

ZOONOTIC CROSSROADS: THE INTERSECTION OF WILDLIFE ECOLOGY AND VECTOR-BORNE PATHOGENS

Madhvee Dhairykar¹, Shobha Jawre², Nengneikim Baite³, and Alok Manna⁴

^{1,2}Nanaji Deshmukh Veterinary Science University, Jabalpur (M.P.), ³College of Veterinary Science and Animal Husbandry, CAU, Selesih, ⁴Wildlife Institute of India, Chandrabani, Dehradun

*Corresponding author email: madhvidhairykar@gmail.com

DOI: <https://doi.org/10.5281/zenodo.21717363>

Abstract

Vector-borne zoonotic diseases represent one of the most significant threats to global public health, accounting for a substantial proportion of emerging infectious diseases worldwide. Wildlife hosts play a pivotal role in maintaining and disseminating pathogens through complex ecological interactions involving arthropod vectors, environmental conditions, and anthropogenic activities. The increasing frequency of zoonotic disease emergence is driven by habitat alteration, climate change, biodiversity loss, globalization, and expanding human–wildlife interfaces. Understanding the ecological mechanisms governing pathogen persistence and transmission is essential for predicting disease outbreaks and developing effective control strategies. This review examines the relationship between wildlife ecology and vector-borne pathogens, highlighting the roles of reservoir hosts, vector dynamics, environmental drivers, and One Health approaches in disease emergence and management. The synthesis of ecological and epidemiological perspectives provides critical insights into the prevention of future zoonotic threats.

Keywords: zoonosis, wildlife ecology, vector-borne diseases, pathogen spillover, One Health, climate change, reservoirs, vectors

Introduction

Zoonotic diseases, which are naturally transmitted between animals and humans, constitute a major global public health challenge. More than 60% of known human infectious diseases and approximately 75% of emerging infectious diseases originate from animal reservoirs, particularly wildlife (Taylor et al., 2001; Jones et al., 2008). Among these, vector-borne pathogens transmitted by hematophagous arthropods such as mosquitoes, ticks, sand flies, fleas, and biting midges represent a significant proportion of emerging zoonoses. Wildlife species serve as important reservoir hosts, maintaining pathogens in natural ecosystems and facilitating their persistence and transmission through vector populations (Gortázar et al., 2014). Disease emergence is governed by complex interactions among wildlife hosts, vectors, pathogens, and environmental conditions. Anthropogenic factors including deforestation, urbanization, agricultural expansion, habitat fragmentation, biodiversity loss, and climate change have altered these interactions, increasing opportunities for pathogen spillover into domestic animals and human populations (Patz et al., 2004; Keesing et al., 2010; Hassell et al., 2017; Rocklöv & Dubrow, 2020). In particular, climate-driven changes in vector distribution and seasonal activity have expanded the geographic range of several vector-borne diseases, posing new challenges for global disease surveillance and control (Ryan et al.,

2019). Understanding wildlife ecology—including host population dynamics, movement patterns, species interactions, and habitat use—is fundamental to predicting pathogen maintenance and spillover risk (Tompkins et al., 2015; Plowright et al., 2017).

This review examines the intersection of wildlife ecology and vector-borne pathogens, highlighting the ecological processes that drive pathogen persistence, transmission, and spillover. It further discusses the influence of environmental change, the role of wildlife reservoirs and vectors, and the importance of One Health-based surveillance and management strategies for reducing the burden of emerging vector-borne zoonoses.

Mechanisms of Host Competency

A competent reservoir host is a wild animal that can carry and transmit pathogens for long periods without developing severe disease. This ability depends on three main factors: life-history traits, population density, and immune tolerance (Figure 1). Long lifespan, high survival, continued reproduction while infected, and wide movement increase opportunities for pathogen maintenance and spread (Plowright et al., 2016; Luis et al., 2013). Dense, social, and stable populations promote continuous transmission among individuals and facilitate long-term pathogen persistence (Haydon et al., 2002; Keesing et al., 2010). In addition, reservoir hosts possess immune tolerance, which controls pathogen growth while preventing excessive inflammation, allowing chronic infection with little or no clinical illness (Schneider & Ayres, 2008; Mandl et al., 2015) (Figure 2).

Ecological Drivers of Transmission

The relationship between biodiversity and infectious disease transmission remains a subject of considerable debate. The Dilution Effect hypothesis proposes that high biodiversity reduces disease risk by increasing

the proportion of less competent hosts, thereby diluting pathogen transmission and reducing encounters between vectors and highly competent reservoir hosts (Keesing et al., 2006; Ostfeld & Keesing, 2012). In contrast, the Amplification Effect suggests that greater biodiversity can increase disease risk by providing additional hosts and food resources for vectors, enhancing vector survival, abundance, and pathogen transmission, particularly when multiple host species are competent reservoirs (Randolph & Dobson, 2012; Roche et al., 2012). The relative importance of these mechanisms depends on ecosystem characteristics, host competence, vector ecology, and pathogen-specific interactions, indicating that biodiversity can either suppress or enhance disease transmission under different ecological conditions (Salkeld et al., 2013; Halliday & Rohr, 2019).

Environmental Change and Range Expansions

Climate change and habitat fragmentation are altering the geographic distribution of wildlife hosts and disease vectors, enabling them to expand into previously unsuitable areas (Figure 1). Rising temperatures, changing precipitation patterns, and land-use change facilitate shifts in species ranges and modify vector survival, abundance, and seasonal activity (Altizer et al., 2013). As wildlife species, vectors, livestock, and humans increasingly overlap in newly colonized regions, opportunities for pathogen transmission and cross-species spillover increase, leading to the emergence of novel disease hotspots (Jones et al., 2008; Carlson et al., 2022). These environmental changes are expected to accelerate the spread of infectious diseases and complicate disease surveillance and control in both wildlife and human populations (IPCC, 2022; Carlson et al., 2022).

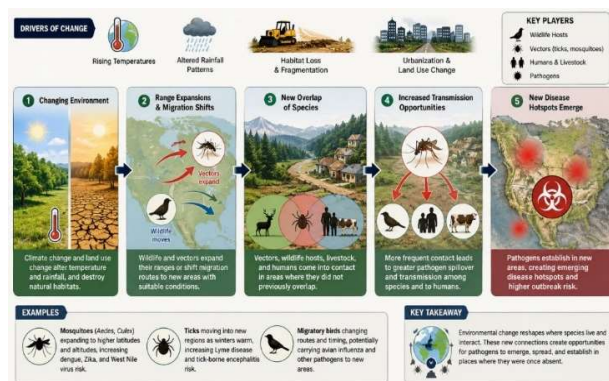


Fig. 1: Environmental change and range expansions (How shifting climates and habitat fragmentation create new disease hotspots)

Vector Ecology and Transmission Dynamics

Arthropod vectors represent the critical link connecting pathogens with susceptible hosts. Vector competence, abundance, feeding behavior, and distribution determine the efficiency of disease transmission. Mosquitoes of the genera *Aedes*, *Anopheles*, and *Culex* transmit numerous pathogens, including dengue virus, malaria parasites, West Nile virus, and Japanese encephalitis virus. Tick species such as *Ixodes*, *Rhipicephalus*, and *Amblyomma* are responsible for transmitting bacterial, viral, and protozoan pathogens affecting both humans and animals. Vector-host interactions are influenced by ecological conditions including temperature, humidity, vegetation structure, and host availability (Plowright et al., 2017). Seasonal fluctuations often regulate vector abundance and pathogen prevalence. Increased vector density can enhance transmission efficiency by increasing contact rates between infected and susceptible hosts. The concept of vector competence encompasses the ability of vectors to acquire, maintain, and transmit pathogens. Genetic variation within vector populations may significantly affect disease dynamics and influence regional differences in transmission risk.

One Health Approaches to Vector-Borne Zoonoses

The 'One Health' framework recognizes the intrinsic interconnectedness of human, animal, and environmental health and emphasizes that the health of each domain is dependent upon the others (Destoumieux-Garzón et al., 2018; World Health Organization [WHO], 2022). Because vector-borne zoonotic diseases emerge through complex interactions among wildlife reservoirs, domestic

animals, arthropod vectors, environmental conditions, and human populations, interdisciplinary collaboration is essential for effective disease prevention, surveillance, and control (Zinsstag et al., 2011; Mackenzie & Jeggo, 2019). One Health strategies integrate wildlife disease surveillance, vector monitoring, environmental assessment, veterinary medicine, public health programs, and ecological research to better understand pathogen transmission dynamics and mitigate disease emergence (Destoumieux-Garzón et al., 2018). Technological advances in molecular diagnostics, remote sensing, geographic information systems (GIS), genomic surveillance, and predictive epidemiological modeling have substantially improved the early detection of emerging pathogens, identification of transmission hotspots, and forecasting of disease outbreaks (Allen et al., 2017; Carlson et al., 2022). Furthermore, coordinated surveillance systems combining ecological, veterinary, and public health data enhance the capacity to detect spillover events and implement timely interventions (Mackenzie & Jeggo, 2019). Successful implementation of the One Health approach requires international collaboration, cross-sectoral data sharing, integrated surveillance systems, and coordinated policies that simultaneously promote biodiversity conservation, sustainable land management, climate resilience, and infectious disease control (WHO, 2022; FAO, UNEP, WHO & WOA, 2022).

Conclusion

The growing emergence and re-emergence of vector-borne zoonotic diseases underscore the critical role of wildlife ecology in understanding pathogen transmission and spillover. Complex interactions among wildlife reservoirs, arthropod vectors, pathogens, and environmental change drive disease emergence, while anthropogenic factors such as climate change, habitat fragmentation, biodiversity loss, and expanding human-wildlife interfaces continue to increase transmission risks. Despite advances in molecular diagnostics, genomic surveillance, and ecological modelling, significant knowledge gaps remain regarding reservoir competence, vector ecology, and the mechanisms underlying cross-species transmission. Addressing these challenges requires long-term ecological surveillance, standardized wildlife health

monitoring, and multidisciplinary research integrating ecology, veterinary science, entomology, epidemiology, and public health. The One Health framework provides a comprehensive approach for managing vector-borne zoonoses by linking human, animal, and environmental health. Strengthening integrated surveillance, predictive risk assessment, and collaborative conservation and public health initiatives will improve early detection, reduce spillover risk, and enhance preparedness for emerging infectious diseases.

References

- Altizer, S., Ostfeld, R. S., Johnson, P. T. J., Kutz, S., & Harvell, C. D. (2013). Climate change and infectious diseases: From evidence to a predictive framework. *Science*, 341(6145), 514–519.
- Carlson, C. J., Albery, G. F., Merow, C., et al. (2022). Climate change increases cross-species viral transmission risk. *Nature*, 607(7919), 555–562.
- Destoumieux-Garzón, D., Mavingui, P., Boetsch, G., et al. (2018). The One Health concept: 10 years old and a long road ahead. *Frontiers in Veterinary Science*, 5, 14.
- One Health Joint Plan of Action (2022–2026): Working together for the health of humans, animals, plants and the environment.
- Gortázar, C., Reperant, L. A., Kuiken, T., et al. (2014). Crossing the interspecies barrier: Opening the door to zoonotic pathogens. *PLoS Pathogens*, 10(6), e1004129.
- Hassell, J. M., Begon, M., Ward, M. J., & Fèvre, E. M. (2017). Urbanization and disease emergence: Dynamics at the wildlife–livestock–human interface. *Trends in Ecology & Evolution*, 32(1), 55–67.
- Haydon, D. T., Cleaveland, S., Taylor, L. H., & Laurenson, M. K. (2002). Identifying reservoirs of infection: A conceptual and practical challenge. *Emerging Infectious Diseases*, 8(12), 1468–1473.
- Jones, K. E., Patel, N. G., Levy, M. A., et al. (2008). Global trends in emerging infectious diseases. *Nature*, 451(7181), 990–993.
- Keesing, F., Belden, L. K., Daszak, P., et al. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. *Nature*, 468(7324), 647–652.
- Keesing, F., Holt, R. D., & Ostfeld, R. S. (2006). Effects of species diversity on disease risk. *Ecology Letters*, 9(4), 485–498.
- 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? *Proceedings of the Royal Society B*, 280(1756), 20122753.
- Mackenzie, J. S., & Jeggo, M. (2019). The One Health approach—Why is it so important? *Tropical Medicine and Infectious Disease*, 4(2), 88.
- Mandl, J. N., Schneider, C., Schneider, D. S., & Baker, M. L. (2015). Going to bat(s) for studies of disease tolerance. *Frontiers in Immunology*, 6, 4.
- Ostfeld, R. S., & Keesing, F. (2012). Effects of host diversity on infectious disease. *Annual Review of Ecology, Evolution, and Systematics*, 43, 157–182.
- Patz, J. A., Daszak, P., Tabor, G. M., et al. (2004). Unhealthy landscapes: Policy recommendations on land use change and infectious disease emergence. *Environmental Health Perspectives*, 112(10), 1092–1098.
- Plowright, R. K., Foley, P., Field, H. E., et al. (2016). Transmission or within-host dynamics driving pulses of zoonotic viruses in reservoir–host populations. *Proceedings of the Royal Society B* (2016).

- Plowright, R. K., Parrish, C. R., McCallum, H., et al. (2017). Pathways to zoonotic spillover. *Nature Reviews Microbiology*, 15(8), 502–510.
- Randolph, S. E., & Dobson, A. D. M. (2012). Pangloss revisited: A critique of the dilution effect and the biodiversity–buffers–disease paradigm. *Parasitology*, 139(7), 847–863.
- Roche, B., Guégan, J. F., Bousquet, F., & Dobson, A. P. (2012). The impact of community organization on vector-borne pathogens. *The American Naturalist*, 181(1), 1–11.
- Rocklöv, J., & Dubrow, R. (2020). Climate change: An enduring challenge for vector-borne disease prevention and control. *Nature Immunology*, 21(5), 479–483.
- Ryan, S. J., Carlson, C. J., Mordecai, E. A., & Johnson, L. R. (2019). Global expansion and redistribution of Aedes-borne virus transmission risk with climate change. *PLoS Neglected Tropical Diseases*, 13(3), e0007213.
- Salkeld, D. J., Padgett, K. A., & Jones, J. H. (2013). A meta-analysis suggesting that the relationship between biodiversity and risk of zoonotic pathogen transmission is idiosyncratic. *Ecology Letters*, 16(5), 679–686.
- Schneider, D. S., & Ayres, J. S. (2008). Two ways to survive infection: What resistance and tolerance can teach us about treating infectious diseases. *Nature Reviews Immunology*, 8(11), 889–895.
- Taylor, L. H., Latham, S. M., & Woolhouse, M. E. J. (2001). Risk factors for human disease emergence. *Philosophical Transactions of the Royal Society B*, 356, 983–989.
- Tompkins, D. M., Carver, S., Jones, M. E., Krkošek, M., & Skerratt, L. F. (2015). Emerging infectious diseases of wildlife: A critical perspective. *Trends in Parasitology*, 31(4), 149–159.
- World Health Organization (WHO). (2022). One Health Joint Plan of Action (2022–2026): Working together for the health of humans, animals, plants and the environment.
- Zinsstag, J., Schelling, E., Waltner-Toews, D., & Tanner, M. (2011). From "One Medicine" to "One Health" and systemic approaches to health and well-being. *Preventive Veterinary Medicine*, 101(3–4), 148–156.

Cite this article:

Madhvee Dhairykar, Shobha Jawre, Nengneikim Baite, and Alok Manna. (2026). Zoonotic crossroads: the intersection of wildlife ecology and vector-borne pathogens. *Vet Farm Frontier*, 03(07), 84–88. <https://doi.org/10.5281/zenodo.21717363>