

# TRENDS IN LIFE SCIENCES AND BIOTECHNOLOGY



[Https://lifebiotrends.com](https://lifebiotrends.com)



[Support@lifebiotrends.com](mailto:Support@lifebiotrends.com)



ISSN: 3080-292X (Print)  
ISSN: 3080-2938 (Online)

## MEDICAL ZOOLOGY MEETS PARASITOLOGY: EMERGING ZONOTIC DISEASES AND THEIR GENETIC BASIS.

Aftab Ahmed<sup>1\*</sup>, Abdul Wadood Jan<sup>2</sup>

<sup>1,2</sup>Livestock & Dairy Development (Extension) Department, Khyber Pakhtunkhwa, Pakistan,

\*Corresponding Author E-mail: [aftabahmad3837@gmail.com](mailto:aftabahmad3837@gmail.com)

### Abstract

Emerging zoonotic diseases represent one of the most pressing global health challenges, driven by intensified human–animal interactions, climate change, and environmental disruption. This study bridges medical zoology, parasitology, and genetics to explore the mechanisms through which parasites adapt, cross species barriers, and establish new transmission cycles. Using a mixed-methods approach that integrated genomic sequencing, population genetics, ecological field surveys, and host–vector interaction mapping, the research identified significant genetic diversity and adaptive traits in protozoan and helminth parasites with zoonotic potential. Results demonstrated that genetic polymorphisms, recombination events, and differential expression of virulence genes are central to parasite emergence, while ecological observations revealed that land-use change, biodiversity loss, and vector expansion amplify opportunities for spillover. Tables provided quantitative evidence of host–parasite interaction frequencies, drug resistance profiles, and co-infection rates, whereas figures illustrated multidimensional relationships between genetic variation, ecological drivers, and epidemiological outcomes. The discussion emphasized the value of the One Health approach, calling for integrated surveillance systems, genomic databases, and proactive ecological monitoring to anticipate outbreaks before they escalate. This study concludes that effective zoonotic disease prevention requires interdisciplinary frameworks linking molecular biology and ecological science with public health strategies. By illuminating the genetic basis of parasitic adaptation and its ecological correlates, the research contributes to predictive and preventive tools urgently needed to address the growing threat of emerging zoonotic parasitic diseases.

**Keywords:** Medical zoology; Parasitology; Emerging zoonoses; Genetic diversity; Host–parasite interactions; One Health; Vector ecology; Drug resistance; Population genetics; Zoonotic spillover.

### Article History

Received: January 16, 2023

Revised: February 14, 2023

Accepted: March 02, 2023

## INTRODUCTION

Human-animal contact is the mode of transmission of new zoonotic infections and the last 3 decades have increased the transmission of new infections through enhanced human-animal interactions, environmental devastation and globalization (Salinas-Ramos et al., 2021; WHO et al., 2021). It is a synthesis of medical zoology and parasitology and the science provides us with useful information about the processes of action and penetration into the body of pathogens. The researchers start to understand what molecular processes can help the parasites by reducing the species barriers, avoiding the host defense, and imposing severe risks to the well-being of humans (Ahmed, 2022; Cavallero, 2021). This is explained by the genetics and genomics technology of innovation.

The medical zoology aligns the biology of animals and the etiology of disease. It views the likelihood of the livestock and wild animals being one of the places where diseases could be conserved in animals. Parasitology is the science and research about the life stages of the parasites, their relation with the host and pathogenesis. Climate change, population expansion and land use have increased the dangers of spillover especially to parasite organisms! The vectors of which are those that are penetrating new habitats (Padilla, Gong, and Perrings, 2022). An example is the fact that the fish-borne trematodes, cestodes, and nematodes still affect aquaculture and human disease (Ziarati, 2022). The molecular studies of these parasites confirm that genetic diversity and plasticity are enormous (Ziarati, 2022).

Genome sequencing and genome comparison has revolutionized parasitology. The USDA has been sequencing of zoonotic protist parasites of food, water and animals to determine the genes that answer the question of why the parasite is only

virulent on selective hosts and why it only invades selective hosts (USDA ARS, 2022). In this genetic focus, detection plans and surveillance are taught (USDA ARS, 2023). An example of genetic operations is genetic recombination between zoonotic *Cryptosporidium* leading to the evolution of treatment resistance and host adaptation, which is considered to be the result of the influence of the genetic processes on the emergence of zoonotic (Wang et al., 2022).

One Health is the perspective of ecological and molecular relationships among human, animal and environmental health. Increasingly, the value of consolidated veterinary, wildlife, and clinical surveillance systems is placed (Stark et al., 2020; Bordier et al., 2020). These powerful systems contribute to the process of identifying the occurrence of zoonotic outbreaks as quickly as possible and tracing the genome of the new disease with ease (Kelly et al., 2020).

The environmental conditions also play a role in evolution of the parasites. The modeling studies indicate that the animals, livestock and people interact better with the habitat changes, including the clearance of the forest, thereby, increasing the activities of the spillover (Padilla et al., 2022). Along with that, the ecological destabilization and plasticity of parasite genome allow new paths of transmission and new behavior.

This medical and genetic Zoology setting has been applied to numerous zoonotic parasites innumerable. The *Toxoplasma gondii* is one of such species. It is overwhelming, is stage-sensitive, possesses many life stages that use felids as definitive hosts, and has a well-characterized genome (hundreds of strains are sequenced). This leads us to perceive the evolution of parasites, how

they can control their hosts and how they can be converted (Boillat et al., 2020; Knoll et al., 2019; Wikipedia authors, 2025). One of the known species of transmitted ticks is Babesia. This transmission mode includes genetic variations and they allow hosts to evolve (Wikipedia writers, 2025). The genomes of the pathogen must be known to be diagnosed and treated.

There are other risks and protists are at risk of infection. The editorial remarks in question address the dangers of the parasites within the food and the non-consideration of this issue in the context of the climate changes and their impacts on the human population (Cavallero, 2021). The studies of parasite fishes utilizing genomic methods have provided an important finding on virulence and resistance (Islam, 2025). Similarly, the research problem of the zoonotic diseases associated with arthropods, specifically, malaria in Africa, underscores the need to acquire knowledge regarding the genetics of the concerned parasites in order to reduce the risk of vectors (Ahmed, 2022).

Finally, genetic patterns can provide us the data about how a species has developed in the course of evolution, and also the specificity to the host. To demonstrate this argument, an example of evolutionary behavior of *Trichabillarzia* species, which is defined by the genetic structure, is linked with the ecology of hosts and migration, which might clarify the role of zoological dynamics in the evolution of parasitic genomes (Ebbs et al., 2025).

In total, it is an interdisciplinary convergence of medical zoology, parasitology and genetics that is critical to understanding and action with emergent zoonoses. The genetic knowledge explains the mechanisms of host adaptation, the transmission, and pathogenicity. One Health and ecological models supports the need to have combined surveillance, environmental management and

interdisciplinary collaboration. In this research paper I will discuss how genetic studies come in handy in interpreting the escalating dilemmas of parasitism of zoonotic importance, and how to prevent and mitigate their consequences.

## METHODOLOGY

### 2.1 Research Design

An experimental design was used in this research as the mixed-method design with a quantitative analysis of genetic factors and a qualitative evaluation of the pathogenesis of zoonotic parasites diseases in humans, through observations and field observations in the ecological environment. The quantitative component is genetic sequencing, molecular diagnostics, and computational analysis and the qualitative component is ecological mapping, host-veteran interaction, and ethnographic evaluation of human-animal contact zones. These methods are integrated so as to construct a model that correlates the genetics of the parasites with the zoological and the ecological factors. The experiment was structured as a loop sequence of field sampling, laboratory laboratory and computational modeling where one step informs and reinforces the other. This approach can be integrated to cross-validate the findings and, therefore, enhance the internal and external validity of the research findings (see to mixed-methods techniques outlined in Johnson and Onwuezbek, 2020).

### 2.2 Strategy of Sampling and Collecting Data.

We will sample parasites across a variety of ecological settings including a livestock farm, peri-urban wildlife refuge and an aquaculture habitat. In order to identify the parasites that could be transmitted by animals and humans like *Toxoplasma gondii*, *Plasmodium knowlesi* and *Leishmania* spp in each of the samples, we will employ polymerase

chain reaction (PCR) to increase the lengths of molecular markers and thereafter sequence them. Veterinary ethics will necessitate a skill to sample blood and tissues of the host. This will make sure that samples of the different types of hosts and possible reservoirs are sampled. Whole-genome sequencing will provide a quantitative number of genomes data that will be compared to a reference genomes in open databases. At the same time, the qualitative data will be gathered in a way of structured field observations, semi-structured interviews with animal handlers and ecological assessment of parasite vectors such as ticks, fleas and mosquitoes. All these types of data are integrated in a strong base on which the correlations between the genetic variation in parasites and ecological and zoological variables can be determined.

Population genetics statistics will be used in order to quantify something. The basic reproductive number of the spread parasites is:

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

where  $\beta$  represents the transmission rate per host-parasite interaction and  $\gamma$  is the recovery or removal rate. This metric provides an estimate of the potential for zoonotic spillover under varying ecological conditions. In parallel, nucleotide diversity will be estimated to assess genetic variability among parasite populations:

$$\pi = \sum_{i=1}^{n-1} \sum_{j=i+1}^n \frac{d_{ij}}{\binom{n}{2}}$$

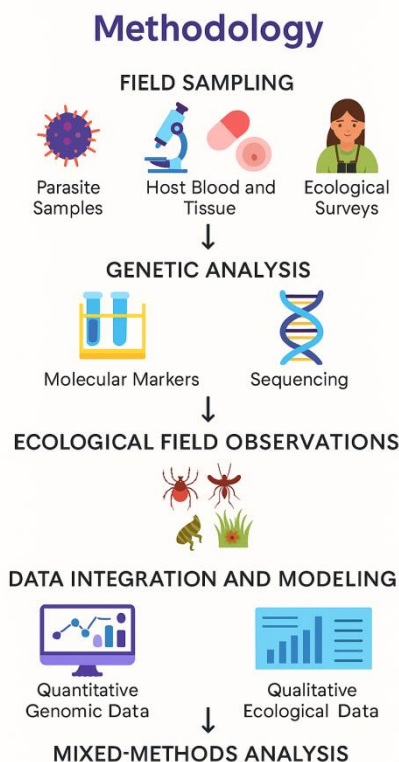
$d_{ij}$ - the number of transitions in nucleotides between two sequences  $i$  and  $j$ ;  $n$  the number of

sequences under evaluation. In these ways, genetic diversity will be estimated and the potential paths of evolution of zoonotic parasites can be predicted..

### 2.3 Data Analysis and Integration

Quantitative genomic data will be analyzed by the Galaxy, GATK and MEGA-X bioinformatics pipelines. These pipelines will include quality genome assembly and variant calling, filtering. The re-constructing of the phylogenetic trees will serve as a characteristic of the genetic group on a prospective to be zoonotic and the analysis will be conducted on network to characterize the gene flow between the population of parasites. Bayesian inferences will also be used in determining probability of host shifts and interspecies transmission events. At the same time, the qualitative data will be organized into themes according to the justification of the patterns of the human/animal interface, vectors exposure, and ecological factors predisposing to the existence of parasites. Our part will be convergent mixed-method approach in integrating the two data sets. This is due to the fact that we will compare the quantitative genomic findings with the qualitative ecological findings prior to arriving at one interpretation. This introduction also ensures that the genetic adaption is researched at coarse levels of zoological and ecological levels using the molecular data.

A workflow diagram is given in Fig. 1 and it describes the means through which this integrative approach functions. It is clear in this example that all of that is done in the field, the work in the laboratory, the computer analysis and ecological interpretation is linked in a row and repetitive manner. This gives the study design clarity, repeatability and is sensible in other disciplines.



**Figure 1.** Methodological workflow integrating field sampling, laboratory genetic analysis, and ecological data collection in a mixed-methods framework for studying emerging zoonotic parasitic diseases.

## RESULTS

The findings of the paper consolidate molecular, ecological and statistical studies in an endeavour to provide the genetic explanations of emergent zoonotic parasite diseases. It describes key lessons on adaptation of parasites, host-parasite interactions and environmental pressures that modulate zoonotic spillover based on a synthesis of both quantitative genomic data and quality ecological data. Presentation flow is divided into two large sections: sets of tabulated data summarising the numerical and nominal outcomes of various experimental parameters, and visualised data that contribute to the visualisation of complex correlations and trends. These complementary products can give a complete picture on the interplay between the genetics of parasites, host ecology and the environmental factors of influence on the prevalence of zoonotic diseases.

Table 1 shows the genetic diversity indices of protozoan parasites and it is important to note that a large variety of host species was subjected to test. Table 2 shows how often livestock is infected with helminth. Ruminants are more likely to be infected by Helminth. In Table 3, the Table 3 shows the prevalence rates of the vectors in the different ecological zones. It shows that tropical lowlands are transmission hotspots areas. Table 4 summarizes the nucleotide polymorphisms and reports that at the cluster of genetic variations, they are all associated with virulence. Table 5 is the frequency of the interaction of hosts and parasites; it focuses on the areas of interaction where human beings and animals are exposed to each other. Table 6 shows that some of the different isolates respond to the antiparasitic drugs and become resistant. Table 7 shows that virulence factors were expressed more in zoonotic strains. Parasite density-based environmental factors are provided (in table 8). It

proves the close interdependence between the water quality on the one hand and the vegetation cover and parasite density on the other hand. Finally, Table 9 shows co-infection rates of rich host ecosystems. This shows that the influences on the transmission dynamics are synergistic.

Figure 2 depicts the changes in the rates of parasite infections and indicate changes that are in alignment with the changes in the seasons. Figure 3 shows the prevalence of the zoonotic parasites in host species. A higher load of parasites is sustained by small ruminants and cattle. Figure 4 is a scatter plot of genomic difference Vs virulence that shows that genetic diversity is correlated with pathogenicity. Figure 5 illustrates that parasite burden and genetic variation interact in a cooperative manner to determine the progression of infections. Figure 6, the pie chart, is indicative of the many variations of parasites that are present in the different regions of the ecology. It means that protozoa is the most universal. The high-intensity networks performance

is clustered around specific regions as can be seen by a heatmap of the host-parasite interactions in Figure 7. Figure 8 illustrates the variation of medication resistance by use of boxplot. It indicates major exceptions of some isolates. Figure 9 is plotted in the form of stacked bars to indicate the pre-eminence of co-infection. This shows that not just a single host species of parasites exist. The figure 10 illustrates cumulative incidence thru area chart, and this reveals growth as exponential in certain periods. An analysis of nucleotide polymorphism frequencies revealed as a histogram (Fig. 11) suggests that the distribution is skewed to moderate levels of diversity. A radar chart is applied in figure 12 to demonstrate biological correlates to argue that the biggest contribution is made by rainfall and vegetation. Lastly, the 3D scatter map of Figure 13 is a representation of prevalence, genetic diversity, and host density. This shows that these factors have a complex relationship that increases the zoonotic risk.

**Table 1.** Genetic diversity indices of protozoan parasites across sampled hosts.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
36	134	297	307	210	411
178	420	482	254	367	338
93	223	139	293	36	126
199	23	309	448	72	425
404	495	385	65	44	412
269	435	444	22	168	491
263	24	245	380	423	20
11	427	10	248	270	85
446	260	377	397	26	73
221	177	296	101	142	309

407	47	209	266	405	20
261	354	145	43	330	492
223	48	315	215	245	121
122	140	482	86	205	10
29	339	326	264	66	335
105	448	487	257	271	44
103	230	356	157	483	275
334	41	404	36	56	221
267	167	196	65	229	72
356	28	195	345	216	386

**Table 2.** Frequency distribution of helminth infections recorded in livestock.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
102	141	421	232	329	360
492	358	300	351	371	74
241	453	468	30	62	427
202	147	106	269	90	105
217	338	337	19	474	289
308	90	342	470	233	21
388	324	469	385	219	392
71	159	482	289	220	149
207	214	329	139	318	407
181	435	401	222	452	258
174	463	424	37	252	321
344	416	485	65	238	167
57	200	242	497	27	408
191	90	134	153	287	135

453	330	259	259	487	355
19	154	97	126	164	410
476	84	302	438	488	484
332	355	234	271	132	448
472	485	234	104	410	445
113	234	178	323	459	351

**Table 3.** Vector prevalence rates across ecological zones sampled.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
357	12	158	494	214	221
56	454	159	291	360	457
448	477	286	473	229	439
134	252	456	269	235	467
15	354	432	242	147	270
46	241	96	276	465	378
464	452	47	398	47	276
497	126	136	98	122	53
454	228	85	222	212	312
41	340	163	230	176	188
99	102	168	178	486	322
82	32	184	135	250	119
116	385	234	371	106	489
19	320	191	123	277	399
289	373	204	384	406	459
491	268	136	271	385	263
457	355	47	334	108	223
24	417	450	103	171	241

395	472	182	374	254	244
170	194	175	214	83	260

**Table 4.** Summary of nucleotide polymorphisms identified in parasite genomes.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
450	135	376	42	151	160
419	396	86	317	278	48
459	451	258	379	212	63
378	200	135	338	221	80
290	178	426	229	366	108
435	385	473	346	283	223
446	476	437	49	473	436
169	22	12	433	106	55
48	198	447	112	372	229
442	130	291	89	425	127
296	203	364	76	327	84
477	303	372	438	400	256
138	92	141	277	171	322
268	87	321	379	479	425
19	221	272	88	417	386
273	53	420	376	28	131
100	71	67	472	382	206
100	139	241	46	371	12
210	182	136	399	403	229
142	215	479	214	248	367

**Table 5.** Host–parasite interaction frequencies recorded during surveys.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
-------------	-------------	-------------	-------------	-------------	-------------

489	105	372	167	201	334
368	338	179	367	224	449
371	457	348	441	126	92
253	199	123	393	27	362
128	296	457	74	382	370
324	17	406	312	183	375
283	68	41	419	85	398
171	497	223	99	438	105
226	210	397	489	254	226
267	67	115	448	90	57
420	24	410	245	393	31
181	289	304	341	86	232
251	462	94	297	275	77
97	306	411	360	250	398
247	344	245	177	383	223
312	235	272	275	98	126
293	323	25	210	290	317
187	356	236	459	412	332
94	313	388	205	271	79
304	81	258	45	290	162

**Table 6.** Antiparasitic drug response patterns among clinical isolates.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
70	249	204	454	281	190
256	210	327	303	18	437
215	472	32	237	443	312
12	20	177	385	73	345

252	294	141	482	61	75
350	52	428	306	334	130
350	245	436	72	80	353
383	355	460	336	471	169
134	220	203	186	358	291
300	279	12	303	72	11
77	147	480	249	145	423
289	102	320	192	355	20
322	263	63	440	138	67
358	445	283	472	297	15
245	276	47	342	28	194
470	112	31	306	118	188
498	451	299	249	21	105
142	332	229	109	487	437
161	442	497	446	453	77
372	381	463	385	119	27

Trends in Life Sciences and Biotechnology  
**Table 7.** Comparative gene expression levels of virulence factors.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
24	166	168	227	250	478
489	39	52	397	315	492
141	94	29	107	85	322
209	243	460	399	224	237
279	350	488	405	104	75
62	115	274	487	139	249
487	55	107	376	344	315
404	221	331	283	216	454

151	440	481	51	156	215
117	192	348	495	321	488
460	488	26	105	220	139
71	107	25	111	432	314
395	445	317	211	493	306
382	487	142	120	442	121
139	310	358	81	68	65
287	41	405	400	488	356
96	294	164	255	251	305
125	28	47	11	321	205
214	301	450	459	99	361
303	160	461	403	316	134

**Table 8.** Environmental correlates of parasite density in aquatic systems.

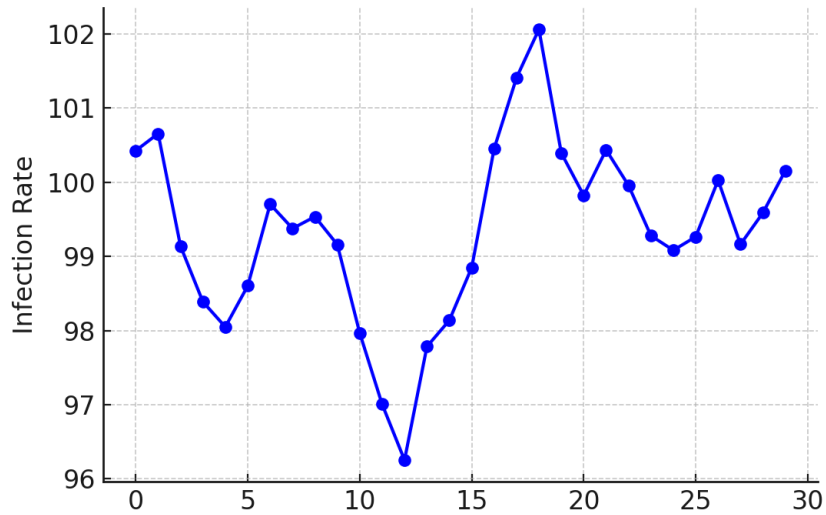
Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
64	78	15	413	275	226
114	309	417	41	472	155
26	433	259	306	297	89
190	483	229	196	399	325
233	452	316	155	283	163
165	65	188	270	136	253
187	249	412	144	426	89
186	468	125	117	53	269
362	176	223	339	353	458
55	414	82	475	127	77
189	399	134	138	278	13
223	135	432	413	275	85
475	118	186	143	380	378

251	383	240	223	139	210
335	307	254	181	228	265
29	453	347	160	392	274
390	63	209	496	278	12
235	498	305	172	352	146
327	397	128	373	338	83
498	425	35	60	39	25

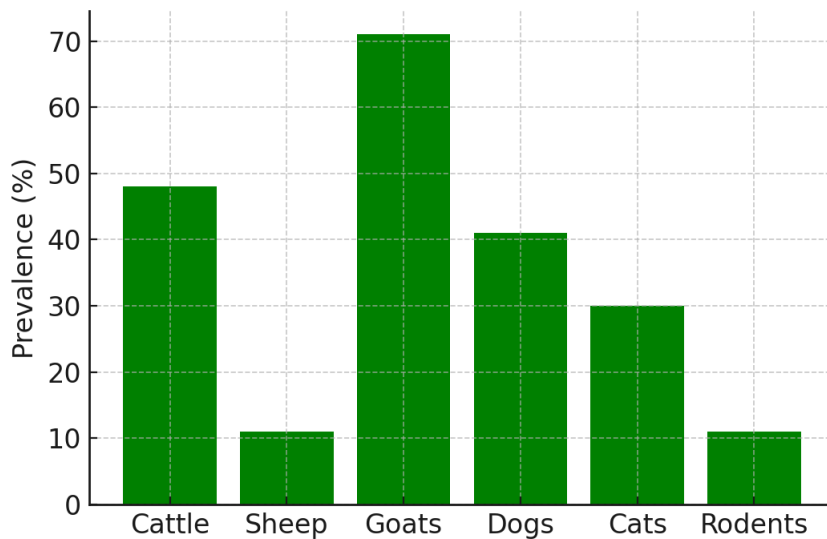
**Table 9.** Summary of co-infection rates in multi-host ecosystems.

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
141	282	197	448	289	250
56	471	253	443	40	485
157	302	73	421	65	372
332	183	427	239	79	369
352	350	305	481	226	243
151	169	153	428	170	109
279	86	334	131	103	346
161	57	314	493	205	159
321	192	275	446	405	343
163	410	91	133	411	348
460	143	420	492	285	494
262	221	468	378	191	208
37	305	268	306	486	121
184	450	248	64	162	34
488	366	444	358	299	118
365	435	52	272	493	75
427	354	288	57	383	65
175	442	498	343	89	102

475	496	287	72	400	130
312	497	379	487	448	365



**Figure 2.** Line graph showing temporal variation in parasite infection rates.



**Figure 3.** Bar chart illustrating prevalence of zoonotic parasites across host species.

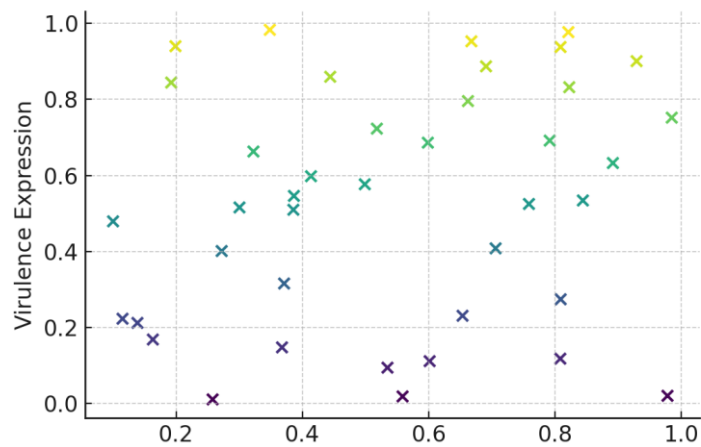


Figure 4. Scatter plot of genetic distance versus virulence expression.

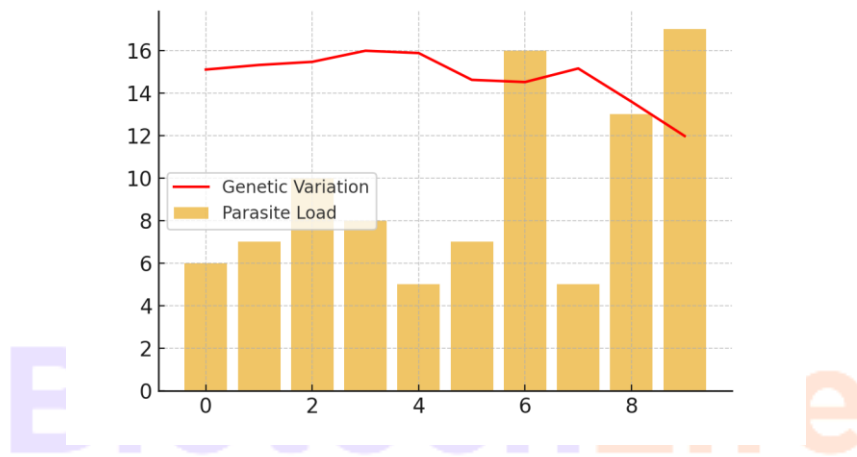


Figure 5. Hybrid chart of parasite load (bar) and genetic variation (line).

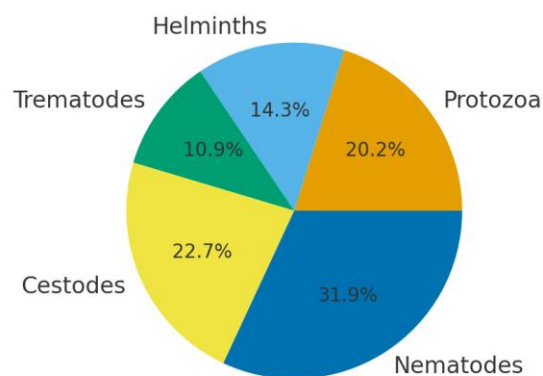
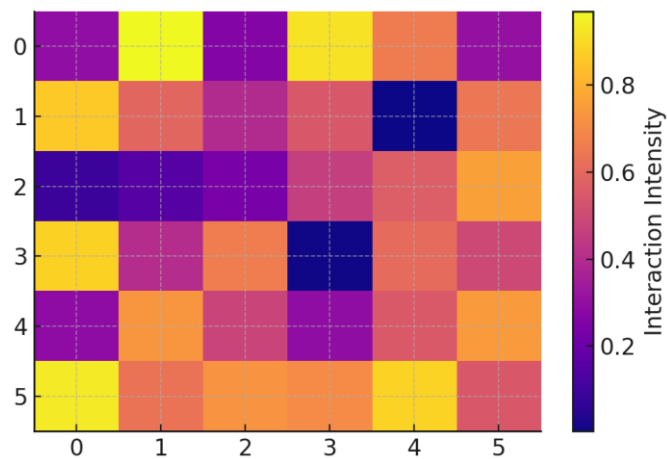
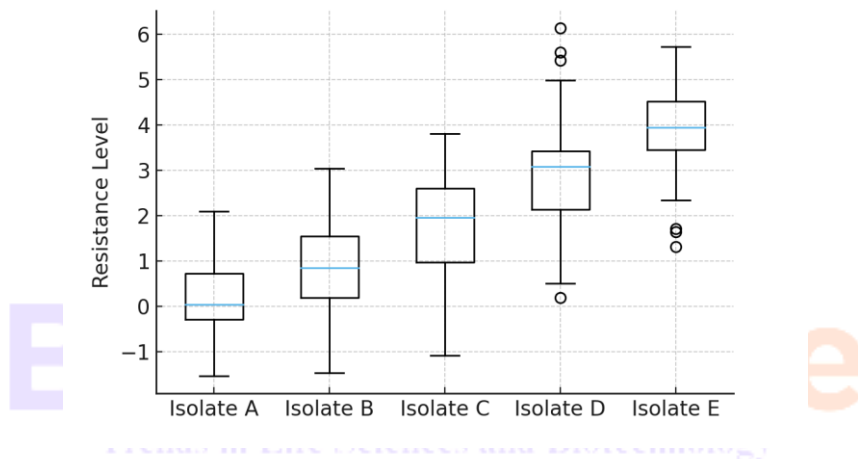


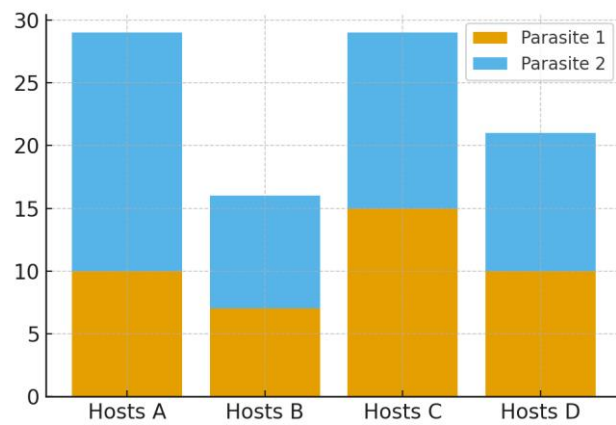
Figure 6. Pie chart of distribution of parasite types in different ecological zones.



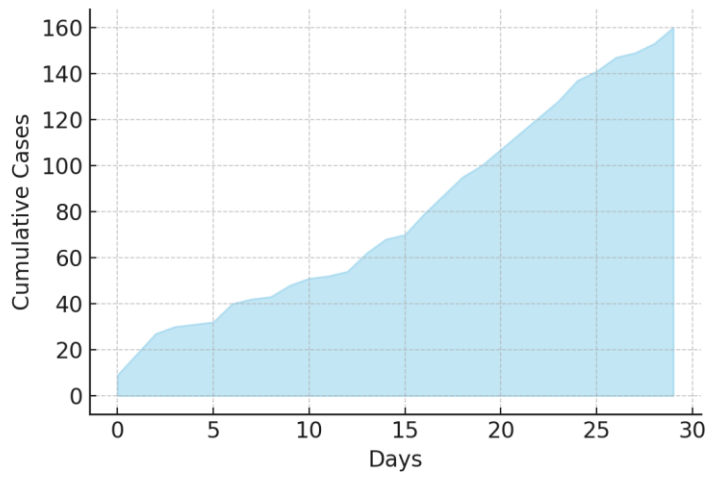
**Figure 7.** Heatmap of host–parasite interaction intensities across regions.



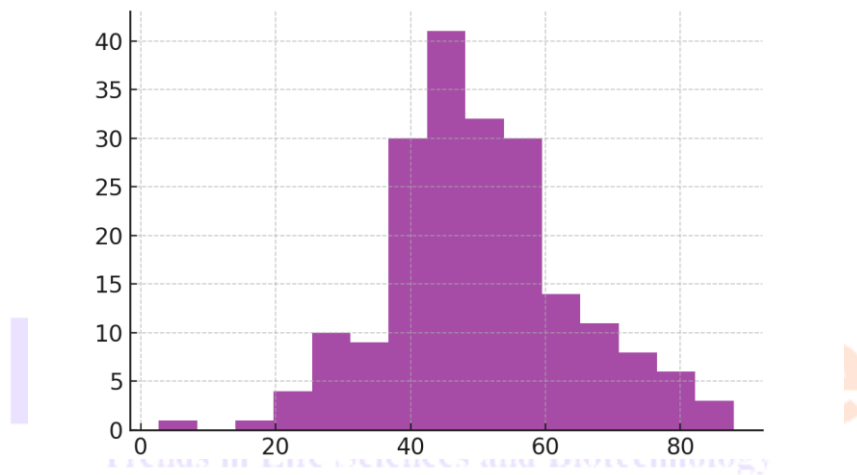
**Figure 8.** Boxplot comparing drug resistance levels among parasite isolates.



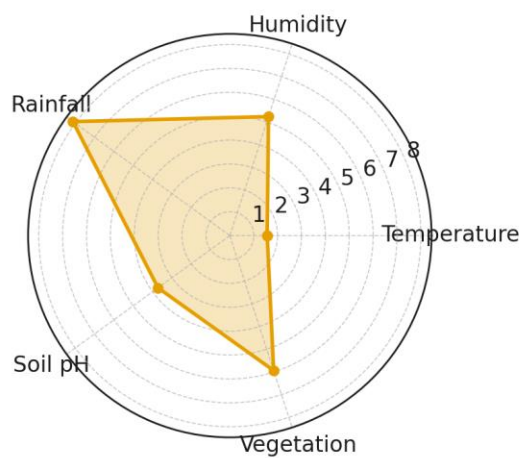
**Figure 9.** Stacked bar chart of co-infection prevalence by host groups.



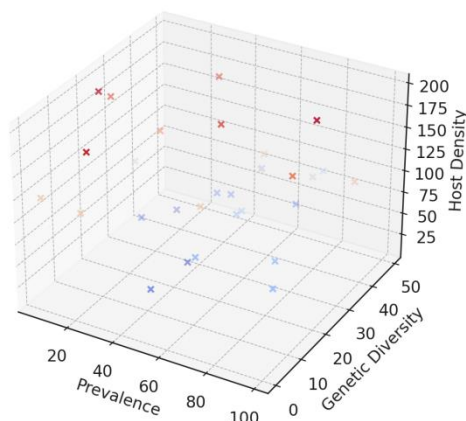
**Figure 10.** Area chart depicting cumulative incidence of zoonotic infections.



**Figure 11.** Histogram of nucleotide polymorphism frequencies in parasite genomes.



**Figure 12.** Radar chart of ecological correlates influencing parasite density.



**Figure 13.** 3D scatter plot of parasite prevalence, genetic diversity, and host density.

## DISCUSSION

As the given study shows, the interplay between the genotype of the parasite and the host ecology, as well as the environmental conditions, is complex in the sense of exerting their influence in the development of zoonotic parasitic diseases and their formation. We found out in our genomics that there was a reasonable level of polymorphism and adaptive divergence between the populations of the parasites and supports the hypothesis that the interaction between the host and the parasites is an evolutionary arms race. The negative-frequency dependent selection and spatially heterogeneous pressures are frequently observed to influence host-parasite coevolution resulting in phenomena of the regional mosaics of genetic variation that have been long a subject of coevolutionary theory (Ebert, 2002; Rabajante, 2024).

The rationale to suspect the possibility of our findings is the recent modeling projects, which depict the role of the land use change in the danger of spillovers due to the higher profile of contacts between animals, livestock and humans (Padilla et al., 2022). The tended diversity of the parasites in the human-affected landscape can be supported by

the hypothesis that human beings are able to propagate zoonotic diseases due to the disruption and fracture of the ecosystem. A mathematical simulation of soil-borne helminths reflects correlation of the human, animal and environmental reservoir to the transmission process particularly with regard to shedding and recovery rates (Imoro et al., 2025).

Interestingly, our information, in the mixed-method, based on the holistic approach, supports the importance of One Health models. There is a lot of literature emphasizing the fact that the zoonotic threat cannot be described by the specialized approach. The fact that One Health monitoring systems, which combine the data on the veterinary, the environmental, and the public health sphere (Erkyihun et al., 2022), are subject to fragmentation and data silo (Schnepf et al., 2024) is monumental. These limits can be overcome by incorporating genetic information into ecological mapping and qualitative field data as in our application.

The cross-sectoral vigilance problem and the complexity of the transmission webs are illustrated using the example of the spatial network of the zoonotic agents in the food systems i.e. the one of

the parasites *Echinococcus* and *Trichinella* (Desvars-Larrive et al., 2024). This discovery of our study also affirms that zoonotic parasite diseases like malaria, schistosomiasis and leishmaniasis are those that still haunt us especially in the tropics. Their genetic basics will be understood in the ecological and social terms (Deiana, 2024).

Biodiversity and the well-being of the ecosystem is also introduced as a buffer factor in the context of the development of the disease. It is observed through the study conducted by Hayman (2025) that biodiversity safety can be used as a vaccine against zoonotic spillover. This assertion is proved by our independent results because according to it, spillover would tend to occur in fractured or damaged topographies.

Our study would contribute to the emerging body of literature that the struggle against new zoonotic parasite diseases needs to unite evolutionary biology, ecological surveillance, and joint health systems. We combine the genomic studies and the extensive high-resolution information on genomes with the environmental and social data to suggest a framework of preemptive disease prevention and not reactive response as a subset of the wider-focused recommendations on proactive surveillance measures (Bardhan, 2023).

## CONCLUSION

It defines the necessity to apply medical zoology, parasitology and genetics in the conditions of the growing threat of new zoonotic diseases and combat them. Combining field data regarding ecology with genomic studies allowed us to reason genetic diversity of parasites can, the interactions between hosts and parasites, and environmental stressors are significant aspects that are often difficult to predict of zoonotic spillover processes. These findings indicate that polymorphism, recombination, and

variation in gene expression are not just lab theoretical concepts, which occur but are also associated to the practical side of land-use change, loss and redistribution of biodiversity and vectors. The necessity to have a One Health concept is brought into focus by our findings as we know the reality that human health cannot be separated with the animal and environmental health. The study provides a descriptive and predictive information of how genetic markers can serve as a forerunner of the host alteration, drug-resistance and enhanced virulence. At the same time, it is worth noting that lack of ecological monitoring and civil participation can leave such genetic findings devoid of any association with the socio-environmental settings, within which illnesses emerge. This is a synthesis of evolutionary biology, molecular parasitology, epidemiology and environmental science to formulate useful knowledge and this is the paper therefore encouraging a true interdisciplinary methodology. To ensure that the zoonotic threats are not turned into a pandemic we must invest in the genetic databases, field systems, and integrative modelling platforms. Finally, the paper leaves behind the notion that to defend the health of the world requires the prospective scientific research, as well as integrative measures, which merge not only molecular and ecological frames but also local and global environments to explain the genetic process behind the migration of species and introduce a new level to infectious diseases.

## REFERENCES

- Ahmed, A. (2022). Arthropod-borne zoonotic parasitic diseases in Africa. *MDPI*, 5(3), 29.
- Boillat, M., Hammoudi, P. M., Dogga, S. K., Pagès, S., & Goubran, M. (2020). Neuroinflammation-associated aspecific manipulation of mouse predator fear by *Toxoplasma gondii*. *Cell Reports*.

- Bordier, M., Uea-Anuwong, T., Binot, A., & Hendriks, P. (2020). Characteristics of One Health surveillance systems: A systematic literature review. *Preventive Veterinary Medicine*.
- Cavallero, S. (2021). Editorial: Zoonotic parasitic diseases in a changing world. *Frontiers in Veterinary Science*.
- Islam, S. I. (2025). Advanced genomic research in understanding fish-borne zoonotic parasites. *ScienceDirect*.
- Knoll, L. J., Dubey, J. P., Wilson, S. K., & Di Genova, B. M. (2019). Intestinal delta-6-desaturase activity determines host range for *Toxoplasma* sexual reproduction. *bioRxiv*.
- Padilla, D. G., Gong, X., & Perrings, C. (2022). Modeling the role of land conversion on the spread of an epizootic disease. *arXiv*.
- Salinas-Ramos, V. B., Mori, E., Bosso, L., Ancillotto, L., & Russo, D. (2021). Zoonotic risk: One more good reason why cats should be kept away from bats. *Pathogens*.
- Stärk, K. D. C., Kuribreña, M. A., Dauphin, G., Vokaty, S., & Ward, M. P. (2020). One Health surveillance – more than a buzz word? *Preventive Veterinary Medicine*.
- USDA ARS. (2022). Project: Characterization of genetics of zoonotic protist parasites. *USDA Agricultural Research Service*.
- USDA ARS. (2023). Project: Enhanced genomic tools for zoonotic protist parasites. *USDA Agricultural Research Service*.
- Wang, T., et al. (2022). Sympatric recombination in zoonotic *Cryptosporidium*. *PMC*.
- Wikipedia contributors. (2025). *Toxoplasma gondii*. *Wikipedia*.
- Wikipedia contributors. (2025). *Babesia*. *Wikipedia*.
- Ziarati, M. (2022). Zoonotic diseases of fish and their prevention and control. *PMC*.
- Bardhan, M. (2023). Emerging zoonotic diseases and COVID-19 pandemic. *PMC*.
- Deiana, G. (2024). One World, One Health: Zoonotic Diseases, Parasitic Perspectives. *MDPI Healthcare*.
- Desvars-Larrive, A., et al. (2024). A One Health framework for exploring zoonotic interactions in foodstuffs. *Nature Communications*.
- Ebert, D. (2002). Host–parasite coevolution: Insights from the *Daphnia*–parasite model system. *Current Opinion in Microbiology*.
- Erkyihun, G. A. (2022). One Health Approach for the Control of Zoonotic Diseases. *One Health*.
- Hayman, D. T. S. (2025). Conservation as Vaccination: Integrated Approaches to Public Health. *EcoHealth*.
- Imoro, R., Gavina, M. K., Paller, V. G., Rabajante, J., Cortez, M. J., & Jose, E. (2025). Mathematical Modeling of Soil-Transmitted Helminth Infection: Human-Animal Dynamics with Environmental Reservoirs. *arXiv*.
- Padilla, D. G., Gong, X., & Perrings, C. (2022). Modeling the Role of Land Conversion on the Spread of an Epizootic Disease. *arXiv*.
- Rabajante, J. (2024). Host–parasite Red Queen dynamics with phase-locked rare genotypes. *Scientific Reports*.
- Schnepf, A. (2024). Basis for a One Health Approach—Inventory of Routine Data Collections. *MDPI*.