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Diseases of humans and their domestic mammals: pathogen characteristics, host range and the risk of emergence

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Pathogens that can be transmitted between different host species are of fundamental interest and importance from public health, conservation and economic perspectives, yet systematic quantification of these pathogens is lacking. Here, pathogen characteristics, host range and risk factors determining disease emergence were analysed by constructing a database of disease-causing pathogens of humans and domestic mammals. The database consisted of 1415 pathogens causing disease in humans, 616 in livestock and 374 in domestic carnivores. Multihost pathogens were very prevalent among human pathogens (61.6%) and even more so among domestic mammal pathogens (livestock 77.3%, carnivores 90.0%). Pathogens able to infect human, domestic and wildlife hosts contained a similar proportion of disease-causing pathogens for all three host groups. One hundred and ninety-six pathogens were associated with emerging diseases, 175 in humans, 29 in livestock and 12 in domestic carnivores. Across all these groups, helminths and fungi were relatively unlikely to emerge whereas viruses, particularly RNA viruses, were highly likely to emerge. The ability of a pathogen to infect multiple hosts, particularly hosts in other taxonomic orders or wildlife, were also risk factors for emergence in human and livestock pathogens. There is clearly a need to understand the dynamics of infectious diseases in complex multihost communities in order to mitigate disease threats to public health, livestock economies and wildlife.

Keywords: pathogen; epidemiology; emerging diseases; zoonoses; wildlife; multihost pathogen

1. INTRODUCTION

Diseases transmitted between human, wild and domestic animal species have important impacts on public health, livestock economies and wildlife conservation. Although from our own perspective diseases of humans seem primarily a concern of humans and their doctors, nearly two-thirds (61%) of human diseases are actually zoonotic, that is they can also infect animals (Taylor *et al.*, this issue). If such diseases can spread widely within the human populations once introduced (e.g. influenza, human immunodeficiency virus and acquired immune deficiency syndrome) or if they spill over frequently from animal reservoirs (e.g. rabies, sleeping sickness), zoonotic infections can have a serious socio-economic impact.

From a conservation perspective, pathogens that can be transmitted across a range of hosts are of great concern for small and endangered populations. Species-specific pathogens that are a major threat to viability are highly unlikely to persist in small populations of endangered hosts (McCallum & Dobson 1995). Thus pathogens that can infect more than one species and persist in another species with a larger host population, have been responsible for virtually all recent outbreaks of disease in endangered species (Murray *et al*. 1999; Daszak *et al*. 2000; Cleaveland *et al*. 2001). For example, domestic dogs were the probable source of rabies virus that decimated populations of both African wild dogs (*Lycaon pictus*) (Gascoyne *et al*. 1993; Alexander *et al*. 1993) and Ethiopian wolves (*Canis simensis*) (Sillero-Zubiri *et al*. 1996; Laurenson *et al*. 1998). Similarly, chimpanzee and mountain gorilla populations have been affected by pathogens such as measles and influenza virus transmitted from humans (Wallis & Lee 1999).

Finally, livestock economies can also be seriously affected by the transmission of pathogens among a range of domestic animal species. Of particular concern are livestock diseases that have the potential for rapid spread and cause widespread mortality, which can have extremely serious socio-economic consequences. These 'transboundary diseases' are classified by the Office International des Epizooties (OIE) (World Organization for Animal Health) into List A and List B (less severe) diseases. Diseases that originate in wildlife reservoirs can also be the source of human–wildlife conflict, when poverty is exacerbated in rural communities that are dependent upon livestock production. In eastern Africa, pastoralists suffer serious losses as a result of transmission of a viral disease (malignant catarrhal fever) from wildebeest to cattle (Thompson 1997). Avoiding cattle contact with wildebeest contributes significantly to poverty among pastoralist people, not only because cattle are unable to access prime grazing lands used by wildebeest, but also because movement restrictions exacerbate tick-borne and helminth disease problems. In Africa, buffalo can act as a reservoir for foot-and-mouth disease (FMD)

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virus transmission to cattle (Thomson 1995; Sutmoller *et al*. 2000). As the presence of FMD in cattle has severe economic consequences for the beef trade, buffalo and cattle in southern Africa are separated by fencing, which in some areas has restricted wildlife movements and caused high mortality. Such conflict is not confined to developing countries. In the UK, one current conflict between cattle farmers and conservation and animal welfare groups stems from the possibility that bovine tuberculosis, caused by *Mycobacterium bovis* may be transmitted between badgers and cows (Krebs 1997).

Against this background it is clear that pathogens that can be transmitted between suites of different host species are of fundamental interest and importance. Although it may seem obvious, at least from a veterinary perspective, that few diseases affect exclusively any one species or group of hosts (Daszak *et al*. 2000), there is a dearth of studies that systematically quantify both pathogen characteristics and their interactions with key features of pathogen–host epidemiology. Here, we aim to rectify this omission by compiling a database of pathogens causing disease in human and domestic mammals. In the first part of the paper, we quantify the extent of multispecies transmission and examine how this varies with pathogen characteristics.

In the past two decades, the emergence of many infectious diseases has attracted increasing attention in humans, domestic animals and wildlife (Institute of Medicine 1992). Emerging diseases are those that have appeared for the first time, or are increasing in incidence, or have been reported in new areas. A number of factors have been proposed to explain disease emergence, including pathogen characteristics (e.g. mutation, recombination, genetic drift), host characteristics (e.g. immunosuppression), host population characteristics (e.g. population size, behaviour, movement) and ecological factors (e.g. changes in agriculture, land-use, urbanization) (Morse 1995; Schrag & Weiner 1995; Morris & Potter 1997).

Among the host–pathogen characteristics, several authors have noted that emerging human diseases are often those that can be transmitted between animals and humans (Morse 1995; Murphy 1998; Palmer *et al*. 1998; Chomel 1998). Only now, however, have zoonotic pathogens been demonstrated, by quantitative analysis, as a risk factor for emergence in humans (Taylor *et al*., this issue). Similarly, it has been noted that many human emerging infections involve free-ranging wildlife, raising suggestions that human encroachment on wildlife habitats may result in increased transmission at the wildlife–human–domestic animal interface (Osburn 1996; Chomel 1998; Daszak *et al*. 2000). Factors such as deforestation, population movements and intrusion of humans and domestic animals into new habitats have resulted in the emergence of several pathogens, such as yellow fever virus, California encephalitis virus (Mahy & Murphy 1998), Ross River virus (Daszak *et al*. 2000) and Marburg and Ebola viruses (Peters *et al*. 1994). However, these accounts have essentially been descriptive and a quantitative evaluation of the relative roles of wildlife and domestic animals in emerging zoonoses has not yet been undertaken.

In the second part of this paper, we aim firstly to identify the animal hosts associated with zoonotic pathogens and secondly to quantify the relative importance of different animal hosts in emerging human diseases. Lastly we identify characteristics of pathogen and host species associated with both emerging domestic mammal diseases and ascertain whether these characteristics are common to mammal diseases that are of greatest socio-economic importance (OIE List A and B diseases).

2. METHODS

(a) *Species database construction*

A database of infectious pathogens causing disease in domestic mammals was compiled from references of livestock (excluding poultry) and domestic carnivore diseases (Radostits *et al*. 1999; Merck 1998; Coetzer *et al*. 1994; Quinn *et al*. 1997; Greene 1998; Soulsby 1982; Urquhart *et al*. 1996; Kassai 1998), following the methodology described by Taylor *et al*. (this issue) for construction of a database of human infectious pathogens. Each pathogen entry was a separate species that was known to be infectious and capable of causing disease in domestic mammals under natural conditions. Domestic mammals included livestock (ungulate species: cattle, sheep, goats, pigs and horses) and carnivores (cats and dogs). Pathogens causing disease in non-mammalian domestic animals were not included.

The domestic mammal database was subsequently combined with a database for human infectious pathogens, which had been developed previously (Taylor *et al*., this issue). Information contained in the combined database comprised the following.

(i) Genus and species name of the pathogen. Nomenclature followed standard references currently available (Bacterial Nomenclature Up-to-Date (Deutsche Sammlung von Mikroorganismen und Zellkuturen GmbH), Index Virum (International Committee on Taxonomy of Viruses) and The CABI Bioscience Database of Fungal Names (Funidex, CABH Bioscience)). Parasite nomenclature was taken from Soulsby (1982). Each species must have appeared in one of the reference texts and appeared in a nomenclature reference source, where available, or appeared in a second of the reference text sources, or appeared in a Web of Science Citation Index search of the last 10 years. Where a genus is known to cause disease in domestic mammals, but no species name was given, the genus name appears in the database followed by 'sp.'.

(ii) Taxonomic grouping. Each pathogen was classified in one of the following categories: viruses (which included prions), bacteria (which included rickettsia), fungi (which included algae), protozoa and helminths.

(iii) Hosts in which disease has been documented. In the combined database, pathogens were classified according to whether they caused disease in livestock, domestic carnivores or humans. These categories were not mutually exclusive.

(iv) Hosts in which infection has been documented. For each pathogen, a list was compiled of host species in which infection (not necessarily disease) had been documented. From this list, several indices of host range were derived: (i) whether infection had been documented in a single- or multiple-host species; (ii) whether infection had been documented in human, domestic or wildlife hosts; (iii) whether infection had been documented in hosts of one or more taxonomic orders; and (iv) the taxonomic grouping of mammal hosts: carnivores, ungulates, primates

(excluding humans), bats, rodents and marine mammals. Insufficient data were available to include other mammalian orders. Additional categories of wildlife hosts included birds and non-mammalian hosts. For human pathogens, the category of multiple-host species was all zoonotic pathogens, which were defined as diseases and infections that are naturally transmitted between vertebrate animals and man, following the World Health Organization (WHO 1959; Palmer *et al*. 1998). This classification differed slightly from that of Taylor *et al*. (this issue), who excluded four organisms with complex life cycles, in which humans are the only definitive host (*Taenia saginata*, *T. solium*, *Sarcocystis hominis* and *S. suihominis*). Because these pathogens can infect and cause disease in other mammalian hosts, they were included in our database as multihost pathogens.

(v) Whether or not the species is emerging in humans. This classification was obtained from the human pathogen database, as described in detail by Taylor *et al*. (this issue).

(vi) Whether or not the species is emerging in domestic mammals. Following the criteria established for human emerging infections, emerging pathogens of domestic mammals were those that have appeared for the first time, or are increasing in incidence, or have been reported in new areas. Information on disease emergence in domestic mammals was obtained from reviews and primary papers of the emerging disease literature (Sanders 1985; Prescott *et al*. 1995; Bolin 1996; Mahy & Murphy 1998; Osburn 1996; Scott *et al*. 1996; Dee 1997; McGrath 1997; Corbel 1997; Chomel 1998; Bello & Abell 1999; MacKenzie 1999; Richt *et al*. 1997; MacLachlan *et al*. 1998; Dubey 1999; Wilson & McOrist 2000; Allan & Ellis 2000; Daszak *et al*. 2000).

(vii) Whether or not the species is the aetiological agent of a disease listed by the OIE. The OIE classifies 'transmissible diseases that have the potential for very serious and rapid spread, irrespective of national borders, that are of serious socio-economic or public health consequence and that are of major importance in the international trade of animals and animal products' as List A diseases and 'transmissible diseases that are considered to be of socio-economic and/or public health importance within countries and that are significant in the international trade of animals and animal products' as List B diseases. In this database, pathogens that were identified as the cause of any of these diseases in mammals were included as OIE-listed pathogens. In some cases (e.g. trypanosomosis), several pathogens were included for a single disease.

(b) *Analysis*

Pathogen characteristics associated with human emerging diseases, domestic-mammal emerging diseases and OIE-listed diseases were examined by comparison of taxonomic division and host range of the pathogen. For 72 human pathogens (eight emerging), non-human animal host species were unknown, although they were known to have a multiple-host range.

Results were expressed as relative risk (RR). The RR of emergence was calculated by dividing the proportion of species that were emerging in a particular category (e.g. which were bacteria, or infected wild animals) by the proportion of species emerging that were not in that category (e.g. which were not bacteria, or did not infect wild animals) (Woodward 1999). Ninety-five per cent confidence intervals (Woodward 1999) were calculated for RRs in the domestic mammal pathogen databases as we considered that the data were less complete than for human pathogens (see Taylor *et al*., this issue).

To investigate the independent effects of pathogen taxonomy and host range on disease emergence, general linear models with binomial errors were used. Disease emergence in each of the pathogen groups was included as a binary response variable. Explanatory variables included taxonomy as a categorical variable and host range as a binary variable. For each of the response variables, taxonomy was added to the model first, followed by host range and finally a taxonomy–host range interaction term. For each pathogen group (human, livestock and domestic carnivore pathogens) three sets of analyses were performed to investigate the effect of interactions between taxonomy and host range, with host range defined as (i) multiple- or single-host pathogens, (ii) infecting one or infecting more than one host order, and (iii) infecting wildlife or not infecting wildlife.

3. RESULTS

(a) *Summary of database*

A total of 1922 species of infectious agent was recorded in the combined database, of which 632 (32.9%) of the pathogens were bacteria, 329 (17.1%) fungi, 499 (26.0%) helminths, 145 (7.5%) protozoa and 317 (16.4%) viruses and prions. Pathogens causing disease in three separate groups of hosts were analysed separately, but these lists were not mutually exclusive. One thousand four hundred and fifteen (1415) pathogens cause disease in humans, 616 cause disease in livestock (cattle, sheep, goats, pigs and horses) and 374 cause disease in domestic carnivores (dogs and cats). The breakdown of pathogens by taxonomy is shown in figure 1*a*. A greater proportion of domestic mammal diseases was caused by helminths and protozoa when compared with human diseases, whereas a lower proportion was caused by fungi and bacteria.

(b) *Host range*

Overall, 1205 (62.7%) of pathogens in the database infect more than one host species. However, multiple-host infections make up a higher proportion of domestic carnivore (90.9%) and livestock (77.3%) pathogens than human pathogens (61.6%) (figure 2). Compared with single-host pathogens, multihost pathogens were more often helminths (36.7% compared with 7.9%) and less often fungi (10.7% compared with 27.8%) and bacteria (26.6% compared with 43.5%).

Multihost pathogens were also classified according to the range of hosts they could infect (humans, domestic mammals and wildlife) and summaries are presented in figure 2. It should be noted that the total number of pathogens infecting wildlife, for example, includes pathogens in three possible categories: (i) human and wildlife, (ii) domestic and wildlife and (iii) human, domestic and wildlife. The category 'domestic' includes both livestock (domestic ungulates) and domestic carnivores.

Across the whole database, when considering three categories of host (i.e. human, domestic animals and wildlife), 1115 out of 1922 (58.0%) of hosts fell into more than one of these categories, and 392 out of 1922 (20.4%) fell into all three. Of the human pathogens, 553 out of 1415 (39.1%) also infected domestic animal hosts

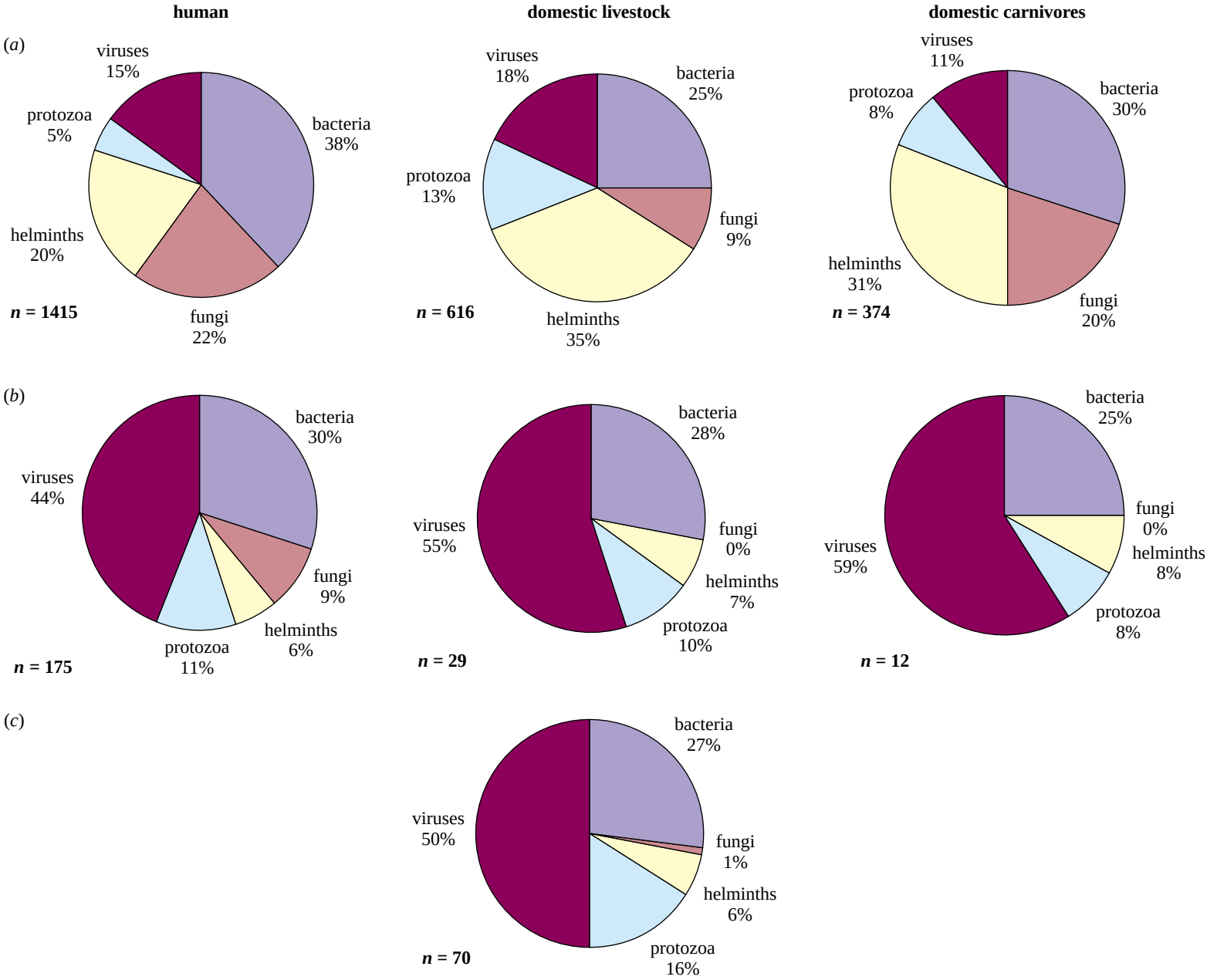

Figure 1. Taxonomic classification of (*a*) all human, livestock and domestic carnivore pathogens, (*b*) emerging pathogens and (*c*) OIE-listed pathogens.

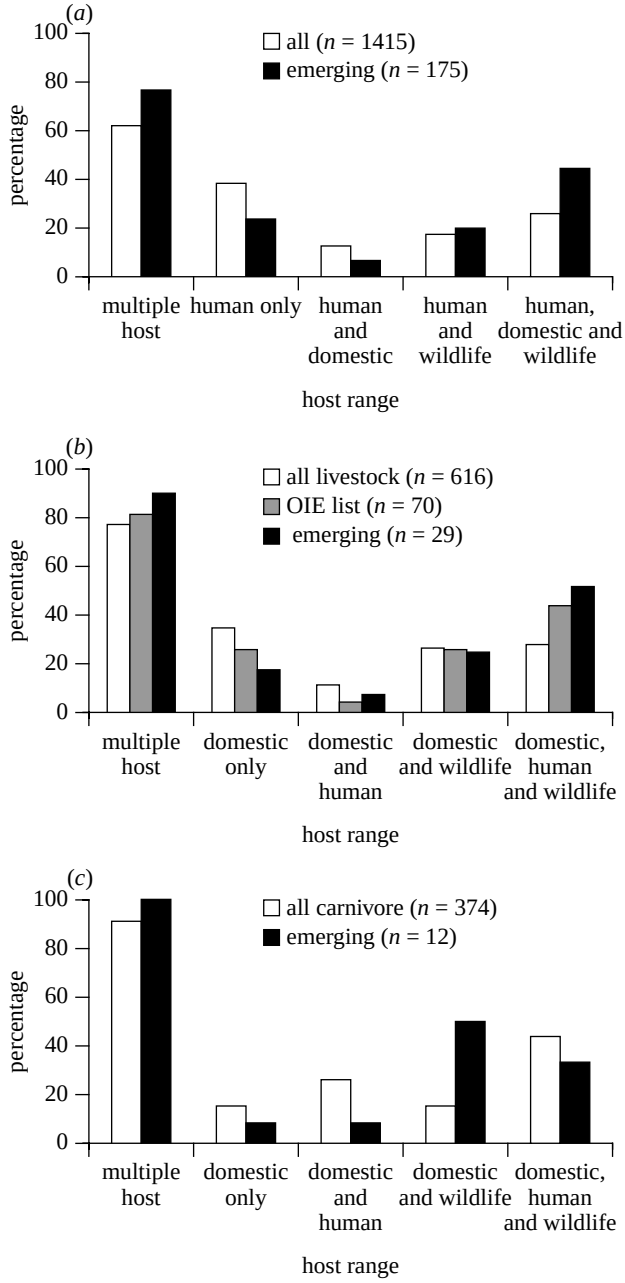

Figure 2. Host ranges for all and emerging (*a*) human, (*b*) domestic livestock and (*c*) domestic carnivore pathogens.

and 620 out of 1415 (43.8%) also infected wildlife hosts, with 373 out of 1415 (26.4%) infecting all three categories. A more detailed breakdown of animal hosts of zoonotic pathogens causing human disease is provided in table 1. Zoonotic pathogens were most often known to have carnivore (43.0%), ungulate (39.3%) or rodent hosts (22.5%), and few were known to have primate hosts (12.9%).

Of the livestock pathogens, 243 out of 616 (39.4%) also infected humans, 335 out of 616 (54.4%) also infected wild animal hosts and 174 out of 616 (28.2%) infected all three categories. In domestic carnivores, 261 out of 374 pathogens (69.8%) also infected humans, 220 out of 374 (58.8%) infected wild animal hosts and 164 out of 374 (43.9%) infected all three categories. Unlike human pathogens, it is of course possible for livestock and carnivore pathogens in the category of domestic hosts only to be multispecies pathogens.

Table 1. Important animal host categories for human zoonoses and emerging human zoonoses.

(Host range detailed represents minimums as full host range for many pathogens may not be known. Diseases for which the animal hosts were completely unknown were excluded ($n = 72$ diseases and 8 emerging diseases).)

host categories	number of zoonotic diseases (total = 800)	number of emerging zoonotic diseases (total = 125)
ungulates	315 (39.3%)	72 (57.6%)
carnivores	344 (43.0%)	64 (51.2%)
primates	103 (12.9%)	31 (24.8%)
rodents	180 (22.5%)	43 (34.4%)
marine mammals	41 (5.1%)	6 (4.8%)
bats	15 (1.9%)	6 (4.8%)
non-mammalian host (includes birds)	109 (13.6%)	30 (24.0%)
birds	82 (10.3%)	23 (18.4%)

(c) *Risk factors for emergence*

In total 196 of the pathogens in the combined database were associated with emerging diseases; 175 in humans, 29 in livestock and 12 in domestic carnivores. Overall a greater proportion of human pathogens has been identified as emerging (12.4%) than livestock pathogens (4.7%) or domestic carnivore pathogens (3.2%). The pathogens responsible for livestock diseases listed by the OIE (Lists A and B) were also analysed for comparison ($n = 70$, 11.3% livestock pathogens), as these by definition cause widespread economic or public health problems and have probably the greatest potential to re-emerge.

(i) *Taxonomy*

Taxonomic breakdowns of emerging diseases of humans, livestock and domestic carnivores and OIE-listed diseases are depicted in figure 1*b*, with the RRs given in table 2*a*. Helminths and fungi were relatively unlikely to be emerging pathogens (RR all 0.36 or lower) and viruses were highly likely to emerge in all groups (RR all 4.34 or higher). Among human pathogens, protozoa were likely to emerge (RR of 2.49), but this was not the case for pathogens of domestic livestock and carnivores.

The viruses were also subdivided into RNA and DNA viruses and their RRs of emergence calculated. Among emerging livestock and OIE-listed pathogens, RNA viruses were more likely to emerge than DNA viruses RRs given in table 2*a*. The same trend was seen among human pathogens, but not among domestic carnivore pathogens, although this latter dataset contained only 7 DNA viruses and only 12 emerging pathogens, making the RR calculations less reliable. Interestingly, an analysis of the viruses in the whole database that were known to infect birds as well as mammals (and thus could make a potentially more difficult host-range transition) revealed that none was DNA and that all 26 were RNA, whereas

Table 2. RR of emergence of human ($n=175$), livestock ($n=70$), carnivore ($n=12$) and OIE-listed diseases ($n=70$).

(Numbers in brackets denote sample sizes for human pathogens or confidence intervals for other pathogens. RRs for RNA and DNA viruses are compared within viruses. Abbreviation: n.a., not applicable.)

taxonomic category	human emerging pathogens	livestock emerging pathogens	OIE-listed pathogens	domestic carnivore emerging pathogens
(*a*) taxonomy				
protozoa	2.49 ($n=19$)	0.77 (0.24–2.50)	1.25 (0.69–2.27)	1.17 (0.14–8.09)
bacteria	0.71 ($n=53$)	1.12 (0.51–2.48)	1.10 (0.67–1.80)	0.76 (0.24–2.50)
helminths	0.24 ($n=10$)	0.14 (0.03–0.56)	0.11 (0.04–0.30)	0.20 (0.03–1.81)
fungi	0.36 ($n=16$)	0.00	0.15 (0.02–1.09)	0.00
viruses	4.34 ($n=77$)	5.66 (2.81–11.43)	4.60 (3.03–7.03)	11.07 (2.75–24.0)
RNA viruses	1.19 ($n=65$)	2.48 (0.75–8.28)	1.94 (0.97–3.89)	0.41 (0.09–1.83)
DNA viruses	0.84 ($n=10$)	0.40 (0.12–1.34)	0.52(0.26–1.03)	2.43 (0.55–10.77)
(*b*) host range				
multiple species	1.97 ($n=133$)	2.55 (0.78–8.30)	1.29 (0.73–2.29)	—[a]
more than one taxonomic order	1.97 ($n=133$)	3.82 (1.66–8.81)	1.36 (0.88–2.12)	0.37 (0.12–1.15)
human	n.a.	2.17 (1.05–4.47)	1.45 (0.93–2.25)	0.31 (0.10–0.96)
wildlife	2.44 ($n=113$)	2.64 (1.14–6.08)	1.96 (1.20–3.18)	3.50 (0.78–15.75)
domestic	1.67 ($n=90$)	n.a.	n.a.	n.a.

[a] All emerging domestic carnivore pathogens are multihost.

Table 3. Deviance (χ^2) associated with each explanatory variable in the full generalized linear model for emergence in humans, livestock and carnivore emerging diseases and OIE-listed diseases.

(Significance levels are $^{****}p < 0.001$, $^{***}p < 0.01$, $^{**}p < 0.05$, $^{*}p < 0.1$. Abbreviation: n.a., not applicable.)

	emerging human diseases	emerging livestock diseases	OIE-listed diseases	emerging carnivore diseases
(*a*) taxonomy (d.f. = 4)	138.7^{****}	31.2^{****}	69.1^{****}	20.4^{****}
(*b*) host range (d.f. = 1)				
single or multiple	13.6^{****}	10.6^{***}	9.4^{***}	3.4^{*}
infects one order or more than one	11.8^{****}	16.5^{****}	4.0^{**}	0.09
infects wildlife or does not infect wildlife	30.0^{****}	12.2^{***}	21.3^{****}	1.24
infects domestic animals	21.0^{****}	n.a.	n.a.	n.a.
(*c*) interaction with taxonomy (d.f. = 4)				
single or multiple	22.9^{****}	1.0	6.5	0.0
infects one order or more than one	25.3^{****}	7.2	7.9	3.2
infects wildlife or does not infect wildlife	17.3^{****}	13.6^{***}	12.5^{**}	6.5
infects domestic animals	14.7^{***}	n.a.	n.a.	n.a.

6.4 DNA and 19.6 RNA viruses would have been expected ($\chi^2=8.51$, d.f. = 1, $p < 0.01$).

(ii) *Host range*

Characteristics of host range differed consistently between all pathogens and the emerging pathogen subset in all groups (figure 2, RRs given in table 2*b*). Pathogens that infected more than one host species were more likely to emerge than single-host species in all groups (RR of 1.29 or higher). Moreover, pathogens that infected more than one order of animal were generally more likely to emerge than those infecting only one order. The exception to this pattern was the domestic carnivore pathogens, where the reverse was true (RR of 0.37). However, as mentioned above, very few domestic carnivore pathogens are regarded as emerging, making calculations of RR less reliable. In all groups, pathogens that also infected wildlife species were more likely to emerge than those without wildlife hosts (RR all 1.96 or higher).

(d) *Statistical analyses*

Disease emergence in humans, livestock and domestic carnivores was significantly associated with pathogen taxonomy (see table 3*a* for χ^2-values and significance levels). Controlling for taxonomy, human and livestock pathogens were more likely to emerge or be listed by the OIE if they could infect more than one species, infect more than one order of host or infect wildlife hosts (table 3*b*). As there were few emerging carnivore pathogens, no further significant explanatory factors could be found, although the ability to infect more than one host approached significance ($p=0.06$).

For human pathogens, the effect of host range differed among taxonomic groups, with emergence associated with multihost pathogens in bacteria and fungi, whereas the opposite was true for helminths and little effect was detected among protozoa and viruses (table 3*c*, see also Taylor *et al.*, this issue). Similarly, for human pathogens, emergence was associated with the ability to infect wildlife

in bacteria, fungi and viruses, but had little effect in helminths and protozoa.

Among the mammal diseases, significant host range–taxonomy interaction terms were only detected between taxonomy and the ability to infect wildlife hosts for emerging livestock pathogens and OIE-listed pathogens (table 3*c*). In the first model, a higher proportion of emerging livestock pathogens also infected wildlife within the bacterial, protozoal and viral pathogens, but the opposite was true of the helminth group. No emerging fungal pathogens were recorded in livestock. Similarly, in the second model, a greater proportion of OIE-listed pathogens also infected wildlife within the bacteria, protozoa and viruses, but not within fungi and helminths. Small samples sizes and thus a lack of power in the analysis suggest these results should be interpreted cautiously.

4. DISCUSSION

We believe this study provides the first quantitative data on the host ranges of human and domestic mammal pathogens and highlights the significance of interactions between populations of human, domestic and wild animal hosts for disease transmission and, particularly, for disease emergence. Although our data may have their limitations and biases, the trends we found were remarkably consistent across the different host groups. Pathogens that can infect more than one host species are extremely common in all host groups, with nearly two-thirds of the pathogens in the database known to fall into this category. Because every host infected by a pathogen will not have been listed in our literature sources, this must be a conservative estimate. Multihost pathogens are therefore of concern to all health workers, whether they care for humans or other animals.

However, we found fewer multihost pathogens that caused disease in humans than in domestic mammals. There are several possible explanations for this finding. First, epidemiological theory predicts that human populations, being larger than other mammal species, could support more single-host pathogens (Anderson & May 1991). Although we believe that this prediction is valid, it seems unlikely that this is the only explanation as differences in host ecology and behaviour and research biases are also likely to be important. For example, there are a greater number of wild species that are closely related to domestic carnivores and livestock than there are wild primate relatives of humans. Furthermore, contact (and thus pathogen transmission) is likely to be more frequent between domestic mammals and their wild relatives than between humans and wild primates.

Biases in research, in particular the single-species approach in human medicine, may also contribute to this finding. Natural infections in humans' closest relatives, wild primates, are poorly studied (Wolfe *et al*. 1998). As we included only instances of natural infection in the database (being epidemiologically more relevant), successful experimental infections of primates were omitted. Thus several of the human pathogens classified as single-host in the database could, in nature, infect multiple hosts, but proof is lacking. The inherent bias of humans in studying themselves in preference to other species is also revealed also by the large number of human pathogens (1415 species) in comparison with pathogens of livestock (616) or domestic carnivores (374); further research might increase the number of domestic mammal pathogens. Finally, a substantial number of human pathogens that were not reported as zoonoses in the medical literature were identified as zoonoses from veterinary reference texts. In summary, while there are fundamental reasons why human pathogens are more likely to persist in a single-host population, further research could reveal that the proportion of human pathogens infecting other hosts is substantially higher than detailed here.

This study also found that over a quarter of pathogens of humans and domestic mammals have a very broad host range and are capable of infecting human, domestic and wildlife hosts. There is therefore clearly great potential for disease issues to be a source of human–wildlife conflict. Disease-control measures may be taken in the best interests of humans or their domestic animals but adversely affect wildlife or, conversely, may place wildlife interests above those of local communities. In either case, conflicts that arise from the need to control pathogen transmission between species are likely to escalate as human populations continue to grow and expand. Furthermore, the potential for a wide range of pathogens to be transmitted from human or domestic animal reservoirs to small and endangered wild animal populations is a serious concern for wildlife conservation.

(a) *Emerging diseases*

To be classified as emerging, a disease must have appeared for the first time, be increasing in incidence, or be reported in new areas or populations. Compared with emerging human diseases, we found relatively few references to emerging diseases of livestock or domestic carnivores in either the emerging disease literature or veterinary texts. We do not have a clear explanation for this, as many of the factors associated with human disease emergence should also apply to domestic mammal pathogens. These include expansion of human (and their domestic animal) populations, encroachment into wildlife areas and changes in agricultural practices. Nevertheless, several factors may underlie this result. For example, domestication and intensification of animal production systems were presumably major factors in the appearance of new domestic animal diseases, but these are generally not recent phenomena and would not have led to the emergence of new diseases in the past 20–30 years. Furthermore, it is possible that humans' anthropocentric approach to infectious disease classification and research has again led to biases in the literature. The concept of emerging infectious diseases appeared only in the late 1980s (Chomel 1998) and has been primarily applied to diseases affecting humans. In the veterinary literature, discussion of emerging disease is more recent and may, at present, be less comprehensive or languishing in the grey literature. Thus in the future, when more domestic mammal diseases have been classified as emerging, we would expect even stronger trends to be found.

Despite these limitations, our analyses identify some clear patterns of pathogen characteristics that appear to be common risk factors for disease emergence across humans, domestic livestock and domestic carnivores. For

a disease to emerge, at least one of two key elements must be in place—the pathogen must be able to come into contact and infect a new host and/or it must be able to spread from host to host (Morse 1995). In this study, pathogen taxonomy was found to influence the probability of emergence. Helminths were relatively unlikely to emerge, despite such a high proportion of helminths being zoonoses and multihost pathogens, both risk factors for emergence and OIE-listed diseases. We do not have a convincing explanation for this finding, although a number of factors may make them unlikely to be classified as emerging. First, they are relatively complex organisms with relatively complex life cycles and longer generation times than microparasites (Anderson & May 1991). Their life-history strategies and epidemiologies may thus intrinsically prevent them from dramatically or suddenly changing their abundance or host range. In addition, in many cases helminths are not extremely virulent or pathogenic and thus are unlikely to cause widespread morbidity or mortality, again making them less likely to be classified as emerging.

In contrast, viruses were a clear risk factor for disease emergence in humans and domestic mammals and for listing by the OIE. One possible explanation for this is the relative difficulty of treating viral diseases. When primary cases of a potentially emerging disease occur, they are often treated symptomatically: broad-spectrum anthelmintics and antibiotics have been widely and effectively used in both humans and domestic mammals. These may have limited the spread of potentially emerging disease caused by helminths, bacteria and protozoa. In contrast, few effective antiviral agents are widely available or used. Thus, diseases caused by viruses may be less easily controlled and thus more likely to spread within a population, to reach a size where they would be deemed emerging. The growing problem of disease re-emergence due to the development of antibiotic or anthelmintic resistance supports this idea.

A further important factor explaining the predilection for viruses to emerge is that mutation rates in viruses are higher than other pathogens (Domingo & Holland 1994) and generation times shorter. Viruses able to evolve more quickly are therefore more likely to be successful at exploiting new niches. This may also explain the greater RR of emergence among RNA viruses, which have higher mutation rates than DNA viruses. The finding that RNA viruses were more likely than DNA viruses to infect birds as well as mammalian hosts also suggests that a fundamental property of RNA viruses may make them more easily transmissible than DNA viruses across species and orders.

The suggestion that mutation rates and pathogen flexibility may be involved in the propensity to emerge is corroborated by the findings that both the ability of a pathogen to infect more than one species and more than one order of host were both risk factors for emergence (table 2*b*). Pathogens that infected wildlife were also twice as likely to emerge as pathogens without wildlife hosts. This is, we think, the first quantitative evidence to support this supposition, which has been widely discussed elsewhere (Osburn 1996; Chomel 1998; Daszak *et al*. 2000).

The quantification of the breadth of host range for many pathogens in this paper, particularly those that are emerging, highlights that research and control of emerging diseases in all hosts requires a holistic multidisciplinary approach. Identification of the factors leading to disease emergence and teasing apart the complex epidemiologies of generalist pathogens can only be achieved by integration of effort among medical, veterinary and wildlife researchers.

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