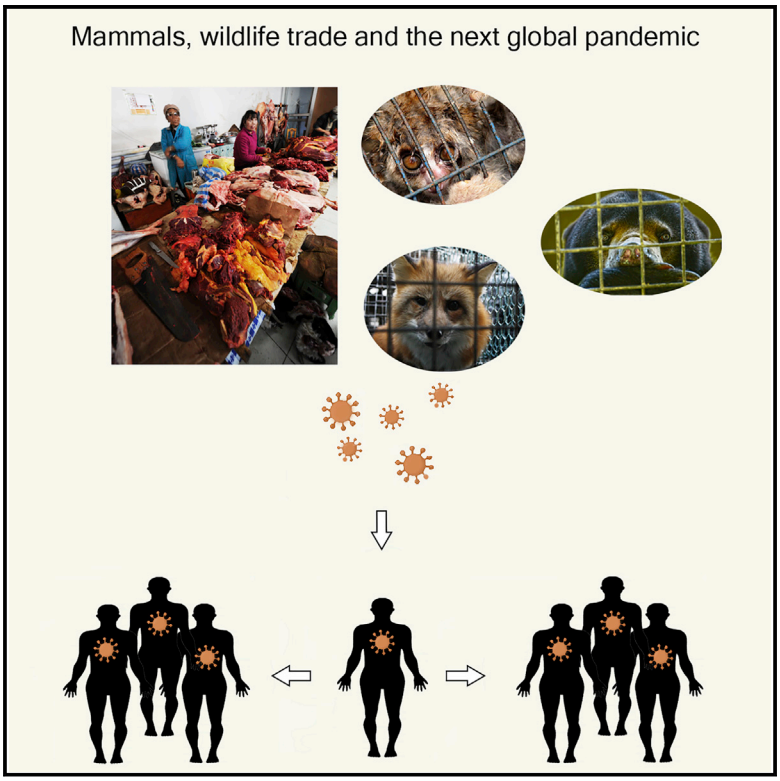
Report

Current Biology

Mammals, wildlife trade, and the next global pandemic

Graphical abstract



Highlights

- A quarter of mammals in wildlife trade host 75% of known zoonotic viruses
- Ungulates, primates, and bats are the major zoonotic reservoirs in wildlife trade
- Not all mammals in wildlife trade host viruses harmful to humans
- Mitigation measures should focus on reservoir species to prevent future pandemics

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In brief

The role of wildlife trade as a source of diseases infectious to humans has long been debated. Shivaprakash et al. show that one-quarter of the mammals in wildlife trade host 75% of known zoonotic viruses, providing some of the first empirical evidence that wildlife trade and zoonotic disease risks are strongly associated.

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Report

Mammals, wildlife trade, and the next global pandemic

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SUMMARY

Most new infectious diseases emerge when pathogens transfer from animals to humans.[1,2] The suspected origin of the COVID pandemic in a wildlife wet market has resurfaced debates on the role of wildlife trade as a potential source of emerging zoonotic diseases.[3–5] Yet there are no studies quantitatively assessing zoonotic disease risk associated with wildlife trade. Combining data on mammal species hosting zoonotic viruses and mammals known to be in current and future wildlife trade,[6] we found that one-quarter (26.5%) of the mammals in wildlife trade harbor 75% of known zoonotic viruses, a level much higher than domesticated and non-traded mammals. The traded mammals also harbor distinct compositions of zoonotic viruses and different host reservoirs from non-traded and domesticated mammals. Furthermore, we highlight that primates, ungulates, carnivores, and bats represent significant zoonotic disease risks as they host 132 (58%) of 226 known zoonotic viruses in present wildlife trade, whereas species of bats, rodents, and marsupials represent significant zoonotic disease risks in future wildlife trade. Thus, the risk of carrying zoonotic diseases is not equal for all mammal species in wildlife trade. Overall, our findings strengthen the evidence that wildlife trade and zoonotic disease risks are strongly associated, and that mitigation measures should prioritize species with the highest risk of carrying zoonotic viruses. Curbing the sales of wildlife products and developing principles that support the sustainable and healthy trade of wildlife could be cost-effective investments given the potential risk and consequences of zoonotic outbreaks.

RESULTS AND DISCUSSION

The COVID-19 pandemic has provided an opportunity for humanity to emphasize the significant and often under-appreciated relationship between people and nature. With millions of lives lost and the world's economy impacted, the focus is on containment of the current outbreak and prevention of future outbreaks.[7–9] Global wildlife trade has drawn considerable public attention,[4,10–14] because it results in direct contact between humans and both wild and domesticated animals that are potential hosts of zoonotic pathogens.[10,11] Annually, upward of one billion direct and indirect contacts among wildlife, humans, and domestic animals result from wildlife trade.[10] The growing demand for wildlife products and modern, faster, and cheaper transportation options via air and water has dramatically increased the potential for cross-species transmission of zoonotic diseases.[10–14]

Recent studies have largely focused on quantifying the magnitude of wildlife trade globally,[6] with limited data on pathogen load of animals involved in legal wildlife trade, which may enable estimates of their potential risk for global health.[5,10–17] Our focus is on zoonotic viruses of mammals because most emerging infectious diseases are more likely to be viral with origins in mammal species. Here we provide the first global analysis of mammals known to be in wildlife trade (including both legally and illegally traded animals)[6] and their associated zoonotic pathogen loads from published data. We compare mammal groups for their potential to carry viral zoonotic diseases via wildlife trade. Further, we also compare wild non-traded and domesticated mammal species as carriers of zoonotic viruses. We first describe the pattern and distribution of viral load (total and zoonotic virus richness) and diversity across mammal taxonomic orders. We then describe the phylogenetic pattern of viral load across mammalian phylogeny to understand whether zoonotic disease risk is concentrated within closely related host taxa in wildlife trade. Finally, we discuss the broader implications of our findings for the global health risk of wildlife trade.

In the last decade alone, viruses have been responsible for several important global pandemics, i.e., COVID-19, Ebola, HIV, Middle East respiratory syndrome (MERS), and severe acute respiratory syndrome (SARS),[1,2,18–20] that have had a significant impact on human health and economic security.[1,4,21,22] Further, mammals and birds alone are thought to host an estimated 1.7 million undiscovered viruses and, of these, 540,000–

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Table 1. Summary of the viruses identified across 1,120 mammal host species

					Total viruses		Zoonotic viruses	
Order	Global richness (domesticated/ nontraded/traded)	No. of host species screened for viruses (domesticated/ nontraded/traded)	No. of host species with zoonotic viruses	Mean no. of hosts/ virus (total/zoonotic)	No.	Mean/host (range)	No.	Mean/host (range)
Rodentia	2,225 (7/1,990/228)	309 (7/246/56)	241	2.9/5.1[a]	355	4.92[a] (1.31)[a]	120	5.25[a] (2.61)[a]
Chiroptera	1,145 (0/957/158)	324 (0/230/89)	213	2.1/7.52[a]	808	12.55[a] (1.10)	65	7.25[a] (2.16)[a]
Primates	417 (0/30/387)	137 (0/11/126)	108	2.26/4[a]	393	11.2[a] (0.90)[a]	81	3.84[a] (1.52)[a]
Cetartiodactyla	270 (24/11/235)	125 (24/17/84)	100	3.6[a]/4.35[a]	238	7.0[a] (1.37)[a]	101	4.33[a] (2.0)[a]
Carnivora	280 (3/57/220)	106 (3/16/87)	107	3.7[a]/4.24[a]	101	3.4 (0.60)	58	4.13[a] (1.09)[a]
Marsupials	329 (0/255/74)	24 (0/11/13)	18	2/2	34	2.9 (0.11)	24	2.04 (0.22)
Lagomorpha	92 (1/42/49)	15 (1/3/11)	13	1.7/1.94	30	3.4 (0.08)	16	1.94 (0.14)
Eulipotyphla	443 (0/430/13)	18 (0/18/0)	11	1.1/1.2	49	4.4 (0.03)	14	1.2 (0.08)
Perissodactyla	17 (0/1/16)	6 (0/6/6)	5	1.83/2.25	12	3.7 (0.04)	4	2.25 (0.04)
Pilosa	10 (0/2/8)	6 (0/1/5)	6	1.9/1.9	11	3.5 (0.03)	11	1.91 (0.10)
Cingulata	21 (0/7/14)	4 (0/3/1)	4	1.43/1.43	7	2.5 (0.02)	7	1.43 (0.04)
Pholidota	8 (0/0/8)	2 (0/1/1)	2	–	2	1.3 (0.01)	1	–
Proboscidea	2 (0/0/2)	2 (1/0/1)	2	1.4/1.5	9	6.5[a] (0.02)	6	1.5 (0.04)
Macroscelidea	17 (0/15/2)	1 (0/1/0)	1	–	1	–	1	–
Scandentia	20 (0/1/19)	3 (0/0/3)	1	1.2/–	11	7.3[a] (0.11)[a]	1	–
Total	5,804 (37/4,326/1,441)	1,120 (37/573/510)	836		1,682		226	

[a]Orders having broader host range and higher mean number of total and zoonotic viruses/host taxa. See also Data S1C.

850,000 viruses could have the ability to infect humans.[23] Our findings may be used to inform policy decisions about wildlife importation and mitigation measures that could promote sustainable and healthy animal trade to prevent potential health risks of wildlife trade.

General trend of viruses across mammals

Our results based on meta-analysis of mammal-virus association and wildlife trade[6] data obtained from the literature survey reveal Rodentia (rodents), Chiroptera (bats), Primates, Cetartiodactyla (even-toed ungulates), and Carnivora (carnivores) to be the major reservoirs of zoonotic viruses among mammals (Figures S1A and S1B; Table 1), and these findings are in line with previous studies.[2,24,25] However, whereas the previous studies have highlighted Rodentia and Chiroptera as the special reservoir of zoonotic viruses among mammals,[26,27] less focus is given to other mammal groups such as Cetartiodactyla and Primates. Our analyses reveal that Cetartiodactyla and Primates also show a broad host range for zoonotic viruses and harbor, on average, more viruses/host species (Table 1). Therefore, in addition to rodents and bats, we suggest Cetartiodactyla and Primates also be considered as important reservoirs of viral zoonotic pathogens. Furthermore, despite weak phylogenetic signal of viral load (total and zoonotic virus richness) across mammalian phylogeny (Figure S2C), Primates, Cetartiodactyla, and Chiroptera tend to share a high load of total and zoonotic viruses among closely related species compared to other orders (Figures S2A and S2B). Our results suggest that specific tips of mammal phylogenies are more likely to carry high viral loads. However, the phylogenetic signal of viral load we detected could be a function of both the incomplete sampling of mammal species for viruses (Table 1) and undiscovered viral diversity in mammals.[28] To date, only a fraction of virus species harbored by mammals have been discovered.[28] Therefore, our incomplete viral diversity data may make the detection of the true phylogenetic signal of viral load difficult.

Association of zoonotic viruses with mammals in wildlife trade

Our analyses of mammal-virus association in wildlife trade suggested structured variation in host richness and total and zoonotic virus richness across mammalian orders (Figures 1 and S1C–S1F; Table S1) and mainly revealed five major findings. First, mammals in wildlife trade had the highest number of both total (878, 52%) and zoonotic viruses (170, 75.2%) compared to domesticated (288, 17%; 117, 52%) and non-traded mammals (846, 50%; 143, 63%). By sharing a large number of known zoonotic viruses, Primates (77, 34%), Cetartiodactyla (62, 27%), and Carnivores (41, 18%) emerge as a major reservoir of zoonotic viruses in current wildlife trade (Figures 1B and S1D), and Chiroptera, Rodentia, and Marsupials are predicted to host high numbers of zoonotic viruses in future wildlife trade (Figures 1B and S1D). Of the 121–244 mammal species predicted to be involved in future wildlife trade,[6] at least 44 of these mammal species host 47 (20%) known zoonotic viruses in our database (Figures 1B and S1D). Therefore, future wildlife trade is expected to increase zoonotic disease risks as novel mammal species get included in wildlife trade. Second, traded and non-traded mammals showed significantly distinct (measured as Bray-Curtis dissimilarity) total and zoonotic virus species composition as compared to domesticated mammals (Figures 2A and 2B). Third, there was greater overlap in the composition of virus species between domesticated and traded mammals than between domesticated and non-traded mammals (Figures 2C and 2D).

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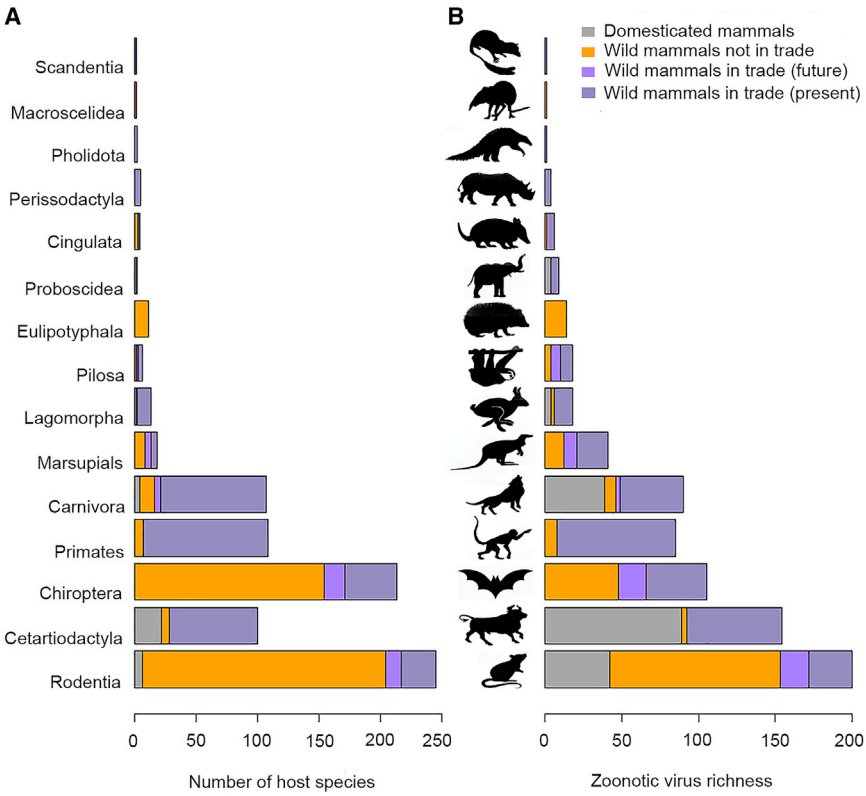

Figure 1. The distribution of host species and zoonotic virus richness across mammalian orders

Number of mammal species hosting zoonotic viruses (A) and total zoonotic viral richness segregated by animal trade category (B): wildlife in trade (present), wildlife in trade (future), wildlife not in trade, and domesticated mammals. See also Figure S1, Data S1, and Table S1.

The high overlap in zoonotic virus composition between domesticated and traded mammals could be driven by taxonomic and phylogenetic relatedness of taxa as they share mammal species from similar taxonomic groups such as Cetartiodactyla and Carnivora. Further, such similarity in virus composition may also indicate the likely role of wildlife trade in the spillover of zoonotic pathogens to domesticated animals, because wildlife markets provide a platform for direct contact between domestic and wild animals, facilitating exchange of zoonotic pathogens.[10] Therefore, domesticated mammals may act as intermediate hosts to transmit zoonotic pathogens from traded wild animals. For example, many zoonotic diseases (swine flu, MERS, Nipah, Menangle, etc.) were transmitted to humans via domesticated animals infected from contact with wildlife species that were sold as food or as pets.[29] Fourth, the 210 mammal species known to have been legally traded between 2012 and 2016[11] alone host 51% of known zoonotic viruses in our database (Figures S1G and S1H). Fifth, Cetartiodactyla (89, 39%), Rodentia (42, 19%), and Carnivora (39, 17%) were the major reservoirs of zoonotic viruses among domesticated mammals, whereas Rodentia (111, 49%) and Chiroptera (48, 21%) were exclusively the major reservoirs of zoonotic viruses for mammals not in wildlife trade (Figures 1B and S1D; Table S1).

In the last few decades, most viral zoonotic diseases have had their origin in wildlife, and their spillover is mainly linked to drivers such as land-use change (LUC) and wildlife trade including hunting for trophies and bushmeat, agriculture expansion, and food industry change.[1,29] While the emergence of many novel viral zoonotic diseases of pandemic potential (SARS, MERS, Ebola, Disease X, etc.), including the ongoing COVID-19 pandemic, is linked to wildlife trade, the debate surrounding wildlife trade as a major factor behind zoonotic disease transmission has heightened the threat of this commerce for human health, economic security, and biodiversity conservation.[4,30] Overall, our findings of a high volume of zoonotic viral pathogens in mammals of wildlife trade compared to domesticated and non-traded mammals implicate wildlife trade as a major mode of zoonotic disease transmission.

For the first time using global-scale analysis of mammal-virus association in wildlife trade as a proxy, we establish a strong link between wildlife trade and zoonotic disease risk. The COVID-19 pandemic has brought the attention and concern of civil society, political leaders, scientists, and conservationists together to zoonotic disease risks of wildlife trade. Given the heightened attention currently given to zoonotic disease risk, our study can inspire the development of mitigation measures that will reduce the health risk of wildlife trade.[31,32] We suggest that similar analyses be undertaken for other vertebrate groups (birds, reptiles, amphibians, and fishes) hosting different zoonotic pathogens (bacteria, viruses, fungi, etc.) to prioritize mitigation efforts at animal groups with high zoonotic disease risk potential. Our findings also confirm that only a few animal groups in wildlife trade host a high number of zoonotic pathogens.[11] As a result, we should focus mitigation attention on the taxonomic groups that represent the greatest risk and not consider all animal groups in wildlife trade as reservoirs of zoonotic pathogens. Such measures can minimize the socioeconomic impact on wildlife-dependent local communities and associated health risks from wildlife trade.[33,34] Even when bans are selectively enforced on zoonotic disease reservoir animal groups, such decisions, rather than preventing the risky trade, often drive the trade underground and encourage criminal activity due to their socioeconomic, livelihood, and food security impact.[33,34] For example, in the Brazilian Amazon alone, wild meat harvested by subsistence hunters provides an estimated $191 million in revenue, second only to timber as a forest product.[35] The 2013–2016 ban on bushmeat in response to the Ebola outbreak resulted in the proliferation of an informal network of bushmeat trade in West Africa.[36] Therefore, vulnerable communities that will be impacted by such a decision must participate in policy and decision-making processes. Before enforcing bans, decision makers should consider alternative livelihoods and food security options to vulnerable communities.[31–34]

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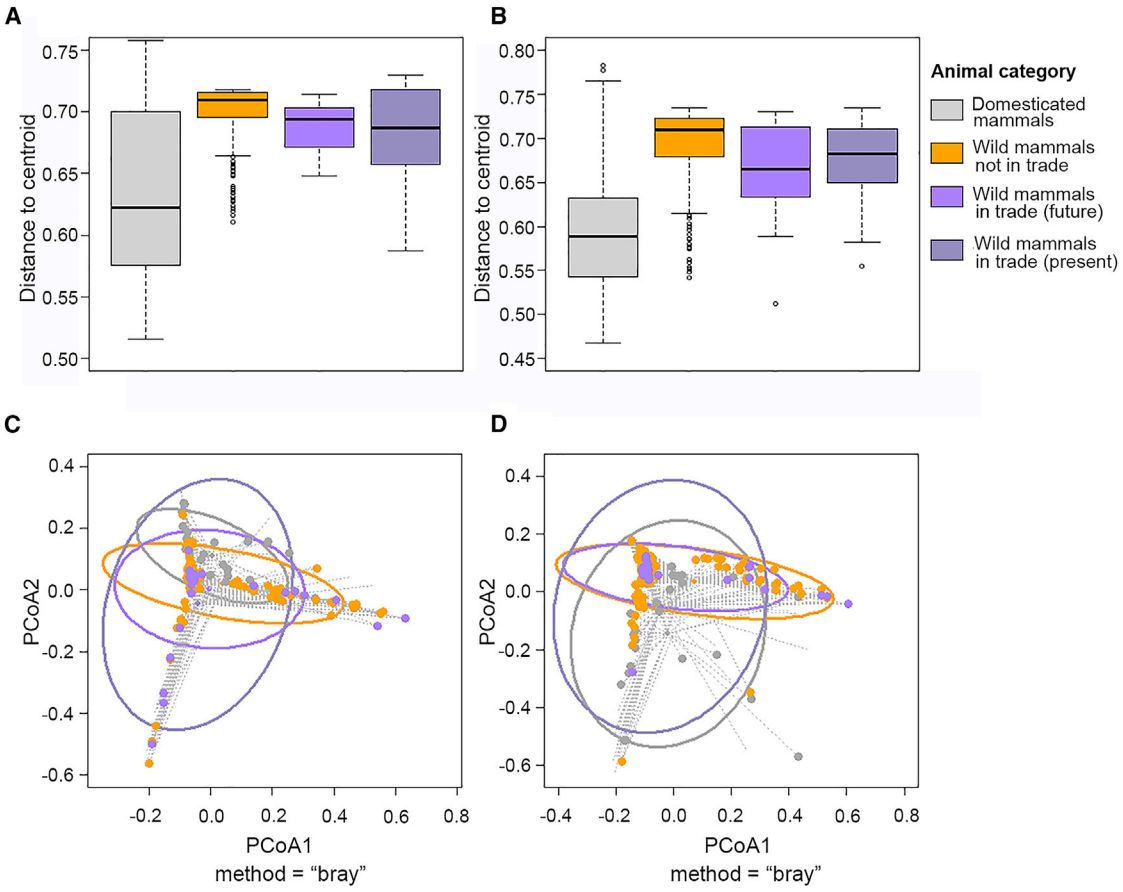

Figure 2. Beta diversity of total and zoonotic viruses among domesticated, traded, and non-traded mammals

Total and zoonotic virus similarity and turnover presented as a boxplot (A and B) and as principal-coordinate analysis (C and D). There was a significant difference in total (ANOVA: $F1;3 = 36.77$, $p = 0.0009$) and zoonotic (ANOVA: $F1;3 = 17.6$, $p = 0.0009$) virus diversity between wildlife in trade (present), wildlife in trade (future), wildlife not in trade, and domesticated, with traded (present and future) and non-traded mammals having a higher diversity (measured as Bray-Curtis dissimilarity) of zoonotic viruses than domesticated mammals. See also Data S1B.

Thus, to both prevent zoonotic disease transmission and limit economic hardships to rural communities, national and international wildlife trade should focus mitigation actions and policy specific to preventing zoonotic disease transmission on animal groups with high pathogenic load as a precautionary step. As per our analysis, regulations must keep rodents, bats, primates, ungulates, carnivores, and marsupials out of wildlife trade (Figure 1; Table 1). Further, to be cost effective, surveillance and monitoring of zoonotic pathogens in wildlife trade could focus on these high-risk animal groups.

We acknowledge several important caveats in this study. First, our estimates of total viruses and zoonotic virus richness per mammalian host species are based on current literature, reports, and databases, which are incomplete. Thus, our viral diversity estimates among domesticated, traded, and non-traded mammals are also incomplete. For example, in mammals alone it is estimated that there are a minimum of 320,000 undiscovered viruses.[28] Therefore, continued research effort will increase the discovery of new viruses from mammals. As the understanding of virus diversity changes, we would expect to see a corresponding change in the interpretation of the current study as appropriate. Second, the ability to detect the true number of viruses in an animal group is a function not only of the number of species screened but the number of individuals sampled per species. Thus, sample size significantly influences discovery of true viral diversity in an animal group.[28,37] The virus and mammal species databases utilized in the current study have significant variability in the number of animals sampled for each species, and virus richness is positively correlated with sampling effort ($R^2 = 0.60$, $p < 0.0001$). Moreover, a higher number of species are screened for viruses from speciose animal groups such as rodents and bats (Table 1). Further, we also recognize more targeted screening of domesticated (100%) and traded (36%) mammals for viruses than compared to non-traded (13%) mammals (Table 1). Therefore, we recognize that estimates of viral diversity across mammalian orders and among domesticated, non-traded, and traded mammals in the current study are potentially influenced by sampling bias. Future efforts should attempt to improve sampling of mammal species viral composition to remove the potential for sampling bias. Finally, studies that contain data on mammal-virus associations and are not published likely limit our ability to accurately estimate viral diversity across mammalian orders. Thus, encouraging better data sharing on open data platforms would help in validation of our findings

and improve detection of more zoonotic reservoirs in wildlife trade. Again, as the understanding of virus diversity improves, we would expect to see a corresponding shift in mitigation recommendations as needed. Despite these caveats, the analyses reported in this study have broad potential to assist in mitigation of zoonotic disease transmission via wildlife trade.

From our findings, it is clear that wildlife trade (legal or illegal) is a significant factor in the global spread of zoonotic and emerging infectious diseases. It is unarguably among the top-ranking modes of transmission.[16,17] Further, the observed zoonotic virus load in many mammal species predicted to be under future risk of wildlife trade[6] suggests potential risk of zoonotic disease transmission via wildlife trade will only increase in the future. However, managing wildlife trade is only part of the solution to prevent future zoonotic pandemics. An equally important threat for wildlife-linked zoonotic diseases is LUC from forests to other uses, such as industrialized agriculture expansion, infrastructure development, and urbanization.[1,29,30,36,38] Drivers of deforestation and fragmentation mediate direct contact between humans and wildlife, resulting in the direct transmission of zoonotic infections. The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) Workshop Report on Biodiversity and Pandemics reports that LUC is a globally significant driver of pandemics and has caused the emergence of more than 30% of new diseases reported since 1960.[39] Thus, the recommended focus toward wildlife trade should not divert our attention from other prominent threats linked to biodiversity and the emergence of zoonotic disease from continued habitat loss and fragmentation.[40] Given the extent of past LUC[41] and projections of future LUC associated with human development patterns,[42] addressing both risk factors hand in hand is necessary to prevent future pandemics.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

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SUPPLEMENTAL INFORMATION

Supplemental information can be found online at https://doi.org/10.1016/j.cub.2021.06.006.

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AUTHOR CONTRIBUTIONS

Conceptualization, K.N.S., K.S.B., S.P., and J.M.K.; data, K.N.S.; methodology, K.N.S.; analysis, K.N.S. and S.S.; writing, K.N.S., K.S.B., S.S., S.P., and J.M.K.

DECLARATION OF INTERESTS

The authors declare no competing interests.

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STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Deposited data		
Wildlife trade, and domestication data, total and zoonotic virus richness data for 1120 mammals. See Data S1A	[1,2,6,11,24–26,43–59,60,61]	N/A
Virus association data compiled for 1081 mammals. See Data S1B	[1,2,11,24–26,43,45–59,60,61]	N/A
Taxonomy, zoonotic status, and host range (species and orders) data for 1682 mammal viruses. See Data S1C	[2,24,26,43,62]	N/A
Number of individuals sampled for 301 mammal species for virus screening and their corresponding virus richness data. See Data S1D	[26]	N/A
The dated phylogenetic tree generated for 1083 mammals (deposited in DRYAD).	[63]	https://doi.org/10.5061/dryad.fxpnvx0rm
Software and algorithms		
VertLife	[63]	http://vertlife.org/data/mammals/
R	[64]	3.0.2
Phytools	[65]	3.5.0
Vegan	[66]	2.4-3

RESOURCE AVAILABILITY

Lead contact

Requests for further information will be fulfilled by the Lead Contact: K. Nagaraju Shivaprakash (shivaprakash.kn@tnc.org).

Materials availability

This study did not use or generate any new material.

Data and code availability

All datasets (full list of host–virus associations, total and zoonotic virus richness, mammals grouped by domestication, and wildlife trade (i.e., traded, and non-traded mammals), and mammal phylogenetic tree) needed to fully replicate and evaluate our study results are available in the Supplemental information and at DRYAD data repository (https://doi.org/10.5061/dryad.fxpnvx0rm).

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Our study subject was mammals and their associated viruses. A total of 1682 viruses associated with 1120 mammal species were assembled from following references.[1,2,11,24–26,43,45–59] Other data used in the analysis include mammals known to be in current and future wildlife trade, which is qualitative data obtained from following studies[6,11] and phylogenetic tree for 1083 mammals generated using online tool VertLife (http://vertlife.org/data/mammals).

METHOD DETAILS

Database

We updated the published mammal-virus association database[2] with additional data collected from the scientific literature on viruses listed as occurring in any mammal species (except humans) using the Web of Science and Scopus electronic library database. The updated database has 1682 viruses distributed among 1120 mammalian host species, of which 1141 (67%) viruses had at least one mammalian host reported at the species level (Data S1A and S1B). Viruses were recognized to species level, based on the International Committee on the Taxonomy of Viruses database (ICTVdb). Host taxonomy conforms to Mammal Species of the World, 3rd edition (MSW3) database.[67] We included all reliable virus-host associations reported in the literature, regardless of the method (polymerase chain reaction (PCR), virus isolation, or serology) used to detect the virus. Viruses exclusive to humans (60 viruses), viruses showing evidence for replication within the host species, and Human viruses that have been recognized in animals (reverse

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zoonoses) (7 viruses) were excluded. The zoonotic status of individual virus species was obtained by combining records of detected human infections from following studies,[2,24,26,43,62] and additional literature searching. Of the 1682 viruses in the database, 226 (13.4%) were zoonotic, and of which 19% (n = 44) of zoonotic viruses had at least one identified mammal host species (Data S1C).

Overall, our mammal-virus association database suggests that, among 5804 globally known extant mammal species,[63] there is published evidence for only 19.3% (n = 1120) of mammal species as hosts of viruses. Of these 5804 species, only 14.4% host zoonotic viruses. Thus, our finding increases the previous estimate from 609 (10.4%) to 836 (14.4%) species, increasing 4%. The number of viruses detected in each mammalian species was summed to estimate total and zoonotic virus richness for each species and order and for traded, non-traded and domesticated mammal category. Total viral richness was calculated as the number of unique ICTV-recognized viruses found in a given host species, and zoonotic viral richness was defined as the number of unique ICTV-recognized viruses in a given host species that were also detected in humans in our database.

The main objective of the present study is to quantify the zoonotic risk of the wildlife trade. Therefore, we categorized 1120 mammal species hosting viruses in our database into four categories: mammals presently in wildlife trade, mammals at risk of future wildlife trade, mammals not in wildlife trade, and domesticated mammals. Here, we have divided wild mammals into traded and non-traded mammal category. We identified domesticated mammals following the list of domestic animal species from the Food and Agriculture Organization (FAO),[44] and mammals presently in wildlife trade were identified using published data.[6] They have compiled wildlife trade data from two of the most comprehensive databases on wildlife trade: The Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and the International Union for Conservation of Nature Red List of Threatened Species (IUCN Red list).[6] Using the IUCN application programming interface platform, study classified all vertebrate taxa, including mammals, as being traded as pets and/or products.[6] Based on phylogenetic relatedness, body size, and traded species per family, the study also predicted vertebrate species that have high potential to be in the wildlife trade in the future.[6] In our analysis, we categorized mammals at risk of future wildlife trade with > 90% probability (n = 244).[6] Of the 1120 mammal host species in our database, 447 (40%) were in the present wildlife trade, 63 (7%) were at risk of future wildlife trade, 37 (3.3%) were domestic, and the rest 573 (49.7%) species were non-traded wild mammals. We also obtained globally the most traded mammal species list to quantify their zoonotic load.[11] The study[11] utilized wildlife trade query between 2012 to 2016 from the CITES trade database to identify 210 most traded wild mammal species. Of these 210 taxa, 122 species hosted at least one virus species, and 108 species hosted at least one zoonotic virus in our mammal-virus association database (Data S1A).

Comparative phylogenetic analyses

We obtained dated phylogeny for 1083 of 1120 mammal species in our database from VerLife.org tool (http://vertlife.org/phylosubsets/). The tool uses recently published species-level dated mammal phylogeny[63] and prune and construct dated phylogeny for a list of taxa provided by the user. Briefly, the mammal phylogeny[63] includes 5,804 extant and 107 recently extinct species in credible sets of 10,000 trees. The VerLife tool has two credible sets of 10,000 trees each for tip dating and node dating. We used a credible set of 1000 node dated (17 fossil calibrations) trees for all our comparative phylogenetic analyses, and results were averaged across these 1000 trees.

First, to test whether the distribution of viral load (total and zoonotic virus richness) across host mammal species in our database is constrained by their phylogenetic relatedness, we estimated the phylogenetic signals of both total (sum of non-zoonotic and zoonotic viruses) and zoonotic virus richness using Pagel's λ.[68] The λ value varies from 0 to 1, and $\lambda = 1$ suggests a strong phylogenetic dependence of variable or trait. Whereas $\lambda > 0$ corresponds to some degree of trait lability and $\lambda = 0$ imply that there is no phylogenetic dependence. We tested for significance in the phylogenetic signal assessed by Pagel's λ (null hypothesis of $\lambda = 0$) by 1,000 randomizations of species names in phylogeny under the ARD (variable transition rate) model. The significance was assessed with a likelihood ratio test.[65,68] The likelihood ratio test compares the likelihood of λ calculated from the true tree to the likelihood of 0. The function of these methods is available in the R package phytools.[65] Further, to examine the phylogenetic pattern of viral load among mammal host species, we mapped both total viral richness and zoonotic virus richness on the phylogeny of mammal host species in our database using stochastic character mapping (SIMMAP), as implemented in the R phytools function contMap.[65]

QUANTIFICATION AND STATISTICAL ANALYSIS

Chi-square test for mammal-virus association

We tested the association and distribution of viral load across mammalian orders among four groups (mammals presently in wildlife trade, mammals at risk of future wildlife trade, mammals not in wildlife trade, and domesticated mammals) using Chi-Square (X^2) analysis implemented in R package (version 3.0.2).[64]

Diversity analysis of total and zoonotic viruses

To understand the diversity of total and zoonotic virus species among four groups of mammals, we quantified beta diversity (i.e., variability in virus species composition between mammals in domestication, wildlife trade, and not in wildlife trade) using the function 'betadisper' implemented in R package Vegan.[66] This function creates a distribution of null values of the test statistic, which is

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compatible with the null hypothesis of no significant differences in multivariate dispersion between two or more groups. We tested the difference in virus species composition among four mammal groups by comparing the average of the calculated dissimilarities (here Bray–Curtis matrices) of virus species assemblages between the four groups using the F-test. P values were computed from 999 permutations of the taxa-to-taxa dissimilarities based on virus composition between the four groups. All statistical analyses were conducted using R (version 3.0.2).[64]