

Genetic Diversity of Zoonotic Viruses and their Ability to Jump the Species Barrier

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ABSTRACT

This chapter goes into detail about the complicated world of infectious viruses, focusing on their wide range of genetic variations and the things that allow them to infect different species. Living things on Earth are all linked, and these germs, which have caused pandemics in the past, show how connected everything is. Zoonotic diseases, which include many different pathogens, are a problem for everyone around the world because they hurt people's health, crops, and budgets. This chapter talks about different types of zoonotic viruses, how they spread, and why a "One Health" method is essential for effective prevention. A look at the past shows how terrible viral animal diseases have been, from the Spanish pandemic to more recent epidemics like SARS and MERS, along with COVID-19. Recent progress in genetics, epidemiology, and surveillance of illnesses is a big part of solving these problems. This shows how important it is for people, animals, and the world to work together. Zoonotic viruses are essential for more than just health care; they also affect the economy, the environment, and society. Outbreaks have a significant effect on the economy because they affect manufacturing, foreign trade, and consumer spending. Healthcare systems are essential for managing diseases, so money needs to be spent on infrastructure, studies, and ways to keep diseases from happening. Zoonotic viruses have an ecological impact on environments and animal populations, which makes conservation efforts even more critical. Five primary examples are used to show how genetic variation in zoonotic viruses can be used to show how adaptable they are and what this means for diagnosis, treatment, vaccine creation, and healthcare preparedness. It is talked about with examples of how immune evasion, interferon-gamma blocking, genetic recombination, cross-species contact, and reservoir hosts can allow species to jump barriers. The chapter stresses how complicated zoonotic viruses are and how important it is to have a complete knowledge of inherent, ecological, and host-related factors. Experts in people, animals, and the environment must work together as part of the One Health plan to lessen the effects of these viruses on people and animals around the world. Animal-to-human viruses are studied because they are harmful to humans and because they show how different parts of life on Earth are linked.

Key words: Zoonotic viruses, Genetic diversity, Pandemics, Disease transmission, Cross-species interaction, Interconnected nature, Viral spillover, Public health, Genetic recombination.

CITATION

Noor BA, Basit MA, Akram MS, Ali A, Kasli MAF, Khan AMA, Rehman A and Ahmed I, 2023. Genetic diversity of zoonotic viruses and their ability to jump the species barrier. In: Aguilar-Marcelino L, Zafar MA, Abbas RZ and Khan A (eds), Zoonosis, Unique Scientific Publishers, Faisalabad, Pakistan, Vol 3: 676-686. <https://doi.org/10.47278/book.zoon/2023.133>

CHAPTER HISTORY

Received: 12-May-2023 Revised: 09-July-2023 Accepted: 20-Aug-2023

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1. INTRODUCTION

Infectious illnesses have fascinated and challenged scientists and public health officials with animal origins that may spread to people. These mysterious diseases can cross species barriers and penetrate human society because of this. The zoonotic viruses at the center of these enigmas are microscopic infectious organisms that can hop from animals to humans. This chapter explores zoonotic viruses and why they can cross species barriers (Tomes 2023). The existence of zoonotic viruses serves as a continual reminder of the interconnected nature of all life on Earth. Diseases from other species serve as a sobering reminder that we all inhabit the same planet. From past terrible pandemics to current difficulties, the development of zoonotic viruses has impacted human history. Protecting global health requires more than just an intellectual interest in the genetic variety of these viruses and the mechanisms behind their capacity to leap species borders. To better understand these deadly foes, we shall delve into the complexities of zoonotic viruses in the next sections (Tomori and Oluwayelu 2023).

Zoonosis, often known as zoonotic illnesses or infections, represents the complex relationship between animal and human health. It includes viruses, bacteria, parasites, fungi, and prions that can cause illness. Zoonotic illnesses can cause pandemics in humans, a dangerous consequence of our relationship with animals. These diseases spread in several ways. They can spread by direct contact with diseased animals, polluted food or water, animal excreta, or arthropod vectors like ticks and mosquitoes. Animals often silently sustain viruses without showing symptoms and secretly transmit them to humans. Pathogens, whether viral (flu, HIV, Ebola), bacterial (Salmonella, Lyme disease), parasitic (malaria, toxoplasmosis), fungal (ringworm), or prionic (variant Creutzfeldt-Jakob disease), present unique challenges to containment and eradication (Haruna et al. 2023). Zoonotic illnesses affect public health, agriculture, and economies worldwide, causing illness, death, and economic turmoil. Their unrelenting development, highlighted by the SARS-CoV-2 virus-caused COVID-19 pandemic, reflects changing human-animal interactions, landscapes with deforestation and urbanisation, and agricultural practices. The "One Health" approach to zoonosis requires collaboration between human, animal, and environmental experts to address the complex relationship between them. Thus, zoonosis awareness and knowledge are essential for protecting public health and the fragile balance of life shared by many species (Toyoshima et al. 2020). Zoonotic illnesses can impact biodiversity in multiple ways, one of which is by reducing or eradicating animal populations. Ebola virus epidemics in Africa have wiped out great ape populations, which are critical to forest ecosystems. Moreover, harming animal populations can have far-reaching consequences for ecosystems. It can disrupt food webs, change predator-prey dynamics, and alter species composition, leading to ecological imbalances. Human interference, such as illegal animal trade and habitat degradation, is often the reason behind the spread of zoonotic viruses. As people come into closer contact with animals due to loss of habitat and intrusion into wildlife territories, the risk of disease transmission

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increases. To mitigate the ecological impact of zoonotic viruses, the conservation of species, preservation of habitat, and adoption of sustainable practices are all crucial.

2. A BRIEF HISTORY OF VIRAL ZOO NOTIC DISEASES

Viral zoonotic illnesses have a long and convoluted history because of the many ways in which infectious organisms have jumped from one species to another. Scientists believe that animals have harbored viruses like influenza, smallpox, and measles for many years, leading to their evolution. Millions of people lost their lives in the devastating Spanish flu (H1N1) epidemic that hit the world in the twentieth century (Begeman et al. 2023).

Diseases such as severe acute respiratory syndrome (SARS), Middle East Respiratory Syndrome (MERS), and the continuing COVID-19 pandemic put emerging coronaviruses in the spotlight as we entered the 21st century. The increasing contact between humans and animals, the loss of habitat due to deforestation, and the ease with which people and things may travel around the world all contribute to the dynamic character of zoonotic dangers in our interconnected world. Scientific progress in genetics, epidemiology, and disease surveillance has helped address these issues by illuminating the dynamics of viral changes. This information highlights the critical need for proactive monitoring, research, and a collaborative One Health approach, bringing together experts in human health, animal health, and environmental health to manage the dynamic nature of zoonotic diseases and lessen their global and societal impacts (Niemi et al. 2022).

2.1 SIGNIFICANCE OF ZOO NOTIC VIRUSES

Zoonotic viruses are important beyond labs and clinics. These mysterious viruses, which may jump from animals to people, affect many aspects of our environment. They suffer economic disruptions that damage industry and trade. They demonstrate healthcare system resilience and the need for readiness and reaction. Zoonotic viruses cause fear, influence behaviour, and illuminate social dynamics. They threaten agricultural output and food supply. Additionally, these viruses create ecological shadows that might decimate wildlife populations and change ecosystems. They emphasize the need for global collaboration, improved research, and public health measures as disease indicators. Zoonotic viruses affect the economy, health, environment, and society, requiring a complex and cohesive strategy to reduce their impact (Parkhe and Verma 2021).

2.2. ECONOMIC

The effects of zoonotic viruses on international trade, manufacturing, and, ultimately, consumer spending are too widespread to ignore. Both affluent and poor countries might suffer significant economic losses as a result of these pathogenic pathogens. Healthcare expenditures associated with treating infected persons, increased demands on medical infrastructure, and the deployment of expensive containment measures like quarantines are all examples of the direct economic consequences that might result from a zoonotic outbreak (Rahman et al. 2020).

Further, they pose a threat to vital economic areas. For instance, when zoonotic infections break out in animals, it can lead to culling, trade restrictions and decreased productivity in the agriculture sector. Pandemics like avian flu or foot-and-mouth disease can lead to the killing of animals, jeopardizing food security. When a zoonotic disease breaks out, it can halt exports, limit travel, and lower customer trust in the safety of items from the affected region. Companies, employees, and international trade are all impacted by the resulting interruptions to supply networks. Further, zoonotic infections can have an

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adverse effect on the local economy by discouraging tourists from visiting places where outbreaks have been recorded. To reduce the financial burden of zoonotic viruses and protect public health, it is crucial to invest in monitoring, research, and preventative measures (McNeely 2021).

2.3 HEALTHCARE

(Keesing and Ostfeld 2021) When it comes to managing diseases, particularly those brought on by zoonotic viruses, healthcare plays a key role in society. It covers a wide range of medical assistance, from routine checkups to more complex procedures, from diagnosis to preventative care. Zoonotic illnesses can represent major hazards to public health. Hence, it is crucial to have a reliable healthcare system in place for their early identification, diagnosis, and treatment.

When a zoonotic disease suddenly spreads, it may put a tremendous strain on the healthcare system and even overwhelm hospitals and doctors. Effective management of these situations requires ready access to adequate infrastructure, medical supplies, and qualified healthcare staff. Vaccination drives, public health education, and epidemic monitoring are all crucial parts of healthcare that are sometimes overlooked in favour of treating the sick. Healthcare systems also play an important role in R&D, which is necessary for the development of vaccines and therapies for zoonotic viruses. Healthcare infrastructure investment on a national and international scale is essential for dealing with these new dangers, protecting people and places, and decreasing the spread of zoonotic illnesses (Mohapatra et al. 2022).

2.4 ECOLOGICAL EFFECTS

Wildlife populations and ecosystem health are inextricably linked to the ecological consequences of zoonotic viruses. The spread of these viruses from animals to people has the potential to have devastating effects on ecosystems (Ribas et al. 2023). The reduction or extinction of animal populations is only one way that zoonotic illnesses can have an effect on biodiversity. Great ape populations, which are vital to forest ecosystems, have been wiped out by Ebola virus epidemics in Africa. Furthermore, if animal populations are harmed, it can have far-reaching consequences for ecosystems. Food webs can be thrown off kilter, and changes in predator-prey dynamics and species composition throw ecological processes off kilter. Many zoonotic viruses spread because of human interference, such as the illegal trade in animals or the degradation of natural habitats. As people come into more fantastic touch with animals due to habitat loss and intrusion on wildlife territories, this proximity raises the possibility of disease transmission. Conservation of species, preservation of habitat, and implementation of sustainable practices are all necessary to mitigate the ecological impact of zoonotic viruses. The probability of zoonotic spillover events can be reduced, and the ecological balance essential to sustain life on Earth can be preserved by protecting ecosystems and conserving the health of wildlife populations (Bezerra-Santos et al. 2021).

2.5 ZOONOTIC VIRUSES

Several viruses may spread from animals to people, and this has serious implications for public health. Here are a few prominent ones:

2.5.1. INFLUENZA VIRUSES

Depending on the type, the influenza virus can cause seasonal epidemics or even global pandemics, with consequences including moderate to severe respiratory symptoms and even pneumonia (Javanian et al. 2021).

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2.5.2. CORONAVIRUSES

The SARS-CoV-2-induced COVID-19 pandemic has produced a wide range of symptoms, from simple respiratory problems to life-threatening pneumonia and multiple organ failure throughout the world (Abdel-Moneim 2020).

2.5.3. EBOLA VIRUS

High death rates are typically associated with epidemics of the Ebola virus, which causes severe hemorrhagic fever in humans (Jacob et al. 2020).

2.5.4. HIV (HUMAN IMMUNODEFICIENCY VIRUS)

HIV (Human Immunodeficiency Virus) targets the immune system, weakening it over time and, if untreated, leading to AIDS, which increases the risk of contracting opportunistic infections and malignancies (Wu et al. 2021).

2.5.5. RABIES VIRUS

Confusion, paralysis, and hallucinations are only some of the neurological signs of rabies, which can quickly progress to death if not treated quickly enough (Lian et al. 2022).

2.5.6. HANTAVIRUSES

Humans can contract deadly respiratory illnesses from hantaviruses, such as hantavirus pulmonary syndrome (HPS) and hemorrhagic fever with renal syndrome (HFRS) (D'Souza et al. 2020).

These examples underscore the importance of understanding and monitoring zoonotic viruses to mitigate the risk of outbreaks and protect global health.

2.6 CATEGORIES OF ZOOTIC VIRUSES

Origin, mode of transmission, and illness manifestations are only a few of the factors that may be used to classify zoonotic viruses. Common types of zoonotic viruses include:

2.6.1. RESPIRATORY ZOOTIC VIRUSES

Airborne droplets often spread these viruses and cause infections in the respiratory system. Certain coronaviruses, adenoviruses, and influenza viruses (including H1N1 and H5N1), as well as SARS-CoV-2 and MERS-CoV, are prime examples.

2.6.2. VECTOR-BORNE ZOOTIC VIRUSES

Arthropods like mosquitoes and ticks act as vectors for the spread of these viruses to people. The Zika virus, West Nile virus, and other encephalitis viruses are only a few examples.

2.6.3. GASTROINTESTINAL ZOOTIC VIRUSES

These viruses can infect the digestive tract and are commonly spread by tainted food or water or by coming into touch with infected animals. Viruses that cause stomach and intestinal illness are one example.

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2.6.4. HEMORRHAGIC FEVER ZONOTIC VIRUSES

Contact with infected animals or their body fluids is a common route of transmission for these viruses, which can cause life-threatening bleeding problems. The Ebola virus, the Marburg virus, and the Lassa virus are only a few examples.

2.6.5. VECTOR-BORNE FLAVIVIRUSES

A group of viruses spread mostly by *Aedes* mosquitoes; they include dengue, yellow fever, and chikungunya.

2.6.6. OTHERS

Many zoonotic viruses exist that cannot be simply classified. Nipah, Hendra, and other poxviruses are among them.

These groups show how many distinct kinds of zoonotic viruses there are and how many ways they may infect people. For the sake of public health and disease prevention, it is crucial to have a firm grasp of these classifications and the dangers they pose (Zhang et al. 2020).

3. GENETIC DIVERSITY IN ZONOTIC VIRUSES

To fully grasp the versatility, transmission, and impact of zoonotic viruses on public health, an appreciation of their genetic diversity is essential. The genetic complexity of five well-known zoonotic viruses is discussed here: SARS-CoV-2 (Coronavirus), HIV-1 (a subtype found in the Democratic Republic of the Congo), Influenza A Virus, Ebola Virus, and Rabies Virus.

3.1 SARS-COV-2 (CORONAVIRUS)

As evidenced by the COVID-19 pandemic caused by SARS-CoV-2, genetic diversity among zoonotic viruses is critically important. The genome of this member of the family *Coronaviridae*, a coronavirus, is around 30,000 nucleotides long and consists entirely of single-stranded RNA. The virus apparently evolved genetic modifications that allowed it to spread efficiently from human to human once it emerged from an animal reservoir. Mutations in the spike protein, which interacts with the human ACE2 receptor, are the primary source of genetic variety in SARS-CoV-2. Transmission, immune evasion, and vaccination efficacy can all be influenced by the genetic fingerprints left by different strains of the same virus. Natural selection, immunological pressure, and host adaptability are all thought to be responsible for these alterations. The fact that new lineages are constantly forming demonstrates the virus's adaptability (Malik 2020).

Because certain mutations might modify a virus's sensitivity to therapy, diverse genetic lineages also provide difficulties for vaccine development and antiviral medicines. Tracking genetic variation and guiding public health efforts to battle a pandemic necessitates global monitoring and sequencing of virus genomes.

3.2 HIV-1 IN THE DEMOCRATIC REPUBLIC OF CONGO

HIV-1, the virus responsible for AIDS, has a lot of genetic variation, especially among its subtypes and recombinant forms. Subtype B is more abundant in North America and Western Europe, whereas Subtype C is more prevalent in Southern Africa. The HIV spectrum is on full display in the Democratic Republic of

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the Congo (DRC) in Central Africa. Subtype D and recombinant variants are the most common types in the DRC. These recombinants are the product of gene exchange between different subtypes that occur when many subtypes infect the same host. The ramifications of this genetic variety for diagnosis, therapy, and vaccination development are significant. Vaccine candidates and antiretroviral medication regimens must take into account geographical differences in order to be effective. Studies conducted in the DRC provide insight into the complex dynamics between HIV subtypes and the difficulties posed by controlling viral populations with such a wide range of genetic diversity in the worldwide battle against AIDS (Rubio-Garrido et al. 2020).

3.3 INFLUENZA A VIRUS

The influenza A virus, like other members of the family *Orthomyxoviridae*, is very adaptable genetically. When two distinct influenzas A strains infect a host, the virus's eight RNA segments allow for genetic reassortment. This reassortment generates fresh strains with the potential to spread worldwide. Subtypes of influenza A viruses are defined by differences in their surface hemagglutinin (H) and neuraminidase (N) proteins. Seasonal flu epidemics and the infrequent appearance of pandemic viruses are both facilitated by the continual mutation and reassortment of these subtypes. The reassortment of genes from human, pig, and avian influenza viruses, for example, caused the 2009 H1N1 influenza pandemic. Point mutations in the H and N genes cause antigenic drift, necessitating regular revisions of flu vaccinations to keep up with circulating strains. The selection of vaccine strains, monitoring, and pandemic preparedness all rely on a thorough knowledge of the genetic variety of influenza A viruses. The worldwide health effect of these extremely adaptable viruses is a major concern, and current research seeks to forecast their development and lessen it (Liu et al. 2020).

3.4 EBOLA VIRUS

Recent Ebola virus outbreaks in Africa have highlighted the family's genetic diversity. Different species of Ebolavirus have somewhat different variations of the virus's single-stranded RNA genome. There are five different types of Ebolaviruses, but the one that causes the worst sickness in humans is the Zaire ebolavirus. The virulence and ease of transmission of Zaire ebolavirus are affected by genetic polymorphism within the virus itself. For instance, the Makona subtype of Zaire ebolavirus was responsible for the 2014 West African epidemic. Diagnostics, therapy, and vaccine development are all affected by the Ebola virus's genetic diversity. Diagnosing and treating diseases successfully requires targeting conserved areas of the genome. Vaccines against Ebola that are effective against several strains of the virus are still being developed (Woolsey and Geisbert 2021).

3.5 RABIES VIRUS

Lyssaviruses, like the one that causes rabies, consist of a single strand of RNA. In comparison to other RNA viruses, it is notable for its low levels of genetic variation and high genetic stability. The phylogenetic study, however, has shown genetic subgroups within lyssaviruses. There are public health consequences associated with the rabies virus's genetic diversity, particularly when considering variant-specific vaccinations. Rabies variations linked with distinct animal reservoirs may influence the choice of treatment and vaccination. In order to comprehend transmission patterns and locate high-risk locations, monitoring rabies virus genetic variation is essential. Data is useful for developing effective vaccine and control tactics, which will ultimately lead to the eradication of an ancient but still lethal zoonotic virus. In

conclusion, the genetic diversity of zoonotic viruses is a key factor in the way these pathogens have evolved, adapted, and affected human and animal populations. This variety provides a window into the ever-changing world of zoonotic viruses and their intricate genetic landscapes, which is essential for diagnostics, therapy, vaccine development, and public health preparation (Coertse et al. 2021).

4. FACTORS ENABLING SPECIES BARRIER JUMPING

Complex molecular and genetic processes are involved in the process by which zoonotic viruses are able to infect both animals and humans (Dhama et al. 2020). Some of the reasons and mechanisms at play, along with some relevant instances, are outlined below:

4.1 ESCAPING IMMUNE SYSTEM

Transmission of zoonotic viruses from animals to people relies heavily on the viruses' capacity to escape the immune system. These viruses are able to infect new host species because of a complex procedure involving many immune evasion mechanisms. Changing the surface proteins of the virus through genetic variants is an essential tactic for evading the host immune system. Because of this diminished recognition, the virus is able to establish itself within the host without being seen during the early stages of infection (Abdullah et al. 2021).

Some viruses produce targeted proteins to circumvent the immune system. To impede the host's immune response, HIV-1 creates proteins, including Vpu and Nef, which down-regulate critical cell surface receptors involved in immune detection. One typical strategy used by zoonotic viruses is antigenic variation. Because they may undergo fast genetic changes that modify the epitopes on their surface proteins, viruses might evade the host immune system's ability to generate an effective response because antibodies may no longer detect the mutated virus. More than that, certain viruses inhibit antiviral immune signalling pathways. Some viruses, for instance, are able to suppress the host's production of interferons, which are vital antiviral signalling molecules (Forni et al. 2021).

Dendritic cells and macrophages are two examples of host immune cells that may be manipulated by zoonotic viruses, leading to an immunosuppressive environment that prevents adaptive immune responses from being activated. Because of this, the virus is able to create long-lasting infections while remaining hidden from immune monitoring. There are instances where these viruses cause immunological tolerance in the host, thereby teaching the immune system to ignore the infection. Constant exposure to the virus, especially in endemic areas, can lead to this condition, which is typical of chronic viral infections (Blum et al. 2020).

4.2 COUNTERING INF GAMMA

To better infect new species, zoonotic viruses often develop strategies to neutralise interferon-gamma (IFN- γ), a vital part of the host immune response. IFN- γ is essential for antiviral defences because it sets off a chain reaction of immune responses to fight against viruses. However, when its activity levels are too high or undergo mutations, it can constitute a barrier to viral reproduction and spread. The IFN- γ responses of hosts can be modulated or suppressed by the methods that zoonotic viruses have evolved. These viruses are better able to infect new host species and thrive in their specific biological contexts if they are able to change their genetic makeup. This approach of immune evasion allows zoonotic viruses to overcome the robust host immune system, allowing for effective transmission across species and the possibility for long-term expansion into new host populations. To adapt and emerge, zoonotic viruses

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must strike a delicate balance between being detected by the immune system and taking advantage of the host's resources (Liu et al. 2022).

4.3 GENETIC RECOMBINATION

An essential mechanism in virology, genetic recombination contributes significantly to the creation of new, potentially more dangerous zoonotic viruses. Hybridization is the process by which they exchange genetic material from two or more distinct viral strains or variations, giving rise to a new hybrid virus with a distinct genetic composition. Because it can help a virus adapt to infect new host species, this mechanism is of particular importance in the context of zoonotic illnesses. During the co-infection of a host cell, viral fragments of the genome (either RNA or DNA) can swap places, a process known as genetic recombination. This can happen if they infect the host with two separate but related viruses or two different strains of the same virus. These viruses' genetic material can mingle during replication, producing recombinant viruses containing features from both parental strains (Rockett et al. 2022).

Genetic recombination may drastically alter the capacity of a virus to identify and connect to host cell receptors, to elude the host immune system, and to multiply successfully in the new host. By rearranging their genes, zoonotic viruses may quickly adjust to the specific conditions of a new host species, which can boost viral dissemination and virulence. Therefore, genetic recombination is essential in the ever-changing process of zoonotic spillover and the formation of infectious illnesses with the potential to become pandemic. In order to forecast and reduce the hazards associated with zoonotic viruses, it is crucial to understand and monitor these recombination processes (Szpara and Van Doorslaer 2021).

4.4 CROSS-SPECIES INTERACTION

Pathogens such as viruses, bacteria, and parasites can be spread from one species to another through "cross-species contact," which is defined as contact between members of various animal species, including humans. The introduction of microorganisms that might cause zoonotic illnesses requires intimate interaction between animals and people. Wildlife trade, farming, hunting, and habitat intrusion are just a few of the places where species meet and mingle. These conditions allow infections to cross across from animals to humans or between species of animals. Factors enhanced the danger of zoonotic disease transmission, such as growing urbanization, deforestation, and changes in land use. For the early diagnosis and control of emerging infectious illnesses, it is essential to gain an understanding of the dynamics of cross-species interaction and the hazards associated with it. This is because it reveals how viruses may breach species barriers and potentially lead to outbreaks and pandemics (Warpeha et al. 2020).

4.5 RESERVOIR HOSTS

In order for zoonotic viruses to jump genetic species boundaries, reservoir hosts play a crucial role. These hosts act as natural reservoirs since they may carry the virus for long periods without showing any symptoms. The genetic adaptations and interactions that take place during this cohabitation have the potential to result in spillover events into other host species, including humans. Reservoir hosts may play many roles in the genetic development of zoonotic viruses. They maintain a constant supply of the virus, which boosts the potential for mutation and genetic diversity. It is recognised that genetic exchange and recombination are facilitated by the wide variety of related viruses seen in some reservoir hosts, such as bats for coronaviruses. These alterations to the viral genome may improve the virus's capacity to adapt

to new host species by allowing it to recognise and attach to receptors, avoid detection by the immune system, and multiply (Van Brussel and Holmes 2022).

Zoonotic viruses essentially employ reservoir hosts as "genetic melting pots," amassing mutations that might improve their adaptation to new hosts. Because of this genetic variation, zoonotic viruses are able to successfully spread to humans and other mammals, resulting in the formation of infectious illnesses. In order to forecast and prevent zoonotic disease outbreaks, an understanding of these genetic relationships is crucial (Holmes 2022).

5. CONCLUSION

In conclusion, the intricate interaction of genetic, ecological, and host-related variables underpinned the phenomena of zoonotic viruses. Because they can suddenly appear and spread throughout populations, zoonotic illnesses pose a serious risk to world health. Viruses are able to detect and exploit new host species thanks to genetic modifications generated by mutation and recombination. Genetic diversity is encouraged, and a source of potential spillover events is provided by the presence of natural reservoir hosts, which typically keep these viruses asymptotically. Viruses' abilities to attach to host receptors and elude immune responses can be improved by changes in viral surface proteins, a consequence of the genetic variety that accumulates inside reservoir hosts.

Furthermore, possibilities for zoonotic viruses to overcome species barriers are facilitated by variables such as host range extension, cross-species interaction, and modifications in ecological landscapes. The spread of infectious diseases from wild animals to domesticated ones and then to people is called "zoonotic spillover," and it has become more of a concern as a result of increased human-animal interactions brought about by urbanization, deforestation, and shifts in agricultural techniques. Arthropods like mosquitoes can act as conduits for the spread of disease from animal reservoirs to human populations through vector-borne transmission.

Variables increased the likelihood of newly discovered viruses infecting vulnerable human hosts, such as behavioural and cultural patterns, international travel, and alterations in the global environment. Because of antibiotic resistance, zoonotic microorganisms can now spread between species despite attempts to contain them. Understanding the genetic, ecological, and immunological variables involved in zoonotic spillover is crucial in this age of increased human-animal interactions and global interconnection. It helps us spot potential danger zones so we can take preventative measures against the spread of zoonotic illnesses. To combat the persistent risk of zoonotic viruses and safeguard the health of human and animal populations throughout the world, a one Health strategy that prioritizes cooperation between human health, animal health, and environmental specialists is necessary.

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