RESEARCH ARTICLE | ECOLOGY

Mutilation of the tree of life via mass extinction of animal genera

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Significance

We are in the sixth mass extinction event. Unlike the previous five, this one is caused by the overgrowth of a single species, *Homo sapiens*. Although the episode is often viewed as an unusually fast (in evolutionary time) loss of species, it is much more threatening, because beyond that loss, it is causing rapid mutilation of the tree of life, where entire branches (collections of species, genera, families, and so on) and the functions they perform are being lost. It is changing the trajectory of evolution globally and destroying the conditions that make human life possible. It is an irreversible threat to the persistence of civilization and the livability of future environments for *H. sapiens.* Instant corrective actions are required.

Abstract

Mass extinctions during the past 500 million y rapidly removed branches from the phylogenetic tree of life and required millions of years for evolution to generate functional replacements for the extinct (EX) organisms. Here we show, by examining 5,400 vertebrate genera (excluding fishes) comprising 34,600 species, that 73 genera became EX since 1500 AD. Beyond any doubt, the human-driven sixth mass extinction is more severe than previously assessed and is rapidly accelerating. The current generic extinction rates are 35 times higher than expected background rates prevailing in the last million years under the absence of human impacts. The genera lost in the last five centuries would have taken 18,000 y to vanish in the absence of human beings. Current generic extinction rates will likely greatly accelerate in the next few decades due to drivers accompanying the growth and consumption of the human enterprise such as habitat destruction, illegal trade, and climate disruption. If all now-endangered genera were to vanish by 2,100, extinction rates would be 354 (average) or 511 (for mammals) times higher than background rates, meaning that genera lost in three centuries would have taken 106,000 and 153,000 y to become EX in the absence of humans. Such mutilation of the tree of life and the resulting loss of ecosystem services provided by biodiversity to humanity is a serious threat to the stability of civilization. Immediate political, economic, and social efforts of an unprecedented scale are essential if we are to prevent these extinctions and their societal impacts.

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Over the last century the pace of many human activities has so accelerated (1), and human overpopulation grown so severe (2, 3), to have created a dramatic global environmental transformation. Most natural ecosystem have been highly modified or have disappeared altogether, and the abundance of wildlife has been greatly reduced (4–9). In well-studied major taxonomic groups, thousands of species and myriad populations have vanished (10–16). The precise number of recent extinctions is impossible to know, but current animal species extinction rates are estimated to be hundreds or thousands of times higher than the background rates that prevailed for millions of years prior to the agricultural revolution (11, 13, 17, 18). The number of vertebrate species known to have become extinct (EX) in the last 500 y would have taken some 10,000 y to vanish under background extinction rates (11). Data on most invertebrates and plants are even scantier; however, some groups also show substantial mutilation (13, 19). To "mutilate" is to cause serious damage, and anthropogenic rapid removal of branches from the tree of life is causing such damage. Furthermore, the potential losses of thousands of endangered (EN) vertebrate species and genera in this century dwarf the damage done in the last 500 y (10, 20–22). At least a third of land vertebrates are known to have decreasing populations, either through range contraction or shrinking numbers (12). For example, there were around 10,000,000 African elephants at the beginning of the 20th century, and now there are only about 450,000 remaining (23, 24). In several countries, all elephant populations have gone EX, and the great beasts are now absent from many large regions of other countries they once occupied. Surviving populations are scattered and most are declining (25). We are not implying that the eventual extinction of African savannah elephants (or all elephants) is an example of a loss with a likely high cost to future *Homo sapiens*. We are, however, implying that the patterns illustrated by this well-censused iconic animal are likely replicated in many less-prominent organisms in systems essential to the thriving of future people.

It is well understood that losing species affects the global configuration of Darwin's "Tree of Life"—the phylogeny of all living entities. Their disappearance is automatically changing the course of evolution by terminating unique pathways of biological change and has profound consequences on issues as diverse as morphological and ecological distinctiveness, many with negative effects on ecosystem structure and function (26–33). However, because phylogenetic relationships and key data on ecological processes are so unevenly available across taxonomic groups and because of the emphasis on species extinctions (34–37), the scientific literature is lacking an overview of the magnitude and impact of today's already substantial mutilation of the tree of life at higher taxonomic hierarchies.

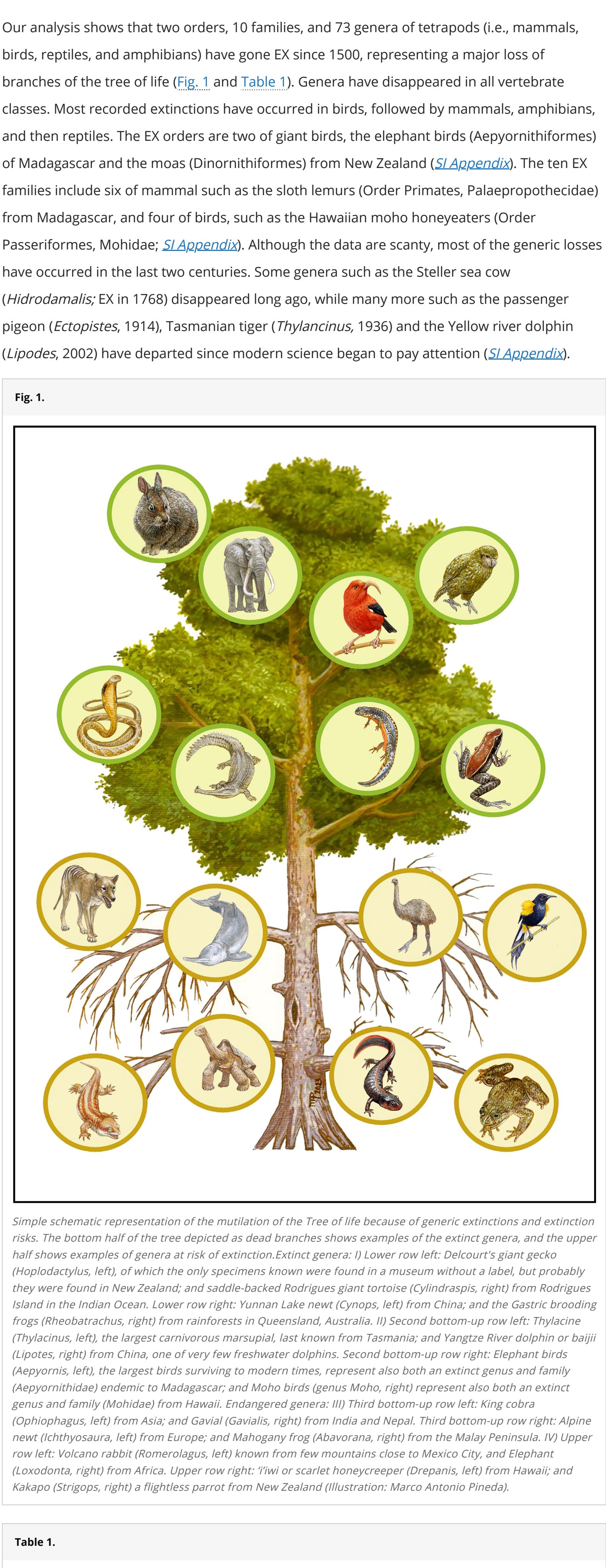
Here, we assess the magnitude of the current extinction crisis on the land vertebrate part of the tree at the generic level in order to investigate patterns of extinction beyond the levels of populations and species We address the following questions: i) What is the magnitude of the current mutilation measured by recent extinction of vertebrate genera?, ii) How do those current *generic* extinction rates compare with the background rates, that prevail in the last million years before human impacts?, iii) What are the patterns of global distribution of extinction and endangerment? and iii) What are the implications of these findings for understanding the likely consequences of the mutilation of the tree of life for the future of biodiversity and *H. sapiens*?

Results

Lost Diversity.

Our analysis shows that two orders, 10 families, and 73 genera of tetrapods (i.e., mammals, birds, reptiles, and amphibians) have gone EX since 1500, representing a major loss of branches of the tree of life (Fig. 1 and Table 1). Genera have disappeared in all vertebrate classes. Most recorded extinctions have occurred in birds, followed by mammals, amphibians, and then reptiles. The EX orders are two of giant birds, the elephant birds (Aepyornithiformes) of Madagascar and the moas (Dinornithiformes) from New Zealand (*SI Appendix*). The ten EX families include six of mammal such as the sloth lemurs (Order Primates, Palaeopropithecidae) from Madagascar, and four of birds, such as the Hawaiian moho honeyeaters (Order Passeriformes, Mohidae; *SI Appendix*). Although the data are scanty, most of the generic losses have occurred in the last two centuries. Some genera such as the Steller sea cow (*Hidrodamalis*; EX in 1768) disappeared long ago, while many more such as the passenger pigeon (*Ectopistes*, 1914), Tasmanian tiger (*Thylancinus*, 1936) and the Yellow river dolphin (*Lipodes*, 2002) have departed since modern science began to pay attention (*SI Appendix*).

Fig. 1.



Simple schematic representation of the mutilation of the Tree of life because of generic extinctions and extinction risks. The bottom half of the tree depicted as dead branches shows examples of the extinct genera, and the upper half shows examples of genera at risk of extinction.Extinct genera: I) Lower row left: Delcourt's giant gecko (Hoplodactylus, left), of which the only specimens known were found in a museum without a label, but probably they were found in New Zealand; and saddle-backed Rodrigues giant tortoise (Cylindraspis, right) from Rodrigues Island in the Indian Ocean. Lower row right: Yunnan Lake newt (Cynops, left) from China; and the Gastric brooding frogs (Rheobatrachus, right) from rainforests in Queensland, Australia. II) Second bottom-up row left: Thylacine (Thylacinus, left), the largest carnivorous marsupial, last known from Tasmania; and Yangtze River dolphin or baijii (Lipotes, right) from China, one of very few freshwater dolphins. Second bottom-up row right: Elephant birds (Aepyornis, left), the largest birds surviving to modern times, represent also both an extinct genus and family (Aepyornithidae) endemic to Madagascar; and Moho birds (genus Moho, right) represent also both an extinct genus and family (Mohidae) from Hawaii. Endangered genera: III) Third bottom-up row left: King cobra (Ophiophagus, left) from Asia; and Gavial (Gavialis, right) from India and Nepal. Third bottom-up row right: Alpine newt (Ichthyosaura, left) from Europe; and Mahogany frog (Abavorana, right) from the Malay Peninsula. IV) Upper row left: Volcano rabbit (Romerolagus, left) known from few mountains close to Mexico City, and Elephant (Loxodonta, right) from Africa. Upper row right: 'i'iwi or scarlet honeycreeper (Drepanis, left) from Hawaii; and Kakapo (Strigops, right) a flightless parrot from New Zealand (Illustration: Marco Antonio Pineda).

Table 1.

Vertebrate generic extinctions since 1500

		Vertebrates			
Taxonomic Level	Total	Mammalia	Aves	Reptilia	Amphibia
Orders	41	14	23	2	2

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Number of taxa at different hierarchical taxonomic levels containing the extinct genera since 1500. Extinct genera include the Extinct (EX), Extinct in the Wild (EW), Possibly Extinct (PE) categories of IUCN (24). For example, the 73 extinct genera belong to 41 orders, of which two are extinct. The highest number of extinct genera belongs to Aves and the lowest to Reptilia.

Background and Current Generic Extinction Rates.

The background generic extinction rate prevailing in the last millions of years, before human impacts has been estimated at 0.75 genus per 10,000 genera per 100 y (Table 2, A. Barnosky, pers. comm.). Presently, there are around 5,418 vertebrate genera, so if the current generic extinction rates were similar to the background extinction rates, they would be equal to 0.4 genus per 5,418 genera per 100 y. Under those rates, one vertebrate genus should be expected to become EX in roughly 250 y (i.e., two in the last 500 y), but the background time for one extinction for particular vertebrate classes varies from 550 y for birds to 2,500 y for amphibians (Table 2). This variation is related to the observed number of extinctions and the total number genera in each class.

Table 2.

Generic vertebrate background extinction rates

Generic Vertebrate Background Extinction Rates (Source of mammal background A. Barnosky, pers comm.)			
	Number of Genera	Extinction Rate per 100 y	Expected years to observed one genus extinction

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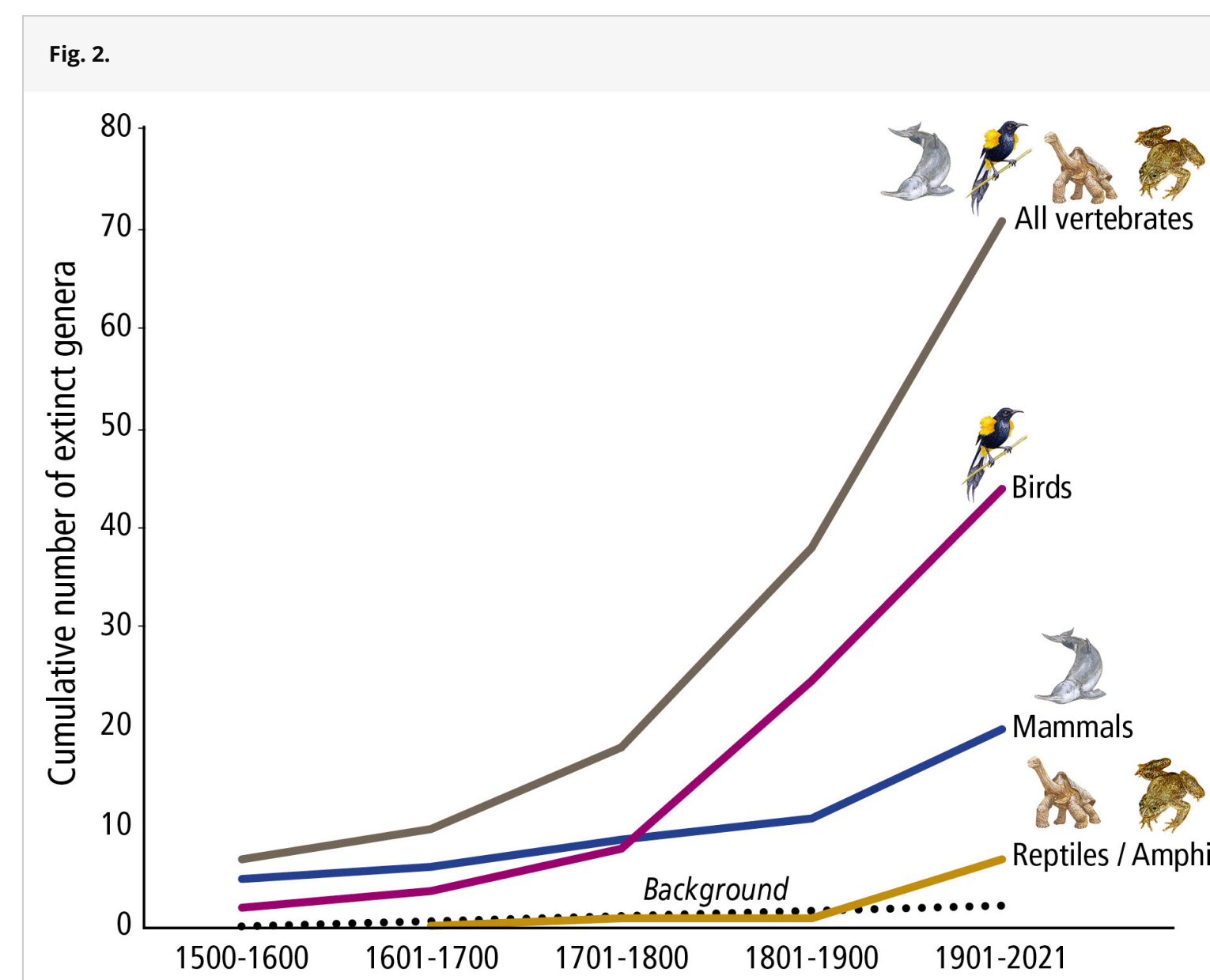
The table shows the current extinction rates if they were similar to the estimated background extinction rates for mammals in the last million years (i.e., 0.75 genus per 10,000 genera per 100 y; A. Barnosky pers. comm). The variation of the current extinction rates is related to the number of genera both in all vertebrates and in each class.

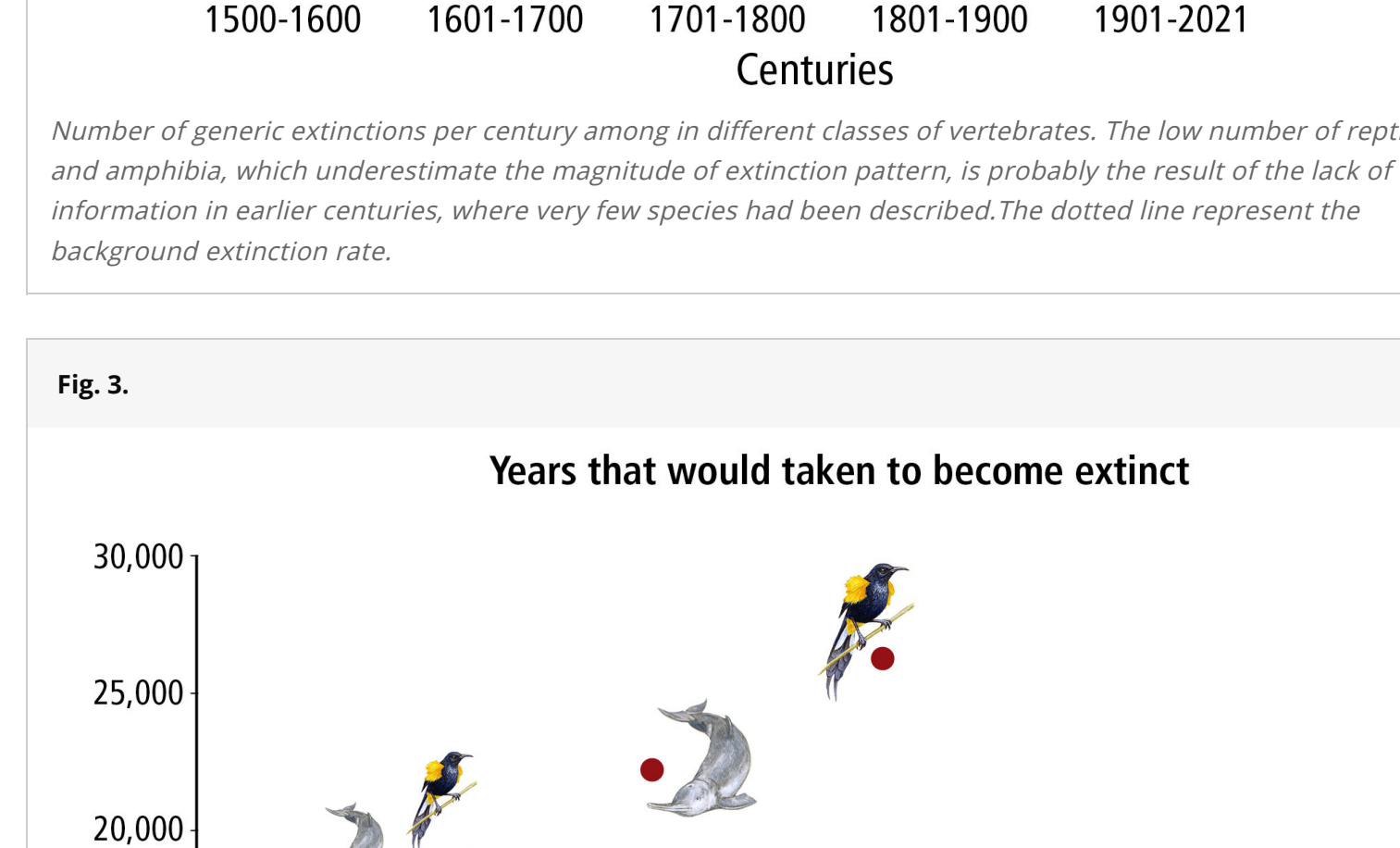
The actual generic current extinction rates are, however, much higher than the background ones. Instead of losing the expected two vertebrate genera in 500 y (i.e., between 1500 to 2022), at least 73 genera became extinct in that period, indicating that the observed extinction ratio is 35 times higher than the background rate prevailing over the last few million years (Table 3 and Fig. 2). This means that the genera lost in the last five centuries should have taken roughly 18,000 y to become extinct under the background rate. Variation among groups shows an even more sobering scenario, because extinct mammals and birds, for example, would have taken 23,000 and 26,000 y respectively, to become extinct under normal "background" conditions (Table 3 and Fig. 3).

Fig. 2.



Number of generic extinctions per century among in different classes of vertebrates. The low number of reptiles and amphibia, which underestimate the magnitude of extinction pattern, is probably the result of the lack of information in earlier centuries, where very few species had been described.The dotted line represent the background extinction rate.

Fig. 3.



Number of years that would have taken for vertebrate genera to become extinct under the background extinction rate prevailing in the last million years. The number of years for all extinct vertebrate genera is 18,000 y. Reptiles and amphibians have fewer extinct genera, so their values are much smaller that mammals and birds.

Table 3.

Comparison of background, historic, and projected (to 2100) number of generic vertebrate extinctions

Vertebrates				
A) Total	B) Extinct	C) Calculated number	D) Ratio (realized/ expected	E) Years that would have

EXPAND FOR MORE

The projections suggest that the already massive losses will show a great increase in the mutilation of the tree of life if the endangered genera become extinct in this century. The 1800 to 2100 section was calculated with the sum of the extinct genera plus the currently endangered (in parenthesis) ones. Number on column E has been rounded.

What will be the magnitude of the sixth mass extinction by the end of the century if the biological annihilation continues and all EN monotypic genera are lost? If current biological annihilation continues and all EN monotypic genera become by the end of this century the generic extinction rates would be unprecedented in the last 66 million y, being 354 times larger for all land vertebrates when compared to background extinction rates (Table 3) and would vary from 86 times in reptiles to 511 times in mammals. In other words, projected losses of genera over three centuries (1800 to 2100) would have taken 106,000 y for all vertebrates and up to 153,000 y for mammals to become EX under the normal, background, rates. Over these geologic time scales, rates of speciation would approximately balance background extinctions, but this cannot occur when extinction rates are so greatly increased.

Endangered Diversity.

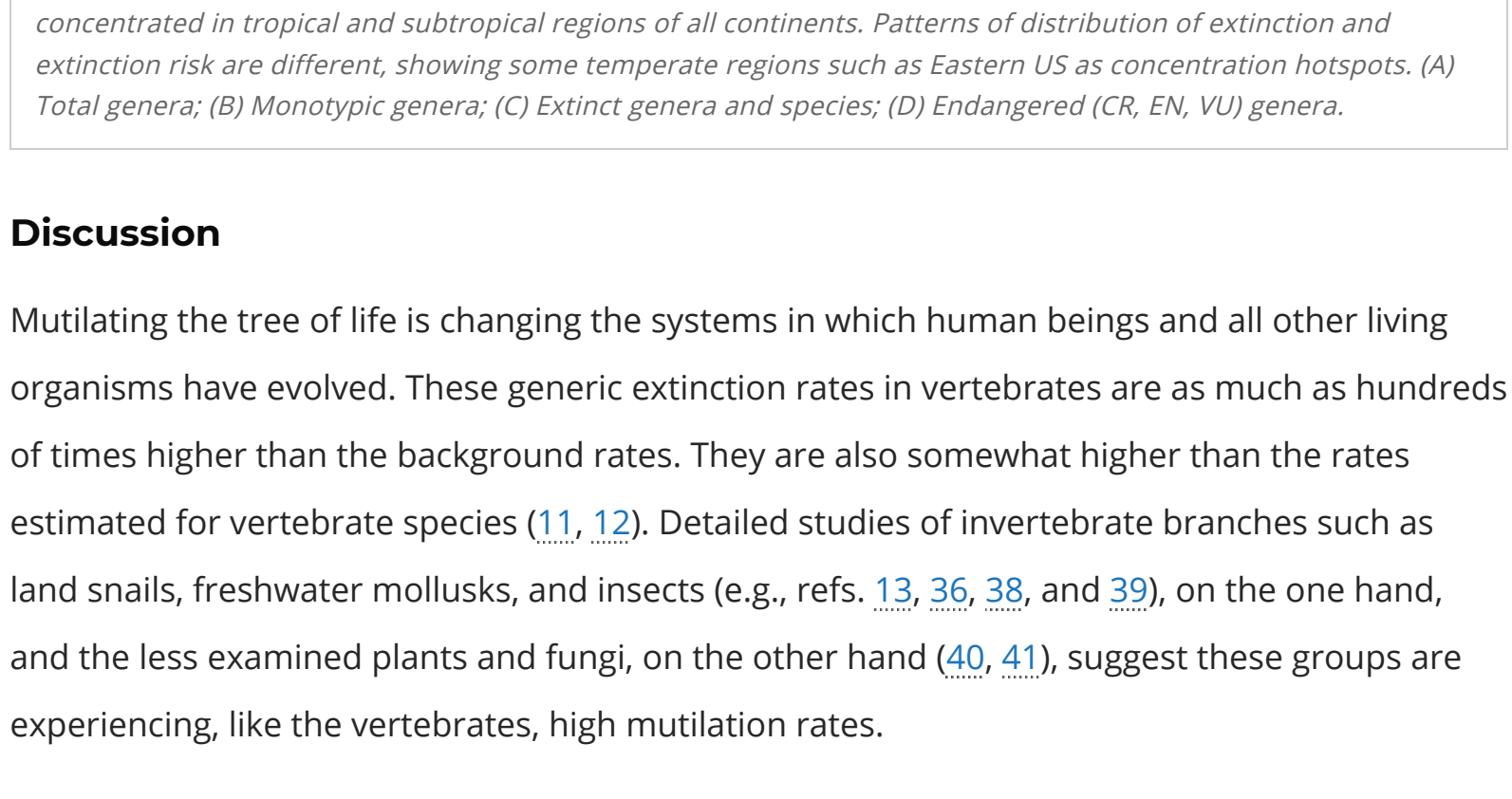
In order to be very conservative in evaluating the potential loss of evolutionary diversity, we restrict our analysis to monotypic genera whose single species is EN.

There are 1,830 monotypic genera (34% of all genera), belonging to 372 families and 63 orders. Ordinarily, the extinction of the one species of these genera would have a greater impact in the tree of life than losing one species in a species-rich genus. At least 370 (20%) of these monotypic genera or other polytypic genera with few species that are already EN. Most of the monotypic ones are birds (137, 37% of the EN genera), followed by mammals (126, 34%), reptiles (59, 16%), and then amphibians (48, 13%). Interestingly, many of those genera at risk represent the largest, more widespread, vertebrate animals, that very likely have profound impacts on ecosystem function and services. Some examples of those monotypic genera are the Sumatran rhino (*Dicerorhinus*), the kakapo (*Strigops*), the gavial (*Gavialis*), and Archey's frog (*Leiopelma*).

Geographic Trends in Generic Losses.

Vertebrate genera that have already gone EX were found on all continents except Antarctica, with major concentrations in regions of each continent, particularly in the tropics (Fig. 4A). The global patterns of total genera and monotypic genera are, surprisingly, rather similar (Fig. 4 *A* and *B*). The subtropical and tropical regions of the Americas, Asia and Africa had both rich total and monotypic genera diversity. Interestingly, EN genera have somewhat similar patterns of distribution, but the regions with high endangerment are different (Fig. 4*C*). Finally, extinctions of genera (and species and populations) have very different distributions (Fig. 4*D*). For example, an area of high concentration of extinctions is the eastern United States, which is not a global region of high diversity. Our maps clearly show that tropical regions in the Americas (from southern Mexico to southern Brazil and northern Argentine), sub-Saharan African, and southern Asia from China and Bhutan to Sumatra and Borneo, are the ones concentrating extant monotypic genera. Therefore, they should be considered primary regions for conservation if a goal is preserving evolutionary potential.

Fig. 4.



Patterns of distribution of extinct and extant land vertebrate genera. Most genera and monotypic ones are concentrated in tropical and subtropical regions of all continents. Patterns of distribution of extinction and extinction risk are different, showing some temperate regions such as Eastern US as concentration hotspots. (A) Total genera; (B) Monotypic genera; (C) Extinct genera and species; (D) Endangered (CR, EN, VU) genera.

Discussion

Mutilating the tree of life is changing the systems in which human beings and all other living organisms have evolved. These generic extinction rates in vertebrates are as much as hundreds of times higher than the background rates. They are also somewhat higher than the rates estimated for vertebrate species (11, 12). Detailed studies of invertebrate branches such as land snails, freshwater mollusks, and insects (e.g., refs. 13, 36, 38, and 39), on the one hand, and the less examined plants and fungi, on the other hand (40, 41), suggest these groups are experiencing, like the vertebrates, high mutilation rates.

Earth has already lost and is now missing significant twigs and branches of the tree of life, losing evolutionary morphologies, ecological roles, and ecosystem functions depending on them, among many other things. This mass extinction is transforming the whole biosphere, possibly into a state in which it may be impossible for our current civilization to persist. The mutilation is eroding the generic library, with consequences on ecosystem functioning and services, including primary productivity, the biogeochemical cycles, and species interactions, among many other (42–46). Absent taxa include genera ranging from evolutionary oddities with very restricted geographic ranges such as the gastric brooding frogs (*Rheobatrachus*) to widespread ones like passenger pigeons (*Ectopistes*). Lacking knowledge of the evolutionary and ecological roles of threatened vertebrates does not preclude us from seeing that it is essential for humanity to take immediate action. After all, we and all other species have evolved together thriving within a stable tree of life (47).

Although the gastric brooding frogs lived in a very small area of Queensland human-dominated rainforest in Australia, their extinction to human pressures represent an instance of loss of opportunity for humanity. Their reproduction systems were unique; the females swallowed the newly fertilized eggs and brooded the tadpoles in their stomachs, which were converted into wombs (48). The frogs were a wonderful model for studying human diseases such as acid reflux and related cancers because the frogs' stomach acid had to be turned off to protect the brood (48, 49). But now they are lost to us as experimental models. Interestingly, many species and genera with functional ecological traits fundamental for the provision of ecosystem goods and services are rare as the gastric breeding frog (43).

The loss of a widespread genus can have, instead, an impact on the function of an entire ecosystem. The anthropogenic extinction of the passenger pigeons narrowed human diets in the northeastern North America and altered ecosystem structure over wide areas. Along with other extinctions and population declines (e.g., cougars and wolves) and resultant shifts in rodent communities, the region likely became ripe for outbreaks of many zoonotic infectious diseases such as the tick-borne spirochete (*Borrelia burgdorferi*) which causes Lyme disease, a nasty and increasingly common human malady (50, 51).

Indeed, there is substantial reason to believe that the destruction and geographic homogenization of the biosphere that accompanies the mutilation of the tree of life at the generic and other taxonomic levels is increasing pandemic disease risk for all macroorganisms including *H. sapiens* (52–54). That is the case of emerging zoonotic diseases such as ebola, Marburg virus, hantavirus disease, Mers, Sars, and Covid (55, 56). For example, in the last decades, the negative relationship between North American bird diversity and human infection by the recently introduced West Nile virus provides another example (52). So does likely health impacts of the removal of large portions of the anuran branch of the tree of life over much of the globe. It has not been well studied, but in Central America the loss of populations of mosquito-gobbling frogs have been accompanied by surges in human malaria (57).

During past mass extinctions there was no species with the power or interest to stop extinctions, and no conscious stake in maintaining biodiversity. Today there is a species that should know it is not able to wait millions of years for its life-support systems to be restored after a mass extinction. Ironically, the scale that species' activities is the sole cause of today's biological holocaust. What is crystal clear is that the trajectory of the dimming future of civilization will be directed in part not just by the overall loss of biodiversity but by the pattern of our mutilation of the tree of life. The scientific community understands this existential problem, so it is time generate public understanding into policy action while there is still a rapidly disappearing window of opportunity to act. What happens in the next two decades will very likely define the future of biodiversity and *H. sapiens*.

Materials and Methods

The list, conservation status, and maps of geographic range of EX and EN genera were obtained from the International Union for the Conservation for Nature (IUCN) and BirdLife International (accessed via http://www.iucn.org and http://www.birdlife.org in March 2022), and other sources (e.g., refs. 14, 16, 58, and 59). It is important to indicate that there is not scientific consensus on the validity or conservation status of some genera. For example, *Lipodes* is considered EX since 2002 but IUCN still considered Critically endangered (CR) (24). In general, we followed IUCN, but in several cases, we have to use other sources (*SI Appendix*). EX genera in our study include those in the IUCN categories of EX, Extinct in the Wild, and Possible EX. EN genera included monotypic ones considered as CR and EN by IUCN. The estimated the background extinction rates for mammal genera in the last million years, 0.75 genus per 10,000 genera per 100 y, were generously provided by Anthony Barnosky (see ref. 17 for methodology to obtain the background rates). To create global maps displaying the distribution ranges of all groups, we overlapped and combined the individual distribution ranges using ArcGIS 10.1. For this process, we employed a Behrmann equal-area global grid with a cell size of 96.5 km × 96.5 km (approximately equivalent to 1° at the equator). After excluding grid cells containing less than 50% of the continental surface, we conducted our analysis using a total of 14,615 cells on a global scale.

Data, Materials, and Software Availability

All study data are included in the article and/or *SI Appendix*.

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Author contributions: G.C. and P.R.E. designed research; performed research; analyzed data; and wrote the paper.

Competing interests: The authors declare no competing interest.

Supporting Information

Appendix 01 (PDF)

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