biases caused by changes of taxonomic expertise over time, we re-filtered the initial GBIF query without excluding records without a species ID, then counted the number of records with or without a species id per year. To analyze trends at continental level, we added a "Continent" field to the base dataset via table joining to a list of countries, country codes and continents from https://datahub.io/JohnSnowLabs/country-and-continent-codes-list. We then repeated the analyses splitting the dataset by continent. To show trends in equitability of species abundance across records over time, we calculated Pielou's evenness index (26), $J=\Sigma p_i \ln(p_i)/\log(S)$ for $i=1$ to S, the total number of species, for each year between 1900 and 2018, using the diversity functions from the package `vegan`(40). To calculate the percentage contribution of each species to each year's records, we generated a count table of records per species (rows) and year (columns) and used the `colPerc` function from the `tigerstats` package (41). Then, the contribution of a single species (e.g., *Apis mellifera*) was plotted as a function of year; an exponential curve was fit to the points of the plot using the `lm` function from the R base `stats` package.

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Footnotes

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Data and materials availability: Occurrence record data used in this paper can be downloaded from https://doi.org/10.15468/dl.h52qyh and https://doi.org/10.15468/dl.o73fzx; original sources traced via GBIF.org. The R language script used to analyze the data and generate the plots is available as Supplementary Materials.

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Figures and figure legends

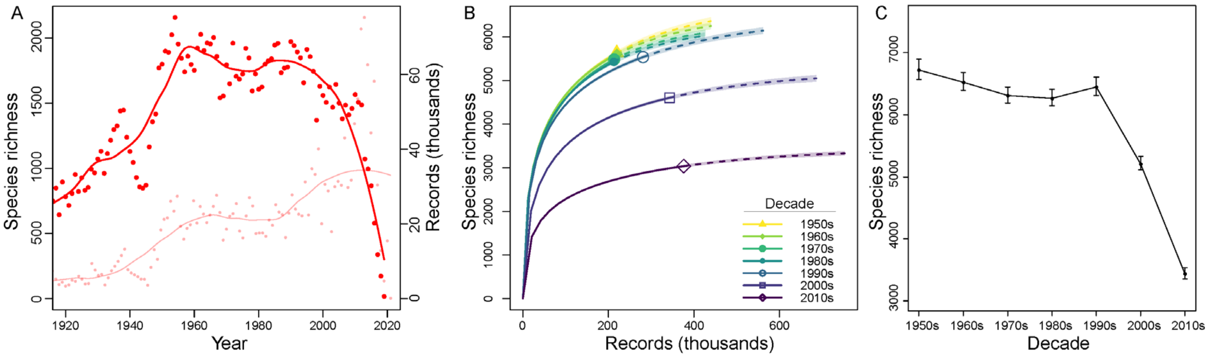


Fig. 1. Despite increasing number of specimen records, the number of worldwide recorded bee species is sharply decreasing. (A) Number of species (bold dots and line, left axis) and specimens (light dots and line, right axis) of worldwide Anthophila (bees) GBIF records of preserved specimens. (B) Chao's interpolation/extrapolation (iNEXT) curves based on worldwide Anthophila (bees) GBIF records of preserved specimens. Data were grouped by decade for the period 1950-2019. The symbols show actual number of specimen records and separate interpolated (left, full line) from extrapolated (right, dashed line) regions of each curve. (C) Values of the asymptotic richness estimator by decade (error bars mark upper and lower 95% confidence intervals).

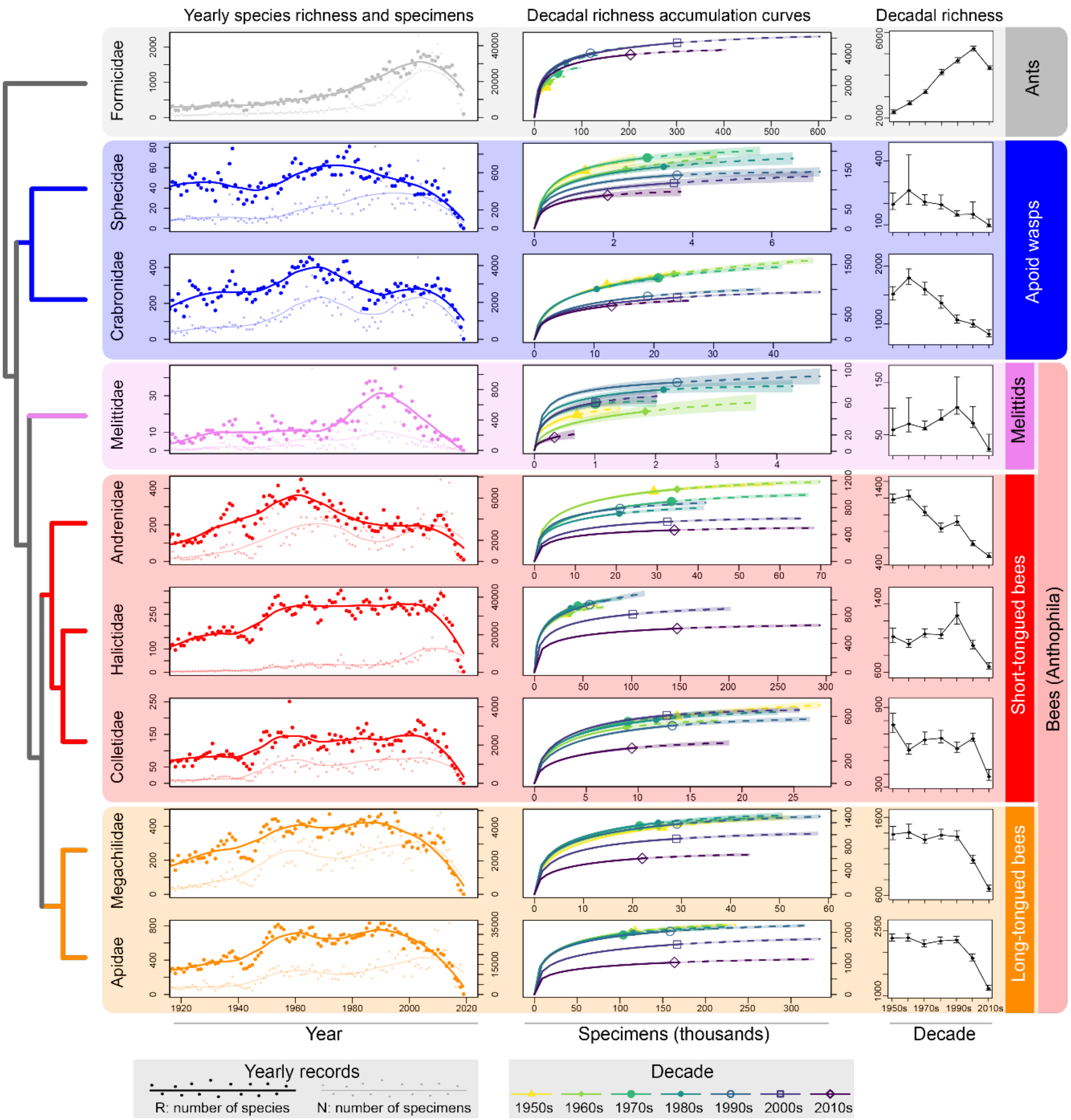
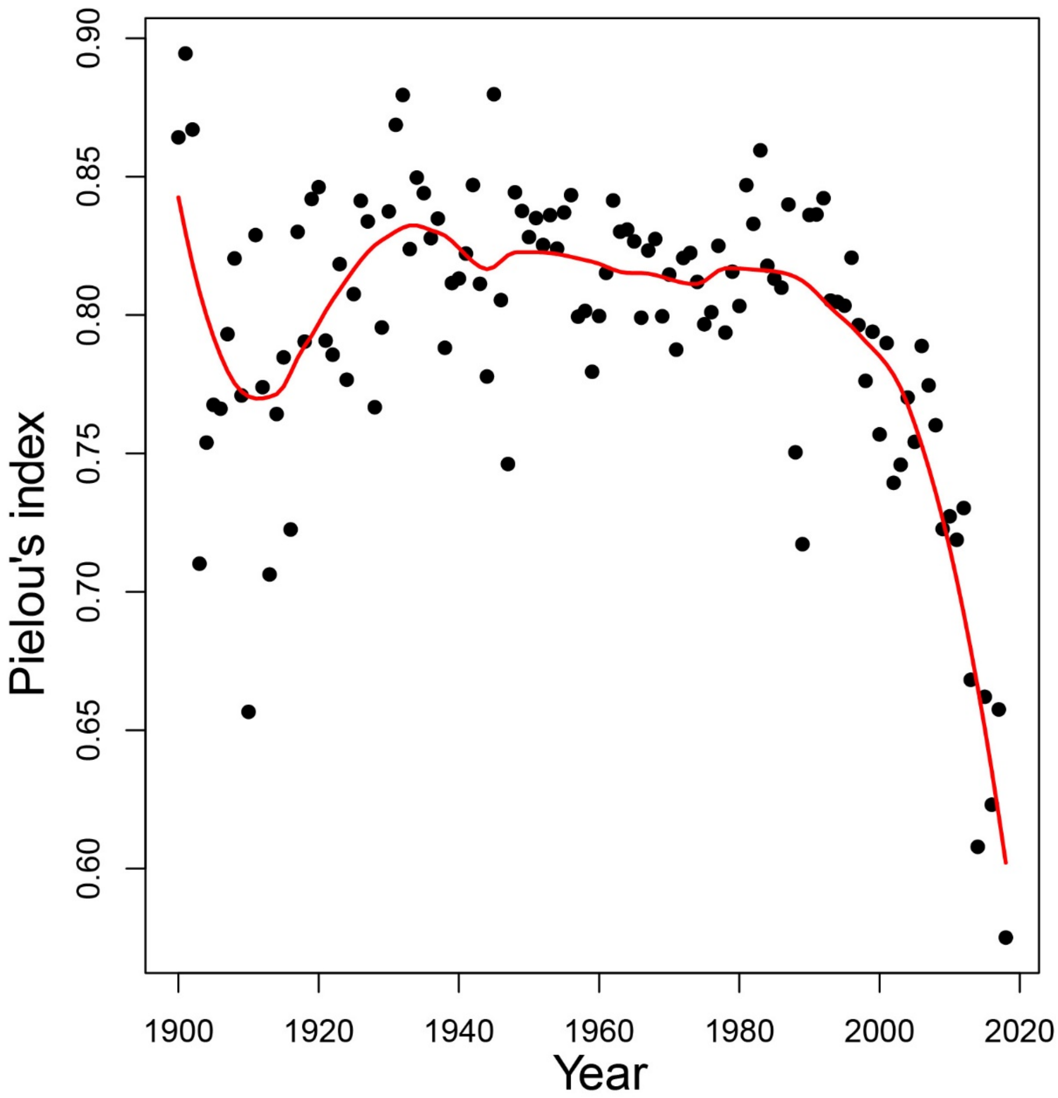


Fig. 2. Decline patterns in worldwide records of bees are generalized but phylogenetically structured. Phylogenetic relationships among each of the six families of bees (Anthophila, lower six rows), two related families of non-flower associated apoid wasps (2nd and 3rd rows), and the less related, highly specious ant family (top row). Plots on the left row show number of species (bold dots and line, left axis) and specimens (light dots and line, right axis) in GBIF records; plots on the middle row shows Chao's interpolation/extrapolation curves based on GBIF records, grouped by decade for the period 1950-2019; plots on the right row

show asymptotic estimates of richness by decade for the same period (error bars mark upper and lower 95% confidence intervals).



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402 **Fig. 3.** Overall representation of worldwide bee species on global records is becoming increasingly uneven over time. Estimate of Pielou's index of sample evenness per year since the year 1900 for worldwide preserved bee specimen records found the GBIF database. Points represent yearly values; the red curve shows a loess smoothed trend line.

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