

BATS: Originators of Most of the Zoonotic Pathogens

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ABSTRACT

Bats are an important host of various viruses. Bats have a role as reservoir hosts for various types of viruses and they can transmit these viruses to humans and other animals via their secretions and excretions. Immunological changes are induced in bats after flight. Such phenomenon may play a part in the origination of endemic infections, having significant manifestations of zoonosis. Spillover is when bat pathogens cross-species transmission into other species. Bats are also capable of causing airborne diseases through bugs that feed on bat blood or stool. Viruses from Bats can enter the host cell by attaching itself to cell receptors, thereby infecting it with viruses or viral DNA. viral genome replication is done through the making of negative strain RNA which forms the basis of creating new virus genomes. A virus replicates its genomic RNA by interacting with the 5' and 3' termini of its genome. Upon completion of the replication process by the viral proteins, they subsequently release newly synthesized virions that can then go on to infect neighboring cells before spreading through the entire host's body system. It is important to understand how viruses can jump from animals to mankind to facilitate targeted surveillance, detecting emerging diseases in good time, and designing relevant vaccines and treatment methods. In brief, this chapter discusses the importance of bats in virus transmissions, how the immune system responds to bat flight, and how coronaviruses multiply in host cells. These mechanisms are central in diagnosing, treating, and preventing bat-borne zoonotic diseases.

Keywords: Bats, Zoonosis, Viral infections, Cross-species transmission, Immune response. Anthropogenic land-use change.

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1. INTRODUCTION

Humans are not the only creation living on this planet rather this world is full of different kinds of creatures other than humans such as animals, plants, birds, insects, and microbes. All these creations live and interact with each other to survive. These interactions can be advantageous, and species get benefits from each other in a healthy interaction. Sometimes these interactions can be hazardous because one species can carry some pathogens which transmit different diseases to the other species. Humans interact with different animals to feed in order to get protein and other nutrients needed for their growth and survival (Rosenberg 2015).

Bats have been known to be the rational originators of most zoonotic microorganisms (pathogens). Their fascinating physiology has an immediate impact. They are known to be the primary warm-blooded animals that can fly, and have a high metabolic rate, which grants them to convey a lot of energy. Moreover, they have a unique safe system that licenses them to get through diseases that would be lethal to various animals. Likewise, bats are known to be the transporters of different befolement, including the Ebola sickness, Mar-burg infection, Nipah illness and Hendra tainting. These diseases are known to cause difficult ailments in individuals and various animals (Brook and Dobson 2015). The legitimization for why bats are carriers of these diseases is that they have a unique resistant system that licenses them to persevere through the contaminations without turning out to be sick. This suggests that they can convey the contaminations for a long time without showing any secondary effects. The close relationship of bats with individuals and various animals has similarly added to the spread of these diseases (Phan and Nguyen 2020). Bats are known to roost in caves, trees, and designs, which are a concept close to human settlements. This plans that there is a high chance of contact between individuals and bats, which can provoke the transmission of these contaminations. The use of bat meat and bat guano as a fertilizer has moreover been associated with the transmission of these contaminations (Guth and Mollentzn 2022). In specific social orders, bat meat is seen as a delicacy, and it is eaten rough or cooked. This can incite the transmission of the contaminations from the bat to human. The use of bat guano as fertilizer (compost) has moreover been associated with the transmission of contaminations. It is rich in enhancements, and used as manure in numerous districts of the planet. Regardless, the guano can be corrupted with contaminations, which can provoke the transmission of the diseases to individuals and various animals. Bats are known to spread contaminations of zoophytic imaginable in more than one manner. One way is through direct contact with individuals or animals (Hayman and Bowen 2013).

Bats can convey diseases in their spit, urine, and manure, which can be imparted to individuals or animals through bites, scratches, or contact with dirty surfaces. Another way that bats can spread diseases is through eating bat meat. As Bats are eaten as food in specific social orders, and the meat can be contaminated with diseases. This can similarly provoke the transmission of contaminates, as the guano can be corrupted with the diseases (Schneeberger and Voigt 2016). Bats can also spread contaminates through the air. A few contaminants can be shed in bat droppings and urine, which can dry and become airborne. When the droppings or urine of bats are distributed, the disease can become airborne and accidentally taken in by individuals or animals. In this way, bats can spread contaminants through bugs that feed on bat blood or stool. A couple of bugs, similar to mosquitoes and ticks, can profit from bats and subsequently eat individuals or animals, spreading the diseases meanwhile (Schneeberger and Voigt 2016).

2. ZOONOTIC DISEASES

When transferred naturally from animals to people and vice versa, several microorganisms that cause illnesses can infect both vertebrate animals and humans. (Rahman et al. 2020). The natural transmission of infectious diseases from animals to humans due to different pathogens is called zoonosis (Wang and

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Crameri 2014), and the term "zoonotic pathogens" refers to pathogens that primarily spread illness when they come into contact with people (Cross et al. 2019).

Zoonotic diseases spread by bats are not new because several viruses have previously caused various outbreaks. Yet, due to limited outbreaks, these diseases were not identified as zoonotic, and a pathogen may remain unnoticed if it does not result in a large-scale disease outbreak (Wang and Crameri 2004).

Infectious organisms including viruses, bacteria, parasites, fungi, prions (Wang and Crameri, 2004), protozoa, and many other pathogens are responsible for different zoonotic diseases (Rahman et al. 2020). More than half of infectious diseases in humans are transferred from animals and this number is continuously increasing due to multiple reasons like different human activities (Cross et al. 2019). Anthrax, TB, plague, yellow fever, and influenza are just a few illnesses that have been transmitted to people through domestic animals, poultry, and cattle during the past ten years. Zoonotic diseases could have detrimental impacts on people's health and the economy, and the upward trend in their frequency is expected to continue (Wang and Crameri 2004). Zoonoses have a substantial negative influence on the environment, industry, and the economy at large. (White and Razgour 2020).

3. HUMAN ACTIVITIES AND ZOONOSIS

Human activities are involved in the sharp rise of zoonotic diseases from wildlife species due to different activities like the destruction of animal habitats and agricultural changes etc. (Wang and Crameri 2004). In the same way, a wide range of geological and biological causes, including changing the climate, industrialization, animal movement, commerce, tourism, and vector biology, have had a substantial influence on the development, recurrence, spread, and pattern of zoonoses (Rahman et al. 2020). The spread of these disorders and the danger of transmission have been exacerbated by recent land-use changes (LUC), such as deforestation and agricultural expansion, which are the aspects that are expected to expand in future owing to human population growth and rising resource demand (White and Razgour 2020).

4. OUTBREAK OF ZOONOSIS

Since more than 75% of new illnesses are zoonotic in nature, zoonotic diseases are no longer rising, rather they are now posing a severe threat to the entire planet (Field 2009). When diseases from a vector species infect its host species, zoonosis develops (Brierley et al. 2016). Bats are the second most species-rich order of animal, with more than 1,200 species spread throughout the world. After it was discovered that bats in Australia were the natural reservoir of Henda virus, there has been a huge rise in researcher's interest in bats by considering it as the reservoir of numerous important known and undiscovered zoonotic viruses. Since bats are so diverse, zoonotic infections can spread easily among them. Their capacity to fly helps them to disseminate these infections over a huge geographical area (Wang and Crameri 2014). As a result, both scientists and general public have become more interested in the origin of zoonotic viruses from bats (Voigt and Kingston 2015). Previously the outbreaks of zoonotic diseases have often been attributed to bats. Since bats are hosts of more than 200 zoonotic viruses, many of which are RNA-based and have considerable genetic variety, these viruses are able to significantly adapt to shifting environmental conditions. (Allocati et al. 2016).

5. GENOMIC VERIFICATION

To generate a strong hypothesis regarding bats as a source of different zoonotic diseases (specifically coronavirus), genomic studies were made which supported that bats are likely to be the natural host of

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Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and *MERS*-like viruses in Asia and South Africa. The discovery of a little polymerase chain reaction (PCR) fragment in the Egyptian tomb bat (*Taphozous perforates*) in Saudi Arabia, provided more evidence in favor of this notion. In addition to the above-mentioned bat zoonotic viruses, several other previously unidentified viruses have been found in the past two decades. Other viruses with a history of zoonotic transmission, include the Menangle virus in Australia and the related Tioman and Melaka viruses in Malaysia. In addition to these, there are other related bat reoviruses as well. Large numbers of bat viruses, including lyssaviruses, parainfluenza viruses, hantaviruses, hepaciviruses, and pegiviruses, have also been linked to recognized human illnesses. Several additional paramyxoviruses, coronaviruses, astroviruses, adenoviruses, and herpesviruses are also documented (Wang and Crameri 2014). These viruses mostly reside inside the bats and then transferred to different organisms where they cause different zoonotic diseases (Hayman 2016).

6. CLASSIFICATION OF ZOONOSIS

Zoonotic diseases are classified into many different types depending upon the conditions in which these diseases spread into different species, such as direct zoonosis and reverse zoonosis (Rahman et al. 2020).

7. DIRECT ZOONOSIS

Humans can get infections from animals either directly or indirectly. Diseases spread by direct zoonoses are those that transfer from animals to humans directly through the environment or other means of transmission. A well-known illustration of direct zoonoses is the virus known as avian influenza, which travels from animals to people through droplets or fungal spores. Additionally, rabies which is one of the deadliest zoonotic illnesses, transmitted when infected animals can bite people and directly transmit viruses to them (Rahman et al. 2020).

8. REVERSE ZOONOSIS

Animals typically infect humans with zoonotic diseases. However, some stories claimed that humans can infect animals as well. Such conditions are referred as reverse zoonoses. Examples of such pathogens include methicillin-resistant *Staphylococcus aureus* (MRSA), *Campylobacter* spp, and influenza A virus (Rahman et al. 2020).

9. CLASSIFICATION BASED ON ETIOLOGY

Based on etiology, zoonoses are classified into:

- i. Bacterial zoonoses (such as Anthrax, Tuberculosis, Lyme disease, and Plague)
- ii. Viral zoonoses (such as rabies, Ebola, and Avian Influenza)
- iii. Parasitic zoonoses (such as Trichinosis, Malaria, and Echinococcosis),
- iv. Fungal zoonoses (such as Ringworm)
- v. Rickettsia zoonoses (such as Q-fever),
- vi. Chlamydial zoonoses (such as Psittacosis),
- vii. Mycoplasma zoonoses (*Mycoplasma pneumoniae* infection),
- viii. Protozoal zoonoses (Toxoplasmosis) (Rahman et al. 2020).

10. ZOONOTIC DISEASES CAUSED BY BATS

Many individual bats are captured repeatedly over time as part of a standard method in bat-borne disease research, and their samples are taken (such as blood, urine, feces, or saliva) and examined for the presence of viruses using PCR or serology (Giles et al. 2021). Research has proved that there are many zoonotic pathogens that make bats as their host and then transmit different diseases to humans and other animals (Giles et al. 2021).

A well-known and well-established virus in the family Rhabdoviridae is rabies virus (RABV), which is still one of the most significant zoonotic infections linked to bats (Voigt and Kingston 2015). This bat-associated virus belongs to the genus *Lyssavirus*, one of the six negative-sense RNA virus genera that make up the Rhabdoviridae family. At least 14 distinct species of the *Lyssavirus* genus are found in bats, which are believed to be the viruses' original hosts. The first recorded instance of the rabies virus (RABV) occurred in 1911, and it was bat-to-human transmission (Allocati et al. 2016).

Hendra virus disease is another example of a zoonotic disease transmitted by bats. Bats are the reservoir hosts for Henipa viruses, according to viral isolation from pteropodid bats and experimental genomic analyses of virus (Voigt and Kingston 2015) and it is most likely spread by eating food, drinking pasture water, or drinking feed that has been contaminated by the feces, saliva, or urine of sick bats (Allocati et al. 2016). This virus also affects horses, who serve as its intermediate hosts and produces a deadly illness in them. This virus caused the Hendra virus (HeV) illness in Australia in 1994, 20 horses and 2 individuals experienced problems in just two weeks, which led experts and high-ranking officials to launch a thorough investigation. Despite the presence of numerous novel zoonotic viruses in the human population, including the extremely dangerous Hendra virus and its close sibling Nipah virus (NiV), their ability to spread to non-reservoir species is only moderately effective (Wang and Crameri 2014).

In 1999, researchers in Malaysia found the second henipaviruses, Nipah virus (NiV), in pigs and encephalitic pig workers (Voigt and Kingston 2015). It is an encapsulated, single-stranded, negatively skewed, non-segmented RNA virus with helical symmetry. The virus circulates between fruit bats, pigs, and humans as well as between pigs to pigs and man. Fruit bats serve as a natural reservoir for Nipah infections (Singh et al. 2019). The Henipavirus genus is the most noteworthy group of Paramyxoviridae viruses found in bats (Voigt and Kingston 2015). Menangle virus (genus *Pararubulavirus*) is the fourth zoonotic virus in the family Paramyxoviridae transmitted by bats (Van Brussel and Holmes 2022).

Coronaviruses were initially discovered in animals of the genus *Miniopterus*, although their zoonotic potential is unknown (Voigt and Kingston 2015). The family Coronaviridae and order Nidovirales both contain single-stranded positive-sense RNA viruses with genomes between 16 and 31 kb, (Hernández-Aguilar et al. 2021). Coronavirus has different strains, including severe acute respiratory syndrome, Middle East Respiratory Syndrome, and Coronavirus. Additionally, it has been proposed that coronaviruses are borne by bats, and genetic research has supported this theory (Hu et al. 2015). Coronavirus is the most recent global zoonotic pandemic which disturbed the whole world and damaged the world economy. The primary host of the coronavirus is bats, and these bats transferred this virus to humans and caused a global pandemic (Hu et al. 2015).

A well-known filovirus, Ebola virus, is responsible for severe hemorrhagic fever in humans, high fatality rates, and fast transmission across the communities in Africa (Voigt and Kingston 2015). Negative-strand RNA viruses with no segments are known as filoviruses. These viruses are filamentous, enclosed particles of varying lengths (Filo, from the Latin *filum* meaning thread). The filovirus genomes generally measure 19 kb in size (Olival and Hayman 2014). Another study has connected filoviruses to the ecology of bats. Anti-EBOV antibodies and EBOV RNA were found in various fruit bat species; and it was discovered that the Ebola virus disease is spread from bats to people through direct contact or through bat feces (Fiorillo et al. 2018).

11. BIOCHEMICAL PATHWAY OF VIRUS TRANSMISSION

The only mammals capable of power-driven flight are Bats, which makes Bats able to migrate across a wider area than other land mammals (Durai et al. 2015). It is important to note that Mammals belong to the second largest category, including bats, which are found all over the world. The phylogenetic study divided bats into two significant suborders, the Yinpterochiroptera, including five Rhinolophoidea (micro-bat) families and one Pteropodidae (mega-bat) and the Yangochiroptera, which had a total of thirteen (micro-bat) families (Durai et al. 2015). Also, the capacity of bats to migrate has importance in disease transmission, and it is suggested that flying provides a selective pressure for cohabitation with viruses. This theory is supported by the fact that a few extremely dangerous human illnesses have been associated with bats. Bat filoviruses (Marburg virus, mental virus, and ebola virus), henipa viruses (hendra virus and nipah virus), lyssaviruses (rabies virus) and CoVs (SADS-CoV, SARS -CoV, and MERS -CoV), among others that have been thoroughly described, represent a danger to human health (Durai et al. 2015). A thorough examination of the interactions between mammalian hosts and viruses revealed that Bats are substantially more likely than other mammalian orders to contain animal disease viruses. Because the hosts cells' translational and transcriptional patterns, cytoskeleton, cell cycle, and apoptotic pathways change as a result of infection with several corona viruses (CoVs). For the same reason inflammation, stress and altered immunological responses, and altered pathways of coagulation may also be brought on by CoV infection. The balance between the genes that are up-and down-regulated may be the key to understanding how these viruses induce disease. Unquestionably by putting part of viral proteins in the nucleus of the host cell, Corona Virus (CoV) may be able to regulate the cell machinery during the cytoplasmic replication of its genome in a microenvironment protected by a membrane. Both cap-dependent and cap-independent processes are used by CoVs to start the translation (Isakbaeva et al. 2004). When a negative strand of sub-genomic mRNA is extended during CoV transcription, discontinuous RNA synthesis (template switching) takes place. The RNA chaperone activity of CoV proteins may aid in the initiation of template switching. Proteins from both cells and viruses are needed for transcription and replication (Isakbaeva et al. 2004).

A better understanding of the biochemical pathway of virus transmission, replication and possible outcomes of viral infection, have been described by the most recent virus outbreak in the world i.e., Corona Virus transmission. The coronavirus (CoV) causes significant morphological and metabolic alterations in infected cells. Virus enters a host cell by attaching to its receptors present on the surface of cell, and made some conformational changes in the vial protein. Non-enveloped viruses enter through penetration and enveloped virus enter by fusing with cell membrane or by endocytosis. This process is completed by injecting viral DNA into the host cell. Once DNA is in the host cell it will start multiplying. In the same way recognition of the 5' and 3' ends of the RNA genome by cellular and viral proteins may be necessary for CoV transcription and replication. Like positive-strand RNA viruses, in CoV genome replication is also carried out by the production of negative-strand RNA, it serves as a template for the production of new viral genomes (Isakbaeva et al. 2004). According to mapping experiments using MHV (Major Histocompatibility Virus) defective-interfering (DI) RNAs, replication of DI RNA requires 470 nucleotides from the 5' end and 436 nucleotides from the 3' end. Additionally, positive-strand synthesis requires both ends of the genome, whereas the synthesis of the negative-strand needs the final fifty-five nucleotides from the 3' end and the poly(A) tail. Hence, the replication signal at the 3' end of the genome interacts with replication signals at the 5' end to exert the influence on the synthesis of RNA since it is the final area of the genome that the viral polymerase reaches during the synthesis of positive-strand RNA. This knowledge has led to the hypothesis that during RNA replication, the genome's 5' and 3' ends interact (Wiersinga and Rhodes 2020). Normally when viral proteins replication process in a host cell is completed, it releases its newly synthesized molecules called

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virions to start infection in extracellular adjacent cells and slowly whole host body is infected and when most of the host's body cells get infected it starts showing symptoms through which one can try to identify the cause of illness (Wiersinga and Rhodes 2020). Fig. 1 shows the bat viral symphony and the replication in flight.

12. CROSS-SPECIES TRANSMISSION OF BAT PATHOGEN

Cross-species transmission, also known as interspecific transmission, host jump, or spillover the spread of a transmissible pathogens, such as by means of a virus, across masses that belong to different species.

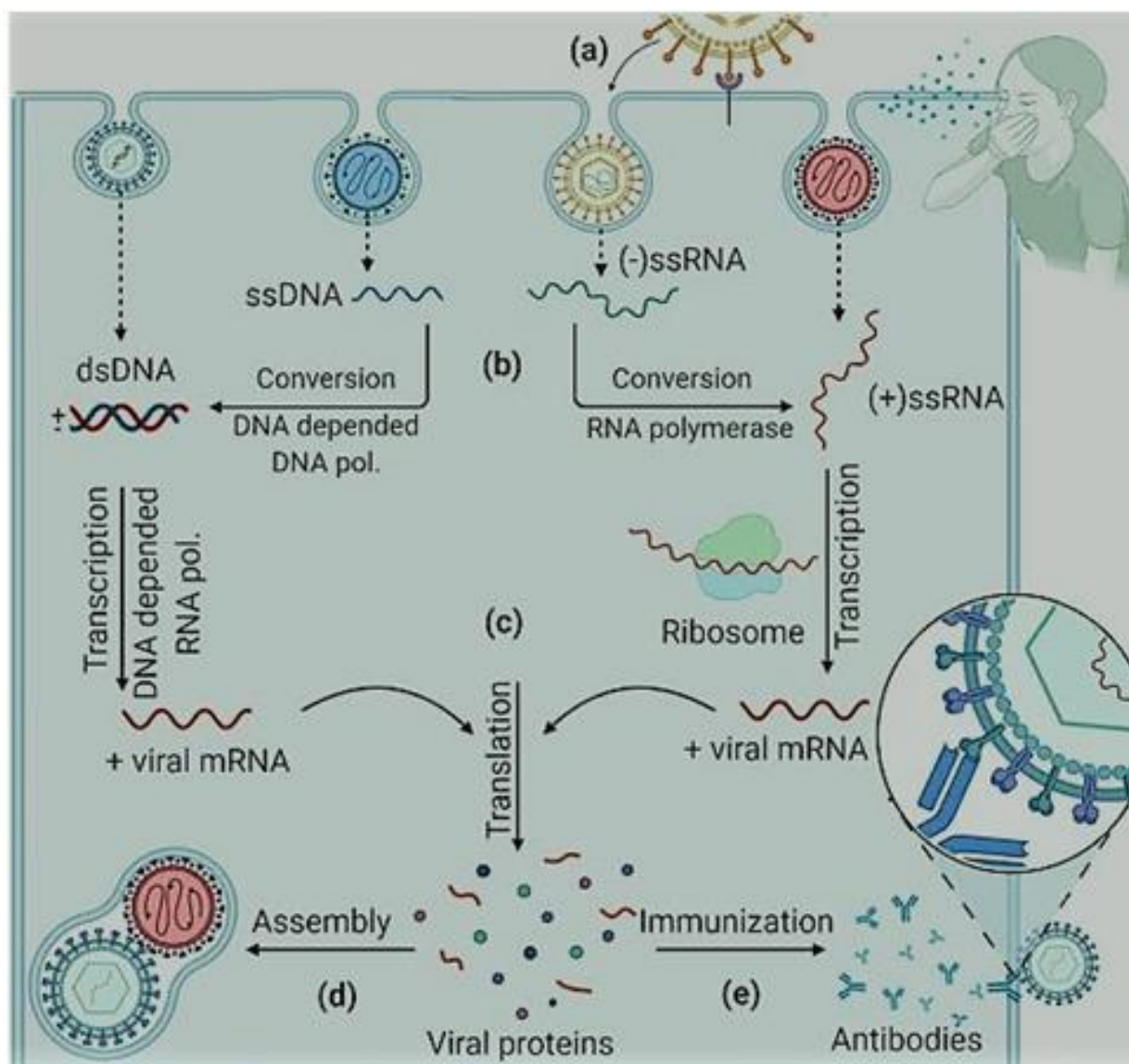


Fig. 1: Bat Viral Symphony: Replication in Flight

In fact, the bacterium may get indisposed in the new host once it has been introduced, or it may develop the capability to infect people of the same kind, permitting it to proliferate throughout the new

population. Although the peculiarities are typically focused on virology, cross-species spread can occur with bacteria or other types of viruses. Contact between the bacterium and the congregation and the operative infection of an underlying specific host, which may result in augmentation, are steps involved in transferring microorganisms to new multitudes equally. Contact between the bacteria and the host, as well as the primary infection of an underlying specific host, which may result in replication, are both processes in transferring microorganisms to other populations (Faria et al. 2013).

Clearly though stages involved in the transmission of microbes to new hosts include direct interaction between the virus and the host, effective contamination of original specific host, which may cause development of an epidemic, as well as microbe's variation within the first or original host, that may give the capability for effectively dispersion among populations of the new host as well as microbial diversity within the initial or original host, which may allow for effective dissemination among subsequent host populations (Allocati et al. 2016).

Because of the similarity of the hosts' immunologic defenses, the degree of evolutionary link across classes influences the likelihood that a microbe will be disseminated among them. The bulk of human zoonotic transmissions, for example, come from numerous warm-blooded animals., although some distantly related forms of microbes, such as plant diseases, may not be capable of contaminating humans in any way. Other factors that influence spread rates include topographical proximity and intraspecies behavior. Hence the risk of viral overflow is expected to rise as land use expands due to environmental changes and topographical challenges (Brierley et al. 2016).

When a disease that is typically present in bats is spread to another species, such as humans or other animals, it is referred to as the cross-species spread of bat infections. Ebola virus, SARS-CoV-2, and Nipah virus are a few bat-borne viruses that have been spread to people. To stop epidemics in the future and safeguard the public's health, it is crucial to research and comprehend these kinds of transmissions. Bats can carry various viruses and infections, making them a natural host for such pathogens. When bats and other animals come into close contact, bats may spread infections to other species, including humans. This happens because of their proximity. As human populations expand and encroach on bat habitats, the likelihood of human-bat interactions increase, there are more opportunities for bats and people to come into contact, which can result in the spread of viruses carried by bats (Brook and Dobson 2015).

Indeed, intermediate host is one of the important means in spreading viruses other than direct contact. In rare instances, the pathogen could be able to directly infect people or other animals without the aid of a host in between. Once the pathogen has been transferred to a new host, it could be able to adapt and reproduce there, which could result in sickness or illness (Chan et al. 2013).

Usually when a pathogen is transferred to a new host, it can adapt and multiply there, causing disease. Researching and understanding infectious diseases is critical for stopping future epidemics and protecting public health. By understanding how viruses jump from animals to humans, scientists can identify potential hotspots and high-risk species, allowing for targeted surveillance and early detection of emerging diseases. Additionally, studying these transmissions can help in the development of vaccines and treatments to mitigate the impact of future outbreaks. (Brook and Dobson 2015).

13. ECOLOGICAL AND PHYSIOLOGICAL PERSPECTIVE ON BATS AS RESERVOIR OF VIRUS

The Bats (Chiroptera), serving as ingrained reservoir hosts of different types of virus species, including scores of eminent zoonosis, have undergone a dramatic transformation to accommodate an extensive variety of viruses as their hosts. On the other hand, this flying mammal suggests the confluent attributes which can be concept to be the end result of powerful restraints on natural choice imposed by means of the demands of powered flight, which include scaled-down body length, intensified metabolic rate and

antioxidant potential, improved lifespan, and a few atypical immunological capabilities as compared to different non-flying mammals (Brook and Dobson 2015).

Because, bat, the only mammal adept at flying, hold significant importance in viral spillovers due to their ability to fly long distances, allowing the transmission of infamous viruses and their divergent forms among humans and other animals. The elevated body temperature and metabolic rate alongside flight expedite the stimulation of the immune system of bats on the basis of a biological clock. Thus, ultimately the descriptive factor for the evolution of viral infections in bats without the production of overt clinical signs of illness could be flight. During the flying activity, the physiological temperature of the bat's body rises above 40°C, inducing a febrile body response that stimulates interferon production, helper T-cell mobilization, agitation, participation in cytotoxic activities, and other immune responses. When any virus challenges a bat, the 15-16 folds proportional increase in its metabolic rate during flight may augment a fundamental price of soaring metabolic rate in order to activate an immune response (Calisher et al. 2006). Due to these recurrent properties, increased body temperature, and metabolism corroborate viruses to survive and resist the innate immune response inside the bat's body. Table 1 highlights the body temperature of various bat species during flight.

Table 1: Body temperature of various bat species during flight

Bat species	Body temperature during flight(°C)
<i>Miniopterus sp.</i>	41.1 ± 0.45
<i>Myotis yumanensis</i>	40.0-40.8
<i>Carollia perspicillata</i>	40.2 ± 0.8
<i>Hypsignathus monstrosus</i>	37.2-40.0
<i>Eptesicus fuscus</i>	41.3 ± 2.1
<i>Mops condylurus</i>	40.5 ± 1.1

Interestingly, Bats produce echolocation by sending forth high-frequency sound pulses and listening to the resulting echo. An aftermath of this echolocation activity is the diffusion of saliva, mucus, or oropharyngeal fluids in the environment, allowing the dispersion of viruses that replicate in the buccal cavity or airways of other vertebrates and mammals. Also, Hibernation is a period of extended deep sleep or dormancy that allows bats to survive the cold winter with less energy and food. So, Bats lower their body temperature and metabolic rate during hibernation from November to mid-May but may wake up briefly for foraging. Resultantly, this perspective leads to molecular co-adaptations in viruses, favoring the co-existence of viruses in their Bat hosts for a very long duration. As far as Bats habitats are concerned, roosts are sites for mating, hibernating, and rearing young; they promote social interactions and offer protection from adverse weather and predators. Living in closer proximity plays a significant role in increasing viral diversification. The co-roosting grounds may encompass the Bat species that don't usually come in physical contact with each other outside the roosts, encouraging the dissemination and sustenance of different viruses in different species and making possible the host-virus shift (Field et al. 2004).

Most importantly an anthropogenic environment of Bats refers to the human-modified habitats and landscapes that Bats encounter and use. These factors influence bat distribution, abundance, diversity, and physiology. Usually Bats live in a densely population manner, making it easy for viruses to spill over into other mammals. The mostly documented lifetime of bats is nearly three and a half folds longer than any non-flying placental mammal with a homogenous body size. For this reason, the longer life span of Bats and the possibility of developing persistent viral infections without showing overt signs helps the maintenance and transmission of viruses in other vertebrates. Meanwhile the intense oxidative stress at the mitochondrial respiratory chain level produced during flight and high-

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performance DNA repair helps the Chiroptera to evade viral infections effectively (Calisher et al. 2006). Fig. 2 shows the flight-Induced oxidative stress and robust DNA repair which are the key to Chiroptera's viral resilience.

As a rule, the Bat's immune system tolerates viral invasion for several months without developing clinical signs. Species of Bats showing longer periods of immunity have more chances of being seropositive to viruses. While the evolution of flight in Bats produces a unique set of antiviral immune responses, controlling the virus propagation and limiting reckless inflammatory responses in its body. On the whole, an antiviral immune pathway known as the "STING-interferon pathway" is waived off in the bat's body, maintaining enough immunity against viral infections without triggering a heightened immune response (O'Shea et al. 2014).

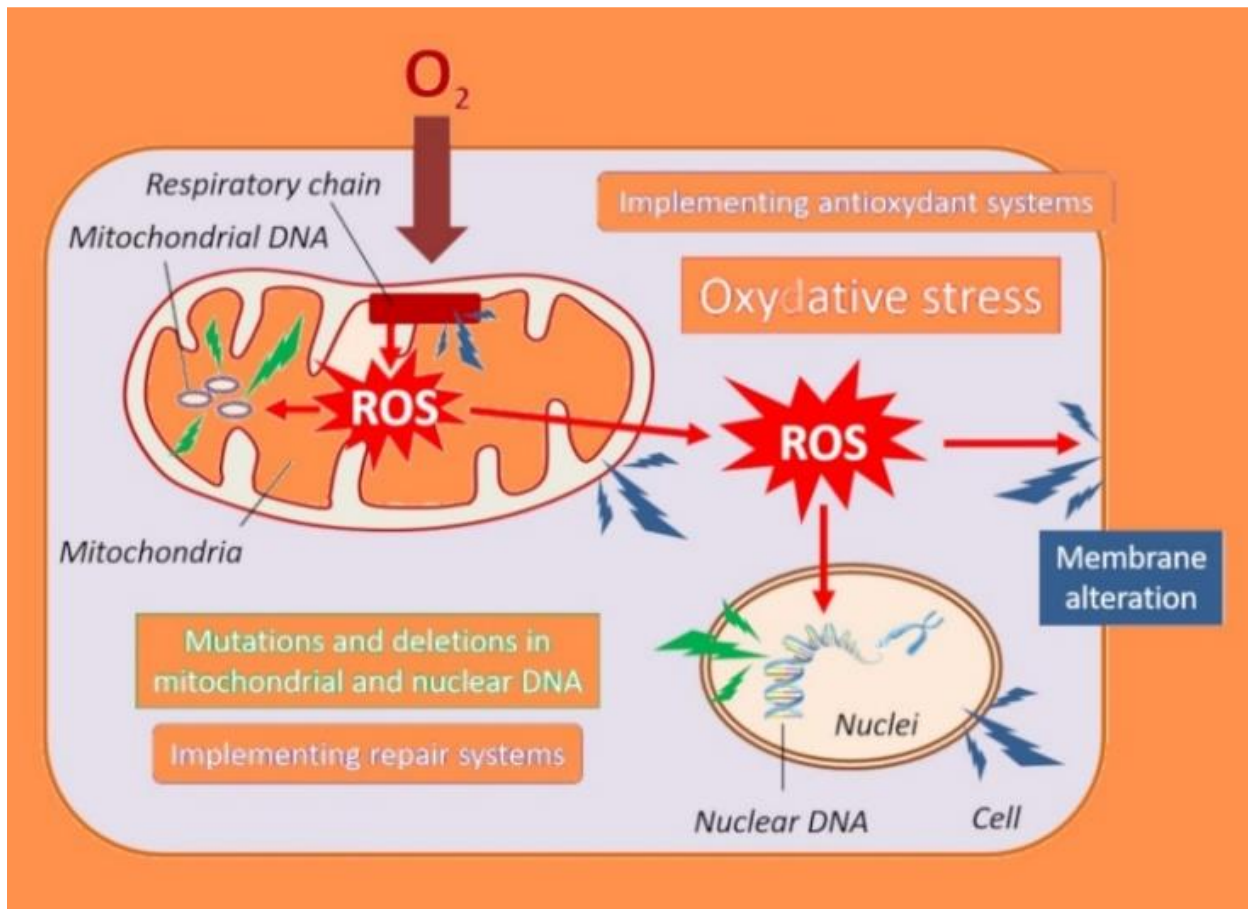


Fig. 2: Flight-Induced Oxidative Stress and Robust DNA Repair: The Key to Chiroptera's Viral Resilience

14. CONCLUSION

Bats are likely progenitors of the majority of zoonotic organisms. This is the result of their extraordinary physiology, behavior, and close relationship with humans and various creatures. As, bats are notorious vectors of zoonotic diseases that carry pandemics such as SARS, MERS, and the novel coronavirus. These pandemics have changed the global pattern of disease spread. Meanwhile the use of bat meat and the use of bat guano as excrement (feces) have also been implicated in the transmission of these infections.

Provided that, every possible precaution should be taken to prevent the transmission of these contaminations to humans and animals. Furthermore, it is also very important to take measures to prevent the spread of these infections to both humans and other organisms.

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