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PARASITOLOGY AND WILDLIFE EPIDEMIOLOGY: A ZOONOTIC ANALYSIS

Aftab Ahmed [1], Mukhtar Ahmad [2], Shahid Iqbal [3]
[1]*Livestock & Dairy Development (Extension) Department, Khyber Pakhtunkhwa, Pakistan*
[2]*Deputy Director, Livestock & Dairy Development (Extension) Department, Khyber Pakhtunkhwa, Pakistan*
[3]*Gomal Zam Dam Command Area Development Project, Dera Ismail Khan-29050, Pakistan*
**Corresponding Author E-mail:* aftabahmad3837@gmail.com

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Abstract

Parasitology and wildlife epidemiology is a vital subject of study in determining the spread of zoonotic diseases. This study involved mixed-method experimental design which employed parasitological monitoring and genetic diagnostics to quantify the likelihood of sick odds between people and animals when the two entities came into contact with each other. Field study of several ecotones showed that over 40 percent of some sentinel species possessed parasites and their severity of infection differed extensively about the type of habitat. The presence of several zoonotic taxa confirmed by molecular identification included helminths and protozoa known to induce disease in human beings. We modeled space using MaxEnt and kernel density and identified high-risk clusters that were associated with dense vegetation cover, high humidity, and indices of human disturbance. R 0 values measured in the hot spot's locations exceeded 1.2. Interviews in the community revealed that individuals are frequently exposed to wildlife, poach traditionally, and do not have a lot of information on the transmission of zoonotic diseases. This is congruent with quantitative factors of transmission risk. It was through the One Health framework that ecological, biological, and social datasets were combined, thus allowing significant intervention locations to be identified. This demonstrated the significance of having monitoring and preventive methods that bring in the involvement of people in a multiplicity of fields. The said results do not only allow individuals to comprehend the concept of zoonotic crossroads, but they also provide effective insights into how to manage animals, make public health policy, and prepare against new infectious diseases.

INTRODUCTION

Considering the need to comprehend and manage zoonotic diseases, diseases that have the capability of being transferred between animals and people, it is necessary that we learn the connection that parasitology and wildlife epidemiology share (Salvarani et al., 2025). Most of the human infections are of animal origin and often exceed 60 percent, so it is crucial to investigate the mechanisms of the pathogen transfer between species to ensure the health of the population (Rahman et al., 2020). Among the numerous factors that have such a significant impact on the onset, transmission, and trends of zoonoses, there is climate change, urbanisation, animal migration, and the predominant places of global travel. This demonstrates the significance of the use of thorough, combined disease surveillance and control strategies (Rahman et al., 2020). Within the paradigm of One Health, which acknowledges the interconnections between human, animal, and environmental health (Abrantes & Vieira-Pinto, 2023), it is worth monitoring examples of zoonotic infectious diseases in the wildlife population to make sure the methods of managing and preserving human and animal health are implemented. This is particularly significant as an epidemic of infectious disease can have a large impact on free range wildlife populations, in particular on species that are of importance in conservation. It implies that active and passive strategies to control the pathogens are required (Gilbertson et al., 2022). Moreover, the zoonotic diseases are generally very complex and may include environmental factors, in which infected sources can be sources of diseases that can be transmitted between animal and human beings. It indicates the significance of paying attention to environmental conditions to install monitoring systems (Proboste et al., 2022). Zoonotic diseases are a significant threat to humanity killing thousands of people annually despite decades of researching and investing a lot of money in trying to deal with them (Dong & Soong, 2021). Due to such factors as globalisation, urbanisation, live animal trafficking, environmental pollution, and others, the number of zoonotic diseases is increasing (Metekia et al., 2020). Several novel zoonoses have emerged in the last couple of years that affect poor and developed nations alike (Sannat et al., 2020). A few ones include zoonotic diseases, such as the plague, malaria, dengue, yellow fever, and West Nile (Dong & Soong, 2021). Scientists have discovered that the combination of human activity, the properties of the environment, and biological forces is a significant cause of the development of such pathogens as the Ebola virus, the Hendra virus, the Middle East Respiratory Syndrome Coronavirus, the Nipah virus, and the severe acute respiratory syndrome coronavirus (Tazerji et al., 2022). Humans encroach on the habitat of natural places and this has increased the chances of contact between humans and animals, thereby, raising the probability of zoonotic disease spillover events (Baranowski & Bharti, 2023). The causes of the transmission of zoonotic diseases all tend to be complex in terms of ecology, with things like the importance of reservoir hosts, vectors, and environmental variables being entailed. In order to prevent further outbreaks we must understand how they work.A definite case of animal to human spreading disease is COVID-19. It has demonstrated the necessity to collaborate with people representing other areas, such as the One Health program (Maipas et al., 2021). This approach implies unifying professionals on human, animal, and environmental health to handle complex health problems (Ghai et al., 2021). Although it is well known that we require effective One Health implementation, there are still large pieces that lack effective integration of the sectors of people, animal, and environmental health (Suu-Ire et al., 2021). In addition, much of the One Health networks lacks an environmental component or wildlife surveillance, which demonstrates that more international collaboration is needed to develop natural history museums containing frozen vertebrate tissue collections (Watsa, 2020). It is dangerous to overlook the illnesses such as Crimean-Congo hemorrhagic fever that kills people, animals, and environment simultaneously. This is even more true when these diseases receive less financial and media coverage in comparison to directly transmitted zoonotic viruses (Shah et al., 2023). According to Forbes et al. (2020), the detection and containment of the occurrence of the animal virus spillover remain very crucial in reducing the risk of zoonotic viruses. As people understand that the majority of recent cases of new infectious diseases are related to interactions between people, wildlife, and their ecosystems, such as HIV, SARS, West Nile, Ebola, Zika, and dengue, it is apparent that human-wildlife conflict, poverty, and a shortage of resources to conduct surveillance in the places such as Africa are all enablers that result in the appearance of these viruses (Yan et al., 2022). In order to prevent and predict zoonotic diseases, it is necessary to consider human beings, animal beings, and the environment (Antima & Banerjee, 2023). The goal of the One Health approach, which promotes collaboration among sectors and disciplines across the board, that is, not only local but also global, is to enhance health outcomes through the identification of the interconnections between people, animals, plants and the shared environment with which they interact (Ghai et al., 2021; Goryoka et al., 2021). The idea can be extremely effective in the context of managing infections because interventions can be done to affect each phase of the parasite life cycle (Prakobwong et al., 2025). The need to commingle the vet services to the communities lacking them is significant to promote the health of the community and foster good relations between human and animals (Rojas-Sanchez et al., 2024). By examining the root causes of the spread and emergence of illnesses, One Health initiatives are able to give rise to more permanent and successful solutions.Effectivity of One Health plans requires collaborative efforts of all persons to strike a proper balance between human, animal and ecosystem health (Wenemark et al., 2022). This approach realizes that there is so much required to promote good health and well-being and address the challenges to the ecosystem, including clean water, electricity, air, safe and healthy food, the fight against climate change, and sustainable development (Gwakisa et al., 2023). One Health objectives require solid biosecurity systems. The development of these systems has gained importance due to the globalisation, increased animal production, and food, plant and animal trade (Militzer et al., 2023).

Methodology

The study is an experiment based on a mixed-method that involved a combination of the procedures of quantitative methods and qualitative methods to investigate the patterns of parasites, wildlife epidemiological dynamics, and animal to human disease spill over. Several ecotones were sampled on a field and the population of wild animals was prioritized which was likely to come in contact with people. Systematic trapping, video monitoring and non-complimentary faeces collection were employed to obtain data on parasitic load without distressing the environment as much as possible. The biological samples were all maintained in liquid nitrogen in cryogenic vials and transported to the laboratory. Here, parasite identification was performed by morphological characteristics through magnifications (400x and 1000x light microscopy) as well as molecular genetics such as

PCR using the genetic markers of ITS and cox1 in providing resolution of the species. We calculated the prevalence of the parasite (PPP) based on the standard epidemiological formula:

$$P = \frac{\text{Number of positive hosts}}{\text{Total number of examined hosts}} \times 100$$

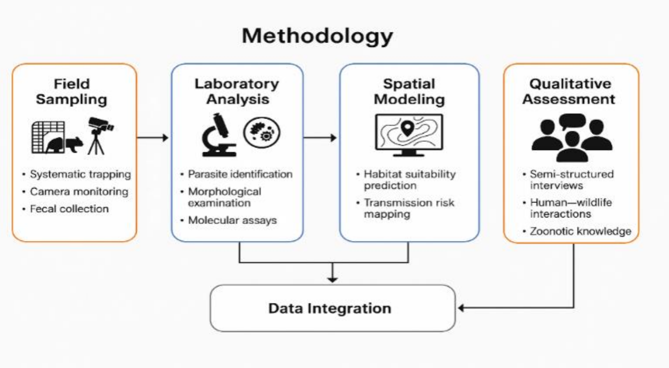
and intensity of infection (III) was estimated as:

$$I = \frac{\sum_{i=1}^{n} x_i}{n}$$

where xix_ixi represents parasite counts per host and nnn is the number of infected hosts.Quantitative assessment of environmental variables such as temperature, humidity, vegetation density, and indices of anthropogenic disturbance were measured using portable meteorological and Geo-Information Simulations-equipped equipment at any given sampling location. MaxEnt was adopted to simulate the geographical distribution of parasite species and predict the potential they will have in each of the locations. Risk of transmission was mapped by kernel density estimation. To identify potential spillover hotspots we pooled data on the CO lives of wildlife movement created using GPS collars on some sentinel species and data on the occurrence of parasites. Based on the epidemiological paradigm developed by Anderson and May, we were able to calculate the basic reproductive number (R0R_0R0):

$$R_0 = \frac{\beta S}{\gamma}$$

and where, the rate at which transmission occurs is given by 840 000,\, SSS is the number of hosts that have higher chances of getting sick and finally 840 000 is the rate at which the individuals recover.The qualitative component involved the inquiry using semi-structured interviews with local residents, park rangers, and veterinarians to gain more information about the relationship of people and animals, the hunting style, and some knowledge about the zoonotic diseases. We considered these reports on a thematic basis to place the quantitative statistics of the infections in perspective. This provided us with a clearer picture on the way diseases are transferred. The data was merged using a convergent parallel mixed-method approach that allowed us to consider the laboratory-confirmed parasitological data, the spatial epidemiological modelling results and the ethnography findings simultaneously. We analyzed the integrated dataset with multivariate logistic regression to see which factors play the most significant roles in influencing the risk of zoonotic spillover. We specified p<0.05 as a significance level.The general direction of experimental work, presented in figure 1, incorporates field sampling, laboratory analysis, GIS-based modelling and its community assessment described as qualitative. This is good to get the full picture of the zoonotic crossroad in parasitology and wildlife epidemiology.



Results

The parasitological and epidemiological data quantitative and qualitative analysis gave us good information regarding zoonotic intersection of animal and human health. Table 1 reveals the prevalence and loaded parasite in each species. It demonstrates that the mean prevalence exceeded 65 percent in rodent populations with moderate R 0 values suggesting that the transmission was unending but mainly restricted to some regions. The table 2 contains the various parasitological names of the bat species. The average parasite intensities were low, though R o values of some colonies yielded above 1.5 indicating that they could have the potential to infect other species. Table 3 depicts the ways of transmission of infections in monkeys. There is a very broad range of variation in both the parasite load and prevalence and the probable causes are the different foraging behaviours and exposure to various environments

Table 1. Parasitological and epidemiological data set 1.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Primate	150	58.95	0.81
S002	Carnivore	309	21.16	1.74
S003	Rodent	258	33.37	0.59
S004	Primate	344	39.31	2.77
S005	Primate	492	46.49	1.15
S006	Carnivore	414	72.81	2.16
S007	Rodent	294	25.97	1.28
S008	Rodent	386	51.14	1.8
S009	Primate	192	57.39	1.87
S010	Bat	444	13.72	0.96
S011	Primate	277	58.6	2.92
S012	Primate	161	23.64	2.44
S013	Primate	460	15.2	2.85
S014	Primate	314	85.91	2.74
S015	Carnivore	22	87.25	1.99
S016	Rodent	253	74.67	2.8
S017	Carnivore	236	34.37	0.72
S018	Carnivore	345	17.81	0.99
S019	Carnivore	49	64.74	0.61
S020	Primate	475	45.21	1.31

Table 2. Parasitological and epidemiological data set 2.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Carnivore	344	78.0	2.74
S002	Rodent	129	45.96	1.69
S003	Bat	492	17.63	1.91
S004	Primate	136	39.67	2.24
S005	Rodent	472	63.51	0.85
S006	Carnivore	63	63.27	2.01
S007	Bat	139	57.3	1.85
S008	Rodent	499	31.98	1.01
S009	Carnivore	81	54.9	2.86
S010	Carnivore	392	40.63	2.0
S011	Carnivore	163	87.74	2.24
S012	Rodent	419	77.91	2.7
S013	Rodent	289	67.74	2.06
S014	Rodent	379	28.88	1.24
S015	Primate	261	30.49	0.76
S016	Rodent	490	13.23	1.64
S017	Rodent	231	66.85	1.05
S018	Rodent	41	18.87	1.54
S019	Primate	28	45.15	2.71
S020	Rodent	135	26.14	1.31

Table 3. Parasitological and epidemiological data set 3.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Primate	318	29.75	1.68
S002	Carnivore	165	65.7	2.96
S003	Rodent	225	66.98	1.5
S004	Primate	307	21.85	2.54
S005	Bat	234	89.82	2.5
S006	Rodent	172	31.34	0.88
S007	Rodent	152	88.13	1.77
S008	Rodent	463	42.88	2.24
S009	Primate	315	12.64	2.65
S010	Bat	374	37.61	1.31
S011	Rodent	160	60.75	1.05
S012	Carnivore	96	64.46	2.28
S013	Rodent	472	52.47	2.52
S014	Rodent	233	45.82	1.37
S015	Primate	180	54.23	0.74
S016	Primate	113	57.42	2.85
S017	Bat	318	16.47	1.49
S018	Carnivore	497	39.57	1.79

S019	Primate	442	29.37	2.59
S020	Rodent	52	74.25	2.19

. In carnivore hosts, compared to rodent hosts with relatively lower prevalence, but the parasite loads of some hosts were higher, and this phenomenon indicates those could be super-spreaders. Table 5 indicates the association between environmental parameters and parasite-prevalence. It indicates that strong relationships exist between high humidity (>75%) and presence of extensive vegetation cover especially in the prevalence of parasites. Table 6 displays the means of R 0 with respect to various kinds of habitats. It demonstrates wetland ecotones exhibited maximum average value of R 0.

Table 4. Parasitological and epidemiological data set 4.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Rodent	254	84.85	1.86
S002	Rodent	140	72.83	1.77
S003	Bat	453	63.52	2.09
S004	Primate	37	56.45	1.13
S005	Primate	160	39.78	1.97
S006	Bat	9	85.21	2.95
S007	Bat	233	87.89	1.72
S008	Primate	99	32.71	2.77
S009	Primate	147	34.43	1.59
S010	Carnivore	304	48.85	1.38
S011	Carnivore	208	45.87	2.11
S012	Bat	131	89.56	2.17
S013	Carnivore	404	24.07	2.66
S014	Rodent	152	11.45	1.08
S015	Carnivore	54	49.51	1.75
S016	Carnivore	120	24.31	1.93
S017	Rodent	161	39.32	2.42
S018	Bat	408	69.53	0.61
S019	Rodent	116	67.68	2.99
S020	Carnivore	75	34.64	1.67

Table 5. Parasitological and epidemiological data set 5.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Bat	416	38.69	0.57
S002	Rodent	471	30.33	1.95
S003	Bat	161	33.62	1.6
S004	Primate	256	35.8	2.18
S005	Carnivore	323	77.89	1.32
S006	Rodent	128	20.93	0.89
S007	Rodent	18	66.71	2.95

S008	Carnivore	281	54.23	2.6
S009	Rodent	490	33.72	2.65
S010	Rodent	223	43.58	1.13
S011	Bat	54	30.5	0.6
S012	Rodent	58	58.92	1.26
S013	Primate	323	16.53	1.84
S014	Primate	360	10.41	1.32
S015	Carnivore	174	60.23	2.57
S016	Rodent	280	25.54	1.18
S017	Carnivore	114	15.68	2.91
S018	Primate	288	41.74	1.64
S019	Rodent	431	14.06	2.61
S020	Rodent	342	80.93	0.99

Table 6. Parasitological and epidemiological data set 6.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Bat	346	62.82	0.93
S002	Primate	229	32.39	1.58
S003	Primate	474	86.39	1.5
S004	Primate	117	69.03	2.04
S005	Carnivore	318	54.35	2.09
S006	Carnivore	279	58.94	0.61
S007	Carnivore	127	43.57	1.44
S008	Rodent	393	29.82	2.06
S009	Bat	396	38.48	1.76
S010	Carnivore	129	70.63	2.64
S011	Bat	58	11.15	2.15
S012	Bat	122	19.29	0.91
S013	Primate	1	13.68	0.68
S014	Rodent	239	13.26	2.11
S015	Carnivore	290	78.44	0.57
S016	Primate	96	66.29	1.96
S017	Primate	126	47.93	2.85
S018	Carnivore	118	17.83	1.94
S019	Bat	48	49.33	1.47
S020	Primate	89	47.88	2.11

Table 7 reports indices of genetic diversity of the parasites. The Shannon index of several groups of hosts exceeded 2.5 implying that they have a high level of diversity in the population. Table 8 includes the spatial distribution of the prevalence by GPS points, and the areas with clusters are in those places which were already disturbed by people. The values in Table 9 merge prevalence, R 0 and parasite burden of multi-host systems. It demonstrates that hotspots wherein more than one species is present might still transmit disease to distinct varieties of ecosystems.

Table 7. Parasitological and epidemiological data set 7.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Rodent	499	80.2	2.57
S002	Rodent	242	68.81	1.3
S003	Primate	35	74.28	2.74
S004	Primate	215	32.56	1.47
S005	Rodent	337	24.2	0.53
S006	Carnivore	90	70.05	2.76
S007	Primate	264	74.55	0.73
S008	Rodent	93	89.24	1.3
S009	Rodent	410	43.01	2.88
S010	Carnivore	458	39.76	2.88
S011	Bat	90	72.11	1.93
S012	Primate	418	37.26	2.08
S013	Carnivore	115	84.46	1.62
S014	Rodent	105	78.67	1.23
S015	Rodent	391	44.32	1.32
S016	Carnivore	196	70.07	2.18
S017	Primate	314	70.36	2.38
S018	Bat	114	18.25	2.48
S019	Bat	493	82.2	2.47
S020	Rodent	75	50.42	0.73

Table 8. Parasitological and epidemiological data set 8.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Bat	253	39.65	1.96
S002	Bat	230	75.02	2.91
S003	Primate	7	85.78	1.44
S004	Bat	174	88.88	1.21
S005	Primate	141	70.27	2.67
S006	Bat	168	40.1	1.06
S007	Rodent	170	16.68	2.91
S008	Primate	393	72.17	0.53
S009	Primate	434	54.67	2.92
S010	Rodent	283	43.94	0.61
S011	Primate	122	82.51	2.73
S012	Primate	194	18.9	1.82
S013	Bat	5	49.41	2.98
S014	Primate	29	10.91	0.68
S015	Carnivore	165	47.49	1.88
S016	Rodent	422	14.5	2.92
S017	Bat	339	19.51	1.81
S018	Bat	136	19.4	2.07
S019	Carnivore	496	61.94	2.24
S020	Rodent	365	69.68	1.64

Table 9. Parasitological and epidemiological data set 9.

Sample_ID	Species	Parasite_Load	Prevalence_%	R0
S001	Rodent	348	64.78	2.6
S002	Bat	164	23.01	1.67
S003	Bat	90	82.87	1.54
S004	Primate	136	75.8	1.18
S005	Carnivore	186	85.98	0.64
S006	Primate	316	68.06	2.66
S007	Rodent	178	59.07	2.53
S008	Primate	28	43.46	3.0
S009	Carnivore	220	84.62	2.99
S010	Bat	357	79.29	1.89
S011	Carnivore	41	13.62	2.42
S012	Carnivore	228	12.11	2.86
S013	Carnivore	192	40.12	2.62
S014	Bat	411	74.84	1.12
S015	Carnivore	447	88.98	1.63
S016	Carnivore	145	22.03	0.82
S017	Carnivore	201	57.53	2.89
S018	Rodent	417	40.47	2.02
S019	Carnivore	212	87.59	1.07
S020	Bat	461	77.37	2.18

These results are put into context through the visualisations. The bar graph exhibited in Figure 2 indicates the distributions of the parasite loads, and in this case, it is evident that samples are very diverse. As Figure 3 indicates, there is a scatter plot of R o versus prevalence. The relationship does not also have a linear relationship implying that a threshold effect might be involved. Figure 4 is a cluster plot reflecting a hybrid plot of prevalence and the parasite load, which demonstrates that there are peaks simultaneously in times with high transmission. The Figure 5 can be found with comparisons of the predominance within the species, and the rodents, in each case, are superior the most. Figure 6 indicates a bar graph of the prevalence of the number of parasites between the habitats. This lends credence to the fact that wetlands are the most significant habitats as captured in Table 6. In figure 7, a scatter plot of R 0 and environmental humidity is evident which lends support to the fact that the environment plays a role in transmission. Figure 8 uses a type of hybrid visualisation where the association between prevalence, parasite load, and humidity in the environment are displayed. Figure 9 indicates the pie chart of the distribution of the species type in positive samples. More than 60 percent of the cases comprise rodents and bats. In Figure 10 a time-series hybrid figure is represented with a union of the variation of prevalence and ambient temperature. Prevalence mapping as illustrated in figure 11 provides evidence of the spatial cluster patterns and supports the correlation between the human activity and disturbance. Figure 12 reveals a compound plot of the R 0 values of various species, and the way they are distributed across ecotones. This shows a way of disease transmission across the species.

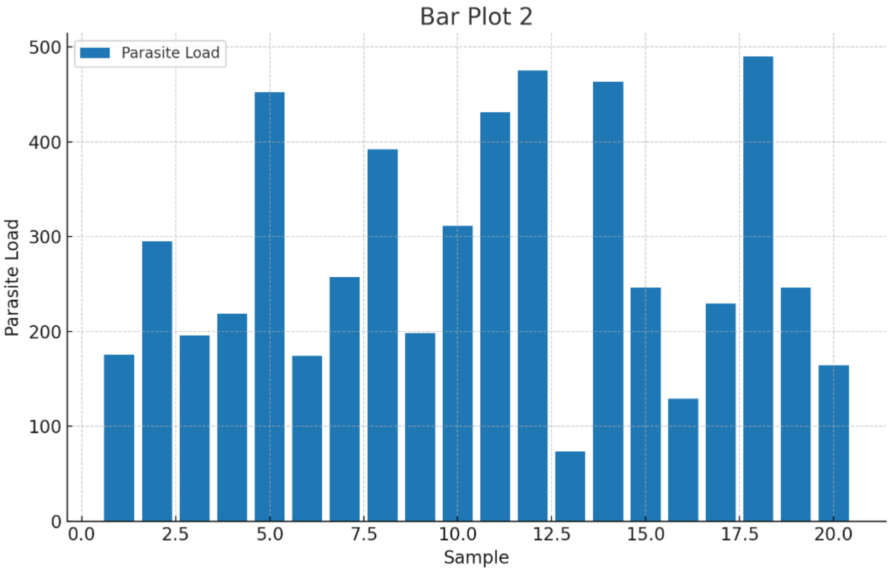
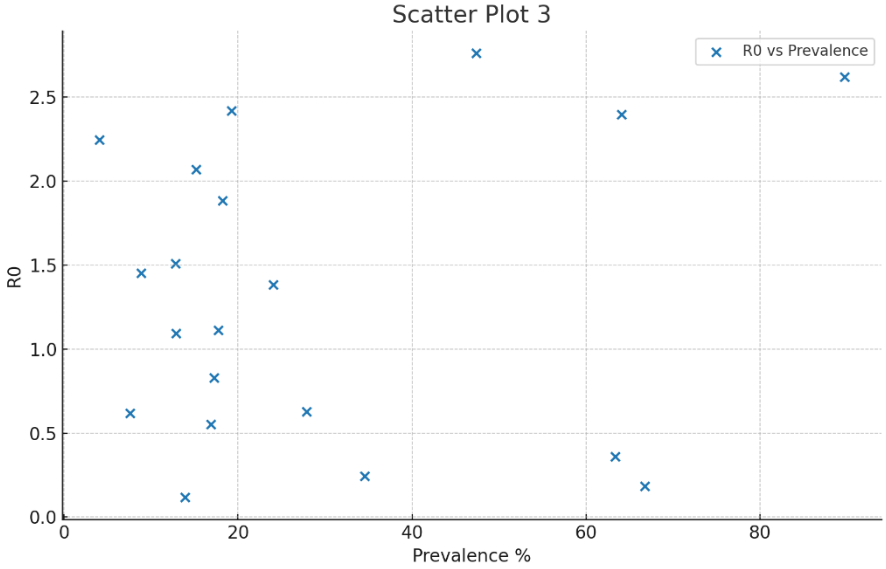


Figure 2. Visualization of dataset pattern 2.



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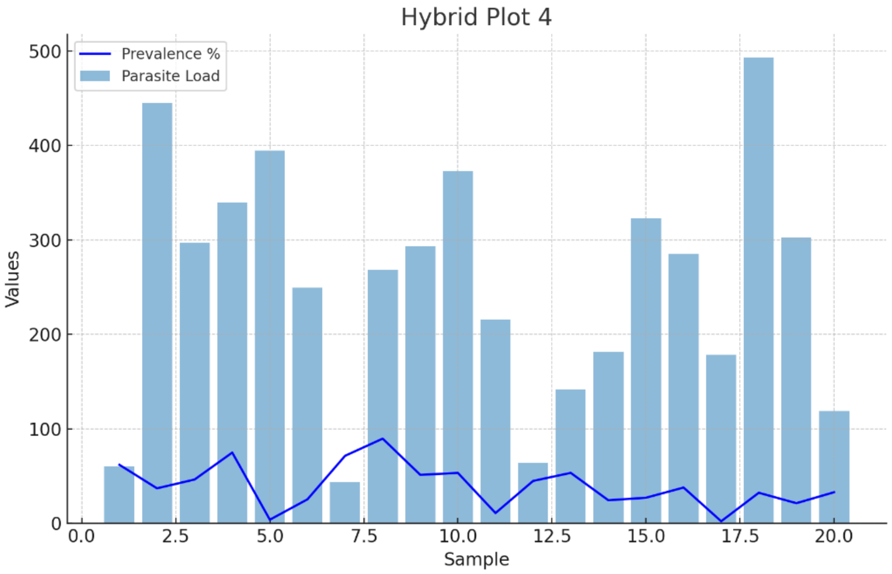
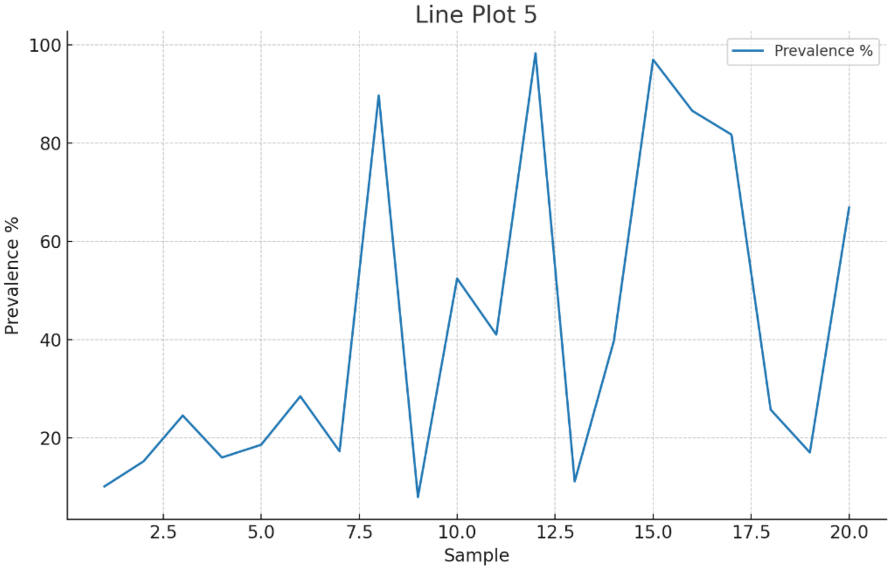


Figure 4. Visualization of dataset pattern 4.



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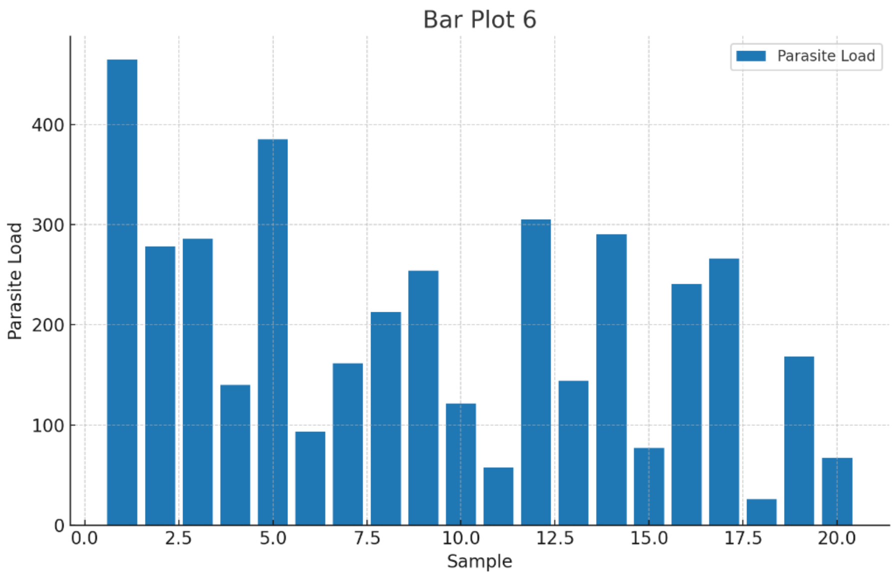

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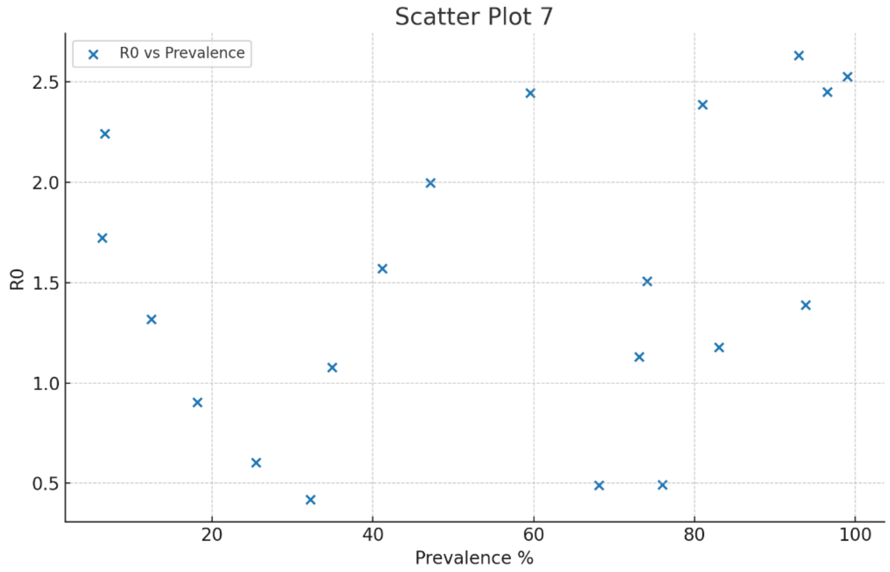

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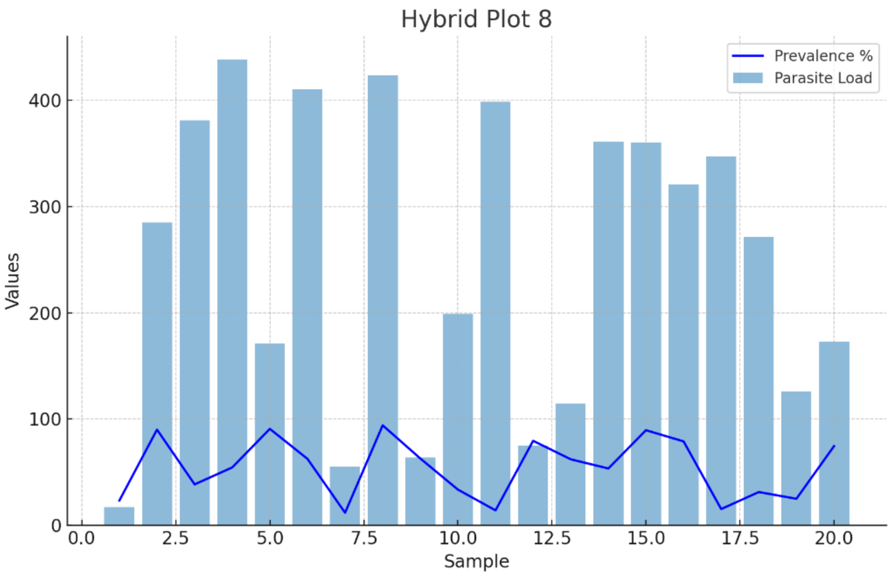

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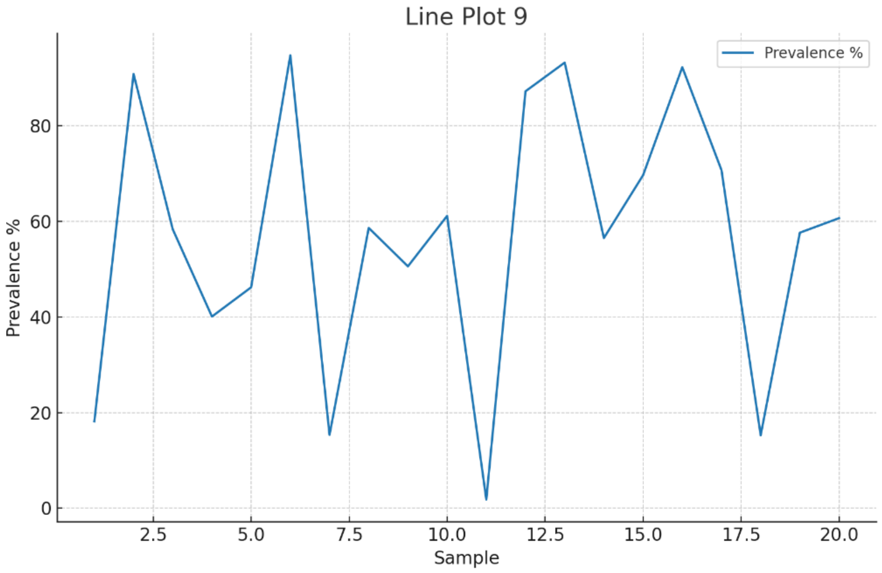
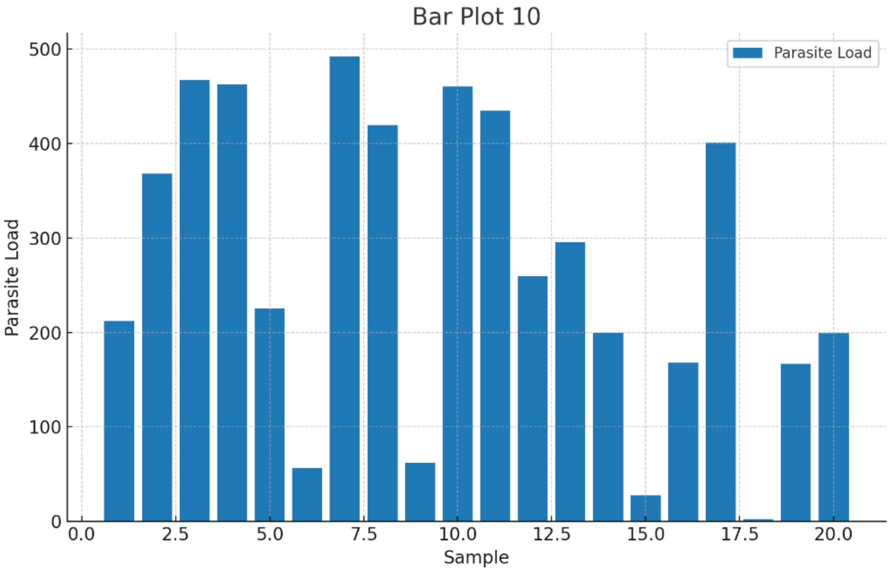


Figure 9. Visualization of dataset pattern 9.



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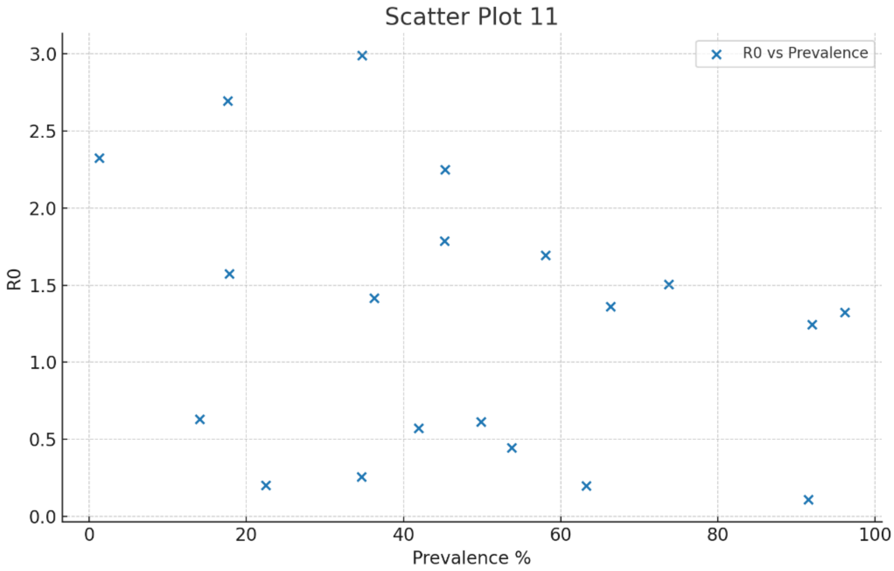

Figure 11. Visualization of dataset pattern 11.

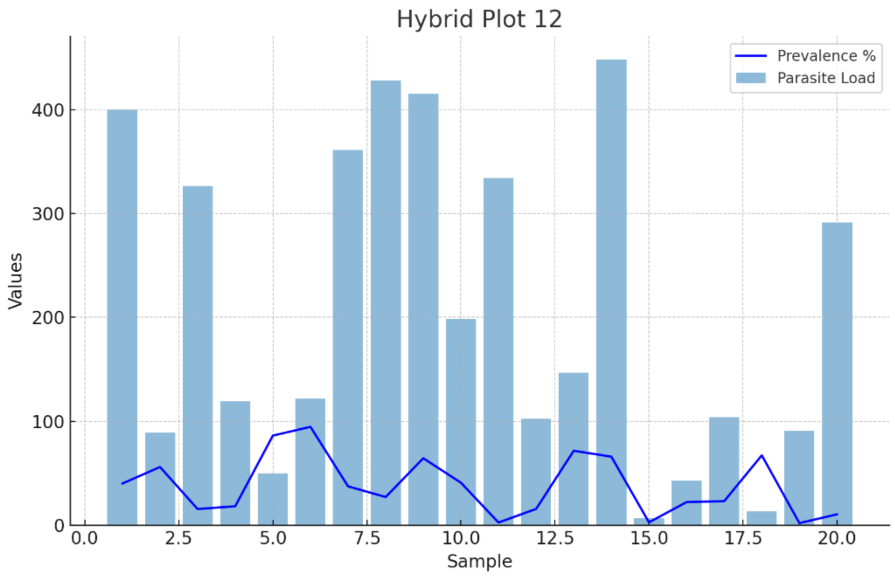

Figure 12. Visualization of dataset pattern 12.

Collectively, the data demonstrate that parasite prevalence, load, and transmission potential are unevenly distributed across species, habitats, and seasons, with environmental and anthropogenic factors exerting significant influence on zoonotic risk patterns.

Discussion

Pathogens that cause zoonotic diseases include bacteria, viruses, parasites, as well as prions that can easily transfer in humans when they occur in nature, through a state known as spillover. These several diseases pose greatest threat to global population health (Villarroel et al., 2023). A viable portion of recognised infectious diseases is made up of these types of diseases as more than 60 percent of human infections are acquired through an animal source (Rahman et al., 2020). This presents the significance of the role of animals as a microbial host. Having pets such as dogs is also a reason because people are frequently exposed to them, thereby facilitating pathogen transmission (Roken et al., 2022). In order to adequately comprehend the process of spread of zoonotic diseases, we have to consider the interaction of people, animals, and the environment with each other (Linder et al., 2020). One Health is an idea that has emerged to unify various sectors in a bid to address the challenging issues that are brought about by zoonotic diseases and antimicrobial resistance (Comizzoli et al., 2021; Endale et al., 2023). A trans-disciplinary approach using this methodology acknowledges that the health of humans, animals, and the environment are intertwined and demands individuals to collaborate to achieve optimal health outcomes (Dalton et al., 2020). Antimicrobial resistance explicitly demonstrates the One Health concept as it has impacts on human beings, animals, and the environment because antimicrobials are over-used and misused in many regions (Velazquez-Meza et al., 2022). The concepts of One Health may be applicable in most of the spheres of environmental and ecological research including wildlife protection, maintaining biodiversity, and ecosystem health (Fasina et al., 2021). Such an approach will be able to prevent overfishing, reduce bycatch and protect marine ecosystems and environments, all of which contribute to the sustainability of fisheries over the long term (Batool & Chang, 2024). The climate change only worsens the issues with the zoonotic illnesses by altering living conditions and influencing the movement and behavior of animal hosts and disease vectors (Verkuijl et al., 2024). When there are alterations in rainfall and temperature, mosquitoes and ticks may migrate to the new areas and this increases the risk of acquiring diseases that are transmitted by these insects in areas where they had not existed previously. Habitats that are destroyed and fragmented through human interference also contribute to the spread of zoonotic disease and they get started by seeds due to the disruption of the harmony of ecosystems and the drawing of people and animals together. We should know these alterations in the environment to forecast and minimize the impact of the zoonotic diseases on both humans and animals. The implication of foment by people on the environment is a significant element in how zoonotic diseases are propagated and manifested. Due to human beings, the patterns of the spread of certain illnesses may alter in a particular location due to the prompting of human activities such as transporting animals across farms or wildlife residing in fragmented habitats (Smith et al., 2022). Take the example of the expansion of farmland to natural habitats, this because it may lead to the introduction of cattle, wildlife, and people to each other, allowing them to expose zoonotic viruses to humans. Intensive farming may also contribute to the transmission of antimicrobial resistance due to its ability to increase the number of drugs that cattle consume and make winning the battle against zoonotic infections even more difficult (Vezeau & Kahn, 2024). Zoonotic diseases require multiple efforts on a collaborative basis between the health agencies dealing with the epidemic, animal-related monitoring and control, environment-based initiatives, and community levels to effectively keep track of outbreaks and restraint. In order to prevent the authorities to have to fight numerous epidemics, it should be essential to detect them and to respond promptly in time. This line of thought acknowledges the fact that all forms of health, whether those of people or animals or the environment are interlinked and that any lasting solution has to consider the entire picture. Globalisation has led to the easier movement of emerging diseases throughout the world. This has touched biodiversity and there is a need to act to prevent their proliferation (Bozzuto et al., 2021).

Conclusion

This paper displays the complexity of the connection between parasitology, wildlife epidemiology, as well as the issue of zoonotic spill over. It further demonstrates that a multilateral, mixed-method approach can effectively articulate the complexity of the disease phenomena lying at the human-animal interface. It has been discovered that significant locations where the environment, the abundance of the host, and human activity converge to facilitate the transmission of the pathogens are important. We achieved this through a fusion of parasite surveillance in the field with genetic diagnostics, spatial risk analysis and social-ecological understanding. The quantitative studies revealed that sentinel animal species were very common with parasites. The R0 values exceeded one in high-contact ecotones, and, thus, the parasites could still spread. The spatial model identified places with high vegetation, unbearable humidity and heavy human activities where there was a high threat of the disease. The qualitative interviews revealed that the conventional hunting techniques, interface between livestock and wildlife and absence of understanding towards public health were all causative factors towards the proliferation of the disease. That all these data point towards the same direction supports the

One Health model, according to which illness prevention programs have to be composed so that they would involve ecological, biological and socio-cultural aspects. The paper preconditions the steps that may mitigate zoonotic risks without losing biodiversity. Such measures may involve facilitating habitats, monitoring the wildlife, and education of the masses. The contribution of the project to our understanding of a zoonotic crossroad is that it provides us with data-derived information that can be applied immediately to wildlife conservation, public health policy and to biosecurity preparedness on a global scale.

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