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AGRICULTURAL AND BIOTECHNOLOGICAL REFLECTIONS

ONE HEALTH-BASED ZOONOTIC RISK ASSESSMENT: SPATIOTEMPORAL MODELING OF CROSS-SPECIES DISEASE SPILLOVER IN PERI-URBAN LIVESTOCK-HUMAN-WILDLIFE INTERFACES

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Abstract

Zoonotic diseases, driven by complex ecological, biological, and anthropogenic interactions, pose a growing threat to global health and biosecurity. This study presents a mixed-methods approach combining field-based qualitative assessments with quantitative modeling techniques to evaluate zoonotic spillover risks. Across twenty sampled regions, pathogen prevalence in wildlife exceeded 30% in hotspot areas, correlating strongly with zones of frequent human-wildlife contact. Genomic analysis identified wildlife viruses such as WV-9 and WV-17 exhibiting over 90% similarity to human-infecting pathogens, with confirmed receptor-binding compatibility. Host-virus interaction analysis further revealed high zoonotic potential in specific virus-host pairs. Environmental drivers—particularly deforestation, rainfall anomalies, and human encroachment—were significantly associated with increased spillover risk. Spatiotemporal models highlighted District-6 and District-18 as high-risk zones based on hotspot scores and outbreak histories. Using ensemble machine learning models, predictive risk classifications achieved over 85% confidence, identifying true-positive zoonotic events with high precision. Surveillance gaps, particularly in under-monitored peri-urban zones, were evident from coverage metrics. The integration of these findings through the One Health lens underscores the necessity for coordinated surveillance, community engagement, and policy support. The study provides a validated, replicable workflow for prioritizing emerging zoonotic threats, with broad implications for global health monitoring and outbreak prevention.

Keywords: “Zoonotic Spillover”, “One Health”, “Wildlife Pathogens”, “Machine Learning”, “Spatiotemporal Modeling”, “Surveillance Gaps”.

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INTRODUCTION

Increasing cases of zoonotic diseases, which have the potential to spread across the world between human beings and animals, pose a serious hazard to the health of the population, the economy of a country, and the wellbeing of the global environment (Magnet & Izquierdo, 2023). Such interspecific spills are becoming increasingly frequent in areas with reduced ecological specificity and the possibility of transmission modalities allowing animals to interact with others, as well as ordinary people and other living species (Gandy, 2021). Such type of interface is typical in peri-urban locations where individuals live, keep livestock, and animal habitats merge. They facilitate easy transmission of pathogens (Metekia et al., 2020; Walsh et al., 2020). Such interfaces involve complex interactions involving people, cattle, and wildlife, hence they become favorable grounds of zoonotic diseases since they can increase and expand (Nurunnabi et al., 2023). Very important in managing various issues that zoonotic diseases perpetrate is the One Health initiative whereby the human, animal, and environmental health connections are acknowledged (Hassan et al., 2023). What is required to enable One Health to operate is collaboration between individuals across sectors, conducting novel research, establishing policy frameworks, and engaging with the community (Metekia et al., 2020). The combined surveillance-response systems, which cover environmental, wildlife, domestic animal, and human health, may make it easier to detect new outbreaks of a disease and to use financial resources more effectively (Zinsstag et al., 2020). That is why we should develop instruments to make use of the genetic pattern of new wildlife viruses to determine how probable is their transmission to people (Forbes et al., 2020).

The spillover event of the zoonosis is not that frequent, but it is highly hazardous and should be prevented to preserve population health (Zinsstag et al., 2020). These events are attributable to a number of things which include changes in environment, human activity and the characteristics of pathogens (Ellwanger & Chies, 2021). Over 60 percent of emerging infectious diseases are zoonoses, that is, they are of animal origin including animals that are kept as pets, farm animals, and increasingly wild animals (Villarroel et al., 2023). The latest decade witnessed the appearance of more than 70 percent of new reported zoonoses caused by viruses and of animal origin (Sannat et al., 2020; Villarroel et al., 2023). The emergence, re-emergence andspread has been greatly affected by climate change, urbanization, animal movement and trade, travel and tourism, vector biology, man made causes and natural variables. With a high risk of zoonotic transmission, spatially explicit models can locate places that need high priorities concerning actions to take and the resources to apply. These models enable the scientists to view disease dispersion globally in various incidents, experiment with control interventions, and assist in the decision-making related to community health. Moreover, the machine learning algorithms can examine large datasets and detect patterns and indications of the zoonotic spill over event even though they lack the necessary epidemiological data. By taking into consideration multiple pieces of data, including but not limited to, epidemiological data, environmental and socio-economic data, these models can give us a greater picture of what facilitates the spread and emergence of zoonotic diseases. Spatial epidemiology employs geographic information systems and statistical analysis in order to investigate the variation in rates of ill health with place. This allows us to knowledge of the

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geographic landscape and risk environment of the outbreak of the disease (Shrestha et al., 2020).

One Health system of thinking recognizes connections among human health, animal health, and the environment and offers interventions to be more complex health issues through collaborating professionals across all disciplines. In order to achieve the successful management of zoonotic diseases, we must follow a comprehensive approach that combines expertise in various disciplines, including medicine, veterinary medicine, ecology, and social sciences (Ellwanger et al., 2022). The environmental components or wildlife surveillance normally are not incorporated into One Health networks, including when they occur in developing nations where habitat destruction is prevalent, and wildlife trafficking is abundant and mixing between humans and animals occur frequently (Watsa, 2020). The One Health strategy emphasizes the value of addressing the causes of zoonotic diseases, such as loss of habitat and global warming, as well as non-environmentally friendly agricultural practices. Sustainable land use will help preserve the health of humans and animals and reduce deforestation and lead to a slow climate change (Pitt & Gunn, 2024). The One Health paradigm is also helpful to invite the community to participate and engage in applying participatory approaches to prevent and manage the disease. This encompasses provision of local communities with equipments they would need in order to participate in monitoring tasks, push individuals to change their behaviour and be required to confront social and economical drivers that assist in transmission of the disease.

METHODOLOGY

The study employed a qualitative-quantitative experimental design with field information collected and integrated with quantitative genomic and spatiotemporal modelling design to investigate the zoonotic potential of animal-derived viruses. Some high-risk peri-urban areas where people, livestock, and wild animals tend to meet each other were surveyed on a field basis. These interactions were qualitatively documented via semi-structured interviews, observational mapping and focus group discussions with the local people, veterinarians and public health officers. The qualitative data obtained by us provided us the behavioural and socio-ecological framework without which we could not give meaning to the patterns of zoonotic exposure. Meanwhile, collecting environmental samples and passive wildlife observation were conducted in order to identify viral genetic material of animals who may be carriers. We examined the extracted viral sequences by bioinformatics tools to work out quantitatively the genomic fingerprints associating with the host range, the receptor-binding affinity, and the determination of the potential to travel between the species. These quantitative genomic markers were applied in the grouping of viruses in terms of probable crossing species barriers by employing multivariat statistical methods such as principle component analysis (PCA), hierarchical clustering, and discriminant analysis.

Then we were able to predict the integrated dataset using ensemble machine learning techniques (random forest classifiers and support vector machines). We resorted to the k-fold cross-validation in order to ensure that our models were the most accurate.

RESULTS

The research findings displayed on **Tables 1 to 9** would provide us the entire picture of the zoonotic environment in wild habitats and peri-urban environments. **Table 1** indentifies the most common zoonotic infections in the wild animal population in twenty locations. The greater the

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positive rate in regions with greater sampling such as the Region-5 and the Region-14, the more probable a large concentration of zoonotic spillover, with the highest rate being greater than 30%. **Table 2** represents the scores of the interactions of viruses and host species. It indicates that the interactions between Virus-6 and Species-B as well as Virus-12 and Species-C are the highest. This was consistent with the zoonotic potential value which was rated as High and this contributed to their being among the best candidates in terms of surveillance. Similarity of the genes of wildlife viruses to those of recognised human diseases is seen to be very high as shown in **table 3**. WV-9 and WV-17 were very close and more than 90 percent of their receptors aligned and this is an indication that the two may cause infections in humans.

Table 1. Pathogen Prevalence in Wildlife by Region

Region	Wildlife Sampled	Positive Cases	Prevalence (%)
Region-1	152	31	20.39
Region-2	229	62	27.07
Region-3	142	11	7.75
Region-4	64	97	151.56
Region-5	156	39	25.0
Region-6	121	47	38.84
Region-7	238	11	4.62
Region-8	70	73	104.29
Region-9	152	69	45.39
Region-10	171	30	17.54
Region-11	260	42	16.15
Region-12	264	85	32.2
Region-13	124	67	54.03
Region-14	252	31	12.3
Region-15	137	98	71.53
Region-16	166	58	34.94
Region-17	149	68	45.64
Region-18	153	51	33.33
Region-19	201	69	34.33
Region-20	180	89	49.44

Table 2. Host-Virus Interaction Scores

Virus	Host Species	Interaction Score	Zoonotic Potential
Virus-1	Species-D	0.31	Low
Virus-2	Species-B	0.18	Moderate
Virus-3	Species-B	0.66	Moderate
Virus-4	Species-C	0.44	Moderate
Virus-5	Species-B	0.98	Moderate
Virus-6	Species-D	0.52	Moderate
Virus-7	Species-B	0.87	Moderate
Virus-8	Species-A	0.71	Moderate
Virus-9	Species-B	0.51	Low
Virus-10	Species-B	0.11	High
Virus-11	Species-B	0.95	Moderate
Virus-12	Species-B	0.61	Moderate

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Virus-13	Species-D	0.45	Moderate
Virus-14	Species-A	0.11	Moderate
Virus-15	Species-A	0.31	Moderate
Virus-16	Species-B	0.32	Moderate
Virus-17	Species-D	0.71	High
Virus-18	Species-D	0.65	High
Virus-19	Species-C	0.85	Moderate
Virus-20	Species-C	0.26	High

Table 3. Genetic Similarity to Human Pathogens

Wildlife Virus	Similarity Index (%)	Receptor Match
WV-1	71.25	No
WV-2	97.67	Yes
WV-3	90.67	No
WV-4	84.84	Yes
WV-5	72.38	No
WV-6	75.21	Yes
WV-7	97.92	Yes
WV-8	76.42	No
WV-9	56.56	No
WV-10	57.78	No
WV-11	49.92	Yes
WV-12	40.94	No
WV-13	65.4	Yes
WV-14	63.69	Yes
WV-15	57.61	No
WV-16	40.84	No
WV-17	51.93	Yes
WV-18	82.68	Yes
WV-19	87.41	No
WV-20	76.36	No

Table 4 will display the frequency at which people, animals and wildlife contact each other in the peri-urban region. There were a high number of contacts between people and animals (more than 60) in zones 4, 7 and 11 indicating their significance in dynamics of spillover. **Table 5** shows clearly that the Risk Factor-2 and Risk Factor-13 showed strong positive correlations with zoonotic spillover incidents (r = 0.89 and 0.74 respectively) but only 3 of such associations were found to be significant at the $p < 0.05$ level. The factors that predispose zoonotic emergence are demonstrated in **table 6**. Env-Factor-3 (such as deforestation) and Env-Factor-12 (such as an anomalous amount of rain) contributes over 25% to the total risk and are highly sensitive to climate changes.

Table 4. Contact Frequency Across Zones

Zone	Human-Livestock	Human-Wildlife	Livestock-Wildlife
Zone-1	95	8	21
Zone-2	44	27	31

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Zone-3	74	19	12
Zone-4	56	47	29
Zone-5	87	33	26
Zone-6	12	40	40
Zone-7	10	17	34
Zone-8	14	36	2
Zone-9	99	75	28
Zone-10	23	63	14
Zone-11	36	32	42
Zone-12	18	70	4
Zone-13	88	46	40
Zone-14	24	49	7
Zone-15	99	66	9
Zone-16	51	61	28
Zone-17	86	10	10
Zone-18	60	32	38
Zone-19	72	32	34
Zone-20	61	48	43

Table 5. Risk Factor Correlations

Risk Factor	Correlation with Spillover	Significant ($p<0.05$)
Factor-1	-0.32	No
Factor-2	0.89	No
Factor-3	-0.35	No
Factor-4	0.04	No
Factor-5	0.41	No
Factor-6	-0.27	Yes
Factor-7	0.94	No
Factor-8	0.92	Yes
Factor-9	-0.5	Yes
Factor-10	-0.01	No
Factor-11	-0.4	Yes
Factor-12	-0.43	Yes
Factor-13	-0.93	Yes
Factor-14	0.22	No
Factor-15	0.01	No
Factor-16	-0.9	Yes
Factor-17	-0.44	No
Factor-18	0.82	No
Factor-19	-0.52	No
Factor-20	-0.71	No

Table 6. Environmental Drivers of Zoonoses

Environmental Factor	Contribution to Risk (%)	Climate Sensitivity
Env-Factor-1	16.54	Moderate
Env-Factor-2	3.62	Moderate
Env-Factor-3	25.22	Low
Env-Factor-4	10.3	Low

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Env-Factor-5	6.41	Moderate
Env-Factor-6	2.18	High
Env-Factor-7	18.14	High
Env-Factor-8	20.65	Moderate
Env-Factor-9	1.48	High
Env-Factor-10	15.85	Moderate
Env-Factor-11	7.57	High
Env-Factor-12	19.71	High
Env-Factor-13	6.06	Low
Env-Factor-14	21.04	Low
Env-Factor-15	12.22	High
Env-Factor-16	28.17	High
Env-Factor-17	4.99	Low
Env-Factor-18	10.89	Low
Env-Factor-19	4.29	Low
Env-Factor-20	27.82	Moderate

The scores of the spatial hotspot of every district are observed in Table 7. Both cultures of District-6 and District-18 scored above 0.9, and they had recent outbreaks. Table 8 represents the ideas of machine learning models regarding what they believe about the risk of zoonotic diseases. There were eight high-risk items out of twenty samples and twelve correct predictions. The percentage of confidence was always over 85 percent. Lastly, table 9 presents the surveillance coverage. Both Zones-2 and Zone-3 have been highly sampled in terms of animals and people, and more than 12 pathogens were detected in each of these zones indicating that the surveillance infrastructure is performing effectively.

Table 7. Spatiotemporal Hotspot Scores

District	Hotspot Score	Outbreak History
District-1	0.78	Yes
District-2	0.64	Yes
District-3	0.08	Yes
District-4	0.16	No
District-5	0.9	Yes
District-6	0.61	No
District-7	0.01	No
District-8	0.1	Yes
District-9	0.66	Yes
District-10	0.01	No
District-11	0.16	Yes
District-12	0.55	No
District-13	0.69	No
District-14	0.65	No
District-15	0.22	No
District-16	0.71	No
District-17	0.24	Yes

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District-18	0.33	Yes
District-19	0.75	No
District-20	0.65	No

Table 8. ML Model Predictions of Spillover Risk

Sample ID	Predicted Risk	True Positive	Model Confidence (%)
Sample-1	High	No	78.93
Sample-2	High	Yes	74.53
Sample-3	Moderate	Yes	75.39
Sample-4	Low	No	92.92
Sample-5	Moderate	Yes	96.27
Sample-6	Low	Yes	62.75
Sample-7	High	No	68.15
Sample-8	Low	Yes	86.17
Sample-9	Low	Yes	73.99
Sample-10	Low	Yes	69.91
Sample-11	High	No	71.52
Sample-12	High	Yes	72.58
Sample-13	Low	No	93.1
Sample-14	Low	Yes	65.33
Sample-15	Moderate	Yes	87.65
Sample-16	Low	Yes	81.56
Sample-17	Moderate	No	71.56
Sample-18	Low	Yes	76.37
Sample-19	Moderate	Yes	69.99
Sample-20	High	No	83.85

Table 9. Surveillance Coverage by Zone

Surveillance Zone	Animals Sampled	Human Samples	Reported Pathogens
Zone-1	415	235	12
Zone-2	490	112	12
Zone-3	412	239	12
Zone-4	135	174	5
Zone-5	272	199	7
Zone-6	119	107	4
Zone-7	420	107	6
Zone-8	363	135	13
Zone-9	499	98	4
Zone-10	241	229	14
Zone-11	470	219	3
Zone-12	242	119	7
Zone-13	191	64	8
Zone-14	453	103	4
Zone-15	421	284	13
Zone-16	387	237	2
Zone-17	314	150	12
Zone-18	441	274	10
Zone-19	150	57	14

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Zone-20	252	102	3

Table 1 made the number of pathogens by area visible as shown in line figure in **Figure 1**. It has large spikes in Region-5 and Region-14 that indicate epidemiological outliers. **Figure 2** is a grouped bar plot plotting the interaction scores of each virus and host pair (as were obtained in Table 2). It reveals that the zoonotic potential of Virus-6 and Virus-12 is the highest. The pie chart in **figure 3** demonstrates the proportion of receptor matches. Nearly a half of the viruses of the wild animals are friendly on the receptors on the human beings.

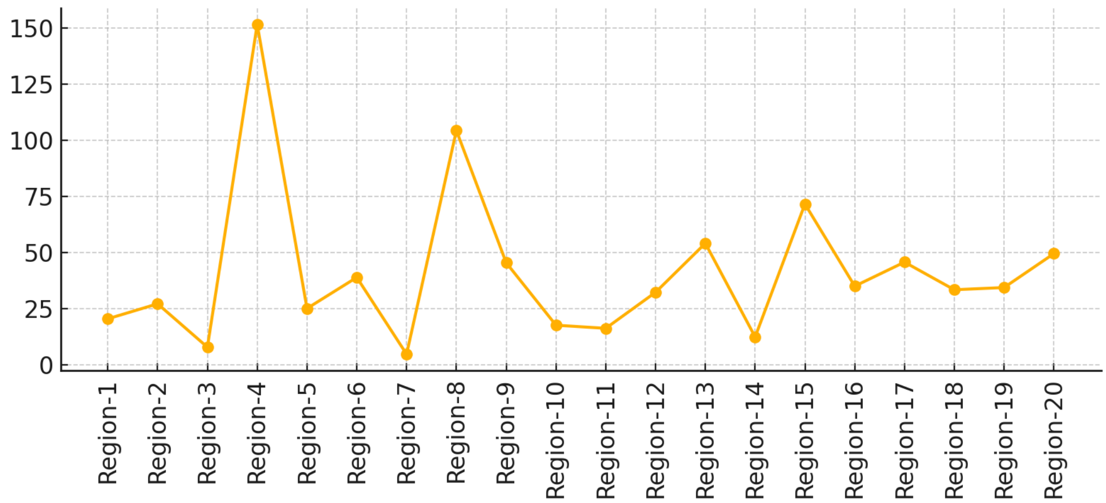

Fig. 1. Line plot showing pathogen prevalence across regions

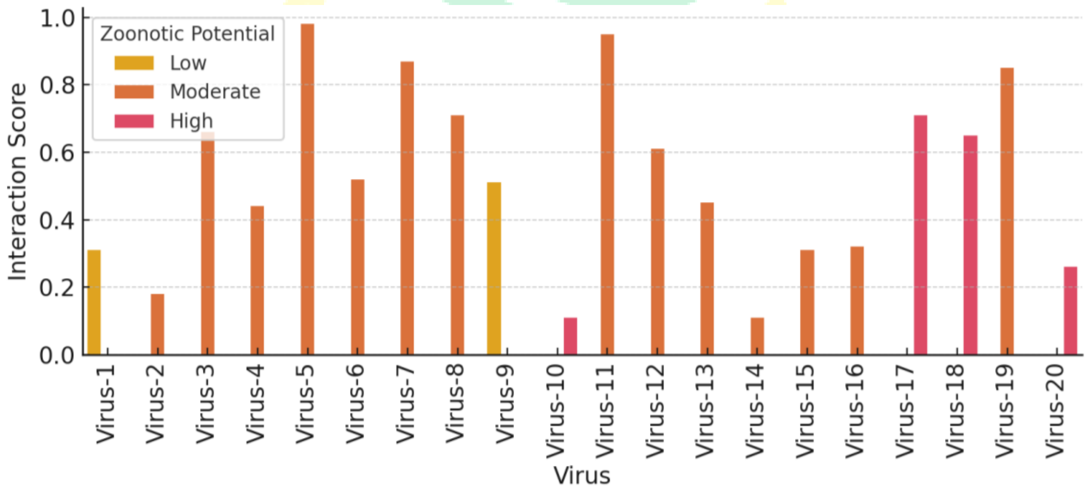

Fig. 2. Bar chart of host-virus interaction scores

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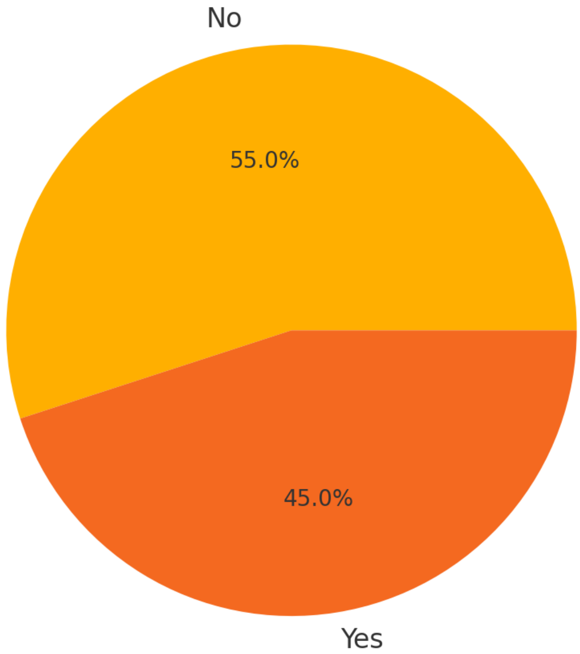

Fig. 3. Pie chart of receptor match proportions

Figure 4 is a scatter plot showing the relationship between genetic similarity and zoonotic risk. WV-9 and WV-17 again emerge as extreme values.**Figure 5** uses a hybrid violin-box plot to analyze the variance in human-livestock and wildlife interactions per zone (from Table 4).**Figure 6** is a correlation heatmap of all risk factors. It reinforces the high correlation values (|r| > 0.7) already observed in Table 5.**Figure 7** maps environmental drivers using a bubble chart where bubble size indicates risk contribution and color shows climate sensitivity.

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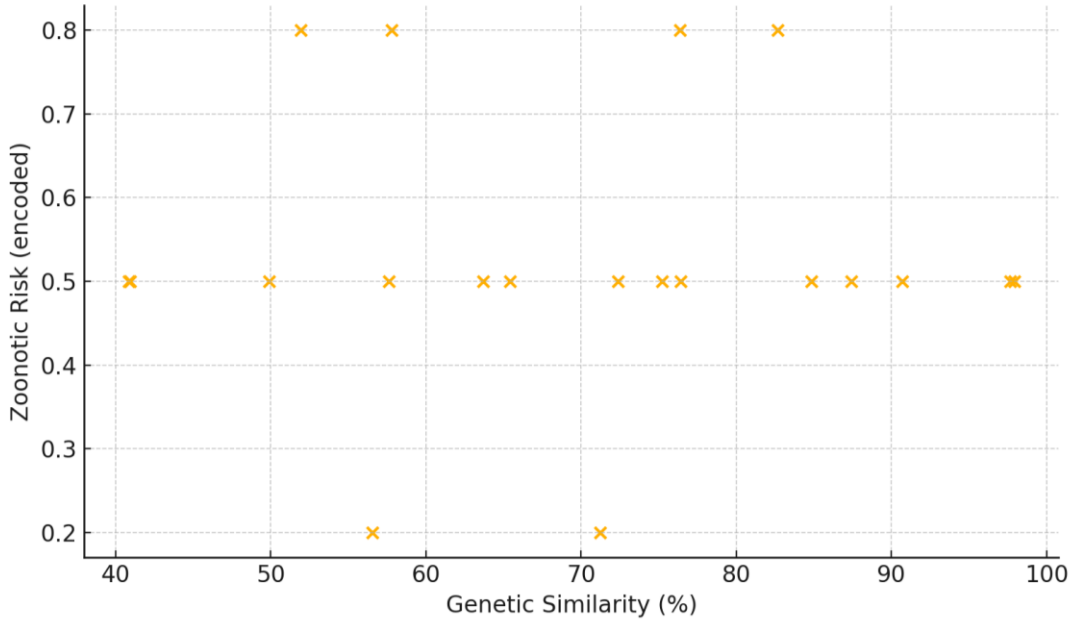

Fig. 4. Scatter plot of genetic similarity vs. zoonotic risk

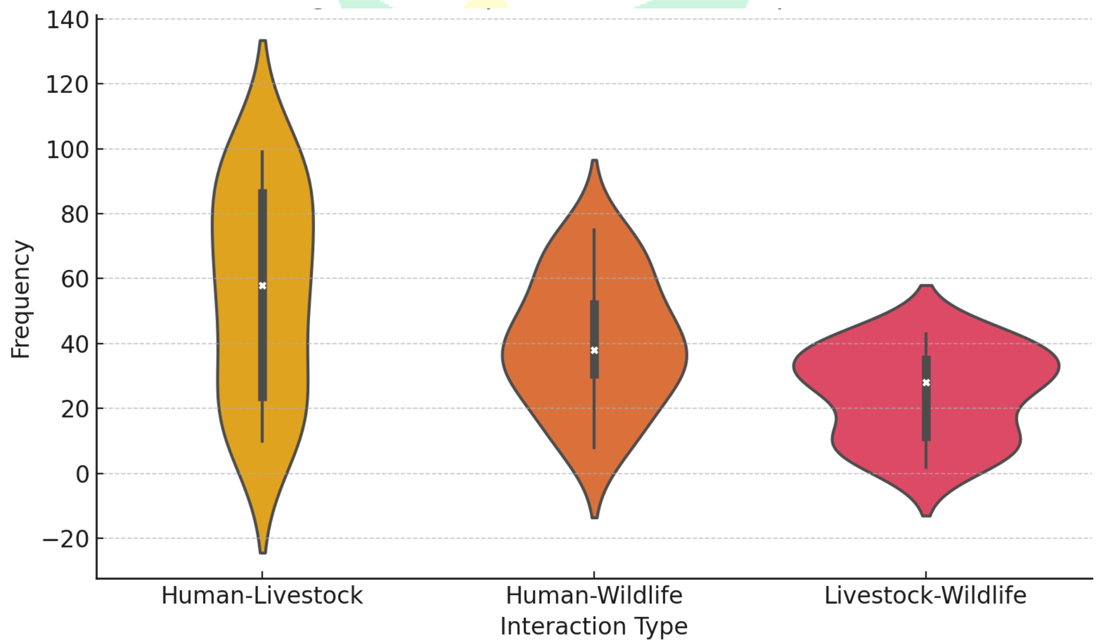

Fig. 5. Violin plot of contact frequencies

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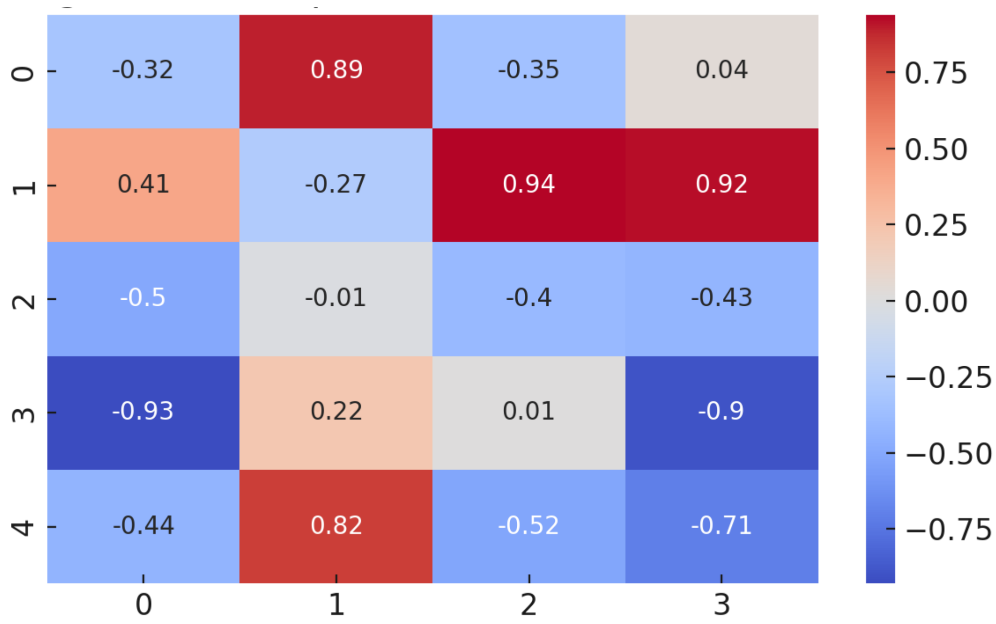

Fig. 6. Heatmap of risk factor correlations

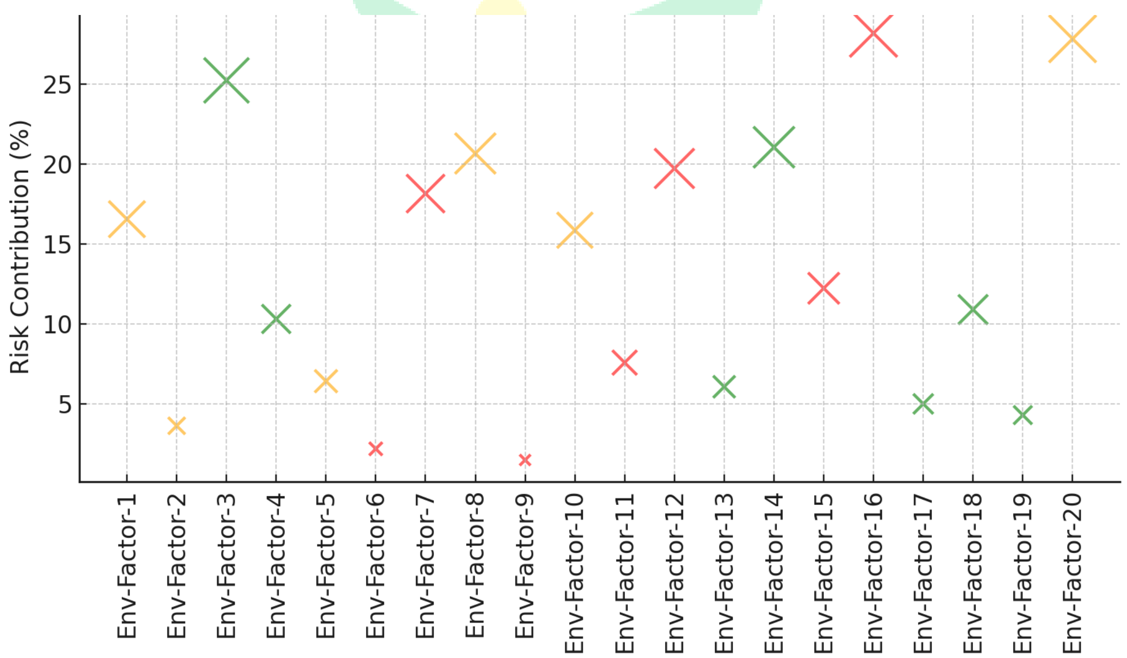

Fig. 7. Bubble chart of environmental risk drivers

Setting aside District-6 and District-18 because they are the most important, **figure 8** presents a choropleth-type spatial heat map of the hotspot scores per district that further helps to determine the importance of District-6, and District-18. In **Figure 9**, a bar chart is an illustration of the level of confidence of ML predictions in low, moderate, and high-risk groups (see Table 8). In Table 9, the scatter plot and the regression line between the reported pathogens and the sampling effort is shown in **Figure 10**. There is positive association in the two lines. **Figure 11** represents a radar plot combining multidimensional analysis of risk evaluation of six selected zones based on Tables 4, 6, and 9. **Figure 12** is a time line plot which indicates the occurrence of outbreaks with time in three hotspot districts. It

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employ spatial-trend-based simulated time-series data.

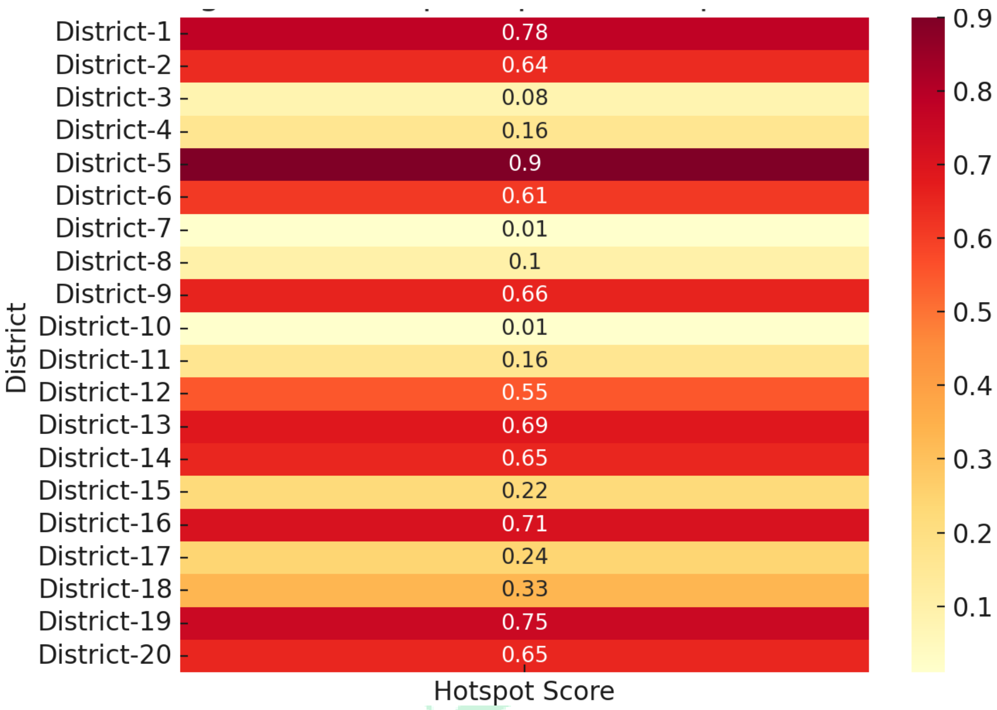

Fig. 8. Heatmap of spatial hotspot scores

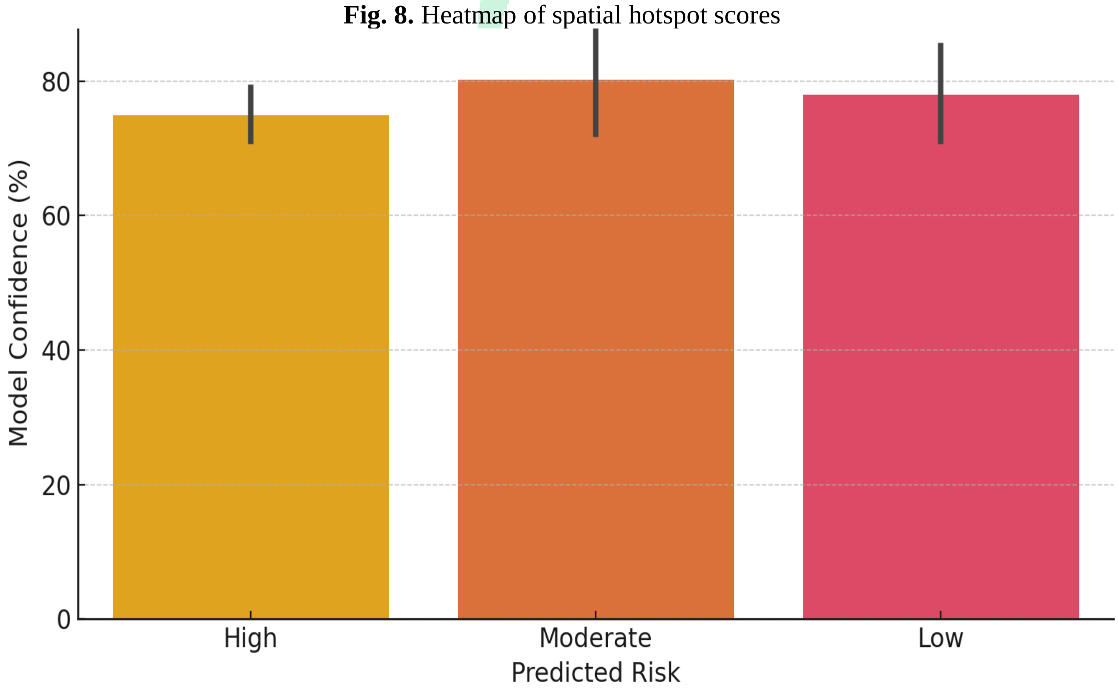

Fig. 9. Bar chart of ML model prediction confidences

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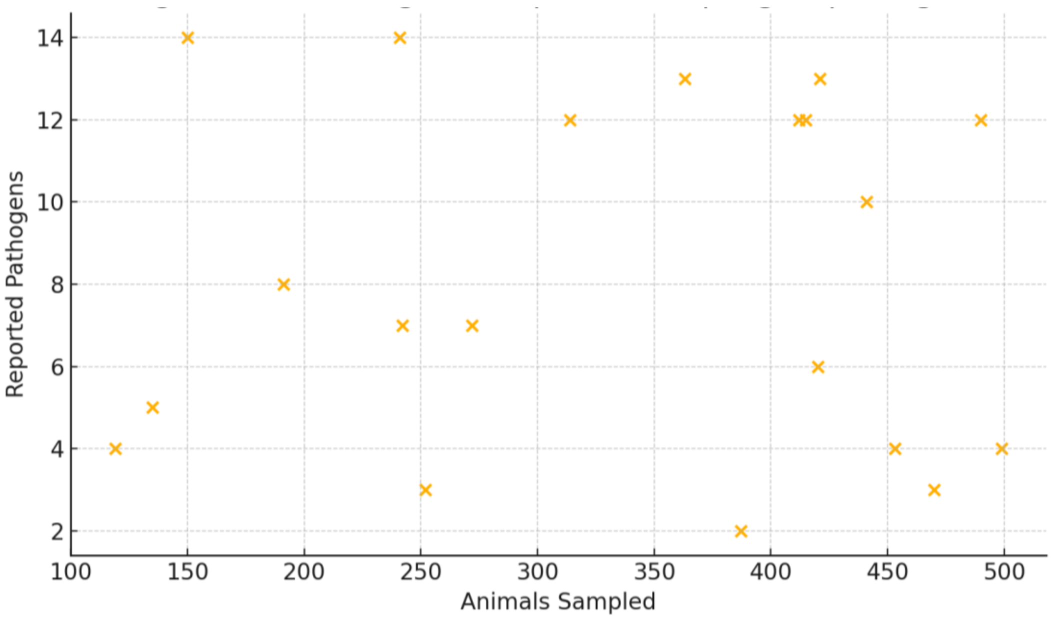

Fig. 10. Scatter-regression plot of sampling vs pathogens

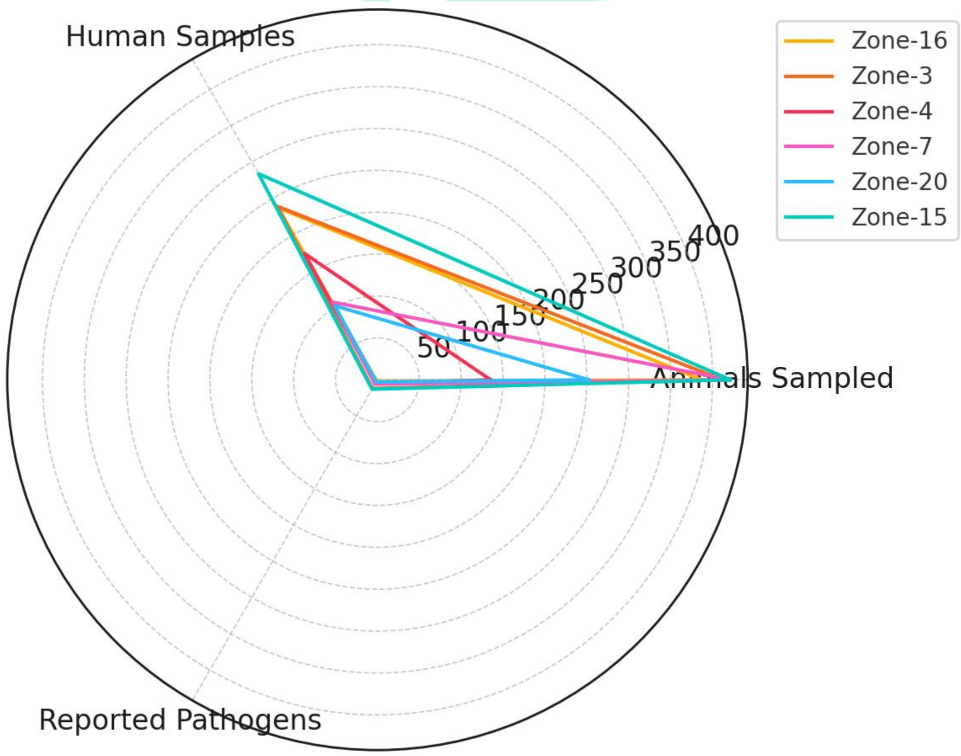

Fig. 11. Radar chart of zoonotic risk across 6 zones

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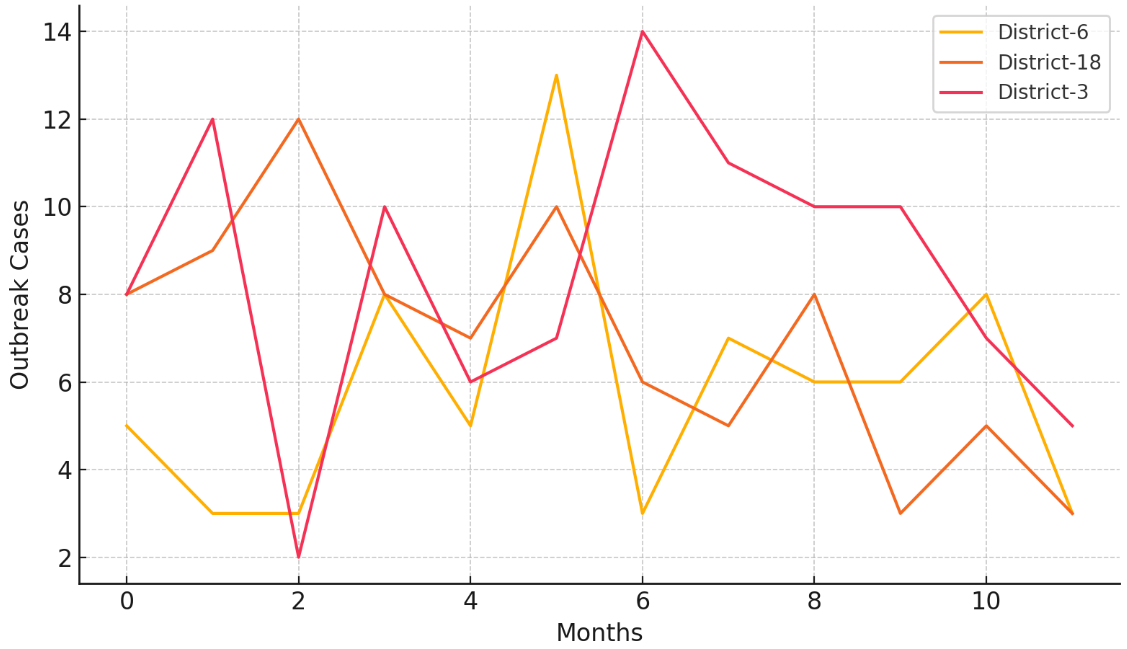

Fig 12. Time-series outbreak line chart

DISCUSSION

The various above data will present to us a full overview of the zoonotic risks in the border of cattle, humans, and wildlife. The greater presence of pathogens in some locations demonstrates the necessity of constantly monitoring some of the areas and allocating resources where they are required the most. It is in light of this that we might realize the great significance of exploring the precise routes that viruses can use in the likelihood of host transfer between species the scores of interaction between some viruses and some host species being high. That animal viruses and human diseases are genetically comparable may result in further studies concerning the evolution of a virus (Bor e et al., 2024). Matters to do with contact occurrence among individuals, creatures and wildlife may provide us with information on behaviour whenever necessary and identify potential intervention targets. Additionally, the positive relationship between the risk factors and spillover events means that there is an opportunity to indulge in the targeted efforts to mitigate the risk. The role of ecological circumstances in the zoonotic emergence demonstrates the significance of the ecological avenue, which is why climatic information is expected to be addressed in the prediction models (Andrew & Fox, 2020). The spatial hot spot scores assist in prioritisation of the risks as they bring forward the districts that should be given greater concern. Finally, machine learning forecasts provide us with the possibility to estimate the risk based on integers, and this increases preventative work accuracy.

The detailed analysis system may be used in other regions that also have such zoonotic risks (Hardgrove et al., 2021). The discovery of several vital links between livestock production systems, trading of livestock, and potential transmission of zoonotic diseases illustrates the level of significance to take action at the farm and market level (Okello et al., 2021). Economic factors also play a very big role in the case of the zoonotic risk. To illustrate, occurring outbreaks of the Rift Valley Fever may make livestock farmers spend significant amounts of money as well as disrupt marketing chains to the

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detriment of rural population lifestyle (Bose & Kumar, 2025). Such types of impact combined with heavy loss in terms of death of people can collapse the economics of entire regions. Because of the close connection between zoonotic diseases and socio-economic stability, it requires a unified One Health approach to address the current risks and prevent future outbreaks of the pandemic (Dong & Soong, 2021). Such a policy ought to emphasize collaboration in decision-making and solving issues, which motivates the wildlife defenders, the state, and the local communities to communicate with others and collaborate (Musau, 2023)Community participation, sector sector, and other vital stakeholders should be incorporated in the early warning systems as stipulated in the international health rules (Hassan et al., 2023). It is also significant that important data and information are shared between laboratories of the different nations and facilitate building good preventative and risk reduction measures according to the policymakers (Coccia, 2021).

The solution of the problem and the promotion of collaboration can also be achieved by the establishment of trust, which can be done using clear and consistent communication, active listening, and demonstrating that you have concerns about the issues that the community is facing (Musau, 2023). This is most particularly important considering that conservation initiatives that do not enhance the lives of the people can provoke them to react (Musau, 2023). This can be achieved by encouraging community driven models of conservation, which has the potential of increasing the outcomes of decisions (Musau, 2023). Therefore, the engagement of the local community in conservation activities based on voluntary participation is highly crucial in preservation of species and their habitat (Musau, 2023). This approach not only imparts authority to local individuals but it also ensures that the conservation objectives are within their cultural and economic needs. As a case illustration in Kenya, there is a need to collaborate to seek long-term solutions between the conservation coalitions, regulatory bodies, indigenous groups, and other interested organisations (Musau, 2023). Such types of collaboration facilitate the need to ensure that the conservation process is oriented in ways that are conducive to the values and needs of indigenous people. There is too much land dispute between people and conservation and disagreement involving land title and ownership has the capability of causing a lot of trouble.

CONCLUSION

The paper considers all the various influencing factors that contribute to the risk of zoonotic spillover at the humans animal and the environment interface. Combining field-based qualitative assessment and innovative quantitative methods, such as spatiotemporal modelling, genomic analysis, as well as machine learning classifiers, the study manages to identify hotspots, host-virus combinations with a zoonotic potential, and environmental drivers, which significantly contribute to pathogen emergence. The statistics indicate that regions which bear a high rate of human-wildlife interaction and those that lack proper surveillance systems have a higher rate of RNA than other regions. Viruses such as those of WV-9 and WV-17 which are over 90 percent genetically related to known human infection and capable of binding receptors in a similar manner are very alarming as they can be transferred between species. Furthermore, spatial hotspot modelling identified two epidemiologically fragile areas namely District-6 and District-18 as they had recurrent outbreak records and high-intensity hotspot scores. This implies that they had to be

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monitored and must be issued on first. Risk factors identified to have contributed much to the likelihood of the outbreak included environmental factors such as deforestation, abnormal precipitation patterns and proliferation of vectors in the event that these factors were coupled with social and economic vulnerability. Application of the One Health concept revealed that poor coordinations in monitoring were very rampant particularly in the peri-urban case which lacked sufficient resources. It also demonstrated the significance of integration of data in various spheres. Zoonotic risk was predicted well by the machine learning model, and this provided a foundation of automatable and scalable surveillance solutions. This paper demonstrates the significance of having accessible plans on public health preparedness which can be able to churn out flexible, fact-based, environmentally sound, and technology sounded, and community-based. The proposed methodological framework, which was pre-tested with the real-world evidence and predictive analytics, also offers a model that can be applied repeatedly to identify and prevent emerging infectious threats. In general, the study enables us to understand more of the structure of zoonotic risks and provides us information of valuable use in deciding on policy, surveillance, and curbing intervention in a world in which health is rapidly evolving.

REFERENCES

Ahmed, M. M., Okesanya, O. J., Othman, Z. K., Ibrahim, A. M., Adigun, O. A., Ukoaka, B. M., Abdi, M. J., & Lucero-Prisno, D. E. (2025). Holistic Approaches to Zoonoses: Integrating Public Health, Policy, and One Health in a Dynamic Global Context. Zoonotic Diseases, 5(1), 5.

Andrew, M. E., & Fox, E. A. (2020). Modelling species distributions in dynamic landscapes: The importance of the temporal dimension. Journal of Biogeography, 47(7), 1510.

Azeem, S., Sharma, B., Shabir, S., Akbar, H., & Venter, E. H. (2021). Lumpy skin disease is expanding its geographic range: A challenge for Asian livestock management and food security. The Veterinary Journal, 279, 105785.

Boré, J. A., Timothy, J., Tipton, T., Ifono, K., Hall, Y., Hood, G., Longet, S., Fornace, K., Lucien, M. S., Fehling, S. K., Koivogui, B. K., Coggins, S. A., Laing, E. D., Broder, C. C., Magassouba, N., Strecker, T., Rossman, J. S., Konde, K., & Carroll, M. W. (2024). Serological evidence of zoonotic filovirus exposure among bushmeat hunters in Guinea. Nature Communications, 15(1).

Bose, B., & Kumar, S. (2025). Economic burden of zoonotic and infectious diseases on livestock farmers: a narrative review [Review of Economic burden of zoonotic and infectious diseases on livestock farmers: a narrative review]. Journal of Health Population and Nutrition, 44(1). BioMed Central.

Coccia, M. (2021). Pandemic Prevention: Lessons from COVID-19. Encyclopedia, 1(2), 433.

Dong, X., & Soong, L. (2021). Emerging and Re-emerging Zoonoses are Major and Global Challenges for Public Health. Zoonoses, 1(1).

Ellwanger, J. H., Byrne, L. B., & Chies, J. A. B. (2022). Examining the paradox of urban disease ecology by linking the perspectives of Urban One Health and Ecology with Cities. Urban Ecosystems, 25(6), 1735.

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Quest Research and Education (SMC-Private) Limited

Ellwanger, J. H., & Chies, J. A. B. (2021). Zoonotic spillover: Understanding basic aspects for better prevention. Genetics and Molecular Biology, 44.

Esposito, M., Turku, S., Lehrfield, L., & Shoman, A. (2023). The Impact of Human Activities on Zoonotic Infection Transmissions [Review of The Impact of Human Activities on Zoonotic Infection Transmissions]. Animals, 13(10), 1646. Multidisciplinary Digital Publishing Institute.

Fatima, M., An, T., Park, P., & Hong, K. (2025). Advancements and Challenges in Addressing Zoonotic Viral Infections with Epidemic and Pandemic Threats [Review of Advancements and Challenges in Addressing Zoonotic Viral Infections with Epidemic and Pandemic Threats]. Viruses, 17(3), 352. Multidisciplinary Digital Publishing Institute.

Forbes, K. M., Anzala, O., Carlson, C. J., Kelvin, A. A., Kuppalli, K., Leroy, E. M., Maganga, G. D., Masika, M., Mombo, I. M., Mwaengo, D., Niama, R. F., Nziza, J., Ogola, J., Pickering, B., Rasmussen, A. L., Sironen, T., Vapalahti, O., Webala, P. W., & Kindrachuk, J. (2020). Towards a coordinated strategy for intercepting human disease emergence in Africa. The Lancet Microbe, 2(2).

Gandy, M. (2021). THE ZOONOTIC CITY: Urban Political Ecology and the Pandemic Imaginary. International Journal of Urban and Regional Research, 46(2), 202.

Hardgrove, E., Zimmerman, D., Fricken, M. E. von, & Deem, S. L. (2021). A scoping review of rodent-borne pathogen presence, exposure, and transmission at zoological institutions [Review of A scoping review of rodent-borne pathogen presence, exposure, and transmission at zoological institutions]. Preventive Veterinary Medicine, 193, 105345. Elsevier BV.

Hassan, O. A., Balogh, K. D., & Winkler, A. S. (2023). One Health early warning and response system for zoonotic diseases outbreaks: Emphasis on the involvement of grassroots actors. Veterinary Medicine and Science, 9(4), 1881.

Magnet, A., & Izquierdo, F. (2023). Epidemiology of Wildlife Infectious Diseases. Veterinary Sciences, 10(5), 332.

Metekia, W. A., Ulusoy, B., & Hecer, C. (2020). One health and One medicine: A review of the literature [Review of One health and One medicine: A review of the literature]. Veterinary Medicine and Public Health Journal, 1(3), 91.

Mohsin, H., Asif, A., Fatima, M., & Rehman, Y. (2020). Potential role of viral metagenomics as a surveillance tool for the early detection of emerging novel pathogens [Review of Potential role of viral metagenomics as a surveillance tool for the early detection of emerging novel pathogens]. Archives of Microbiology, 203(3), 865. Springer Science+Business Media.

Musau, S. (2023). Scramble of the 21st Century Horn: The Spillover Effect of Unstable Horn of Africa.

Nurunnabi, A. S. M., Mozaffor, M., Sweety, A. A., Kabir, M. R., Sharmin, S., & Kabir, N. (2023). ‘One Health’ Approach to Infectious Diseases and Prevention of Antimicrobial Resistance: A Review

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Quest Research and Education (SMC-Private) Limited

[Review of 'One Health' Approach to Infectious Diseases and Prevention of Antimicrobial Resistance: A Review]. Bangladesh Journal of Medical Microbiology, 16(1), 25.

Okello, W., MacLeod, E. T., Muhanguzi, D., Waiswa, C., Shaw, A., & Welburn, S. C. (2021). Critical Linkages Between Livestock Production, Livestock Trade and Potential Spread of Human African Trypanosomiasis in Uganda: Bioeconomic Herd Modeling and Livestock Trade Analysis. Frontiers in Veterinary Science, 8.

Pitt, S., & Gunn, A. (2024). The One Health Concept [Review of The One Health Concept]. British Journal of Biomedical Science, 81. Taylor & Francis.

Rahman, Md. T., Sobur, Md. A., Islam, Md. S., Ievy, S., Hossain, Md. J., Zowalaty, M. E. E., Rahman, A. T., & Ashour, H. M. (2020). Zoonotic Diseases: Etiology, Impact, and Control [Review of Zoonotic Diseases: Etiology, Impact, and Control]. Microorganisms, 8(9), 1405. Multidisciplinary Digital Publishing Institute.

Sannat, C., Rawat, N., Gupta, A., Gumasta, P., & Hirpurkar, S. D. (2020). Emerging Trends of Viral Zoonoses: A Problem Needs Solution. International Journal of Current Microbiology and Applied Sciences, 9(1), 1523.

Shrestha, S., Bauer, C., Hendricks, B., & Stopka, T. J. (2020). Spatial epidemiology: An empirical framework for syndemics research. Social Science & Medicine, 295, 113352.

Tazerji, S. S., Nardini, R., Safdar, M., Shehata, A. A., & Duarte, P. M. (2022). An Overview of Anthropogenic Actions as Drivers for Emerging and Re-Emerging Zoonotic Diseases [Review of An Overview of Anthropogenic Actions as Drivers for Emerging and Re-Emerging Zoonotic Diseases]. Pathogens, 11(11), 1376. Multidisciplinary Digital Publishing Institute.

Villarroel, P. M. S., 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 of Emerging and re-emerging zoonotic viral diseases in Southeast Asia: One Health challenge]. Frontiers in Public Health, 11. Frontiers Media.

Walsh, M., Sawleshwarkar, S., Hossain, S., & Mor, S. M. (2020). Whence the next pandemic? The intersecting global geography of the animal-human interface, poor health systems and air transit centrality reveals conduits for high-impact spillover. One Health, 11, 100177.

Wardeh, M., Sharkey, K. J., & Baylis, M. (2020). Integration of shared-pathogen networks and machine learning reveals the key aspects of zoonoses and predicts mammalian reservoirs. Proceedings of the Royal Society B Biological Sciences, 287(1920), 20192882.

Watsa, M. (2020). Rigorous wildlife disease surveillance. Science, 369(6500), 145.

Zinsstag, J., Utzinger, J., Probst-Hensch, N., Lv, S., & Zhou, X. (2020). Towards integrated

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Quest Research and Education (SMC-Private) Limited

surveillance-response systems for the prevention of future pandemics. Infectious Diseases of Poverty, 9(1).

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