
ARE BATS REALLY “SPECIAL” AS VIRAL RESERVOIRS? WHAT WE KNOW AND NEED TO KNOW

Kevin J. Olival¹, Cristin C. Weekley², and Peter Daszak¹

¹*EcoHealth Alliance, New York, NY, USA*

²*Graduate Group in Epidemiology, University of California,
Davis, CA, USA*

11.1 INTRODUCTION

The notion that bats are “special” or “unique” as reservoir hosts for viral pathogens has recently become in vogue in both the media and scientific literature (Dobson, 2005; Wang *et al.*, 2011; Olival *et al.*, 2012; Luis *et al.*, 2013; O’Shea *et al.*, 2014). This was initially based on the relatively recent finding that a number of high-profile zoonotic viruses (such as severe acute respiratory syndrome coronavirus (SARS-CoV), Ebola and Marburg viruses, and Hendra and Nipah viruses) have bat origins. It has been further developed through the hypothesis that the life history traits of bats compared to other mammals may make them unique and exceptional hosts for viruses (Luis *et al.*, 2013; O’Shea *et al.*, 2014), and with the finding that they harbor more viruses than some other groups of mammals (Luis *et al.*, 2013). However, claims of bats being “special” as viral reservoirs are often made in isolation, without a proper comparative approach that includes data from a wide array of animal taxonomic groups. In this chapter, we extend our previously published preliminary analysis of this issue (Olival *et al.*, 2012), and take a critical and objective look at what may, or may not, make bats “special” as disease reservoirs.

11.2 WHAT FACTORS MAY MAKE A HOST TAXON "SPECIAL" AS A VIRAL RESERVOIR?

In order to make claims that some host taxonomic groups, such as those within a specific mammalian Order, are "special" or "unique" as compared to other taxonomic groups, it is first necessary to define what we mean by "special". There are six criteria that can be used to test whether a given group of mammals differs from others in terms of their importance or significance as disease reservoirs. We use the term taxonomic group to generally refer to any hierarchical taxonomic level which can be compared to others in the same level, for example a genus as compared to other host genera, or, as often used here, an Order compared to other Orders in the same Class (Mammalia).

1. Greater number of pathogens (greater viral richness) than other taxonomic groups.
2. Higher proportion of zoonotic diseases than other taxonomic groups.
3. Unique set of pathogens as compared to other taxonomic groups.
4. Ecological, behavioral, or life-history traits that differentially favor pathogen diversity as compared to other taxonomic groups.
5. Ecological, behavioral, or life-history traits that differentially favor interspecies transmission or spillover as compared to other taxonomic groups.
6. Unique immune system traits or responses that result in more frequent asymptomatic infection as compared to other taxonomic groups.

11.3 FACTORS THAT MAY CONFOUND INVESTIGATIONS OF WHETHER OR NOT A TAXONOMIC GROUP IS "SPECIAL"

The ability to determine whether a host is "special", based on the above six criteria, is highly dependent on the availability of unbiased and comprehensive datasets for comparable taxonomic groups. With a complete and unbiased dataset, simple statistical approaches can be used to test hypotheses related to the six criteria listed previously (Hypothesis 1: Bats harbor a greater number of viruses than other taxonomic groups). However, the availability of unbiased data is rare, and therefore methods to differentiate certain taxonomic groups over others may be confounded by sampling bias (as in, not distributing pathogen discovery research equally) and other factors that affect probability of detection (for instance, lack of clinical signs or lack of immunological reagents). We address specific research limitations and causes for bias in the comparative analyses next.

11.3.1 Research bias towards certain hosts and pathogens

We examined the number of virus-related research studies published per year for each major mammalian order, through a keyword search of ISI Web of Science including order name, common name, and virus keywords, such as "((chiroptera OR bat*) AND (virus* OR viral))." The number of bat virus studies has grown dramatically, especially in the last 10 years, as compared to some other groups of mammals (Figure 11.1). Other orders, including primates and rodents, have an order of magnitude greater number of

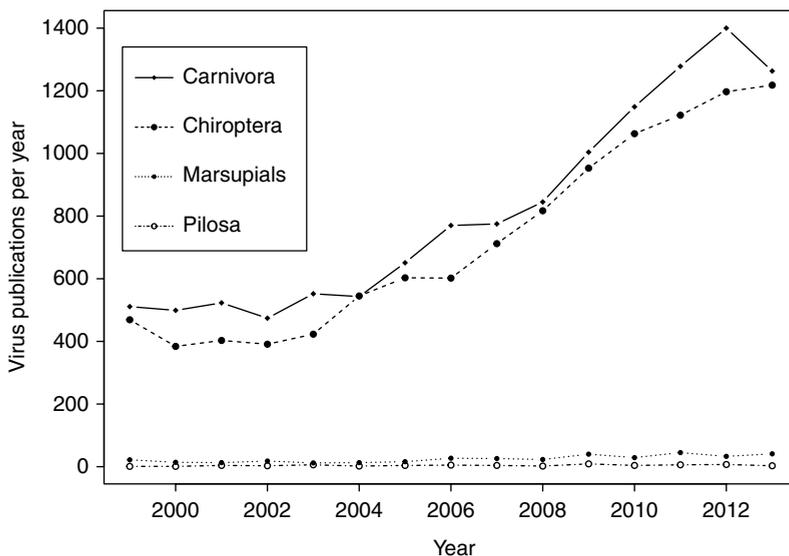


Figure 11.1 Number of virus research papers published per year from 1999–2013 for bats, carnivores, marsupials, and sloths.

studies published than bats; for example, there were 23 012 virus studies on rodents and 70 900 studies on primates in 2013.

However, the bias toward a very large number of studies in rodents and primates may be due to studies using experimental animal models, including *Rattus rattus* and macaques – common viral infection lab models – and may not reflect surveillance in wild species. We find that the number of virus studies published per year for the Order Carnivora is roughly equivalent to the number of papers published on bats – although this too could be biased higher due to lab or domestic animals such as using ferrets for influenza studies, and dogs and cats. Other, less speciose orders like Pilosa (sloths and anteaters), Didelphimorphia (opossums), and Diprotodontia (kangaroos, wallabies, etc.) (Note: ‘Marsupials’ combines these two orders in Figure 11.1), have been subject to very little virus research (‘Marsupials’ 1999–2013, range 12–45 studies per year; Pilosa, range 1–9 studies). Neither of these “control taxonomic groups” has seen the dramatic increase in viral research in recent years that bats, carnivores, rodents, and primates all have. This begs the rhetorical question: Are sloths special? Or any other understudied order of mammals? We know that, overall, Pilosa is a much less diverse order of mammals, but on a per species basis do they harbor more viruses, more unique viruses, or more zoonotic viruses but we just do not know it yet because we have not looked?

11.3.2 Lack of thorough disease ecology studies

One criterion for defining whether a given taxonomic group is “special” would be to assess whether or not humans share some unique ecological interface or likelihood of contact with that group which differs from other groups. For example, bats, due to the synanthropic roosting behavior of many species, have been implicated as being more

likely to come into contact with humans than many other groups of mammals, and overall in Australasia make up a higher proportion of species that use human-modified habitat (McFarlane *et al.*, 2012). While this is true for some species of bat that are adaptable to human dwellings, many species of bat are also obligate forest-dwelling species that need pristine forest for survival. For example, over 125 species of bats, including many obligate forest interior species, have been described from one rich rainforest community in Malaysia (Kingston *et al.*, 2006). Furthermore, while some bat species are capable of roosting and foraging in close proximity to humans, several species of rodents are also tolerant of disturbed habitat and act as common as "peri-domestic" species around the world. In ranking mammalian orders by emerging infectious disease host status and use of human modified habitat, McFarlane *et al.* (2012) found that rodents, primates, and carnivores all had higher odds ratios than bats.

While these literature review studies are important, in order to properly assess levels of wildlife contact with humans, thorough ecological studies and properly designed studies for data collection are needed. Several detailed disease ecology studies of bat-human ecological interaction have been published over the last decade, but these remain limited to a few species. This includes the use of telemetry to identify overlap and habitat use in flying foxes in order to understand the ecology of henipaviruses (Epstein *et al.*, 2009; Newman *et al.*, 2011; Smith *et al.*, 2011) and Reston Ebola virus (de Jong *et al.*, 2013). Geographical information systems (GIS)-based approaches to estimate likelihood of contact and spillover have also been used to estimate risk of Nipah virus spillover at a coarse scale (Hahn *et al.*, 2014a, b). Camera traps have been used to understand specific bat foraging ecology and have led to implementation of a low-tech barrier solution to reduce the risk of Nipah virus transmission via bat contact (Khan *et al.*, 2011). Most recently, under the USAID PREDICT project, we have begun to systematically quantify human contact with bat, primate, and rodent wildlife species across tropical land-use gradients on three continents (in the Brazilian Amazon, Borneo rainforest, and Ugandan Bwindi Rainforest). This project, named Deep Forest, uses a combination of ecological surveys using standardized trapping at each field site and standardized behavioral questionnaires administered to people living around each field site and those who interact with wildlife. Ultimately, these studies are relatively few, and are often preliminary in nature, so it is not yet possible to deduce how frequently people make contact with bats, under what circumstances they do so, and whether this is increasing over time so that it could contribute to increased viral emergence from bats.

11.3.3 The ability to measure immune responses and detect illness in hosts

Reservoirs of zoonotic viruses are typically able to support replication of the viral agent with only minor clinical signs of infection. Some authors have suggested that another criteria defining bats as "special" disease reservoirs is their ability to become infected with diverse viral pathogens, but show no clinical signs. Unfortunately, very few studies have been conducted to test this phenomenon in bats, largely because such trials are difficult to conduct in the field, and usually involve experimental infections of previously uninfected hosts. Clearly, the absence of prior infection cannot be determined with any level of confidence in wild-caught animals. Very few laboratory colonies of bats have been set up, and little work has so far been conducted to test this hypothesis. Experimental

infection studies of *Pteropus* sp. bats with henipaviruses (Halpin *et al.*, 2011; Middleton *et al.*, 2007), recent work on infection in *Rousettus* sp. bats with Marburg virus (Towner, 2013), and other studies have increased our understanding of bat immune response, but are insufficient to fully understand the diversity of host–pathogen interactions involving bats. The results of these studies do not support the claim that bats show no clinical signs when challenged with virus. Rather, these studies are inconclusive to date in this subject, suggesting that they may not be unusually refractory to viral infection and may be similar to other reservoir host–pathogen relationships that have coexisted for long periods of time. One definition of a reservoir host is a species that has coevolved with a given pathogen, and is immunologically conditioned to its infection (Ashford, 2003; Haydon *et al.*, 2002; Olival *et al.*, 2012). For example, rodents have co-evolved with dozens of different Hantaviruses, with most viral strains and species being highly species-specific and seeming to cause only mild pathology in their natural host species. Experimental research on various rodent models has shown that rodents have a similar ability to become infected, shed virus, but show little to no clinical signs when infected with Hantaviruses (Schountz & Prescott, 2014). Does this make rodents special because they do not get sick from Hantaviruses, but other hosts (i.e., humans) will show pathology and die from these viruses? This indeed leads us to a critical and still unanswered scientific question, whether we are talking about bats, rodents, or some other group of mammals: why do some individuals/genotypes/species get sick while others do not? And what can we learn about this process for the benefit of humans? It seems the uniqueness of the bat immune response remains an open question, and we should be reminded that a broader comparative approach is needed.

Another limitation in assessing clinical signs and determining if bats get “sick” or not from viral infection is a lack of bat-specific reagents for immunological studies (See Chapter 14 for further discussion) and of captive bat colonies for experimental work. Recently established captive colonies, such as *Rousettus aegyptiacus* at the Centers for Disease Control (CDC) in the US, are beginning to make experimental work more accessible and these efforts are shedding light on filovirus infections in bats (Olival & Hayman, 2014; Towner, 2013).

Finally, there has been little work so far on defining clinical signs in bats, or the clinical progression of illnesses. Do bats develop the same clinical features as other mammalian hosts? Should we expect elevated temperatures? What are the baseline physiological data we are measuring against? With the exception of a very few bat species kept in captivity (for instance, at Lubee Bat Conservancy and other zoos around the world), we have no idea as to what the physiological parameters for a “healthy bat”, such as temperature or blood cell count, should be. Levinson *et al.* (2013) conducted a literature review to assess if viral discovery efforts targeted clinically “sick” wildlife, and if this was more effective than viral discovery in seemingly healthy wildlife hosts. They first found that only about half of all studies reported the health condition of the host animals. They argue that this can be improved with the inclusion of wildlife veterinarians in viral discovery efforts – and the general move toward more interdisciplinary “One Health” research teams. Second, they found for those studies that did report the health condition of animals, that there was no significant effect on the number of viruses found per host species in those animals that were reported as sick vs. those that were not. Interestingly, they did find that the proportion of hosts that were symptomatic differed by host order. Overall, bats were reported as being asymptomatic more often than

other host groups (Levinson *et al.*, 2013). However, is this due to the fact that sick, wild bats are difficult to detect in the field, or is it a real physiological or immunological effect that was captured in the reported studies? These questions remain unanswered, but it is likely a combination of both factors. More systematic approaches to assessing health status in wildlife are needed to explore this further, rather than reliance on disparate studies published over the years.

11.4 VIRAL DIVERSITY IN BATS COMPARED TO OTHER MAMMALIAN HOSTS

In order to assess whether bats harbor a disproportionate number of viruses compared to other groups of mammals, and whether they harbor a disproportionate number of zoonotic viruses, we updated our literature review and data extraction process that included all literature describing mammalian viruses and their hosts published over the previous 50 years (Olival *et al.*, 2012).

11.4.1 Do bats harbor a disproportionate number of viruses?

In a two order comparison of bats and rodents, Luis *et al.* (2013) found that overall bats harbored 2.71 total viruses per species, and rodents harbored 2.48. While their study did use robust modeling approaches including phylogenetic correction, these values of mean number of viruses per host cannot be taken to suggest that bats really do harbor more virus than other mammals. While accessible, these summary statistics do not properly account for research bias, and further include only comparison of two mammalian orders. To address this latter issue, we used our database of mammalian viruses to examine viral richness across all mammalian orders for which we had data. In Figure 11.2 we summarize the known viral richness for the six most speciose orders. In this broad data set, although mean values will obviously differ between orders, these differences in viral richness across orders are not statistically significant. Thus, using a very large comparative dataset including 593 unique viruses and 768 mammal species from 13 different orders, bats do not stand out as having a significantly greater per-species viral diversity than other mammalian orders.

11.4.2 Do bats harbor a disproportionate number of zoonoses?

In their analysis, Luis *et al.* (2013) also found that bats harbored slightly more zoonotic viruses on a per species basis, 1.79 mean zoonotic viruses per bat species, and 1.48 per rodent species. We also addressed this hypothesis using our large comparative data set to include more than the two orders they looked at. In Figure 11.3 we show the proportion of zoonotic viruses on a per-species basis for each of 13 mammalian orders. As is evident, there is a paucity of data for several orders, including Cingulata, Pilosa, Didelphimorphia, and Eulipotyphyla, even though the proportion of zoonotic viruses for each of these orders is close to 100%. This finding clearly reflects the role of research bias (which we did not correct for here). It is not necessarily the case that these hosts harbor only viruses that can infect humans, but rather that we are biased in our available assays and surveillance priorities towards viruses that infect humans. No doubt each of

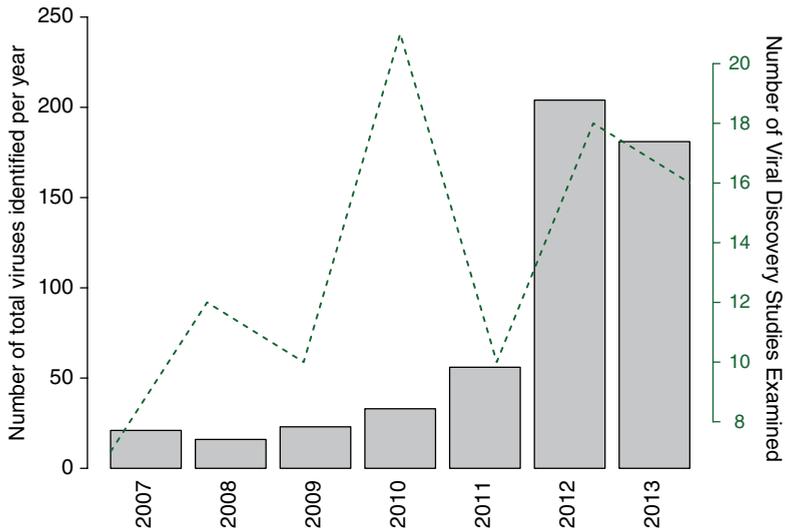


Figure 11.2 Viral discovery publications per year for bats from the past 7 years, and total number of viruses found in those studies (dashed line). Data from Weekley & Olival (in preparation).

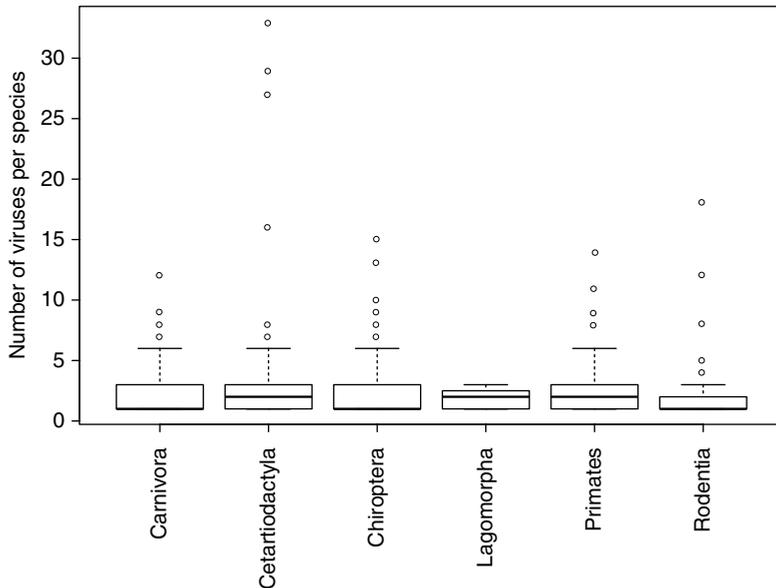


Figure 11.3 Boxplot showing total viral richness, species level data aggregated by order, for over 700 species of mammals across six orders with the most data available. Data updated from Olival *et al.* (2012).

these orders harbors a unique pool of viruses, but to date we have lacked the tools and motivation to describe this viral diversity. For the orders that do have significant data available, we find that bats, rodents, and primates all have a significantly higher proportion of zoonoses than other orders, but the differences between them are not significant (Figure 11.3). Again, our findings do not suggest that bats are more special than either rodents or primates in terms of their ability to harbor zoonotic viruses.

11.4.3 Focused literature review of bat viral discovery efforts from the past 7 years

We conducted a detailed quantitative review of the bat viral discovery literature published between 2007 and 2013, to identify specific variables to better target future viral discovery efforts in bats (Weekley & Olival, unpublished data, in preparation). In this review, data were extracted from 94 bat virus studies, including host species identification, sample types, virus detection methods, and viral identification to at least the family level, and the number of total and novel viruses found per study.

We found that the number of studies have increased over this 7-year period, as have the number of bat species sampled per study, the number of novel and total viruses found by year of publication, and increased reliance on molecular detection methods. Figure 11.4 shows the total number of viruses identified in these studies per year from 2007–2013, and the number of viral discovery studies investigated (dashed line). There is an increasing trend of more studies yielding more total viruses in bats; however this relationship is not significant for several reasons. For example, in 2010 there were a large number of studies published, but most of these were describing single viruses from single host species. Research efforts have shifted to larger discovery studies involving multiple bat host species for a given viral family (Drexler *et al.*, 2012; Anthony *et al.*, 2013b; Quan *et al.*, 2013) and multiple viral families for a given host species (Anthony *et al.*, 2013a). This has resulted in a large increase in viral detection and discovery in bats, which does not relate linearly to research effort as measured by the number of publications per year. This is important, as it may skew findings if using linear methods to correct for research effort, and reflects the surge in viruses discovered in bats over the last two years.

Across the 94 bat studies examined, over 60 000 samples were taken from over 44 000 individual bats comprising 17 families, 110 genera, and 340 species, with 24 viral families identified. The majority of viruses described were found in only four host families (Vespertilionidae, Pteropodidae, Rhinolophidae, and Hipposideridae), with mean viral prevalence highest in feces and tissue samples. These results have important implications for how future viral discovery studies in bats are designed, how samples are collected, what samples should be screened for different viral families, and whether lethal sampling is effective (Weekley & Olival, unpublished data).

11.5 LIFE HISTORY TRAITS: ARE BATS UNIQUE?

Do bats have unique life history and ecological characteristics that make them better positioned to harbor and transmit viruses to humans than other mammals? First, it is important to recognize that bats are an extremely diverse group and have a wide range of life-history traits, morphologies, and ecologies (Nowak, 1999). Thus there are two

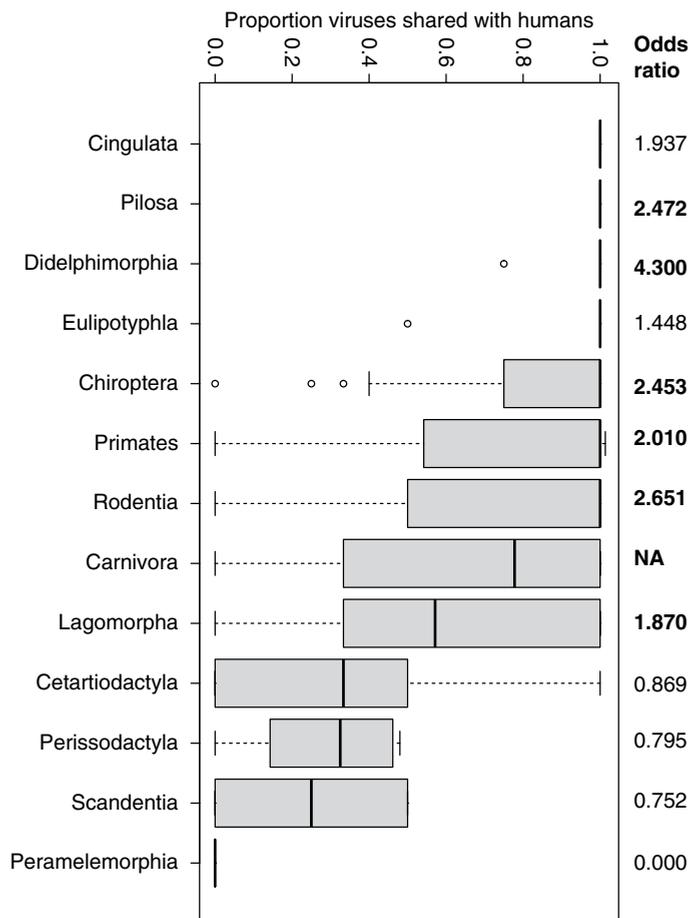


Figure 11.4 Boxplots based on species-level data of proportion of viruses for each species in an Order that are zoonotic. Black bar is median value, box shows interquartile range of proportion of zoonotic viruses across the order. Odds ratio calculated relative to default Order in analysis, Carnivora. Note: while Cingulata, Pilosa, Didelphimorphia, and Eulipotyphla have the highest overall proportion of zoonotic viruses per species, they are also the most data deficient Orders and are highly skewed.

types of comparisons in question. First, there is the *intra*-order comparison; that is, are there specific species of bats that harbor more viruses or more zoonoses than other bat species? Second, the *inter*-order comparison; do bats harbor more viruses because of life history traits that are distinct from all other groups of mammals? Several studies have addressed the former question previously using data acquired from literature reviews, and factors like geographic range area and shape, population structure, sympatric overlap with other hosts, and the use of torpor were each found to be significant in various studies (Turmelle & Olival, 2009; Olival *et al.*, 2012; Luis *et al.*, 2013; Gay *et al.*, 2014). In this chapter, we will take a closer look at the latter question: do bats differ in their life history traits in comparison to other groups of mammals?

At this large, comparative scale, the first thing that comes to mind that sets bats apart from all other mammals is their ability to fly. Bats are the only mammals capable of self-powered flight. Most bats (excluding the family Pteropodidae) have also evolved echolocation as a sensory trait, which they share with marine mammals through convergent evolution. O'Shea *et al.* (2014) proposed an interesting hypothesis that bats' ability to fly may have conferred some unique selective force for dealing with viral infection due to the metabolic rates and elevated body temperatures that are a by-product of the physiologically demanding act of flight. Essentially, these daily, elevated body temperatures may mimic a regular febrile response to limit infections. This hypothesis needs to be tested, but of all the life history traits, self-powered flight is certainly one that sets bats apart from all other mammals. To see whether, across all ~5000 mammalian species, we could identify other life-history traits uniquely different in bats, we analysed species level life-history data from the PanTHERIA database (Jones *et al.*, 2009). Figure 11.5 shows boxplots of species-level data aggregated by mammalian order for life-history traits that have been previously been suggested as significant in influencing viral diversity. Of the six traits examined, the only trait for which bats seem to stand out (though influenced strongly by a series of outlier species), is population group size. The y-axis of Figure 11.5 for Population Group Size was truncated to a maximum group size of 5000 individuals to make the data more visible across orders, but there are a handful of

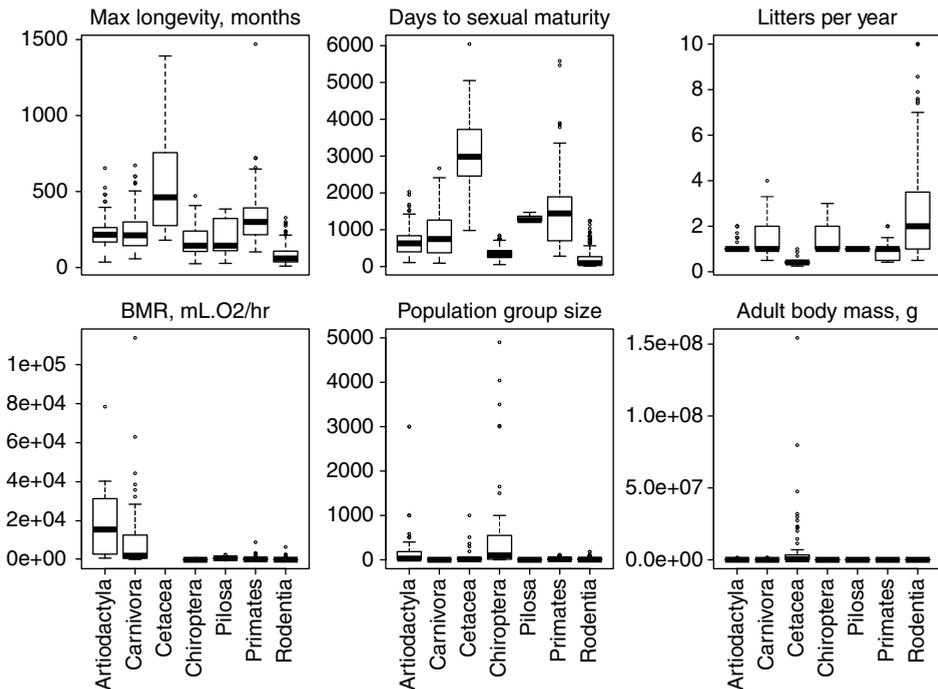


Figure 11.5 Boxplots of life-history trait data from PanTHERIA species-level database, grouped by Order for seven mammalian orders. Bats are not significantly differentiated from other mammals for any of these traits that have been previously suggested to influence viral diversity.

bat species that aggregate in population sizes much larger than this. For example, the Brazilian free-tailed bat and Straw-colored fruit bat are two outliers not shown on the figure, which both have population sizes in the millions. However, while these outliers are often cited as examples of bats having much larger population sizes than all other mammals, the totality of the species-level data shows that there is no statistically significant difference between orders for this trait. In summary, of the life history traits we examined, none seem to clearly set bats apart as unique from other mammals when viewed aggregated across species. It should be noted, however, that we did not examine some traits that have been suggested as being unique in bats because we did not have good comparative data across the groups (for example maximum heart rate or maximum oxygen consumption rate). More comparative research and species-specific data are needed to see how different bats are as a whole for other traits such as these.

11.6 DISTRIBUTION AND DIVERSITY OF BAT VIRUSES, AND WAYS TO TARGET FUTURE DISCOVERY EFFORTS

Whether or not bats are “special”, we know they harbor some viral pathogens of serious consequence to human health. Several zoonotic viruses such as Ebola, Marburg, Nipah, Hendra, Middle East respiratory syndrome, and SARS-like coronaviruses, have bats as the most likely natural reservoirs (Calisher *et al.*, 2006; Ge *et al.*, 2013; Memish *et al.*, 2013; Olival *et al.*, 2012; Olival & Hayman, 2014). Due to the emergence of these high consequence pathogens in human populations, there has been a growing interest in analytical approaches that may begin to forecast bat-borne disease outbreaks and spillover events to other hosts. Can we predict the next bat-borne zoonoses? Can we allocate our surveillance resources to the geographic localities and species most likely to harbor the next big emerging infectious disease?

Brierely *et al.* (personal communication) laid out a framework to identify the drivers of zoonotic bat-borne virus emergence. They divided the processes of disease emergence into principle components and examined drivers at each stage: drivers of pathogen richness, drivers of transmission opportunity and drivers of infection success. This overall structure allows for different aspects of the emergence process to be tested against various potential “drivers”, or causes of virus sharing, using spatial analyses that account for research bias. In this analysis, host diversity and climatic variability seem to drive pathogen richness; while human population density, bushmeat hunting and live-stock production are significant drivers of transmission opportunity between bats and humans. Mapping the outputs of these spatial models for each stage of the emergence process separately can help to identify high priority locations for pathogen discovery in ways that may not overlap with those for public health interventions.

Others have focused on modeling which host species are most likely to harbor more viruses/zoonoses. These studies have given us clues to life history traits that may help predict viral richness within, but not between, different mammalian groups (Altizer *et al.*, 2003; Turmelle & Olival, 2009; Cooper *et al.*, 2012; Luis *et al.*, 2013; Gay *et al.*, 2014). Within bats, results from these studies suggest that species that are more frequently studied (research bias), with more fragmented range area, more structured populations, smaller litter size, larger body mass, and greater longevity and litters per year all may be more likely to harbor zoonoses and virus diversity in general. Species that are sympatric

with a large number of other species are also more likely to harbor a greater diversity of viruses (Luis *et al.*, 2013). Targeting bat species with these traits for viral discovery may prove particularly fruitful, as compared to randomly selecting species for surveillance.

Far less research has been conducted on targeting surveillance at key transmission and ecological interfaces, even for known zoonoses. For example, despite several bat species being identified as the origin of filoviruses, only a handful of studies have investigated the ecology of these bats with respect to viral shedding or high risk contact with people (for a review see Olival & Hayman, 2014). The exception seems to be the henipaviruses, largely due to the high number of outbreaks of Nipah virus in Bangladesh and Hendra virus in Australia identified recently. It is increasingly apparent that spillover of Nipah virus in Bangladesh is largely through the consumption of date palm sap contaminated by bats feeding from sap collection jars (Rahman *et al.*, 2012). In Australia, emergence of Hendra virus has occurred repeatedly via bat to horse viral spillover, followed by human contact with sick horses (Plowright *et al.*, 2011). It is, however, unclear whether these risk factors are responsible for spillover in other countries or are risk factors for other viruses carried by bats. Perhaps one of the challenges to progress is that ecological studies are complex, expensive and require multi-year surveillance to obtain the power necessary to test hypotheses. For example, it took over 5 years of research to identify the most likely underlying driver of Nipah virus emergence in Malaysia (Pulliam *et al.*, 2012). This included field capture and sampling of *Pteropus* bats, satellite telemetry, analysis of climate trends, veterinary epidemiology of pig farms, and complex mathematical modeling of viral dynamics. To understand the broader context of human–bat interactions, and their consequences for viral spillover will require similar long-term studies at geographically disparate sites, and the sampling of multiple species of bats representing the phylogenetic diversity of the Order Chiroptera.

11.7 SUMMARY AND FUTURE RESEARCH

The review presented here, and our literature and data analyses do not give a clear indication of whether bats are “special” for zoonotic viruses – that is, they do not definitively demonstrate that bats do, or do not, harbor a greater diversity of zoonotic or potentially zoonotic viruses than other taxonomic groups or have a greater propensity for spillover of zoonotic viruses. However, it does appear that bats, along with rodents and primates, not only make up the vast majority of mammal species in the world (~70%), but also seem to harbor a high proportion of zoonotic viruses. On the other hand, it is also clear that other mammalian taxonomic groups have had very little viral discovery research conducted on them, and with more dedicated research these groups may also turn out to be important for zoonoses. Our review does suggest that there are major gaps to be addressed before this hypothesis can be tested, particularly in the clinical signs that bats exhibit when infected as “natural” reservoirs, and in the mechanisms by which bat life history traits do or do not make them more likely to be reservoirs. Given the new analyses reported here, and the substantial gaps in other studies, we conclude that the evidence does not yet support the hypothesis that bats are “special” in their relationship with viruses. That said, our analyses provide substantial support that bats rank highly, along with primates, rodents, and potentially other mammalian groups, as hosts for a significant number of known and as-yet undiscovered zoonotic viruses,

many of which are, or may be significant public health threats. Like primates and rodents, bats may not be particularly “special” reservoirs, but simply reservoirs, and therefore should continue to be the focus of viral research and discovery.

REFERENCES

- Altizer, S., Nunn, C. L., Thrall, P. H., *et al.* (2003). Social organization and parasite risk in mammals: Integrating theory and empirical studies. *Annu Rev Ecol Evol Syst* 34, 517–547.
- Anthony, S. J., Epstein, J. H., Murray, K. A., *et al.* (2013a). A strategy to estimate unknown viral diversity in mammals. *MBio* 4 (5), e00598–13.
- Anthony, S. J., Ojeda-Flores, F., Rico-Chávez, O., *et al.* (2013b). Coronaviruses in bats from Mexico. *J Gen Virol* 94, 1028–1038.
- Ashford, R. W. (2003). When is a reservoir not a reservoir? *Emerg Infect Dis* 9, 1495–1496.
- Calisher, C. H., Childs, J. E., Field, H. E., Holmes, K. V. & Schountz, T. (2006). Bats: Important reservoir hosts of emerging viruses. *Clin Microbiol Rev* 19, 531–545.
- Cooper, N., Griffin, R., Franz, M., Omotayo, M. & Nunn, C. L. (2012). Phylogenetic host specificity and understanding parasite sharing in primates. *Ecol Lett* 15, 1370–1377.
- de Jong, C., Field, H., Tagtag, A., *et al.* (2013). Foraging behaviour and landscape utilisation by the endangered golden-crowned flying fox (*Acerodon jubatus*), the Philippines. *Plos One* 8.
- Dobson, A. P. (2005). What links bats to emerging infectious diseases? *Science* 310, 628–629.
- Drexler, J. F., Corman, V. M., Muller, M. A., *et al.* (2012). Bats host major mammalian paramyxoviruses. *Nat Commun* 3, 1–12.
- Epstein, J. H., Olival, K. J., Pulliam, J. R. C., *et al.* (2009). *Pteropus vampyrus*, a hunted migratory species with a multinational home-range and a need for regional management. *J Appl Ecol* 46, 991–1002.
- Gay, N., Olival, K. J., Bumrungsri, S., Siriaronrat, B., Bourgarel, M. & Morand, S. (2014). Parasite and viral species richness of Southeast Asian bats: Fragmentation of area distribution matters. *Int J Parasitol Parasites Wildl* 3, 161–170.
- Ge, X. Y., Li, J. L., Yang, X. L., *et al.* (2013). Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature* 503, 535–538.
- Hahn, M. B., Epstein, J. H., Gurley, E. S., *et al.* (2014a). Roosting behaviour and habitat selection of *Pteropus giganteus* reveal potential links to Nipah virus epidemiology. *J Appl Ecol* 51, 376–387.
- Hahn, M. B., Gurley, E. S., Epstein, J. H., *et al.* (2014b). The role of landscape composition and configuration on *Pteropus giganteus* roosting ecology and Nipah virus spillover risk in Bangladesh. *Am J Trop Med Hyg* 90, 247–255.
- Halpin, K., Hyatt, A. D., Fogarty, R., *et al.* & the Henipavirus Ecology Research Group. (2011). Pteropid bats are confirmed as the reservoir hosts of henipaviruses: a comprehensive experimental study of virus transmission. *Am J Trop Med Hyg* 85, 946–951.
- Haydon, D. T., Cleaveland, S., Taylor, L. H. & Laurenson, M. K. (2002). Identifying reservoirs of infection: A conceptual and practical challenge. *Emerg Infect Dis* 8, 1468–1473.
- Jones, K. E., Bielby, J., Cardillo, M., *et al.* (2009). PanTHERIA: a species-level database of life history, ecology, and geography of extant and recently extinct mammals. *Ecology (Washington D C)* 90, 2648–2648.
- Khan, M. S. U., Hossain, J., Gurley, E. S., Nahar, N., Sultana, R. & Luby, S. P. (2011). Use of infrared camera to understand bats’ access to date palm sap: implications for preventing Nipah virus transmission. *EcoHealth* 7, 517–525.

- Kingston, T., Liat, L. B. & Zubaid, A. (2006). *Bats of Krau Wildlife Reserve*. Kuala Lumpur Penerbit University, Kebangsaan, Malaysia.
- Levinson, J., Bogich, T. L., Olival, K. J., *et al.* (2013). Targeting surveillance for zoonotic virus discovery. *Emerg Infect Dis* 19, 743–747.
- Luis, A. D., Hayman, D. T. S., O’Shea, T. J., *et al.* (2013). A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? *Proc Roy Soc B Biol Sci* 280, 20122753.
- McFarlane, R., Sleigh, A. & McMichael, T. (2012). Synanthropy of wild mammals as a determinant of emerging infectious diseases in the Asian-Australasian region. *Ecohealth* 9, 24–35.
- Memish, Z. A., Mishra, N., Olival, K. J., *et al.* (2013). Middle east respiratory syndrome coronavirus in bats, Saudi Arabia. *Emerg Infect Dis* 19, 1819–1823.
- Middleton, D. J., Morrissy, C. J., van der Heide, B. M., *et al.* (2007). Experimental Nipah virus infection in pteropid bats (*Pteropus poliocephalus*). *J Comp Pathol* 136, 266–272.
- Newman, S. H., Field, H. E., Jong, C. E. d. & Epstein, J. H., (eds) (2011). *Investigating the Role of Bats in Emerging Zoonoses: Balancing ecology, conservation and public health interests*. Rome: Food and Agriculture Organization of the United Nations.
- Nowak, R. M. (1999). *Walker’s Mammals of the World*. Baltimore: Johns Hopkins University Press.
- O’Shea, T. J., Cryan, P. M., Cunningham, A. A., *et al.* (2014). Bat flight and zoonotic viruses. *Emerg Infect Dis* 20, 741–745.
- Olival, K. J., Epstein, J. H., Wang, L. F., Field, H. E. & Daszak, P. (2012). Are bats unique viral reservoirs? In *New Directions in Conservation Medicine: Applied Cases of Ecological Health*, 2nd edn, pp. 195–212. Edited by Aguirre, A. A., Ostfeld, R. S. & Daszak, P. Oxford: Oxford University Press.
- Olival, K. J. & Hayman, D. T. S. (2014). Filoviruses in bats: current knowledge and future directions. *Viruses – Basel* 6, 1759–1788.
- Plowright, R. K., Foley, P., Field, H. E., *et al.* (2011). Urban habituation, ecological connectivity and epidemic dampening: the emergence of Hendra virus from flying foxes (*Pteropus* spp.). *Proc Roy Soc B Biol Sci* 278, 3703–3712.
- Pulliam, J. R. C., Epstein, J. H., Dushoff, J., *et al.* (2012). Agricultural intensification, priming for persistence and the emergence of Nipah virus: a lethal bat-borne zoonosis. *J Roy Soc Interface* 9, 89–101.
- Quan, P. -L., Firth, C., Conte, J. M., *et al.* (2013). Bats are a major natural reservoir for hepaciviruses and pegiviruses. *Proc Natl Acad Sci U S A* 110, 8194–8199.
- Rahman, M. A., Hossain, M. J., Sultana, S., *et al.* (2012). Date palm sap linked to Nipah virus outbreak in Bangladesh, 2008. *Vector-Borne and Zoonotic Diseases* 12, 65–72.
- Schountz, T. & Prescott, J. (2014). Hantavirus Immunology of rodent reservoirs: current status and future directions. *Viruses – Basel* 6, 1317–1335.
- Smith, C. S., Epstein, J. H., Breed, A., *et al.* (2011). Satellite telemetry and long-range bat movements. *PLOS One* 6, e14696.
- Towner, J. S. (2013). Bats as reservoirs of filoviruses (data from recent challenges). In *16th International Bat Research Conference*. San Jose, Costa Rica.
- Turmelle, A. S. & Olival, K. J. (2009). Correlates of viral richness in bats (Order Chiroptera). *EcoHealth* 6, 522–539.
- Wang, L. F., Walker, P. J. & Poon, L. L. M. (2011). Mass extinctions, biodiversity and mitochondrial function: are bats ‘special’ as reservoirs for emerging viruses? *Curr Opin Virol* 1, 649–657.