

WILDLIFE AND VECTOR-BORNE DISEASES: THE TWIN ENGINES OF ZONOTIC EMERGENCE

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Abstract

Wildlife and arthropod vectors are the twin engines that drive much of the world's zoonotic disease. Wild animals serve as the natural reservoirs for the majority of the pathogens that have emerged in people in recent decades, while blood-feeding vectors such as mosquitoes, ticks, fleas and sandflies provide the bridge that carries many of these agents from animals to humans. This review examines both halves of the equation and, crucially, their intersection. We consider why certain wildlife taxa—bats, rodents, primates and birds in particular—are such prolific sources of pathogens, and how human encroachment on natural habitats converts a latent reservoir into an active threat. We then survey the principal groups of arthropod vectors and the diseases they transmit, noting that vector-borne diseases account for more than seventeen per cent of all infectious diseases and over seven hundred thousand deaths each year. The two themes converge in the many vector-borne diseases that are maintained in sylvatic cycles among wild hosts—Kyasanur Forest disease, West Nile fever, plague and the leishmaniases among them—and that spill into people when human, vector and reservoir overlap. We review representative mosquito-borne, tick-borne and other vector-borne diseases, with attention to the Indian context, before discussing the ecological drivers of emergence, the principles of surveillance and control, and the One Health framework within which veterinarians play an indispensable role at the wildlife–vector–human interface.

Keywords: Wildlife reservoirs; vector-borne diseases; arboviruses; ticks; mosquitoes; spillover; Kyasanur Forest disease; One Health

Introduction

World Zoonoses Day, observed each 6 July, is a reminder that human health is bound up with the health of animals and of the environments they share. Within the broad field of zoonotic disease, two elements recur so persistently that they may be regarded as the twin engines of disease emergence: wildlife and arthropod vectors. Wild animals harbour an immense and largely uncharacterised diversity of microorganisms, and a clear majority of the human pathogens that have emerged in recent decades originate in wildlife reservoirs (Jones et al.,

2008; Karesh et al., 2012). Blood-feeding arthropods, meanwhile, transmit a substantial share of the world's infectious disease, ferrying viruses, bacteria and parasites between animal hosts and people (World Health Organization, 2024).

These two engines frequently work in tandem. Many of the most important vector-borne diseases are maintained not in humans but in cycles among wild animals, with people infected only incidentally when they intrude upon, or are intruded upon by, the natural transmission cycle. Kyasanur Forest disease in the forests of India's Western

Ghats, West Nile fever in birds, plague in wild rodents and the leishmaniasis spread by sandflies all illustrate this convergence. This review therefore treats wildlife and vector-borne diseases together. It first considers wildlife as a reservoir of pathogens, then the vectors and the burden of vector-borne disease, then their intersection, and then representative diseases grouped by vector. It closes with the ecological drivers of emergence, the principles of surveillance and control, and the One Health response in which the veterinary profession is central.

Wildlife as reservoirs of disease

Wild animals are the original source of a striking proportion of human infectious disease. More than sixty per cent of human pathogens are shared with animals, and among newly emerging diseases the proportion of wildlife origin is higher still (Figure 1), a pattern documented across successive global analyses of emerging infectious disease events (Taylor et al., 2001; Jones et al., 2008; Daszak et al., 2000). The reasons are partly arithmetic—wild vertebrates vastly outnumber domestic species and carry a correspondingly larger and more varied microbial flora—and partly ecological, in that pathogens long co-adapted to wild hosts may cause little disease in those reservoirs while proving devastating when they reach a novel human host (Figure 1).

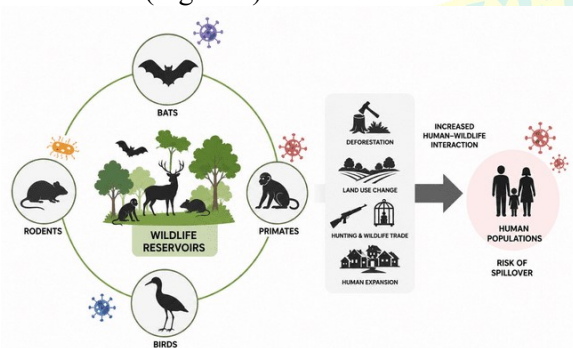


Fig. 1. Conceptual illustration of wildlife reservoirs and the ecological drivers of zoonotic spillover

Wildlife reservoir hosts, including bats, rodents, birds and non-human primates, maintain a wide diversity of zoonotic pathogens in nature. Anthropogenic activities such as deforestation, land-use change, agricultural expansion, wildlife hunting and trade, and increasing human population density

reduce the ecological barriers between wildlife and humans, thereby increasing opportunities for pathogen spillover. Enhanced human–wildlife interactions facilitate the transmission of infectious agents from animal reservoirs to humans, contributing to the emergence and re-emergence of zoonotic diseases. The figure emphasizes the central role of environmental disturbance and human activities in shaping spillover risk within a One Health framework.

A handful of wildlife groups stand out as especially important reservoirs. Bats are remarkable hosts of emerging viruses, harbouring lyssaviruses, the henipaviruses Nipah and Hendra, filoviruses such as Ebola and Marburg, and a great diversity of coronaviruses, apparently tolerating infections that would sicken other mammals (Calisher et al., 2006; Leroy et al., 2005; Halpin et al., 2000; Arunkumar et al., 2019). Rodents are the second great reservoir group, hosting the agents of plague, leptospirosis, hantavirus disease and many others, and analyses of host traits identify them as a likely source of future zoonoses (Han et al., 2015). Non-human primates, our closest relatives, share pathogens readily with people, as seen in the sylvatic cycles of yellow fever and Kyasanur Forest disease and in the origins of human immunodeficiency virus. Wild birds, finally, are the natural reservoir of the avian influenza viruses and of arboviruses such as West Nile and Japanese encephalitis, and their migratory movements can carry pathogens across continents (Kramer et al., 2008).

Crucially, the mere existence of a pathogen in wildlife is not, by itself, a threat to people. The danger materialises when human activity erodes the separation between wild reservoirs and human populations—through deforestation, the expansion of farms and settlements into forest, hunting and the wildlife trade, and the disturbance of habitats that forces wild animals and people into closer and more frequent contact (Figure 1). Spillover, in other words, is as much a consequence of human ecology as of animal biology, a theme developed further below (Plowright et al., 2017).

Vectors and the burden of vector-borne disease

A vector is a living organism, most often a blood-feeding arthropod, that transmits an infectious agent from one host to another. In biological transmission, which characterises the most

important vector-borne diseases, the pathogen multiplies or develops within the vector before being passed on; in mechanical transmission the vector merely carries the agent on its mouthparts or body. The principal vector groups are the mosquitoes, the ticks, the fleas, the sandflies, the triatomine bugs and the tsetse flies, together with mites and lice of lesser importance. Once infected, many vectors remain infectious for life and transmit the pathogen at each subsequent blood meal, which makes them formidable amplifiers of disease (World Health Organization, 2024).

The collective burden is enormous. Vector-borne diseases account for more than seventeen per cent of all infectious diseases and cause over seven hundred thousand deaths every year, falling most

heavily on tropical and subtropical regions and on the poorest populations. Malaria alone, a parasitic infection transmitted by Anopheline mosquitoes, causes on the order of two hundred and fifty million cases and more than six hundred thousand deaths annually, the majority in young children (World Health Organization, 2024). Dengue, the most prevalent viral vector-borne disease, has been estimated through cartographic modelling at around three hundred and ninety million infections each year, of which roughly ninety-six million are clinically apparent, with Asia bearing the greatest share and India alone accounting for a substantial fraction of the global total (Bhatt et al., 2013). The principal vector groups and the diseases they transmit are summarised in Table 1.

Table 1. Principal arthropod vectors and representative vector-borne diseases.

Vector group	Representative vectors	Diseases transmitted
Mosquitoes	Anopheles, Aedes, Culex	Malaria, dengue, chikungunya, Zika, Japanese encephalitis, West Nile fever, Rift Valley fever, yellow fever
Ticks	Haemaphysalis, Hyalomma, Ixodes	Kyasanur Forest disease, Crimean–Congo haemorrhagic fever, Lyme disease, tick-borne encephalitis, babesiosis
Fleas	Xenopsylla	Plague, murine typhus
Sandflies	Phlebotomus	Leishmaniasis (visceral, cutaneous)
Other (mites, tsetse, triatomines)	Trombiculid mites, Glossina, Triatoma	Scrub typhus, African trypanosomiasis, Chagas disease

The intersection: vector-borne diseases with wildlife reservoirs

The deepest connection between this review's two themes lies in the many vector-borne diseases that are maintained in sylvatic, or wildlife, cycles. In such systems the pathogen circulates between wild vertebrate hosts and their arthropod vectors largely independently of humans; people become infected only when they enter the cycle, when an infected vector strays from its usual hosts, or when a “bridge” vector feeds on both wild reservoirs and humans. Because the reservoir persists in wildlife regardless of what happens in people, these diseases cannot be eliminated simply by treating human cases—a feature that

distinguishes them sharply from infections maintained in human or domestic-animal populations.

The consequences are twofold. First, control must engage with the ecology of wild hosts and vectors, not only with human medicine. Second, disturbance of the natural cycle—through land-use change that alters the abundance or distribution of reservoirs and vectors—can abruptly increase human exposure. Several diseases reviewed below, including Kyasanur Forest disease, West Nile fever, plague and the zoonotic leishmaniases, exemplify this wildlife–vector–human triad, and representative examples are collected in Table 2.

Table 2. Selected wildlife-associated vector-borne diseases.

Disease	Pathogen	Vector	Wildlife reservoir / host	Note
Kyasanur Forest disease	KFD virus (flavivirus)	Haemaphysalis ticks	Monkeys, rodents, birds, shrews	Endemic to Western Ghats, India; monkey

				deaths can precede human cases
West Nile fever	West Nile virus (flavivirus)	Culex mosquitoes	Wild birds	Humans and horses are dead-end hosts
Plague	Yersinia pestis	Fleas	Wild rodents	Sylvatic reservoir with periodic spillover
Visceral leishmaniasis	Leishmania spp.	Phlebotomine sandflies	Rodents and canids (zoonotic forms)	Major burden in India (kala-azar)
Crimean–Congo haemorrhagic fever	CCHF virus	Hyalomma ticks	Livestock, hares, ground-feeding birds	High case-fatality; notifiable in India

Major mosquito-borne diseases

Mosquitoes are the most consequential of all disease vectors. Malaria, caused by *Plasmodium* parasites and transmitted by Anopheline mosquitoes, remains among the heaviest infectious-disease burdens on earth and is concentrated in the tropics; although primarily a human-maintained infection, it shares ecological territory with the other mosquito-borne diseases and responds to the same environmental drivers (World Health Organization, 2023). The *Aedes*-borne arboviruses—dengue, chikungunya, Zika and yellow fever—have expanded dramatically with urbanisation and global travel; dengue in particular has become a defining urban-tropical disease, with hundreds of millions of infections each year and a burden that has grown steadily over recent decades (Bhatt et al., 2013).

Several mosquito-borne diseases are intimately tied to animal hosts. Japanese encephalitis, the leading cause of viral encephalitis in much of Asia and a major concern in India, is maintained in a cycle involving water birds and amplifying pig hosts, with *Culex* mosquitoes transmitting the virus to people who are incidental, dead-end hosts. West Nile virus is maintained in an enzootic cycle between wild birds and ornithophilic mosquitoes, spilling over to humans and horses, both of which are dead-end hosts that do not sustain transmission; the geographic spread of West Nile virus across continents is a textbook example of an avian-reservoir arbovirus exploiting migratory birds and competent local mosquitoes (Kramer et al., 2008). Rift Valley fever, transmitted by mosquitoes and affecting livestock and people alike, and yellow fever, with its sylvatic cycle in forest primates, complete a picture in which mosquito-borne disease

repeatedly straddles the wildlife–livestock–human divide.

Major tick-borne diseases

Ticks rival mosquitoes as vectors of zoonotic disease and are of particular importance at the wildlife interface, because they feed across the full range of vertebrate hosts and can maintain pathogens through their life cycle. For an Indian readership the pre-eminent example is Kyasanur Forest disease, a tick-borne viral haemorrhagic fever first recognised in 1957 in the Kyasanur Forest of Karnataka. Caused by a flavivirus and transmitted chiefly by *Haemaphysalis spinigera* ticks, the virus circulates in a sylvatic cycle among monkeys, rodents, shrews and birds; humans are infected incidentally, typically while entering forest fringes, and a die-off of monkeys often precedes human outbreaks, serving as a natural early-warning sentinel. Since its discovery the disease has spread to new districts and states, a spread linked to deforestation, forest fragmentation and increasing human incursion into wildlife habitat (Mourya et al., 2014; Walsh et al., 2019).

Crimean–Congo haemorrhagic fever, also notifiable in India and associated with high mortality, is transmitted by *Hyalomma* ticks and circulates among livestock, hares and ground-feeding birds, with people exposed through tick bites or contact with infected animal tissues, including during slaughter (Mourya et al., 2014). Beyond India, Lyme disease, caused by *Borrelia* spirochaetes transmitted by *Ixodes* ticks and maintained in small mammals and deer, is the most common vector-borne disease of the temperate Northern Hemisphere, while tick-borne encephalitis, babesiosis and anaplasmosis add to the toll. Ticks

also impose a heavy direct burden on livestock through theileriosis, babesiosis and anaplasmosis, linking wildlife, domestic-animal and human health in a single vector group.

Flea-, sandfly- and other vector-borne diseases

Plague, one of the most historically devastating of all diseases, is caused by the bacterium *Yersinia pestis* and transmitted from rodents to people by fleas. It persists in sylvatic cycles among wild rodents across several continents and spills over periodically, a reminder that even an ancient scourge remains a wildlife-maintained, vector-borne zoonosis. The leishmaniasis, caused by *Leishmania* protozoa and transmitted by phlebotomine sandflies, range from self-limiting skin lesions to the lethal visceral form. Visceral leishmaniasis, known in the Indian subcontinent as kala-azar, is caused there by *Leishmania donovani* and transmitted by the sandfly *Phlebotomus argentipes*; globally the disease causes upwards of a million cases and tens of thousands of deaths, with the Indian subcontinent historically among the most heavily affected regions and an active elimination programme under way (Alvar et al., 2012).

Other vector groups round out the picture. Trombiculid mites transmit scrub typhus, a rickettsial disease of growing recognition across rural Asia, including India, with small mammals as reservoirs. Tsetse flies transmit African trypanosomiasis, and triatomine bugs transmit Chagas disease in the Americas, both maintained in part by animal reservoirs. Across this diversity the common thread is unmistakable: a blood-feeding arthropod links an animal reservoir to the human host, and effective control therefore demands attention to all three.

Ecological drivers of emergence and spread

The distribution and intensity of wildlife and vector-borne diseases are powerfully shaped by human-driven environmental change (Figure 2). Deforestation and forest fragmentation, the expansion of agriculture and settlements into wild areas, the construction of dams and irrigation systems that create vector breeding sites, the wildlife trade, and the unprecedented mobility of people and goods all alter where reservoirs, vectors and humans meet. The spread of Kyasanur Forest disease into

new areas of the Western Ghats has been explicitly linked to forest loss and human encroachment, a clear demonstration that land-use change can convert a localised sylvatic infection into an expanding public-health problem (Walsh et al., 2019; Plowright et al., 2017).

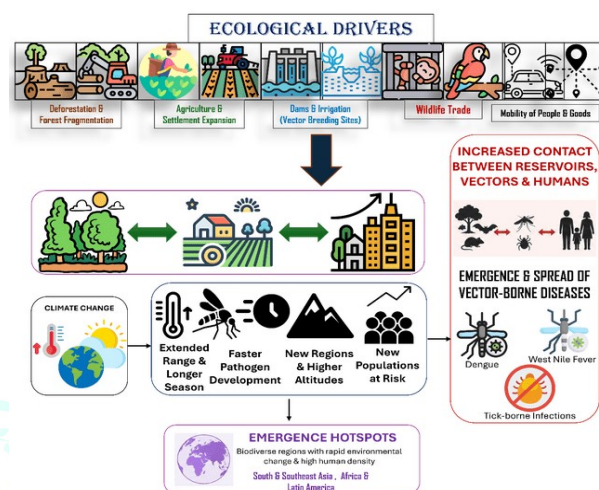


Fig 2. Ecological and climatic drivers influencing the emergence and spread of zoonotic and vector-borne diseases

Human-induced environmental changes, including deforestation, forest fragmentation, agricultural expansion, dam construction, wildlife trade, and increased mobility of people and goods, enhance interactions among wildlife reservoirs, vectors, livestock, and human populations. Climate change further amplifies disease risk by extending vector distribution, accelerating pathogen development, facilitating colonization of new geographic regions and higher altitudes, and exposing previously unaffected populations. These interconnected ecological and climatic drivers contribute to the emergence and spread of vector-borne diseases and create global hotspots of disease emergence, particularly in biodiverse regions undergoing rapid environmental change and population growth.

Climate change adds a further dimension that is especially acute for vector-borne disease, because arthropod vectors and the pathogens they carry are exquisitely sensitive to temperature, humidity and rainfall. Warming can extend the geographic range and lengthen the seasonal activity of mosquitoes and ticks, accelerate pathogen

development within them, and bring vectors into regions and altitudes previously free of them; the resulting shifts threaten to expose new populations to diseases such as dengue, West Nile fever and tick-borne infections (Rocklöv and Dubrow, 2020). Modelling of mammalian range shifts under climate change further predicts thousands of novel encounters between species and new opportunities for spillover in the coming decades, concentrated in the densely populated tropics of Asia and Africa (Carlson et al., 2022). These drivers explain why vector-borne diseases, far from receding, have resurged as a global health problem over recent decades (Gubler, 1998), and why hotspots of emergence cluster in biodiverse, rapidly changing regions that prominently include South and Southeast Asia (Allen et al., 2017).

Surveillance and diagnosis at the interface

Detecting and tracking wildlife and vector-borne diseases requires surveillance that reaches beyond the human clinic into animal populations and the environment. Because many of these diseases are maintained in wildlife, events in animals frequently foreshadow human risk: the die-off of monkeys that precedes human Kyasanur Forest disease, mortality in wild birds that signals circulating West Nile virus, and rodent die-offs that herald plague are all natural sentinels that, if monitored, provide invaluable early warning. Sentinel surveillance in domestic animals—horses for West Nile virus, for example—serves a similar purpose.

Equally important is entomological surveillance: monitoring the abundance, distribution, species composition and infection status of vector populations allows risk to be mapped and interventions to be timed and targeted. Laboratory diagnosis draws on serology, antigen detection and increasingly on molecular methods such as polymerase chain reaction and genomic sequencing, which can identify pathogens in patients, in animal hosts and in pooled vectors alike. The persistent weakness of such integrated, cross-sectoral surveillance in many endemic settings—so that cases and circulating pathogens go undetected—remains one of the principal obstacles to control.

Prevention and control

Control operates simultaneously against the vector, the reservoir and the route of human

exposure. Vector control remains the mainstay for most of these diseases and includes insecticide-treated bed nets and indoor residual spraying against mosquitoes, larval source management to remove breeding sites, the use of acaricides and habitat management against ticks, and, increasingly, integrated vector management that combines methods judiciously to slow the development of insecticide resistance. Personal protection—repellents, protective clothing, prompt tick removal and the avoidance of high-risk habitats during peak transmission—reduces individual exposure, and is the practical advice given, for example, to those entering Kyasanur Forest disease—endemic forests.

Vaccination, where available, complements vector control: a formalin-inactivated vaccine exists for Kyasanur Forest disease, though its effectiveness has been limited, and effective vaccines exist for Japanese encephalitis and yellow fever, while for many other diseases no licensed vaccine is yet available. At the level of the wildlife reservoir, habitat protection and the regulation of activities that increase contact between people, vectors and wild hosts offer a means of reducing risk at its ecological source—an approach that, for sylvatic diseases, is often the only durable one. Underlying all of these measures is the recognition that prevention focused upstream, on the ecological conditions that generate spillover, is generally more effective and more economical than responding to outbreaks once they reach people (Plowright et al., 2017).

One Health and the role of the veterinarian

Diseases that span wildlife, vectors, domestic animals and people cannot be managed from within any single sector, which makes them a paradigm case for the One Health approach. As defined by the international expert panel that advises the global health agencies, One Health is an integrated, unifying approach that seeks to balance and optimise the health of people, animals and ecosystems, recognising their interdependence and the need for collaboration across disciplines (Adisasmito et al., 2022). For wildlife and vector-borne diseases this means linking wildlife biologists, entomologists, veterinarians, physicians, public-health authorities and environmental managers in shared surveillance, joint outbreak investigation and coordinated control.

Veterinarians occupy a uniquely strategic position within this network. They monitor and manage disease in domestic animals that often serve as sentinels or amplifying hosts, they possess expertise in the ecology and control of vectors and of the livestock diseases they cause, they are increasingly engaged in wildlife health and conservation medicine, and they bridge the worlds of farm, forest, laboratory and clinic. Strengthening veterinary capacity in vector surveillance, wildlife health and laboratory diagnosis is therefore not a narrow professional concern but a direct contribution to the early detection and prevention of the next spillover.

Challenges and the way forward

Several obstacles stand in the way of effective control. Surveillance of wildlife and vectors is weak or absent in many high-risk areas, so that circulating pathogens and shifting vector populations go undetected until human cases appear. Diagnostics and vaccines are limited for several important diseases, including Kyasanur Forest disease and Crimean–Congo haemorrhagic fever. Insecticide and acaricide resistance erodes the effectiveness of vector control, and the ecological drivers of emergence—deforestation, land-use change and a warming climate—continue to intensify (Mourya et al., 2014; Rocklöv and Dubrow, 2020). Many of these diseases, moreover, fall disproportionately on poor, rural and forest-dependent communities whose needs struggle to command sustained attention and resources.

The way forward lies in strengthening integrated, cross-sectoral surveillance that couples human, animal, wildlife and entomological monitoring; in investing in diagnostics, vaccines and sustainable vector-control tools; in maintaining

sentinel systems such as monitoring of monkey mortality for Kyasanur Forest disease; and in addressing the upstream drivers of emergence through habitat protection and careful land-use planning. For India in particular, with its rich biodiversity, its extensive forest fringes and agricultural frontiers, and its position within recognised emergence hotspots, building durable One Health capacity at the wildlife–vector–human interface offers protection against both the endemic burden of today and the emerging threats of tomorrow (Allen et al., 2017; Carlson et al., 2022).

Conclusion

Wildlife and arthropod vectors together account for a great share of the world's zoonotic and emerging disease, and they are most dangerous where their cycles intersect with human activity. Wild animals supply the reservoir of pathogens; vectors supply the bridge; and human disturbance of natural habitats repeatedly converts a quiescent sylvatic cycle into a human epidemic. The diseases that result—from the tick-borne haemorrhagic fevers of India's forests to the mosquito-borne arboviruses of its cities and the sandfly-borne kala-azar of its plains—are diverse in their biology but unified in their solution. Vigilant surveillance spanning wildlife, vectors and people; control directed simultaneously at vector, reservoir and exposure; and, above all, the cross-sectoral collaboration embodied in the One Health approach offer the surest path forward. World Zoonoses Day is a fitting moment to recognise that protecting human health is inseparable from understanding the wild animals and the small biting arthropods at the very root of so much disease—and that the veterinary profession stands at the heart of that task.

References

- Adisasmito, W.B., Almuhaire, S., Behraves, C.B., Bilivogui, P., Bukachi, S.A., Casas, N. et al. (2022). One Health: A new definition for a sustainable and healthy future. *PLOS Pathogens*, 18(6), e1010537.
- Allen, T., Murray, K.A., Zambrana-Torrel, C., Morse, S.S., Rondinini, C., Di Marco, M., Breit, N., Olival, K.J. and Daszak, P. (2017). Global hotspots and correlates of emerging zoonotic diseases. *Nature Communications*, 8, 1124.
- Alvar, J., Vélez, I.D., Bern, C., Herrero, M., Desjeux, P., Cano, J., Jannin, J. and den Boer, M. (2012). Leishmaniasis worldwide and global estimates of its incidence. *PLOS ONE*, 7(5), e35671.

- Arunkumar, G., Chandni, R., Mourya, D.T., Singh, S.K., Sadanandan, R., Sudan, P. and Bhargava, B. (2019). Outbreak investigation of Nipah virus disease in Kerala, India, 2018. *The Journal of Infectious Diseases*, 219(12), 1867–1878.
- Bhatt, S., Gething, P.W., Brady, O.J., Messina, J.P., Farlow, A.W., Moyes, C.L. et al. (2013). The global distribution and burden of dengue. *Nature*, 496(7446), 504–507.
- Calisher, C.H., Childs, J.E., Field, H.E., Holmes, K.V. and Schountz, T. (2006). Bats: important reservoir hosts of emerging viruses. *Clinical Microbiology Reviews*, 19(3), 531–545.
- Carlson, C.J., Albery, G.F., Merow, C., Trisos, C.H., Zipfel, C.M., Eskew, E.A., Olival, K.J., Ross, N. and Bansal, S. (2022). Climate change increases cross-species viral transmission risk. *Nature*, 607(7919), 555–562.
- Daszak, P., Cunningham, A.A. and Hyatt, A.D. (2000). Emerging infectious diseases of wildlife – threats to biodiversity and human health. *Science*, 287(5452), 443–449.
- Gubler, D.J. (1998). Resurgent vector-borne diseases as a global health problem. *Emerging Infectious Diseases*, 4(3), 442–450.
- Halpin, K., Young, P.L., Field, H.E. and Mackenzie, J.S. (2000). Isolation of Hendra virus from pteropid bats: a natural reservoir of Hendra virus. *Journal of General Virology*, 81(8), 1927–1932.
- Han, B.A., Schmidt, J.P., Bowden, S.E. and Drake, J.M. (2015). Rodent reservoirs of future zoonotic diseases. *Proceedings of the National Academy of Sciences USA*, 112(22), 7039–7044.
- Jones, K.E., Patel, N.G., Levy, M.A., Storeygard, A., Balk, D., Gittleman, J.L. and Daszak, P. (2008). Global trends in emerging infectious diseases. *Nature*, 451(7181), 990–993.
- Karesh, W.B., Dobson, A., Lloyd-Smith, J.O., Lubroth, J., Dixon, M.A., Bennett, M. et al. (2012). Ecology of zoonoses: natural and unnatural histories. *The Lancet*, 380(9857), 1936–1945.
- Kramer, L.D., Styer, L.M. and Ebel, G.D. (2008). A global perspective on the epidemiology of West Nile virus. *Annual Review of Entomology*, 53, 61–81.
- Leroy, E.M., Kumulungui, B., Pourrut, X., Rouquet, P., Hassanin, A., Yaba, P., Délicat, A., Paweska, J.T., Gonzalez, J.-P. and Swanepoel, R. (2005). Fruit bats as reservoirs of Ebola virus. *Nature*, 438(7068), 575–576.
- Mourya, D.T., Yadav, P.D. and Patil, D.Y. (2014). Highly infectious tick-borne viral diseases: Kyasanur forest disease and Crimean–Congo haemorrhagic fever in India. *WHO South-East Asia Journal of Public Health*, 3(1), 8–21.
- Plowright, R.K., Parrish, C.R., McCallum, H., Hudson, P.J., Ko, A.I., Graham, A.L. and Lloyd-Smith, J.O. (2017). Pathways to zoonotic spillover. *Nature Reviews Microbiology*, 15(8), 502–510.
- Rocklöv, J. and Dubrow, R. (2020). Climate change: an enduring challenge for vector-borne disease prevention and control. *Nature Immunology*, 21(5), 479–483.
- Taylor, L.H., Latham, S.M. and Woolhouse, M.E.J. (2001). Risk factors for human disease emergence. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 356(1411), 983–989.
- Walsh, M.G., Mor, S.M., Maity, H. and Hossain, S. (2019). Forest loss shapes the landscape suitability of Kyasanur Forest disease in the biodiversity hotspots of the Western Ghats, India. *International Journal of Epidemiology*, 48(6), 1804–1814.
- World Health Organization. (2023). *World Malaria Report 2023*. Geneva: World Health Organization.
- World Health Organization. (2024). *Vector-borne diseases: Fact sheet*. Geneva: World Health Organization.

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