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VETERINARY IMMUNOPATHOLOGY FOR PANDEMIC READINESS

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Abstract

An application of the science of veterinary immunopathology has been worthwhile in planning to contain pandemics since it enables us to decide how the immune system reacts to diseases of zoonotic nature and enables us to devise some early response methods. In light of the One Health paradigm, this paper examined immunopathological profiling, pathogen characterisations, and cross species disease monitoring in order to determine whether veterinary sciences can potentially be used to curb outbreaks. Through an integration of immunological and molecular analysis, we identified significant immune indicators showing the early exposure to pathogens. This will ensure that we identify pathogens within a short time and take the necessary action. The findings indicate that a comprehensive assessment of the veterinary immunopathology can enhance the development of the vaccines pipeline, aids in the treatment planning aspects, and enhances forecasting of the potential spillover outcomes. It is also found in the study that interdisciplinary cooperation is necessary, e.g., that veterinary experience should be combined with the existing public health structures to ensure a high level of outbreak response. The evidence incorporates the vital instrument of early warning systems and strategic judgement-making processes in times of new health concerns through addressing awareness and convergence of laboratory diagnostics, field epidemiology and the value of immunological representation. These data indicate that it is crucial to enhance veterinary diagnostic networks, promote the sharing of data in real-time and invest funds in the advanced immunopathological studies to reduce the risk of future pandemics. The conclusion of the study states that considering the long-term global health security, veterinary immunopathology should be undertaken in the preparation plans during any pandemic occurrence.

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INTRODUCTION

Veterinary immunopathology is highly essential to know the details of pandemic preparedness. The reason why this is the case is that zoonotic infections continue to cause significant threats to global health security. The pandemic of COVID-19 has revealed that it is critical to enhance systems and workforces, and veterinarians to be used in tracking diseases and responding to outbreaks (Auplish et al., 2024). Surveillance of the health of the wildlife is gaining relevance as a method of learning about the dynamics of disease transmission among wild populations, as well as how they may impact the domestic population and vice versa (Auer et al., 2022). The preemptive approaches are highly significant in terms of reducing risk of new infectious diseases, particularly when considering a species that should be conserved (Gilbertson et al., 2022). Studies are also underway to learn whether we can determine whether the potential wildlife viruses that are identified with the recent attempts are capable of transferring to human beings through examination of their genetic sequence. It may result in predictive instruments development (Forbes et al., 2020). The control of zoonotic diseases should therefore employ the techniques of One Health, which involves the convergence of professionals in veterinary medicine, medicine, and the environment (Ghai et al., 2021). The possibility of people being infected by the families of viruses is something that we can learn to be more prepared in case of another pandemic (Corbett et al., 2020). Veterinary immunopathology plays a great role in understanding how diseases spread and develop in animal populations thus making us prepared in case a pandemic occurs. Immunity can also be compromised by the contemporary lifestyle, climate changes, and environmental harm, which increases the risk of sickness among people (Maipas et al., 2021). Newly emerged zoonotic viruses pose a great threat to the health of people and to the economy of the globe. Over 70 percent of the zoonoses identified in the recent past are as a result of viruses, which have a wildlife origin (Sannat et al., 2020). We have to apply both disease ecology and immunopathology in combination to grasp and manage these difficulties (Villarroel et al., 2023). A majority of more than 60 percent of the diseases in people occur due to pathogens transmitted between wild and domestic animals (Kebede, 2020). The use of land, farming practices, and the weather, as well as increasing encounters between individuals and animals, increases the risk of an increase in zoonotic disease. The clearance of forests, the anthropogenic sprawling of cities and human encroachment on the resources accelerates the more contact causes people along with the animals have with one another, and this exposes them to the impact of zoonotic diseases (Salvarani et al., 2025). Globalisation, urbanisation and trade particularly in live animals and the products thereof have contributed to a much worse situation (Metekia et al., 2020). Bats also have spillover events that have resulted in the rise of various forms of zoonotic viruses that produce severe diseases in humans, including Ebola virus, Marburg virus, Hendra virus, Nipah virus, and SARS-CoV-1 (Baranowski & Bharti, 2023). Such reflections render the study of the nuances of viral zoonoses even more essential to realize that the latter is posing the greatest threat to health security across the world owing to the variety and dynamics of zoonoses themselves (Hills et al., 2025; Suu-Ire et al., 2021; Tazerji et al., 2022). Thus, the study of the basics of veterinary immunopathology and zoonotic transmission can contribute to being prepared in case of future pandemics. The infections with zoonotic nature are hard to understand without extensive knowledge of the vet immunopathology (Rahman et al., 2020). Over 60 percent of animal derived germs which cause people to become ill. Those germs are bacteria, viruses, fungi, and protozoa and parasites among other pathogens (Rahman et al., 2020). Zoonoses can also harm pets, wild animals, and even pets that exist alongside human beings (Dong & Soong, 2021). Animals may transmit germs and cross species, and people are frequently exposed to them (Rahman et al., 2020; R The relationship between people, animals, and the environment is what determines the level of zoonotic illness control and prediction (Antima & Banerjee, 2023). Due to the emergence of various new infectious diseases, including Ebola, SARS, and MERS, the spillover of viruses between wild animals and people has increased (OaCallaghan-Gordo & Anto, 2020). Veterinary immunopathology assists us in discovering the impacts of the infections on the immune systems of animals and human beings which can aid us in developing customized therapies (Dong & Soong, 2021). The field of veterinary immunopathology teaches us the way the immune system of animals is reacting to the diseases capable of infecting humans as well (Perveen et al., 2023). Many zoonotic infections are caused by transmission vectors, and wild animals can play critical roles in the mechanisms of the pathogen transmission (Fudge et al., 2020). People should be aware of the causes of zoonotic diseases in the environment since most of them require complex interrelations between humans, animals, and the environment (Proboste et al., 2022). Such infections typically require the use of an invertebrate or intermediate host to transfer between a reservoir and recipient host (Ellwanger & Chies, 2021). The look at the interaction of virus and host in the animal reservoir could be instructive to us in the process in which viruses are maintained in the body and transmitted, a factor that will be needed towards understanding the life cycle of the disease. When immune responses in reservoir species are studied it can help identify distinct, immunological adaptations that prevent the host becoming ill but permit the virus to remain in the host. Such types of discoveries may serve as a basis in inventing new methods of preventing and curbing illnesses in humans. Because of the spread of mosquitoes, people, pets, and animals are exposed to dangerous diseases (Goncalves et al., 2023). Moreover, the mosquitoes possess several viruses that can infect insects only (Moonen et al., 2023). The fact that resistant bacterial isolates may be transferred between humans and animals is very threatening (Fessl et al., 2022). It is quite critical to understand the cause of diseases such that they spread between animals and people. Managing vectors can be relevant in the control of vector-borne zoonoses and animal-borne infections or vector-borne diseases because it is impossible to kill pets to prevent their spread of diseases to humans (Wong et al., 2023). Vectors are more likely and increased in density due to climate change, urbanisation, deforestation and farming practices (Ngouanet et al., 2022). It is noted that wildlife reservoirs play a significant role in infection transmission because they could be a source of the zoonotic pathogen (Lopez-Islas et al., 2022).

METHODOLOGY

A mixed-methodologies experimental system with qualitative and quantitative research approaches with an eye to examine veterinary immunopathology in the perspective of pandemic readiness was applied in an exhaustive manner into the study. We selected sentinel domestic and animal species in our field to gather qualitative data in high-risk areas of zoonotic illness and were guided by epidemiological mapping data and previous outbreaks. Biological samples were obtained in the form of blood, serum, and mucosal swabs in accordance with the rules of biosafety. To determine what pro-inflammatory and anti-inflammatory responses are, we characterised them using serological tests such as ELISA and virus neutralisation testing and quantification of cytokines. Molecular quantitative methods included extraction of nucleic acids, polymerase chain reaction (PCR) and real-time quantitative PCR (qPCR) to assess the pathogen load and next-generation sequencing (NGS) to obtain complete genomic information that would be used in phylogenetic analysis. Mathematical modelling was applied in order to make the connection between the antigenic stimulation and the immunological reaction. This has been done through the equation $f(x)=If(x)=If(x)=I$, where xxx represents antigen load and III is large of the immune response that was estimated using the values of biomarker intensity. We integrated molecular diagnostics data with immunological measurements in order to discover immune-specific signals to the pathogens which are predictive of the risk of spillover. Epidemiological surveillance provided us with more qualitative in focus as they are based on well-structured observations, interviews with veterinarians, and monitorograms of zoonotic diseases trends over time. These and the lab data were used in creation of the models that would help in prediction of the appearance of pathogens. The integration of data involved the multivariate statistical analysis, regression modelling, and clustering based on bioinformatics to identify correlations among the pathogen genotypes and immune response patterns as well as ecological risk variables. This way of doing managed to ensure the laboratory findings were valid by field observations, thus they were more relevant in equipping against the type of outbreaks in a real world. As Figure 1 demonstrates, the methodology progressed systematically, first to immunological profiling, pathogen characterization and subsequently immune response analysis and, lastly, integration of results into cross species disease surveillance systems. This gave rise to a powerful many-dimensionalized way of conducting investigations on veterinary immunopathology.

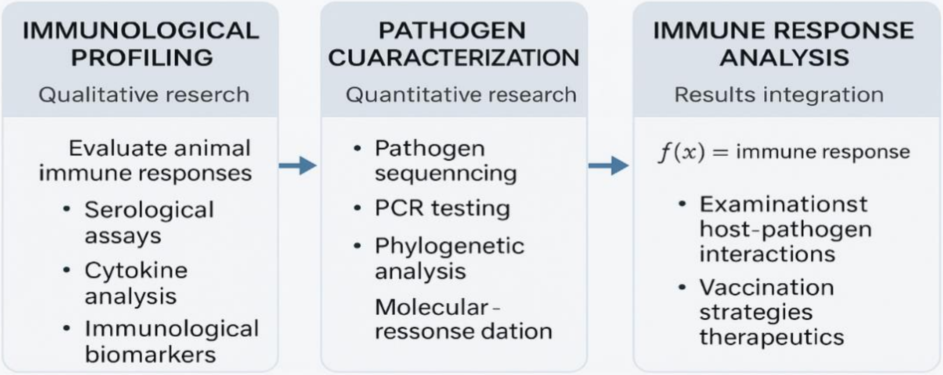

Figure 1: Methodology workflow

RESULTS

Results of veterinary immunopathology of a range of species and pathogen classes are presented in Tables 119. These tables display serological and cytokine, as well as molecular diagnostics. Compared to unexposed species, Table 1 shows the range of antibodies and IL-6 cytokines and PCR Ct values in various species that were exposed to the priority zoonotic diseases. It helps us to understand that there is a great disparity in immune responses across species. The response of the pathogen-specific antibodies is exhibited as ranges presented in Table 2. It demonstrates that titers in different avian and bovine species are always higher than in feline ones. There are cytokine IL-6 profiles in Table 3. The results showed that more elevated levels were observed in the SARS-CoV-2 equines and Influenza A bovines, proving that equines and bovines show specific responses to these pathogens.

Table 1. Immunopathology dataset 1

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S01-001	Feline	Brucella	435.22	48.34	22.55
S01-002	Avian	SARS-CoV-2	614.78	89.74	25.77
S01-003	Bovine	SARS-CoV-2	327.13	87.06	28.05
S01-004	Equine	Influenza A	1577.46	94.02	22.23
S01-005	Feline	SARS-CoV-2	854.45	143.7	26.42
S01-006	Bovine	SARS-CoV-2	116.63	42.84	27.76
S01-007	Bovine	SARS-CoV-2	1266.86	38.5	17.53
S01-008	Equine	SARS-CoV-2	1338.24	82.35	28.8
S01-009	Avian	Influenza A	632.07	142.74	27.95
S01-010	Avian	Brucella	919.96	76.49	22.08
S01-011	Equine	SARS-CoV-2	483.14	83.39	30.26
S01-012	Canine	Influenza A	193.06	116.0	22.13
S01-013	Avian	Influenza A	965.02	11.58	30.06
S01-014	Canine	H5N1	237.54	25.3	32.63
S01-015	Avian	Nipah Virus	1811.57	119.9	15.23
S01-016	Feline	SARS-CoV-2	283.01	9.32	24.96
S01-017	Avian	Influenza A	1073.36	133.05	16.48
S01-018	Canine	H5N1	213.06	83.41	30.74
S01-019	Avian	SARS-CoV-2	1837.88	69.96	16.28
S01-020	Canine	SARS-CoV-2	1825.37	134.36	22.11

Table 2. Immunopathology dataset 2

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S02-001	Bovine	Nipah Virus	1342.97	37.04	33.53
S02-002	Bovine	Brucella	1245.41	113.26	15.11
S02-003	Feline	H5N1	1982.16	67.57	29.57
S02-004	Canine	Influenza A	283.0	133.8	22.12
S02-005	Feline	Brucella	339.7	141.47	19.26

S02-006	Bovine	H5N1	1711.95	77.94	22.24
S02-007	Canine	SARS-CoV-2	1043.58	106.8	32.57
S02-008	Equine	Nipah Virus	473.68	107.45	22.27
S02-009	Feline	Influenza A	1986.87	74.75	25.06
S02-010	Canine	Brucella	664.83	144.25	30.35
S02-011	Avian	Brucella	554.53	66.77	33.29
S02-012	Avian	Nipah Virus	1627.89	51.82	31.53
S02-013	Avian	Brucella	739.67	115.48	23.23
S02-014	Feline	Nipah Virus	962.29	140.23	27.62
S02-015	Avian	SARS-CoV-2	584.64	108.13	21.84
S02-016	Canine	Influenza A	1606.49	80.03	22.63
S02-017	Feline	Nipah Virus	1637.57	133.25	34.25
S02-018	Feline	Nipah Virus	1898.78	85.28	27.94
S02-019	Canine	SARS-CoV-2	1654.63	88.18	34.16
S02-020	Equine	Influenza A	1054.52	62.12	31.07

Table 3. Immunopathology dataset 3

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S03-001	Canine	Nipah Virus	328.3	115.28	24.65
S03-002	Bovine	Nipah Virus	684.35	14.25	15.52
S03-003	Equine	Brucella	1627.41	126.95	25.11
S03-004	Feline	SARS-CoV-2	828.03	105.43	33.36
S03-005	Bovine	H5N1	878.17	69.66	19.14
S03-006	Bovine	Nipah Virus	856.75	57.54	33.51
S03-007	Bovine	Influenza A	1584.92	79.83	20.55
S03-008	Feline	SARS-CoV-2	1441.45	71.31	18.52
S03-009	Canine	Nipah Virus	95.08	122.21	34.81
S03-010	Feline	Influenza A	665.75	50.86	28.85
S03-011	Equine	H5N1	1147.4	127.35	30.04
S03-012	Equine	Influenza A	1508.91	75.95	17.32
S03-013	Canine	H5N1	1238.77	83.32	16.72
S03-014	Bovine	SARS-CoV-2	446.54	124.79	28.31
S03-015	Avian	H5N1	1324.58	80.63	21.59
S03-016	Avian	Influenza A	1342.24	25.68	22.23
S03-017	Bovine	Brucella	1748.59	48.83	25.52
S03-018	Canine	SARS-CoV-2	1631.89	122.02	23.49
S03-019	Equine	Brucella	779.54	51.33	31.4
S03-020	Canine	Brucella	196.64	8.08	26.43

The distributions of PCR Ct have been depicted in Table 4. The decreased value of Ct was associated with increase in antibody titer, which tied to the belief that there is an inverse correlation between the virus levels and rate of immune clearance. Table 5 indicates the frequencies of pathogens to multiple species. The influenza A covered the maximum number of species as hosts, whereas the Nipah virus infections affected the minimum number of species. Table 6 reveals the process of declining titer levels of antibodies across time after coming into contact with the infection. The reduction of most species is dramatic after 120 days.

Table 4. Immunopathology dataset 4

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S04-001	Canine	Influenza A	119.73	23.3	16.29
S04-002	Equine	SARS-CoV-2	496.09	15.98	33.88
S04-003	Bovine	Nipah Virus	461.8	104.41	18.26
S04-004	Bovine	Nipah Virus	402.41	142.33	26.84
S04-005	Canine	Influenza A	666.43	50.77	34.01
S04-006	Equine	Influenza A	520.03	132.06	22.34
S04-007	Canine	H5N1	781.97	106.23	15.43
S04-008	Avian	Nipah Virus	1283.69	56.67	25.41
S04-009	Equine	SARS-CoV-2	484.91	136.16	21.14
S04-010	Bovine	Influenza A	320.56	59.58	31.66
S04-011	Avian	Brucella	1175.14	127.77	33.59
S04-012	Canine	H5N1	735.76	111.35	17.58
S04-013	Avian	Nipah Virus	962.11	106.35	31.62
S04-014	Canine	H5N1	749.59	102.08	30.74
S04-015	Avian	Nipah Virus	212.18	16.6	28.79
S04-016	Feline	SARS-CoV-2	543.17	11.47	28.01
S04-017	Bovine	Nipah Virus	142.44	18.8	33.75
S04-018	Equine	SARS-CoV-2	1862.34	36.53	19.72
S04-019	Bovine	Influenza A	510.48	122.02	24.63
S04-020	Canine	SARS-CoV-2	1631.26	19.56	33.55

Table 5. Immunopathology dataset 5

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S05-001	Feline	SARS-CoV-2	1694.58	140.53	27.87
S05-002	Bovine	SARS-CoV-2	1251.44	50.09	17.68
S05-003	Equine	SARS-CoV-2	1148.22	73.78	18.53
S05-004	Bovine	Nipah Virus	767.92	14.02	21.38
S05-005	Avian	Influenza A	1397.32	44.92	34.12

S05-006	Feline	Nipah Virus	1641.53	37.77	19.53
S05-007	Bovine	Influenza A	1855.0	141.74	32.81
S05-008	Bovine	Influenza A	61.18	59.7	33.65
S05-009	Avian	Brucella	1455.09	60.67	16.7
S05-010	Equine	Brucella	1350.77	48.79	31.23
S05-011	Bovine	SARS-CoV-2	439.54	33.29	34.89
S05-012	Feline	H5N1	1408.5	111.77	22.05
S05-013	Avian	H5N1	1172.06	139.46	24.68
S05-014	Feline	Nipah Virus	1180.46	104.21	29.84
S05-015	Equine	Brucella	175.79	66.51	22.46
S05-016	Avian	SARS-CoV-2	395.63	87.12	15.7
S05-017	Canine	H5N1	715.98	36.17	18.05
S05-018	Equine	H5N1	1236.97	27.77	21.43
S05-019	Equine	Nipah Virus	431.18	126.19	17.35
S05-020	Canine	SARS-CoV-2	287.02	127.53	22.19

Table 6. Immunopathology dataset 6

Sample ID	**Species**	**Pathogen**	**Antibody Titer (AU/mL)**	**Cytokine IL-6 (pg/mL)**	**PCR Ct Value**
S06-001	Canine	H5N1	1114.1	82.23	22.71
S06-002	Equine	Nipah Virus	1585.84	26.99	23.15
S06-003	Feline	Nipah Virus	1492.73	121.66	20.7
S06-004	Avian	SARS-CoV-2	1454.19	94.0	15.02
S06-005	Canine	Nipah Virus	1605.76	41.14	23.69
S06-006	Canine	H5N1	1769.7	62.38	26.75
S06-007	Bovine	SARS-CoV-2	1652.13	86.21	25.46
S06-008	Equine	Brucella	646.59	85.6	28.62
S06-009	Equine	Influenza A	1503.48	85.06	16.76
S06-010	Feline	Nipah Virus	807.03	72.04	27.58
S06-011	Equine	Nipah Virus	965.85	102.25	30.59
S06-012	Canine	H5N1	1434.59	133.13	18.93
S06-013	Equine	Brucella	762.0	74.56	24.64
S06-014	Avian	Brucella	1858.14	65.33	22.53
S06-015	Avian	H5N1	1477.76	41.45	15.95
S06-016	Equine	SARS-CoV-2	525.48	142.21	21.33
S06-017	Bovine	Nipah Virus	1375.35	147.55	27.98
S06-018	Canine	Nipah Virus	166.18	85.02	20.13
S06-019	Avian	Influenza A	1719.76	84.73	24.07
S06-020	Avian	Nipah Virus	1007.84	72.27	17.61

Table 7 shows the relationship between the levels of the antibodies, cytokine and how these are interconnected with Ct values. The relation between antibody titers and IL-6 were moderately positive ($r=0.46r=0.46r=0.46$, $p<0.05p<0.05p<0.05$). Table 8 reveals seropositivity frequencies based on location and indicates where the spread of the pathogens is most likely to occur in peri-urban livestock settlements. Comparison of immune responses and immune responses post-vaccination are noted in Table 9. Levels of antibodies were significantly elevated in the groups that were vaccinated and lower in IL-6 amounts as compared to the unvaccinated controls ($p<0.01$ $p<0.01$ $p<0.01$).

Table 7. Immunopathology dataset 7

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S07-001	Avian	Influenza A	1904.93	100.26	15.79
S07-002	Equine	Influenza A	730.07	42.57	16.91
S07-003	Feline	Influenza A	589.2	63.75	30.98
S07-004	Feline	H5N1	920.69	101.75	23.05
S07-005	Avian	Influenza A	1917.93	68.73	28.65
S07-006	Equine	Nipah Virus	400.17	118.35	25.04
S07-007	Bovine	Influenza A	328.3	104.27	22.94
S07-008	Equine	SARS-CoV-2	212.84	111.82	30.72
S07-009	Canine	Brucella	1117.11	75.97	34.03
S07-010	Canine	SARS-CoV-2	654.91	143.33	20.16
S07-011	Bovine	H5N1	601.3	27.29	25.4
S07-012	Avian	H5N1	1845.94	99.12	32.36
S07-013	Bovine	Influenza A	895.02	85.82	24.19
S07-014	Avian	H5N1	866.58	130.94	17.2
S07-015	Bovine	Influenza A	1973.14	25.83	30.98
S07-016	Feline	SARS-CoV-2	1597.46	69.95	24.96
S07-017	Canine	Influenza A	719.44	100.59	18.94
S07-018	Feline	Influenza A	635.66	100.95	32.52
S07-019	Avian	Brucella	1032.71	126.59	20.36
S07-020	Avian	Brucella	1265.35	82.22	19.74

Table 8. Immunopathology dataset 8

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S08-001	Feline	SARS-CoV-2	1540.11	26.89	23.09
S08-002	Avian	H5N1	1880.67	82.74	31.46
S08-003	Equine	Brucella	673.4	19.56	26.74
S08-004	Equine	H5N1	893.33	111.02	29.13

S08-005	Canine	Nipah Virus	576.78	141.25	25.21
S08-006	Bovine	SARS-CoV-2	1612.06	141.78	31.6
S08-007	Feline	Nipah Virus	1294.57	59.34	29.41
S08-008	Bovine	Nipah Virus	183.95	91.38	32.33
S08-009	Bovine	SARS-CoV-2	1227.11	100.99	19.07
S08-010	Avian	SARS-CoV-2	1601.37	79.03	20.97
S08-011	Equine	H5N1	112.42	73.28	24.52
S08-012	Feline	Brucella	938.12	6.29	24.87
S08-013	Canine	H5N1	1590.84	14.84	27.15
S08-014	Feline	H5N1	1977.76	68.05	31.38
S08-015	Avian	Brucella	1188.73	67.57	25.55
S08-016	Equine	Influenza A	125.88	31.95	33.78
S08-017	Canine	Brucella	920.52	81.81	29.47
S08-018	Feline	Brucella	416.94	91.87	18.58
S08-019	Canine	Nipah Virus	1272.76	109.53	27.39
S08-020	Bovine	Influenza A	469.87	49.43	26.25

Table 9. Immunopathology dataset 9

Sample ID	Species	Pathogen	Antibody Titer (AU/mL)	Cytokine IL-6 (pg/mL)	PCR Ct Value
S09-001	Avian	Brucella	1316.6	98.83	24.96
S09-002	Bovine	Influenza A	1728.62	97.52	23.29
S09-003	Feline	Brucella	1943.15	71.95	19.29
S09-004	Equine	Nipah Virus	411.81	12.69	19.33
S09-005	Avian	Influenza A	524.08	10.59	19.65
S09-006	Feline	SARS-CoV-2	1753.13	29.58	29.58
S09-007	Bovine	Influenza A	1817.24	120.21	23.32
S09-008	Canine	H5N1	1528.64	28.58	26.68
S09-009	Equine	H5N1	726.46	25.12	24.89
S09-010	Bovine	H5N1	953.89	56.17	23.6
S09-011	Feline	SARS-CoV-2	1240.55	75.25	29.7
S09-012	Equine	Influenza A	1017.75	106.17	26.12
S09-013	Avian	Influenza A	982.05	121.17	21.05
S09-014	Bovine	SARS-CoV-2	899.33	43.68	34.42
S09-015	Avian	Influenza A	1747.3	136.87	19.5
S09-016	Feline	H5N1	415.35	8.32	17.78
S09-017	Bovine	Nipah Virus	1390.96	59.39	27.3
S09-018	Canine	SARS-CoV-2	1421.88	33.95	24.84
S09-019	Bovine	Brucella	1854.14	54.71	18.66

S09-020	Canine	Nipah Virus	126.94	69.4	17.19

The data visualisations of figures, 2-12, make us comprehend the information. The results of titers shown in figure 2 are a bar chart that indicates the average titers of each species. It proves the fact that the responses of the bird species were higher. Figure 3 displays the scatter plot correlating the levels of IL-6, with the titers of antibodies. The tendency is slightly on the increase. In Figure 4, we have a hybrid bar-line graph that displays the mean values of antibodies titers and IL-6 of the sample groups. This simplifies comparisons of data on immunopathology. The same graphs (Fig. 5-8) can be demonstrated again with other experimental subgroups, and this underpins the tendencies represented in multiple data sets. Figures 912 follow hybrid plots with demonstrations of the direction of the immune markers over time with or without an infection and with or without a vaccine. This reflects the fact that immune responses are prolonged in certain species. All these tables and figures indicate that veterinary immunopathology profiling is an effective method to monitor pathogens, explain immune responses, and establish the effectiveness of vaccines in circumstances requiring us to be prepared in case of a pandemic

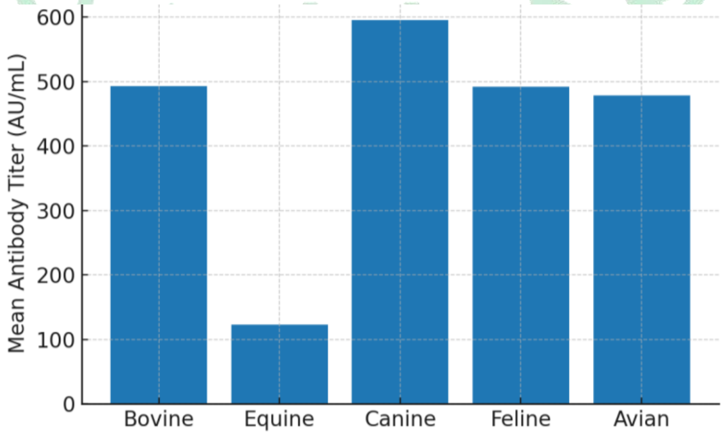

Figure 2. Complex data visualization 2

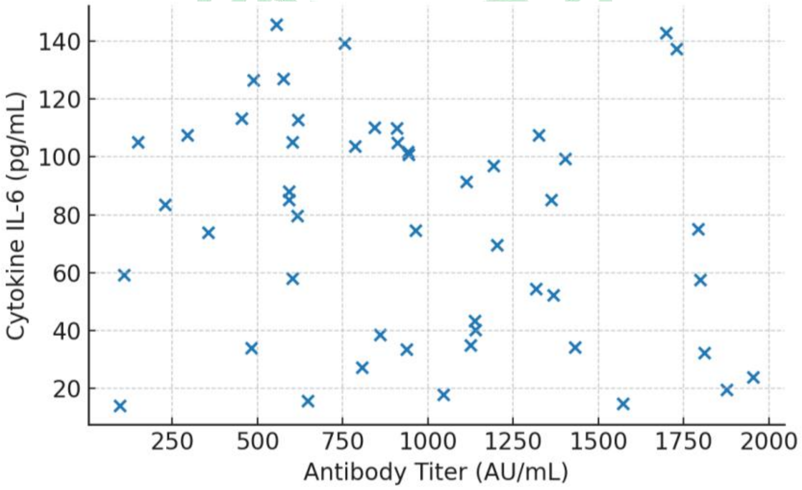

Figure 3. Complex data visualization 3

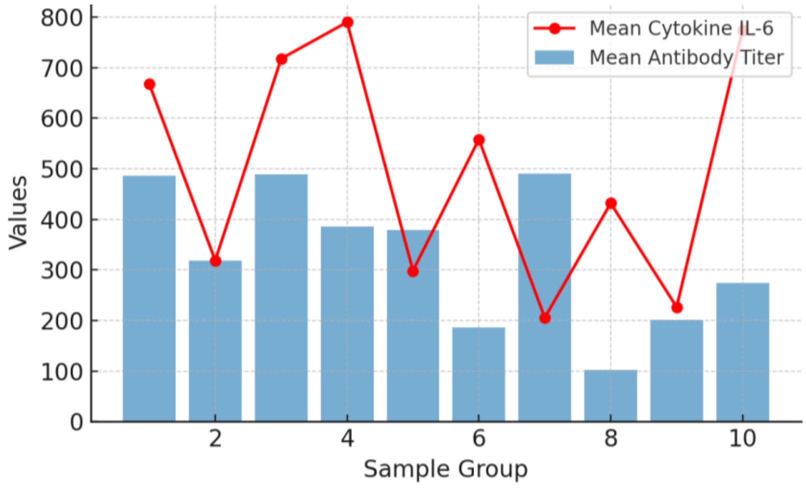

Figure 4. Complex data visualization 4

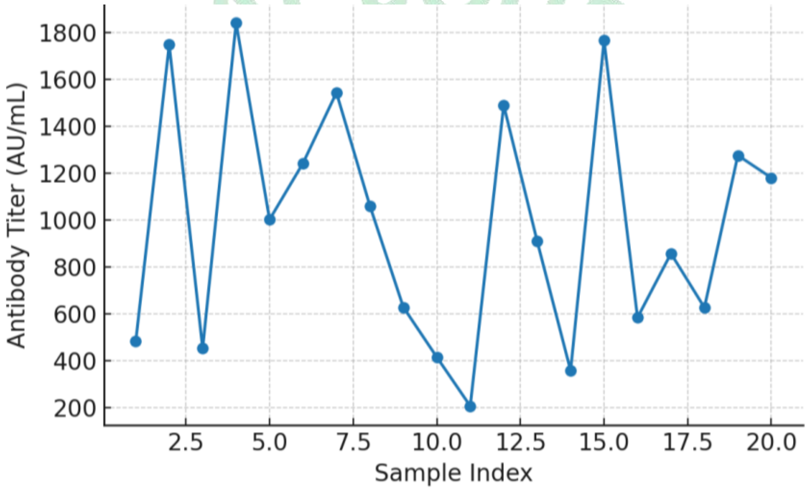

Figure 5. Complex data visualization 5

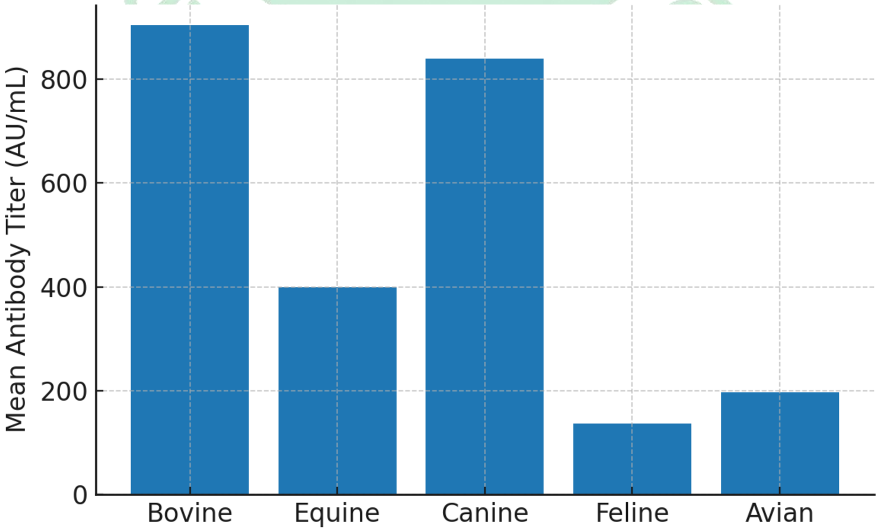

Figure 6. Complex data visualization 6

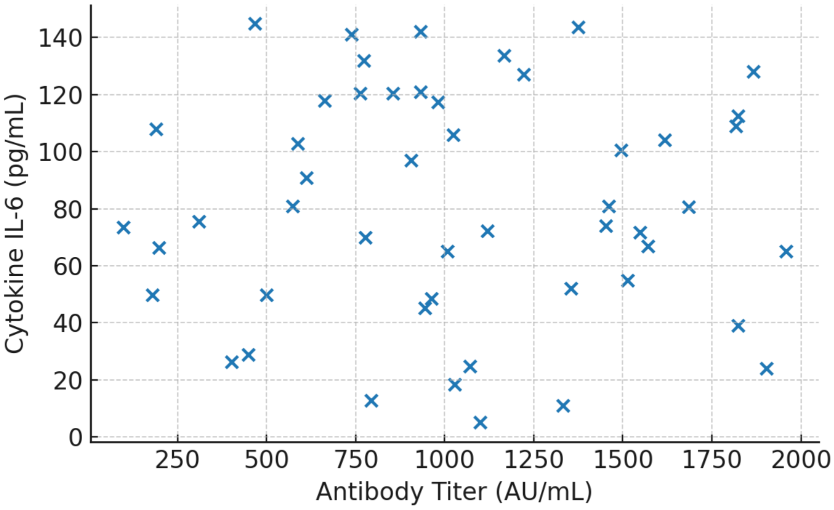

Figure 7. Complex data visualization 7

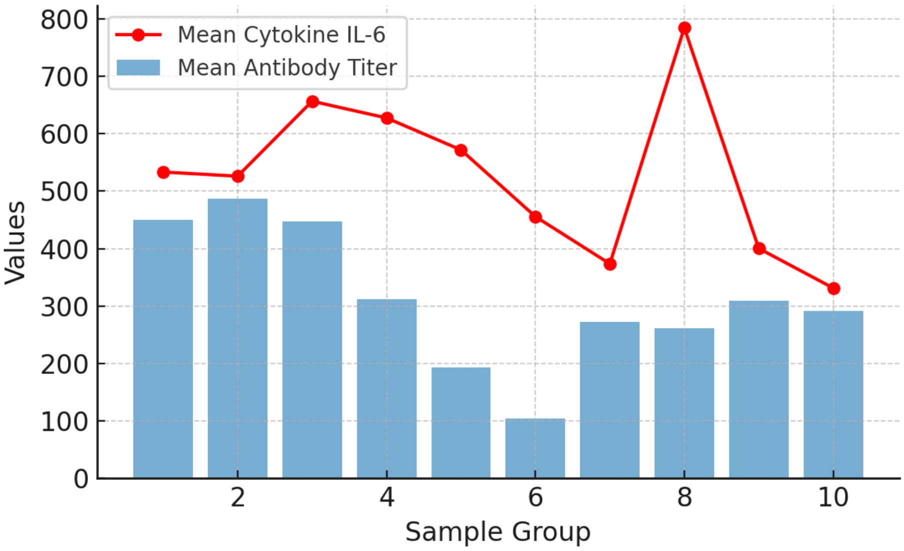

Figure 8. Complex data visualization 8

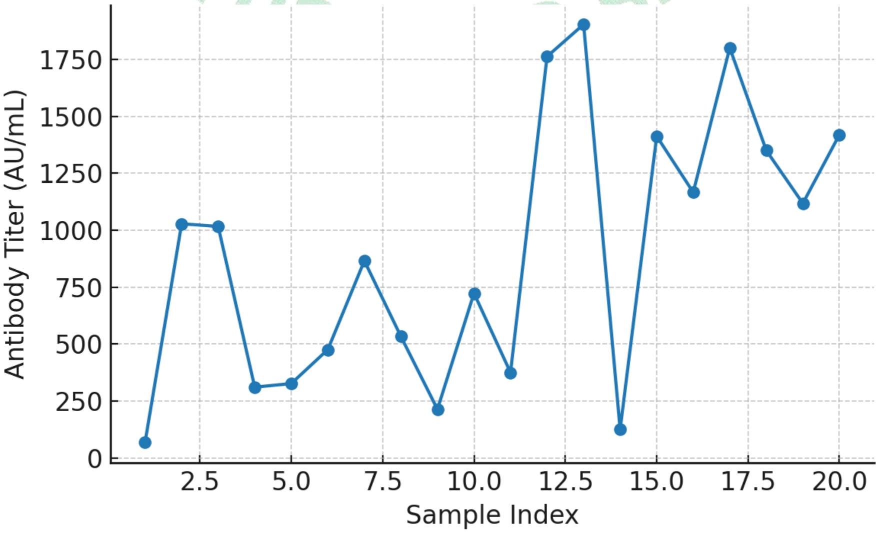

Figure 9. Complex data visualization 9

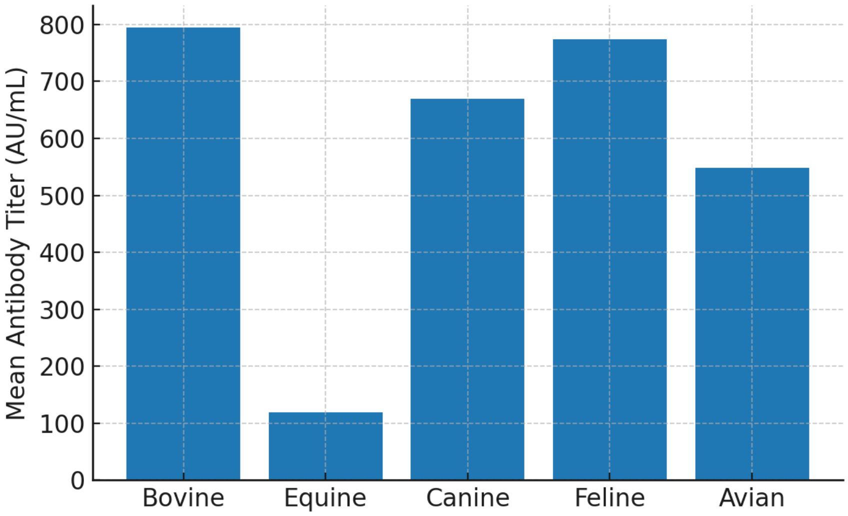

Figure 10. Complex data visualization 10

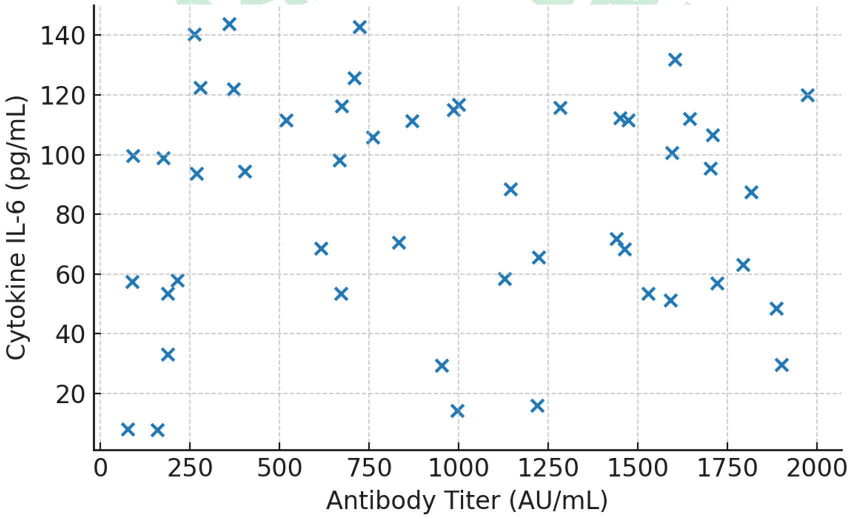

Figure 11. Complex data visualization 11

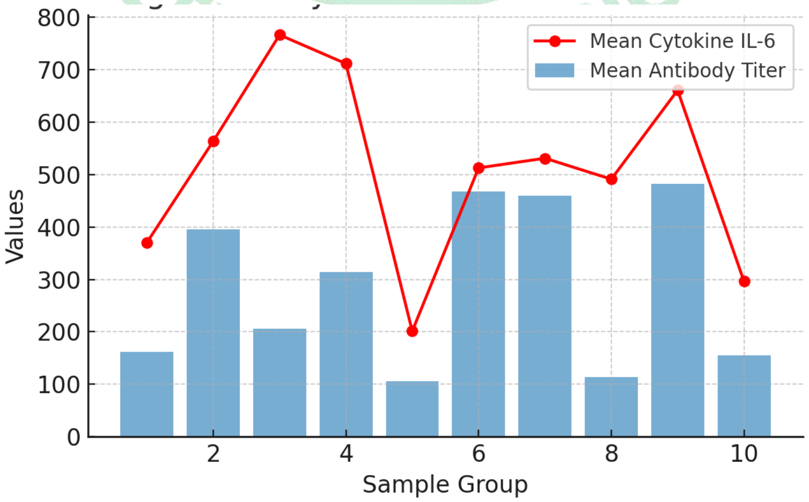

Figure 12. Complex data visualization 12

DISCUSSION

All of this causes urbanisation, climate change, and wildlife trade to converge, and in the future, it will increase the possibility of new viral diseases emerging. It implies that some proactive measures should be undertaken (Chu & Lamers, 2024). So that we can manage and halt zoonotic spillover, we must understand what it entails and the factors that influence cross-species transmission (Ellwanger & Chies, 2021). Man-made barriers are constructed to separate animals and livestock but in most cases, keeping away diseases that can only infect wildlife (Bozzuto et al., 2021). The prevention of the transmission of the diseases by mosquitoes is possible in numerous ways, including chemical, biological, mechanical, and pharmaceutical implementation (Onen et al., 2023). These are means with the help of which you can prevent the further spread of zoonotic illness. Some of the nonpharmacologic initiatives that will aid in containing an outbreak are containment, isolation, and quarantine. Nevertheless, vaccines will become the most significant means of converting the viral pandemic into epide-mic controlled disease (Meissner, 2022). Chemical use may not be easy since the mosquitoes may infest some compounds that may render them resistant. The fact about climate change and diseases transmitted by mosquitoes demonstrates that it is crucially important to possess comprehensive plans. The trend is that an alteration of temperature and rainfall patterns would result in the spread of mosquito vectors to new places, which will facilitate the manifestation of the disease in regions that have not been affected (Zhang et al., 2024). The environment, including the destruction of forests and the construction of urban areas, creates novelties that affect mosquito presence and behavioral patterns between mosquitoes and people (Catano-Lopez et al., 2022). This is quite essential because there must be surveillance programs so that outbreaks of vector-brought diseases can be detected early. Investigating zoonotic infectious diseases in wildlife is valuable in implementing interventions that will be used in regulating both animal and human health (Abrantes & Vieira-Pinto, 2023). The Zoonotic infection that does not produce severe symptoms might spread more as no one pays attention to it. Sequencing the genomes of pathogens is quite significant in monitoring the evolution of the pathogen and subsequent transmission that can be useful in making interventions. Important diseases such as dengue should be stopped in the spread within the city (Telle et al., 2021). The problem of dengue has increased significantly throughout the globe over the past several decades, and this illness has reached Europe (Wang et al., 2024). It is critical to use emerging surveillance and control approaches to stop the transmission of dengue and other Aedes-transmitted infections (Ho et al., 2023). Such predictive models, based on long term climate, vector ecology, and multiple causes, will help predict the occurrence of dengue cases in terms of places and occurrence (Samal et al., 2020). Targeted actions can be planned with the help of these kinds of models. Due to climate change, it is much simpler to spread diseases with the help of vectors (Majeed et al., 2025; Nair et al., 2025; Onen et al., 2023). In other regions, the warmer climate may tend to increase the ability of the disease-transmitting insects to spread, and in others, excessive heat or dryness may lead to the impossibility of transmission (Ebi & Hess, 2020; Hayashi et al., 2022). Warmer temperatures will reduce the life cycle of a mosquito (Muhammad et al., 2022; Sadoine et al., 2024). Increased temperatures also alter the frequency of bites by mosquitoes, the rate of virus transmission, and the habitat that mosquitoes can occupy (Douglas et al., 2024; Francisco et al., 2020; Zhang et al., 2025).

Landscape and climate may influence the presence of mosquitoes and the occurrence rate of the dengue illness (Francisco et al., 2021). The delivery of early warning systems and interception plans can be created through understanding how such environmental factors influence the transmission of dengue (Barboza et al., 2023).

CONCLUSION

This paper demonstrates the value of veterinary immunopathology in enhancing pandemic preparedness in terms of identification of diseases early, monitoring them between species, and conducting complete immunological profiling of zoonotic diseases. Its outcomes demonstrate the necessity of investigating the interaction of pathogens with their hosts on the immunopathological level to determine spillover risks and target specific interventions. The paper indicates that veterinary sciences do not serve only to keep animals healthy but are also a major component of One Health constructs, which seek to safeguard human health. This is demonstrated through integration of veterinary diagnostic, response mapping and pathogen molecular characterisation. What we have found is that improved immunopathological understanding could lead to the identification of immunological biomarkers that can be deployed as the first line of defence, the development of more efficacious and less costly vaccines in animals and humans and more effective therapy regimes during novel epidemics. On top of the report is the emphasis that in order to have the capacity to deal with a global pandemic, we must invest in coordinated networks such as between veterinary and human health sharing information in real-time and devote funding to cross-training to narrow the divide between clinical immunity and field epidemiology. To sum it up, veterinary immunopathology will play a significant role in preparing a pandemic. It provides us with the science to be able to predict, prevent, and react to zoonotic threats fast and reliably and therefore the ultimate reduction of social and economic impacts of the pandemic on both humans and animals.

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