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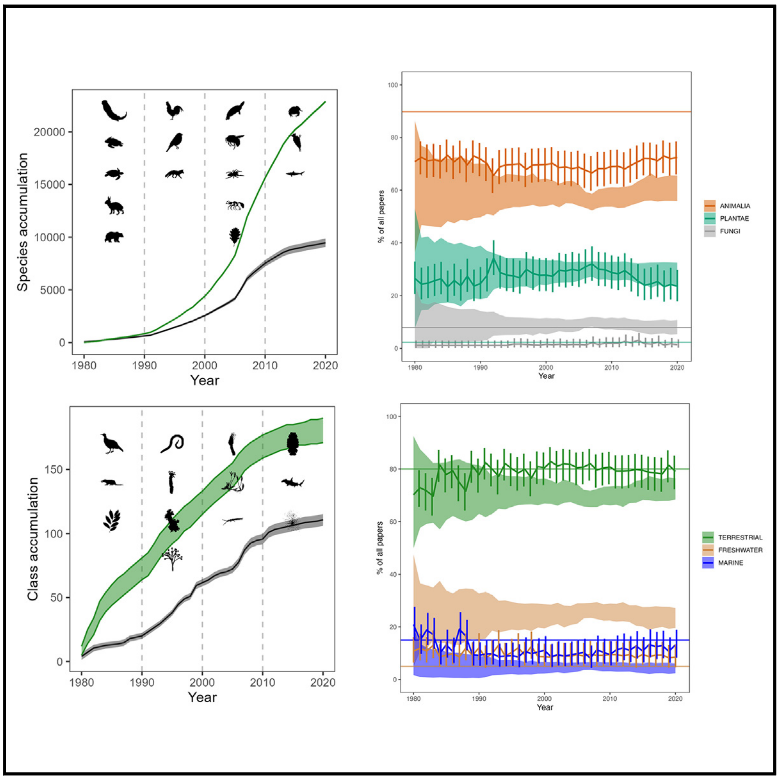
# Global trends and biases in biodiversity conservation research

## Graphical abstract



## Highlights

- Biases in conservation research have not changed over time
- Conservation research increasingly focuses on the same suite of species
- Conservation status of a species does not seem to predict research attention
- Targeted funding of understudied systems is necessary to even out research imbalance

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## In brief

Conservation biology research seems biased toward popular species and ecosystems, with seemingly little attention paid to within-species (genetic) diversity. By looking through thousands of conservation-focused research articles, we found that these biases have been notably consistent over the last four decades. We saw that some of the most-studied species have low conservation risk, and some are domesticated animals. Animals and terrestrial ecosystems are consistently over-represented while plants, fungi, and freshwater ecosystems remain under-represented.

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Article

# Global trends and biases in biodiversity conservation research

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**SCIENCE FOR SOCIETY** While efforts to conserve biodiversity are increasing, research and conservation efforts are unequally allocated across different scales of biodiversity, with within-species diversity receiving the least overall attention. One potential solution is to realign funding priorities to promote efforts across different scales, from genetic to species to ecosystem. With limited funding, prioritization approaches seek to maximize impact by returning to ongoing conservation efforts or focusing on high-profile species. However, these approaches reinforce biases against more equitable allocation because a lack of knowledge about understudied groups can be seen as detrimental to conservation success and prohibitively expensive. This study shows that these biases in conservation research are long standing and still ongoing, which will ultimately lead to an uneven loss of biodiversity. Deliberate funding and targeted efforts are needed to investigate both understudied species and ecosystems.

## SUMMARY

Efforts to conserve biodiversity have been hampered by long-standing biases, including a disproportionate focus on particular taxa and ecosystems with minimal attention to underlying genetic diversity. We assessed whether these biases have persisted over the past four decades by analyzing trends in 17,502 research articles published in four top conservation-focused journals. Overall, we found that historical biases in conservation biology research remain entrenched. Despite increasing numbers of conservation articles published each decade from 1980 to 2020, research effort has increasingly focused on the same suite of taxa. Surprisingly, some of the most-studied species in these conservation articles had low conservation risk, including several domesticated animals. Animals and terrestrial ecosystems are consistently over-represented while plants, fungi, and freshwater ecosystems remain under-represented. Strategically funding investigations of understudied species and ecosystems will ensure more effective conservation effort across multiple levels of biodiversity, alleviate impediments to biodiversity targets, and ultimately prevent further extinctions.

## INTRODUCTION

Biodiversity loss continues to accelerate despite decades of international conservation initiatives aimed at its prevention. Human impacts are a key factor, resulting in Earth's sixth mass extinction event[1–3]; current extinction rates in the Anthropocene Epoch are 10–100 times greater than in the last 10 million years.[4] Halting biodiversity loss has therefore become a global priority.[5] To address this priority, an international treaty, The United Nations Convention on Biological Diversity (CBD), was established in 1993 and ratified by 196 Nations. In 2010, the CBD outlined a Strategic Plan to reverse the loss of biodiversity by 2020. This treaty included a specific target of preventing any further extinction of *threatened species* (Aichi targets; key terms are italicized and defined in Table 1). Despite many conservation efforts aimed at this target, extinction rates continue to accelerate,[4] with up to 40% of species in particular groups or habitats predicted to disappear in the 21st century.[2,6,7] This raises the question: Why are conservation efforts not meeting CBD targets?

One issue that could be hampering biodiversity protection is long-standing biases in conservation research effort. An overarching goal of CBD is to conserve multiple *levels of biodiversity*, specifically genetic, species, and ecosystem diversity. Conservation efforts at different levels of biodiversity can be critical as threats occur at different scales (e.g., localized inbreeding versus ecosystem disruption), so this stated goal parallels calls from the greater scientific community to promote integrative efforts across these different scales. Historically, genetic diversity has received the least attention when compared with species or ecosystem diversity.[9] However, recent improvements in the accessibility of molecular techniques have made it easier to conduct genetic research. Taxonomic biases have also long persisted in conservation biology research. Across species, vertebrates have received the most attention, with plants and invertebrates receiving much less attention, while fungi, archaea, bacteria, and other microbial life are rarely considered.[10–12] Such taxonomic biases could mean that population declines in understudied species go unnoticed, leading to *silent extinctions*.[13] These biases begin within the mapping of species distributions,[14] skewing priorities at the earliest stages of conservation planning.

Although the CBD emphasizes conserving biodiversity across all ecosystems, most of the focus has been on terrestrial ecosystems. While terrestrial environments house more than 80% of Earth's total biomass (mostly terrestrial plants), the marine environment houses 78% of animal biomass yet receives <10% of conservation research effort. Marine environments constitute 99% of the world's habitat by volume and support twice as many phyla than land (with 15 exclusively marine phyla), including an estimated 15%–25% of the world's species.[15–21] This bias was first identified in the 1980s when the field of conservation biology was in its infancy.[15] While some of the underlying causes for biases against aquatic research have been addressed through technological innovation and greater ecosystem access, it is unclear if these improvements have reduced research bias over time.

Given that taxonomic and ecosystem biases have long been recognized as an impediment to biodiversity conservation, we need to know whether any of these biases have diminished.[22] With the 2022 UN Biodiversity Conference (COP 15) establishing the post-2020 framework for conserving biodiversity, it is particularly timely to assess whether efforts to conserve biodiversity have become less biased and more representative of global ecosystems and taxa across the tree of life. To this end, we examined temporal trends in *conservation research efforts* across three levels of biodiversity identified in the CBD: genetic, species, and ecosystem. Conclusions are based on an analysis of more than 17,000 research articles published in four well-established international conservation biology journals: *Biodiversity & Conservation* (2021 Impact Factor 4.3), *Biological Conservation* (2021 Impact Factor 7.5), *Conservation Biology* (2021 Impact Factor 7.6), and *Conservation Letters* (2021 Impact Factor 10.1) (Figure S1A). We first examined how evenly research effort was distributed across species and ecosystems over time. Then, we assessed bias based on how representative these efforts were; we compared the distribution of research effort with what would be expected from a random sampling of global databases of species (Global Biodiversity Information Facility [GBIF]) and their conservation status (International Union for Conservation of Nature [IUCN]). For example, if 80% of species diversity is found in terrestrial environments,[19,20] was more or less than 80% of the research effort focused there? We can thus determine if conservation research efforts have become more representative of the tree of life and global distribution of ecosystems over time.

## RESULTS

Our analysis of research effort in four leading conservation biology journals reveals an increase in taxonomic bias over time. From 1980 to 2020, there was a 35-fold increase in the number of published research articles (Figure S1A); however, the number of new study species has not kept pace with expectations (Figure 1). The accumulation curve for new species studied increases until the mid-2000s but then reaches an inflection point in that decade, beyond which the number of new species studied has decreased. Overall, there were significantly fewer species (2.4×), families (2.7×), and classes (1.6×) studied in the focal journals over the 40 years than would be expected based on a random sample of GBIF-listed species in each of the past four decades (all t tests: $p < 0.001$). For example, we estimate that 9,462 species (95% quantiles: 9,061–9,864 species) were studied in the four journals between the years 1980 and 2020. In contrast, we would expect 22,878 species (95% quantiles: 22,860–22,896 species) to have been studied based on a random sample of GBIF species. Furthermore, the difference between the observed and randomly generated accumulation curves has grown in each successive decade at all three taxonomic levels (all Tukey multiple pairwise comparisons: $p < 0.001$). Despite the continued increase in research papers, and the large number of species that have been studied overall, the number of new species studied each decade has declined and now seems to be approaching an asymptote (Figure 1).

A closer examination of which species were most studied (both per decade and overall) revealed a core group of 27

**Table 1. Definition of key terms used in this study**

| Term | Definition as used in this study |
|---|---|
| Bias/representativeness | level of agreement between conservation research effort and proportional occurrence of taxa/study systems/habitats within key databases (GBIF and IUCN) |
| Conservation research effort | proportion of taxa/system/habitat focused articles published over time (per year and per decade) across four conservation biology journals: *Biodiversity & Conservation*, *Biological Conservation*, *Conservation Biology*, and *Conservation Letters* |
| Charismatic megafauna/flora | species (generally large and conspicuous), that have high recognizability and/or popular appeal and are used to promote funding and awareness of conservation goals[8] |
| Levels of biodiversity | three levels of biodiversity, ranging from fine to broad scale, are discussed; the finest level is genetic diversity, which refers to the differences between individuals within a species; species diversity refers to the number of species found within a discrete habitat; and the broadest level, ecosystem diversity, refers to the variability in habitats within a geographic region |
| Silent extinction | undocumented loss of diversity leading to the seemingly sudden extirpation of a known species |
| Threatened species | any species falling into one of the following IUCN Red List categories: Vulnerable; Endangered; Critically Endangered |

over-represented species (Figure 2). These 27 species represent 0.0008% of all GBIF-listed species and yet feature in 8.5% of all research articles published between 1980 and 2020 in the four conservation biology journals. Vertebrates represent 89% of these most-studied species and yet equate to less than 4% of all GBIF species. Furthermore, the most-studied species are not dominated by those at higher risk of extinction. Rather, 50.6% of the most-studied species are listed as least concern or not evaluated by the IUCN Red List of Threatened Species; 22.2% are domesticated animals.

There was no improvement in research effort bias at higher taxonomic levels across the study period. Although there were slight changes over time in the percentage of articles devoted to each of the three assessed taxonomic kingdoms, animals were always studied more often than plants and fungi (Figure 3). Overall, there was a greater focus on animals (median = 70.3%; 95% quantiles = 66.7%–74.1%) versus plants (median = 27.4%; 95% quantiles = 22.9%–31.8%), and fungi (median = 1.45%; 95% quantiles = 1.22%–2.44%). Comparison with a random selection of GBIF species (i.e., null model) revealed that animals were over-represented in conservation biology journal articles in every decade considered (Wilcoxon's signed rank tests; all $p < 0.001$). Animals were studied an average of 11.1% more than expected (95% quantiles = 1.63%–21.0%). There were small changes in the focus on animals over time, decreasing from 71.7% in the 1980s to 70.1% in the 1990s (Wilcoxon's test; $p = 0.0145$), then increasing from 68.6% to 71.5% from the 2000s to 2010s (Wilcoxon's test; $p = 0.0145$). Plants were slightly under-represented compared with the null model in three of the four previous decades (by 0.5%–2.9%; Wilcoxon's signed rank tests; all $p < 0.001$) but slightly over-represented in the 2000s (by 0.4%; $p < 0.001$). Studies involving fungi were rare, being consistently under-represented compared with a random selection (Wilcoxon's signed rank tests; all $p < 0.001$). However, fungi did attract slightly more attention over time: fungal studies increased significantly with each successive decade: from 1.22% in the 1980s, 1.27% in the 1990s, 1.53% in the 2000s, and 1.54% in the 2010s (Wilcoxon's test, $p < 0.03$ for all comparisons).

Traditionally, conservation biology research has focused mainly on terrestrial ecosystems, and this trend has persisted from 1980 to 2020 (Figure 4). Terrestrial species were the focus of 80% of studies overall, with consistent focus among decades (pairwise Wilcoxon's post-hoc test; $p > 0.18$). In comparison, there was significantly less focus on marine (11%) or freshwater (9%) species across every decade (pairwise Wilcoxon's post-hoc tests; all $p < 0.001$). There was a similar focus on marine and freshwater species across most decades, except in the 1980s and 2010s when there was significantly more focus on marine species versus freshwater species (pairwise Wilcoxon's post-hoc tests; $p = 0.007$ and $p < 0.001$, respectively).

Compared with the IUCN list of species, research articles have over-represented terrestrial and marine species while under-representing freshwater species. In the 1980s, terrestrial species were featured 5% more than expected based on random sampling of IUCN species. This rose to 14% more in the 2000s (pairwise Wilcoxon's post-hoc test; $p < 0.001$), but then improved slightly (back to 12%) in the 2010s ($p < 0.001$). Surprisingly, even though marine species represented only ~11% of research articles, that proportion was higher than expected from a random sampling of IUCN species across all decades (all $p < 0.001$). In contrast, freshwater species were significantly under-represented across all decades (all $p < 0.001$), becoming slightly more under-represented from the 1980s (15% less than expected) to the 2000s (19% less).

Study system biases are also apparent at a finer habitat scale. Forests were the most-studied habitat, present in 24% of journal articles (Figure 5). While there was significantly more focus on forests than any of the other 15 IUCN-defined habitats (pairwise Wilcoxon's post-hoc tests: all $p < 0.001$), forest-dwelling species were actually under-represented compared with the number of randomly selected IUCN-listed species across all decades (pairwise Wilcoxon's post-hoc tests: all $p < 0.001$). Most other habitats were consistently over-represented in research articles (Figure 5) compared with what would be expected from habitats where IUCN-listed species live: grassland, artificial terrestrial, marine neritic, shrubland, marine intertidal, marine coastal/supratidal, marine oceanic, artificial aquatic/marine, desert, and introduced vegetation all had greater representation in research articles compared with null expectations across all decades (pairwise Wilcox's post-hoc tests; all $p < 0.001$).

Furthermore, there has been little improvement in this bias over the survey period (1980–2020). Although there were slight changes in bias from one decade to the next in most habitats, only three were consistently biased in the same direction: shrubland became more biased whereas marine intertidal and marine coastal/supratidal became less biased over all four decades tested (pairwise Wilcoxon's post-hoc tests: $p < 0.001$).

The finest level of biodiversity (genetic diversity) has received the least attention. According to our targeted text search for genetics-associated words, genetics research in conservation biology journals increased from an average of less than 3% of journal articles prior to 1980 to a peak of 20% in 1996 (Figure 6). Since that peak, genetics-based research has trended down to 7%–10% of recent articles (Figure 6). When we validated our genetics text search with a manual check (see methods), we found an overall accuracy of 97.2%, with 2.8% false positives and no false negatives (Table S1). This suggests that we may still be slightly overestimating its occurrence.

## DISCUSSION

Overall, we found that historical biases in research efforts to conserve biodiversity remain entrenched. Despite the long-standing need to adjust research efforts to cover a broader range of taxa, our results show that the opposite has happened: effort has increasingly focused on the same suite of species through four decades. Vertebrates represented the majority (89%) of the 27 most-studied species (Figure 2), even though vertebrates comprise less than 4% of all known species. Why is this taxonomic bias getting worse? Potentially, this bias reflects preferences that have led to more funding for vertebrate research.[23] During the initial growth of the field of conservation biology, mammals were the most over-represented study group (1987–2001[10]), and our study shows that this has not changed. Mammals comprise seven (eight if *Canis lupus* and *Canis familiaris* are considered separately) of the 10 most-studied species in the last decade (2010–2019). Five of these seven mammals are *charismatic megafauna* that are within the top 15 species of greatest public interest[22]: *Panthera tigris* (Tiger), *Panthera leo* (Lion), *Canis lupus* (Wolf), *Panthera pardus* (Leopard), and *Ursus arctos* (Brown

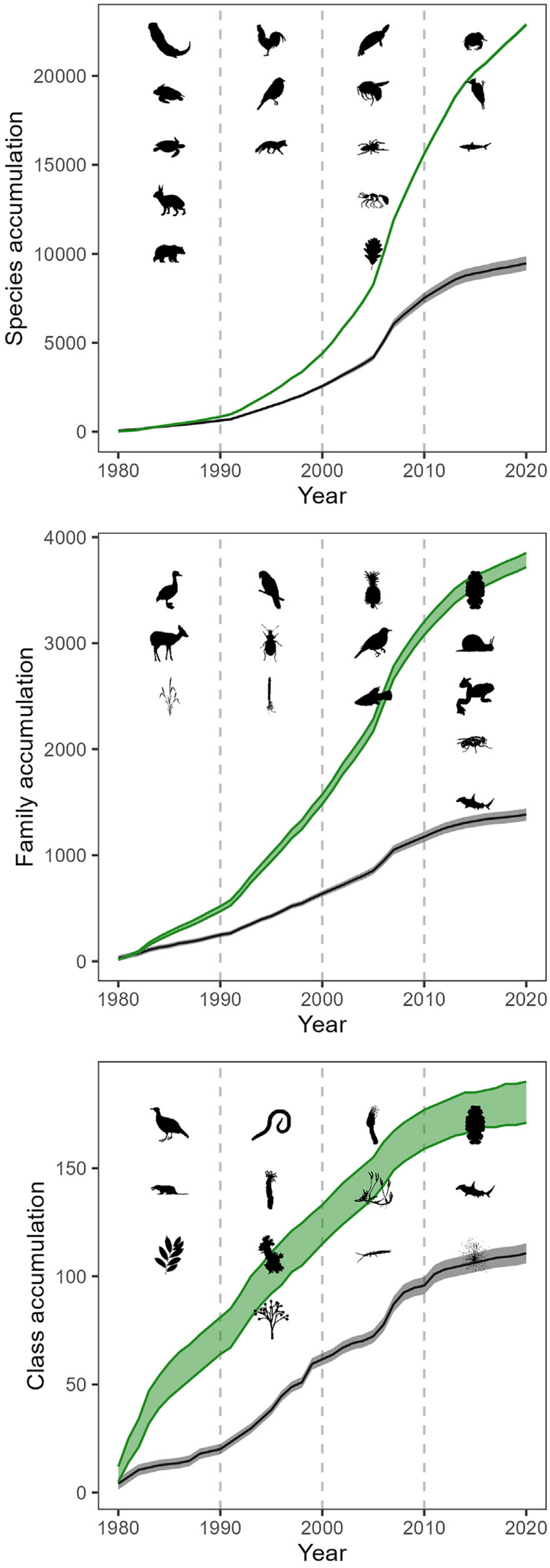

**Figure 1. Taxonomic research accumulation over time**

Accumulation curves showing the number of new taxa studied each year from 1980 to 2020 in conservation biology research articles (black lines and gray ribbons) compared with a null model (green ribbons), measured at three taxonomic scales: species, family, and class. The black lines are the predicted numbers of new taxa and gray ribbons are 95% quantiles around those predictions based on a comparison between automated text searches and manual text searches of a subset of articles. Green ribbons represent 95% quantiles from 1,000 random samples of the Global Biodiversity Information Facility (GBIF) species list. Silhouettes are the top 3 (including more if tied) most commonly studied new taxa for each decade (i.e., not studied in previous decades). Taxa names and attributions for silhouettes (from phylopic.org) are shown in Table S2. All silhouettes are under either CC0 1.0 Universal Public Domain Dedication or Public Domain Mark 1.0 licenses. Note that some of the 95% quantiles are small making the ribbons difficult to discern from the lines (e.g., gray ribbons at the species and family level; green ribbon at the species level).

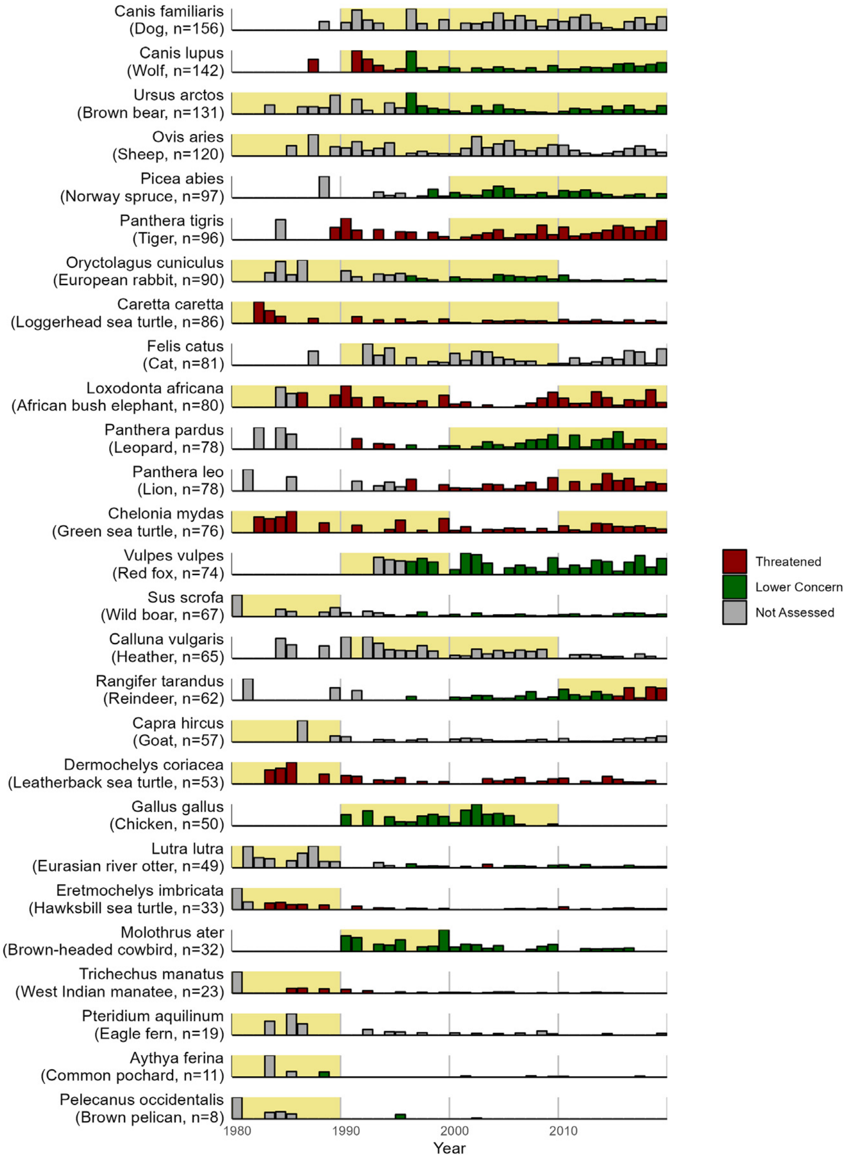

**Figure 2. Most commonly studied species in conservation between 1980 and 2020**

Relative proportions over time of the 27 most commonly studied species in conservation biology journals. The top 10 species were identified for each decade based on the percentage of research articles where each species name was found in four conservation biology journals from 1980 to 2020. Species are listed from the most to least published across all years, with their common names and total number of research articles in which they were studied (*n*). Each bar represents the percentage of articles in each year relative to all years for that species, with yellow backgrounds highlighting species that were in the top 10 for that decade. Bars are colored based on their International Union for Conservation of Nature (IUCN) status each year: red, threatened; green, lower concern; gray, not assessed.

bear). Perhaps not surprisingly, the most-studied species are also the most popular. Long-standing taxonomic biases in research efforts could, thus, be driven by societal preferences.[24] When comparing publication trends with a random null model, we assumed that as the field grew in terms of the number of researchers and articles written, a greater number of nascent conservation biologists would gravitate toward previously understudied systems to establish their niche. Publication trends since at least the mid-2000s have not shifted to incorporate more diverse taxonomic representation, perhaps due to a shift in the field of conservation biology at that time toward more policy-oriented discussions and away from ecology-focused research.[25]

Two possible limitations of our methodology should be considered when interpreting our results. First, the articles published in these four prominent English-language journals do not reflect the entire body of conservation research being conducted across all scales. It is possible that more articles focused on lesser-studied species can be found in unpublished studies or regional journals. A valuable follow-up to our study could be conducted on, for example, lower impact or regional journals that contain valuable conservation information (e.g., *Pakistan Journal of Zoology*, *Pacific Science*, *South African Journal of Science*, *Atoll Research Bulletin*, *Revista de Biologiá Tropical*, *Oikos*). Another limitation may arise from perceptions about conservation priorities. While this subject is complex and beyond the purview of our study, some priorities are widely accepted, such as range size as a valuable predictor of extinction risk. More relevant to our analysis is the recognition that top predators and herbivores are key to maintaining ecosystem health and are therefore prioritized in conservation efforts. Many of the 27 most-studied species (Figure 2) can be classified as top predators and herbivores and are also likely key to nutrient cycling within ecosystems. This contributes to the apparent curtailment of taxonomic diversity in conservation research. The individual conservation outcomes of more intense research focus on these 27 most-studied species are not easily summarized. The lack of a simple relationship between conservation effort and IUCN Red List status could be the result of several underlying issues including (1) compartmentalization of conservation units (e.g., reindeer being globally listed as ‘‘least concern’’ but regionally ‘‘threatened’’), (2) lack of synchrony or lags between research output and conservation response, and (3) multi-faceted system-specific relationships between IUCN Red List status, local politics, and funding (in addition to research effort) resulting in inconsistencies in the direction of responses. Despite these potential limitations, the value of our analyses lies in the robust

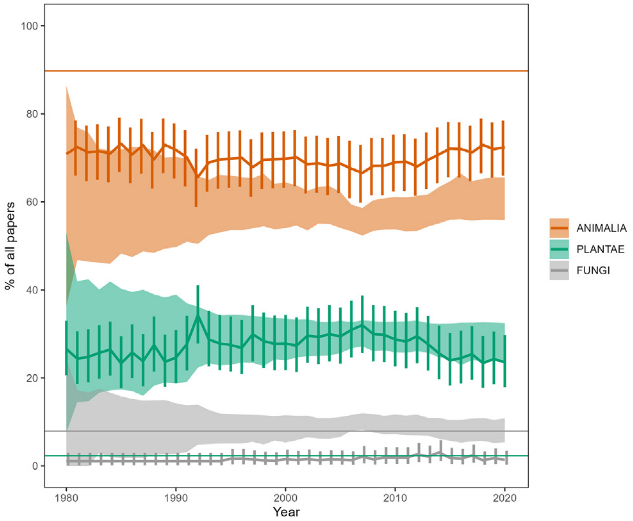

**Figure 3. Changes over time in broad taxonomic focus**

Temporal patterns (1980–2020) in the percentage of conservation biology research articles focused on each of three key taxonomic kingdoms. Research articles were surveyed from four leading conservation journals and categorized based on the ecosystem of the study species (see methods). Solid lines are observed percentages (after correcting based on comparisons between automated and manual text searches), with error bars representing uncertainty around those observations (95% quantiles; see methods for full description). Ribbons represent the 95% quantiles from 1,000 random subsamples of species from the GBIF species list (i.e., null model). Solid horizontal lines represent rough estimates of extant species proportions occupying each kingdom from Grosberg et al.[19] (89.8% Animalia, 2.3% Plantae, 7.9% Fungi).

documentation of consistently highly skewed research priorities for conservation.

From a species conservation perspective, we found it surprising that many of the conservation research articles were focused on species with low conservation priority (according to their IUCN Red List status). Heavily researched species of low conservation concern may support a focus on problematic species: those that cause conservation problems via ecosystem disruption (invasive, domesticated, or overpopulated), or exhibit behaviors detrimental to human interests. For example, 22% of the most-studied species are domesticated and not at risk of extinction even though these species comprise less than 1% of total species diversity.[26] Domesticated species can cause biodiversity loss through predation, competition, and habitat destruction.[27] Indeed, many of the domesticated species on our list of most-studied taxa also top the list of invasive predators that have caused the most biodiversity loss.[27] For example, the most represented species in our analysis (Figure 2) was the domesticated dog (*Canis familiaris*), which is frequently included as a keyword in articles where dogs are discussed as predators or competitors of species of conservation concern or closely related to threatened species (e.g., wolves). While such a focus on problematic species seems reasonable, it may drive taxonomic bias. However, this might also simply be indicative of a general barrier to the study of threatened species because they are rare (and thus require more resources to adequately study) as well as having tighter permit restrictions compared with common and non-listed species. Studying non-threatened species may be quicker, easier, and provide effective proxies to understanding the decline and recovery of threatened species, particularly if they are close relatives.

Conservation efforts remain uneven across ecosystems, with the majority of research articles focused on terrestrial ecosystems. Comparisons with the IUCN database suggests that studies in terrestrial and marine ecosystems are over-represented, and those focused on freshwater systems remain under-represented. These findings align with the historic bias, with the exception being marine studies. Traditionally, marine studies were considered to be under-represented.[15–18,22] A likely explanation for this discrepancy is that the IUCN database could also be under-representing marine species due to the difficulty of identifying and assessing marine species, most of which are undescribed. For example, a third of known marine invertebrates cannot be evaluated by the IUCN due to inadequate population data.[28] When compared with past estimates of global proportions of species per ecosystem (80% terrestrial, 15% marine, and 5% freshwater[19]), studies focused on marine species (11%) are actually under-represented (Figure 4). The lack of research effort in aquatic systems reflects a general lack of funding and shortage of specialists on taxa within these ecosystems as well as increased logistic challenges of surveying underwater compared with on land. For example, the relatively low proportion of publications on marine species (~10%) aligns with the small proportion of funding allocated for marine research and the proportion of journal editors, conference presenters, and specialist panel members that focus on marine systems.[16,17,29] Thus bias in research effort may reflect the disproportionate distribution of researchers, funding, and accessibility across ecosystems. Other factors that we have not examined in depth are likely also contributing to the biases we detected. For example, there are known publication biases associated with geography, language, and author identity.[30–33]

Some improvements through time are apparent, specifically in addressing the traditional lack of research effort directed at genetic diversity, the finest level of biodiversity. This improvement was evident by an increase in the proportion of genetic studies published in conservation biology journals from ~1980 to 1996 (Figure 6). Although the trend reversed after 1996, this is almost certainly due to the increased availability of scientific journals specializing in molecular methods applied to ecological, conservation, and evolutionary applications. Indeed, the decline in our surveyed journals after 1996 coincided with the arrival of three molecular-focused journals: *Molecular Ecology* (1992), *Molecular Phylogenetics and Evolution* (1992), and *Conservation Genetics* (2000). Consequently, genetic studies in the field of conservation biology may have continued to increase after 1996, but articles were split between conservation-focused and molecular-focused journals. Indeed, analyses of articles published in the aforementioned journals and other molecular journals show that genetic studies relevant to the field of conservation biology continued to increase after 1996.[34] Despite the apparent increase in genetic-focused conservation research, biases persist within these studies. For example, an increasing proportion of genetic studies purported for conservation are focused on species that are not threatened with extinction[9,34]; instead,

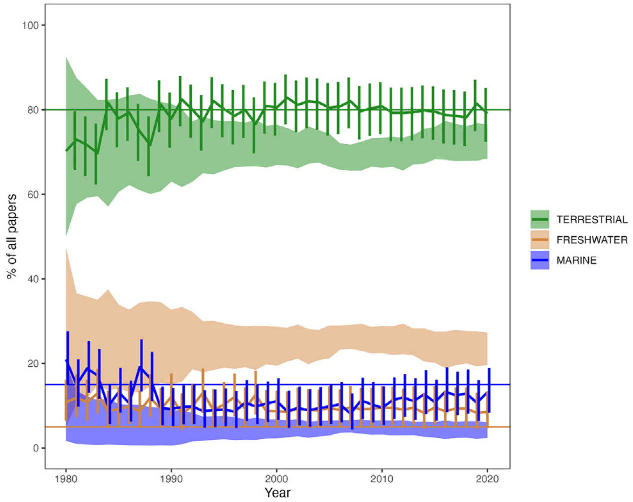

**Figure 4. Changes over time in broad study system focus**

Temporal patterns (1980–2020) in the percentage of conservation biology research articles focused on each of the three study systems. Research articles were surveyed from four leading conservation journals and categorized based on the ecosystem of the study species (see methods). The solid lines are the observed proportion of journal articles after correcting for differences between automated and manual searches, with error bars representing the uncertainty around those corrections (95% quantiles; see methods for full description). Ribbons represent the 95% quantiles of percentages found from 1,000 random subsamples of all species included in the IUCN species list (i.e., null model). Solid horizontal lines represent estimated proportions of extant species in each study system from Grosberg et al.[19] (80% terrestrial, 15% marine, 5% freshwater).

species within such studies tend to be of economic (e.g., agricultural), rather than conservation importance.[9] Thus, while there has been an improvement in the amount of effort directed toward genetic diversity, the usefulness of these studies for conserving biodiversity may be compromised by other motivations.

What are the consequences of these research biases? For taxonomic and ecosystem biases, our ability to conserve understudied groups is limited; thus, biodiversity loss (including *silent extinctions*, Table 1) is more likely compared with well-studied groups.[13,35] The implications of an increasing bias in genetic studies toward non-threatened species is that resources are deflected from species in most need of genetic research.[9,34] Threatened species (particularly those with low or declining population abundance) are most vulnerable to reductions in genetic diversity, probably the most important component for adapting to future challenges.[36–38] Ultimately these conditions will influence which species perish. Bias in research priorities is likely to contribute to bias in extinction patterns.

While efforts to conserve biodiversity continue to increase, it remains challenging to ensure that research and conservation efforts are proportionally allocated across all levels of biodiversity. One potential solution is to realign funding priorities, so they are proportionally allocated. However, funding is limited, and prioritization approaches often maximize conspicuous conservation returns (e.g., triage[39]) or focus on high-profile species. These approaches could inadvertently reinforce biases because a lack of knowledge about understudied groups could be seen as detrimental to conservation success and increase the costs of remedial efforts. Similarly, allocating funding based on the IUCN Red List of Threatened Species could still reinforce underfunding of understudied groups if data is not available to adequately conduct formal IUCN evaluations. To address this issue, alternative methods have been devised to identify understudied species that are threatened.[13,40]

Our study shows the persistence of long-standing biases in research to conserve biodiversity.[9,23,26,34,41] These biases remain and will ultimately lead to uneven loss of biodiversity as understudied groups decline and disappear—some species before they are even identified and described. Understanding how current conservation practices, funding allocation processes, and researchers themselves reinforce these biases should help level the playing field across taxa and ecosystems. Specifically, increasing the amount of funding allocated to understudied species and ecosystems will ensure a more equitable effort to conserve biodiversity across scales and help address impediments to CBD targets.

## EXPERIMENTAL PROCEDURES

### Resource availability

#### *Lead contact*

Further information and requests for resources should be directed to the lead contact, Áki Jarl Láruson (aki.jarl.laruson@hafogvatn.is).

#### *Materials availability*

This study did not generate new unique materials.

#### *Data and code availability*

Data files and accompanying code (R scripts) used for the analysis have been deposited at Zenodo [https://doi.org/10.5281/zenodo.10815720] and are publicly available as of the date of publication.

### Method details

To identify patterns in conservation research effort over time, and potential biases in that effort, we compiled data sourced from articles tagged specifically as research articles (as opposed to commentary or policy papers) published in four of the longest running conservation biology research journals: *Biodiversity & Conservation* (2021 Impact Factor 4.3), *Biological Conservation* (2021 Impact Factor 7.5), *Conservation Biology* (2021 Impact Factor 7.6), and *Conservation Letters* (2021 Impact Factor 10.1) (Figure S1A). Using the online databases Scopus and Web of Science, we found 17,502 research articles published between 1968 and 2020 in these four journals (see Figure S1A). We used information about the content of each of these research articles (e.g., title, abstract, keywords) to determine the focus of articles in three areas: study taxa, study environment (ecosystem and habitat), and whether the study included genetic analyses.

#### *Study taxa and system*

We extracted taxonomic and ecosystem data from research articles in two ways: (1) manually searching through the text of a subset of articles, and (2) using automated text searches of all articles. We subsequently corrected our automated search results, and estimated their uncertainty, by comparing our automatic and manual search results.

For our manual search, we selected a stratified random subset of 3,210 research articles published between 2000 and 2015 (representing ~33% of all articles in these journals from those years), with approximately equal representation for each year and each journal within each year. We read through each of the randomly selected articles to identify whether they focused on any specific taxonomic groups (species or kingdom) and study systems (i.e., marine, freshwater, and/or terrestrial).

For our automated searches, we searched Scopus and Web of Science manuscript fields (titles, abstracts, and keywords) for any and all species names that matched with an entry in the GBIF and/or the IUCN databases.

**Figure 5. Changes over time in specific habitat focus**

Temporal patterns (1980–2020) in conservation biology research effort per habitat, organized from the most to least overall research effort. Research effort is based on the IUCN “Habitats” assigned to species found in research articles published in four conservation biology journals (see methods). The solid lines are the percentages for each habitat in research articles. Ribbons represent the 95% quantiles of percentages found from 1,000 random subsamples of all species included in the IUCN species list (i.e., null model).

In total, we found 9,733 unique species mentioned in 9,004 articles (i.e., 51% of all 17,502 scientific articles searched). For every article with a species name assigned, we used information in the GBIF database to assign higher level taxonomic groups (family, class, and kingdom). To automatically assign ecosystems, we limited our automatic search to species in the IUCN database, since IUCN designates “systems” for each species. On a finer scale, we also assigned each species identified in the articles to one of 16 “habitats” designated in the IUCN species list (excluding “unknown habitat” and “other habitat”). Since there are fewer species listed in the IUCN database than in GBIF, we were only able to assign study systems and habitats to a smaller subset of 5,833 IUCN-listed species within 7,719 articles (Figure S1B).

Although we compiled data for research articles from as early as 1968, missing information (e.g., keywords and abstracts) meant that the percentage of articles in which we were able to identify species was much lower in the earlier years. To ensure that we were obtaining a representative sample of the articles, we used 1980 as the earliest cutoff for our taxonomic and study system analysis because there was a sudden increase in the number of articles in which a species was identified after 1980 (Figure S1).

We estimated uncertainty and error in the automatic search results by comparing the manual and automated datasets. Focusing on the subset of articles overlapping both datasets, we used either linear regression models (for species, family, and class accumulation) or beta regression models (for % of articles within kingdoms or study systems) to compare the manual assignments (response variable) with the automatic assignments (predictor variable). For the percentage of articles within each taxonomic kingdom and study system, we also included an interaction term to account for potential differences in relationships and errors for each kingdom and study system, respectively. We then used the resulting linear or beta regression models to generate predictions of what we would expect to have found if we manually searched each article, with estimated uncertainty around those predictions (95% quantiles), given the results of the automatic search.

### *Taxonomic analysis*

To explore how much conservation research effort was devoted to new taxa in each year (as opposed to studying the same taxa repeatedly), we created accumulation curves at three taxonomic scales: species, family, and class. As a basis for comparison, we also generated accumulation curves for null models at the same three taxonomic levels, simulating a random selection of study organisms. To generate these null models, we randomly selected the same number of species from the GBIF species list as was studied in each article, and repeated that process 1,000 times for each article. We generated accumulation curves for the 1,000 iterations and calculated the 95% quantiles around those accumulation curves, allowing us to compare the observed accumulation curves with a random expectation. We also generated 1,000 samples of the observed accumulation curve data by randomly sampling from a normal distribution based on results from the manual to automatic model fits. We summarized the data by decade and used t tests to evaluate whether the observed accumulation curves were significantly different from random expectations for each decade. To assess whether there was any change in bias over time, we subtracted the observed from the expected data and used one-way ANOVAs with Tukey multiple pairwise-comparison post-hoc tests to assess whether there was an increase or decrease in those differences from one decade to the next. To further assess which species represented the greatest focus over time, we identified the most frequently studied species (top 10) across the entire dataset and in each decade. In the case of ties within the top 10, all tied species were included.

On a broader taxonomic scale, we calculated the percentage of articles in each year that focused on particular kingdoms. Three kingdoms were represented well enough for this analysis: Animalia, Plantae, and Fungi. Only 3% of species in the GBIF database were not represented by one of these three kingdoms; this small percentage represents a deep-seated taxonomic bias which we are unable to properly account for here. To calculate the percentages from each of the three kingdoms, we used the total number of articles each year in which at least one species was found as the denominator. If an article included multiple kingdoms, then each kingdom was given proportional value. For example, if a study included a plant and an animal species, each was assigned half of the proportional value of that article in that year. To assess differences in proportional effort devoted to each kingdom over time, we compared these percentages by decade using Kruskal-Wallis and pairwise Wilcoxon’s post-hoc tests with false discovery rate. However, since equal effort is not necessarily what we should expect, we also created null models at the kingdom level using the same random selection process as the

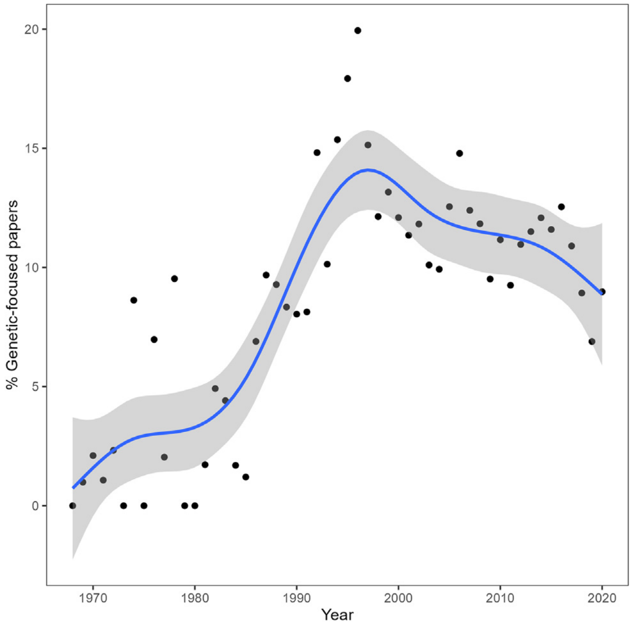

**Figure 6. Changes over time in genetics focus**

The percentage of genetic articles published in four conservation biology journals from 1968 to 2020. Points represent the percentage of all articles each year that contained genetics-associated words in their title, abstract, or keywords. Also shown is a generalized additive model (GAM) fit to the data (blue line), with 95% confidence intervals (gray ribbon).

accumulation curves but assigning each species to their corresponding kingdom. To test if the proportional effort devoted to each kingdom differs from random, we subtracted the 1,000 null percentages from the observed percentages for each kingdom in each year, then used Kruskal-Wallis tests and pairwise Wilcoxon's post-hoc tests to assess whether there were significant differences among kingdoms each decade.

### *Study system and habitat analysis*

To determine whether there were biases in research effort toward particular study systems or habitats, we analyzed the relative effort devoted to each over time. As with our kingdom-level analysis, we maintained proportional representation across articles and years by calculating and comparing the percentage of articles in each year that were devoted to each study system or habitat. For the denominator, we only included articles for which at least one study system or habitat could be applied. For any articles that included multiple study systems or habitats, we proportionally assigned partial value to each. For example, if a study included species that covered all three study systems (terrestrial, marine, and freshwater), each was assigned a third of the proportional value of that article in that year. As in the taxonomic analyses, we generated null models using 1,000 random samples, but using IUCN species instead of GBIF since the IUCN database was used to assign study systems and habitats. We compared the observed and null percentages of articles focused on each study system or habitat in each year using Kruskal-Wallis tests with pairwise Wilcoxon's post-hoc tests.

### *Genetic studies—Identification and analysis*

We used a targeted text search to assess trends in the number of genetics-focused conservation articles over time. We first developed the following regular expression to find words related to terms such as "GENE," "GENETICS," "DNA," "RNA," and "MOLECULAR": "\\bGENE\\b|\\bGENET\\w*|\\bDNA\\w*|\\bMDNA\\w*|\\bMTDNA\\w*|\\bRNA\\w*|\\bMOLECUL\\w*." We further refined this expression to remove the following exact matches that could refer to the common name of an animal (genet) within the genus Genetta: "GENET," "GENETTA," "GENETS." We applied this refined search expression to the titles, abstracts, and keywords of all articles to determine what percentage of articles in each year included a genetic component. We then used a generalized additive model (GAM) to explore trends in the percentage of genetics-focused articles over time.

To validate our targeted search for genetics-associated words, we manually checked a subset of 10% of the papers from two years: 1996 and 2019. We identified a random stratified sample of 10% of the papers from each journal within each of these years, resulting in a total of 106 papers (32 in 1996 and 74 in 2019). We chose 1996 as it was the year with the highest proportion of genetic papers according to our automated text search, reasoning that it would give us the best chance of identifying true and false positives. We then chose 2019, as the year after 1996 with the lowest proportion of genetic papers according to our automatic search, in an attempt to identify false negatives (e.g., papers that used more contemporary genetics-associated words that we did not include in our automated search). We manually read through each paper within the 10% sample to validate whether or not they involved any genetic component. We then compared the automatic text search with the manual assignments to estimate the percentage of false positives (papers identified in the text search as being genetics focused but are not) and the percentage of false negatives (papers identified in the text search as not being genetics-focused but are) and an overall accuracy (true positives + true negatives/# observations).

## SUPPLEMENTAL INFORMATION

Supplemental information can be found online at https://doi.org/10.1016/j.crsus.2024.100082.

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## AUTHOR CONTRIBUTIONS

Conceptualization: J.-P.A.H., P.F.C., and J.D.D.; data curation: I.R.C., J.-P.A.H., P.F.C., J.L.W., and A.J.L.; formal analysis: I.R.C. J.-P.A.H., and A.J.L.; funding acquisition: J.-P.A.H. and A.J.L.; investigation: I.R.C., J.-P.A.H., P.F.C., J.D.D., J.L.W., and A.J.L.; methodology: I.R.C., J.-P.A.H., P.F.C., J.D.D., and A.J.L.; project administration: I.R.C., J.-P.A.H., J.L.W., and A.J.L.; software: I.R.C. and A.J.L.; supervision: I.R.C., J.-P.A.H., and A.J.L.; validation: I.R.C., J.-P.A.H., P.F.C., J.D.D., J.L.W., P.A.A., R.B., S.C., R.R.C., M.I., E.C.J., I.K., E.M.N., T.M.S., and A.J.L.; visualization: I.R.C. and A.J.L.; writing – original draft: I.R.C., J.-P.A.H., and A.J.L.; writing – review & editing: I.R.C., J.-P.A.H., B.W.B., P.F.C., J.D.D., J.L.W., P.A.A., R.B., S.C., R.R.C., M.I., E.C.J., I.K., E.M.N., T.M.S., and A.J.L.

## DECLARATION OF INTERESTS

The authors declare no competing interests.

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