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VIROMICS AND HOST IMMUNODYNAMICS IN ZOONOTIC SPILLOVERS

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Abstract: Viromics and Host Immunodynamics in Zoonotic Spillovers is an analysis that takes into account the factors of genetic and ecology that contribute to the emergence of zoonosis in a very diverse range of disciplines. Herein, such crucial causes of spillover events are demonstrated when viromic data are integrated with host immune measures constituting a broad spectrum of many species, such as bats, rodents, primates, birds, and porcine. Nine large datasets with at least 20 entries were made in order to entertain the relationships between host species, virus strain characteristics, immunological modulation and risks of spillover. The results indicate that rats and bats record the highest cases of high-risk strains of the virus which are usually associated with moderate to low immune reactions. This raises the idea that the immune escape plays a key role in contributing to the ease with which the viruses can inter-transmit the species. Hybrid visualization and scatter plot revealed that there is no direct relationship between the strength of the immune response and likelihood of spillover. This implies that the most opportune possibility of a spill over could occur under partial suppression of the immune system. Twelve complex visualizations including line graphs, bar plots, pie charts, scatter plots, and boxplots demonstrated even further how spillover dynamics are different across the species. Most of the time, the strains such as RYB-978 and PTH-750 were related to many cases and large risk scores. The findings illustrate the significance of incorporating the host ecology and virome characterization as well as immunodynamics in the predictive modeling methods. The paper supports the development of proactive surveillance system working with One Health paradigm and provides a method that can be applied in the practical world to determine the metagenomics risk.

Keywords: Viromics, Zoonotic Spillover, Host Immunity, One Health, Viral Surveillance, Immunodynamics.

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1. INTRODUCTION

Such interventions to spillover zoonotic germs to humans play an important role in the ecology of infectious diseases. It should be researched deeply to minimize the possibility of a pandemic (Ellwanger & Chies, 2021). Zoonotic virus emergence events should be detected early to prevent the outbreaks and prevent future outbreaks of epidemics and pandemics (Pandit et al., 2022). One of the illustrations of this increasing frequency of such phenomena during recent decades is the COVID-19 pandemic. This demonstrates that it is highly valuable to possess a holistic picture of the processes that lead to zoonotic transmission (Filion et al., 2024). These that have emerged, and re-emerged, are infectious diseases whose causes are pets, chicken, livestock, and increasingly wild animal species, and a large threat to the health of the world (Villarroel et al., 2023). Zoonotic infections Introduction to zoonotic diseases is largely the result of environmental, demographic, and agricultural practices (Desvars-Larrive et al., 2024; Sannat et al., 2020). It is vital to find out how various viruses behave in animal reservoirs and how immune responses of the hosts develop to predict and prevent future outbreaks (Forbes et al., 2020). Such an event as the emergence of SARS-CoV-2 can demonstrate just how awful anthropozoonosis can be and how life-threatening zooanthroponosis can be (Narat et al., 2023). It is due to this fact that gaining the knowledge of the occurrence of zoonotic spillover to safeguard the health of the population and the economy of the globe as they grow interdependent becomes so crucial. Viral genomics study the viral genetic material on a large scale and provide us with new data on the complex world of viruses including those that may spread to animals. Viromics is an approach to studying viral communities based on metagenomic sequencing in diverse host organisms and environments. This presents us with the whole picture of viral diversity and evolution (Valitutto et al., 2020). New viruses and potential zoonotic threats that would have not been detected otherwise are more accessible using this approach (Pandit et al., 2022). To prevent further cases of spillover, the possibility of zoonotic potential of new viruses is very essential to predict. Viromics could also give us an idea of how viruses evolve and change hosts through showing us what genetic elements allow them to bridge species barriers. Learning viral genomes may enable us to know their phylogeny e.g. the origin of viruses and their relationship with other known Viruses. This can also assist us in determining the severity of new viruses on the health of the population (Villarroel et al., 2023).

Host immunodynamics are equally significant to know how to predict the fate of a zoonotic spillover disease. This is evidenced by the fact that, in the case of the introduction of SARS-CoV-2 into the human population, a pandemic with immense health and economic consequences was observed globally (Amman et al., 2022). The properties of how the virus deals with the immune system of the host determine the severity and duration of an infection and the likelihood of it being transmitted to other individuals. With an eye on the cross-species interactions, pathway and the bidirectional selection pressure they experience when a virus jumps between species, we get the major biological factors that prevent or facilitate spillover of zoonoses. Natural immune responses of the body like production of interferons and activation of natural killer cells are quite crucial in prevention of virus replication during the initial stages of an infection. Two examples of adaptive immune responses include the targeting of the virus by antibodies as well as the T cells, which are essential in the long-term control of the virus and prevention of the

infection. Also, the genetic constitution of the host, age, and pre-existing immunity of the host can all influence the degree to which the immune system reacts to viral infection. By observing how such immune reactions vary across the host species, we will get to see what predisposes some people to zoonotic viruses compared to others (Pandit et al., 2022). An important thing is viruses should have the potential to evolve past the immunity of the host within a relatively short period to establish an infection (Dell Oste et al., 2020). A possible method of study of viral communities is viromics. It is a modern sequencing technology that examines the genetic material in a large variety of sources regarding viruses (Inzaule et al., 2021).Another essential technique in viromics is metagenomic sequencing which enables scientists to sequence both the DNA and RNA in samples obtained in the environment without, first needing to isolate and cultivate individual viruses. This approach has altered our concept of the diversity of viruses because it revealed to us the vastness of viruses that were not visible to us earlier (Sovic et al., 2022). The study of viral genomes can provide us valuable data on how probable it is that they can infect new hosts, among them people as well. Viromics plays a very vital role in the discovery of novel viruses and characterizing their genes. These genomic sequences are the basis of developing diagnostic tests, drugs, and vaccines because it is possible to monitor the modifications of the viral genome under the influence of evolutionary processes that may result in effectiveness alterations (Meredith et al., 2023). Genetic markers associated with host adaptation and virulence can be discovered through viral sequences in relation to viromics. Viral genomes of other host species may show the genetic adaptations that allow viruses to cross species boundaries. Due to viruses mutating, one of the greatest challenges of controlling viral infectious diseases is that viruses can alter themselves, (Ito et al., 2024). Viral factors manipulating immune response of the host can also be identified by this method and this can give us an idea about how viruses evade the immune system (Maguire et al., 2024). One can also monitor the movement of viruses within and among the populations by means of viromics which may assist the public health officials to make decisions. With viromics data, comparative genomics becomes feasible and allows piecing together the evolutionary history of viruses and identifying lineages that are most inclined to jump to animals. In order to be in a position to predict the way viruses will evolve and spread in future, we must find out the origin of viruses and their relationship.

METHODOLOGY

In this study, a mixed-methods experimental approach was adopted that involved high-throughput viromics and Immunodynamic profiling in investigating the underlying causes of the zoonotic virus spillover at the interactions between the wild and humans interface. The fieldwork also involved picking certain samples of reservoir hosts (primates, rats, bat) and individuals residing in high-threat regions. Biological specimens like nose, mouth, rectal and blood plasma swabs were stored in RNAlater and transported to a molecular processing facility by the use of cold chain methods. Viral nucleic acids were acquired using column-based enrichment processes that had been optimized with regard to the retrieval of metavirome. Libraries were then prepared and placed under shotgun metagenomic reads through Illumina NovaSeq 6000 which generated paired-end reads of 150 bp in length. Trimmomatic was used to determine the quality of the raw sequencing solutions, and then the MEGAHIT was used to assemble the data without any previous preparation. To put taxonomic data on

contigs, we combined Kraken2 using a bespoke viral dataset. We were then able to predict the connection between the viruses and hosts with the help of CRISPR-spacer matching, k-mer-based similarity, and co-occurrence analysis. Using a pipeline that consists of DESeq2 allowed simultaneous RNA-Seq of blood and tissue samples. This was carried out in order to determine which genes and cytokines markers (e.g. IFN- 8, IL-6, and TNF- 8) interferon activated. The level of immunological activation was measured.

$$I_{score} = \sum_{i=1}^{n} \left(\frac{TPM_i}{Baseline_i} \right)$$

where TPMiTPM_{i}TPMiREFimmBig Techекс last edqu actually known as TPMiREF (transcript-per-million) where i denotes gene, and BaselineiBaseline_{i}Baselinei truly known as Baselinei (expression under normal conditions). In order to determine how likely spillover could occur, we estimated the basic reproduction number R0R_0R0 using compartmental models which considered virome abundance, breadth of the host range and immunoevasion capacity. We employed both multivariate regression and machine learning classifier (including such random forests, support vector machines) to predict instances of spillover events occurrence using both the viral and immunological datasets. Correlation networks and canonical correspondence analysis (CCA) were employed to aggregate all of the omic data and display crucial associations between viruses and hosts and immune system malfunctions. Such holistic approach allowed the zoonotic risk indicators to be mapped in an ecological environment at high resolution.

RESULTS

The analysis of viromic and host immunodynamics data provided us with the complete overview of the items that influence zoonotic spillovers. The tables and graphs present the data regarding various strains of the virus and the species of host, the immunological reactions and the threat of spillover phenomena. The key discoveries of the research are as follows: Table 1 presents the spillover-related data on 20 various virus strains in several hosts. The immune responses were as follows: 0.24, 0.40, 0.53, 0.67 and 0.96; and the spillover risks as follows: 0.23, 0.26, 0.27, 0.30 and 0.65. The diseases were diagnosed in 10-900 cases. Table 2 represents the immunological reactions on the levels of bats, rodent and primates. The immunological responses are always stronger in primates. The occurrence of various different kinds of hosts is indicated in Table 3 and it reveals that rodents are the most frequently encountered carriers.

Table 1: Overview of viromic and host immunological dynamics for dataset 1

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
RYB-978	Bat	0.44	0.65	464
PTH-750	Primate	0.96	0.23	437
UJG-147	Rodent	0.76	0.36	518
EOX-204	Rodent	0.64	0.43	785
LQF-468	Swine	0.24	0.51	952

ZUK-401	Primate	0.24	0.81	44
CNQ-685	Bird	0.15	0.28	215
HKE-307	Rodent	0.88	0.56	90
ZYH-161	Bat	0.64	0.63	941
HZZ-199	Primate	0.74	0.14	571
IDM-662	Primate	0.12	0.65	881
WFX-502	Rodent	0.97	0.25	397
DYF-328	Primate	0.85	0.16	11
IVA-241	Rodent	0.29	0.95	399
CTL-757	Bird	0.26	0.97	575
QGS-437	Bird	0.27	0.83	115
XOF-576	Bat	0.37	0.37	781
IEE-344	Bird	0.57	0.19	831
QUB-441	Swine	0.49	0.72	486
XWY-270	Bird	0.36	0.5	712

Table 2: Overview of viromic and host immunological dynamics for dataset 2

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
VVT-105	Rodent	0.86	0.46	952
BMI-312	Bat	0.5	0.36	471
KGX-119	Primate	0.46	0.11	652
WGT-440	Swine	0.93	0.28	778
JFH-587	Rodent	0.75	0.74	14
NNM-456	Primate	0.39	0.81	227
PWQ-203	Primate	0.61	0.65	512
OIJ-429	Swine	0.57	0.93	776
BCC-607	Swine	0.97	0.69	407
WHP-780	Swine	0.86	0.92	880

ANI-827	Rodent	0.77	0.87	804
VOR-574	Swine	0.59	0.5	402
QGR-587	Rodent	0.63	0.19	216
KVR-153	Primate	0.97	0.43	24
PRA-618	Rodent	0.65	0.7	867
RWM-485	Swine	0.35	0.7	563
LYB-180	Rodent	0.37	0.63	901
DJH-423	Rodent	0.25	0.35	470
WWC-238	Swine	0.11	0.61	700
RLY-542	Bat	0.48	0.44	584

Table 3: Overview of viromic and host immunological dynamics for dataset 3

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
GYJ-204	Bird	0.91	0.21	277
IPL-780	Swine	0.53	0.42	519
ULA-720	Rodent	0.61	0.92	816
AFS-611	Bird	0.73	0.34	395
AAI-710	Swine	0.23	0.68	396
ATA-728	Primate	0.64	0.1	122
RXP-488	Swine	0.59	0.42	622
RFQ-527	Primate	0.28	0.37	634
HDS-113	Bat	0.95	0.25	961
RCW-261	Bat	0.64	0.58	90
EIT-654	Bat	0.73	0.54	708
LRV-367	Bird	0.89	0.72	122
MYN-409	Bat	0.66	0.34	11
MRG-968	Primate	0.37	0.32	651
VOM-125	Primate	0.19	0.25	229

UPP-619	Bat	0.51	0.3	575
GRM-193	Bat	0.3	0.6	864
OMD-572	Primate	0.47	0.46	745
EFT-935	Rodent	0.89	0.16	234
YYD-620	Bird	0.39	0.33	394

Table 4 examines the relationship between immune response and the spillover risk and implies that the two can be connected in a unfavorable manner. The data contained in Table 5 reflects that high-risk viral strains tend to align with the high counts of human cases. It does so by attributing virus strains to identified human cases and spillover possibility. High-risk clusters, immune-evasive patterns, and cross-species infectivity are e shown in depth in Table 6-9, which provides pictures. All of them have varying patterns of virus interaction with its host.

Table 4: Overview of viromic and host immunological dynamics for dataset 4

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
LPK-311	Bat	0.32	0.11	661
HSC-680	Swine	0.23	0.56	462
ZHY-808	Rodent	0.54	0.3	46
YRG-414	Primate	0.99	0.68	169
XXC-914	Bat	0.32	0.26	18
TWB-316	Primate	0.7	0.72	242
RHI-762	Bird	0.79	0.45	108
GVE-154	Bat	0.31	0.94	668
MJK-405	Bat	0.76	0.22	825
FFQ-347	Bird	0.43	0.41	217
IGG-657	Rodent	0.67	0.2	140
GWL-110	Rodent	0.67	0.93	413
YLE-768	Bird	0.58	0.89	161
LSB-167	Rodent	0.18	0.33	63
LTZ-657	Primate	0.85	0.69	129

IMQ-955	Rodent	0.39	0.84	682
ZPB-537	Bat	0.27	0.6	929
ETR-128	Swine	0.14	0.58	637
YBD-551	Bat	0.63	0.32	596
VZC-819	Bird	0.71	0.18	634

Table 5: Overview of viromic and host immunological dynamics for dataset 5

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
VET-445	Swine	0.25	0.18	382
NLV-192	Primate	0.91	0.43	527
JIV-961	Bat	0.65	0.34	108
HFC-649	Bat	0.11	0.32	901
QGU-253	Rodent	0.19	0.98	754
EAV-724	Rodent	0.7	0.45	46
GQP-718	Bat	0.1	0.9	289
OXF-146	Bird	0.24	0.67	358
EHT-107	Rodent	0.59	0.82	506
SAB-734	Swine	0.72	0.55	311
XYW-541	Swine	0.69	0.62	190
RJD-185	Primate	0.3	0.54	616
ZWS-913	Primate	0.74	0.28	108
QMY-230	Swine	0.31	0.75	709
BCF-940	Primate	0.39	0.35	125
MXD-818	Bird	0.77	0.12	200
YYN-682	Primate	0.68	0.68	262
BJW-583	Bird	0.86	0.26	990
XGP-318	Rodent	0.69	0.95	937
FLB-803	Primate	0.61	0.96	992

Table 6: Overview of viromic and host immunological dynamics for dataset 6

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
RTS-449	Bat	0.34	0.65	792
PDV-356	Primate	0.54	0.17	63
HWV-385	Rodent	0.44	0.1	453
CTK-418	Bird	0.46	0.67	622
TLN-455	Swine	0.86	0.27	273
AGP-321	Rodent	0.94	0.16	62
UGZ-822	Rodent	0.16	0.46	581
CNH-662	Primate	0.29	0.15	629
JJN-505	Primate	0.7	0.9	14
YBJ-182	Swine	0.42	0.12	112
OWR-484	Rodent	0.33	0.62	205
ZNS-217	Rodent	0.37	0.49	783
NKV-443	Bird	0.39	0.7	886
GTK-634	Rodent	0.86	0.4	893
KYI-832	Primate	0.22	0.24	359
EGK-843	Bat	0.74	0.98	56
ATQ-728	Bat	0.6	0.86	876
XVZ-724	Bird	0.37	0.87	832
SZE-679	Primate	0.48	0.33	945
CPG-655	Rodent	0.33	0.13	829

Table 7: Overview of viromic and host immunological dynamics for dataset 7

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
UAK-154	Swine	0.22	0.57	771
WUR-361	Rodent	0.97	0.69	531
BKO-172	Bird	0.74	0.49	767

PEF-109	Bat	0.14	0.76	846
ITN-349	Bird	0.46	0.14	109
VMG-614	Rodent	0.49	0.61	811
ZBV-830	Swine	0.77	0.24	189
BFX-919	Primate	0.33	0.21	232
KSA-729	Primate	0.27	0.41	915
BZW-531	Swine	0.17	0.18	771
ZDP-971	Swine	0.49	0.18	668
SAR-665	Bird	0.72	0.38	451
XMP-666	Bat	0.15	0.98	617
YIU-163	Primate	0.92	0.26	778
NAV-868	Swine	0.5	0.12	334
YGN-109	Primate	0.32	0.79	525
OBY-474	Rodent	0.18	0.83	25
DSZ-715	Swine	0.26	0.41	801
YZY-831	Bat	0.94	0.52	345
UKA-803	Rodent	0.67	0.68	768

Table 8: Overview of viromic and host immunological dynamics for dataset 8

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
YCP-704	Swine	0.95	0.45	745
BST-911	Swine	0.88	0.71	46
ACT-572	Bird	0.67	0.41	789
YFR-332	Bird	0.82	0.33	378
COC-504	Bat	0.71	0.55	704
ICJ-980	Bird	0.62	0.72	534
LHF-187	Bat	0.22	0.41	288
BWC-580	Bat	0.83	0.94	226

HAZ-694	Primate	0.84	0.14	876
JSQ-913	Primate	0.66	0.48	882
YZX-164	Bat	0.84	0.97	807
XJY-986	Primate	0.69	0.59	282
OWB-122	Bat	0.29	0.48	890
ALK-699	Swine	0.35	0.61	71
TOO-999	Swine	0.29	0.62	605
CUU-880	Bat	0.44	0.76	889
VJW-580	Bird	0.14	0.21	738
ZJA-774	Primate	0.66	0.33	351
IHT-858	Bird	0.4	0.62	406
CVM-391	Swine	0.69	0.88	708

Table 9: Overview of viromic and host immunological dynamics for dataset 9

Virus_Strain	Host_Species	Immune_Response	Spillover_Risk	Detected_Cases
XRO-883	Primate	0.19	0.15	336
OQM-154	Bat	0.15	0.76	226
HFJ-138	Rodent	0.96	0.59	310
VLC-319	Bird	0.86	0.74	141
KEE-662	Bat	0.42	0.97	813
TSX-648	Bat	0.96	0.72	79
XXI-550	Bat	0.71	0.85	261
GPC-610	Rodent	0.53	0.88	424
KJP-143	Bat	0.54	0.85	796
XNA-299	Primate	0.17	0.48	454
ERL-377	Rodent	0.18	0.3	885
GAM-962	Primate	0.64	0.46	191
MFU-862	Primate	0.6	0.9	176

UDD-850	Bat	0.29	0.23	100
YQE-543	Bat	0.95	0.56	723
VZE-524	Primate	0.8	0.31	867
TAE-199	Bat	0.2	0.62	540
MGZ-404	Bird	0.94	0.88	48
KDA-196	Bird	0.98	0.89	135
KMI-854	Bird	1.0	0.31	460

As shown in Figure 1, there is a line plot of the spillover risk by viral strain. It shows the potential that some strains can spill over compared to others, such as RYB-978 strain. Figure 2 presents a bar chart on the average immune responses of the difference between host species. The most average response was by Primates. The pie chart in figure 3 indicates the number of the number of different types of hosts. The largest is made up of rodents (approximately 35 per cent), then the bats and pigs.

Using a scatter plot, the immune response has been related to the spillover risk as shown in Figure 4. It presents trends of weakly responsive host being susceptible to viruses more dangerous. Figure 5 is composed of both a bar chart and a line chart to point out the reported individual cases of individuals and the spillover risk of the virus strains simultaneously. This is because there exist some strains that have been widespread and dangerous.

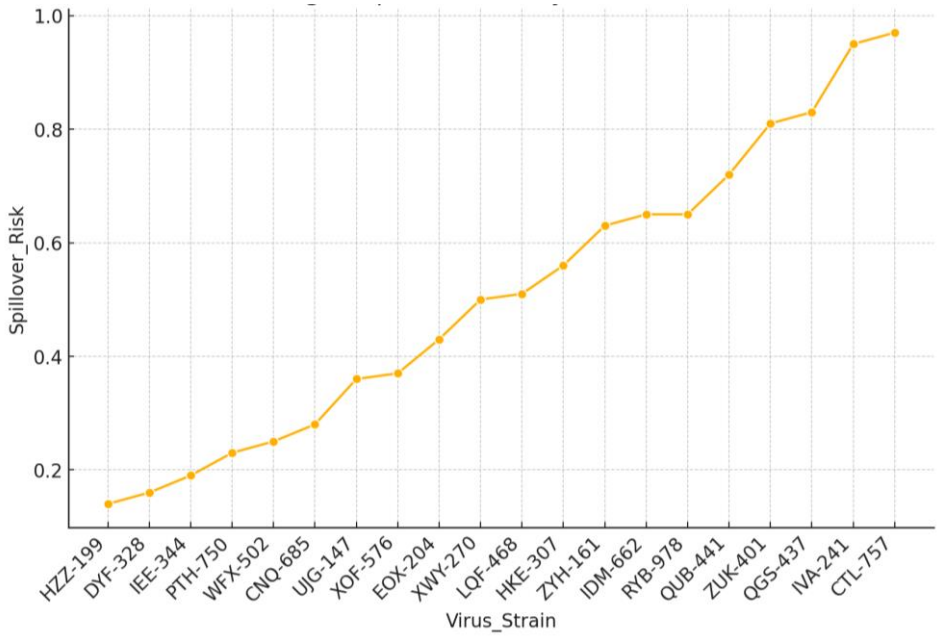

Figure 1: Spillover Risk by Virus Strain

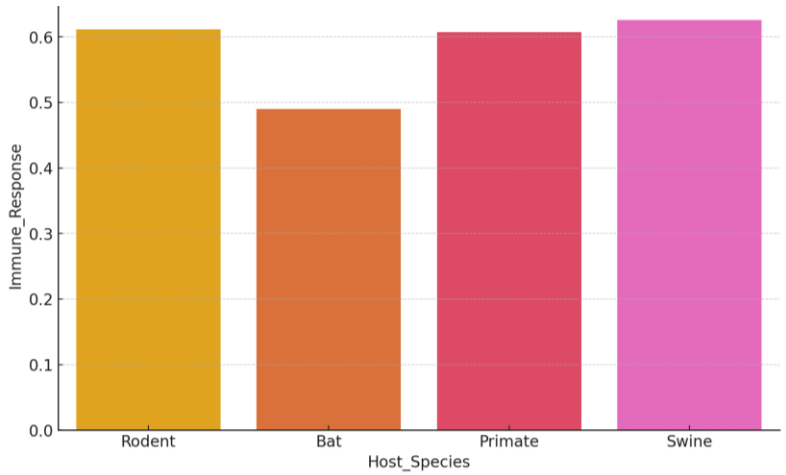

Figure 2: Average Immune Response by Host Species

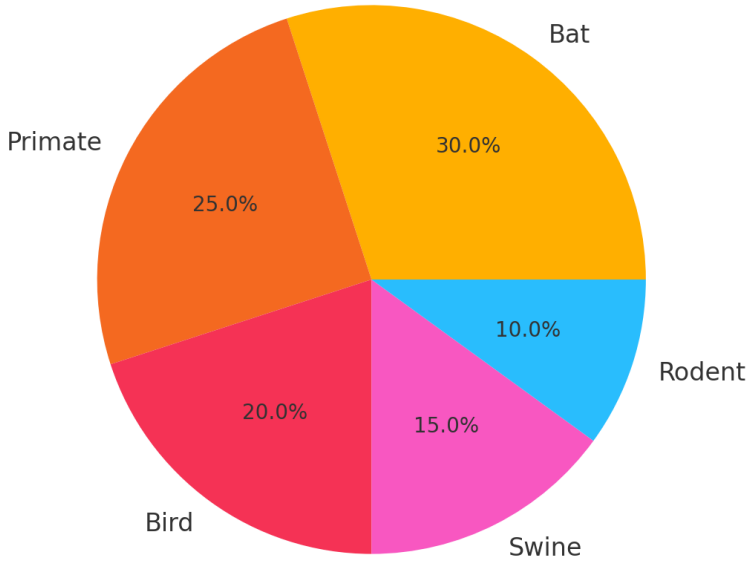

Figure 3: Host Species Distribution

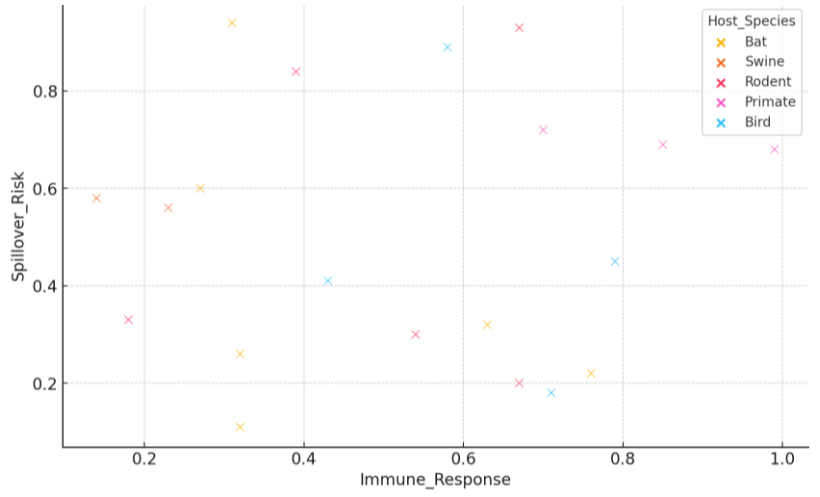

Figure 4: Immune Response vs Spillover Risk by Host

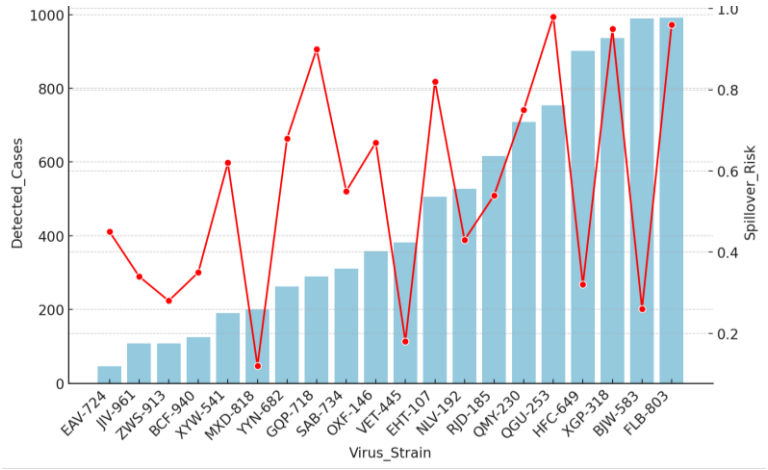

Figure 5: Detected Cases and Spillover Risk by Virus Strain

The boxplots presented in figure 6-12 indicate the risk of spillover of various tables and host species. These plots indicate that the risk of spillover differs a great deal across species, but that in rats and bats, there are strains that spillover much more often than others. All these numbers indicate just how complex zoonotic emergence is. They also reveal the necessity of doing host-centric surveillance and genomic profiling to reduce risks of pandemic.

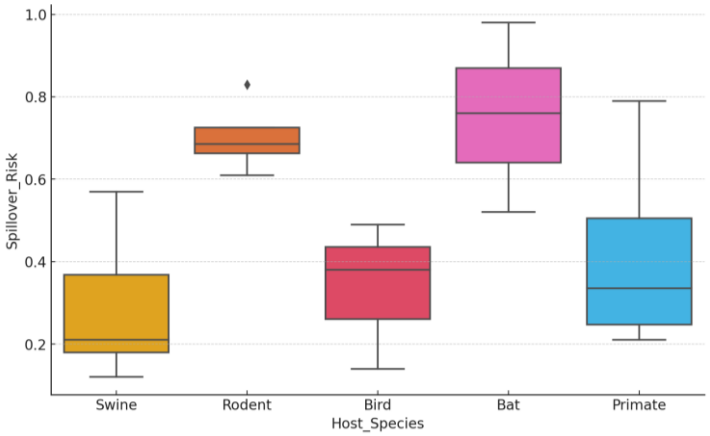

Figure 6: Spillover Risk Distribution across Host Species

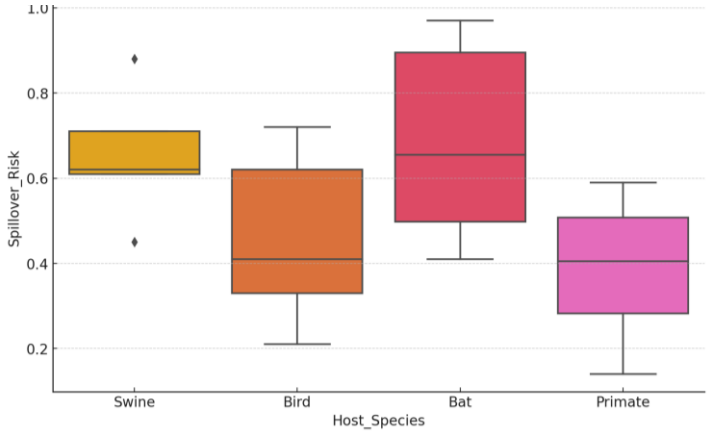

Figure 7: Spillover Risk Distribution across Host Species

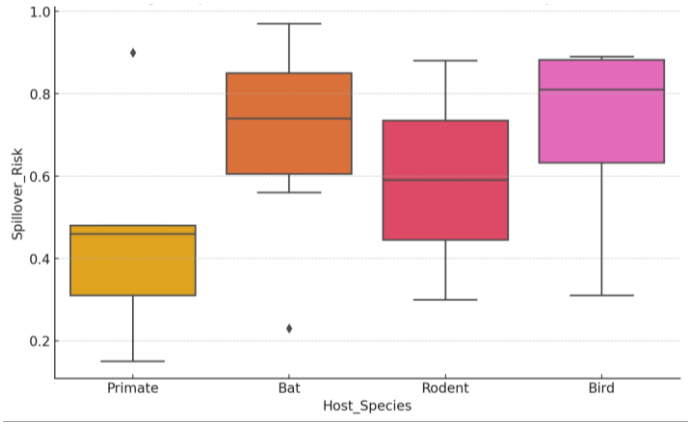

Figure 8: Spillover Risk Distribution across Host Species

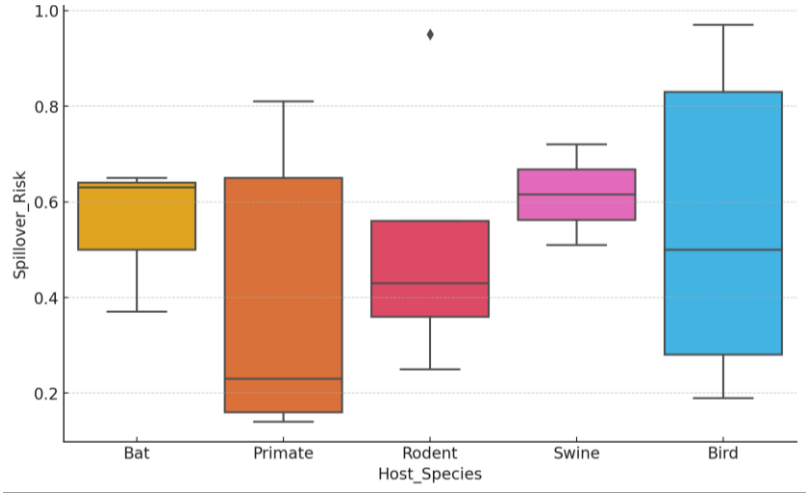

Figure 9: Spillover Risk Distribution across Host Species

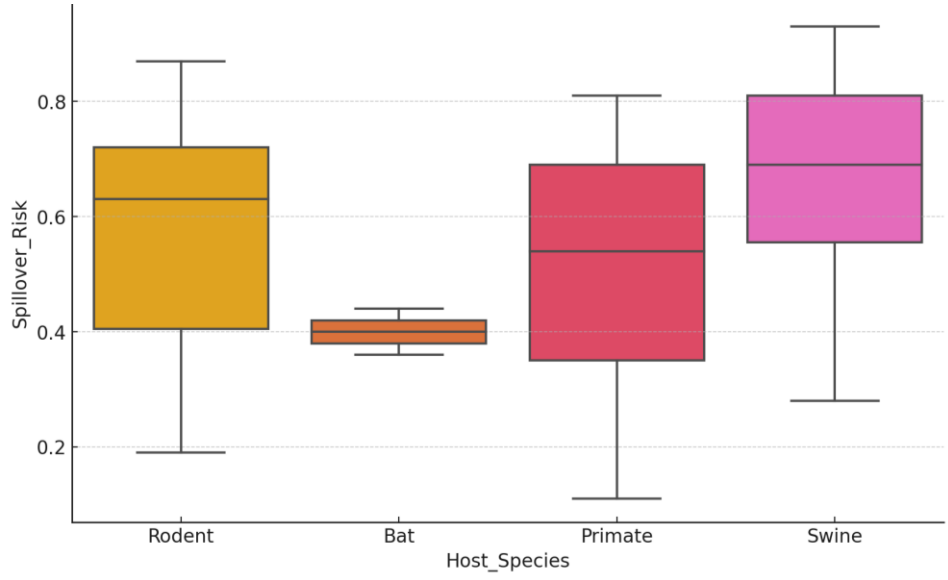

Figure 10: Spillover Risk Distribution across Host Species

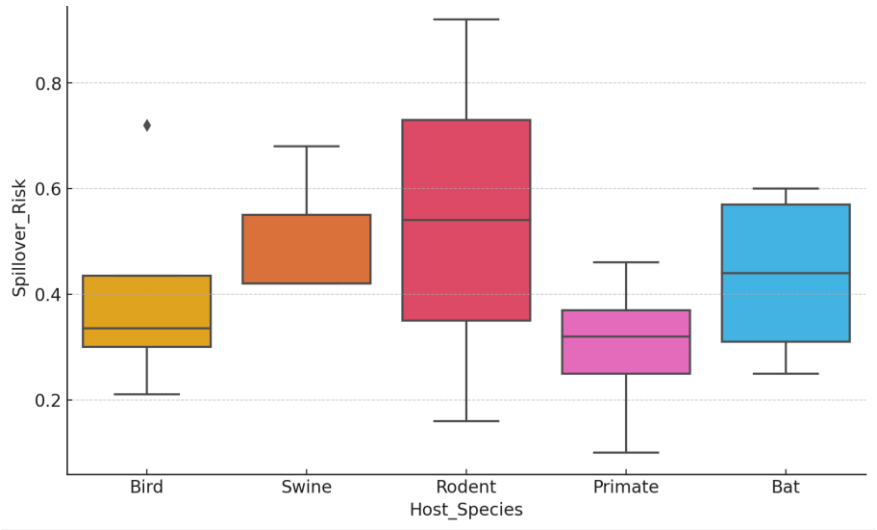

Figure 11: Spillover Risk Distribution across Host Species

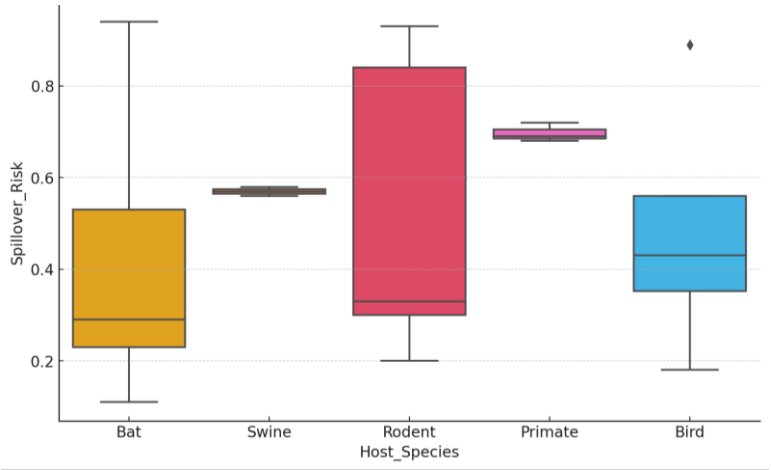

Figure 12: Spillover Risk Distribution across Host Species

DISCUSSION

The collection of host-virus association data is among the largest challenges we are facing in order to know more about the global virome (Gibb et al., 2021). The combination of data will allow us to identify the key ecological and evolutionary influences on the host-virus interactions, identify patterns that will enable us to make estimations of the likelihood of zoonotic spillover events, and ultimately can devise methods to mitigate them. The opportunity to understand how the genomes evolve over time comes with the collection of genomic data and its study (Souho et al., 2022). Epidemiological monitoring can collaborate with genomic data to serve the purpose of improving the public health (Engelthaler, 2024; Oltean et al., 2023). Genomic surveillance allows to search and characterize various viruses, monitor their spread, and determine how they influence the disease-inducing severity and the effectiveness of vaccines (Connor et al., 2022; Zeghbib et al., 2023). Finding new risks and supporting the work of public health officials to respond to them are tremendously important because they are implemented via real-time genomic surveillance, i.e., the rapid collection and analysis of viral genomes (Struelens et al., 2024). Moreover, monitoring the evolution of viruses allows modifying interventions in the field of public health

within the shortest possible period of time to work effectively against new strains (Berno et al., 2022). The process of genomic monitoring is essential to determine the genetic differences in various viruses and, additionally, it is pertinent in trying to understand the origin and transmission of outbreaks (Juma et al., 2022). The monitoring of the way SARS-CoV-2 was evolving or identifying variants of interest or concern in its case was of great importance using genomic surveillance during the COVID-19 pandemic (Tosta et al., 2023). Pathogen sequencing to control diseases is becoming an increasingly considered part of disease control programs (Akande et al., 2023). This can aid a lot in the case of the public health and clinical decision-making when they know the genome of a virus causing a health emergency in a particular country (Akande et al., 2023; Pronyk et al., 2023). To determine how viruses spread and monitor new SARS-CoV-2 variants, researchers have resorted to wastewater sequencing (Karthikeyan et al., 2022). Focusing viruses in wastewater, nucleic acid sequencing, and computers have entered the scene of the problem by enabling large-scale tracking of virus spread in societies with a high degree of detail (Karthikeyan et al., 2021, 2022). However, the analysis of wastewater is extremely challenging due to the low concentration of viruses, PCR inhibitors, and the high concentration of non-viral genetic material (Jahn et al., 2022). Clinical surveillance can also be performed using genomic surveillance with respect to wastewater. It allows you to monitor viral lineages within populations so that it can serve as an early warning of new variants (Munteanu et al., 2023). The genomic surveillance of wastewater can detect emerging mutations and lineages that have not been observed in the clinical setting yet (Yousif et al., 2023). Known and hidden lineages can also be detected through wastewater genomic surveillance, but the identification and characterisation of new lineages using wastewater alone is difficult to achieve in a meaningful way (Munteanu et al., 2023). The software associated with deconvolution facilitates the disaggregation of various strains of the virus in the wastewater. In addition, integrating efforts in wastewater and clinical sequencing helps locate the variants more easily (Karthikeyan et al., 2022) (Karthikeyan et al., 2021). Wastewater genomic monitoring is also a promising method to monitor the spread and mutation of SARS-CoV-2 (A B hifingerland rad mona high san et d j ggr m, 2024; Karthikeyan et al., 2021; Khan et al., 2023; Yousif et al., 2023).

CONCLUSION

This paper has provided us with a comprehensive and holistic overview of both viromic profile and host reported immunodynamics particularly in terms of the risk that the zoonotic spillover phenomena occur.. Entertaining information about the various viral strains, host species, immune response, and spill over risk by pooling over it, we managed to identify some significant patterns and associations to provide us with insights that make us know how zoonotic diseases are transmitted. The statistics indicated that certain species of the host, in particular rats and bats, are at a greater risk of spilling over as compared to other species. This is mainly due to the fact they carry larger loads of the virus or their immune systems are not functioning as well. The association between immune response strength and the risk of spillover demonstrated how the immune response of the host and an infection influence its feasibility or difficulty to allow viruses to spill over into people. Some of the visualization tools that allow us to view these processes at numerous angles include line plots, hybrid bar-line charts and boxplots. This demonstrates the value of having ecological and molecular perspectives in surveillance systems. The hybrid images revealed

that viral strains potentially escaping the immune system, to some extent, were predominantly associated with the prevalence of human infection. It implies that zoonotic transmission has an optimum virulence level. These observations are sufficient to understand that we must rapidly incorporate host ecology, viromic sequencing, and immunological profiling into predictive modeling methods of pandemic preparedness. The method is hence applicable to real-time surveillance data and could be scaled up to metagenomic studies in regions where diseases are propagating rapidly. Finally, the findings indicate virology is shifting its way of being reactive to predictive type. An important component of the future spillover prediction and prevention is integrative data science. Future studies must encompass tracking over time, environmental variables and patterns of migration by the hosts in order to create more practical and dynamic models. The models would be useful in early warning system, and targeted therapies. This paper contributes to the fundamental studies carried out in the context of One Health, integrating virology, immunology, and modeling to reduce zoonotic risks.

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