

Understanding how social, environmental, and etiological factors shape (re)emerging infectious
disease outbreaks

A Dissertation Presented for the
Doctor of Philosophy
Degree
The University of Tennessee, Knoxville

Muhammad Belal Hossain

August 2025

DEDICATION

To my father, Yousuf, who dreamed of my higher education, was always strict about my schooling and whose unwavering support continues to guide my path. Even in your absence, your memory is a light I carry forward.

and

to my daughter Susana, whose bright eyes, boundless curiosity, and wonderfully funny spirit fill my life with laughter and love. Your tiny thoughts about every aspect of our lives are a joy to watch and remind me daily of the wonder of learning and the beauty in small moments. I love your drawings.

With deepest love and gratitude.

ACKNOWLEDGEMENTS

I would like to begin by expressing my sincere gratitude to the Department of Ecology and Evolutionary Biology (EEB) at the University of Tennessee Knoxville. The faculty, staff, undergraduate and graduate students have provided incredible support throughout my time in the program. I am especially thankful for the collaborative spirit, stimulating academic environment, and the many opportunities to grow as a researcher and educator. Being part of the EEB community has been one of the most enriching aspects of my graduate school journey.

I am deeply grateful to my advisor, Dr. Nina Fefferman, who was the greatest inspiration throughout my Ph.D. Her steady guidance, thoughtful mentorship, and unwavering belief in my potential shaped both my academic direction and personal development. I will carry forward the lessons I learned under her mentorship with great pride. I also extend heartfelt thanks to my committee members, Dr. Mona Papes, Dr. Mark Wilber, Dr. Sebastian Stockmaier, and Dr. Phoebe Tran. Their academic guidance, thoughtful feedback, and continuous support were instrumental to the success of this dissertation. I am also thankful to all my past and current lab mates in the Fefferman Lab for their collaboration, intellectual engagement, and friendship throughout the years. A special thank you goes to John and Courtney for being such wonderful friends. Your kindness, humor, and consistent support helped me navigate the most difficult moments of graduate school with a lighter heart.

To my wife, Sharmina, thank you for your love, patience, and unwavering support. I am also forever grateful to my family. To my mother, Sakia, for her unconditional love and endless prayers. To my sister, Marzina, who has always been my greatest cheerleader. To my brothers, Shahadat and Iqbal, thank you for your steady encouragement. To my nephews and niece, Juhayer, Jarif, and Shana, your humor and energy from New Jersey and Dhaka always brought me joy and relief. I deeply appreciate my extended family for believing in me and supporting me over the years.

To my graduate school friends, EEB peers, research collaborators, the broader UTK community, and all my Knoxville friends, thank you for the fellowship, shared experiences, and conversations that made this journey more fulfilling. Your presence gave me strength and belonging. I also thank my many table tennis partners for moments of joy, focus, and mental

clarity. And to my undergraduate students, thank you for inspiring me with your energy and curiosity. Teaching you was a highlight of my graduate career.

To everyone who supported me in this journey—through your time, care, words, or presence—thank you. This accomplishment is shared with all of you.

ABSTRACT

Emerging infectious diseases (EIDs), over 60% of which are zoonotic, represent a growing threat to human health, development, and ecological stability. Their emergence is shaped by complex interactions among environmental change, human activity, and social vulnerability, particularly in low-resource settings. This dissertation investigates the ecological, social, and environmental determinants of EID risk through three integrated studies.

The first chapter examines public health communication in two geographically and socially vulnerable island communities: Shahpori Island, Bangladesh, and Gaya Island, Malaysia. Both face high burdens of vector-borne diseases yet have limited access to healthcare and surveillance systems. While awareness was generally low, residents of Gaya Island demonstrated significantly greater knowledge and preventive behaviors. Factors such as education, age, and marital status emerged as significant predictors of disease knowledge. Inadequate understanding on mosquito ecology highlights the urgent need for culturally tailored, community-based interventions.

The second chapter presents a systematic meta-analysis of global risk factors for human anthrax. The analysis reveals that occupational exposures such as handling infected carcasses, butchering moribund animals, and consuming contaminated meat greatly increase infection risk. These behaviors are often rooted in poverty, limited veterinary infrastructure, traditional practices, and inadequate public health outreach. Addressing these structural drivers is essential for effective anthrax prevention and control, especially in endemic rural settings.

The third chapter uses ecological niche modeling to project current and future climatic suitability for 14 bat species identified as putative reservoir hosts of Nipah virus. Based on WorldClim climate data and Maxent modeling under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060, the models predict substantial shifts and expansions in climatically suitable habitats. These changes signal increasing risk of zoonotic spillover in new areas, reinforcing the importance of climate-sensitive surveillance and early warning systems.

Together, these studies integrate communication research, epidemiological synthesis, and spatial modeling to inform a One Health approach to EID prevention. The findings emphasize the urgency of climate-informed surveillance, risk communication, and cross-sectoral preparedness strategies for vulnerable populations.

Table of Contents

INTRODUCTION	1
CHAPTER I: Public health communication on emerging vector-borne disease risk in remote regions of South and Southeast Asia	11
Abstract	12
Introduction.....	13
Methods.....	14
Results.....	16
Discussion	18
References.....	21
Appendix I	25
CHAPTER II: Risk factors for human anthrax infection on a global scale: Understanding how outbreaks converge from animal husbandry, socioeconomic conditions, and cultural practices .	33
Abstract	34
Introduction.....	35
Methods.....	37
Results.....	38
Discussion	42
References.....	46
Appendix II	50
CHAPTER III: Ecological niche models of Nipah virus-associated bats: Predicting current and future climatic suitability in endemic and emerging risk zones	66
Abstract	67
Introduction.....	68
Methods.....	70
Results.....	73

Discussion	76
References.....	81
Appendix III.....	89
Appendix IIIA.....	107
CONCLUSION	121
VITA	123

LIST OF TABLES

Table 1.1 Comparative sociodemographic characteristics between Shahpori and Gaya islands...	25
Table 1.2 Population knowledge concerning vector-borne disease transmission, symptoms, and other factors among the respondents between two islands	26
Table 1.3 Population attitude and prevention practices of vector-borne disease between two islands	27
Table 1.4 Predictors of vector-borne disease knowledge, attitude and practices among residents of both islands in Bangladesh and Malaysia.....	29
Table 1.5 Comparative model fit statistics.....	30
Table 2.1 Characteristics of included studies on risk factors associated with human anthrax infection	50
Table 2.2 Newcastle-Ottawa Quality Assessment table for included studies	57
Table 3.1 WorldClim variables list used in the ecological niche	89

LIST OF FIGURES

Figure 1.1 Map of the study area in Gaya Island, Sabah, Malaysia	31
Figure 1.2 Map of the study area in Shahpori Island, Cox's Bazar, Bangladesh.....	32
Figure 2.1 PRISMA diagram showing selection of articles for the meta-analysis	58
Figure 2.2 Forest plot showing associations between exposure to raw meat and anthrax infection in humans.....	59
Figure 2.3 Forest plot showing associations between skinning sick or moribund animals and anthrax infection in humans.....	60
Figure 2.4 Forest plot showing associations between butchering sick or moribund animals and anthrax infection in humans.....	61
Figure 2.5 Forest plot showing association between slaughtering or presence at slaughtering time of sick or moribund animals and anthrax infection in humans.....	62
Figure 2.6 Forest plot showing associations between handling carcass or animal by-products of sick or moribund animals and anthrax infection in humans	63
Figure 2.7 Funnel plot assessing publication bias for studies evaluating raw meat exposure or consumption as a risk factor for anthrax infection.....	64
Figure 2.8 Funnel plot assessing publication bias in studies evaluating handling of carcasses and exposure to animal by-products as a risk factor for anthrax infection.....	65
Figure 3.1 Pixel-wise changes in climatic suitability for <i>Pteropus medius</i>	90
Figure 3.2 Pixel-wise changes in climatic suitability for <i>Pteropus vampyrus</i>	91
Figure 3.3 Projected gain and loss of climatic suitability for <i>Pteropus medius</i> based on binary threshold maps across future climate scenarios.....	92
Figure 3.4. Projected gain and loss of climatic suitability for <i>Pteropus vampyrus</i> based on binary threshold maps across future climate scenarios.....	93
Figure 3.5. Pixel-wise changes in climatic suitability for <i>Pteropus neohibernicus</i>	94

Figure 3.6. Pixel-wise changes in climatic suitability for <i>Pteropus alecto</i>	95
Figure 3.7. Pixel-wise changes in climatic suitability for <i>Pteropus scapulatus</i>	96
Figure 3.8. Pixel-wise changes in climatic suitability for <i>Pteropus poliocephalus</i>	97
Figure 3.9. Pixel-wise changes in climatic suitability for <i>Pteropus conspicillatus</i>	98
Figure 3.10. Pixel-wise changes in climatic suitability for <i>Pteropus hypomelanus</i>	99
Figure 3.11. Pixel-wise changes in climatic suitability for <i>Rousettus amplexicaudatus</i>	100
Figure 3.12. Pixel-wise changes in climatic suitability for <i>Rousettus leschenaultii</i>	101
Figure 3.13. Pixel-wise changes in climatic suitability for <i>Cynopterus sphinx</i>	102
Figure 3.14. Pixel-wise changes in climatic suitability for <i>Hipposideros larvatus</i>	103
Figure 3.15. Pixel-wise changes in climatic suitability for <i>Dobsonia magna</i>	104
Figure 3.16. Pixel-wise changes in climatic suitability for <i>Eidolon helvum</i>	105
Figure 3.17. Project species richness of NiV-associated bats under baseline and future climate scenarios.....	106
Figure S1. Projected climatic suitability for <i>Pteropus medius</i> under baseline and future climate scenarios.....	107
Figure S2. Projected climatic suitability for <i>Pteropus vampyrus</i> under different climate and emission scenarios	108
Figure S3. Projected climatic suitability for <i>Pteropus alecto</i> under different climate and emission scenarios.	109
Figure S4. Projected climatic suitability for <i>Pteropus scapulatus</i> under different climate and emission scenarios	110
Figure S5. Projected climatic suitability for <i>Pteropus poliocephalus</i> under different climate and emission scenarios.....	111
Figure S6. Projected climatic suitability for <i>Pteropus neohibernicus</i> under different climate and emission scenarios	112

Figure S7. Projected climatic suitability for <i>Pteropus conspicillatus</i> under different climate and emission scenarios	113
Figure S8. Projected climatic suitability for <i>Pteropus hypomelanus</i> under different climate and emission scenarios	114
Figure S9. Projected climatic suitability for <i>Rousettus amplexicaudatus</i> under different climate and emission scenarios.....	115
Figure S10. Projected climatic suitability for <i>Rousettus leschenaultii</i> under different climate and emission scenarios.....	116
Figure S11. Projected climatic suitability for <i>Cynopterus Sphinx</i> under different climate and emission scenarios	117
Figure S12. Projected climatic suitability for <i>Hipposideros larvatus</i> under different climate and emission scenarios.....	118
Figure S13. Projected climatic suitability for <i>Eidolon helvum</i> under different climate and emission scenarios.....	119
Figure S14. Projected climatic suitability for <i>Dobsonia magna</i> under different climate and emission scenarios.....	120

INTRODUCTION

The world is passing through a crucial time in the context of emerging infectious diseases (EID), especially zoonotic infections. EIDs pose a substantial burden on global economies, animals, and public health, particularly where disease surveillance is inadequate, human density is high, and resources are constrained (Jones et al., 2008). Various factors have been identified as drivers of EID events over time such as altered ecosystems, agricultural intensification, wildlife trade, and rapid urbanization which constantly poses risk to multiple mammalian hosts including human populations (Bradley et al., 2007; Horby et al., 2014). In the past century, EID events were dominated by zoonoses with over 71% originated from wildlife and or animal populations such as HIV, severe acute respiratory syndrome (SARS), Ebola, anthrax, and Nipah virus. The likelihood of the origin of EID events is significantly increasing over time (Jones et al., 2008).

Social determinants play a pivotal role in the transmission, prevention, and control of infectious diseases. Factors such as socioeconomic status, education, and access to healthcare impact both individual susceptibility to infections and the capacity for effective management. Marginalized communities have limited healthcare access and lower health literacy, and often face disproportionate burdens of disease (Marmot et al., 1991). Social behaviors such as travel patterns, urbanization, and population density, also influence the spread of infections.

Urbanization, for instance, often creates densely populated environments which are conducive to rapid pathogen transmission (McMichael et al., 2000). Moreover, cultural practices and public health strategies such as vaccination and disease surveillance are crucial in shaping disease dynamics. Environmental factors further influence infectious disease patterns. Climate change, alterations in land use, and environmental degradation can modify the habitats of vectors and pathogens, leading to the emergence of infectious disease in previously unaffected regions. For example, rising temperatures and shifting precipitation patterns can extend the geographical range of mosquitoes, thereby increasing the incidence of malaria and dengue fever (Gething et al., 2010). Additionally, deforestation and urban sprawl can disrupt ecosystems which increase human exposure to zoonotic diseases (Faust et al., 2018).

The intersection of social, environmental, and etiological factors creates a complex landscape for infectious disease dynamics. For instance, the spread of vector-borne diseases is influenced by both environmental conditions and social behaviors, as well as public health infrastructure (Ma et

al., 2022). The rise of emerging infectious diseases, such as COVID-19, underscores the necessity of a comprehensive understanding of these interconnected factors. A holistic approach that integrates social, environmental, and etiological perspectives is essential for effective disease surveillance, prevention, and response strategies.

This dissertation investigates how social, environmental, and etiological elements converge to shape the emergence and re-emergence of infectious diseases, focusing on three distinct, however interconnected areas: public health communication on vector-borne diseases in remote regions of Southeast Asia, the determination of risk factors for anthrax infections in humans, and the prediction of future climatic suitability of Nipah virus animal reservoir hosts. Each chapter is analyzed through the lens of these key factors, aiming to shed light on how diseases emerge and persist in different settings. Vector-borne diseases (VBDs) are one of the major public and animal health challenges of the twenty-first century. Pathogens resulting in VBDs are transmitted by the bite of infected arthropods, such as mosquitoes, fleas, sandflies, black flies, ticks, and bugs (Hill et al., 2005).

VBDs account for more than 17% of all cases of infectious diseases resulting in more than 700,000 deaths per year worldwide (Rocklöv et al., 2020). A significant number of VBDs are prevalent in Asia such as dengue, malaria, chikungunya, leishmaniasis, yellow fever, lymphatic filariasis, Japanese encephalitis, Zika fever, and schistosomiasis (Chala et al., 2021; Servadio et al., 2018). In recent years, highly infectious fatal tick-borne diseases such as Crimean-Congo hemorrhagic fever, Kyasanur forest disease, and tick-borne encephalitis have also emerged in South and Southeast Asia (Devendra et al., 2014; Subramaniam et al., 2021).

VBDs pose substantial threat to all nations, irrespective of their socio-economic status, disease surveillance programs, and prevention policies, and risk tends to be high where surveillance effort is low especially in low-income and middle-income countries. Bangladesh and Malaysia are two nations with high population density and rapid urbanization that have been experiencing outbreaks of VBDs, with the most alarming outbreaks including dengue, Zika virus infection, and chikungunya viral fever. Dengue remains a significant mosquito-borne disease in both countries, with numerous outbreaks between 2010 and 2023 resulting in thousands of cases and several hundred deaths annually (AbuBakar et al., 2022; Hossain et al., 2023; Hsan et al., 2019; Teng et al., 2001). Furthermore, the geographic range of emerging VBDs, such as Zika virus

fever, Japanese encephalitis, and yellow fever have expanded their territories in South and Southeast Asia with routine detection in both countries (Khoo et al., 2022; Maluda et al., 2020; Paul et al., 2020; Rahman et al., 2019). Although recent progress has made in malaria prevention in both Bangladesh and Malaysia, substantial challenges persist due to rise of anti-malarial drug resistance. Emerging strains of *Plasmodium falciparum* resistant to artemisinin-based combination therapies continue to complicate treatment efforts and threaten malaria control in these regions (Chin et al., 2020; Johora et al., 2021; Subramaniam et al., 2021). Moreover, the region faces challenges in obtaining comprehensive data due to inadequate disease surveillance, diagnostics, low/middle economic resources, and limited public health awareness.

The first chapter focuses on public health communication strategies addressing emerging VBDs in two distinct yet similarly challenging settings: Shahpori Island in Bangladesh and Gaya Island in Malaysia.

Anthrax, caused by *Bacillus anthracis* bacterium, is a globally distributed, underreported, soil-borne zoonotic disease. It is estimated that between 20,000 to 100,000 cases of anthrax occur every year predominantly in impoverished and rural parts of the world, resulting in severe economic losses (Swartz et al., 2001). The spores of *B. anthracis* remain viable in the environment for decades, facilitating the persistence of natural infection cycle from animal to human populations (Hugh-Jones et al., 2009). Although there are four types of anthrax infection that can occur, cutaneous and gastrointestinal types of anthrax cases are most common, typically caused by handling and slaughtering of infected livestock or butchering and eating of contaminated meat (Carlson et al., 2018).

Outbreaks of *B. anthracis* occurs worldwide and are of concern for animal conservation, wildlife management, livestock production, and public health (Turner et al., 2013). These outbreaks are influenced by various factors such as animal husbandry practices, anthropogenic activities, soil and climate characteristics, and inadequate carcass disposal methods. Mechanical vectors such as blood-feeding flies (tabanids), may also play a role in the transmission cycle of the disease (Hugh-Jones et al., 2009).

In the past, anthrax outbreaks are consistently linked with poor animal husbandry practices and consumption of contaminated meat butchered from a moribund livestock (Hugh-Jones et al., 2009). Human activities such as butchering moribund livestock, selling/marketing infected meat

and animal by-products, and cultural activities also drive anthrax outbreaks. Because anthrax spores can remain viable in the soil for decades, animal husbandry practices such as feeding unwashed grass and grazing on the land for extended periods especially in the dry season are presumed to be key risk factors for anthrax outbreaks in animals (Munang'andu et al., 2012). There is scientific evidence demonstrating that animal slaughtering during the festivals can increase the likelihood of the occurrence of outbreaks where resources are constrained, and disease awareness is low. It is quite evident from the historical data that social and cultural factors were implicated in anthrax outbreaks such as in Georgia and Bangladesh (Chakraborty et al., 2012; Kracalik et al., 2013). Socio- economic drivers such as education, healthcare access, and income levels significantly impact the ability of affected communities to respond to anthrax outbreaks. In low-income settings, poor access to vaccines for livestock or delays in seeking medical treatment for infected individuals exacerbate the outbreak conditions. Anthrax poses serious risks in agricultural communities where contact with infected animals is frequent (Islam et al., 2013).

The second chapter aims to conduct a meta-analysis of risk factors for anthrax infection in humans integrating data from different regions and socio-economic contexts. The analysis will identify common patterns of risk and vulnerability with a focus on occupational exposure, environmental conditions, and socio-economic factors. Occupational exposure, particularly among farmers and veterinarians, is a well- established risk factor for anthrax infection (Rao et al., 2019). This chapter will explore how different practices in livestock handling, slaughtering, meat consumption, and processing animal by-products affect transmission risks. By synthesizing data across multiple studies, this chapter aims to provide a comprehensive understanding of anthrax outbreak dynamics and offer insights into effective interventions.

Nipah virus (NiV) is an emerging zoonotic virus that poses a significant threat to public health due to its high mortality rate among infected individuals and its potential for widespread outbreaks. First identified during an outbreak in Malaysia in 1998, NiV has since caused outbreaks in Bangladesh, India, the Philippines, and Singapore. The range of henipaviruses including Hendra and Cedar viruses extend throughout the geographic range of Pteropodid bats to Australia, Indian Ocean islands, and sub-Saharan Africa (Kessler et al., 2018; Olival et al., 2020). NiV is primarily transmitted to humans through close contact with infected animals,

particularly fruit bats (*Pteropus* species), which serve as natural reservoirs of the viruses. Human-to-human transmission has also been documented, raising concerns about the potential of NiV to cause sustained outbreaks in densely populated regions (Gurley et al., 2007). Since the emergence of NiV, recurrent outbreaks of NiV have been reported in several South and Southeast Asian countries including Bangladesh and India, with fatality rates ranging from 40% to 75% (Arunkumar et al., 2019; Nikolay et al., 2019). The unpredictable nature of these outbreaks, coupled with the absence of a specific treatment or vaccine, underscores the urgent need to understand the environmental and ecological drivers that influence the distribution and transmission of the viruses.

It is recognized that NiV is hosted by various *Pteropus* fruit bats species with partially overlapping ranges across countries of South and Southeast Asia (Breed et al., 2013). There are many bat species implicated with NiV virus transmission and outbreaks. In Bangladesh, *Pteropus medius* (formerly known as *P. giganteus*) frequently visit date palm trees to consume sap, potentially contaminating date palm sap by licking the shaved area of the tree, urinating or defecating in the collection pots, or even trapped and/or dying in the pot (Khan et al., 2010). These bats often roost in regions with high human population density, fragmented forests, and supplemental food sources from residential fruit trees (Hahn et al., 2014). Until recently, researchers have put enormous efforts into understanding the ecological drivers that facilitate the spillover events from bats to humans. Studies have demonstrated that 53% of annual variation in winter spillovers events can be attributed to winter temperatures which may influence bat behavior, physiology, and human risk behaviors (McKee et al., 2021). The current distribution of *Pteropus* bats is ubiquitous in Asia and Africa, therefore, future spillover of NiV in human populations is likely to emerge in new territories.

REFERENCES

- AbuBakar, S., Puteh, S. E. W., Kastner, R., Oliver, L., Lim, S. H., Hanley, R., & Gallagher, E. (2022). Epidemiology (2012-2019) and costs (2009-2019) of dengue in Malaysia: a systematic literature review. *International journal of infectious diseases*, 124, 240-247.
- Arunkumar, G., Chandni, R., Mourya, D. T., Singh, S. K., Sadanandan, R., Sudan, P., & Bhargava, B. (2019). Outbreak Investigation of Nipah Virus Disease in Kerala, India, 2018. *J Infect Dis*, 219(12), 1867-1878. doi:10.1093/infdis/jiy612

- Bashar, K., Al-Amin, H., Reza, M. S., Islam, M., Asaduzzaman, & Ahmed, T. U. (2012). Socio-demographic factors influencing knowledge, attitude and practice (KAP) regarding malaria in Bangladesh. *BMC Public Health*, 12, 1-13.
- Bradley, C. A., & Altizer, S. (2007). Urbanization and the ecology of wildlife diseases. *Trends Ecol Evol*, 22(2), 95-102. doi:10.1016/j.tree.2006.11.001
- Breed, A. C., Meers, J., Sendow, I., Bossart, K. N., Barr, J. A., Smith, I., . . . Field, H. E. (2013). The distribution of henipaviruses in Southeast Asia and Australasia: is Wallace's line a barrier to Nipah virus? *PLoS One*, 8(4), e61316. doi:10.1371/journal.pone.0061316
- Carlson, C. J., Getz, W. M., Kausrud, K. L., Cizauskas, C. A., Blackburn, J. K., Bustos Carrillo, F. A., . . . Stenseth, N. C. (2018). Spores and soil from six sides: interdisciplinarity and the environmental biology of anthrax (*Bacillus anthracis*). *Biol Rev Camb Philos Soc*, 93(4), 1813-1831. doi:10.1111/brv.12420
- Chakraborty, A., Khan, S. U., Hasnat, M. A., Parveen, S., Islam, M. S., Mikolon, A., . . . Hossain, M. J. (2012). Anthrax outbreaks in Bangladesh, 2009-2010. *Am J Trop Med Hyg*, 86(4), 703-710. doi:10.4269/ajtmh.2012.11-0234
- Chala, B., & Hamde, F. (2021). Emerging and Re-emerging Vector-Borne Infectious Diseases and the Challenges for Control: A Review. *Front Public Health*, 9, 715759. doi:10.3389/fpubh.2021.715759
- Chin, A. Z., Maluda, M. C. M., Jelip, J., Jeffree, M. S. B., Culleton, R., & Ahmed, K. (2020). Malaria elimination in Malaysia and the rising threat of *Plasmodium knowlesi*. *J Physiol Anthropol*, 39(1), 36. doi:10.1186/s40101-020-00247-5
- Devendra, T. M., Pragma, D. Y., & Deepak, Y. P. (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. Retrieved from <https://iris.who.int/handle/10665/329715>
- Faust, C. L., McCallum, H. I., Bloomfield, L. S. P., Gottdenker, N. L., Gillespie, T. R., Torney, C. J., . . . Plowright, R. K. (2018). Pathogen spillover during land conversion. *Ecol Lett*, 21(4), 471-483. doi:10.1111/ele.12904

- Gething, P. W., Smith, D. L., Patil, A. P., Tatem, A. J., Snow, R. W., & Hay, S. I. (2010). Climate change and the global malaria recession. *Nature*, 465(7296), 342-345. doi:10.1038/nature09098
- Gurley, E. S., Montgomery, J. M., Hossain, M. J., Bell, M., Azad, A. K., Islam, M. R., . . . Breiman, R.F. (2007). Person-to-person transmission of Nipah virus in a Bangladeshi community. *Emerg Infect Dis*, 13(7), 1031-1037. doi:10.3201/eid1307.061128
- Hahn, M. B., Epstein, J. H., Gurley, E. S., Islam, M. S., Luby, S. P., Daszak, P., & Patz, J. A. (2014). Roosting behaviour and habitat selection of *Pteropus giganteus* reveals potential links to Nipah virus epidemiology. *J Appl Ecol*, 51(2), 376-387. doi:10.1111/1365-2664.12212
- Hill, C. A., Kafatos, F. C., Stansfield, S. K., & Collins, F. H. (2005). Arthropod-borne diseases: vector control in the genomics era. *Nature Reviews Microbiology*, 3(3), 262-268. doi:10.1038/nrmicro1101
- Horby, P. W., Hoa, N. T., Pfeiffer, D. U., & Wertheim, H. F. L. (2014). Drivers of Emerging Zoonotic Infectious Diseases. In A. Yamada, L. H. Kahn, B. Kaplan, T. P. Monath, J. Woodall, & L. Conti (Eds.), *Confronting Emerging Zoonoses: The One Health Paradigm* (pp. 13-26). Tokyo: Springer Japan.
- Hossain, M. S., Noman, A. A., Mamun, S., & Mosabbir, A. A. (2023). Twenty-two years of dengue outbreaks in Bangladesh: epidemiology, clinical spectrum, serotypes, and future disease risks. *Tropical Medicine and Health*, 51(1), 1-14.
- Hsan, K., Hossain, M. M., Sarwar, M. S., Wilder-Smith, A., & Gozal, D. (2019). Unprecedented rise in dengue outbreaks in Bangladesh. *The Lancet Infectious Diseases*, 19(12), 1287.
- Hugh-Jones, M., & Blackburn, J. (2009). The ecology of *Bacillus anthracis*. *Mol Aspects Med*, 30(6), 356-367. doi:10.1016/j.mam.2009.08.003
- Islam, M. S., Hossain, M. J., Mikolon, A., Parveen, S., Khan, M. S., Haider, N., . . . Luby, S. P. (2013). Risk practices for animal and human anthrax in Bangladesh: an exploratory study. *Infect Ecol Epidemiol*, 3. doi:10.3402/iee.v3i0.21356

- Johora, F. T., Elahi, R., Nima, M. K., Hossain, M. S., Rashid, H., Kibria, M. G., . . . Alam, M. S. (2021). Persistence of Markers of Chloroquine Resistance in *Plasmodium falciparum* in Bangladesh. *Am J Trop Med Hyg*, 104(1), 276-282. doi:10.4269/ajtmh.20-0415
- Jones, K. E., Patel, N. G., Levy, M. A., Storeygard, A., Balk, D., Gittleman, J. L., & Daszak, P. (2008). Global trends in emerging infectious diseases. *Nature*, 451(7181), 990-993. doi:10.1038/nature06536
- Kessler, M. K., Becker, D. J., Peel, A. J., Justice, N. V., Lunn, T., Crowley, D. E., . . . Plowright, R. K. (2018). Changing resource landscapes and spillover of henipaviruses. *Ann N Y Acad Sci*, 1429(1), 78-99. doi:10.1111/nyas.13910
- Khan, M. S., Hossain, J., Gurley, E. S., Nahar, N., Sultana, R., & Luby, S. P. (2010). Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. *Ecohealth*, 7(4), 517-525. doi:10.1007/s10393-010-0366-2
- Khoo, H.-Y., Lee, H.-Y., Khor, C.-S., Tan, K.-K., bin Hassan, M. R., Wong, C. M., . . . bin Jeffree, M. S. (2022). Seroprevalence of Zika virus among forest fringe communities in peninsular Malaysia and Sabah: General population-based study. *The American Journal of Tropical Medicine and Hygiene*, 107(3), 560.
- Kracalik, I. T., Malania, L., Tsertsvadze, N., Manvelyan, J., Bakanidze, L., Imnadze, P., . . . Blackburn, J. K. (2013). Evidence of Local Persistence of Human Anthrax in the Country of Georgia Associated with Environmental and Anthropogenic Factors. *PLOS Neglected Tropical Diseases*, 7(9), e2388. doi:10.1371/journal.pntd.0002388
- Ma, J., Guo, Y., Gao, J., Tang, H., Xu, K., Liu, Q., & Xu, L. (2022). Climate Change Drives the Transmission and Spread of Vector-Borne Diseases: An Ecological Perspective. *Biology (Basel)*, 11(11). doi:10.3390/biology11111628
- Maluda, M. C. M., Jelip, J., Ibrahim, M. Y., Suleiman, M., Jeffree, M. S., Aziz, A. F. B., . . . Ahmed, K. (2020). Nineteen years of Japanese encephalitis surveillance in Sabah, Malaysian borneo. *The American Journal of Tropical Medicine and Hygiene*, 103(2), 864.

- Marmot, M. G., Smith, G. D., Stansfeld, S., Patel, C., North, F., Head, J., . . . Feeney, A. (1991). Health inequalities among British civil servants: the Whitehall II study. *Lancet*, 337(8754), 1387-1393. doi:10.1016/0140-6736(91)93068-k
- McKee, C. D., Islam, A., Luby, S. P., Salje, H., Hudson, P. J., Plowright, R. K., & Gurley, E. S. (2021). The Ecology of Nipah Virus in Bangladesh: A Nexus of Land-Use Change and Opportunistic Feeding Behavior in Bats. *Viruses*, 13(2). doi:10.3390/v13020169
- McMichael, A. J. (2000). The urban environment and health in a world of increasing globalization: issues for developing countries. *Bull World Health Organ*, 78(9), 1117-1126.
- Merow, C., Smith, M. J., & Silander Jr, J. A. (2013). A practical guide to MaxEnt for modeling species' distributions: what it does, and why inputs and settings matter. *Ecography*, 36(10), 1058-1069.
- Munang'andu, H. M., Banda, F., Siamudaala, V. M., Munyeme, M., Kasanga, C. J., & Hamududu, B. (2012). The effect of seasonal variation on anthrax epidemiology in the upper Zambezi floodplain of western Zambia. *J Vet Sci*, 13(3), 293-298. doi:10.4142/jvs.2012.13.3.293
- Nikolay, B., Salje, H., Hossain, M. J., Khan, A., Sazzad, H. M. S., Rahman, M., . . . Gurley, E. S. (2019). Transmission of Nipah Virus - 14 Years of Investigations in Bangladesh. *N Engl J Med*, 380(19), 1804-1814. doi:10.1056/NEJMoa1805376
- Olival, K. J., Latinne, A., Islam, A., Epstein, J. H., Hersch, R., Engstrand, R. C., . . . Daszak, P. (2020). Population genetics of fruit bat reservoir informs the dynamics, distribution and diversity of Nipah virus. *Mol Ecol*, 29(5), 970-985. doi:10.1111/mec.15288
- Paul, K. K., Sazzad, H. M., Rahman, M., Sultana, S., Hossain, M. J., Ledermann, J. P., . . . Fischer, M. (2020). Hospital-based surveillance for Japanese encephalitis in Bangladesh, 2007–2016: Implications for introduction of immunization. *International journal of infectious diseases*, 99, 69-74.

- Rahman, M., Yamagishi, J., Rahim, R., Hasan, A., & Sobhan, A. (2019). East/central/south african genotype in a chikungunya outbreak, Dhaka, Bangladesh, 2017. *Emerging Infectious Diseases*, 25(2), 370.
- Rao, S., Traxler, R., Napetavaridze, T., Asanishvili, Z., Rukhadze, K., Maghlakelidze, G., ... & Salman, M. (2019). Risk factors associated with the occurrence of anthrax outbreaks in livestock in the country of Georgia: A case-control investigation 2013-2015. *PloS one*, 14(5), e0215228.
- Rocklöv, J., & Dubrow, R. (2020). Climate change: an enduring challenge for vector-borne disease prevention and control. *Nature Immunology*, 21(5), 479-483. doi:10.1038/s41590-020-0648-y
- Servadio, J. L., Rosenthal, S. R., Carlson, L., & Bauer, C. (2018). Climate patterns and mosquito-borne disease outbreaks in South and Southeast Asia. *Journal of Infection and Public Health*, 11(4), 566-571.
- Subramaniam, N., Anua, S. M., & Mat, N. F. C. (2021). Knowledge, Attitude and Practices (KAP) On Aedes Mosquito-Borne Diseases Amongst Community Members in Malaysia: A Review. *Malaysian Journal of Medicine & Health Sciences*, 17(2).
- Swartz, M. N. (2001). Recognition and management of anthrax--an update. *N Engl J Med*, 345(22), 1621-1626. doi:10.1056/NEJMr012892
- Teng, A. K., & Singh, S. (2001). Epidemiology and new initiatives in the prevention and control of dengue in Malaysia. Turner, W. C., Imologhome, P., Havarua, Z., Kaaya, G. P., Mfunne, J. K. E., Mpofu, I. D. T., & Getz, W.
- M. (2013). Soil ingestion, nutrition and the seasonality of anthrax in herbivores of Etosha National Park. *Ecosphere*, 4(1), art13. doi:https://doi.org/10.1890/ES12-00245.1

CHAPTER I

Public health communication of emerging vector-borne disease risk in remote regions of South and Southeast Asia

A version of this chapter was originally submitted for publication by Muhammad Belal Hossain: Hossain, M.B., Shimmi, S.C., Parash, M.T.H., Tran, P. Public health communication on emerging vector-borne disease risk in remote regions of South and Southeast Asia. Under review - *Parasitologia*

ABSTRACT

Vector-borne diseases (VBDs) continue to pose a persistent global health challenge, disproportionately impacting low- and middle-income countries where surveillance and healthcare infrastructure are constrained. Within these countries, residents of remote island communities are particularly vulnerable to emerging VBD threats, however, these populations remain critically understudied. A community-based cross-sectional survey was conducted among 300 residents from Shahpori Island, Bangladesh, and Gaya Island, Malaysia, to assess knowledge, attitudes, and practices (KAP) related to VBDs. Socio-demographic predictors of VBD-related knowledge were identified, and KAP outcomes across the two islands were compared, using a structured questionnaire and mixed-effects Poisson regression modeling. Significant disparities were observed between two settings: Gaya Island residents demonstrated a higher level of awareness regarding VBDs and preventive practices compared to Shahpori residents. Education was a strong predictor of VBD knowledge, with individuals possessing secondary education or above exhibiting significantly better knowledge ($\beta = 0.2024$, $p = 0.0003$). Marital status was also a significant factor, with unmarried respondents showing lower levels of knowledge ($\beta = -0.1657$, $p = 0.0372$). Age was positively correlated with VBD knowledge ($\beta = 0.0051$, $p = 0.0119$), indicating gradual increase with age, while income, gender, occupation, and household size were not significantly associated. Despite basic awareness of VBD symptoms and transmission, detailed understanding of mosquito ecology, disease symptoms, and breeding prevention strategies was remarkably poor, especially among Shahpori residents. Our findings highlight critical gaps in VBDs related knowledge and prevention behaviors shaped by socio-economic and educational disparities. Community-focused public health strategies including educational campaigns, establishment of health care infrastructure, access to trained health-care providers, and integrated vector control interventions are urgently needed to enhance resilience against emerging VBD threats such as drug-resistant malaria in remote island populations.

INTRODUCTION

Vector-borne diseases (VBDs) represent a significant global public and animal health challenge in the twenty-first century. These diseases are caused by pathogens transmitted through the bites of infected arthropods, including mosquitoes, fleas, sandflies, black flies, ticks, and bugs (Hill et al., 2005). VBDs account for more than 17% of all cases of infectious diseases, resulting in more than 700,000 deaths per year worldwide (Rocklöv et al., 2020). A significant number of VBDs are prevalent in Asia such as dengue, malaria, chikungunya, leishmaniasis, yellow fever, lymphatic filariasis, Japanese encephalitis, and schistosomiasis (Servadio et al., 2018). Recently, highly infectious fatal tick-borne diseases such as Crimean-Congo hemorrhagic fever, Kyasanur forest disease, and fatal tick-borne encephalitis have emerged in South and Southeast Asia (Mourya et al., 2014; Subramaniam et al., 2021). Despite the significant vector borne disease burden, challenges persist in acquiring comprehensive data due to insufficient disease surveillance, inadequate diagnostics, and limited public health awareness.

VBD poses a risk to all nations, irrespective of their socio-economic status, with vulnerability heightened where disease surveillance programs are absent particularly in low- and middle-income countries. Bangladesh and Malaysia, both characterized by high population density, and rapid urbanization, geographic features conducive to VBD outbreaks, have recently faced significant VBD threats including dengue, Zika virus, and chikungunya. Dengue remains a major concern in both countries, with numerous outbreaks between 2010 and 2023 resulting in thousands of cases and several hundred deaths annually (AbuBakar et al., 2022; Hossain et al., 2023; Hsan et al., 2019; Teng et al., 2001). The geographic range of emerging VBDs, such as Zika virus, Japanese encephalitis, and yellow fever, has also expanded in South and Southeast Asia, with routine detection in both countries (Khoo et al., 2022; Maluda et al., 2020; Paul et al., 2020; Rahman et al., 2019). While malaria was once a major concern, it has been effectively controlled in both nations in recent years, with a decline in mortalities attributed to continuous public health campaigns (Subramaniam et al., 2021).

Despite the significant challenges posed by VBDs to global health, particularly in low- and middle-income countries, control efforts have predominantly targeted urban localities. The challenges are often more severe in remote areas where low literacy rate, social prejudice, climatic vulnerabilities, and inadequate healthcare infrastructures exacerbate the problems.

Remote areas, such as islands and mountainous or hilly regions, present even greater difficulties due to their perceived inaccessibility, harsh weather conditions, and limited resources. Gaya Island, the largest island in the Tunku Abdul Rahman (TAR) Marine Park, situated near Kota Kinabalu in Sabah province of Malaysia, and Shahpori Island in Bangladesh, located across the maritime borders between Bangladesh and Myanmar, share similar geographic characteristics. Both islands are highly vulnerable to climate change, isolated, and constrained by limited resources, resulting in a lack of medical care facilities for residents.

The level of public health preparedness and awareness of disease risks, especially regarding emerging vector-borne diseases, remains largely unknown in these island communities. Given the challenges and resource constraints, understanding how these underserved populations address the threats posed by VBDs is critical for the development of effective prevention, intervention, and control strategies. Moreover, enhancing education and knowledge dissemination about VBDs and mosquito control practices could help change residents' attitudes and encourage the adoption of protective behaviors. Previous knowledge, attitude, and practice (KAP) studies conducted in various regions of Malaysia and Bangladesh have highlighted significant knowledge gaps regarding VBD transmission, prevention, vector biology, and control measures (Bashar et al., 2012). However, most of these studies have been conducted in highly accessible areas, such as cities or municipalities, and have not specifically targeted remote or marginalized island communities or focused on emerging VBDs. Therefore, this study aims to assess the knowledge, attitudes and practices towards VBDs in the remote localities of South and Southeast Asia.

METHODS

Study settings, timeline, & data collection

A community-based cross-sectional survey was carried out in two remote Islands: Gaya Island, Sabah, Malaysia (**Figure 1.1**), and Shahpori Island, Cox's Bazar, Bangladesh (**Figure 1.2**). A total of 300 adult participants (150 from Gaya Island and 150 from Shahpori Island) were enrolled from the local populations of both islands. Participants were selected using a simple random sampling method, with inclusion criteria specifying individuals who were native and had been residents of the study Islands for more than five years. *All tables and figures are located in appendices at the end of each chapter.*

Study participants from the selected communities were recruited between November 2018 and February 2020. Upon explaining the study objectives, participants provided oral consent and completed a questionnaire that had been pretested with 10 community members to assess clarity and identify missing information such as respondent phone numbers, detailed addresses, and household size. The questionnaire covered various aspects of VBDs including demographics; socio-economic characteristics (such as gender, age, marital status, education level, employment status, occupation, income, and number of household members); knowledge and experiences with VBDs; attitudes and practices related to VBD prevention and control. Trained interviewers administered the questionnaire, simplifying questions as needed using the local dialect. In total, six interviewers conducted the fieldwork: three in Shahpori Island, including two veterinarians and one research assistant, and three in Gaya Island, comprising a senior lecturer and two field assistants. All interviewers had prior experience in community-based epidemiological data collection. Participation was entirely voluntary, and no incentives were offered. The study protocol received approval from the University of Malaysia Sabah (UMS) Institutional Review Board for Research, prior to implementation in the field.

Data Analysis

Descriptive statistics were used to summarize the socio-demographic and VBD-related characteristics of participants from Gaya Island, Malaysia and Shahpori Island, Bangladesh. Frequency distributions and percentages were calculated separately for each island and for the combined data across both locations. Comparative analyses were performed to assess socio-demographic differences between the islands, using chi-square tests for categorical variables, independent t-test for continuous variables when normality assumptions were met, and Wilcoxon rank-sum tests when normality assumptions were violated. The normality of continuous variables was assessed using the Shapiro-Wilk test. A questionnaire was administered to 150 residents on each island, focusing on VBD-related questions. For each participant, the percentage of correct answers was calculated to create a continuous outcome variable reflecting overall VBD knowledge. This measure represents the proportion of correct responses out of the total questions answered, providing a continuous measure of VBD knowledge for each participant.

To identify the factors associated with knowledge of VBDs, a mixed-effects Poisson regression model was employed. This approach allowed us to account for both individual-level predictors

and island-level differences between Shahpori and Gaya islands. The fixed effects in the model included demographic variables such as age, gender, education level, income, household size, occupation, and exposure to health communication. Random effects were incorporated to account for variability at the island level, capturing unobserved island-specific factors, as well as individual-level variations in VBD knowledge not explained by the fixed effects. Model fit was evaluated using a range of statistics, including Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), -2 Res Log Pseudo-Likelihood, and Generalized Chi-Square/DF ratio. These fit statistics helped us to assess the adequacy of the model in accounting for the observed data. Specifically, the Generalized Chi-Square/DF ratio of 0.98 indicated a good model fit, with no evidence of over- or under dispersion. The significance of the fixed effects was evaluated through Wald tests or likelihood ratio tests. Statistical significance was considered at $p < 0.05$ for all analyses. Data analysis was conducted using SAS version 9.4.

RESULTS

A total of 300 participants were surveyed, with 150 from each island. There was a significant disparity in the gender distribution between the islands. Due to the absence of female interviewers in Shahpori Island, only one female respondent was included, which resulted in 99.3% of participants from Shahpori Island being male. In contrast, Gaya Island had a balanced gender distribution, with 50% male and 50% female participants. No significant difference in marital status was observed between the islands ($p = 0.5139$) (**Table 1.1**). A higher proportion of respondents from Gaya Island reported higher education levels compared to those from Shahpori Island, with 54.6% of Gaya respondents having completed secondary school or higher, compared to just 22.6% on Shahpori Island ($p < 0.0001$). Gaya islanders also reported significantly higher average monthly incomes (USD 170.97) compared to Shahpori islanders (USD 130.03) ($p < 0.0001$). The mean age of respondents from Shahpori Island (35.64 years) was significantly younger than that of Gaya Island (39.4 years) ($p = 0.0107$), while mean household size did not differ significantly between the islands ($p = 0.9775$).

Knowledge of VBDs varied significantly between the two islands. A significantly higher proportion of Gaya islanders (98.7%) had heard of vector-borne diseases such as malaria, dengue, chikungunya, and other VBDs, compared to 89.3% of Shahpori islanders ($p = 0.001$). While most respondents from both islands recognized fever as a symptom of VBDs, Gaya

islanders demonstrated much greater awareness, with 89.3% correctly identified that fever as a symptom, compared to only 42.7% on Shahpori Island ($p < 0.0001$). Gaya respondents also had a better understanding of the primary cause of these diseases, with 94.7% identifying mosquito bites as the main transmission route, compared to 70% on Shahpori Island ($p < 0.0001$; **Table 1.2**).

A higher proportion of Gaya islanders (42.7%) were aware of the importance of preventing or destroying mosquito breeding sites, while none of the respondents from Shahpori Island were aware of this practice ($p < 0.0001$). Regarding prevention methods, residents of Shahpori Island were more likely to report using bed nets (52.7%) compared to Gaya islanders (24%), whereas Gaya islanders preferred a combination of bed nets and mosquito coils (23.3%). In terms of treatment costs, significantly more Gaya islanders (54%) reported spending money on treatment for mosquito-borne diseases than Shahpori islanders (16%) ($p < 0.0001$). Furthermore, Gaya islanders primarily sought medical care from government hospitals (98.7%), while Shahpori islanders tended to use rural unregistered healthcare providers (61.3%) ($p < 0.0001$; **Table 1.3**).

Significant predictors of KAP regarding VBDs were identified through Poisson regression analysis. Occupation categories did not exhibit significant associations with VBD-related knowledge. Specifically, the β for the "business" category ($\beta = 0.05840$) suggested a marginal increase in VBD knowledge among individuals in this category, but this effect was not statistically significant ($p = 0.4042$) (**Table 1.4**). Similarly, the occupation categories "private job" ($\beta = -0.02526$), "housewife" ($\beta = -0.03913$), and "other occupation" ($\beta = 0.01046$) showed no significant associations with VBD knowledge, with p-values exceeding 0.05 ($p = 0.7621$, $p = 0.6980$, and $p = 0.8770$, respectively). Education was identified as a significant predictor of VBD knowledge, attitudes, and practices. Individuals with higher education levels (secondary school or above) demonstrated significantly better knowledge of VBDs ($\beta = 0.2024$, $p = 0.0003$). Marital status was also a significant predictor, with unmarried or single respondents exhibiting lower knowledge levels compared to their married counterparts ($\beta = -0.1657$, $p = 0.0372$). Age was a positive predictor of VBD knowledge, with each additional year of age contributing to a slight increase in VBD awareness ($\beta = 0.005125$, $p = 0.0119$).

Income did not emerge as a significant predictor of VBD knowledge, as the negative β ($\beta = -0.00017$) suggested a marginal decrease in VBD knowledge with higher income, but this effect

was not statistically significant ($p = 0.5589$). Household members/size also did not significantly impact VBD knowledge ($\beta = 0.001985$, $p = 0.8086$). Gender was also not significant (**Table 1.4**).

DISCUSSION

Our study revealed considerable disparities in knowledge, attitude, and prevention practices regarding VBDs between the islands of Shahpori (Bangladesh) and Gaya (Malaysia), despite their similar remote geographical settings. The socio-economic and educational status significantly differed between the two islands. Only 22.6% of Shahpori residents had completed their post-high school education, whereas 54.6% of Gaya residents had attained a similar level of education. Education has long been recognized as a key determinant of health, and our findings align with previous studies that suggest a correlation between low educational attainment and limited VBD-related knowledge (Aerts et al., 2020; Alobuia et al., 2015; Nava-Doctor et al., 2021; Shafie et al., 2016). While both islands have a limited number of educational institutions, Shahpori Island suffers from an insufficient provision of educational facilities in contrast to its counterpart.

The occupational distribution among the residents of both islands exhibited similarities, encompassing roles such as small-scale business owners, day laborers, low-income private service, housewife, fishermen, and farmers. In Gaya, many participants were housewives but contributed to the family income by selling handmade mats, crafts made from shells and other sea products in the nearby market. A small proportion of these homemakers made shell ornaments and sold them in the nearby municipalities for their livelihood. The residents of Gaya often commuted to Kota Kinabalu, the capital of Sabah, where they engaged in various occupations such as day laborers, small-scale business, or shopkeepers. Meanwhile, we observed a slightly different pattern in Shahpori Island, where all the participants were predominantly male, with men playing the primary role in supporting family income. Most of our respondents were day laborers in Gaya Island (38%). Residents from both islands frequently commute to nearby municipalities by engine boat or speed boat, however, during dry season, residents of Shahpori can commute to the mainland on foot.

Despite these socio-economic differences, participants from both islands exhibited a basic level of awareness regarding VBDs, with only a small fraction of respondents (6%) reporting no prior knowledge or having never heard of mosquito-borne diseases. In our study, 12.3% of

respondents were unaware of symptoms associated with emerging VBDs such as Zika virus and Chikungunya. The majority of the participants on both islands recognized that mosquito bites could lead to mosquito-borne diseases, consistent with the findings reported in different other settings in both countries and other geographic regions of different countries (Fritzell et al., 2016; Jaramillo Ramírez et al., 2017; Pandit et al., 2010). Interestingly, only 2.6% of our respondents were aware of other potential causes of VBDs other than mosquito bites, suggesting significant gaps in understanding the broader etiologies of VBDs.

In terms of preventive measures, Gaya Island residents demonstrated better awareness than those from Shahpori counterparts. However, both populations lack knowledge of the detailed life cycle of mosquitoes, mosquito breeding sites, and the natural history of the diseases. While respondents from both islands recognized mosquito bites as a key risk factor and reported using preventive measures such as mosquito nets and repellents, the actual prevalence and implementation of these measures were relatively low compared to other regions (Kulkarni et al., 2017; Morse et al., 2019). The disparity in prevalence may arise from spatial and socioeconomic discrepancies, limited resources, and the rural nature of these areas. Strategies to prevent the mosquito breeding sites are not commonly adopted in the rural areas of Bangladesh, although some urban areas have implemented mosquito breeding prevention measures (Sizear et al., 2019). However, at Shahpori island, these practices have never been adopted. Similarly, while there is a comprehensive mosquito prevention program in operation in urban areas of Malaysia, no such program has been reported on Gaya Island (Haque et al., 2008).

The medical infrastructure and diagnostic capabilities on both islands are significantly limited as reflected in our study findings. While all individuals on Gaya Island reported receiving medical treatment at government health facilities, residents of Shahpori predominantly sought medical care from rural, non-registered practitioners or minimally educated rural pharmacy staff, with government and private healthcare facilities serving as secondary options. The absence of registered medical practitioners in both locations indicates a significant healthcare infrastructure gap. Notably, Gaya Island does not have any 'bomoh' or traditional village healers commonly found in other rural areas of Malaysia (Haque et al., 2008). The absence of these traditional healers suggests that Gaya residents neither rely on nor perceive traditional healers as primary healthcare providers. This contrasts with the situation on Shahpori Island, where participants

frequently depend on non-registered rural practitioners due to the lack of registered medical professionals and infrastructure. Access to healthcare on Shahpori is particularly challenging, as residents must undertake strenuous journeys to the nearest municipality to receive medical care. Previous research in Bangladesh has shown a preference among the majority of individuals to seek medical care from rural, non-registered practitioners, attributed to inadequate medical infrastructure, high poverty rates, and limited availability of registered medical physicians (Sizear et al., 2019).

Although respondents from both islands have limited knowledge about VBDs including their causes, symptoms, and preventive measures, they demonstrated positive attitudes toward VBD prevention. This may be linked to the significant public health implications of VBDs, and the existence of some awareness initiatives disseminated through mass media channels. However, these efforts remain remarkably insufficient given the severe adverse effects of VBDs. Most importantly, VBDs frequently evade diagnosis due to the absence of well-equipped laboratories, technicians, and trained medical professionals, leading to treatments based on presumptive diagnoses or left untreated. Furthermore, Shahpori Island is particularly vulnerable due to ongoing refugee crisis, socio-political unrest, armed conflicts, inadequate immunization, massive ecological degradation, and reports of drug-resistant malaria in the regions (Haque et al., 2013; Nima et al., 2022).

This study has some limitations, including a relatively small sample size and the exclusion of female participants from Shahpori Island due to logistical challenges. As a result, the gender comparison between the islands was not possible, which limits the generalizability and warrants careful interpretation of the findings. Additionally, the random selection of participants in these remote island territories was based on transportation convenience, which may have introduced sampling bias.. Nevertheless, our study provides valuable insights into the gaps in knowledge and prevention practices related to VBDs in remote islands of South and Southeast Asia. These findings underscore the need for targeted public health interventions tailored to the unique socio-economic and geographic contexts of these populations. Furthermore, the implementation of integrated vector control programs is critical for mitigating the health risks associated with VBDs in these vulnerable communities. Coordinated outreach and educational campaigns, particularly those focused on increasing awareness of mosquito breeding sites and encouraging appropriate

medical care-seeking behaviors, are crucial steps toward improving the prevention and management of VBDs on both islands.

REFERENCES

- AbuBakar, S., Puteh, S. E. W., Kastner, R., Oliver, L., Lim, S. H., Hanley, R., & Gallagher, E. (2022). Epidemiology (2012-2019) and costs (2009-2019) of dengue in Malaysia: a systematic literature review. *International journal of infectious diseases*, 124, 240-247.
- Aerts, C., Revilla, M., Duval, L., Paaijmans, K., Chandrabose, J., Cox, H., & Sicuri, E. (2020). Understanding the role of disease knowledge and risk perception in shaping preventive behavior for selected vector-borne diseases in Guyana. *PLOS Neglected Tropical Diseases*, 14(4), e0008149.
- Alobuia, W. M., Missikpode, C., Aung, M., & Jolly, P. E. (2015). Knowledge, attitude, and practices regarding vector-borne diseases in Western Jamaica. *Annals of global health*, 81(5), 654-663.
- Bashar, K., Al-Amin, H., Reza, M. S., Islam, M., Asaduzzaman, & Ahmed, T. U. (2012). Socio-demographic factors influencing knowledge, attitude and practice (KAP) regarding malaria in Bangladesh. *BMC Public Health*, 12, 1-13.
- Fritzell, C., Raude, J., Adde, A., Dusfour, I., Quenel, P., & Flamand, C. (2016). Knowledge, attitude and practices of vector-borne disease prevention during the emergence of a new arbovirus: implications for the control of chikungunya virus in French Guiana. *PLOS Neglected Tropical Diseases*, 10(11), e0005081.
- Haque, A. (2008). Culture-bound syndromes and healing practices in Malaysia. *Mental Health, Religion and Culture*, 11(7), 685-696.
- Haque, U., Glass, G. E., Haque, W., Islam, N., Roy, S., Karim, J., & Noedl, H. (2013). Antimalarial drug resistance in Bangladesh, 1996-2012. *Trans R Soc Trop Med Hyg*, 107(12), 745-752. doi:10.1093/trstmh/trt088
- Hill, C. A., Kafatos, F. C., Stansfield, S. K., & Collins, F. H. (2005). Arthropod-borne diseases: vector control in the genomics era. *Nature Reviews Microbiology*, 3(3), 262-268.

- Hossain, M. S., Noman, A. A., Mamun, S., & Mosabbir, A. A. (2023). Twenty-two years of dengue outbreaks in Bangladesh: epidemiology, clinical spectrum, serotypes, and future disease risks. *Tropical Medicine and Health*, 51(1), 1-14.
- Hsan, K., Hossain, M. M., Sarwar, M. S., Wilder-Smith, A., & Gozal, D. (2019). Unprecedented rise in dengue outbreaks in Bangladesh. *The Lancet Infectious Diseases*, 19(12), 1287.
- Jaramillo Ramírez, G. I., & Álvarez, L. S. B. (2017). Knowledge, attitudes and practices regarding dengue, chikungunya, and zika and their vector *Aedes aegypti* in Villavicencio, Colombia. *The Open Public Health Journal*, 10(1).
- Khoo, H.-Y., Lee, H.-Y., Khor, C.-S., Tan, K.-K., bin Hassan, M. R., Wong, C. M., . . . bin Jeffree, M. S. (2022). Seroprevalence of Zika virus among forest fringe communities in peninsular Malaysia and Sabah: general population-based study. *The American Journal of Tropical Medicine and Hygiene*, 107(3), 560.
- Kulkarni, M. M., Jacob, G. P., Kamath, A., Guha, S., & Ramireddy, M. (2017). Knowledge, attitude and practices regarding mosquito borne diseases among adults in Udupi District, Karnataka.
- Maluda, M. C. M., Jelip, J., Ibrahim, M. Y., Suleiman, M., Jeffree, M. S., Aziz, A. F. B., . . . Ahmed, K. (2020). Nineteen years of Japanese encephalitis surveillance in Sabah, Malaysian borneo. *The American Journal of Tropical Medicine and Hygiene*, 103(2), 864.
- Morse, W., Izenour, K., McKenzie, B., Lessard, S., & Zohdy, S. (2019). Perceptions and practices of mosquito-borne diseases in Alabama—is concern where it should be? *BMC Public Health*, 19, 1- 9.
- Mourya, D. T., Yadav, P. D., & 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.
- Nava-Doctor, J. E., Sandoval-Ruiz, C. A., & Fernández-Crispín, A. (2021). Knowledge, attitudes, and practices regarding vector-borne diseases in central Mexico. *Journal of ethnobiology and ethnomedicine*, 17, 1-14.

- Nguyen-Tien, T., Pham, L. T., Vu, D. T., Tran, S. H., Vu, L. T., Bui, V. N., . . . Nguyen-Viet, H. (2021). Knowledge and practice on prevention of mosquito-borne diseases in livestock-keeping and non- livestock-keeping communities in Hanoi city, Vietnam: A mixed-method study. *PLoS One*, 16(2), e0246032.
- Nima, M. K., Mukherjee, A., Sazed, S. A., Hossainey, M. R. H., Phru, C. S., Johora, F. T., . . . Halder, K. (2022). Assessment of *Plasmodium falciparum* Artemisinin Resistance Independent of kelch13 Polymorphisms and with Escalating Malaria in Bangladesh. *mBio*, 13(1), e0344421. doi:10.1128/mbio.03444-21
- Pandit, N., Patel, Y., & Bhavsar, B. (2010). Awareness and practice about preventive method against mosquito bite in Gujarat. *Healthline*, 1(1), 16-20.
- Paul, K. K., Sazzad, H. M., Rahman, M., Sultana, S., Hossain, M. J., Ledermann, J. P., . . . Fischer, M. (2020). Hospital-based surveillance for Japanese encephalitis in Bangladesh, 2007–2016: Implications for introduction of immunization. *International journal of infectious diseases*, 99, 69-74.
- Rahman, M., Yamagishi, J., Rahim, R., Hasan, A., & Sobhan, A. (2019). East/central/south african genotype in a chikungunya outbreak, Dhaka, Bangladesh, 2017. *Emerging Infectious Diseases*, 25(2), 370.
- Rocklöv, J., & Dubrow, R. (2020). Climate change: an enduring challenge for vector-borne disease prevention and control. *Nature Immunology*, 21(5), 479-483.
- Servadio, J. L., Rosenthal, S. R., Carlson, L., & Bauer, C. (2018). Climate patterns and mosquito-borne disease outbreaks in South and Southeast Asia. *Journal of Infection and Public Health*, 11(4), 566-571.
- Shafie, A., Roslan, M. A., Ngui, R., Lim, Y. A. L., & Sulaiman, W. Y. W. (2016). Mosquito Biology and Mosquito-Borne Disease Awareness Among Island Communities In Malaysia. *Journal of the American Mosquito Control Association*, 32(4), 273-281, 279. Retrieved from <https://doi.org/10.2987/16-6604.1>
- Sizear, M. M. I., Nababan, H. Y., Siddique, M. K. B., Islam, S., Paul, S., Paul, A. K., & Ahmed, S. M. (2019). Perceptions of appropriate treatment among the informal allopathic

providers: insights from a qualitative study in two peri-urban areas in Bangladesh. BMC Health Services Research, 19(1), 424. doi:10.1186/s12913-019-4254-3

Subramaniam, N., Anua, S. M., & Mat, N. F. C. (2021). Knowledge, Attitude and Practices (KAP) On Aedes Mosquito-Borne Diseases Amongst Community Members in Malaysia: A Review. Malaysian Journal of Medicine & Health Sciences, 17(2).

Teng, A. K., & Singh, S. (2001). Epidemiology and new initiatives in the prevention and control of dengue in Malaysia.

APPENDIX I

TABLES

Table 1.1. Comparative socio-demographic characteristics between Shahpori and Gaya islands

Variables		Shahpori Island N=150 n (%)	Gaya Island N=150 n (%)	Total (combined for both islands) N = 300 n (%)	<i>p</i> value
Gender identity	Male	149 (99.3)	75 (50)	224 (74.7)	
	Female	1 (0.7)	75 (50)	76 (25.3)	
Marital status	Single	20 (13.3)	24 (16)	44 (14.7)	0.5139
	Married	130 (86.7)	126 (84)	256 (85.3)	
Education level	Low (elementary)	116 (77.3)	68 (45.3)	184 (61.3)	<0.0001
	High (secondary and above)	34 (22.7)	82 (54.7)	116 (38.7)	
Current occupation	Business	47 (31.3)	18 (12)	65 (21.7)	<.0001
	Day labor	57 (38)	22 (14.7)	79 (26.3)	
	Private service	24 (16)	11 (7.3)	35 (11.7)	
	Housewife	0 (0)	50 (33.3)	50 (16.7)	
	Other occupation	22 (14.7)	49 (32.7)	71 (23.6)	
Mean age in years		35.64	39.4	37.52	0.0107
Mean household members		6.63	6.77	6.69	0.9775
Mean income (USD)		130.03	170.97	150.5	<.0001

Statistical significance at the $p < 0.05$ level is indicated in bold.

Table 1.2. Population knowledge concerning vector-borne disease transmission, symptoms, and other factors among the respondents between two islands

Characteristics/ Questions	Shahpori Island N=150 n (%)	Gaya Island N=150 n (%)	Total N=300 n (%)	<i>p</i> value
Have you ever heard about malaria/ dengue/chikungunya/ Zika/ yellow fever/ Japanese encephalitis/ filariasis or other emerging vector-borne disease?				
Yes	134 (89.3)	148 (98.7)	282 (94)	0.001
No	16 (10.7)	2 (1.3)	18 (6)	
How long have you known about vector-borne emerging disease?				
Mean duration (in months)	17.06	27.77		0.8616
Do you know the symptoms of vector-borne diseases?				
Fever	64 (42.7)	134 (89.3)	198 (66)	<0.0001
Fever with shivering, joint pain, rash, lymph node swelling, seizure, convulsion, eye problems, or anemia	50 (33.3)	14 (9.3)	64 (21.4)	
Other compatible symptoms	0 (0)	1 (0.7)	1 (0.3)	
Do not know	36 (24)	1 (0.7)	37 (12.3)	
Do you know about the possible causes of vector-borne emerging diseases?				
Mosquito bite	105 (70)	142 (94.6)	247 (82.4)	<0.0001
Not maintaining environmental cleanliness	0 (0)	4 (2.7)	4 (1.3)	
Reasons unrelated to mosquitoes or cleanliness	0 (0)	4 (2.7)	4 (1.3)	
Do not know	45 (30)	0 (0)	45 (15)	
Do you know why someone can get infected with vector-borne diseases?				
Bite from a mosquito	103 (68.7)	132 (88)	235 (78.4)	<0.0001
Exposure to flies, ticks, or insects	1 (0.7)	0 (0)	1 (0.3)	
Not maintaining cleanliness in the surrounding environment	0 (0)	7 (4.7)	7 (2.3)	
Do not know	46 (30.6)	11 (7.3)	57 (19)	

Statistical significance at the $p < 0.05$ level is indicated in bold.

Table 1.3. Population attitude and prevention practices of vector-borne disease between two islands

Characteristics/ Questions	Shahpori Island N=150 n (%)	Gaya Island N=150 n (%)	Total N=300 n (%)	<i>p</i> -value
Do you know how to prevent or control mosquito-borne diseases?				<0.0001
Prevent or destroy breeding site of mosquito	0 (0)	64 (42.7)	64 (21.3)	
Using bed nets	79 (52.7)	36 (24)	115 (38.3)	
Using mosquito repellent coils	24 (16)	3 (2)	27 (9)	
Combination of bed nets and coils	0 (0)	35 (23.3)	35 (11.7)	
Others	0 (0)	9 (6)	9 (3)	
Do not know	47 (31.3)	3 (2)	50 (16.7)	
How do you confirm/diagnose a case of mosquito-borne disease?				<0.0001
Presence of fever	28 (18.7)	144 (96)	172 (57.3)	
Blood test results	23 (15.3)	0 (0)	23 (7.7)	
Do not know	99 (66)	5 (3.3)	104 (34.7)	
Others/traditional	0 (0)	1 (0.7)	1 (0.3)	
Have you ever spent money on the treatment of mosquito-borne diseases?				<0.0001
Yes	24 (16)	81 (54)	105 (35)	
No	95 (63.3)	68 (45.3)	163 (54.3)	
Unsure/ Don't know	31 (20.7)	1 (0.7)	32 (10.7)	
Where do you usually seek medical treatment?				<0.0001
Government hospital	10 (6.7)	148 (98.7)	158 (52.7)	
Private health-care Center	3 (2)	2 (1.3)	5 (1.7)	
Rural unregistered health-care provider	92 (61.3)	0 (0)	92 (30.6)	
Unsure/ family or neighbors' suggestion	45 (30)	0 (0)	45 (15)	
What are the measures you would like to take to tackle vector-borne disease in future?				<0.0001
Destroying larva/mosquito breeding sites	1 (0.7)	49 (32.7)	50 (16.7)	

Table 1.3 continued

Using bed nets	92 (61.3)	47 (31.3)	139 (46.3)	
Administering insecticide & practice of bed nets	3 (2)	1 (0.7)	4 (1.3)	
Mosquito repellent coil	9 (6)	33 (22)	42 (14)	
Others/traditional protective measures	0 (0)	17 (11.3)	17 (5.7)	
Do not know	45 (30)	3 (2)	48 (16)	
Where could you receive treatment if you were diagnosed with a mosquito-borne disease?				<0.0001
Government hospital	44 (29.3)	150 (100)	194 (64.7)	
Private hospital or health-care center	6 (4)	0 (0)	6 (2)	
Unregistered health-care providers/ pharmacy salesperson	55 (36.7)	0 (0)	55 (18.3)	
Do not know	45 (30)	0 (0)	45 (15)	

Statistical significance at the $p < 0.05$ level is indicated in bold.

Table 1.4. Predictors of vector-borne disease knowledge, attitude and practices among residents of both islands in Bangladesh and Malaysia

Variables		Estimate	Standard Error	t-value	Pr > t
Occupation	Business	0.05840	0.06991	0.84	0.4042
	Private job	-0.02526	0.08337	-0.30	0.7621
	Housewife	-0.03913	0.1007	-0.39	0.6980
	Other occupation	0.01046	0.06752	0.15	0.8770
	Day labor (Ref)	0			
Education	High (high school and above)	0.2024	0.05489	3.69	0.0003
	Low (elementary - ref)	0			
Marital status	Unmarried or single	-0.1657	0.07914	-2.09	0.0372
	Married (Ref)	0			
Gender	Female	0.04335	0.08104	0.53	0.5931
	Male (Ref)	0			
Age (in years)		0.005125	0.002025	2.53	0.0119
Income (USD)		-0.00017	0.000287	-0.59	0.5589
Household size		0.001985	0.008190	0.24	0.8086

Statistical significance at the $p < 0.05$ level is indicated in bold.

Table 1.5. Comparative model fit statistics

Fit Statistic	Poisson	Negative binomial
-2 Log Likelihood	1422.77	1463.00
AIC	1446.77	1489.00
AICC	1447.87	1490.29
BIC	1491.01	1536.93
CAIC	1503.01	1549.93
HQIC	1464.48	1508.19
Pearson Chi-Square	276.94	358.75
Pearson Chi-Square / DF	0.98	1.27

FIGURES

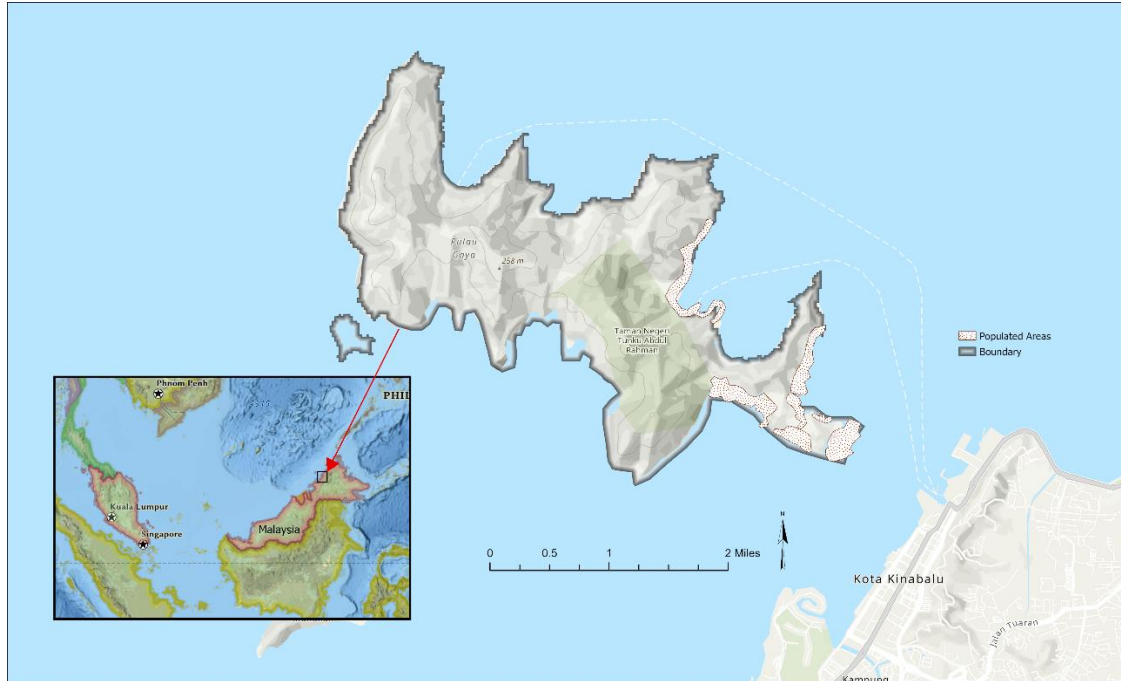


Figure 1.1. Geographic location of the study area on Gaya Island, Sabah, Malaysia

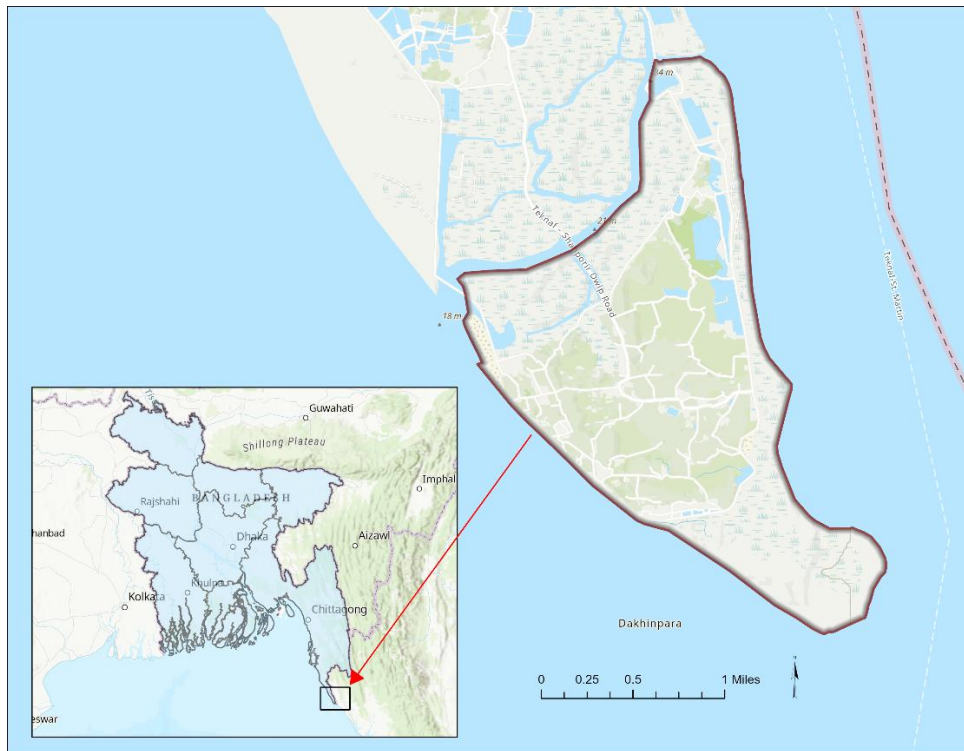


Figure 1.2. Geographic location of the study area on Shahpori Island, Cox's Bazar, Bangladesh

CHAPTER II

Risk factors for human anthrax infection on a global scale: Understanding how outbreaks converge from animal husbandry practice, socioeconomic conditions, and cultural practices

ABSTRACT

Anthrax, caused by *Bacillus anthracis*, remains a significant zoonotic disease across the globe disproportionately affecting rural populations reliant on livestock farming. Despite the availability of vaccines for humans and animals, and preventive measures, anthrax outbreaks continue to occur due to convergence of inadequate animal husbandry practices, socioeconomic vulnerabilities, and cultural traditions. To inform targeted public health interventions, a comprehensive global synthesis of the risk factors for human anthrax is urgently needed. A systematic review and meta-analysis were performed in accordance with PRISMA guidelines. PubMed, Embase, Web of Science, Scopus, and Google Scholar were searched for case-control studies reporting odds ratios (ORs) for human anthrax risk factors published between January 1900 and February 2025. Studies were screened based on predefined inclusion criteria, and data were independently extracted by two investigators. A random-effects model was employed for meta-analysis to assess pooled risk estimates across various exposure-related, socioeconomic, and cultural factors. A total of 18 studies were included, primarily from Africa, Asia, and Europe. Our analysis identified several significant risk factors for human anthrax infection. Direct exposure to raw meat from infected animals was strongly associated with an increased risk (OR = 5.79, 95% CI: 4.04-8.31), along with direct contact activities such as skinning (OR = 5.64, 95% CI: 3.73-8.52), butchering (OR = 6.54, 95% CI: 3.26-13.09), and handling carcasses or by-products of infected animals (OR = 4.13, 95% CI: 2.88-5.92). Presence during the slaughter of an infected or moribund animal was also a significant risk factor (OR = 5.16, 95% CI: 2.54-10.49). Furthermore, socio-cultural factors such as religious permissions and demographic characteristics substantially increased anthrax risk (OR = 10.50, 95% CI: 5.44-20.23). While heterogeneity varied by risk factor, it remained generally low to moderate, supporting the consistency of findings across diverse settings. Our study underscores the strong associations between human anthrax infection and exposure-related, socioeconomic, and cultural risk factors. Effective prevention strategies should prioritize improved livestock management, enhanced biosecurity systems, community education on safe animal handling practices, particularly the handling of moribund livestock or dead animals of unknown origin, and strengthened veterinary services. Future research should focus on region-specific interventions and conduct longitudinal studies to assess the effectiveness of anthrax risk reduction efforts.

INTRODUCTION

Anthrax, caused by *Bacillus anthracis*, is a globally distributed zoonotic disease that disproportionately affects impoverished, rural communities dependent on livestock farming. Estimates suggest that anthrax causes between 20,000 to 100,000 cases annually worldwide, primarily in regions with limited veterinary care and public health infrastructure (Morton N. Swartz, 2001). Approximately 1.83 billion peoples and 1.1 billion livestock live within regions of anthrax risk (Carlson et al., 2019). Despite being preventable through livestock vaccination and improved animal management practices, anthrax outbreaks continue to pose risks especially in settings where animal husbandry practices intersect with socioeconomic and cultural factors. The transmission of anthrax to humans typically occurs through direct contact with infected animals or contaminated animal products, underscoring the importance of understanding the dynamics of animal husbandry practices and other factors that contribute to these risks (Beyer et al., 2009; Kasradze et al., 2018; Traxler et al., 2019).

The relationship between animal husbandry and anthrax outbreaks is multifaceted. Direct exposure to infected animal products through different processes, such as slaughtering, butchering, skinning, or handling of raw meat without protective measures, remains the most common route of infection in many rural communities. Poor biosecurity, inadequate hygiene practices during slaughter, lack of protective equipment, improper carcass disposal and insufficient livestock vaccination, have been linked to increased incidence of human infections (Beyer et al., 2009). In regions where livestock are kept in close proximity to humans, the risk for zoonotic transmission escalates, particularly in the absence of proper veterinary oversight and effective public health interventions (Islam et al., 2013; Kracalik et al., 2013). These conditions are prevalent in parts of sub-Saharan Africa, Asia, and Eastern Europe, where anthrax continues to be a recurrent public health problem. Furthermore, environmental factors such as soil pH, rainfall, and climatic variability influence the sporulation of the *B. anthracis* spores, correlating with the resurgence of anthrax in livestock and humans (Kracalik et al., 2013; Ndolo et al., 2022).

Socioeconomic conditions also critically shape community vulnerability to anthrax infection especially in resource-poor settings. Communities with limited access to healthcare, education, and veterinary services are at a heightened risk as they lack the resources to implement

preventative measures or respond effectively to outbreaks. Economic pressures often lead farmers to engage in risky practices such as raising unvaccinated animals in the household/farms or neglecting biosecurity protocols, further exacerbating the likelihood of anthrax transmission (Bodenham et al., 2021). Cultural practices also significantly influence both animal husbandry and public health responses to anthrax. In some regions, traditional beliefs regarding livestock management, disease prevention, and vaccination are reliant on governance leading to inadequate preventive measures (Kracalik et al., 2014). In regions where livestock play a central role in religious and social traditions, disease prevention measures such as the culling of infected animals or the avoidance of consuming potentially contaminated meat may be disregarded because of cultural norms and financial investment (Islam et al., 2021; Mugo et al., 2021). Additionally, cultural events such as rituals, celebrations, and the slaughtering of sick or moribund animals to mitigate economic losses often involve handling or consuming animal products, which makes targeted control efforts difficult and increase the risk of exposure to *B. anthracis* (Chakraborty et al., 2012; Gurbanov et al., 2010; Kasradze et al., 2018).

The continued spread of anthrax globally is exacerbated by environmental factors, including the persistence of *B. anthracis* spores in the soil where they can remain viable for years under certain conditions (Carlson et al., 2018). In regions with frequent outbreaks, contaminated land or grazing areas, along with inadequate agricultural practices, create a cycle of infection in endemic areas (Biswas et al., 2012). Once soil becomes contaminated, it becomes a source of exposure to both livestock and humans (Driciru et al., 2020). In such areas, anthrax outbreaks are often cyclic, with periods of disease following environmental changes that favor the survival of *B. anthracis* spores (Barandongo et al., 2023).

Understanding the risk factors for human anthrax infection necessitates an interdisciplinary approach that combines epidemiological data, socioeconomic analysis, and cultural anthropology across various regions. Although numerous studies have examined the risk factors leading to anthrax outbreaks (Kasradze et al., 2008; Nayak et al., 2019; Chowdhury et al., 2024), these papers focus on specific regions or isolated incidents, limiting the generalizability of findings across diverse socio-economic and environmental contexts. A global meta-analysis of anthrax risk factors allows identification of common patterns of infection and vulnerabilities that transcend regional differences. This comprehensive approach will provide valuable insights into

our understanding on broader dynamics of anthrax transmission, informing evidence-based strategies to mitigate future outbreaks. Policymakers and public health officials can leverage these findings to design targeted interventions such as improving access to veterinary services, safe handling of sick or moribund animals, promoting safe carcass disposal, and increasing disease awareness through community outreach. A nuanced understanding of global anthrax transmission drivers will facilitate the development of effective, localized public health strategies aimed at reducing the disease burden particularly in underserved populations.

METHODS

Search strategy and selection criteria

This meta-analysis followed preferred reporting for systematic reviews and meta-analysis (PRISMA) guidelines (Page et al., 2021). Two investigators (Muhammad Belal Hossain and Mariah Pearle Dee) independently conducted a comprehensive literature search across PubMed, Embase, Cochrane, Embase, Scopus, and Google Scholar for studies published between January 1900 and February 2025. Search terms included combinations such as “anthrax risk factors,” “anthrax outbreaks,” “risk factors for human anthrax,” and “anthrax case- control studies,” along with “odds ratio” and related terms to capture studies reporting risk estimates for human anthrax infection. Duplicate results were removed. Only peer-reviewed articles were included; conference abstracts and preprints were excluded from the analysis. The screening process involved two stages; First, titles and abstracts of retrieved citations were evaluated independently by both investigators to exclude irrelevant studies to anthrax. In the second stage, the full texts of potentially eligible studies were reviewed based on predefined criteria. Any disagreements were resolved through discussion or consultation with a third expert. Eligible studies were included if they met the following criteria: (1) involved human populations with anthrax infection, (2) reported confirmed or probable anthrax cases, (3) included case-control studies, (4) provided odds ratios (ORs) as risk estimates, and (5) were published in any language. The exclusion criteria included: (1) duplicates, (2) studies with incomplete data, (3) studies with fewer than three cases, (4) low-quality studies measured by Newcastle-Ottawa Scale (NOS < 7), and (5) studies focusing solely on animal anthrax cases. After rigorous screening, all studies included in the meta-analysis were synthesized, as presented in **Table 2.1**.

Data extraction and quality assessment

Extracted data included study characteristics (author, year, study design, location), population details (age, gender, sample size), exposure or risk factors, and reported outcomes, particularly ORs with 95% confidence intervals (CIs). The quality of each study included in the meta-analysis was independently assessed by two investigators according to the NOS (Stang, 2010). Studies scored above seven according to NOS were included for the analysis (**Table 2.2**).

Data Analysis

Meta-analysis was performed using Stata v18.0. The primary effect measure for dichotomous outcomes was the OR with a 95% CI, quantifying the association between risk factors and human anthrax infection. Heterogeneity was assessed using the Q statistic and I^2 index, with values classified as low (<25%), moderate (25-50%), or substantial (>50%). The ORs for each risk factor were pooled with the random-effects model because the studies included in this meta-analysis represented samples from different populations. Summary statistics were expressed as ORs and 95% CIs. Forest plots were generated using *meta forestplot* command in Stata to visualize pooled ORs and 95% CIs for each risk factor for the studies included in the analysis using a random-effects model. Sensitivity analyses were conducted by sequentially excluding individual studies to assess the robustness of pooled estimates. τ^2 quantified between-study variance, while I^2 indicated the proportion of variability due to heterogeneity. The H^2 measure reflected the ratio of total variance to sampling variance, with values >1 indicating more variability than expected by chance. The Cochran's Q test assessed variability among study results, with significant results ($P < 0.05$) indicating heterogeneity. Z statistic tested the significance of the overall pooled effect size (ES). Sensitivity analyses were performed to examine the robustness of the results by removing each study one at a time and recalculating the pooled OR, identifying any studies that significantly influenced the overall effect estimate. Publication bias was assessed using funnel plots for visual symmetry inspection. Begg's and Egger's tests were applied for statistical evaluation.

RESULTS

Our systematic search initially identified 3,292 records, which were reduced to 1,773 after removal of duplicates. Title and abstract screening excluded studies unrelated to anthrax,

yielding 404 articles for further review. After excluding letters, abstracts, conference proceedings, theses, and studies with incomplete data, 92 full-text articles were assessed for eligibility. Of these, 18 met the inclusion criteria and were retained for quantitative synthesis. The study selection process is outlined in **Figure 2.1**, with key characteristics of the included studies presented in **Table 2.1**. Most studies were conducted in Africa (n=12), Asia (n=4), and Europe (n=2). Importantly, not all 18 studies contributed data to every risk factor analysis; each meta-analysis was conducted using the subset of studies that reported extractable data for the specific exposure of interest. Only studies that provided outcome data stratified by exposure status (e.g., case vs control or exposed vs unexposed) were included in the corresponding pooled analyses.

Exposure to raw meat

The forest plot in **Figure 2.2** presents a meta-analysis evaluating the risk factor of "exposure to raw meat from infected animals" for anthrax infection in humans, based on data from 10 studies. The odds ratios (ORs) and 95% confidence intervals (CIs) for each study are displayed on the right. The pooled OR, represented by the diamond at the bottom, is 5.79 (95% CI: 4.04–8.31), indicating a significant association between exposure to raw meat from infected animals and an increased likelihood of anthrax infection ($p = < 0.0001$). There is no evidence of heterogeneity among the studies ($I^2 = 0\%$, $p = 0.70$), suggesting consistency across the study results. Notably, individual studies such as Nayak P (2019) and Freda A (2021) report high ORs of 14.50 and 16.00, respectively, highlighting a strong association in these settings. Studies like Chirundu D (2009) and Chowdhury S (2024) contributed significantly to the overall weight of the analysis, as evidenced by their precise estimates, as indicated by the larger squares representing their weight in the forest plot. Overall, the meta-analysis demonstrates a robust and significant link between exposure to raw meat from infected animals and the increased odds of anthrax infection.

Skinning of slaughtered animal

The forest plot in **Figure 2.3** presents a meta-analysis of the risk factor "skinning of slaughtered/infected animals" for human anthrax infection, summarizing data from five studies. The pooled OR is 5.64 (95% CI: 3.73–8.52), indicating a significant association between skinning infected animals and an increased risk of anthrax infection ($p = 0.00$). The analysis shows no significant heterogeneity ($I^2 = 0\%$, $p = 0.94$), suggesting that the study results are

highly consistent across regions. Studies such as Freda A (2021) and Chowdhury S (2024) contributed the most weight to the overall effect estimate, as reflected by their larger square sizes, with ORs of 5.00 and 6.01, respectively. Chadambuka A (2017) reported a higher OR of 8.90, but with a wider confidence interval, indicating more variability in that study. Overall, this meta-analysis underscores the strong association between skinning infected or moribund animals and the increased risk of anthrax infection in humans.

Butchering of slaughtered animal

The forest plot in **Figure 2.4** presents a meta-analysis of the risk factor "butchering of slaughtered or infected animals" for anthrax infection in humans, based on data from five studies. The pooled OR is 6.54 (95% CI: 3.26–13.09), indicating a significant association between butchering infected animals and an increased risk of anthrax infection ($p = < 0.0001$). The heterogeneity is moderate ($I^2 = 30.41\%$, $p = 0.19$), suggesting some variability across the studies, but it is not substantial. Significant contributions came from Freda A (2021) and Mwenye KS (1996), with ORs of 22.00 and 29.00, respectively, indicating a very high risk in these studies, though Mwenye KS had a larger confidence interval, reflecting greater uncertainty. Studies such as Gombe NT (2010) and Chadambuka A (2017) reported lower ORs but still demonstrate significant risks. Overall, this meta-analysis emphasizes a strong positive association between butchering infected or moribund animals and the likelihood of contracting anthrax in humans.

Slaughtering or presence during slaughtering of animal

A total of five studies were included in the meta-analysis to assess the OR for the risk factor 'slaughtering or presence at slaughtering site of an infected animal' and human anthrax case (**Figure 2.5**). The pooled OR from a random-effects model was 5.16 (95% CI: 2.54, 10.49), indicating that individuals involved in slaughtering or present at the slaughtering site of an infected animal were more than five times as likely to contract anthrax compared to those who were not exposed. The studies included in the analysis showed some variability in the ES. Navdarashvili A (2016) reported an OR of 7.30 (95% CI: 2.92-18.24), contributing 24.21% weight to the pooled analysis. Brian K (2023) found a notably higher OR of 51.00 (95% CI: 4.24-613.87), though it contributed a smaller weight (6.78%) due to the wide confidence interval. Migisha R (2010) reported an OR of 5.74 (95% CI: 1.39- 23.75), contributing 15.46% weight.

Chowdhury S (2024) estimated an OR of 2.29 (95% CI: 1.30-4.03), contributing the highest weight (32.37%) to the overall ES. Kwizera P (2024) reported an OR of 5.30 (95% CI: 1.84-15.30), contributing 21.29% weight to the overall ES. The heterogeneity among studies was substantial with an I^2 value of 54%, and a τ^2 of 0.32, suggesting that the variability in ESs is likely due to differences in study populations, study sites, methodologies, and/or other factors. The Q-test for heterogeneity was significant ($Q(3) = 9.93$, $p = 0.04$), further confirming the presence of heterogeneity among the studies. However, the test for overall effect size (z-test) was statistically significant ($z = 4.53$, $p = 0.00$), confirming the robustness of the pooled OR.

Handling of carcasses or animal by-products

Six studies were included in the meta-analysis to evaluate the effect of handling carcasses or animal by-products as a risk factor for anthrax infection. The pooled estimate from the random-effects model was 4.13 (95% CI: 2.88–5.92), indicating that individuals involved in handling infected carcasses or animal by-products were almost four times more likely to contract anthrax compared to those who did not engage in such activities (**Figure 2.6**). The effect sizes varied among the studies. Freda A (2021) reported an effect size of 6.90 (95% CI: 2.99–15.93), contributing 16.41% of the weight to the pooled estimate. Kasradze A (2018) found an effect size of 4.36 (95% CI: 2.61–7.27), contributing the largest weight to the overall estimate at 35.45%. Mwenye KS (1996) reported an effect size of 5.00 (95% CI: 0.90–27.84), contributing the lowest weight at 4.26%, due to the wide confidence interval. Nigusse A (2021) reported an effect size of 3.22 (95% CI: 1.71–6.08), contributing 25.57% to the overall estimate. Makurumidze R (2021) found an effect size of 1.80 (95% CI: 0.69–4.70), contributing 12.68% to the pooled estimate. Kwizera P (2024) reported an effect size of 11.00 (95% CI: 2.59–46.77), contributing 5.91% of the weight. The heterogeneity among studies was low, with an I^2 value of 13% and a τ^2 of 0.03, suggesting minimal variability in the effect sizes across the included studies. The Q-test for heterogeneity was not statistically significant ($Q(4) = 6.76$, $p = 0.24$), confirming low heterogeneity. The overall ES was statistically significant, as indicated by the z-test ($z = 7.70$, $p = 0.00$), demonstrating a strong association between handling carcasses or animal by-products from infected animals and the risk of anthrax infection.

Socio-economic and cultural factors

Across the six studies reviewed, several individual risk factors for anthrax infection were identified, however, differences in how these variables were defined and the small number of studies per factor prevented grouped analysis. One study reported that being male was associated with higher risk, while two studies identified age (under 20 years) as a significant factor for contacting anthrax. Two studies also found that religious or cultural permission to consume potentially contaminated meat increased risk, and one study reported that attending social gatherings was linked to infection. For some risk factors like skinning, slaughtering, or being present during slaughter, too few studies were available to draw meaningful conclusions or conduct meta-analysis. Only one study reported associations with chronic health conditions such as obesity, hypertension, smoking, and alcohol use. A few other factors such as living near pastoralist routes, buying beef from informal butcheries, or recent travel to an outbreak area, were each reported by a single study and could not be grouped with others. These gaps highlight the need for more consistent data collection and reporting in future anthrax outbreak investigations.

DISCUSSION

This meta-analysis provides comprehensive assessment of significant associations between various exposure-related risk factors and the likelihood of anthrax infection in humans. Our findings highlight the critical public health implications of activities involving raw meat and animal handling particularly in regions where anthrax is endemic. The pooled OR of 5.79 (95% CI: 4.04-8.31) for exposure to raw meat from infected animals indicates a substantial risk factor for anthrax infection, consistent with findings from previous studies (Aceng et al., 2021; Nayak et al., 2019). The absence of heterogeneity among the studies ($I^2 = 0\%$, $p = 0.70$) reinforces the validity of these findings suggesting that the risk associated with consuming raw meat is a widespread issue across regions.

Individual studies such as those by Nayak (2019) and Freda (2021), reported elevated odds ratios of 14.50 and 16.00 respectively, indicating that certain populations may face even greater risks due to localized factors, such as cultural practices and limited access to veterinary services (Chowdhury et al., 2024). These results align with previous research that identified dietary practices and lack of awareness as key contributors to anthrax risk (Migisha et al., 2021). Public

health interventions must therefore focus on educating communities about the dangers of handling and consuming raw meat from potentially infected animals.

Our analysis of skinning and butchering infected animals revealed significant associations with anthrax infection with pooled ORs of 5.64 (95% CI: 3.73-8.52) and 6.54 (95% CI: 3.26-13.09), respectively. The low heterogeneity for skinning ($I^2 = 0\%$, $p = 0.94$) and moderate heterogeneity for butchering ($I^2 = 30.41\%$, $p = 0.19$) suggest that while the risk from these activities remain consistent, certain contextual factors such as education, access to personal protective equipment (PPE), and local regulations may modulate the risk. Studies from Freda (2021) and Mwenye (1996) reported exceptionally high ORs (22.00 and 29.00), emphasizing the urgent need for improved safety practices among butchers or people involved with skinning and butchering of an infected livestock (Aceng et al., 2021; Mwenye et al., 1996). Previous research has similarly highlighted the risks faced by individuals engaged in slaughtering and butchering infected animals (Islam et al., 2021; Kasradze et al., 2018). Enhanced biosecurity training, implementation of personal protective measures, and rigorous regulatory oversight are essential steps to mitigate these risks. Our findings indicate that being present during the slaughtering of infected animals significantly increases the risk of anthrax infection, with a pooled OR of 5.16 (95% CI: 2.54-10.49). The substantial heterogeneity among studies ($I^2 = 54\%$, $\tau^2 = 0.32$) suggests variability in effect sizes due to differences in populations, methodologies, and other factors. The exceptionally high OR reported by Kibwika (2023), along with others, suggests that certain contexts pose heightened risks (Kibwika et al., 2023). This finding points to the necessity of educating individuals about the dangers of slaughtering moribund/infected animals and enforcing biosecurity measures at slaughterhouses and during communal slaughter events (Chadambuka et al., 2017).

Handling carcasses and animal by-products also represents a critical risk factor, with a pooled OR of 4.13 (95% CI: 2.88-5.92) further underscoring the danger posed by exposure to infected carcasses and animal by-products. The low heterogeneity among studies ($I^2 = 13\%$) strengthens these findings, indicating that the risk associated with handling contaminated materials is universally applicable (Nigusse et al., 2023). These results highlight the need for stringent hygiene protocols and protective measures for individuals involved in handling carcasses of unknown causes of death. Community health programs should focus on educating these

individuals about proper handling techniques and the critical importance of using PPE to prevent infection, echoing recommendations from previous studies (Islam et al., 2021; Kasradze et al., 2018; Subedi et al., 2024). Importantly, our study advances understanding by statistically synthesizing evidence across regions and eco-epidemiological contexts, offering a more precise estimate of risk magnitude. This level of quantification enables stronger, evidence-based, and data-driven justification for intervention strategies. Moreover, our findings emphasize the global relevance/universality of this risk, cutting across endemic zones, occupational group and outbreak conditions, thereby, reinforcing the need for globally standardized hygiene protocols and prevention guidelines. Community health programs should prioritize educational outreach on safe carcass handling, the use of PPE, and the avoidance of contact with animals found dead from unknown causes. These results not only bolster earlier findings but also extend them by consolidating fragmented evidence into robust, actionable framework, enabling more targeted and science-backed public health messaging in endemic and at-risk regions.

Although a wide range of risk factors have been associated with anthrax infection, our meta-analysis focused specifically on direct exposure-related factors. Socio-demographic and behavioral variables such as age, sex, religious permission, and participation in social gatherings were excluded from the pooled analysis due to substantial variability across studies, incomparable measurement, and insufficient number of contributing studies (fewer than three per factor). As a result, these factors were not incorporated in the quantitative synthesis. These variables represent distinct social or cultural practices rather than comparable exposures, often reflect culturally specific practices or population-level dynamics, rather than discrete and quantifiable exposure. As such, these factors were narratively described rather than pooled in the meta-analysis. This approach ensures that the meta-analysis reflects methodologically consistent risk factors that are directly linked to anthrax transmission pathways such as handling or consuming raw meat, butchering, or slaughtering moribund infected animals. Previous studies have shown that individuals engaged in livestock management often lack awareness of anthrax risks which further heightens their susceptibility (Migisha et al., 2021). Thus, public health initiatives should focus on educational efforts that consider socio-economic contexts, improving access to veterinary services and resources for at-risk populations.

While the findings from this meta-analysis are robust, certain limitations need to be acknowledged. Variability in methodologies, spatio-temporality of the studies, and reliance on self-reported data may influence the reliability of the results. Publication bias remains a potential concern, particularly given the tendency for studies with non-significant results to remain unpublished. To address this, we conducted publication bias diagnostics using funnel plots and statistical tests. Although, a minor asymmetry was observed likely due to inclusion of small number of studies, we did not find strong evidence of public bias, supporting the overall reliability of the pooled estimates. Furthermore, the evolving nature of anthrax epidemiology necessitates continuous surveillance and research to identify trends and emerging risk factors especially on injectional anthrax, a rare but serious form of anthrax observed among people who inject drugs, resulting from direct inoculation of anthrax spores into deep tissue (Palmateer et al., 2012). Longitudinal studies assessing the impact of public health interventions on reducing anthrax incidence will provide valuable insights into future effective prevention strategies.

This meta-analysis advances current understanding by quantifying the strength of associations between specific exposure-related risk factors and anthrax infection across diverse geographic and epidemiological contexts. Our pooled synthesis highlights the relative magnitude of animal husbandry and occupational behaviors, such as handling raw meat or participation of animal slaughter in a group, and butchering activities, offering a clearer evidence base for prioritizing targeted public health intervention to mitigate the risk. By pointing out six distinct exposure activities, all of which showed significant associations, this study allows for differentiation of high-risk practices, enabling more focused risk communication and behavioral messaging. Notably, the consistency of these association across varied ecological settings emphasize the global relevance of these findings and reinforces the value of cross-sectoral One Health strategies. The analysis also reveals critical gaps in the literature, particularly the insufficient and heterogenous reporting of socio-demographic and behavioral variables, which limited quantitative synthesis for those domains. To address these limitations, we will require more standardized epidemiological study designs, structured outbreak and case investigations, improved surveillance methods, and enhanced data collection frameworks. By prioritizing educational campaigns, enhancing safety practices, and providing socio-economic support, we can effectively reduce the incidence of anthrax infections and safeguard vulnerable communities from this preventable zoonotic disease.

REFERENCES

- Aceng, F. L., Ario, A. R., Alitubeera, P. H., Neckyon, M. M., Kadobera, D., Sekamatte, M., . . . Zhu, B. P. (2021). Cutaneous anthrax associated with handling carcasses of animals that died suddenly of unknown cause: Arua District, Uganda, January 2015-August 2017. *PLoS Negl Trop Dis*, 15(8), e0009645. doi:10.1371/journal.pntd.0009645
- Barandongo, Z. R., Dolfi, A. C., Bruce, S. A., Rysava, K., Huang, Y. H., Joel, H., ... & Turner, W. C. (2023). The persistence of time: the lifespan of *Bacillus anthracis* spores in environmental reservoirs. *Research in Microbiology*, 174(6), 104029.
- Beyer, W., & Turnbull, P. C. (2009). Anthrax in animals. *Mol Aspects Med*, 30(6), 481-489. doi:10.1016/j.mam.2009.08.004
- Biswas, P. K., Islam, M. Z., Shil, S. K., Chakraborty, R. K., Ahmed, S. S., & Christensen, J. P. (2012). Risk factors associated with anthrax in cattle on smallholdings. *Epidemiol Infect*, 140(10), 1888-1895. doi:10.1017/s0950268811002408
- Bodenham, R. F., Mtui-Malamsha, N., Gatei, W., Woldetsadik, M. A., Cassell, C. H., Salyer, S. J., . . . Fasina, F. O. (2021). Multisectoral cost analysis of a human and livestock anthrax outbreak in Songwe Region, Tanzania (December 2018-January 2019), using a novel Outbreak Costing Tool. *One Health*, 13, 100259. doi:10.1016/j.onehlt.2021.100259
- Carlson, C. J., Getz, W. M., Kausrud, K. L., Cizauskas, C. A., Blackburn, J. K., Bustos Carrillo, F. A., . . . Stenseth, N. C. (2018). Spores and soil from six sides: interdisciplinarity and the environmental biology of anthrax (*Bacillus anthracis*). *Biol Rev Camb Philos Soc*, 93(4), 1813-1831. doi:10.1111/brv.12420
- Carlson, C. J., Kracalik, I. T., Ross, N., Alexander, K. A., Hugh-Jones, M. E., Fegan, M., . . . Blackburn, J. K. (2019). The global distribution of *Bacillus anthracis* and associated anthrax risk to humans, livestock and wildlife. *Nature Microbiology*, 4(8), 1337-1343. doi:10.1038/s41564-019-0435-4
- Chadambuka, A. (2017). Risk factors for contracting anthrax in Ntabeni South ward of Kwekwe District, Zimbabwe, 2016. *Texila International Journal of Public Health*, 5(4), 1-10.

- Chakraborty, A., Khan, S. U., Hasnat, M. A., Parveen, S., Islam, M. S., Mikolon, A., . . . hygiene. (2012). Anthrax outbreaks in Bangladesh, 2009–2010. 86(4), 703.
- Chowdhury, S., Islam, M. S., Haider, N., Hossain, M. B., Alam, M. A., Sharif, M. A. R., . . . Haque, F. (2024). Risk factors associated with cutaneous anthrax outbreaks in humans in Bangladesh. 12. doi:10.3389/fpubh.2024.1442937
- Driciru, M., Rwego, I. B., Ndimuligo, S. A., Travis, D. A., Mwakapeje, E. R., Craft, M., . . . Pelican, K. (2020). Environmental determinants influencing anthrax distribution in Queen Elizabeth Protected Area, Western Uganda. PLoS One, 15(8), e0237223. doi:10.1371/journal.pone.0237223
- Gurbanov, S., & Akhmedova, S. (2010). Especially dangerous infections in Azerbaijan. In Emerging and Endemic Pathogens: Advances in Surveillance, Detection and Identification (pp. 39-43): Springer.
- Islam, M. S., Hasan, S. M. M., Salzer, J. S., Kadzik, M., Haque, F., Haider, N., . . . Gurley, E. S. (2021). Human exposures to by-products from animals suspected to have died of anthrax in Bangladesh: An exploratory study. Transbound Emerg Dis, 68(4), 2514-2520. doi:10.1111/tbed.13921
- Islam, M. S., Hossain, M. J., Mikolon, A., Parveen, S., Khan, M. S., Haider, N., . . . Luby, S. P. (2013). Risk practices for animal and human anthrax in Bangladesh: an exploratory study. Infect Ecol Epidemiol, 3. doi:10.3402/iee.v3i0.21356
- Kasradze, A., Echeverria, D., Zakhshvili, K., Bautista, C., Heyer, N., Imnadze, P., & Mirtskhulava, V. (2018). Rates and risk factors for human cutaneous anthrax in the country of Georgia: National surveillance data, 2008-2015. PLoS One, 13(2), e0192031. doi:10.1371/journal.pone.0192031
- Kibwika, B., Namulondo, E., Aanyu, D., Nuwamanya, Y., Rek, J., Kiza, D., . . . Komugishai, M. Anthrax outbreak associated with handling and consuming meat from animals that died suddenly, Ibanda District, Uganda, May 2023.

- Kracalik, I., Abdullayev, R., Asadov, K., Ismayilova, R., Baghirova, M., Ustun, N., . . . Blackburn, J. K. J. P. n. t. d. (2014). Changing patterns of human anthrax in Azerbaijan during the post-Soviet and preemptive livestock vaccination eras. 8(7), e2985.
- Kracalik, I. T., Malania, L., Tsertsvadze, N., Manvelyan, J., Bakanidze, L., Imnadze, P., . . . Blackburn, J. K. J. P. n. t. d. (2013). Evidence of local persistence of human anthrax in the country of Georgia associated with environmental and anthropogenic factors. 7(9), e2388.
- Migisha, R., Mbatidde, I., Agaba, D. C., Turyakira, E., Tumwine, G., Byaruhanga, A., . . . Kirunda, H. (2021). Risk factors for human anthrax outbreak in Kiruhura District, Southwestern Uganda: a population-based case control study.
- Mugo, B. C., Lekopien, C., & Owiny, M. (2021). 'We dry contaminated meat to make it safe': An assessment of knowledge, attitude and practices on anthrax during an outbreak, Kisumu, Kenya, 2019. PLoS One, 16(11), e0259017. doi:10.1371/journal.pone.0259017
- Mwenye, K. S., Siziya, S., & Peterson, D. (1996). Factors associated with human anthrax outbreak in the Chikupo and Ngandu villages of Murewa district in Mashonaland East Province, Zimbabwe. Cent Afr J Med, 42(11), 312-315.
- Nayak, P., Sodha, S. V., Laserson, K. F., Padhi, A. K., Swain, B. K., Hossain, S. S., . . . Dash, K. C. (2019). A cutaneous Anthrax outbreak in Koraput District of Odisha-India 2015. BMC Public Health, 19(3), 470. doi:10.1186/s12889-019-6787-0
- Ndolo, V. A., Redding, D. W., Lekolool, I., Mwangangi, D. M., Odhiambo, D. O., Deka, M. A., . . . Wood, J. L. N. (2022). Drivers and potential distribution of anthrax occurrence and incidence at national and sub-county levels across Kenya from 2006 to 2020 using INLA. Scientific Reports, 12(1), 20083. doi:10.1038/s41598-022-24589-5
- Nigusse, A. T., Amaha, M. H., Hailu, T. T., Gebremariam, H. G., Cazzoletti, L., Zanolin, M. E., . . . Alemayohu, M. A. (2023). Human anthrax outbreak and associated factors in the horrific siege of Tigray, Ethiopia. IJID One Health, 1, 100013. doi:https://doi.org/10.1016/j.ijidoh.2023.100013

- Page, M. J., Moher, D., Bossuyt, P. M., Boutron, I., Hoffmann, T. C., Mulrow, C. D., . . . McKenzie, J. E. (2021). PRISMA 2020 explanation and elaboration: updated guidance and exemplars for reporting systematic reviews. *BMJ*, 372, n160. doi:10.1136/bmj.n160
- Palmateer, N. E., Ramsay, C. N., Browning, L., Goldberg, D. J., & Hutchinson, S. J. (2012). Anthrax infection among heroin users in Scotland during 2009-2010: a case-control study by linkage to a national drug treatment database. *Clin Infect Dis*, 55(5), 706-710. doi:10.1093/cid/cis511
- Stang, A. (2010). Critical evaluation of the Newcastle-Ottawa scale for the assessment of the quality of nonrandomized studies in meta-analyses. *Eur J Epidemiol*, 25(9), 603-605. doi:10.1007/s10654-010-9491-z
- Subedi, D., Pantha, S., Jyoti, S., Gautam, B., Kaphle, K., Yadav, R. K., . . . Dhakal, S. (2024). Anthrax in Humans, Animals, and the Environment and the One Health Strategies for Anthrax Control. *Pathogens*, 13(9). doi:10.3390/pathogens13090773
- Swartz, M. N. (2001). Recognition and Management of Anthrax — An Update. 345(22), 1621-1626. doi:doi:10.1056/NEJMr012892
- Traxler, R. M., Napetvaridze, T., Asanishvili, Z., Geleishvili, M., Rukhadze, K., Maghlakelidze, G., . . . Reynolds, D. (2019). Knowledge, attitudes, and practices related to anthrax and animal care: A case-control study in Georgia. *PLoS One*, 14(10), e0224176.

APPENDIX II

TABLES

Table 2.1 Characteristics of included studies on risk factors associated with human anthrax infection

Sl. #	Study	Study design	Population & type of infection	Country	Main findings	Analysis methods	Remarks
1	Freda A 2021	Case-control	Cutaneous anthrax	Uganda	Skinning: 5 (2.3-11), butchering: 22 (5.5-89), carrying carcass of livestock: 6.9 (3-16)	Logistic regression	
2	Nayak P 2019	Case-control	Cutaneous anthrax	India	Eating meat of ill cattle (OR: 14.5, 95% CI: 1.4–85.7) and with close handling of carcasses of ill animals such as burying, skinning, or chopping (OR: 342, 95% CI: 40.5–1901.8). Significant associations between eating and handling ill animals and presence of anthrax-like organisms in cutaneous lesions.	Logistic regression	3 human deaths, CFR 4%
3	Ana K 2018	Retrospective analysis of surveillance data	Cutaneous anthrax	Georgia	Handling animal products (aOR 4.36, 95% CI 2.61–7.26) and living near pastoralist routes (aOR 2.74, 95%CI 1.57–4.76) were associated with cutaneous anthrax	Multiple logistic regression	8 years data: 2008-15

Table 2.1 continued

4	Traxler R 2019	Descriptive statistics & matched case-control	Cutaneous	Georgia	Cases had lower odds of burying a suddenly dead animal compared to all controls (Odds Ratio [OR]: 0.32, 95% Confidence interval [CI]:0.12, 0.88) and area controls (OR: 0.32, 95% CI: 0.11, 0.91). Cases had higher odds of ever having human anthrax or knowing another person who had anthrax compared to all controls (OR: 4.56, 95% CI: 1.45, 14.30) and area controls (OR: 7.16, 95% CI: 1.52, 33.80).	Conditional logistic regression	
5	Makurumidze R 2021	Outbreak investigation & case-control	Cutaneous	Zimbabwe	Multivariable analysis demonstrated that meat sourced from other villages [vs butchery, OR = 15.21, 95% CI (2.32–99.81)], skinning [OR = 4.32, 95% CI (1.25–14.94)], and belonging to religions that permit eating meat from cattle killed due to unknown causes or butchered after unobserved death [OR = 6.12, 95% CI (1.28–29.37)] were associated with contracting anthrax	Multivariate unconditional logistic regression	

Table 2.1 continued

6	Gombe N 2010	Case-control	Cutaneous	Zimbabwe	Eating contaminated meat (OR = 7.7, 95% CI 2-29.8), belonging to a household with cattle deaths (OR= 9.7, 95% CI 2.9-33), assisting with skinning anthrax infected carcasses (OR= 5.4(95% CI 1.7-17), assisting with meat preparation for drying (OR = 5(95%CI 1.9-13.9), assisting with cutting contaminated meat (OR = 4.8(95% CI 1.7-13.2), having cuts or wounds during skinning (OR = 19.5, 95% CI 2.4-159) and belonging to a village with cattle deaths (OR = 6.5(95%CI 1.3-32) were significantly associated with anthrax	Logistic regression	
7	Kutmanova A 2022	Retrospective chart review	Meningitis anthrax	Kyrgyzstan	Underlying medical conditions, such as obesity 10.5 (4.1–26.9), hypertension 18.1 (5.5–59.6), and COPD 2.7 (1.1–6.4), diabetes 13.7 (2.3–∞), and tobacco and alcohol use, as potential risk factors for severe anthrax and anthrax meningitis	Logistic regression	
8	Migisha R 2021	Case-control	Cutaneous	Uganda	slaughtering of anthrax infected animals (aOR=5.74;	Logistic regression	

Table 2.1 continued

					95%CI: 1.39-23.8), consuming of anthrax infected meat (aOR=6.4; 95%CI: 1.53- 6.7) and being male (aOR=12.8; 95%CI: 3.31-49.1)		
9	Dhliwayo TH 2022	Descriptive statistics, case-control	Cutaneous & gastrointestinal	Zimbabwe	Independent risk factor for contracting anthrax was eating under-cooked meat (aOR = 12.2, 95% CI: 1.41-105.74, p = 0.023)	Multivariate logistic regression	
10	Wondmnew T 2023	Case-control	Cutaneous	Ethiopia	The probability of developing anthrax among people who had unvaccinated animals was higher than in those who didn't have unvaccinated animals with an AOR = 8.113 (95% CI 1.685-39.056) and the probability of getting anthrax in relation to people's awareness of anthrax was AOR = 0.114 (95% CI 0.025-0.524)	Logistic regression	
11	Brian K 2023	Case-control	Cutaneous & gastrointestinal	Uganda	Consuming meat of an animal that died suddenly (AOR 22.3 CI 3.5-139), slaughtering animal that died suddenly (AOR 51 CI 4.2-608.5)	Multivariate logistic regression	
12	Mwakapeje ER 2018	Case-control	Cutaneous	Tanzania	In the younger group (1-20 years), the odds of being infected were 25 times higher in the	Logistic regression	

Table 2.1 continued

					exposed group compared to the unexposed (OR= 25, 95% CI = 1.5-410). The odds of exposure in the old group (≥ 20 years) were three times lower in the exposed group compared to the unexposed (OR = 3.2, 95% CI = 1.28-8.00). age-group, sleeping on animal's skins, contacting with infected carcasses through skinning and butchering, and not having formal education were linked to exposure for anthrax		
13	Nigusse AT 2023	Case-control	Cutaneous, gastrointestinal, & inhalation	Ethiopia	Being less than 15 years old (AOR = 21.34; 95% CI 8.67-52.5), eating sick animal raw meat (AOR = 5.49; 95% CI: 1.18-25.66), having a sick person in the household (AOR = 2.07 95% CI:1.13-3.76), bringing meat of sick animal 1.87 (1.04-3.35), expose to animal by-products 3.22 (1.71-6.09). On the other hand, burying and burning sick or dead animals showed a protective effect (AOR = 0.48; 95% CI: 0.23–0.98)	Multivariate logistic regression	8 human deaths

Table 2.1 continued

14	Chadambuka A 2017	Case-control	Cutaneous	Zimbabwe	Skinning OR = 8.9 (95% CI 2.32-33.8) and butchering OR = 3.2 (95% CI 1.07-9.58). Not handling anthrax infected carcasses was protective OR = 0.06 (95% CI 0.01-0.3), having no cuts OR = 0.04 (95%CI 0.003-0.28) and having no cattle deaths in the household OR = 0.12 (95% CI 0.03-0.45)	Logistic regression	
15	Lonogan K 2017	Case-control	Gastrointestinal	Philippines	Twenty-nine suspect cases were identified. All ate meat of dead water buffalo. Majority (15, 52%) were males. Age ranges from 6-77 years (Median: 17). Eating uncooked meat of dead animal (AOR=6, 95% CI:1.7-18.4) was a risk factor	Multivariate logistic regression	
16	Chowdhury S 2024	Outbreak investigation & case-control	Cutaneous & gastrointestinal	Bangladesh	Persons who had a cut injury (aOR 19.04, CI: 4.08–88.86), weighed raw meat (aOR 5.73, CI: 3.03–10.83), mixed bones and meat (aOR 4.64, CI: 3.03–7.09), observed livestock slaughtering (aOR 2.86, CI: 2.02–4.04), had direct contact to an anthrax suspected livestock (aOR 2.68, CI:1.61–4.45),	Multivariate logistic regression	

Table 2.1 continued

					slaughtered livestock (aOR 2.29, CI: 1.3–4.02), and who did not wash hands with soap and water after direct contact (aOR 2.57, CI: 1.89–3.5)		
17	Nakanwagi M 2020	Case-control	Gastrointestinal	Uganda	Ate beef purchased exclusively from butchery during the week before illness onset (MOR = 46, 95%CI = 4.7–446); 8.0% of case-patients and 3.0% of controls ate beef purchased from butchery and elsewhere (MOR = 19, 95%CI = 1.0–328)	Conditional logistic regression	
18	Kwizera P 2024	Case-control	Cutaneous	Uganda	People who slept on the hides of animals (OR=11, 95% CI:2.6-47) and those who were involved in slaughter (OR=5.3,95%CI:1.8-15). There was a dose-response effect for persons who slaughtered, skinned and carried (OR=19, 95% CI:2.6-136), slaughtered and carried (OR=13,95%CI:2.2-78) and those who slaughtered and skinned (OR=8.1,95%CI:2.1-31).	Logistic regression	

Table 2.2 Newcastle-Ottawa Quality Assessment table for included studies

Study	Selection	Comparability	Outcome	Total	Quality of the study
Freda A 2021	***	**	***	8	High
Nayak P 2019	***	**	***	8	High
Ana K 2018	***	**	***	8	High
Traxler R 2019	***	***	***	9	High
Makurumidze R 2021	***	**	***	8	High
Gombe N 2010	***	***	***	9	High
Kutmanova A 2022	***	**	***	8	High
Migisha R 2021	***	**	***	8	High
Dhliwayo TH 2022	***	**	***	8	High
Wondmnew T 2023	***	**	**	7	High
Brian K 2023	***	**	***	8	High
Mwakapeje ER 2018	***	***	***	9	High
Nigusse AT 2023	***	***	***	9	High
Chadambuka A 2017	***	***	***	9	High
Lonogan K 2017	***	**	***	8	High
Chowdhury S 2024	***	**	***	8	High
Nakanwagi M 2020	***	**	***	8	High
Kwizera P 2024	***	**	***	8	High

*Each star indicates a point for each component. One study can obtain a maximum of four, two and three stars for each component (selection, comparability, outcomes) respectively. Study with a total score of 7 or higher are considered as high-quality studies, and those lower than 5 are considered as low-quality studies.

FIGURE

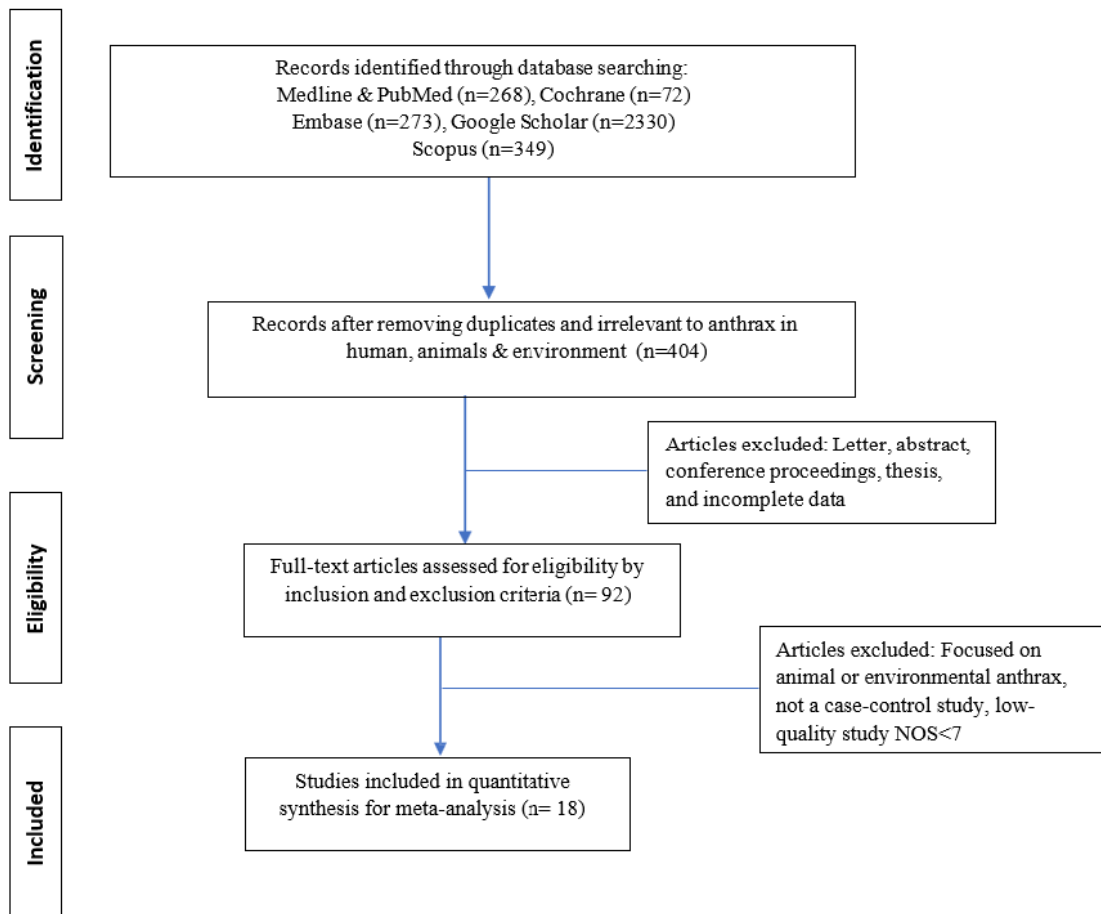
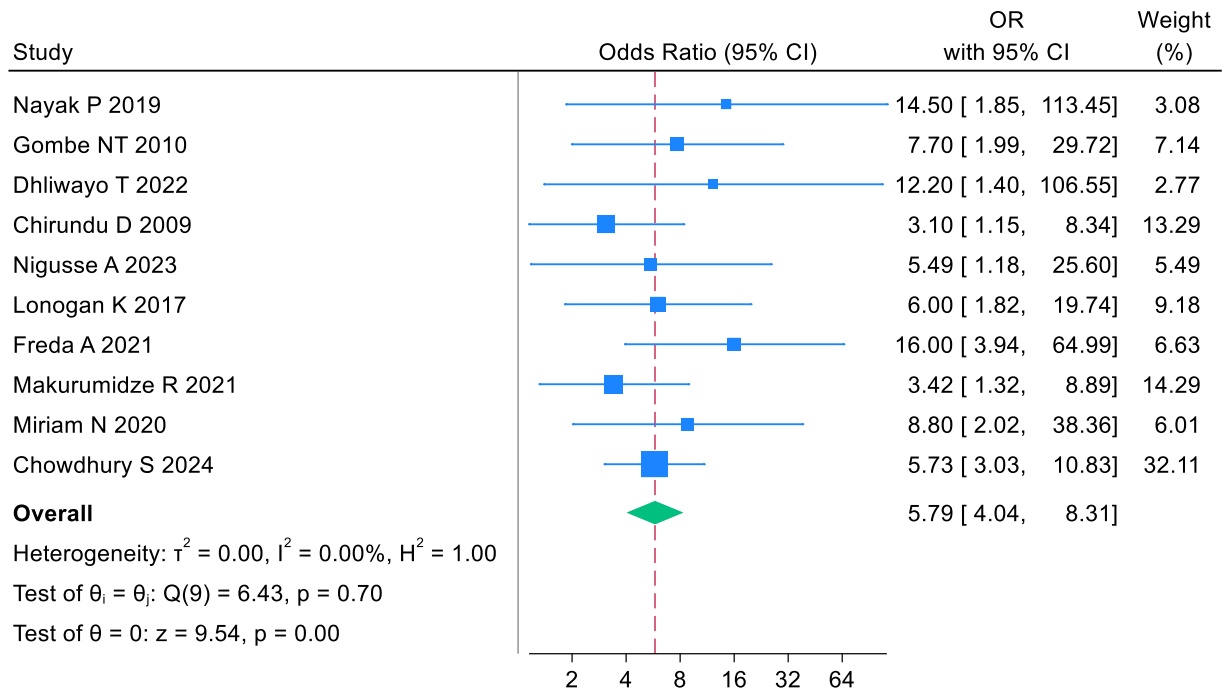


Figure 2.1. PRISMA diagram showing selection of articles for the meta-analysis



Random-effects REML model

Figure 2.2. Forest plot showing associations between exposure to raw meat and anthrax infection in humans

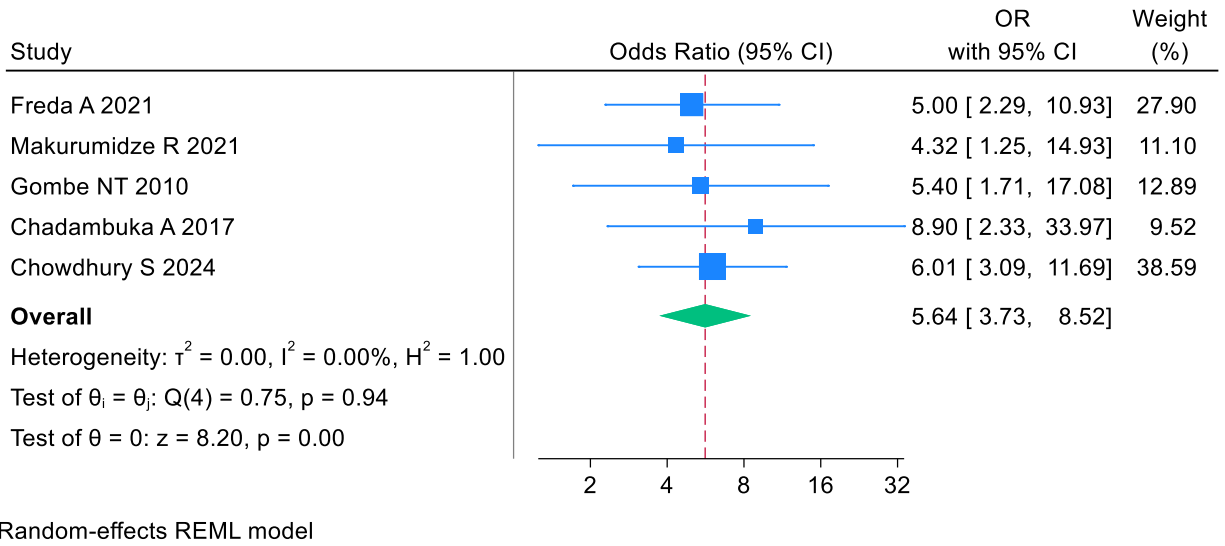


Figure 2.3. Forest plot showing associations between skinning sick or moribund animals and anthrax infection in humans

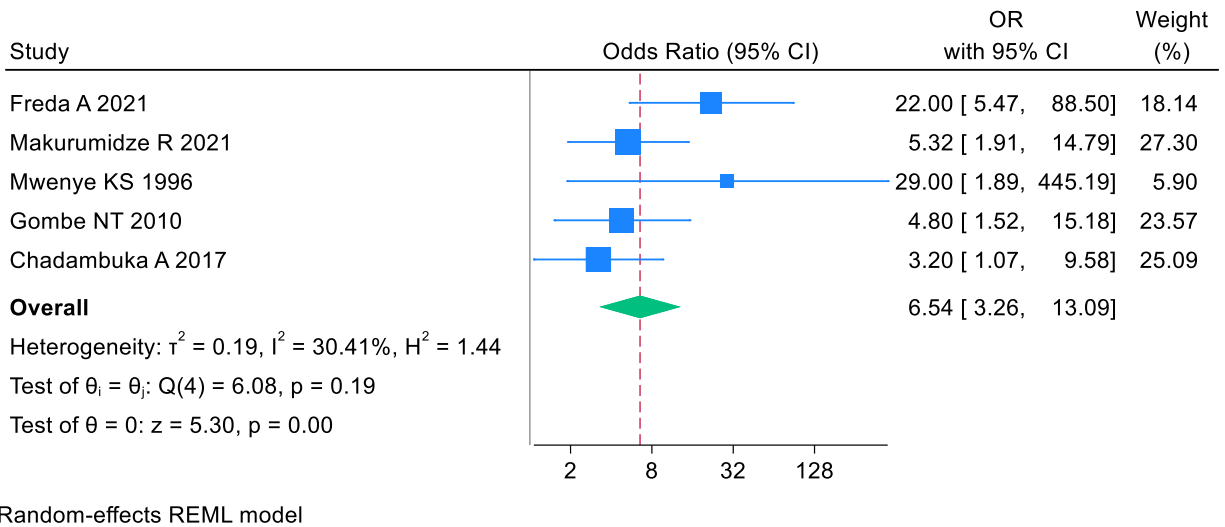


Figure 2.4. Forest plot showing associations between butchering sick or moribund animals and anthrax infection in humans

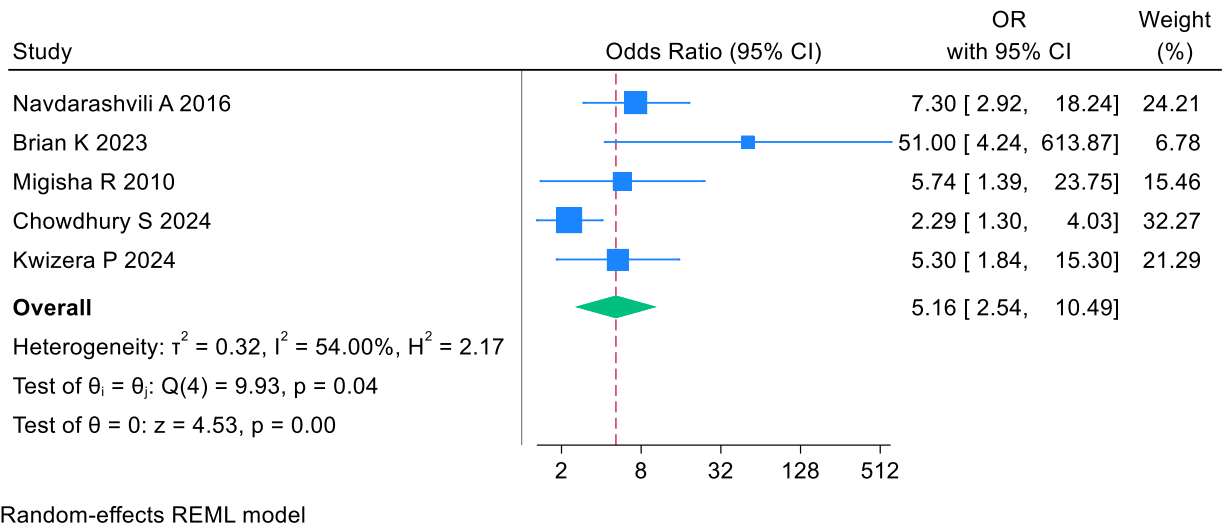


Figure 2.5. Forest plot showing associations between slaughtering or presence at slaughtering time of sick or moribund animals and anthrax infection in humans

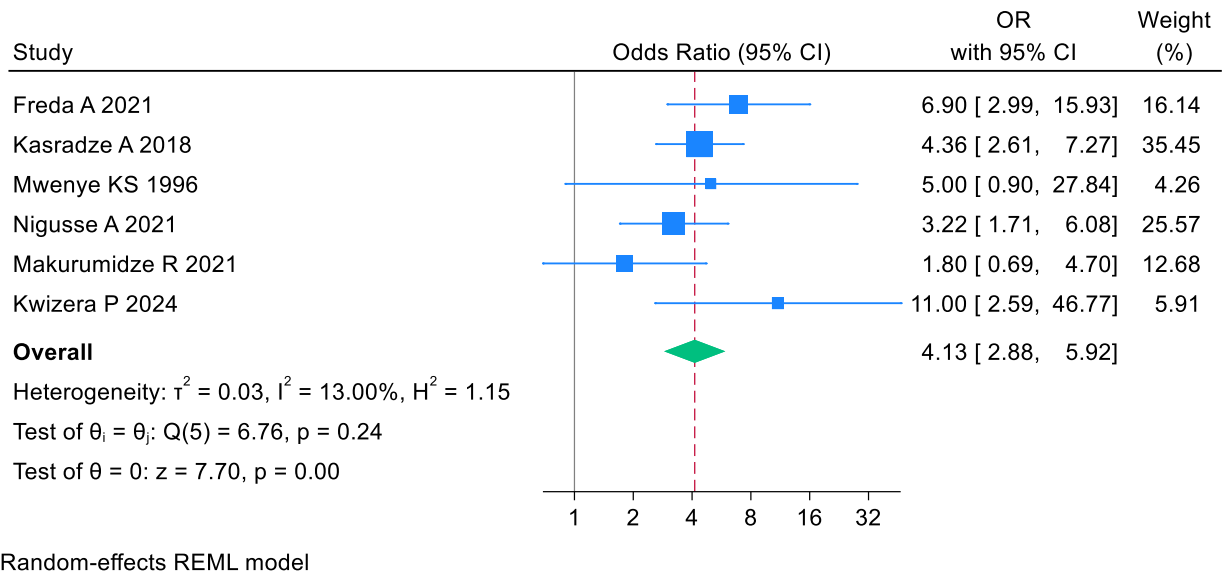


Figure 2.6. Forest plot showing associations between handling of carcass or animal by-products of sick or moribund animals and anthrax infection in humans

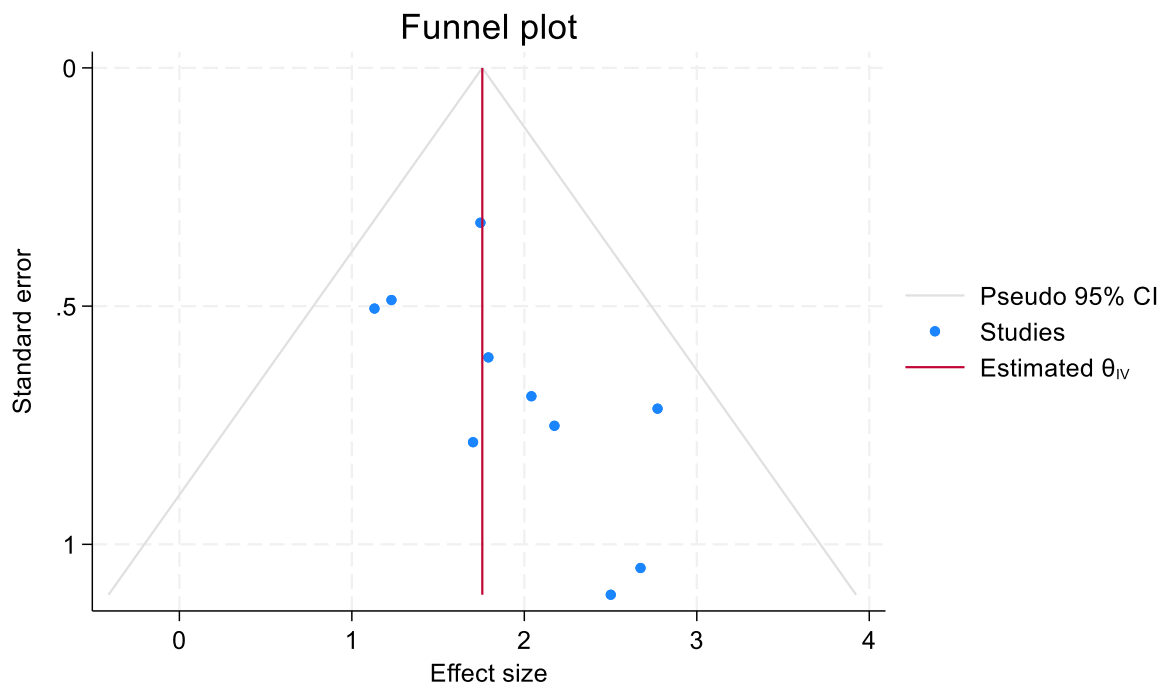


Figure 2.7. Funnel plot assessing publication bias for studies evaluating raw meat exposure or consumption as a risk factor for anthrax infection

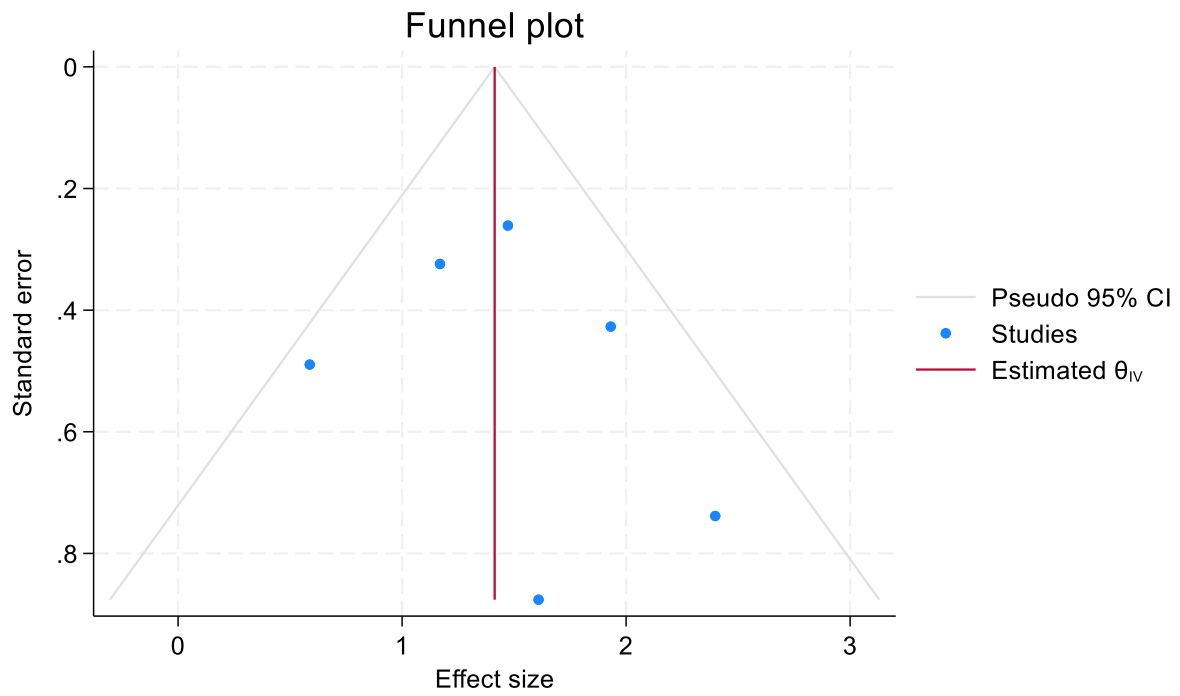


Figure 2.8. Funnel plot assessing publication bias in studies evaluating handling of carcasses and exposure to animal by-products as a risk factor for anthrax infection

CHAPTER III:

Ecological niche models of Nipah virus-associated bats: Predicting current and future climatic suitability in endemic and emerging risk zones

ABSTRACT

Nipah virus (NiV), a deadly zoonotic pathogen with a high case fatality rate and potential for sustained human-to-human transmission, poses a growing global health concern. While fruit bats of the genus *Pteropus* are well-established as NiV reservoirs, multiple other genera of bats have also been implicated in NiV maintenance. Most importantly, the full ecological range of these hosts and the extent to which their distributions may shift under climate change remain underexplored or unknown. Using ecological niche modeling (ENM) technique, current and future climatic suitability were predicted for 14 confirmed NiV reservoir bat species across both endemic and non-endemic regions. To predict climatic suitability distribution of these species and distributional shifts, the occurrence data are integrated in models with current climate conditions. Then the models are projected to future climate conditions under two Shared Socioeconomic Pathways (SSP245 and SSP585) through early (2021–2040) and mid-century (2041–2060) time periods. Our models reveal substantial spatial redistribution in climatic suitability driven by climate change with critical implications for zoonotic spillover risk. *Pteropus medius* and *P. vampyrus*, historically linked to outbreaks in Bangladesh, India, Malaysia, and Singapore, are projected to experience climatic suitability contraction and fragmentation in current hotspot regions. Further, range expansion is anticipated into areas such as northeastern India, eastern Indonesia, Vietnam, and the Himalayan foothills. Island-adapted species such as *Rousettus amplexicaudatus*, indicate range expansions into biodiversity-rich yet surveillance-limited areas of Oceania and Southeast Asia. Meanwhile, generalist species *Cynopterus sphinx* is projected to persist and expand in densely populated agricultural landscapes in South and Southeast Asia. Our study offers a comprehensive spatial forecast of NiV reservoir host dynamics under different climatic change and emission scenarios. The findings emphasize the urgent need for integrating ENM-based disease surveillance with land-use planning, biodiversity conservation, community education, and One Health strategies. Identification of future spillover risk zones, particularly regions where host species ranges overlap, will be crucial for guiding targeted public health interventions, strengthening early warning systems, and mitigating the risk of future NiV outbreaks.

INTRODUCTION

Nipah virus (NiV), a highly virulent zoonotic virus belonging to the genus *Henipavirus* of Paramyxoviridae family, has emerged as a critical public health threat due to its high case fatality rate, broad host range, and potential for sustained human-to-human transmission (Chua et al., 2000). First identified during a large outbreak in Malaysia and Singapore in 1998 and 1999, the virus caused over 100 deaths and prompted the culling of more than one million pigs to contain transmission from infected livestock farms (Paton et al., 1999). Since then, outbreaks in Bangladesh and India have occurred almost annually, with most of the cases linked directly to bat-to-human transmission through food or limited human-to-human transmission (Harit et al., 2006; Hsu et al., 2004; Luby et al., 2009). The reported case fatality rate in Bangladesh and India outbreaks are as high as 91% (Arunkumar et al., 2018; Nikolay et al., 2019). The World Health Organization (WHO) has recognized NiV a priority pathogen under the Research and Development Blueprint due to its epidemic potential and absence of vaccines or effective therapeutics (Mohapatra et al., 2024).

Fruit bats of the family Pteropodidae, particularly species within the genus *Pteropus*, are widely recognized as the natural reservoirs of NiV (Mougari et al., 2022). Multiple studies have detected NiV RNA and antibodies in *P. medius*, *P. vampyrus*, and other frugivorous bat species across South and Southeast Asia, underscoring their essential role in the maintenance and circulation of the virus in wildlife populations (Epstein et al., 2006; Gurley et al., 2017; Olival et al., 2020). In addition, NiV has been identified in several other bat species other than the Pteropodidae family such as in *Cynopterus sphinx*, *Hipposideros larvatus*, *Eidolon helvum*, *Rousettus leschenaultii*, and *Dobsonia magna* (Reynes et al., 2005; Drexler et al., 2009; McKenzie et al., 2003; Hasebe et al., 2012). Beyond Asia, serological and molecular evidence of NiV or NiV-like henipaviruses has been reported in *Eidolon helvum* in Africa and *Pteropus alecto* in Australia (Edson et al., 2019; Juman et al., 2024). These findings strongly suggest that the virus has a broader ecological range than currently observable through human outbreaks and case investigations. Bat ecology plays a pivotal role in shaping the dynamics of NiV spillovers. Frugivorous bats are highly mobile, capable of travelling long distances, and often move in large colonies (Moussy et al., 2013). Their tendency to forage in a fruit orchards or peri-urban areas bring them close contact with humans and livestock. Anthropogenic changes specifically deforestation, habitat fragmentation, agricultural expansion, and rapid urbanization have intensified human-bat

contact, creating ecological interfaces that are conducive to viral transmission (McKee et al., 2021; Singh et al., 2025). In Bangladesh, repeated outbreaks of NiV in humans have been linked to the consumption of raw date palm sap contaminated with bat saliva or urine, specifically in the winter months, highlighting a culturally mediated but ecologically driven transmission pathway (Khan et al., 2010; Luby et al., 2009). Similarly, roosting and foraging behaviors of *Pteropus* bat species near livestock farming in Malaysia were associated with the initial outbreaks (Daszak et al., 2006). Moreover, serological studies confirmed that livestock also can be infected by NiV, which further amplifies the risk of transmission to humans, particularly in rural agricultural settings (Chowdhury et al., 2014).

There is a growing consensus within the scientific community that the current outbreak-based framing of NiV risk is inadequate, as it overlooks the broader ecological and anthropogenic factors that shape host distribution, flight capabilities of the bats, intensified human contact, and viral shedding dynamics (Daszak et al., 2013; Y.-Q. Sun et al., 2024). One of the most consequential drivers of infectious disease emergence is the impact of climate change. Changes in temperature, precipitation, and seasonality can alter bat physiology, reproductive cycles, migration patterns, and roosting behavior, all of which directly influence the spatial and temporal dynamics of bat-borne zoonoses (Daszak et al., 2013; Kumar et al., 2022). For instance, in Australia, El Nino–associated climatic conditions were linked to Hendra virus spillover from *Pteropus* bats to horses, which shares a similar ecology with NiV emergence (Field et al., 2011; Paez et al., 2017).

ENMs, especially those based on ecological niche theory, offer a robust framework for estimating the potential geographic ranges of species under current and future environmental conditions (Peterson, 2001; Sofaer et al., 2019). These models integrate georeferenced occurrence records with environmental covariates, such as temperature and precipitation, to predict areas of climatic suitability for a given species. Among various techniques, MaxEnt (maximum entropy) modeling has demonstrated superior performance for presence-only datasets and has been widely used to model distributions of zoonotic reservoirs including Ebola virus hosts, Lassa fever reservoirs, and SARS-like coronaviruses (Baluma Didier et al., 2024; Phillips et al., 2006; Thibaud et al., 2014). While recent work such as Sun *et al* (Sun et al., 2024) has advanced our understanding of NiV reservoir distributions in known endemic regions of South

and Southeast Asia, these studies have largely focused on a subset of NiV reservoir species. Including non-endemic regions is essential as climate-driven range shifts may enable reservoir species to expand into previously unaffected areas, increasing spillover risk in regions lacking historical exposure or surveillance infrastructures.

To address critical gaps in understanding the spatial ecology of NiV reservoir hosts under future climatic conditions extending to mid twenty first century, ENMs were developed for 14 bat species associated with NiV ecology. Because NiV is a WHO priority pathogen with high case fatality rate, zoonotic in nature, has potential for sustained human-to-human transmission, and causes recurring outbreaks in South and Southeast Asia, understanding how the ecological ranges of its reservoir hosts may shift under future climate scenarios is critical to anticipating spillover risk and devising public health preparedness strategies. Species of the genus *Pteropus* play a central role in NiV ecology. *Pteropus medius* has been repeatedly linked to outbreaks in Bangladesh and India, while *P. vampyrus* and *P. hypomelanus* were associated with the 1998–1999 outbreak in Malaysia and Singapore. Other species such as *Rousettus leschenaultii*, *Dobsonia magna*, *Cynopterus sphinx*, and *Eidolon helvum* may also contribute to viral persistence or amplification, though their epidemiological roles remain largely understudied. We applied ecological niche modeling using species occurrence data and bioclimatic predictors to estimate current (1970–2000) and future (2021–2040 and 2041–2060) climatic suitability under two standardized climate emissions pathways. Our spatial projections identify emerging regions of host convergence, particularly at the interfaces of deforestation, agriculture, and human settlement, that may serve as future hotspots for NiV spillover. This work contributes to the One Health literature by delivering spatial insights essential for forecasting zoonotic risks, enhancing early warning systems and disease preparedness, and guiding targeted interventions in both historically endemic regions and emerging areas at risk.

METHODS

Case definition of NiV-associated bat species

Fourteen bat species associated with NiV ecology were included for ENMs based on documented evidence of involvement in NiV outbreaks, viral detection, serological evidence, or ecological traits indicative of spillover potential. While not all species are confirmed reservoirs, each demonstrated credible indicators of NiV exposure or transmission relevance, supporting

their inclusion in climatic suitability assessments.

Species selection and occurrence data

Fourteen bat species were selected for ENM based on confirmed NiV detection through PCR, serological assays, or virus neutralization tests, as well as compelling ecological or experimental evidence implicating them in NiV maintenance. These species included *Pteropus medius*, *P. vampyrus*, *P. hypomelanus*, *P. poliocephalus*, *P. scapulatus*, *P. conspicillatus*, *P. alecto*, *P. neohibernicus*, *Rousettus leschenaultii*, *R. amplexicaudatus*, *Cynopterus sphinx*, *Eidolon helvum*, and *Dobsonia magna*. Georeferenced occurrence records were obtained from the Global Biodiversity Information Facility (GBIF; www.gbif.org). To ensure data quality, we excluded records with spatial errors, missing temporal data, and duplicates.

Environmental variables and climate data

Nineteen bioclimatic variables were extracted from WorldClim version 2.1 database at 30 arc-second resolutions (~1 km), covering historical baseline (1970–2000) and projected future climate conditions for 2021–2040 and 2041–2060 (**Table 3.1**). Future projections were modeled under two Shared Socioeconomic Pathways (SSPs): SSP245 (moderate emissions scenario) and SSP585 (high emissions scenario), using the Model for Interdisciplinary Research on Climate, version 6 (MIROC6) general circulation model (GCM). WorldClim bioclimatic variables were selected for their ecological relevance for bat distributions, including temperature seasonality, precipitation of the driest month, and mean temperature of the warmest quarter. The geographic extent for model training was defined individually for each species based on occurrence records obtained from the GBIF, aligned with the historical baseline period (1970–2000) to ensure consistency with climatic variables. Models were then projected to broader spatial domains to evaluate potential shifts in climatic suitability under future climate scenarios, including both endemic and non-endemic regions. All environmental layers were processed and clipped using ArcGIS Pro 3.2.1 and converted to ASCII format for use in modeling.

Model generation and evaluation

The climatic suitability distribution models for 14 confirmed NiV reservoir bat species were developed using MaxEnt v3.4.4 and extracted bioclimatic variables, which estimates habitat suitability from presence-only data (Merow et al., 2013). For each species, a random subsampling approach was employed, allocating 70% of occurrence data for model training and

30% for testing purposes. Species occurrence data were uploaded in CSV format, and corresponding environmental predictors (19 bioclimatic variables) were input as ASCII raster layers. Majority of the MaxEnt default settings were retained (regularization multiplier = 1, maximum iterations = 500, convergence threshold = 0.00001, maximum number of background points = 10,000, default prevalence = 0.5, and replicates = 1), except that the output format was set to logistic, and the Jackknife analysis was disabled to reduce computational load. Model performance was assessed using the area under the receiver operating characteristic curve (AUC), where values between 0.7 and 0.9 was considered good predictive performance, and values ≥ 0.9 reflect high accuracy, and models with AUC values below 0.7 were considered suboptimal (Phillips et al., 2008). Binary climatic suitability maps were generated using the “minimum training presence” threshold and projected under both current (1970–2000) and future climate scenarios (SSP245 and SSP585 for 2021–2040 and 2041–2060) to identify spatial patterns and potential shifts in climatic suitability.

Estimating climatic suitability shifts in key reservoir species

Range shift analyses were conducted to assess suitability dynamics for *Pteropus medius* and *P. vampyrus*, two species historically linked to NiV spillover events in Bangladesh–India and Malaysia–Singapore, respectively. Binary raster outputs from MaxEnt for current and future scenarios (SSP245 and SSP585 for 2021–2040 and 2041–2060) were analyzed using the Raster Calculator in ArcGIS Pro. For each species, grid cells were classified as suitability gained (1), lost (100), stable (101), or absent (0). These spatial assessments enabled quantification of projected range shifts and provided critical insight into how climate-driven changes may alter future zoonotic spillover risk. The findings support strategic surveillance planning and public health preparedness within a One Health framework.

Quantifying pixel-level suitability change

To further quantify and visualize climatic suitability shifts, pixel-level changes across climate scenarios were extracted and analyzed using R (v4.3.2). For each species, the pixel-wise change in climatic suitability was computed by subtracting present-day continuous suitability raster from future scenario rasters. Values were aggregated and visualized using *ggplot2* to generate histograms illustrating pixel-level trends across four future scenarios (SSP245 and SSP585 for

2021–2040 and 2041–2060). These histograms provide quantitative metrics of suitability change and complement the broader spatial assessments modeled for each species.

Species richness mapping

Species richness was estimated by summing binary thresholded climatic suitability rasters for all 14 NiV-associated bat species using the Cell Statistics tool in ArcGIS Pro. This method calculated the number of species with climatic suitability per pixel for each time period and climate scenario. Richness maps were generated for the baseline (1970–2000) and future projections (SSP245 and SSP585 for 2021–2040 and 2041–2060) to identify spatial changes in areas of multi-species overlap.

RESULTS

ENMs revealed distinct patterns of climatic suitability for 14 bat species associated with NiV ecology. Under baseline conditions (1970–2000), species distributions were shaped by climatic gradients and regional biogeography. Future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060 time periods, indicated substantial variation across species in terms of shifts in climatic suitability, contraction, and expansion. Three general trends emerged: (1) persistence of climatic suitability in core habitats, (2) directional expansion into newly favorable regions, and (3) contraction in climatically marginal zones.

Within the genus *Pteropus*, *P. medius* and *P. vampyrus* exhibited broadly divergent patterns of future redistribution but with important spatial differences. *P. medius* displayed high baseline suitability across Bangladesh, eastern India, and Sri Lanka, with slight eastward shift extending into coastal Myanmar, Vietnam, the northern Philippines, and Sulawesi. Likewise, a noticeable losses of suitability occurred in inland Bangladesh and eastern India. In contrary, *P. vampyrus*, with a broader baseline range encompassing Peninsular Malaysia, western Indonesia, Philippines, Vietnam, and coastal Thailand, experienced northward and westward expansion. However, a minor losses were projected for southern and northern India, western Peninsular Malaysia, and Java. These spatial shifts are visualized in **Supplementary Figures S1–S2**.

Pixel-wise histograms of continuous climatic suitability changes support these spatial projections. *P. medius* exhibited a left-skewed distribution though difference of values were not prominent (**Figure 3.1**), indicating slight declines in suitability across a large portion of its range.

In contrast, *P. vampyrus* showed a broader distribution with a moderate right skew (**Figure 3.2**), reflecting a greater proportion of areas experiencing suitability gains, particularly under SSP585 scenarios in both future timeframes. Binary change maps (**Figures 3.3 and 3.4**) revealed that while both species retain stable core areas, *P. vampyrus* underwent more extensive redistribution, with significant expansion than *P. medius*, and skewed patterns of gain and loss across Southeast Asia.

Among the remaining *Pteropus* species, four showed consistent suitability gains under both climate scenarios. *P. alecto* and *P. scapulatus*, found along the eastern and northern coasts of Australia, expanded inland and westward under future conditions. *P. poliocephalus*, restricted to southeastern Australia, maintained its coastal core while extending modestly southward and inland. *P. neohibernicus*, native to the northern coast of Papua New Guinea, exhibited the most pronounced expansion into the Bismarck Archipelago and surrounding island groups under SSP585. These spatial changes are detailed in **Supplementary Figures S3–S6**.

Pixel-based histograms for these species (**Figures 3.5–3.8**) revealed distributions concentrated around stable or increasing climatic suitability values. *P. neohibernicus* displayed a completely right skew, indicating uniform gains in suitability across all scenarios, while *P. alecto*, *P. scapulatus*, and *P. poliocephalus* exhibited reasonable to moderate gains with minimal losses. These trends suggest climatic adaptability and potential for range expansion, particularly under high-emission scenarios.

Two other *Pteropus* species exhibited more constrained or divergent responses. *P. conspicillatus*, found in northeastern Queensland and parts of Papua New Guinea, showed minimal future changes in climatic suitability, with slight inland reductions and persistence of suitable conditions in core areas. *P. hypomelanus*, which occurs across the Philippines and eastern Indonesia, retained high suitability in the central Philippines through 2021–2040 but experienced substantial contraction by 2041–2060, especially under SSP585. Losses were concentrated in the southern Philippines and eastern Indonesia (**Supplementary Figures S7–S8**). These patterns were confirmed by pixel histograms: *P. conspicillatus* showed a slight left skewness though changes are very minor and centered near zero (**Figure 3.9**), while *P. hypomelanus* showed a distinct left-skewed distribution (**Figure 3.10**), suggesting increased vulnerability to climate change.

Within the genus *Rousettus*, both species demonstrated general climatic stability with distinct spatial dynamics. *R. amplexicaudatus*, broadly distributed across Southeast Asia and island regions, showed both gains and losses across the Philippines, Sulawesi, and eastern Indonesia, with future suitability expanding into northern Australia and the Lesser Sunda Islands. *R. leschenaultii*, dominant in South Asia and mainland Southeast Asia, exhibited more losses than gain in northern Thailand, central Vietnam, and parts of Myanmar, while maintaining stable core areas in Sri Lanka and eastern India. These spatial patterns are illustrated in **Supplementary Figures S9–S10**.

Despite shared trends of persistence and net gain, the two species differed in the geography and direction of their expansion. *R. amplexicaudatus* showed mixed phenomenon, it experienced marginal losses than gain across island systems, similar pattern was also observed for *R. leschenaultii*, however, the suitability losses were more pronounced for *R. leschenaultii*. Pixel histograms reflect this divergence. *R. amplexicaudatus* (**Figure 3.11**) had a near-symmetrical distribution with modest losses, whereas *R. leschenaultii* (**Figure 3.12**) showed a pronounced left skew, indicating widespread pixel-level suitability losses in some parts of its range. These results suggest a similar climatic resilience for both species withing the genus *Rousettus*.

Among the four remaining genera, spatial responses were generally stable but varied in magnitude. *Cynopterus sphinx* and *Hipposideros larvatus*, both centered in South and Southeast Asia, showed high baseline suitability and only minor inland expansion under SSP585 by 2041–2060. These shifts occurred primarily along the Indo-Gangetic Plain and upland areas of Myanmar and Laos. *Eidolon helvum*, the only African species analyzed, retained suitability across coastal and equatorial regions while expanding into southern and eastern Africa, including Angola and Mozambique. *Dobsonia magna*, found in Papua New Guinea and adjacent islands, expanded into northern Australia and nearby archipelagos under future scenarios.

Supplementary Figures S11–S14 illustrate these spatial dynamics.

Pixel-wise histograms further support these findings. *C. sphinx* showed a tightly centered distribution near zero (**Figure 3.13**), consistent with climatic stability, while *H. larvatus* and *Dobsonia magna* exhibited a moderate left skew (**Figures 3.14** and **3.15**), indicating incremental declines in suitability across parts of its range. In contrast, *E. helvum* displayed modest right-skewed distributions (**Figures 3.16**), suggesting increased suitability across portions of their

range. These differences reflect species-specific interactions between biogeography, ecological flexibility, and climate sensitivity.

Species richness patterns of NiV-associated bats were also evaluated. Under baseline conditions, richness peaked in mainland Southeast Asia, particularly in Vietnam, Thailand, and Laos, where up to six species co-occurred (**Figure 3.17**). Moderate richness levels extended across Peninsular Malaysia, Java, Sumatra, and Borneo, while lower richness values were observed in Indonesia, Papua New Guinea, and northern Australia. Sub-Saharan Africa exhibited uniformly low richness, typically one species. Projected changes in species richness showed spatial consistency with species-level trends. Under SSP245 (2021–2040), richness persisted in Southeast Asia with expansion into Laos, Peninsular Malaysia, Sulawesi, and northern Papua New Guinea. SSP585 scenarios showed similar but slightly more extensive expansion, including into Cambodia and parts of the Lesser Sunda Islands. By 2041–2060, SSP245 projected further spread into southern China and Java, while SSP585 showed intensified hotspots in the Malay Archipelago and substantial gains across eastern Australia. These findings collectively highlight the Southeast Asian tropics as persistent richness hotspots and future areas of multi-species overlap, with the greatest gains occurring under high-emission scenarios. In contrast, continental Africa remained species-poor and relatively unaffected by projected climate shifts.

DISCUSSION

Our study comprehensively modeled current and future distributions of all species associated with NiV ecology across both endemic and non-endemic settings using standardized climate scenarios extending to mid-twenty first century. Understanding the future distribution of bat species that currently serve or have the potential to serve as reservoirs for NiV is critical to predicting and mitigating zoonotic spillover risk. Our ENMs for 14 reservoir bat species, including *Pteropus medius*, *P. vampyrus*, *P. hypomelanus*, *Rousettus* spp., *Cynopterus sphinx*, *Eidolon helvum*, and five other *Pteropus* spp. endemic to Australia and Oceania, under both moderate and high-emissions scenarios, reveal significant shifts in climatic suitability and emphasize the need for monitoring efforts in emerging risk zones. Many species demonstrate notable resilience to climate changes. *Cynopterus sphinx*, a generalist fruit bat common in South and Southeast Asia, retains broad suitability across its current range, matching prior studies showing flexibility to urban and agricultural environments (Shafie et al., 2014). *Eidolon helvum*,

prevalent in Africa and Madagascar, also maintains stable climatic suitability, though predicted range shifts may increase its interface with human populations. Conversely, montane or island specialists, such as *Dobsonia magna*, *P. conspicillatus*, and *P. hypomelanus*, are projected to experience declines in climatic suitability in lower elevations, especially in warmer lowlands, pushing them into upland or cooler island refugia. These patterns reflect global trends in montane species distributions responding to warming temperatures or climate change (Festa et al., 2023; Freeman et al., 2021). These spatial trends were further supported by pixel-wise histogram graphs, which quantified the direction and intensity of change in climatic suitability across each species' distribution.

We focused on *P. medius* and *P. vampyrus*, both historically implicated in NiV outbreaks. In Bangladesh and India, *P. medius* contamination of raw date palm sap remains a primary human infection route (Khan et al., 2010; S. P. Luby et al., 2009). In Malaysia and Singapore, *P. vampyrus*-linked spillovers involved transmission to domestic pigs (Goh et al., 2000; Paton et al., 1999). Under moderate and high emission scenarios, our models show northward and upslope shifts in *P. medius* climatic suitability into the Himalayas and northeastern Indian states by 2041–2060. Simultaneously, high-emission scenarios indicate fragmented climatic suitability in the Gangetic Plain and Bangladesh, areas already known as 'Nipah belt'. This concentration of bats within climatically constrained areas may promote higher bat densities, increase behavioral stress, and elevate the risk of human exposure via date palm sap collection practices, underscoring the need for targeted outreach and interventions around raw date-sap harvesting (Nahar et al., 2012; Rahman et al., 2011). We observed a northward and westward range shift for *P. vampyrus*, from Malaysia and Singapore towards Sumatra and Southern Thailand. This westward shift could heighten the risk of humans and domestic animal interactions at forest–farm interfaces, especially if roosting sites relocate consequently. Historical evidence suggests that livestock, particularly pigs, served as bridging hosts between bats and humans during the initial outbreaks in 1998 and 1999 in Singapore and Malaysia (Chua et al., 2003; Lam et al., 2002). These projections reinforce the need for biosecurity enhancements in regions where climatic suitability of *P. vampyrus* overlaps with agricultural lands, livestock farms and semi-urban environments.

In the border region between Nepal and northern India, climate-driven expansion of *P. medius* and *C. sphinx* are expected to increase bat species diversity along the Himalayan foothills, a region with limited historical disease surveillance but increasing human-wildlife contact. Eastern Myanmar and western Vietnam are predicted to experience overlapping distributions of multiple bat species, including *Rousettus* spp. and *P. vampyrus*, particularly under the high-emissions scenario. This overlap coincides with areas undergoing rapid urbanization and deforestation, landscape changes that are known to facilitate NiV emergence (Pham-Thanh et al., 2022; Saba Villarroel et al., 2023). Similarly, southern Sumatra and Borneo show expanding climatic suitability for *P. vampyrus*, *P. hypomelanus*, and *Rousettus amplexicaudatus*, especially in biodiverse forests increasingly fragmented by agricultural expansion and extensive deforestation (Lubis et al., 2023; Gaveau et al., 2017). The convergence of multiple NiV-associated species in these regions may form ecological “spike zones,” where the probability of interspecies virus transmission and subsequent spillover into human populations is significantly elevated (Degeling et al., 2019; Paterson et al., 2011).

Bat density, physiology, and stress-driven viral shedding, all influenced by habitat disturbance, impact spillover risk (Eby et al., 2023). As climatic shifts and land-use changes lead to contractions in climatic suitability and increased habitat fragmentation, bats may increasingly forage in agricultural zones or form larger communal roosts in anthropogenic landscapes, elevating contact with humans and domestic animals. The movement of NiV-associated bat species across overlapping zones of climatic suitability presents heightened spillover potential, particularly in densely farmed areas. Bangladesh remains a critical example of this risk where outbreaks occur every year with fatalities.

Our study revealed significant insights on all NiV-associated bat species, that build upon earlier ENM efforts focused on South and Southeast Asia. Previous ENM studies such as Hahn et al. (Hahn et al., 2014), Chaibes et al. (Chaibes et al., 2022), Walsh et al. (Walsh et al., 2015), Peterson et al. (Peterson et al., 2015), and Sun et al. (Sun et al., 2024) primarily focused on individual *Pteropus* species such as *P. medius* and *P. lylei* within outbreak affected zones, mostly specific to countries like Bangladesh, Cambodia, India, Malaysia, Singapore Thailand, and Vietnam. These studies emphasized predictive risk of *Pteropus* bats across known endemic regions linked to seasonal food-borne transmission and outbreaks through consumption of raw

date palm sap and livestock mediated transmission. Our study advances the understanding of growing work by systematically modeling fourteen NiV-associated bat species across both endemic and non-endemic settings using different climate and emission scenarios and extending mid-century timeframes. This broader spatial and taxonomic scope allow the scientific and public health researchers to better anticipate how NiV-associated bat distributions and associated zoonotic risk may evolve under global climate change scenarios particularly in the areas not previously recognized as high-risk zone.

Unlike earlier models that often lacked future climate projections with different emission scenarios such as SSP245 or SSP585 and limited to single species, our approach incorporates dynamic climatic suitability shifts over two future time horizons (2021–2040 and 2041–2060) along with two emissions, providing actionable foresight into emerging spillover zones. For instance, our identification of the Himalayan foothills, eastern Indonesia, and coastal Vietnam as future high-risk zone would not have been identified as a potential emerging risk zone using existing studies restricted to current distributions or focused solely on *Pteropus* species. Furthermore, our findings confirm some previously observed trends, such as the resilience of generalist species like *Cynopterus sphinx*, but also highlight new concerns, such as the fragmentation of core climatic suitability zones for *P. medius* in the Gangetic Plain and the westward range shift of *P. vampyrus*, which have not been extensively explored in prior literature (Garg et al., 2023; Mohd-Azlan et al., 2022; Thapa et al., 2024). By modeling shifts in climatic suitability for all NiV-associated bat species across multiple continents, our study enhances the precision of anticipatory public health strategies. Decision-makers and health practitioners can now identify regions not only where bats currently exist or predefined risk zones, but emerging expanding zones of bat-borne zoonotic risk. These include biodiversity-rich, surveillance-limited islands such as Mindanao, Sulawesi, and Sumatra, as well as newly suitable continental areas along the India-Nepal border and across Indochina. These insights are directly relevant for shaping One Health surveillance frameworks, optimizing early warning systems, and informing interventions such as date palm sap harvesting education and food hygiene, enhancement of biosecurity of livestock and food animal farms, and the conservation of ecological corridors in projected high-risk zones.

Species richness projections from our models further reinforce regional risk heterogeneity. Baseline richness peaked in Vietnam, Thailand, and Laos, with future scenarios showing persistence and expansion into Sulawesi, Sumatra, Papua New Guinea, and parts of southern China. SSP585 projections indicated intensified richness hotspots across the Malay Archipelago, eastern India, and eastern Australia, while sub-Saharan Africa remained species-poor and stable. These patterns suggest that Southeast Asia will remain the epicenter of NiV reservoir diversity, with multiple species co-occurring under high-emission future scenarios.

While our ENMs offer important insights into NiV-associated bat hosts, some limitations should be considered interpreting our results. Future climatic suitability projections rely on historical baseline climate data (1970–2000) from WorldClim and may not reflect recent urbanization or land-use changes that affect bat distributions. MaxEnt presence-only modeling, though robust, cannot fully mitigate sampling bias or account for absence data (Lissovsky et al., 2021). Additionally, ENMs do not model bat behavior, immunity, or pathogen dynamics, crucial elements in spillover risk. Incorporating land-use, roost site density, and human population trends would improve future predictive models. Despite limitations, our ENM projections provide valuable information for One Health literature. The models identify newly emerging zones such as the Himalayan foothills and eastern Sumatra, as well as consistent high richness areas such as Vietnam, Thailand, and Laos, where enhanced viral surveillance, early warning systems, and serological sampling of bat populations can inform disease preparedness. Targeted public health education and implementing community-level interventions in traditional date-sap harvesting regions, particularly in areas projected to become more suitable for *P. vampyrus* and *P. medius*, remains crucial in reducing human exposure and preventing spillover events especially in high-risk zones such as Bangladesh and India (Nahar et al., 2012). In regions like Sumatra and other high-suitability landscapes, strengthening farm-level biosecurity, especially in pig husbandry, could prevent cross-species transmission and livestock mediated transmission. As such, future studies that integrate temporally resolved climate data, land use and vegetation dynamics, and metrics of human–animal interface would improve model accuracy and robustness. Despite these constraints, our results emphasize the urgency of implementing integrated, climate-informed One Health strategies. Aligning ecological surveillance, public health preparedness, and conservation of suitable habitats in both endemic and emerging risk

regions will be essential to mitigating the intensifying threat of Nipah virus spillover in a rapidly changing world.

REFERENCES

- Arunkumar, G., Chandni, R., Mourya, D. T., Singh, S. K., Sadanandan, R., Sudan, P., Bhargava, B., People, N. I., & Group, H. S. (2018). Outbreak Investigation of Nipah Virus Disease in Kerala, India, 2018. *The Journal of infectious diseases*, 219(12), 1867-1878.
<https://doi.org/10.1093/infdis/jiy612>
- Baluma Didier, L., Jude, L. L., Franck, E. I., Wang, H., & Wang, X.-L. (2024). Spatial modeling and ecological suitability of Ebola virus disease in Africa. *PLoS One*, 19(10), e0311936.
- Chaiyes, A., Duengkae, P., Suksavate, W., Pongpattananurak, N., Wacharapluesadee, S., Olival, K. J., Srikuhnath, K., Pattanakit, S., & Hemachudha, T. (2022). Mapping Risk of Nipah Virus Transmission from Bats to Humans in Thailand. *Ecohealth*, 19(2), 175-189.
<https://doi.org/10.1007/s10393-022-01588-6>
- Chowdhury, S., Khan, S. U., Cramer, G., Epstein, J. H., Broder, C. C., Islam, A., Peel, A. J., Barr, J., Daszak, P., Wang, L.-F., & Luby, S. P. (2014). Serological Evidence of Hendraviruses Exposure in Cattle, Goats and Pigs in Bangladesh. *PLOS Neglected Tropical Diseases*, 8(11), e3302. <https://doi.org/10.1371/journal.pntd.0003302>
- Chua, K. B. (2003). Nipah virus outbreak in Malaysia. *Journal of Clinical Virology*, 26(3), 265-275. [https://doi.org/10.1016/S1386-6532\(02\)00268-8](https://doi.org/10.1016/S1386-6532(02)00268-8)
- Chua, K. B., Bellini, W. J., Rota, P. A., Harcourt, B. H., Tamin, A., Lam, S. K., Ksiazek, T. G., Rollin, P. E., Zaki, S. R., Shieh, W., Goldsmith, C. S., Gubler, D. J., Roehrig, J. T., Eaton, B., Gould, A. R., Olson, J., Field, H., Daniels, P., Ling, A. E., . . . Mahy, B. W. (2000). Nipah virus: a recently emergent deadly paramyxovirus. *Science*, 288(5470), 1432-1435. <https://doi.org/10.1126/science.288.5470.1432>
- Daszak, P., Plowright, R., Epstein, J. H., Pulliam, J., Abdul Rahman, S., Field, H. E., Smith, C., Olival, K., Luby, S., & Halpin, K. (2006). The emergence of Nipah and Hendra virus: pathogen dynamics across a wildlife-livestock-human continuum. *Disease Ecology: Community structure and pathogen dynamics*, 186-201.
- Daszak, P., Zambrana-Torrel, C., Bogich, T. L., Fernandez, M., Epstein, J. H., Murray, K. A., & Hamilton, H. (2013). Interdisciplinary approaches to understanding disease emergence: the past, present, and future drivers of Nipah virus emergence. *Proceedings of the*

- National Academy of Sciences*, 110(supplement_1), 3681-3688.
- Degeling, C., Gilbert, G. L., Tambyah, P., Johnson, J., & Lysaght, T. (2019). One Health and Zoonotic Uncertainty in Singapore and Australia: Examining Different Regimes of Precaution in Outbreak Decision-Making. *Public Health Ethics*, 13(1), 69-81. <https://doi.org/10.1093/phe/phz017>
- Drexler, J. F., Corman, V. M., Gloza-Rausch, F., Seebens, A., Annan, A., Ipson, A., ... & Drosten, C. (2009). Hendraviruses RNA in African bats. *PloS one*, 4(7), e6367.
- Eby, P., Peel, A. J., Hoegh, A., Madden, W., Giles, J. R., Hudson, P. J., & Plowright, R. K. (2023). Pathogen spillover driven by rapid changes in bat ecology. *Nature*, 613(7943), 340-344. <https://doi.org/10.1038/s41586-022-05506-2>
- Edson, D., Peel, A., Huth, L., Mayer, D., Vidgen, M., McMichael, L., Broos, A., Melville, D., Kristoffersen, J., & de Jong, C. (2019). Time of year, age class and body condition predict Hendra virus infection in Australian black flying foxes (*Pteropus alecto*). *Epidemiology & Infection*, 147, e240.
- Epstein, J. H., Field, H. E., Luby, S., Pulliam, J. R., & Daszak, P. (2006). Nipah virus: impact, origins, and causes of emergence. *Current infectious disease reports*, 8(1), 59-65.
- Festa, F., Ancillotto, L., Santini, L., Pacifici, M., Rocha, R., Toshkova, N., Amorim, F., Benítez-López, A., Dömer, A., Hamidović, D., Kramer-Schadt, S., Mathews, F., Radchuk, V., Rebelo, H., Ruczyński, I., Solem, E., Tsoar, A., Russo, D., & Razgour, O. (2023). Bat responses to climate change: a systematic review. *Biol Rev Camb Philos Soc*, 98(1), 19-33. <https://doi.org/10.1111/brev.12893>
- Field, H., de Jong, C., Melville, D., Smith, C., Smith, I., Broos, A., Kung, Y. H., McLaughlin, A., & Zeddeman, A. (2011). Hendra virus infection dynamics in Australian fruit bats. *PLoS One*, 6(12), e28678.
- Freeman, B. G., Song, Y., Feeley, K. J., & Zhu, K. (2021). Montane species track rising temperatures better in the tropics than in the temperate zone. *Ecol Lett*, 24(8), 1697-1708. <https://doi.org/10.1111/ele.13762>
- Garg, K. M., Chattopadhyay, B., Paramanatha Swami Doss, D., Vinoth Kumar, A., & Kandula, S. (2023). Bat Societies across Habitat Types: Insights from a Commonly Occurring Fruit Bat *Cynopterus sphinx*. In *Urban Bats: Biology, Ecology, and Human Dimensions* (pp. 61-71). Springer.

- Gaveau, D. L., Sheil, D., Husnayaen, Salim, M. A., Arjasakusuma, S., Ancrenaz, M., ... & Meijaard, E. (2016). Rapid conversions and avoided deforestation: examining four decades of industrial plantation expansion in Borneo. *Scientific reports*, 6(1), 3, 2017.
- Goh, K. J., Tan, C. T., Chew, N. K., Tan, P. S. K., Kamarulzaman, A., Sarji, S. A., Wong, K. T., Abdullah, B. J. J., Chua, K. B., & Lam, S. K. (2000). Clinical Features of Nipah Virus Encephalitis among Pig Farmers in Malaysia. *New England Journal of Medicine*, 342(17), 1229-1235. <https://doi.org/doi:10.1056/NEJM200004273421701>
- Gurley, E. S., Hegde, S. T., Hossain, K., Sazzad, H. M. S., Hossain, M. J., Rahman, M., Sharker, M. A. Y., Salje, H., Islam, M. S., Epstein, J. H., Khan, S. U., Kilpatrick, A. M., Daszak, P., & Luby, S. P. (2017). Convergence of Humans, Bats, Trees, and Culture in Nipah Virus Transmission, Bangladesh. *Emerg Infect Dis*, 23(9), 1446-1453. <https://doi.org/10.3201/eid2309.161922>
- Hahn, M. B., Epstein, J. H., Gurley, E. S., Islam, M. S., Luby, S. P., Daszak, P., & Patz, J. A. (2014). Roosting behaviour and habitat selection of *Pteropus giganteus* reveal potential links to Nipah virus epidemiology. *Journal of Applied Ecology*, 51(2), 376-387. <https://doi.org/https://doi.org/10.1111/1365-2664.12212>
- Hasebe, F., Thuy, N. T. T., Inoue, S., Yu, F., Kaku, Y., Watanabe, S., ... & Morita, K. (2012). Serologic evidence of nipah virus infection in bats, Vietnam. *Emerging infectious diseases*, 18(3), 536.
- Harit, A., Ichhpujani, R., Gupta, S., & Gill, K. (2006). Nipah/Hendra virus outbreak in Siliguri, West Bengal, India in 2001. *Indian Journal of Medical Research*, 123(4), 553.
- Hsu, V. P., Hossain, M. J., Parashar, U. D., Ali, M. M., Ksiazek, T. G., Kuzmin, I., Niezgoda, M., Rupprecht, C., Bresee, J., & Breiman, R. F. (2004). Nipah virus encephalitis reemergence, Bangladesh. *Emerg Infect Dis*, 10(12), 2082-2087. <https://doi.org/10.3201/eid1012.040701>
- Islam, M. S., Hasan, S. M. M., Salzer, J. S., Kadzik, M., Haque, F., Haider, N., Hossain, M. B., Islam, M. A., Rahman, M., Kennedy, E., & Gurley, E. S. (2021). Human exposures to by-products from animals suspected to have died of anthrax in Bangladesh: An exploratory study. *Transbound Emerg Dis*, 68(4), 2514-2520. <https://doi.org/10.1111/tbed.13921>
- Juman, M. M., Gibson, L., Suu-Ire, R. D., Languon, S., Quaye, O., Fleischer, G., Asumah, S., Jolma, E. R., Gautam, A., & Sterling, S. L. (2024). Ecological and Reproductive Cycles

- Drive Henipavirus Seroprevalence in the African Straw-Coloured Fruit Bat (*Eidolon helvum*). *Ecology and Evolution*, 14(11), e70555.
- Kasradze, A., Echeverria, D., Zakhshvili, K., Bautista, C., Heyer, N., Imnadze, P., & Mirtskhulava, V. (2018). Rates and risk factors for human cutaneous anthrax in the country of Georgia: National surveillance data, 2008-2015. *PLoS One*, 13(2), e0192031. <https://doi.org/10.1371/journal.pone.0192031>
- Khan, M. S., Hossain, J., Gurley, E. S., Nahar, N., Sultana, R., & Luby, S. P. (2010). Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. *Ecohealth*, 7(4), 517-525. <https://doi.org/10.1007/s10393-010-0366-2>
- Kumar, V. B., Rooney, N., & Carr, A. (2022). Nipah virus from bats-another potential pandemic? Risk mapping the impact of anthropogenic and climate change on the transmission of Nipah virus infection to humans. *medRxiv*, 2022.2002. 2021.22271216.
- Lam, S. K., & Chua, K. B. (2002). Nipah Virus Encephalitis Outbreak in Malaysia. *Clinical Infectious Diseases*, 34(Supplement_2), S48-S51. <https://doi.org/10.1086/338818>
- Lissovsky, A. A., Dudov, S. V., & Obolenskaya, E. V. (2021). Species-Distribution Modeling: Advantages and Limitations of Its Application. 1. General Approaches. *Biology Bulletin Reviews*, 11(3), 254-264. <https://doi.org/10.1134/S2079086421030075>
- Lubis, M. I. (2023). Cascading impacts of deforestation to biodiversity and ecosystem functioning in the tropical rainforests of Sumatra.
- Luby, S. P., Gurley, E. S., & Hossain, M. J. (2009). Transmission of human infection with Nipah virus. *Clin Infect Dis*, 49(11), 1743-1748. <https://doi.org/10.1086/647951>
- Luby, S. P., Hossain, M. J., Gurley, E. S., Ahmed, B.-N., Banu, S., Khan, S. U., Homaira, N., Rota, P. A., Rollin, P. E., & Comer, J. A. (2009). Recurrent zoonotic transmission of Nipah virus into humans, Bangladesh, 2001–2007. *Emerging Infectious Diseases*, 15(8), 1229.
- Mackenzie, J. S., Field, H. E., & Guyatt, K. J. (2003). Managing emerging diseases borne by fruit bats (flying foxes), with particular reference to henipaviruses and Australian bat lyssavirus. *Journal of Applied Microbiology*, 94(s1), 59-69.
- McKee, C. D., Islam, A., Luby, S. P., Salje, H., Hudson, P. J., Plowright, R. K., & Gurley, E. S. (2021). The ecology of Nipah virus in Bangladesh: a nexus of land-use change and

- opportunistic feeding behavior in bats. *Viruses*, 13(2), 169.
- Merow, C., Smith, M. J., & Silander Jr, J. A. (2013). A practical guide to MaxEnt for modeling species' distributions: what it does, and why inputs and settings matter. *Ecography*, 36(10), 1058-1069.
- Migisha, R., Mbatidde, I., Agaba, D. C., Turyakira, E., Tumwine, G., Byaruhanga, A., Siya, A., Ruzaaza, G. N., & Kirunda, H. (2021). Risk factors for human anthrax outbreak in Kiruhura District, Southwestern Uganda: a population-based case control study.
- Mohapatra, P., Nazli Khatib, M., Shabil, M., Rajput, P., Sharma, N., Satapathy, P., Bhopte, K., Jena, D., Sah, S., & Bushi, G. (2024). Addressing the Nipah virus threat: A call for global vigilance and coordinated action. *Clinical Infection in Practice*, 24, 100390.
<https://doi.org/https://doi.org/10.1016/j.clinpr.2024.100390>
- Mohd-Azlan, J., Kaicheen, S. S., & Lok, L. (2022). The Distribution and Community's Perception of Flying Fox, *Pteropus vampyrus* in Limbang, a Transboundary Area in Sarawak. *Tropical Life Sciences Research*, 33(3), 195.
- Mougari, S., Gonzalez, C., Reynard, O., & Horvat, B. (2022). Fruit bats as natural reservoir of highly pathogenic henipaviruses: balance between antiviral defense and viral tolerance. *Current Opinion in Virology*, 54, 101228.
<https://doi.org/https://doi.org/10.1016/j.coviro.2022.101228>
- Moussy, C., Hosken, D. J., Mathews, F., Smith, G. C., Aegerter, J. N., & Bearhop, S. (2013). Migration and dispersal patterns of bats and their influence on genetic structure. *Mammal Review*, 43(3), 183-195.
- Nahar, N., Mondal, U. K., Sultana, R., Hossain, M. J., Khan, M. S. U., Gurley, E. S., Oliveras, E., & Luby, S. P. (2012). Piloting the use of indigenous methods to prevent Nipah virus infection by interrupting bats' access to date palm sap in Bangladesh. *Health Promotion International*, 28(3), 378-386. <https://doi.org/10.1093/heapro/das020>
- Nigusse, A. T., Amaha, M. H., Hailu, T. T., Gebremariam, H. G., Cazzoletti, L., Zanolini, M. E., Hailu, A. B., & Alemayohu, M. A. (2023). Human anthrax outbreak and associated factors in the horrific siege of Tigray, Ethiopia. *IJID One Health*, 1, 100013.
<https://doi.org/https://doi.org/10.1016/j.ijidoh.2023.100013>
- Nikolay, B., Salje, H., Hossain, M. J., Khan, A. K. M. D., Sazzad, H. M. S., Rahman, M., Daszak, P., Ströher, U., Pulliam, J. R. C., Kilpatrick, A. M., Nichol, S. T., Klena, J. D.,

- Sultana, S., Afroj, S., Luby, S. P., Cauchemez, S., & Gurley, E. S. (2019). Transmission of Nipah Virus — 14 Years of Investigations in Bangladesh. *New England Journal of Medicine*, 380(19), 1804-1814. <https://doi.org/doi:10.1056/NEJMoa1805376>
- Olival, K. J., Latinne, A., Islam, A., Epstein, J. H., Hersch, R., Engstrand, R. C., Gurley, E. S., Amato, G., Luby, S. P., & Daszak, P. (2020). Population genetics of fruit bat reservoir informs the dynamics, distribution and diversity of Nipah virus. *Molecular Ecology*, 29(5), 970-985. <https://doi.org/https://doi.org/10.1111/mec.15288>
- Paez, D. J., Giles, J., McCallum, H., Field, H., Jordan, D., Peel, A. J., & Plowright, R. K. (2017). Conditions affecting the timing and magnitude of Hendra virus shedding across pteropodid bat populations in Australia. *Epidemiology & Infection*, 145(15), 3143-3153.
- Palmateer, N. E., Ramsay, C. N., Browning, L., Goldberg, D. J., & Hutchinson, S. J. (2012). Anthrax infection among heroin users in Scotland during 2009-2010: a case-control study by linkage to a national drug treatment database. *Clin Infect Dis*, 55(5), 706-710. <https://doi.org/10.1093/cid/cis511>
- Paterson, B. J., Mackenzie, J. S., Durrheim, D. N., & Smith, D. (2011). A review of the epidemiology and surveillance of viral zoonotic encephalitis and the impact on human health in Australia. *New South Wales Public Health Bulletin*, 22(6), 99-104. <https://doi.org/https://doi.org/10.1071/NB10076>
- Paton, N. I., Leo, Y. S., Zaki, S. R., Auchus, A. P., Lee, K. E., Ling, A. E., Chew, S. K., Ang, B., Rollin, P. E., & Umapathi, T. (1999). Outbreak of Nipah-virus infection among abattoir workers in Singapore. *The Lancet*, 354(9186), 1253-1256.
- Paton, N. I., Leo, Y. S., Zaki, S. R., Auchus, A. P., Lee, K. E., Ling, A. E., Chew, S. K., Ang, B., Rollin, P. E., Umapathi, T., Sng, I., Lee, C. C., Lim, E., & Ksiazek, T. G. (1999). Outbreak of Nipah-virus infection among abattoir workers in Singapore. *The Lancet*, 354(9186), 1253-1256. [https://doi.org/10.1016/S0140-6736\(99\)04379-2](https://doi.org/10.1016/S0140-6736(99)04379-2)
- Peterson, A. T. (2001). Predicting Species' Geographic Distributions Based on Ecological Niche Modeling. *The Condor: Ornithological Applications*, 103(3), 599-605. <https://doi.org/10.1093/condor/103.3.599>
- Peterson, A. T. (2015). Mapping risk of Nipah virus transmission across Asia and across Bangladesh. *Asia Pac J Public Health*, 27(2), Np824-832. <https://doi.org/10.1177/1010539512471965>

- Pham-Thanh, L., Nhu, T. V., Nguyen, T. V., Tran, K. V., Nguyen, K. C., Nguyen, H. T., Ngo Thi, H., & Padungtod, P. (2022). Zoonotic pathogens and diseases detected in Vietnam, 2020–2021. *One Health*, *14*, 100398.
<https://doi.org/https://doi.org/10.1016/j.onehlt.2022.100398>
- Phillips, S. J., Anderson, R. P., & Schapire, R. E. (2006). Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, *190*(3), 231-259.
<https://doi.org/https://doi.org/10.1016/j.ecolmodel.2005.03.026>
- Phillips, S. J., & Dudík, M. (2008). Modeling of species distributions with Maxent: new extensions and a comprehensive evaluation. *Ecography*, *31*(2), 161-175.
<https://doi.org/https://doi.org/10.1111/j.0906-7590.2008.5203.x>
- Rahman, M. A., Hossain, M. J., Sultana, S., Homaira, N., Khan, S. U., Rahman, M., Gurley, E. S., Rollin, P. E., Lo, M. K., Comer, J. A., Lowe, L., Rota, P. A., Ksiazek, T. G., Kenah, E., Sharker, Y., & Luby, S. P. (2011). Date Palm Sap Linked to Nipah Virus Outbreak in Bangladesh, 2008. *Vector-Borne and Zoonotic Diseases*, *12*(1), 65-72.
<https://doi.org/10.1089/vbz.2011.0656>
- Reynes, J. M., Counor, D., Ong, S., Faure, C., Seng, V., Molia, S., ... & Sarthou, J. L. (2005). Nipah virus in Lyle's flying foxes, Cambodia. *Emerging infectious diseases*, *11*(7), 1042.
- Saba Villarroel, P. M., Gumpangseth, N., Songhong, T., Yainoy, S., Monteil, A., Leaungwutiwong, P., Missé, D., & Wichit, S. (2023). Emerging and re-emerging zoonotic viral diseases in Southeast Asia: One Health challenge [Review]. *Frontiers in public health*, *Volume 11 - 2023*. <https://doi.org/10.3389/fpubh.2023.1141483>
- Shafie, N. J., Rahman, N. A., Sah, S. A., Rosely, N. F., & Sufian, M. (2014). Feeding Behaviour of Cynopterus sphinx (Pteropodidae) Under Captive Conditions. *Trop Life Sci Res*, *25*(2), 53-59.
- Singh, D. K., Ragesh, P., & Kumar, S. (2025). Impact of deforestation and environmental degradation on Nipah virus outbreaks: a critical review. *Advances in Computational Methods and Modeling for Science and Engineering*, 269-276.
- Sofaer, H. R., Jarnevich, C. S., Pearse, I. S., Smyth, R. L., Auer, S., Cook, G. L., Edwards, T. C., Jr, Guala, G. F., Howard, T. G., Morisette, J. T., & Hamilton, H. (2019). Development and Delivery of Species Distribution Models to Inform Decision-Making. *BioScience*, *69*(7), 544-557. <https://doi.org/10.1093/biosci/biz045>

- Subedi, D., Pantha, S., Jyoti, S., Gautam, B., Kaphle, K., Yadav, R. K., Ghimire, S., & Dhakal, S. (2024). Anthrax in Humans, Animals, and the Environment and the One Health Strategies for Anthrax Control. *Pathogens*, 13(9).
<https://doi.org/10.3390/pathogens13090773>
- Sun, Y.-Q., Zhang, Y.-Y., Liu, M.-C., Chen, J.-J., Li, T.-T., Liu, Y.-N., Zhang, L.-Y., Wang, T., Yu, L.-J., & Che, T.-L. (2024). Mapping the distribution of Nipah virus infections: a geospatial modelling analysis. *The Lancet Planetary Health*, 8(7), e463-e475.
- Sun, Y. Q., Zhang, Y. Y., Liu, M. C., Chen, J. J., Li, T. T., Liu, Y. N., Zhang, L. Y., Wang, T., Yu, L. J., Che, T. L., Tang, T., Xu, Q., Lv, C. L., Jiang, B. G., Golding, N., Mehlman, M. L., Hay, S. I., Fang, L. Q., & Liu, W. (2024). Mapping the distribution of Nipah virus infections: a geospatial modelling analysis. *Lancet Planet Health*, 8(7), e463-e475.
[https://doi.org/10.1016/s2542-5196\(24\)00119-0](https://doi.org/10.1016/s2542-5196(24)00119-0)
- Thapa, S., Dahal, D. R., Baral, S., Pandey, K., Thapa, T. B., Racey, P. A., Yu, W., & Wu, Y. (2024). Current and future predicted distribution of roosts of the Indian Flying Fox *Pteropus medius* Temmink, 1825 in Nepal.
- Thibaud, E., Petitpierre, B., Broennimann, O., Davison, A. C., & Guisan, A. (2014). Measuring the relative effect of factors affecting species distribution model predictions. *Methods in Ecology and Evolution*, 5(9), 947-955.
- Walsh, M. G. (2015). Mapping the risk of Nipah virus spillover into human populations in South and Southeast Asia. *Transactions of The Royal Society of Tropical Medicine and Hygiene*, 109(9), 563-571. <https://doi.org/10.1093/trstmh/trv055>

APPENDIX III

TABLES

Table 3.1. WorldClim variables list used in the ecological niche models

Code	Variables
BIO1	Annual Mean Temperature
BIO2	Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIO3	Isothermality (BIO2/BIO7) ($\times 100$)
BIO4	Temperature Seasonality (standard deviation $\times 100$)
BIO5	Max Temperature of Warmest Month
BIO6	Min Temperature of Coldest Month
BIO7	Temperature Annual Range (BIO5-BIO6)
BIO8	Mean Temperature of Wettest Quarter
BIO9	Mean Temperature of Driest Quarter
BIO10	Mean Temperature of Warmest Quarter
BIO11	Mean Temperature of Coldest Quarter
BIO12	Annual Precipitation
BIO13	Precipitation of Wettest Month
BIO14	Precipitation of Driest Month
BIO15	Precipitation Seasonality (Coefficient of Variation)
BIO16	Precipitation of Wettest Quarter
BIO17	Precipitation of Driest Quarter
BIO18	Precipitation of Warmest Quarter
BIO19	Precipitation of Coldest Quarter

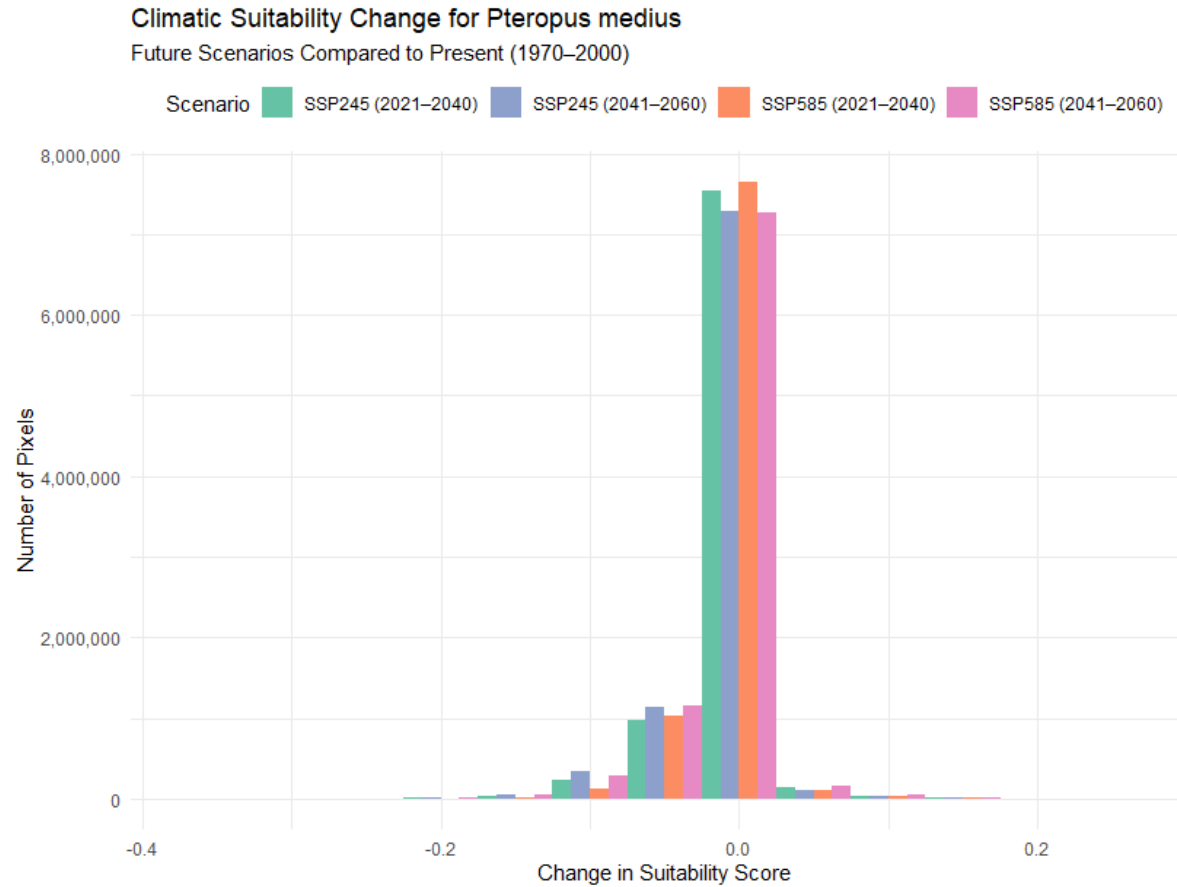


Figure 3.1. Pixel-wise changes in climatic suitability for *Pteropus medius* between the baseline period (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram illustrates the frequency distribution of logistic suitability value changes (future minus present) across all pixels. The distribution is skewed toward negative values, indicating a greater proportion of pixels with reduced climatic suitability. However, the magnitude of most changes remains modest, mostly not exceeding -0.15.

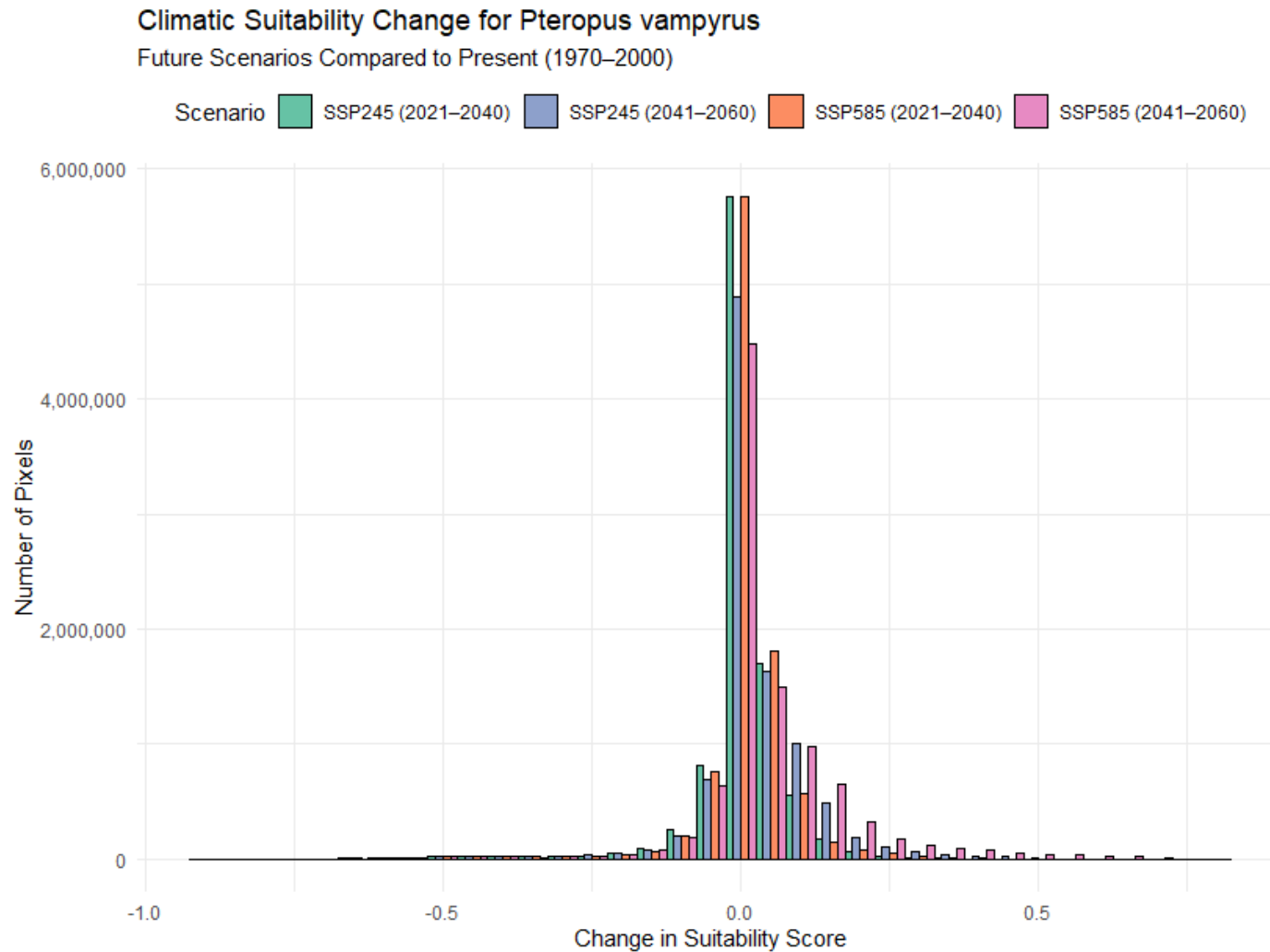
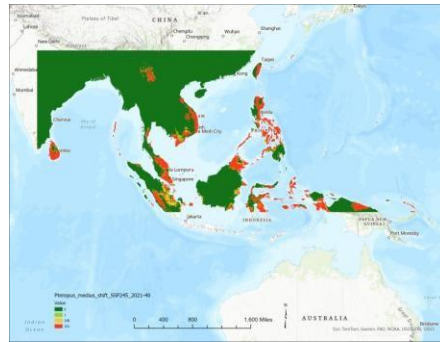
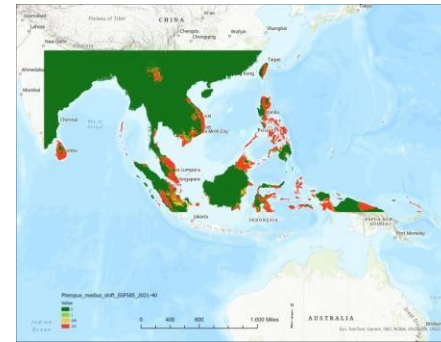


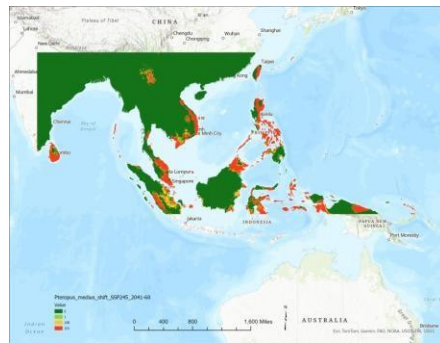
Figure 3.2. Pixel-wise changes in climatic suitability for *Pteropus vampyrus* between the baseline period (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram shows the frequency distribution of logistic suitability value changes (future minus present) across all pixels. The distribution is moderately right-skewed, with a wider spread of positive values, suggesting an overall gain in climatic suitability across many regions, particularly under SSP585 (2041–2060).



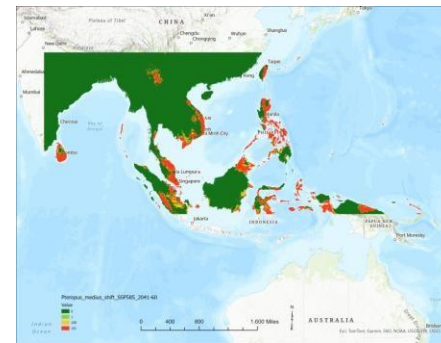
(a) 2021–2040: ssp245



(b) 2021–2040: ssp585

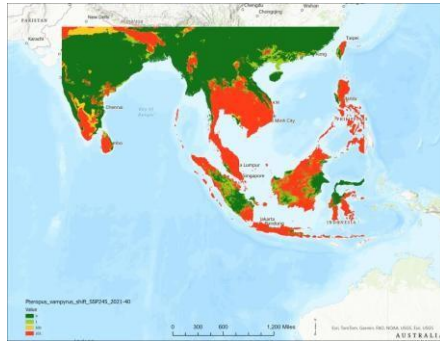


(c) 2041–2060: ssp245

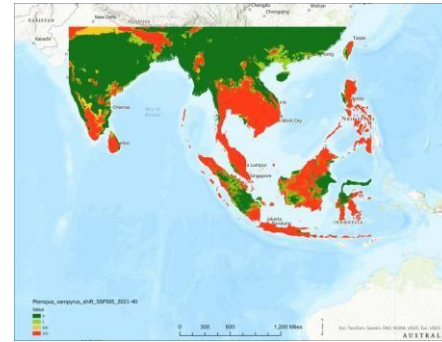


(d) 2041–2060: ssp585

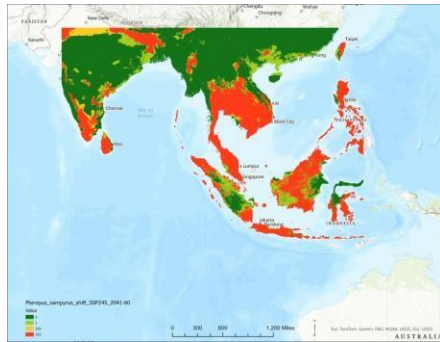
Figure 3.3. Projected gain and loss of climatic suitability for *Pteropus medius* based on binary threshold maps across future climate scenarios. Maps compare future projections to the baseline period (1970–2000) for (a) SSP245: 2021–2040, (b) SSP585: 2021–2040, (c) SSP245: 2041–2060, and (d) SSP585: 2041–2060. Colors represent pixel-wise changes in binary climatic suitability: dark green (0) indicates absence, light green (1) indicates newly gained suitable areas, yellow (100) indicates areas of loss (present suitability not maintained in the future), and red (101) indicates stable suitable areas across both future time periods.



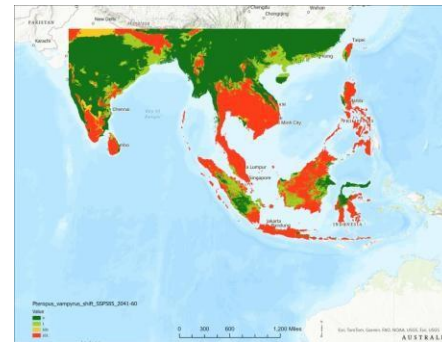
(a) 2021–2040: ssp245



(b) 2021–2040: ssp585



(c) 2041–2060: ssp245



(d) 2041–2060: ssp585

Figure 3.4. Projected gain and loss of climatic suitability for *Pteropus vampyrus* based on binary threshold maps across future climate scenarios. Maps compare future projections to the baseline period (1970–2000) for (a) SSP245: 2021–2040, (b) SSP585: 2021–2040, (c) SSP245: 2041–2060, and (d) SSP585: 2041–2060. Colors represent pixel-wise changes in binary climatic suitability: dark green (0) indicates absence, light green (1) indicates newly gained suitable areas, yellow (100) indicates areas of loss (present suitability not maintained in the future), and red (101) indicates stable suitable areas across both future time periods.

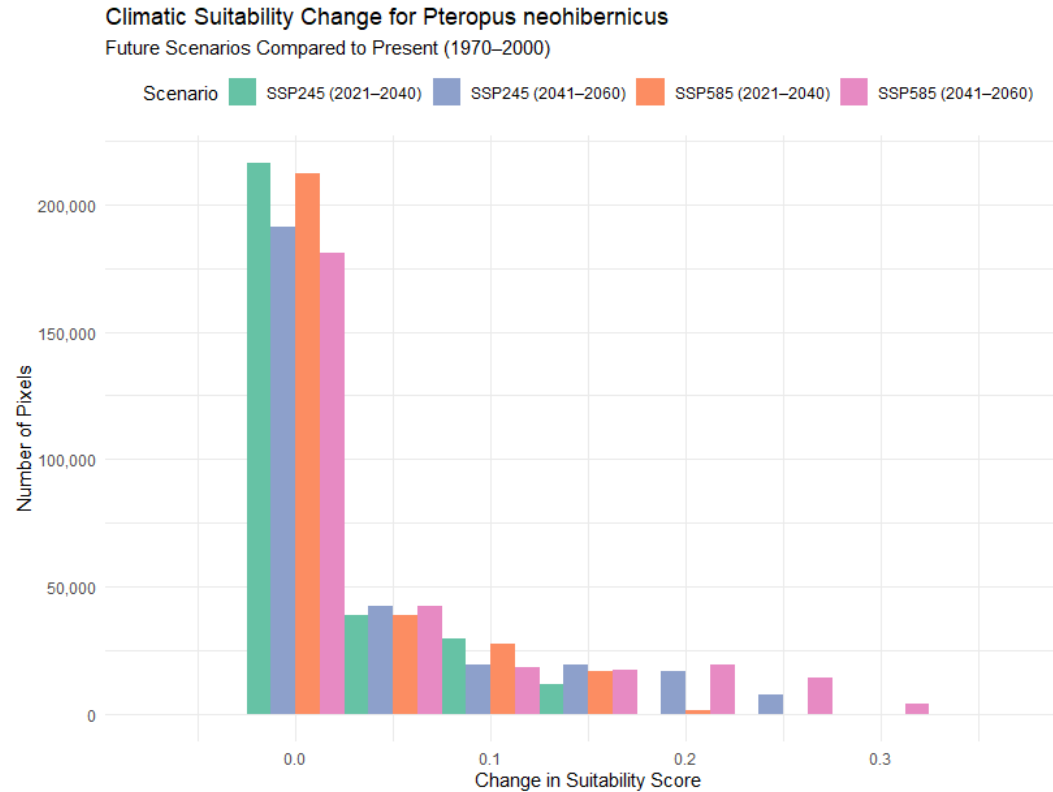


Figure 3.5. Pixel-wise changes in climatic suitability for *Pteropus neohibernicus* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram displays the frequency distribution of logistic suitability changes (future minus present) across all pixels. The distribution is completely skewed to the right, clearly showing gradual increases of pixel gains (primarily in the 0.0–0.3 range), indicating a broader trend of suitability gain under projected climate conditions.

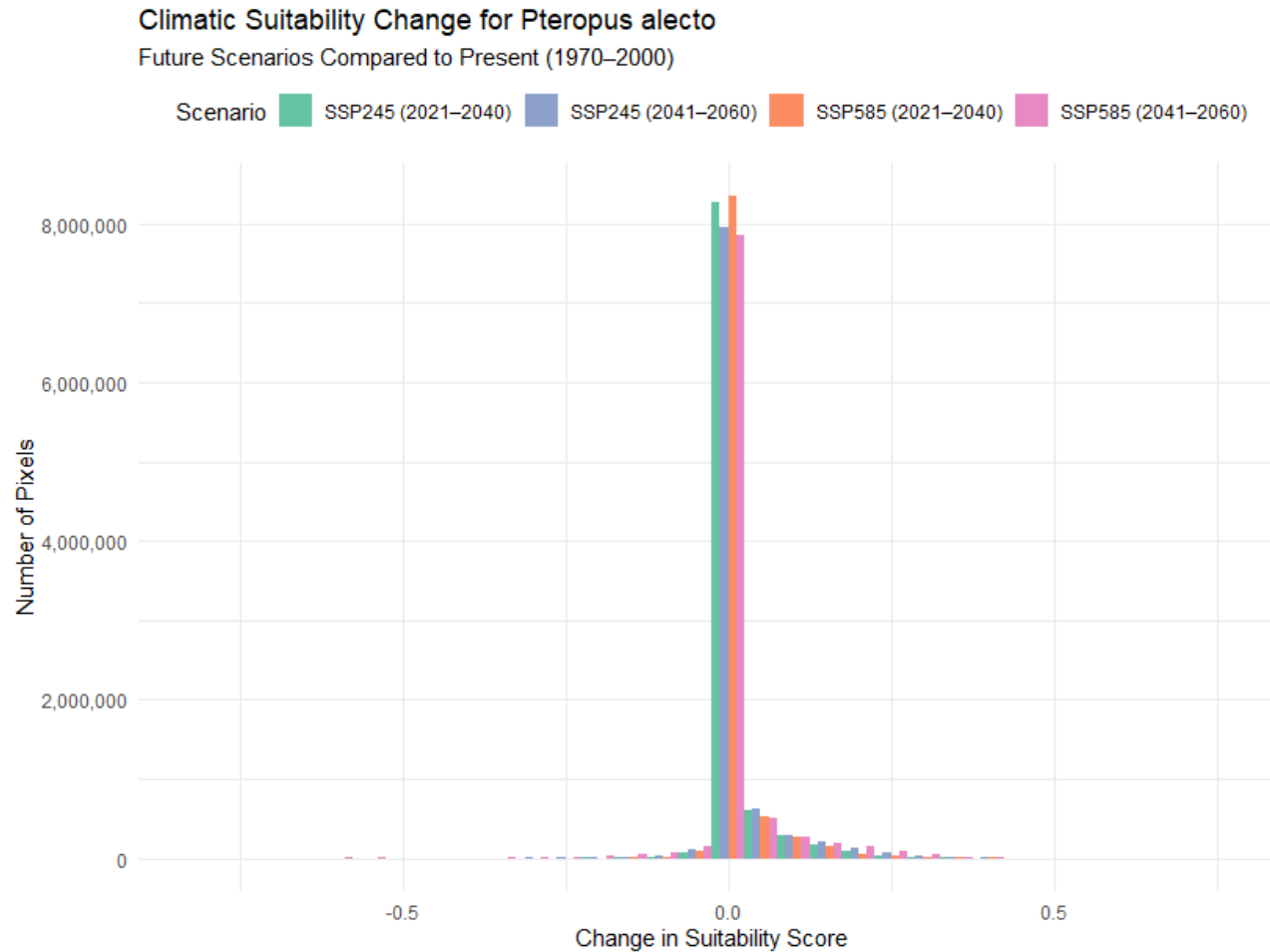


Figure 3.6. Pixel-wise changes in climatic suitability for *Pteropus alecto* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram displays the frequency distribution of logistic suitability value changes (future minus present) across all pixels. The distribution is moderately skewed to the right, suggesting that more pixels are projected to experience gains in climatic suitability under future conditions.

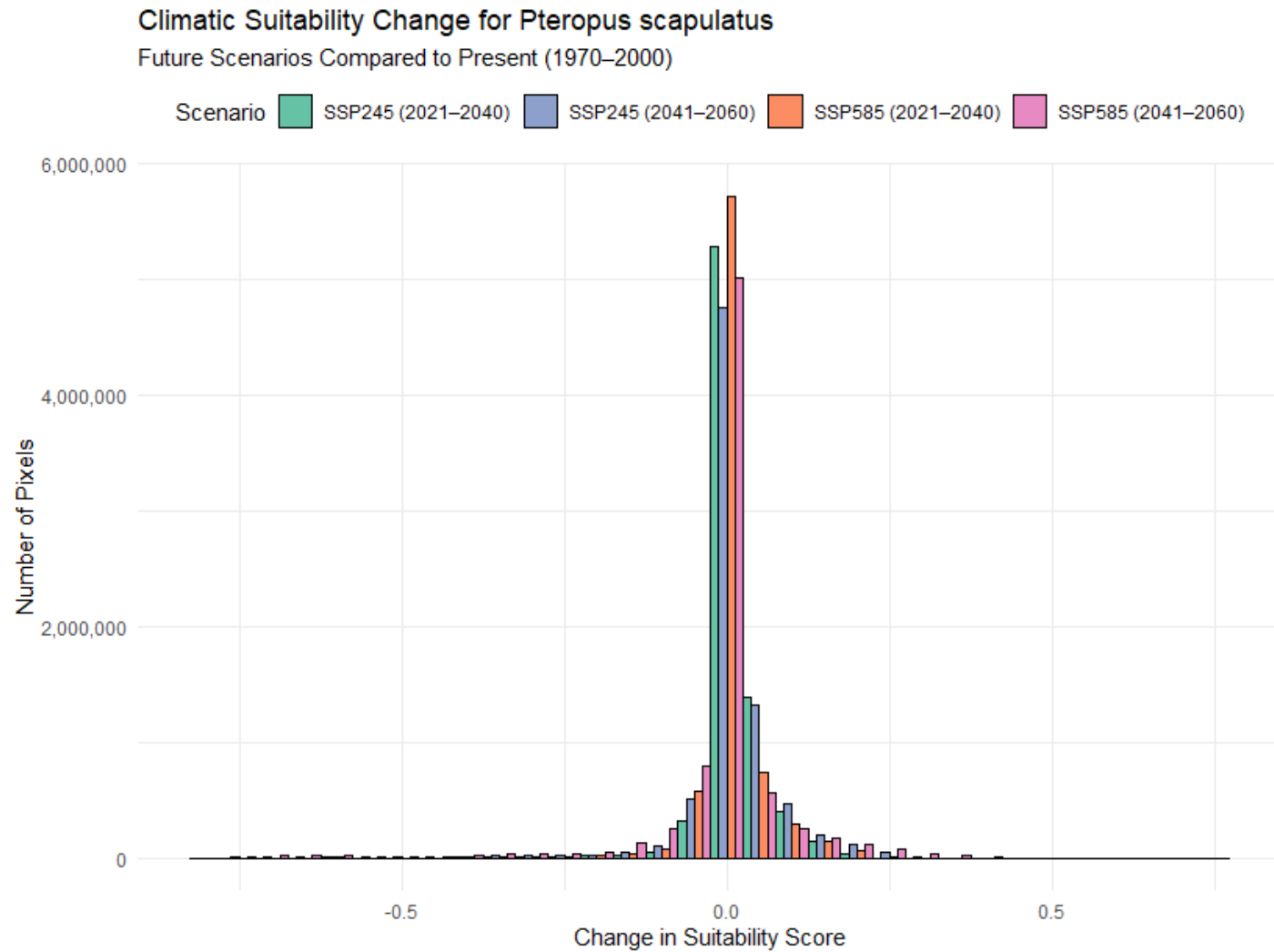


Figure 3.7. Pixel-wise changes in climatic suitability for *Pteropus scapulatus* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram displays the frequency distribution of logistic suitability value changes (future minus present) across all pixels. The distribution is slightly skewed to the right, indicating that more pixels are projected to experience gains in climatic suitability across future scenarios.

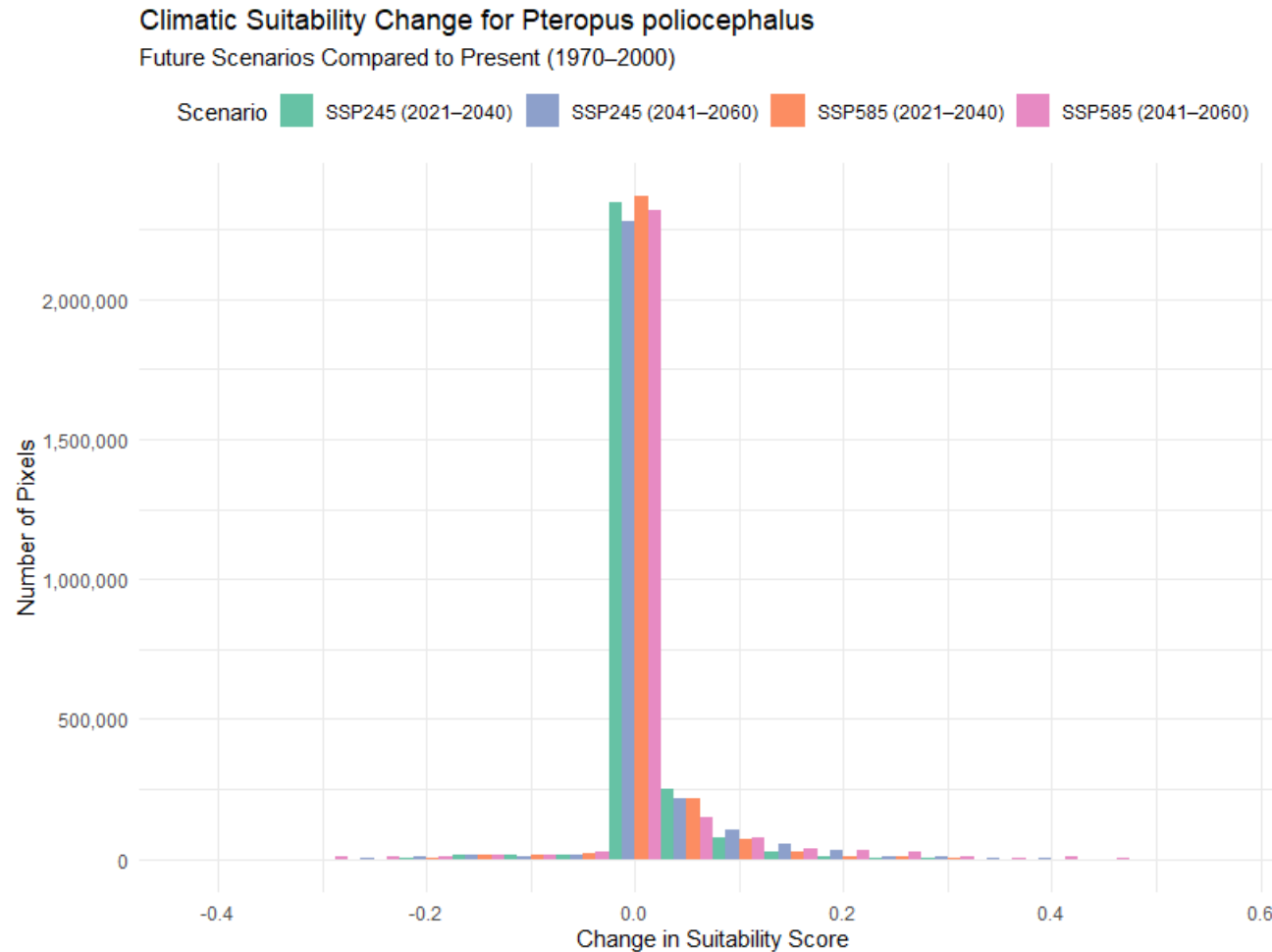


Figure 3.8. Pixel-wise changes in climatic suitability for *Pteropus poliocephalus* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram shows the distribution of logistic suitability value changes (future minus present) across all pixels. The distribution is skewed to the right, indicating that more pixels are projected to experience increases in climatic suitability under future conditions.

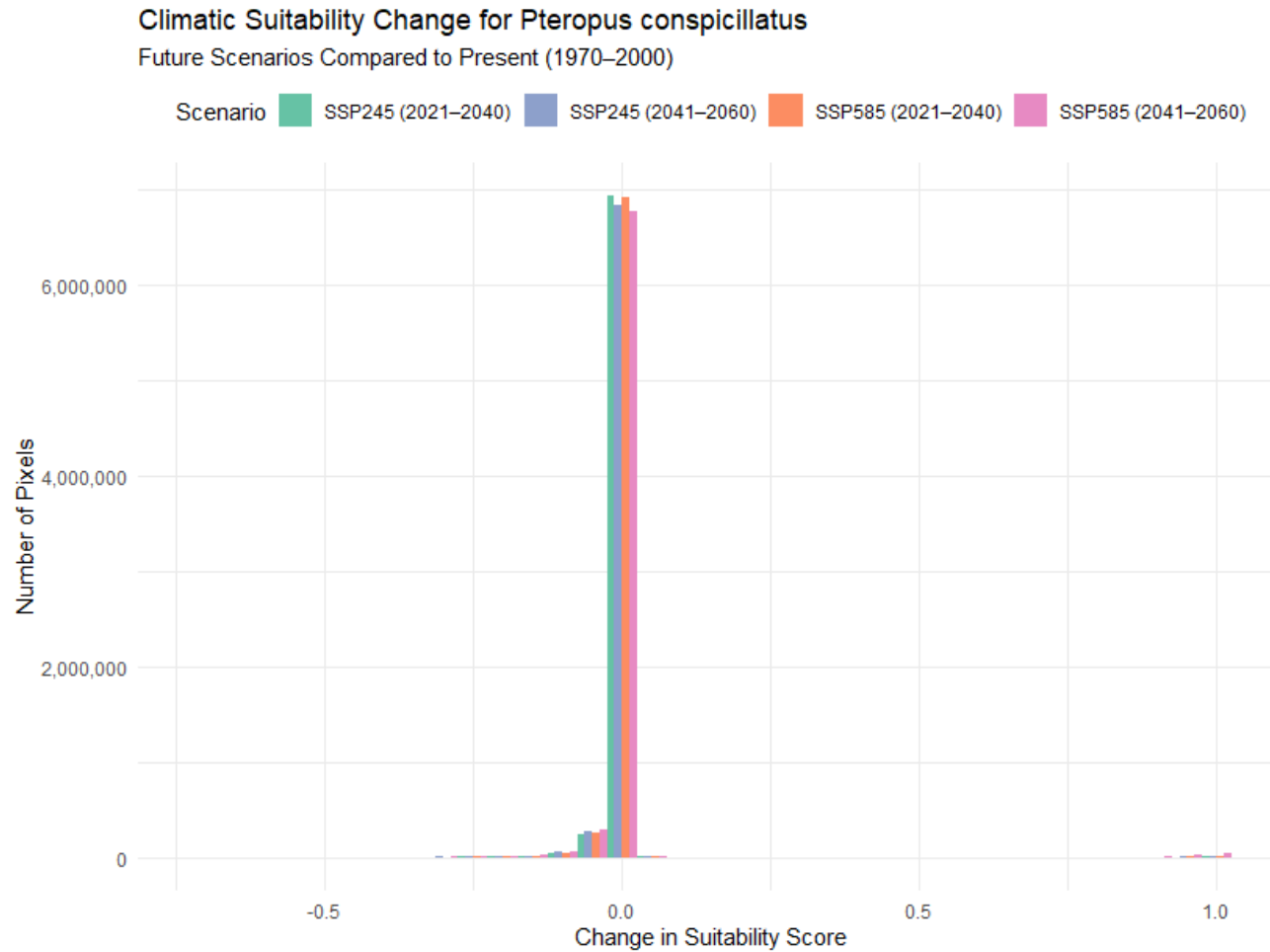


Figure 3.9. Pixel-wise changes in climatic suitability for *Pteropus conspicillatus* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram displays the frequency distribution of logistic suitability changes (future minus present) across all pixels. The distribution is sharply peaked near zero with a distinct left skew, indicating that while most areas remained stable, a greater number of pixels experienced small/minor reductions in climatic suitability.

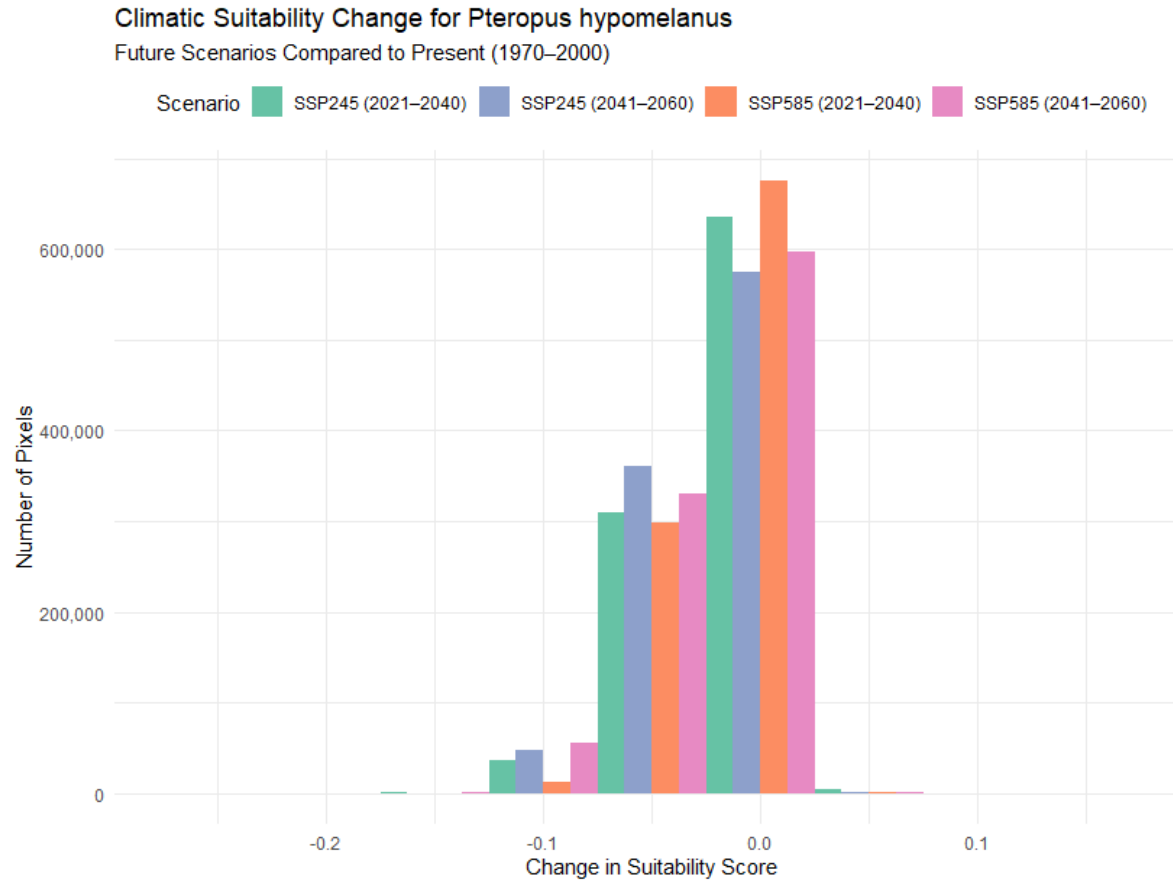


Figure 3.10. Pixel-wise changes in climatic suitability for *Pteropus hypomelanus* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram displays the frequency distribution of suitability score changes (future minus present) across all pixels. The distribution is distinctly left skewed, with most pixels exhibiting moderate declines below -0.1. Very few pixels show positive changes, indicating an overall reduction in climatic suitability across future scenarios.

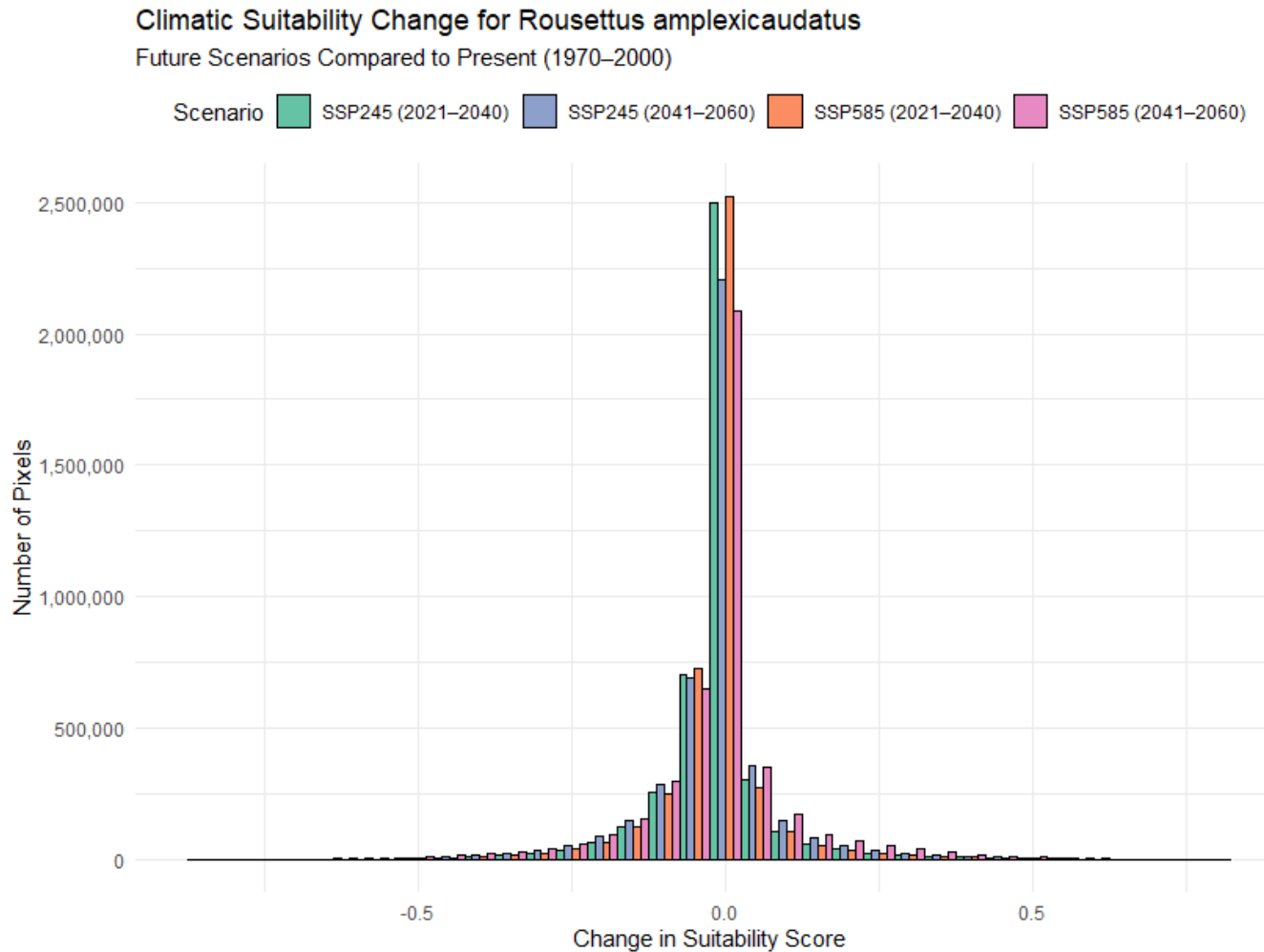


Figure 3.11. Pixel-wise changes in climatic suitability for *Rousettus amplexicaudatus* between baseline (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram displays the distribution of suitability score changes (future minus present) across all pixels. The distribution is approximately symmetric but slightly skewed to the left, indicating that while most pixels exhibit little or no change, a noticeable portion shows negative shifts in climatic suitability. The moderate spread on both sides of zero suggests a mix of pixel-level spread where losses are more noticeable than gains across the projected scenarios.

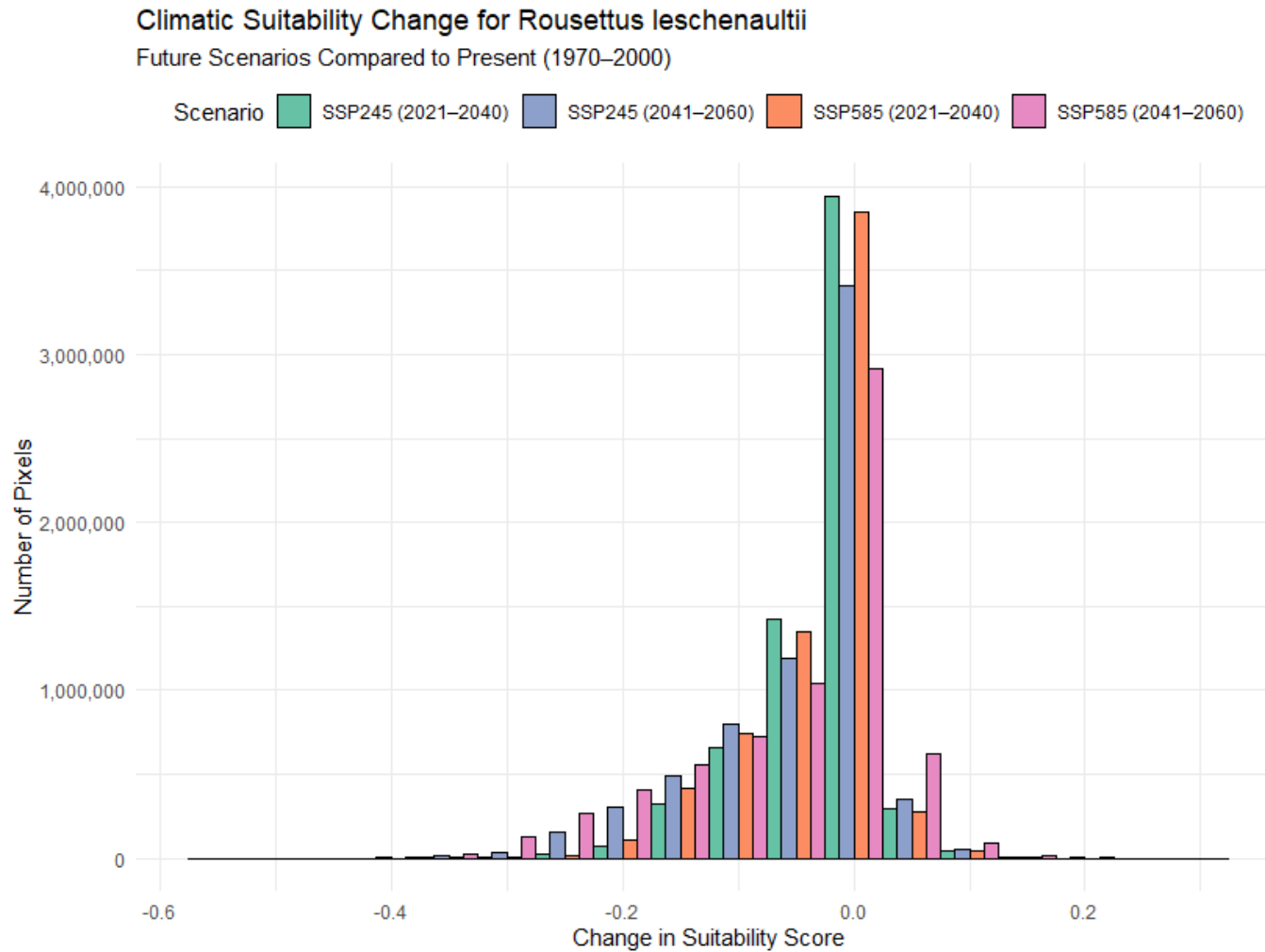


Figure 3.12. Pixel-wise changes in climatic suitability for *Rousettus leschenaultii* between the baseline period (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram illustrates a left-skewed distribution, with a higher concentration of pixels showing negative changes in suitability scores. This indicates that, across all scenarios, more pixels are projected to experience a reduction in climatic suitability relative to the baseline, although modest suitability gains are still present in a smaller subset of pixels.

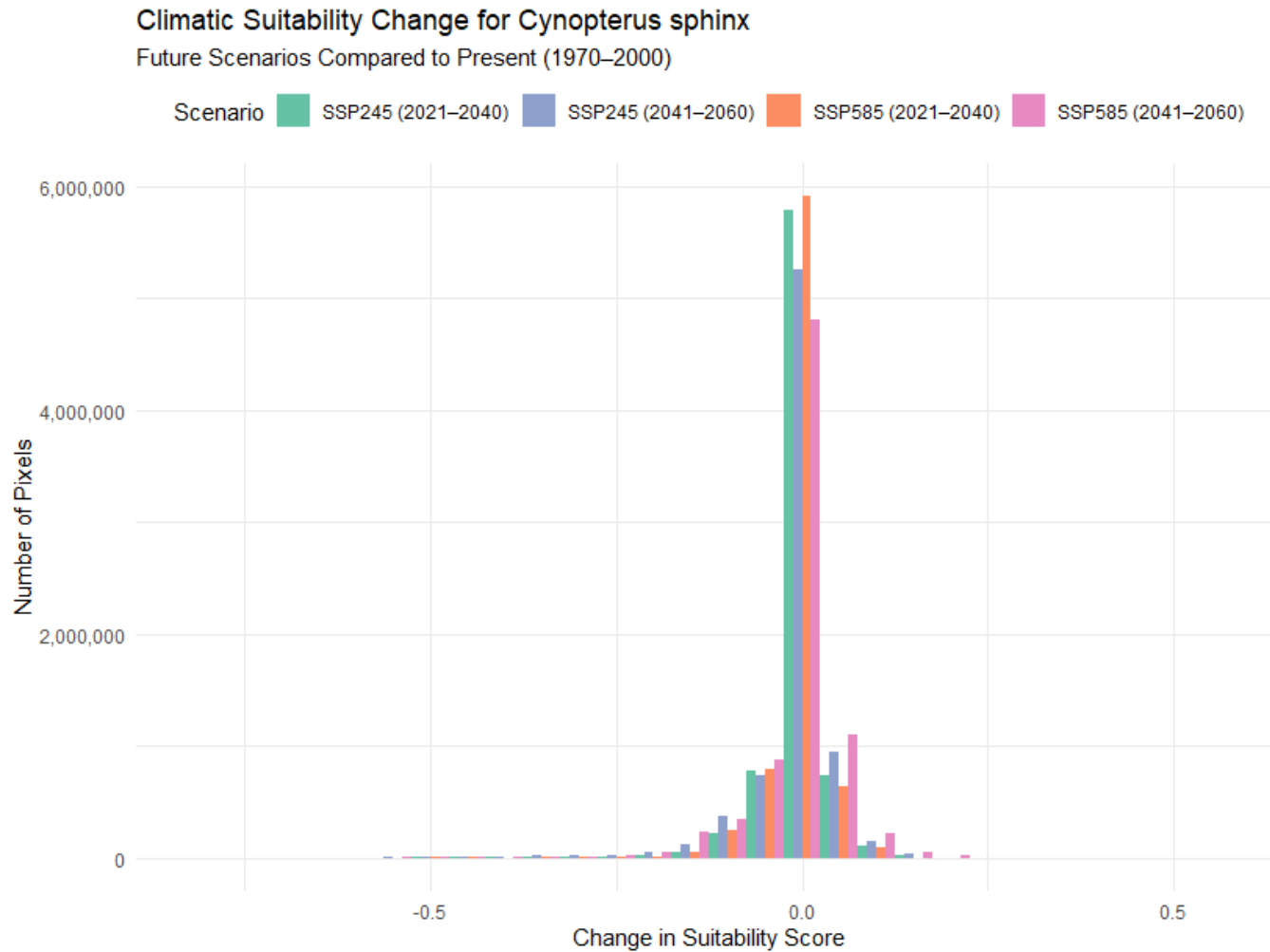


Figure 3.13. Pixel-wise changes in climatic suitability for *Cynopterus sphinx* between the baseline period (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram shows a relatively symmetrical distribution, indicating no notable skew. Most pixel values are concentrated around zero, suggesting minimal net change in climatic suitability across much of the species’ range.

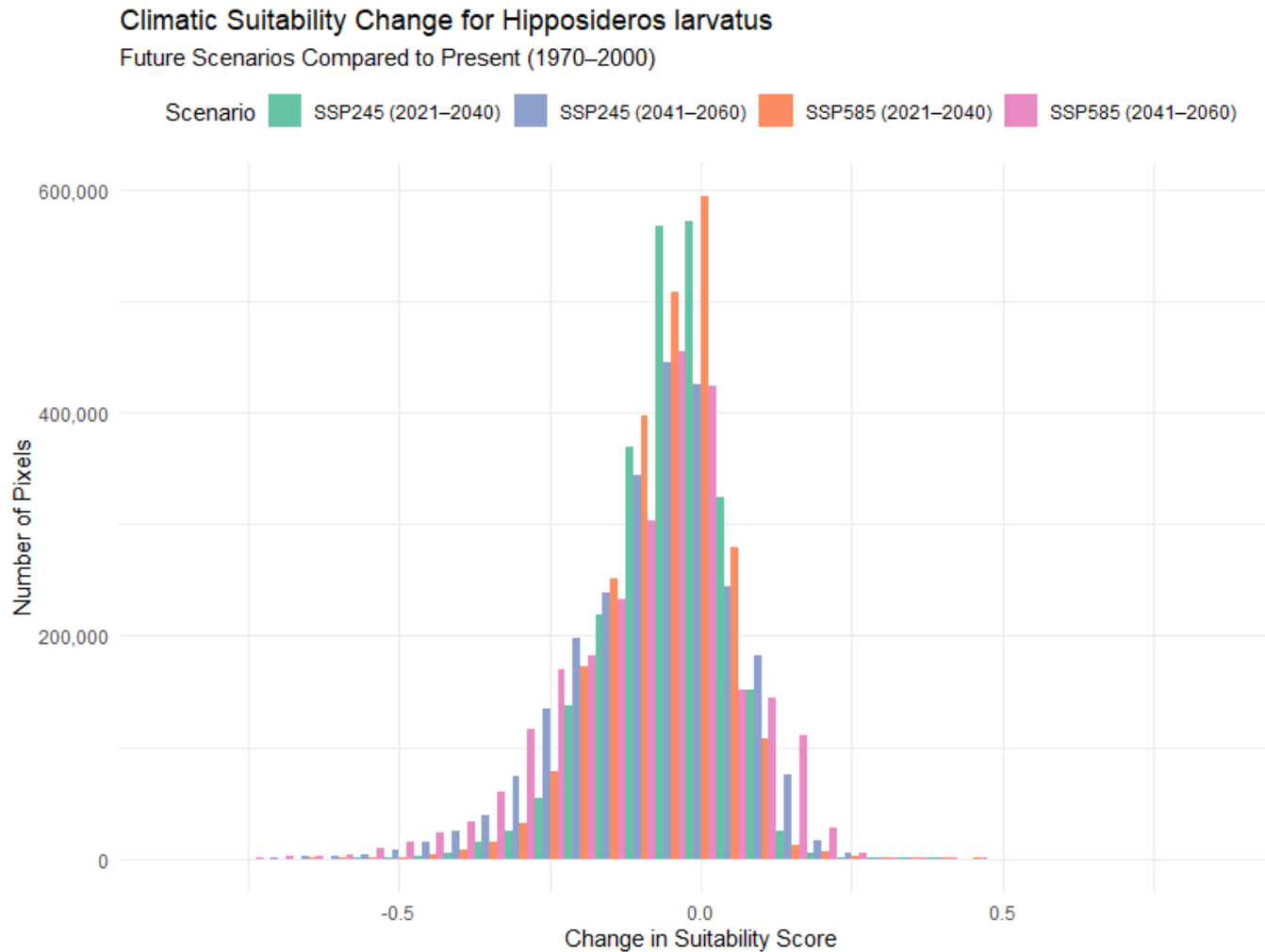


Figure 3.14. Pixel-wise changes in climatic suitability for *Hipposideros larvatus* between the baseline period (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The histogram reveals a moderately left-skewed distribution, with a greater number of pixels showing reductions in suitability. While the majority of pixel values cluster around zero, indicating relative stability in some areas, declines in climatic suitability are more widespread than increases under future climate scenarios.

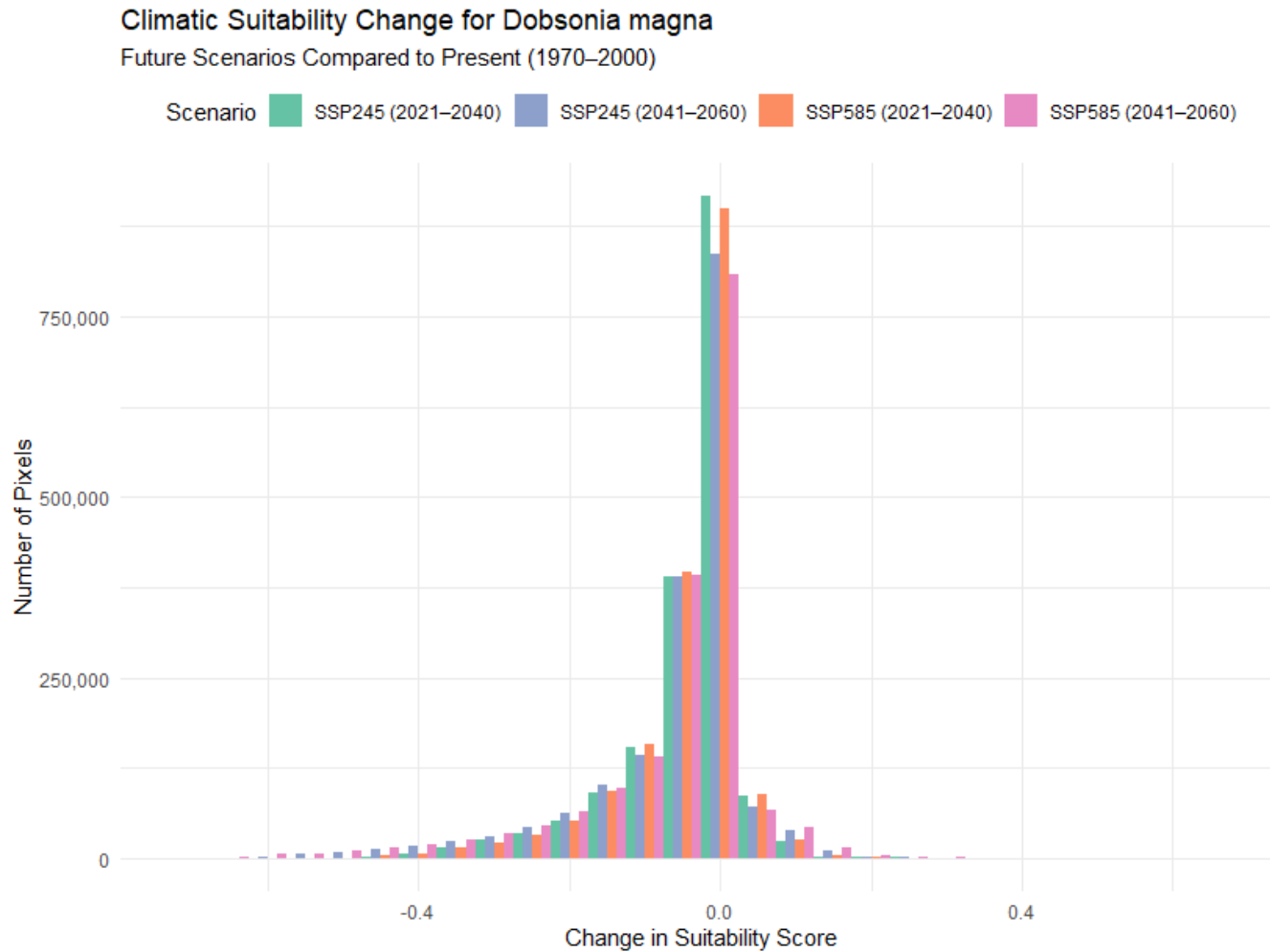


Figure 3.15. Pixel-level changes in climatic suitability for *Dobsonia magna* under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060, relative to the baseline period (1970–2000). The histogram is moderately left-skewed, with a larger proportion of pixels showing reductions in climatic suitability. Although the peak remains centered near zero, the longer negative tail indicates net habitat loss across future scenarios.

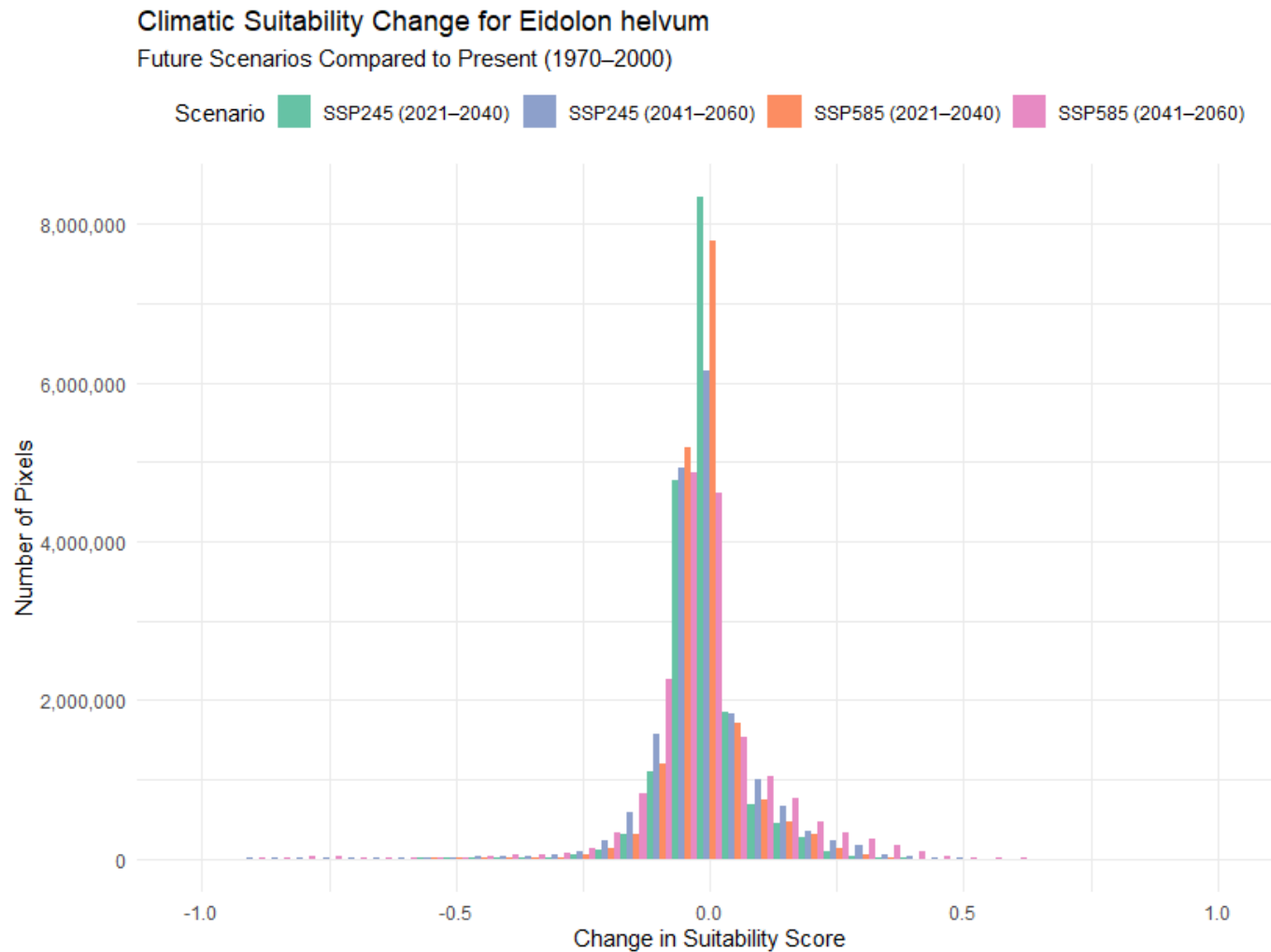


Figure 3.16. Pixel-wise changes in climatic suitability for *Eidolon helvum* between the baseline period (1970–2000) and future projections under SSP245 and SSP585 scenarios for 2021–2040 and 2041–2060. The distribution is slightly right-skewed, reflecting a modest number of pixels with increased suitability. While most values cluster near zero, the positive tail indicates emerging areas of climatic suitability under future climate scenarios.

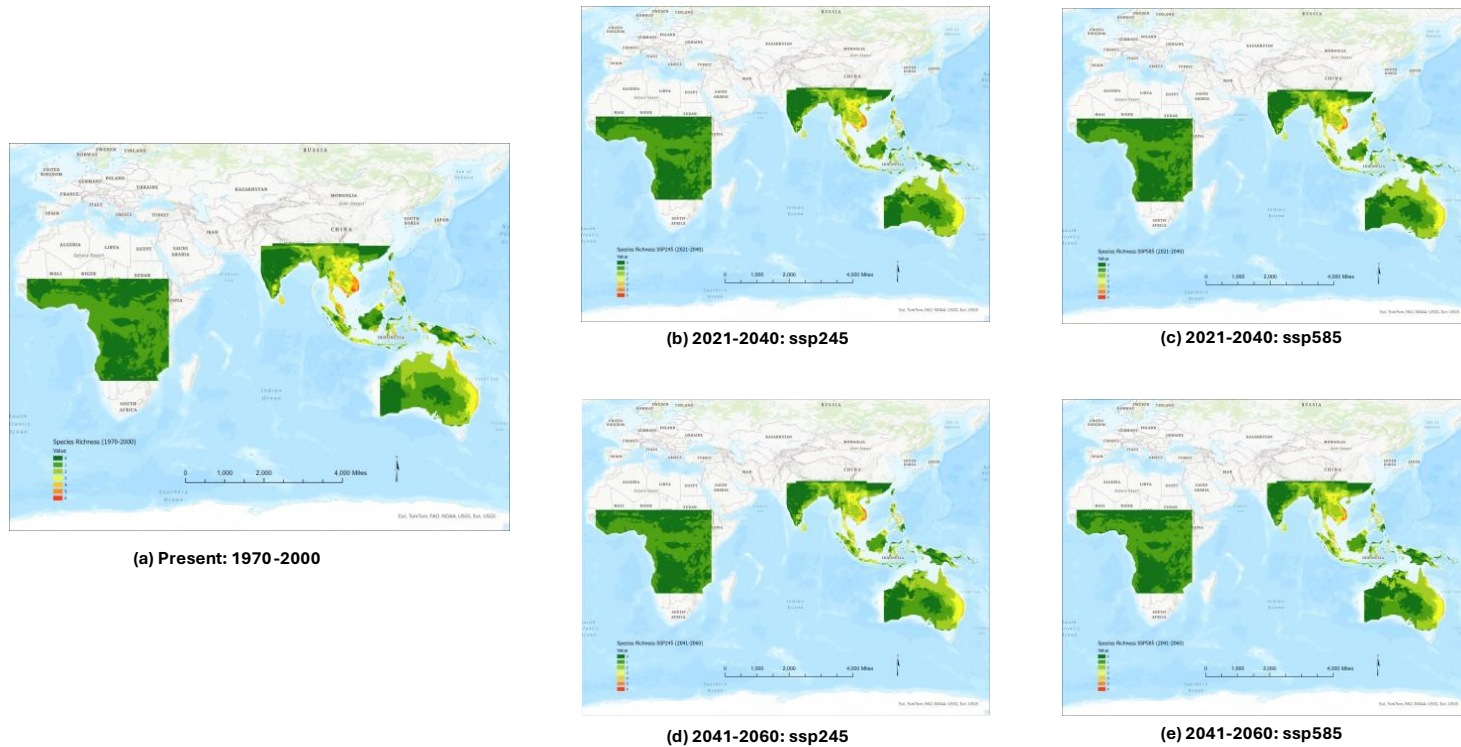


Figure 3.17 Projected species richness of Nipah virus associated bat species under different climate and emission scenarios. Panel (a) shows baseline richness (1970–2000). Panels (b) and (d) represent projected richness under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient indicates the number of overlapping species per grid cell, ranging from 0 (dark green) to 6 (dark red), highlighting areas of potential multi-species concentration under future climatic conditions.

APPENDIX IIIA

SUPPLEMENTARY FIGURES

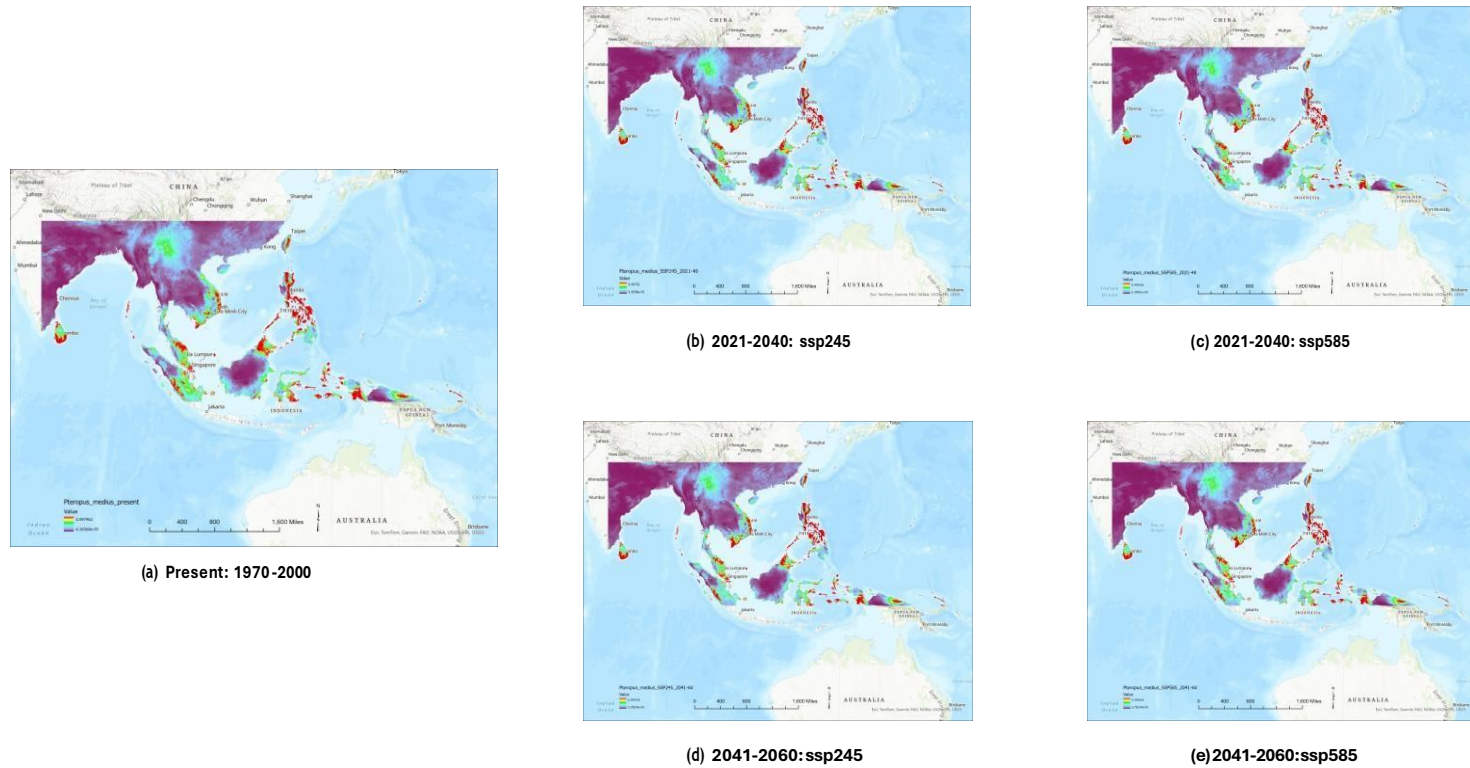


Figure S1. Projected climatic suitability for *Pteropus medius* under baseline and future climate scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

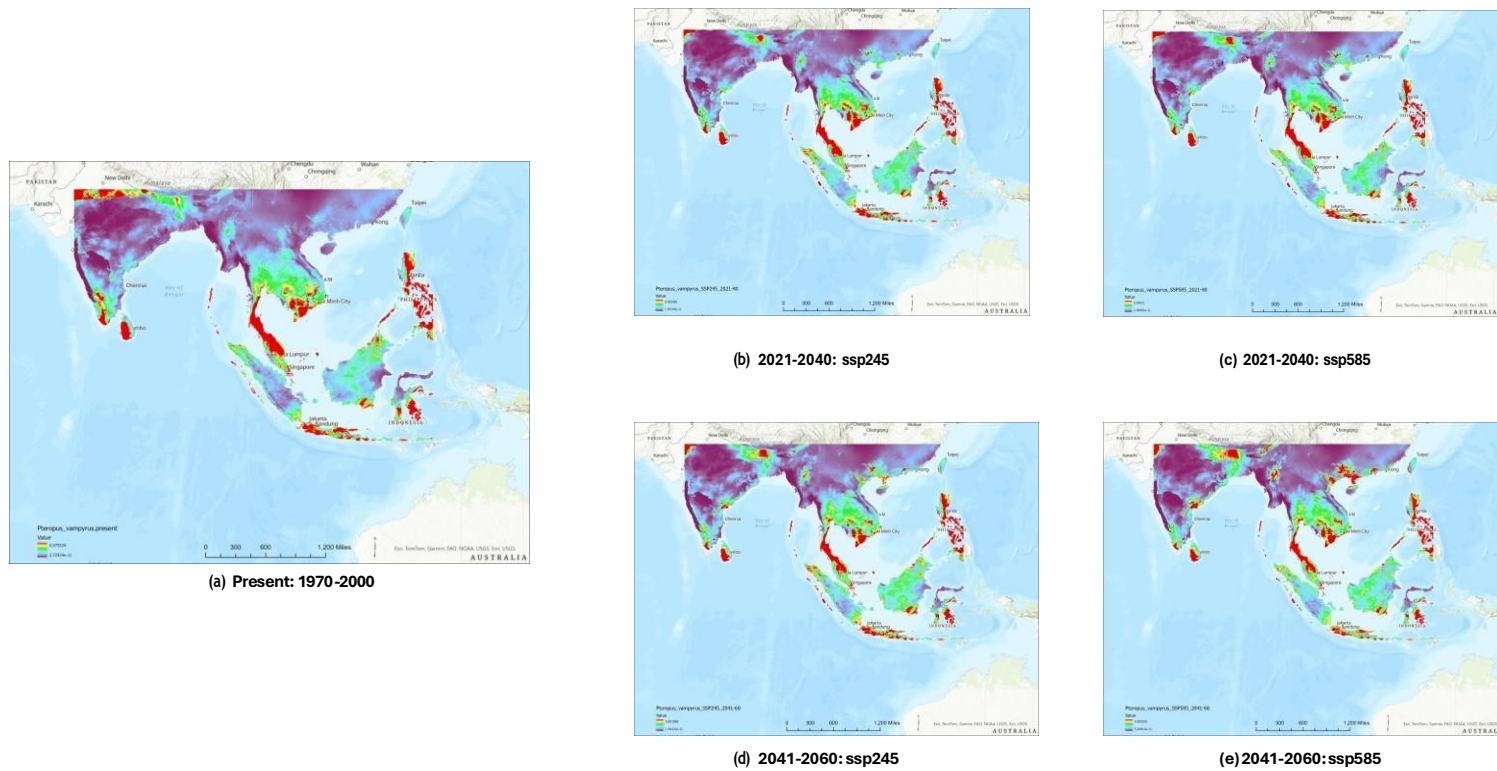


Figure S2. Projected climatic suitability for *Pteropus vampyrus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

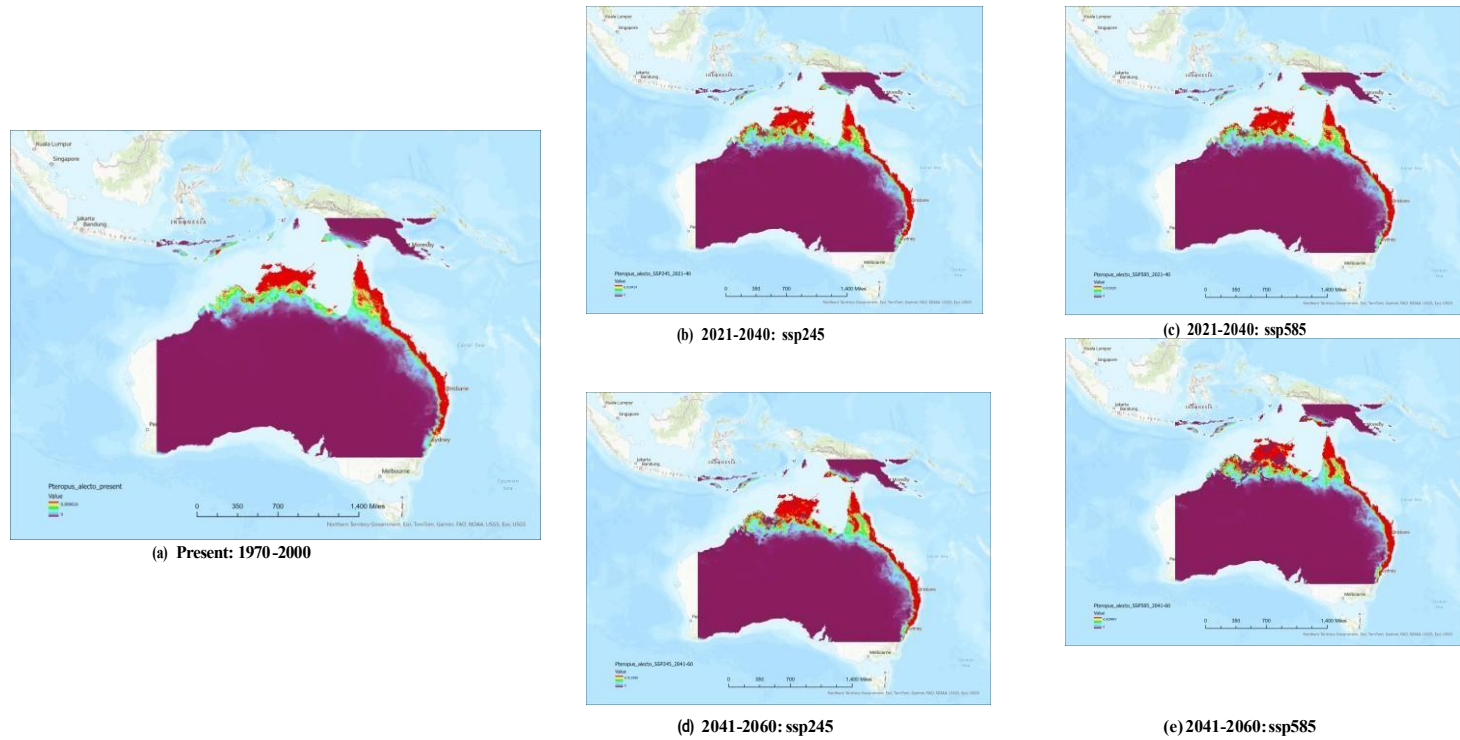


Figure S3. Projected climatic suitability for *Pteropus alecto* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

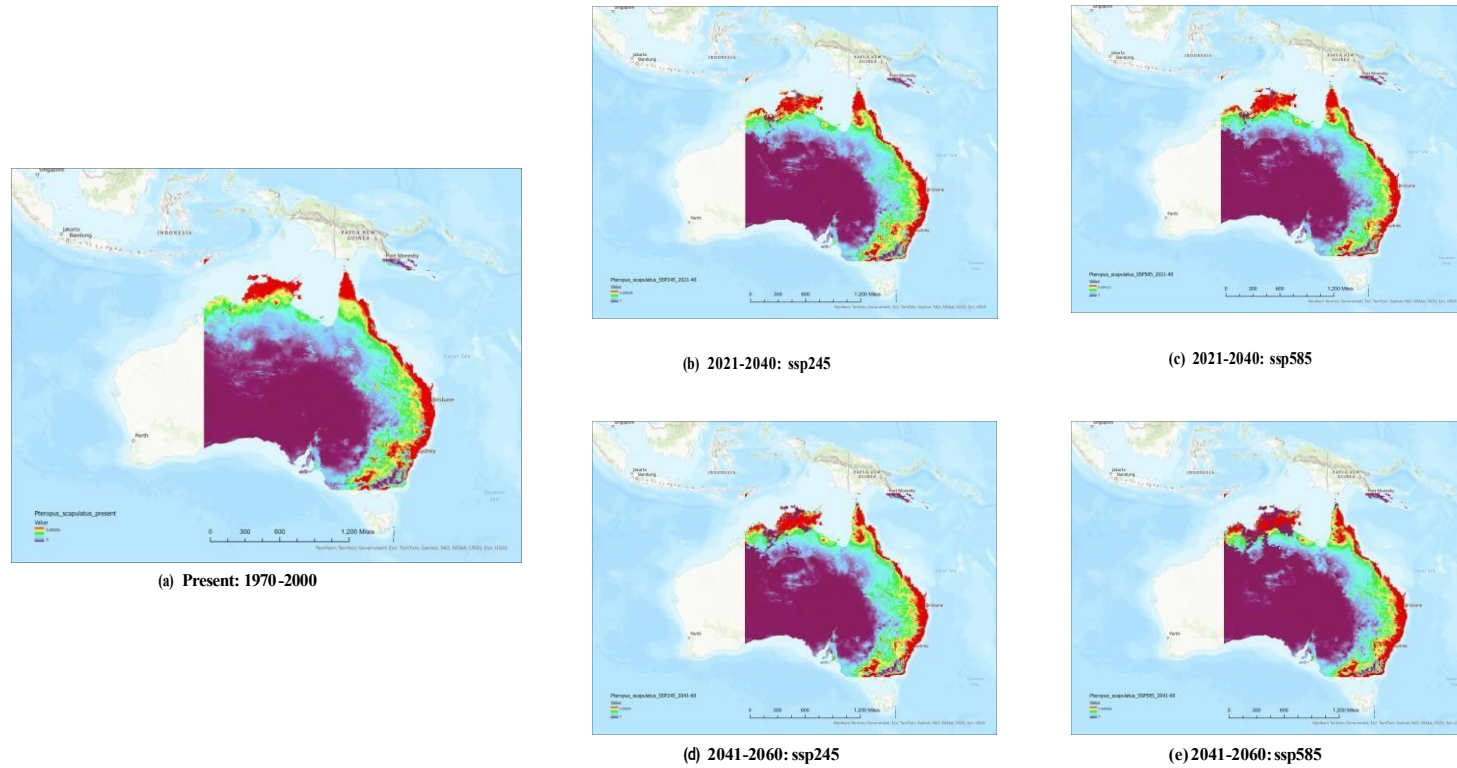


Figure S4. Projected climatic suitability for *Pteropus scapulatus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

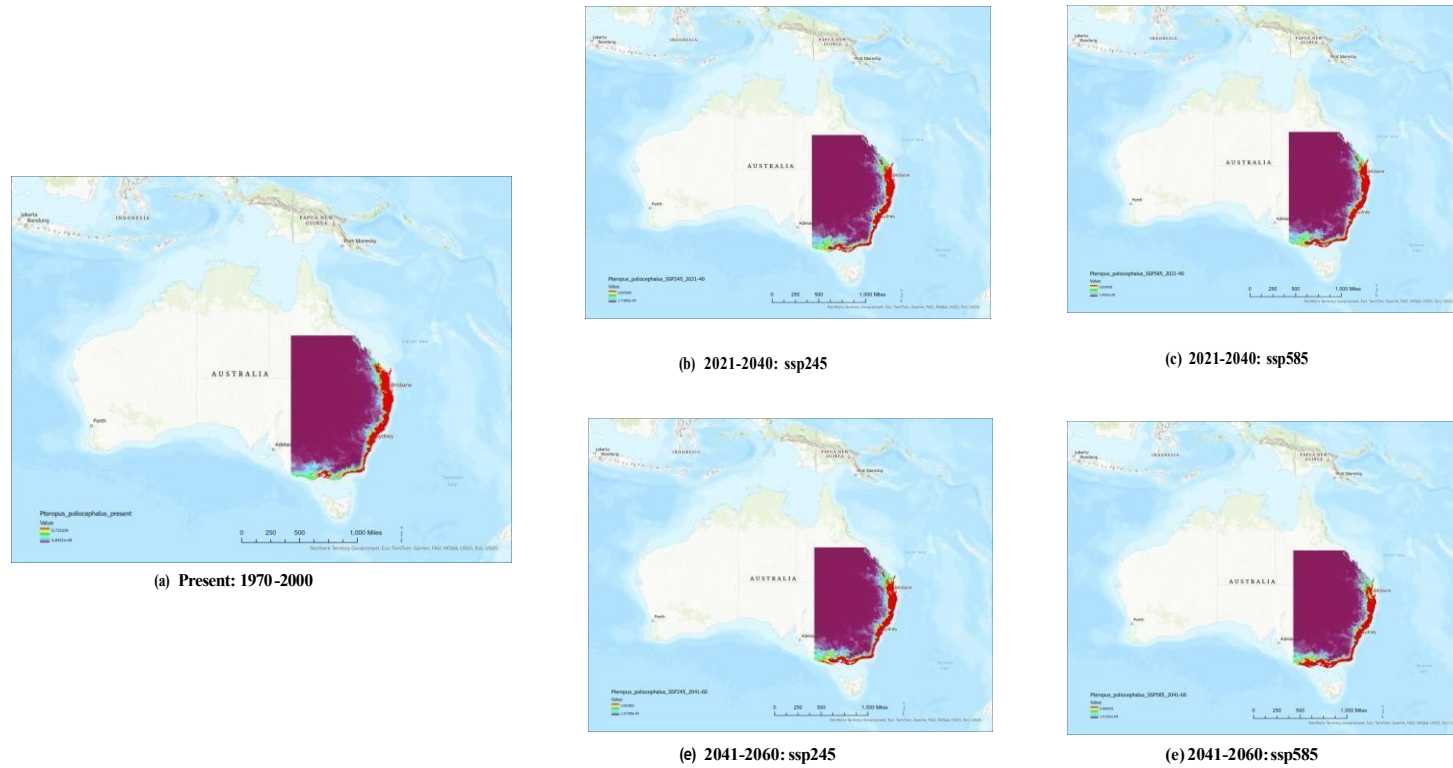


Figure S5. Projected climatic suitability for *Pteropus poliocephalus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

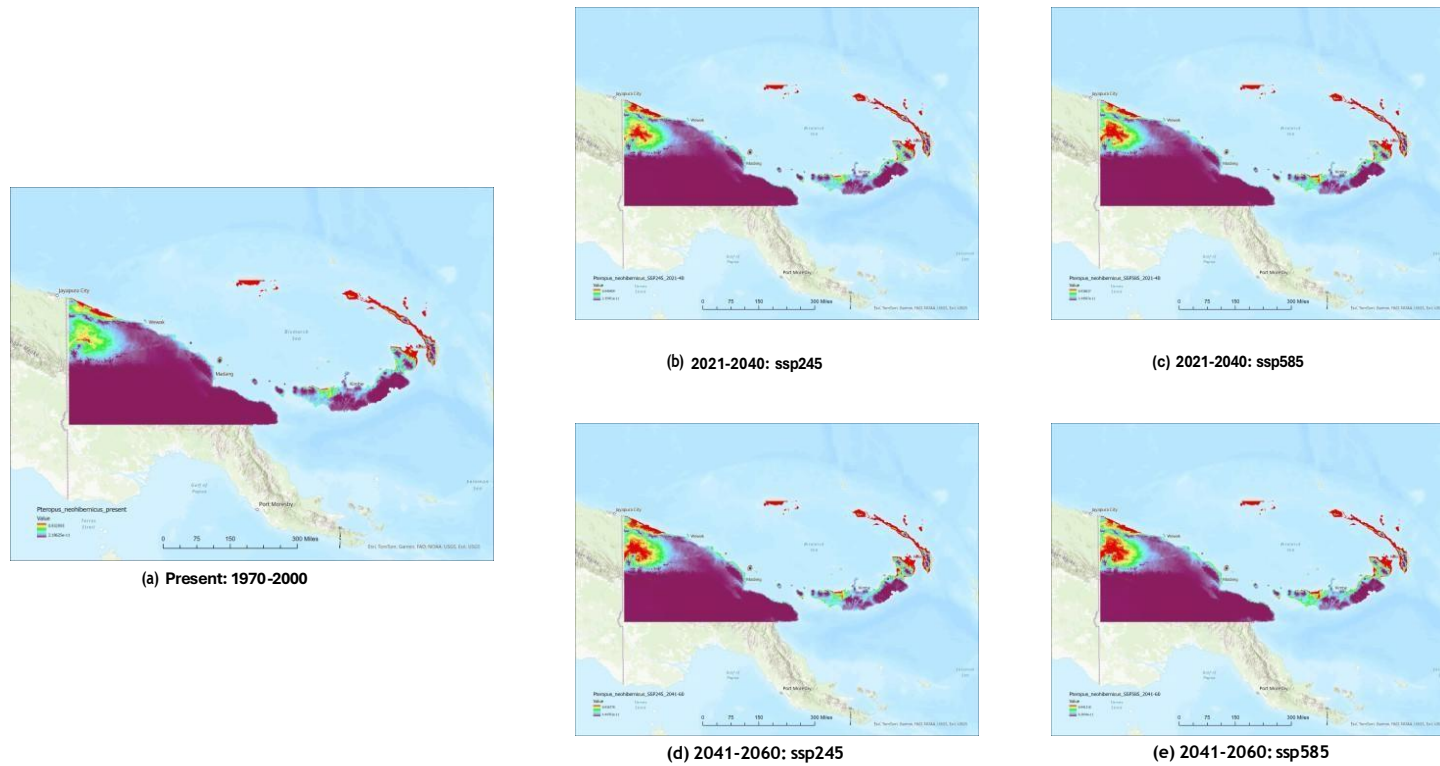


Figure S6. Projected climatic suitability for *Pteropus neohibernicus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

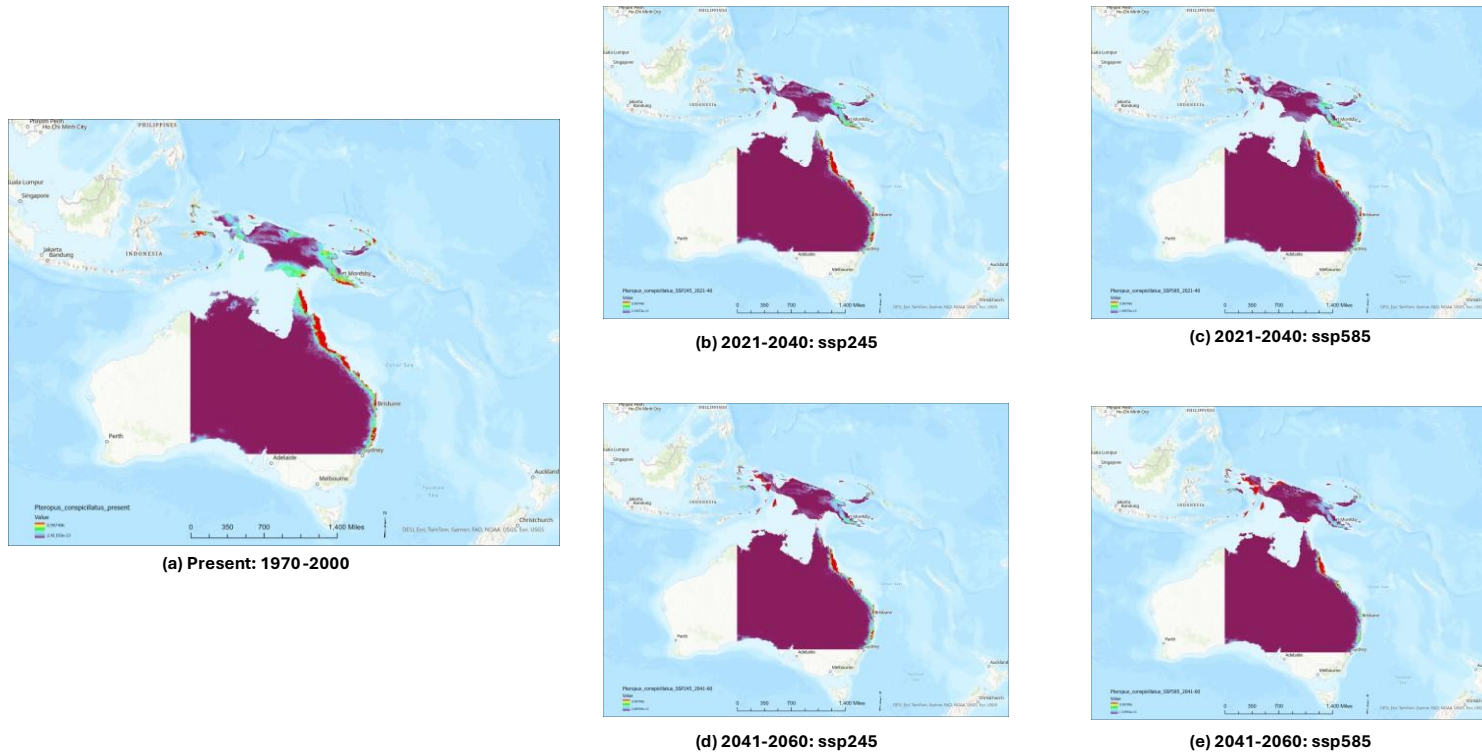


*Figure S7. Projected climatic suitability for *Pteropus conspicillatus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.*

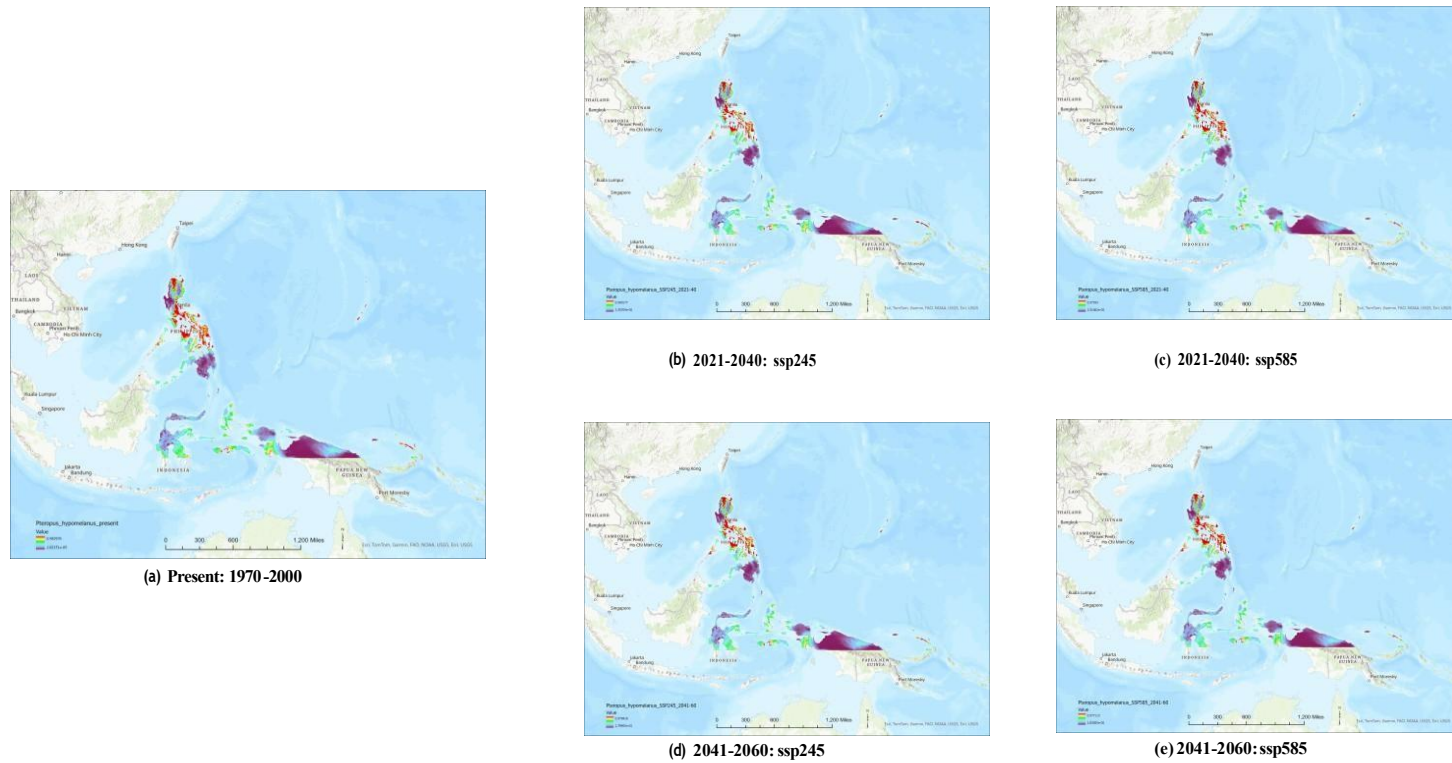


Figure S8. Projected climatic suitability for *Pteropus hypomelanus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

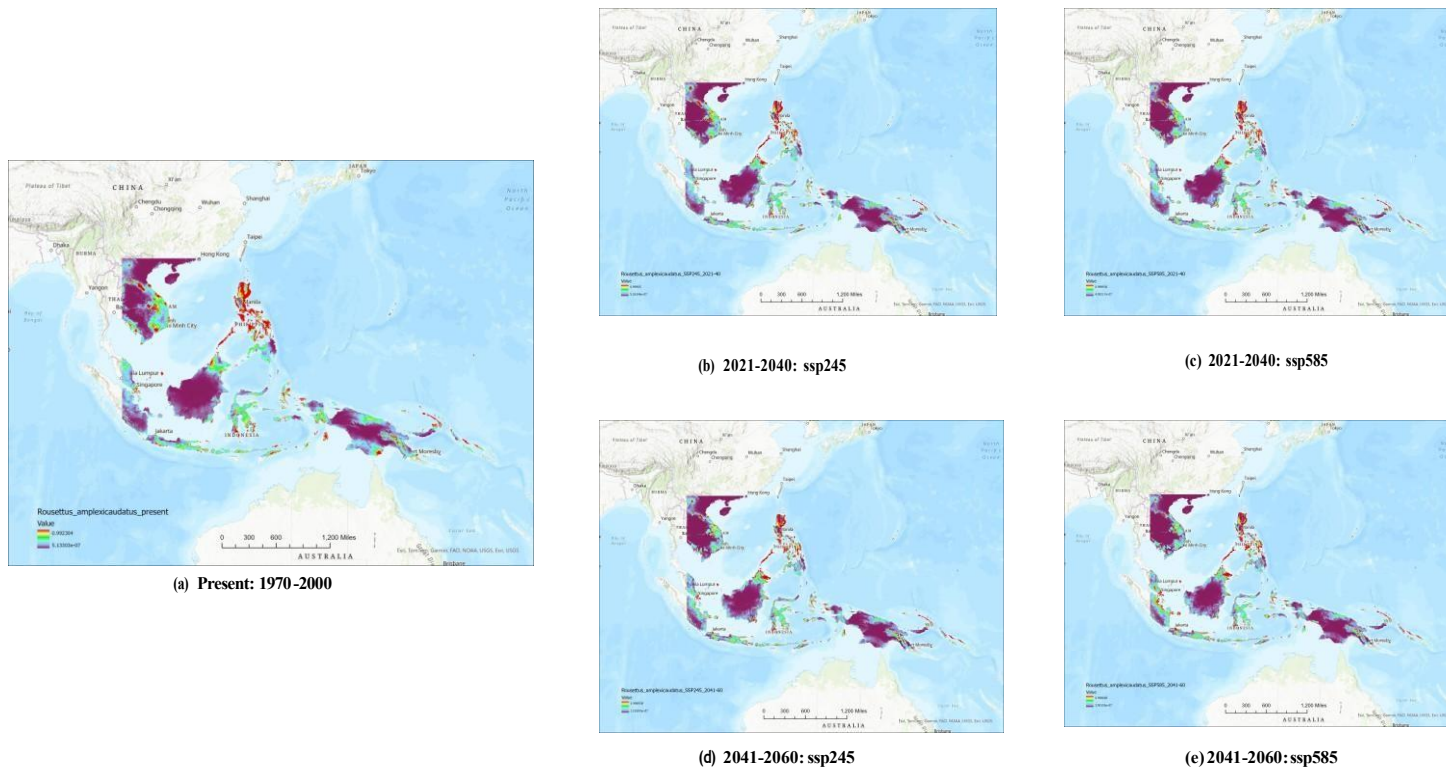
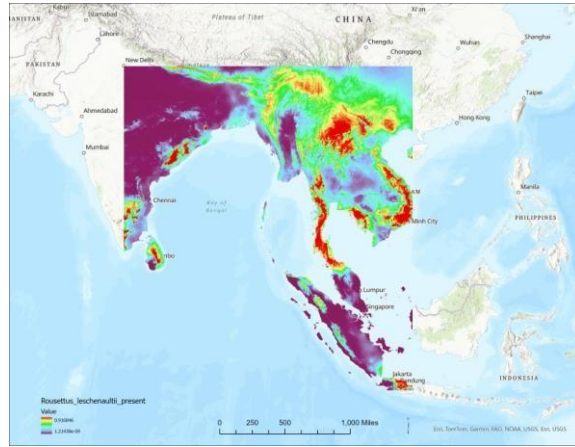
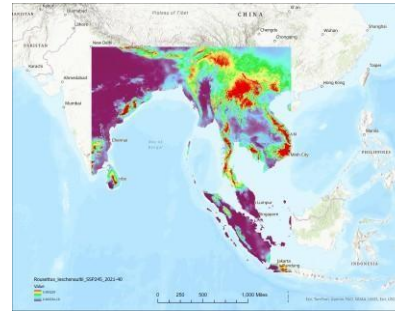


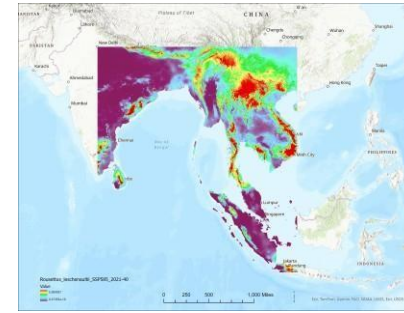
Figure S9. Projected climatic suitability for *Rousettus amplexicaudatus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.



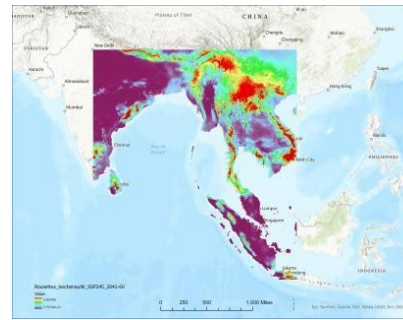
(a) Present: 1970–2000



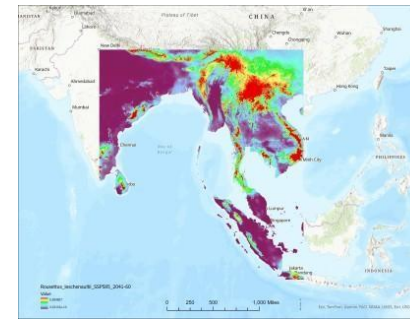
(b) 2021–2040: ssp245



(c) 2021–2040: ssp585



(d) 2041–2060: ssp245



(e) 2041–2060: ssp585

Figure S10. Projected climatic suitability for *Rousettus leschenaultii* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

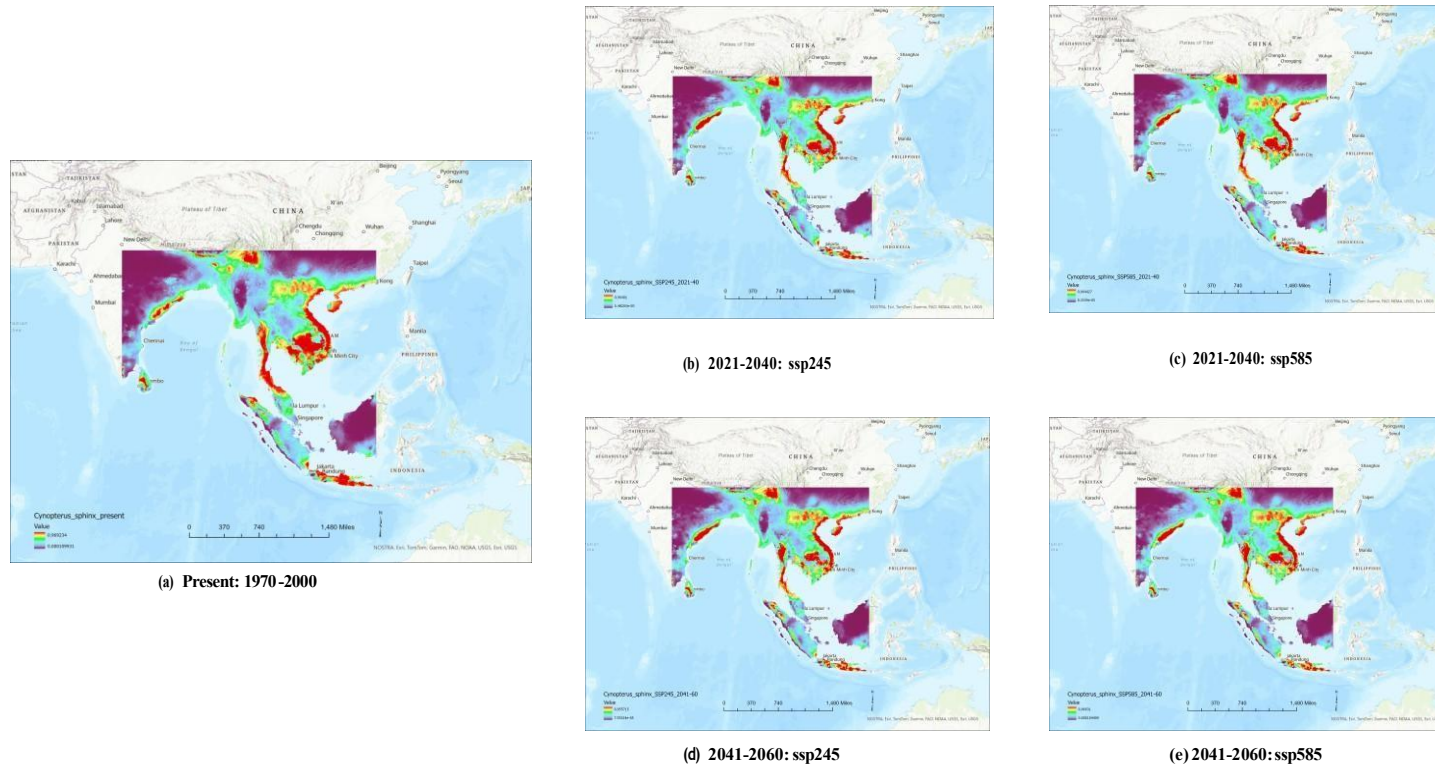


Figure S11. Projected climatic suitability for *Cynopterus Sphinx* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

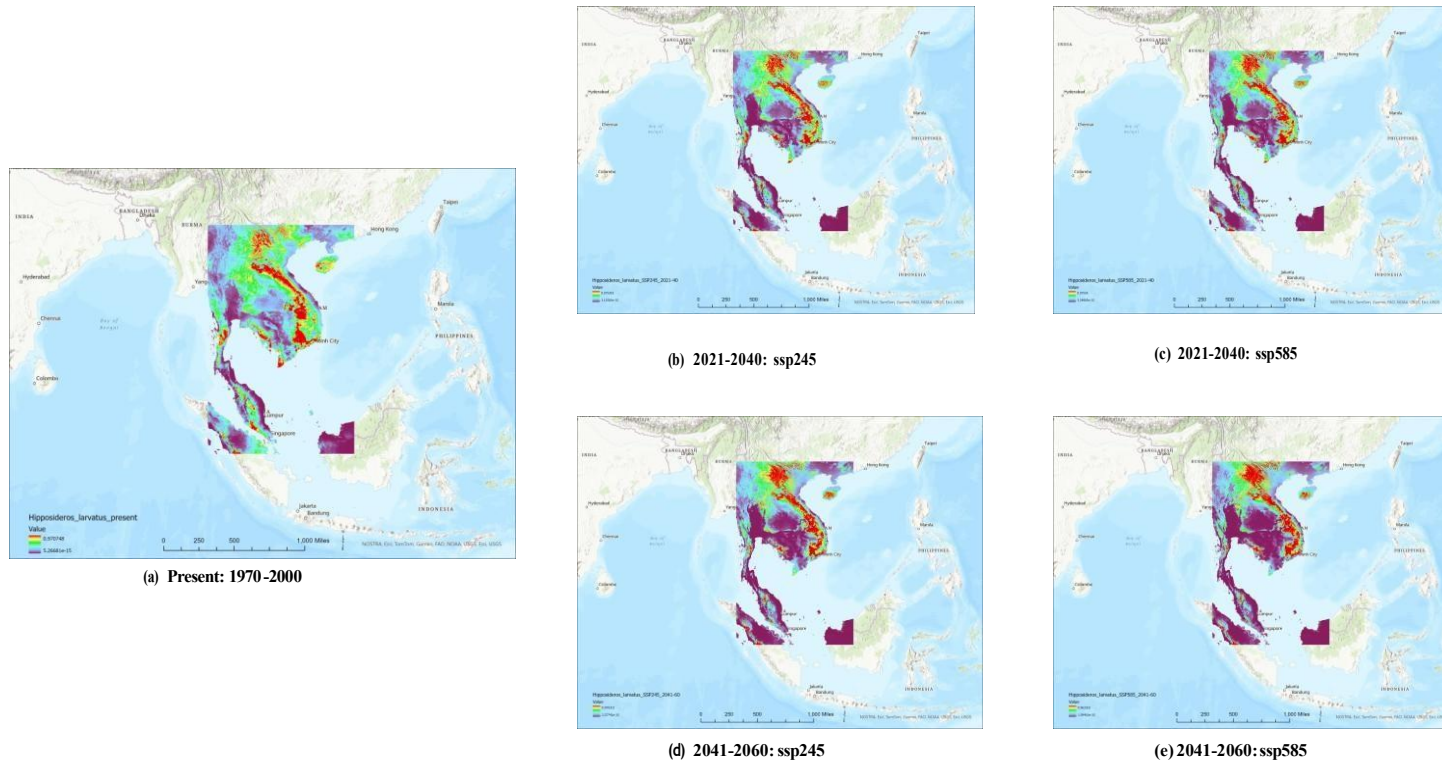
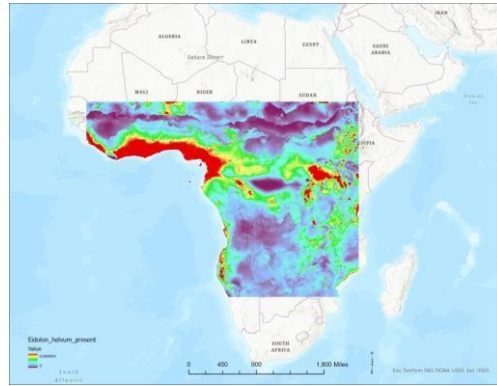
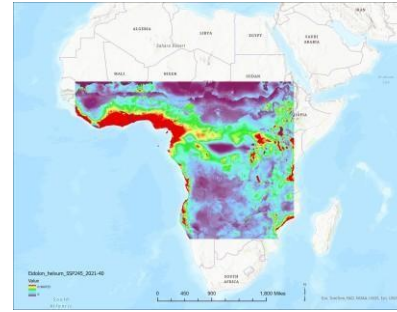


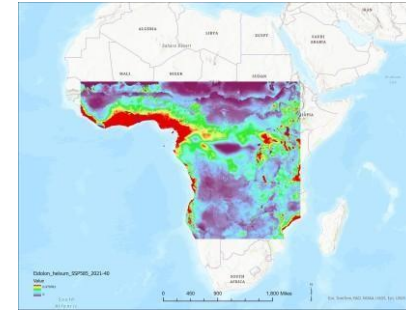
Figure S12. Projected climatic suitability for *Hipposideros larvatus* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.



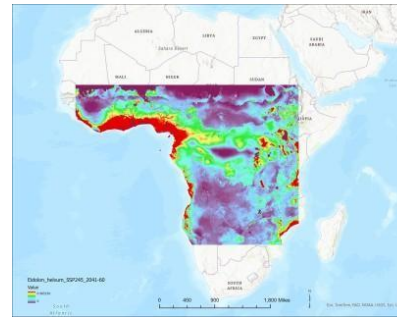
(a) Present: 1970–2000



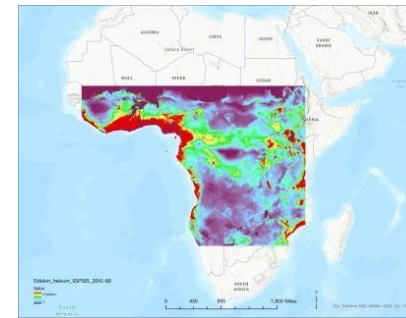
(b) 2021–2040: ssp245



(c) 2021–2040: ssp585



(d) 2041–2060: ssp245



(e) 2041–2060: ssp585

Figure S13. Projected climatic suitability for *Eidolon helvum* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

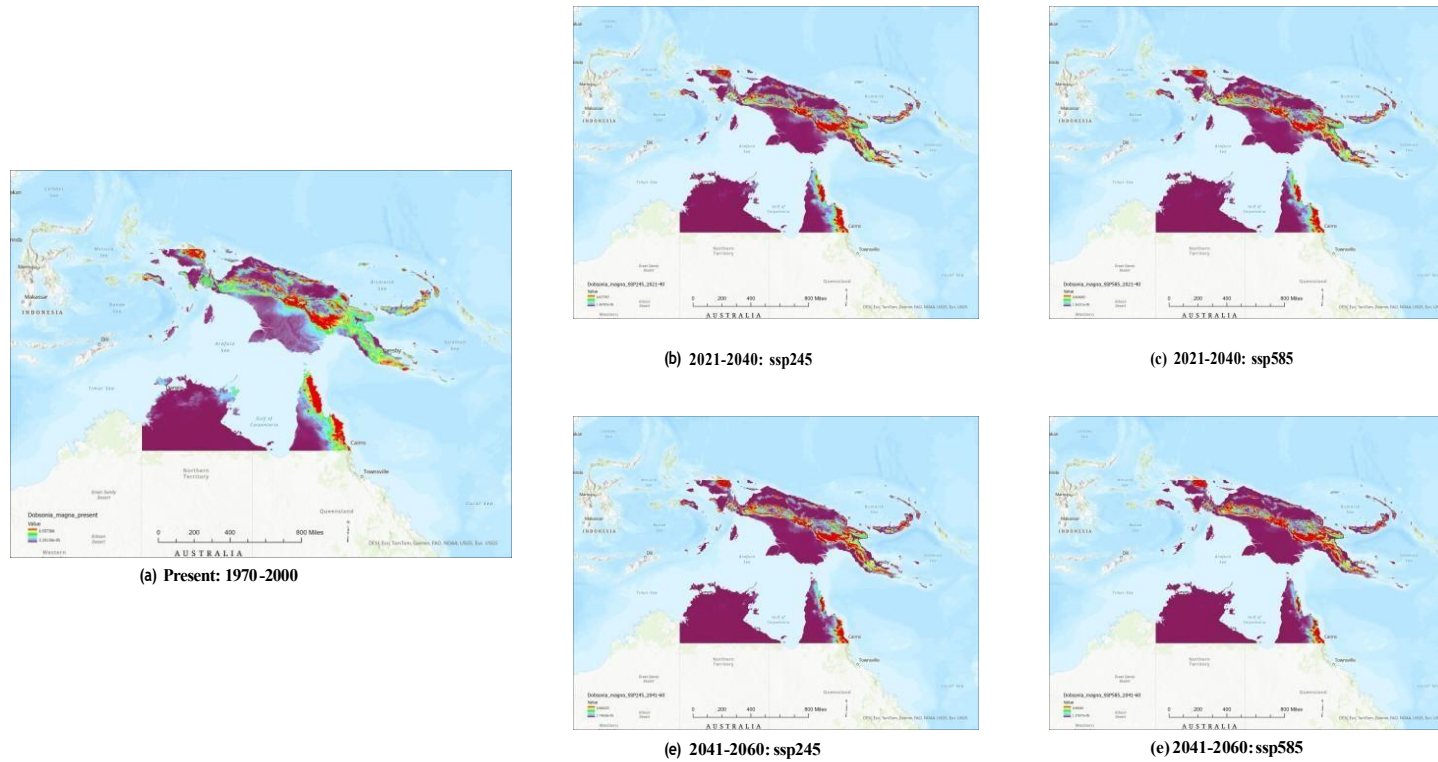


Figure S14. Projected climatic suitability for *Dobsonia magna* under different climate and emission scenarios. Panel (a) shows baseline suitability (1970–2000). Panels (b) and (d) represent projections under SSP245 for 2021–2040 and 2041–2060, respectively, while panels (c) and (e) show projections under SSP585 for 2021–2040 and 2041–2060. The color gradient represents logistic suitability values, ranging from low (dark purple) to high (bright red), indicating the relative probability of climatically suitable conditions across the species' range.

CONCLUSION

This dissertation integrates three distinct but interconnected studies to explore how social, environmental, and etiological factors interact to shape the emergence and persistence of infectious disease threats. By combining field research, meta-analysis, and spatial modeling, it provides a comprehensive and interdisciplinary understanding of risk patterns associated with emerging and reemerging infectious diseases in vulnerable socioecological settings.

The first chapter examined vector-borne disease awareness and prevention practices in two remote island communities in South and Southeast Asia. Despite facing similar ecological conditions, Gaya Island in Malaysia exhibited significantly higher knowledge levels and more robust preventive behaviors than Shahpori Island in Bangladesh. These differences were strongly associated with disparities in education, access to healthcare services, and public health infrastructure. The findings underscore the importance of investing in locally adapted health communication strategies that are culturally relevant and community driven. In geographically isolated and socioeconomically marginalized regions, such targeted interventions can play a crucial role in reducing disease transmission and enhancing resilience against climate-sensitive vector-borne threats.

The second chapter synthesized global literature on anthrax through a systematic meta-analysis to identify key risk factors for human anthrax. It identified occupational exposure, particularly among those who handle, slaughter, or consume moribund and infected livestock, as the strongest and most consistent driver of infection. These behaviors are often rooted in structural vulnerabilities such as poverty, food insecurity, inadequate veterinary infrastructure, insufficient livestock vaccination, and traditional practices. The synthesis of findings from diverse socio-ecological contexts highlights the need for comprehensive prevention strategies that extend beyond individual behavior change. Livestock vaccination programs, improved carcass disposal practices, and culturally appropriate health education are essential components of a broader One Health approach that addresses the interconnected risks to animals, humans, and the environment.

The third chapter used ecological niche models to project the current and future climatic suitability distributions of fourteen bat species associated with Nipah virus ecology and transmission dynamics. The projections, based on mid and high greenhouse gas emission scenarios, revealed substantial range expansions and shifts in climatic suitability across South and Southeast Asia. These changes are likely to increase the frequency and spatial reach of human-bat interactions, particularly in densely populated or agriculturally expanding areas. The results offer important insights into the geographic redistribution of zoonotic risk in a changing climate and emphasize the importance of integrating spatial modeling tools into early warning systems and disease surveillance platforms.

Together, these studies offer a unified framework for understanding and responding to EIDs through the lens of social and environmental vulnerability. Disease risk is shaped not only by pathogen biology, but also by structural inequalities, ecological change, socioeconomic disparities, and gaps in public health capacity. This work affirms a growing consensus that interdisciplinary, cross-sectoral strategies are required to detect, prevent, and respond to emerging zoonoses. A proactive and predictive public health agenda must include investments in education, surveillance, ecological forecasting, and community engagement. By combining local perspectives, global data synthesis, and predictive modeling, this dissertation contributes to a more integrative vision of pandemic preparedness. It highlights the urgency of climate-informed health systems and the value of place-based approaches that prioritize equity, sustainability, and resilience. These findings can inform both national strategies and international frameworks aimed at reducing the risk of future zoonotic spillover events and ensuring that vulnerable populations are not left behind in the evolving landscape of infectious disease threats.

VITA

Belal Hossain is a Ph.D. candidate in Ecology and Evolutionary Biology at the University of Tennessee, Knoxville, where he joined Dr. Fefferman's lab in 2021. Originally from Feni, Bangladesh, Belal holds a Master of Public Health (MPH) in Epidemiology and a Doctor of Veterinary Medicine (DVM). Before starting his doctoral training at UTK, he served as an Assistant Scientist at the International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b), where he worked on infectious disease surveillance, outbreak response, and global health. His research interests lie at the intersection of ecology and epidemiology of emerging infectious disease, and One Health, with a particular focus on ecological drivers of pathogen spillover. Belal is an active member of the Student Coalition of One Health at UTK and is committed to interdisciplinary, community-engaged public health research.