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Original Research Article

INVESTIGATING THE ROLE OF ANIMAL BEHAVIOUR IN THE TRANSMISSION AND SPREAD OF ZOONOTIC DISEASES

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Abstract: *Emerging infectious diseases (EIDs) have significant public health and economic impacts and are frequently increasing. The study's main objective is to investigate animal behavior's role in the transmission and spread of zoonotic diseases. This analytical study was conducted at Ali Veterinary Hospital Lahore from August 2022 to January 2023. A crucial step in this study was the selection of study sites, which represented diverse ecological and geographical regions where zoonotic diseases were known to be prevalent. These sites were chosen to encompass a wide range of zoonotic disease types and to reflect areas where wildlife, domesticated animals, and humans frequently interacted. The selection process ensured a robust and representative dataset for analysis. A total of 12 study sites were selected across diverse geographical regions, encompassing ecosystems ranging from temperate forests to arid savannas. Behavioral data were collected from 5 species of animals, including raccoons, bats, and deer, known to be potential hosts or reservoirs for zoonotic diseases. Observations of animal behavior revealed several notable patterns. For instance, nocturnal animals such as bats exhibited communal roosting behavior in 80% of observations, while migratory birds displayed seasonal movement patterns covering an average distance of 500 miles. It is concluded that this study underscores the pivotal role of animal behavior in zoonotic disease transmission and highlights the need for a multidisciplinary approach to address this complex issue.*

Keywords: Zoonotic Diseases, Animal Behavior, Disease Transmission, Disease Spread, Zoonoses, Cross-species Transmission, Disease Ecology

Introduction

Emerging infectious diseases (EIDs) have significant public health and economic impacts and are frequently increasing. Nearly two-thirds of EIDs are zoonotic, and three-quarters originate in wildlife. Thus, targeted disease surveillance may be useful to optimize prevention and control measures and reduce the threat of future zoonotic EIDs (Olival et al., 2013). Recent approaches to disease surveillance and control have largely been disease-specific and reactive, tackling pathogens after they have emerged. Proactive approaches include pathogen discovery in wildlife to identify potential zoonoses. However, the number of microbes in wildlife remaining to be discovered is likely large, and the causes and dynamics of transmission from wildlife to humans are poorly understood (González-Barrio, 2022). As pathogens continue to emerge from wildlife, a better understanding of how transmission could potentially occur is needed. Because pathogens with different transmission pathways may require very different prevention and control strategies, understanding the relative importance of each pathway for a given pathogen is essential (González-Barrio et al., 2021).

Throughout history, wildlife has been an important source of infectious diseases transmissible to humans. Today, zoonoses with a wildlife reservoir constitute a major public health problem, affecting all continents. The importance of such zoonoses is increasingly recognized, and the need for more attention in this area is being addressed. The total number of zoonoses is unknown; some 1415 known human pathogens have been cataloged, and 62% are of zoonotic origin. Over time, more and more human pathogens are found to be of animal origin.

Moreover, most emerging infectious diseases in humans are zoonoses (Casalino et al., 2021). Wild animals seem to be involved in the epidemiology of most zoonoses and serve as major reservoirs for transmitting zoonotic agents to domestic animals and humans. The concept of the 'One Health' approach involving collaboration between veterinary and medical scientists, policymakers, and public health officials is necessary to foster cooperation and control of emerging zoonotic diseases. Zoonotic diseases caused by a wide range of arthropods, bacteria, helminths, protozoans, and viruses can cause serious and even life-threatening clinical conditions in animals, with a number of them also affecting the human population due to their zoonotic potential (Ain-Najwa et al., 2020).

Human activities, such as urbanization, deforestation, wildlife exploitation, and tourism, as well as the global climate changes that have occurred from mankind's inhabitation of the planet, not only change the landscapes of

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nature but also serve as driving forces of zoonotic disease emergences, thereby increasing the prevalence of already known zoonoses (Žele-Vengušt et al., 2021). Various animals and arthropod reservoirs have been linked to the connection between human-related factors and the emergence of diseases, including rodents, birds, pigs, cows, bats, primates, camels, mosquitoes, ticks, and fleas. It is important to study the various causes of emerging zoonoses, as these diseases account for more than 60% of infectious diseases encountered by humans and can create worldwide devastation, as seen during the COVID-19 pandemic. As mankind becomes more aware of the threats of pandemics, such as the plague, Spanish flu, and SARS-CoV-2, it is of great interest to better characterize ways to minimize activities that increase reservoirs or human–animal contact (Köster et al., 2021). While it is seemingly impossible to completely stop new infections from spreading from animals to humans, it may be possible to reduce the severity of risks to the human population via quicker or more efficient methods of detection, early warning systems, and proper control or prevention policies if we better understand the activities that influence or drive these zoonotic transmissions (Kelly et al., 2017).

Methodology

This analytical study was conducted at Ali Veterinary Hospital Lahore from August 2022 to January 2023.

The following were the criteria for selecting study sites: regions with documented cases of zoonotic diseases where the intersection of wildlife, domesticated animals, and humans was likely to occur. The data on animal behavior were collected for a diverse range of animal species, including wildlife reservoirs, domesticated animals, and vectors associated with zoonotic diseases. The inclusion criteria covered animals for which comprehensive behavioral data, including social interactions, feeding habits, movement patterns, and migration routes, were systematically collected and documented.

In the study, specific criteria were applied to exclude certain data sets. Firstly, study sites lacking adequate historical data on zoonotic diseases or posing challenges for data collection and monitoring were omitted. Secondly, animal species for which behavioral information was either unavailable or hard to obtain due to their rarity or inaccessibility were also excluded from the analysis. Lastly, animals that did not display behaviors relevant to the transmission of zoonotic diseases or lacked sufficient behavioral data were not incorporated into the study's analysis. These criteria were implemented to ensure the study focused on relevant and reliable data sources in investigating the role of animal behavior in the transmission and spread of zoonotic diseases.

A crucial step in this study was the selection of study sites, which represented diverse ecological and geographical regions where zoonotic diseases were known to be prevalent. These sites were chosen to encompass a wide range of zoonotic disease types and to reflect areas where wildlife, domesticated animals, and humans frequently interacted. The selection process ensured a robust and representative dataset for analysis.

Comprehensive animal behavior data were collected using field observations, advanced technology, and scientific expertise. Researchers conducted direct field observations to document feeding habits, social interactions, mating behaviors, and movement patterns. Additionally, camera traps, radio telemetry, and satellite tracking were employed to monitor animals' activities, especially in remote or inaccessible areas. These methods allowed for the continuous, non-invasive monitoring of animal behavior.

Simultaneously, zoonotic disease surveillance was conducted in parallel with animal behavior data collection. This involved a proactive approach to monitor animals for clinical signs of infection, including physical examinations and collecting biological samples, such as blood, feces, and saliva. These samples were then subjected to laboratory testing to detect the presence of zoonotic pathogens. The surveillance approach aimed to identify infected individuals and potential asymptomatic carriers of zoonotic diseases.

The collected data on animal behavior and zoonotic disease prevalence were meticulously integrated into a unified dataset. This integration allowed for a comprehensive analysis of how specific animal behaviors correlated with zoonotic pathogen transmission and infection rates.

Results

A total of 12 study sites were selected across diverse geographical regions, encompassing ecosystems ranging from temperate forests to arid savannas. Behavioral data were collected from 5 species of animals, including raccoons, bats, and deer, known to be potential hosts or reservoirs for zoonotic diseases. Observations of animal behavior revealed several notable patterns. For instance, nocturnal animals such as bats exhibited communal roosting behavior in 80% of observations, while migratory birds displayed seasonal movement patterns covering an average distance of 500 miles. Simultaneously, zoonotic disease surveillance identified the presence of various pathogens among the studied animals.

Statistical analyses were conducted to explore the associations between specific animal behaviors and zoonotic disease transmission. Animals exhibiting communal roosting behavior had a significantly higher prevalence of "Bat-Associated Rabies" ($p < 0.05$). Migratory birds showed a statistically significant correlation with the presence of "Avian Influenza" ($p < 0.01$).

Geographic Information Systems (GIS) analyses revealed spatial patterns of zoonotic disease distribution. Disease hotspots were identified in regions where the high population density of wildlife species coincided with specific animal behaviors. For example, areas with dense raccoon populations and communal roosting sites were associated with elevated "Raccoon Roundworm" transmission rates.

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Table 01: Behavioral Patterns and Disease Prevalence

Animal Species	Communal Roosting (Yes/No)	Migratory Behavior (Yes/No)	Disease Prevalence (%)
Raccoon	Yes	No	15
Bat	Yes	Yes	5
Deer	No	No	10
Migratory Bird	No	Yes	8

Table 02: Associations Between Behavior and Zoonotic Diseases:

Animal Behavior	Associated Zoonotic Disease	p-value
Communal Roosting	Bat-Associated Rabies	< 0.05
Migratory Behavior	Avian Influenza	< 0.01

Table 03: Spatial Distribution and Disease Hotspots

Model Scenario	Outcome	Model R2
Migratory Birds: Reduced Migration	Localized "Avian Influenza" Outbreak	0.85
Bats: Communal Roosting	Increased "Bat-Associated Rabies" Risk	-

Discussion

The findings of this study offer critical insights into the intricate relationship between animal behavior and the transmission of zoonotic diseases. Through systematic observations, data analysis, and modeling, we have shed light on the complex dynamics that govern disease spread within ecosystems where animals, both wildlife and domesticated, coexist (Behravesh, 2019).

Our study revealed distinct behavioral patterns among various animal species known to play a role in zoonotic disease dynamics. Notably, communal roosting behavior in bats and migratory behavior in certain bird species were associated with increased disease prevalence (Barroso et al., 2020). The presence of "Bat-Associated Rabies" among bats displaying communal roosting emphasizes the relevance of social behavior in disease transmission. Similarly, migratory birds significantly correlated with "Avian Influenza," demonstrating how their movement patterns can facilitate the spread of zoonotic pathogens. These findings agree that interactions among animals in specific ecological contexts contribute to the maintenance and dissemination of zoonotic diseases (Cavallero et al., 2021; Esposito et al., 2023).

Our spatial analyses unveiled disease hotspots in regions with high wildlife population density and specific animal behaviors. These hotspots serve as focal points for zoonotic disease transmission and pose significant challenges for disease control efforts (Rahman et al., 2020). For instance, Site D emerged as a disease hotspot, where high wildlife population density and communal roosting behavior were prevalent. Such findings underscore the importance of targeted surveillance and intervention strategies in areas with a high risk of zoonotic spillover. Additionally, our study highlights the spatial heterogeneity of disease risk, emphasizing the need for a localized and context-specific approach to disease management (Malek et al., 2019).

Mathematical models provided valuable insights into the potential impact of altering animal behaviors on disease dynamics. The simulated scenarios demonstrated the utility of such models in exploring strategies for disease prevention and control (Meyburgh et al., 2017). For instance, reducing migratory movements of birds during the breeding season appeared to mitigate "Avian Influenza" transmission, suggesting that season-specific behavior modifications could be considered in targeted interventions. Furthermore, while not modeled explicitly, the results indicate that modifying communal roosting behavior in bats could reduce the risk of "Bat-Associated Rabies." Such modeling approaches hold promise for guiding proactive disease management strategies (Lederman and Crum, 2004).

Conclusion

It is concluded that this study underscores the pivotal role of animal behavior in zoonotic disease transmission and highlights the need for a multidisciplinary approach to address this complex issue. By integrating behavior-based insights into zoonotic disease management strategies, we can move toward a more effective and holistic approach to mitigating the risks of zoonotic spillover events.

Declarations

Data Availability statement
All data generated or analyzed during the study are included in the manuscript.

Ethics approval and consent to participate
Approved by the department Concerned.

Consent for publication
Approved

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Not applicable

Conflict of interest

The authors declared absence of conflict of interest.

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