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## BAT TRANSMITTED VIRAL ZOOSES: AN ENIGMA TO BE RESOLVED

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### ABSTRACT

Bats, an ancient and diverse group of ecologically important mammals have recently attracted more attention as an important reservoir for several lethal zoonotic viral infections of humans and animals. Although they provide essential beneficial ecological services such as eating vast quantities of disease-carrying insects like mosquitoes and pollinating economically important plants, they have been maligned for harbouring numerous zoonotic viruses. An accurate knowledge of pathogen, host and disease dynamics, mechanisms of pathogen persistence and ecological factors underlying the disease emergence and reasons and timing of spill over to humans would help in forecasting the occurrence of such diseases and formulating possible preventive and mitigation strategies. In this article, we look at a few zoonotic disease epidemics that are thought to have originated from bats. Factors that permitted these viruses to “jump” the species barrier from bats to other animals, as well as a specific adaptation

in bats that may allow them to harbour these viruses without causing serious illness in them were also speculated.

**Keywords:** Bats, Chiroptera, Emerging epidemics, Viral zoonoses, Virus

### INTRODUCTION

Bats, the only known mammals capable of flying forms the second largest order of mammals, with around 1301–1331 species (Simmons, 2005) and outnumbered only by rodents (Teeling *et al.*, 2005). Nonetheless, they account for roughly one-fifth (20 per cent) of all mammals with new species being continually described. They could be found all over the planet, with the exception of a few remote oceanic islands like Tahiti and the polar areas, however they do breed inside the Arctic Circle (Rydell, 1989).

Taxonomically, bats are classified as part of the order *Chiroptera* (Greek: *cheir*-hand; *pteron*-wing) and, as the name implies, have morphological and physiological adaptations for

powered flight. The order *Chiroptera* is further subdivided into two suborders: *Megachiroptera* (Megabats), which includes a single *Pteropodidae* family (42 genera, 166 species), and *Microchiroptera* (Microbats), which includes 16 *Chiroptera* bat families (135 genera, 759 species). Megabats primarily consume fruits, whilst microbats primarily consume insects, with some also consuming birds, lizards, frogs, fish, or blood (vampire bat) (Aguirre *et al.*, 2003 and Patterson *et al.*, 2003).

Regardless of whether they are depicted as a negative emblem, bats serve as the keystone species on which other wildlife and flora rely heavily for fertilisation, pollination, seed dispersal, and pest population control. They pollinate a wide range of economically important flowering plant species as well as commercial crops (Whittaker *et al.*, 1992 and Kelm *et al.*, 2008). They keep an eye out for pests and insects (Leelapaibul *et al.*, 2005 and Kalka *et al.*, 2008). A single bat can swallow enough insects equal to its body weight. Since the excreta and excrement are high in nutrients, bat excreta (guano) are being used as a natural fertiliser. They are also used in traditional medicine (Walker, 2005 and Ashwell and Walston, 2008). Indeed, they are regarded as the keystone species on which many other species rely for existence. As a result, it would be an

impractical proposition to eliminate them from the ecosystem as it might result in the collapse of the entire ecosystem for want of essential linkages that supports the sustenance of the systems.

The problem of zoonosis probably commences when humans destroy bat habitats or as a result of undue interference in their dwelling place. As the bat roosts in large colonies, these viruses are likely to be transmitted from one bat to another. When bats move from one fruit to another, they may leave their secretions through saliva, urine and faeces. Consumption of bat meats or fruits that carries heavy viral load contaminated by secretions and excretions of bats or accidental contact through some intermediate animals or human beings, may result in disease transmission and spill over ((Zohdy *et al.*, 2019).

Bats have long been established as reservoir hosts and vectors for rabies and associated with lyssaviruses in humans and animals (Streicker *et al.*, 2010). Bats have become a focus of attention as possible reservoirs of several emerging pathogens, including SARS-like viruses (Li *et al.*, 2005) Hendra virus (Halpin *et al.*, 2000), Ebola virus (Leroy *et al.*, 2005), Marburg virus (Towner *et al.*, 2007), Nipah virus (Reynes *et al.*, 2005) and most likely the newly arrived global pandemic, the 2019 novel coronavirus (Lu *et al.*, 2020).

Currently there are almost 200 different types of genetically diverse viruses that have been hosted by bats over several decades (Moratelli and Calisher, 2015). Bats host more zoonotic viruses per species than do rodents and most of the resulting zoonoses have high profile spillover incidents of extreme human pathogenicity (Dobson, 2005). The ecological drivers of pathogen spillover and the emergence of novel hosts, including humans, is the result of interplay between numerous complex processes. Knowing the host ecology and the human-animal interface elements are significant in identifying the pathogenic spillover events (Haymann *et al.*, 2013).

### **Uniqueness of bats in relation to infectious diseases**

Bats are diverse, abundant mammalian species that have co-evolved with humans and serve as a reservoir to numerous infectious agents, mostly viruses. They function as intact reservoirs, with the diseased animals displaying only minor signs of illness. However, they occasionally breach the frontier, resulting in new, far more vulnerable viral infections in humans and other species, ultimately leading to dreadful zoonotic outbreaks (Gupta *et al.*, 2021).

Bats, the only flying mammal, have various other characteristics that set

them apart from other mammals, including a long lifespan relative to body size, a low incidence of carcinogenesis, and an amazing ability to host viruses without causing clinical disease (Irwing *et al.*, 2021). In this section, we address the processes that support host defence system of bats and immunological tolerance, as well as the implications for human health and disease.

The capacity of bats to harbour a wide range of viruses, including the most recent coronaviruses (SARS-CoV-2 viruses), may be due to their ability to effectively manage host responses to infection. Bats can escape severe immunological pathology in response to most viral infections due to ecological conditions, biological features, or their underlying unique immune systems. The immune system of bats is unique, which makes them perfect virus incubators. Bats are the only gifted mammal that can fly. This gift has provided them with an additional distinct edge in the form of a stronger immune system. Flying is a strenuous exercise that generates a lot of heat. This can result in an accumulation of free radicals, a reactive chemical that can damage tissue. To keep this reactive waste from injuring bat tissues, sophisticated defensive mechanisms have been created. This also aids the bat's defence against lethal illnesses and disorders. During a virus

attack, bats create a chemical called alpha interferon, which stimulates other cells to boost up their defences. To circumvent this defence, the virus begins to replicate rapidly and is highly transmissible. As a result, even if a virus reaches a bat, it is likely to trigger a hyperactive immune response (Olival *et al.*, 2012).

Although these viruses can be tolerated by bats, they can be fatal to other mammals such as humans and other domesticated species. Humans, unlike bats, do not have a quick immune response, and the virus load becomes lethal. Furthermore, a virus that has been exposed to bats' superior hypervirulent immunological response has little to do with entering and surviving in considerably weaker immune system of humans. In humans, the virus finally infects the cell machinery and begins to multiply instantly, resulting in human infection and mortality (Olival *et al.*, 2012). Any stress that disrupts bats' natural ecology causes them to shed even more viruses in their saliva, urine, faeces, and so on, culminating in emergence of novel zoonotic infections.

## **DISEASE OUTBREAKS LINKED TO BATS**

Bats as human virus reservoirs were recognized as early as the 1920s when rabies was detected in bats in South and Central America (Sulkin and Allen,

1974), but bats were not well known as carriers of emerging zoonotic viruses until the mid-1990s. The number of bat viruses identified, rapidly expanded following the detection of henipavirus and severe acute respiratory Syndrome Coronavirus (SARS-CoV). The following are some of the important diseases linked to bats.

### **(a) Marburg hemorrhagic fever**

The first outbreak of Marburg virus in African green monkeys during 1967, were suspected to have encountered from fruit bats on the shores of Lake Victoria before shipment from Uganda (Smith *et al.*, 1982). Furthermore, the genetic analysis demonstrated that the Marburg virus isolated from the infected mine workers was highly similar to those circulating in the *Rousettus aegyptiacus* (Egyptian bats) population.

### **(b) Ebola hemorrhagic Fever**

The fruit bats of the *Pteropodidae* family, maintains the deadly viral haemorrhagic fever in the enzootic cycle from which the infection spreads to primates. Primates become seriously ill due to viral infection, and close proximity to these primates can serve as a source of infection for humans. The virus can then cause major deaths and fatalities in humans and is associated with human-to-human transmission. During 2014-2016,

the largest global epidemic of Ebola virus occurred in West African countries, which later spread to the central part of African range of ecosystems all over the globe.

**(c) Severe acute respiratory syndrome coronavirus (SARS-CoV)**

Severe acute respiratory syndrome coronavirus emerged in late 2002 and represents the first public health emergency of 21st century (Berger *et al.*, 2004). As early as 2003, 8422 people had been diagnosed in 30 countries with 916 deaths and a fatality rate of 11 per cent (WHO, 2003). Palm civets have been found to be infected with SARS virus in live animal markets and restaurants in Guangdong province in southern China. Civets are possibly the host for amplification and/or adaptation. Later on, Wang *et al.* (2006) identified several horseshoe bat species (*Rhinolophus* sp.) as the reservoir host for a large number of viruses that have a close genetic relationship with the SARS CoV.

**(d) Middle East respiratory syndrome coronavirus (MERS-CoV)**

Since the first recorded outbreak in 2012, the MERS-CoV has posed a significant public health threat. Most of the diseases have arisen in the Middle Eastern countries of the Arabian Peninsula. It was assumed, on the basis of phylogenetic research, that MERS, like many other

coronaviruses, originated in bats (De Benedictis *et al.*, 2014).

**(e) Nipah virus**

The past two decades have reported regular outbreaks of Nipah virus with a mortality rate of up to 70 per cent in both humans and animals across different parts of the world. The bats of genus *Pteropus* have been identified as the natural reservoirs of infection, with the proximity to bats being regarded as one of the important reasons behind the emergence of Nipah Virus (Ochani *et al.*, 2019).

**(f) Other bat-borne viruses**

In addition to major bat-borne zoonotic viruses, a significant number of previously unknown viruses with significant zoonotic potential have been discovered in recent decades (e.g., Menangle virus in Australia and the related Tioman and Melaka viruses in Malaysia, and other related bat reoviruses) (Kohl *et al.*, 2012). Moratelli and Callisher (2015) have identified about 27 different virus families that have been linked directly or indirectly to bats, the most important of which are the Hantavirus, Hepadnavirus, Flavivirus and Henipavirus. The potential for public health risks to these viruses has yet to be unraveled. Therefore, it would be wise to keep a close surveillance on their possible spillover.

**(g) 2019 novel Coronavirus**

The phylogenetic analysis of the ongoing global pandemic, 2019-nCoV which has claimed around 5,027, 183 lives all over the world (WHO, 2021) till date (November 5, 2021) by Lu *et al.* (2020) suggests that this virus is a sufficiently divergent new human-infecting beta coronavirus and probably bats might be the original host for this virus facilitating the emergence of the virus in humans.

**PREVENTION AND CONTROL OF BAT BORNE ZONOSIS**

Though the complete elimination of the human and bat interaction is impossible, it is probable to manage how these encounters occur (Stone, 2011). The abundance and widespread distribution of bats makes the prevention and control of bat borne diseases complex. Epidemiological investigation of zoonotic diseases reported to be associated with bats is based on effective monitoring and surveillance of the free range of bats (Dhaka and Vijay, 2018). This could be accomplished by observational field study and behavioural study involving population dynamics of bats followed by morphological identification and sequence analysis. Spatial and temporal sero-epidemiological and molecular investigations may be conducted in bats and in susceptible domestic animals to detect antibodies to important emerging

zoonotic pathogens, based on which the epidemiologists would be able to best predict the factors that determine the dynamics of zoonotic infections.

Like any other emerging disease, bat-borne zoonoses also exist in a finely balanced host-pathogen interaction among wildlife, domestic animals and human populations. Therefore, any changes in the environment or host behaviour provides the pathogen an effective bridge to spill over from the natural host to a susceptible host and spread more easily between them (Morens *et al.*, 2004). In Southeast Asia, anthropogenic hazards such as deforestation, urbanisation and hunting for consumption or crop protection have been recognized as serious threats (Mickleburgh *et al.*, 1992). This frequently puts the bat population under stress, modifies the foraging, roosting, and behavioural patterns, widens the ecological niche, and brings them closer to livestock and humans. Therefore, minimizing direct or indirect contact with the natural host, improving biosecurity measures and rapid disease detection and diagnosis is of paramount importance for the prevention and control of the disease as well as its spill over to animals and man.

Bat-borne zoonoses could be prevented to some extent by promoting a sustainable land use pattern, avoiding the



encroachment of human and domestic animals to the potential risk areas of the reservoirs (Haymann *et al.*, 2013) and avoidance of risky behaviours such as handling of wild bat or keeping bats as pets. Contact exclusion with bats in humans can be achieved through multidisciplinary orientation programmes and public health awareness programmes to raise awareness on the need to avoid bat hunting and use of safe techniques along with personal protective equipments (PPE) in cases of emergency (Jong *et al.*, 2011). Early detection and rapid response are the key strategies to contain many of these outbreaks. Prompt surveillance, early detection, emergency preparedness and rapid response are the key strategies to contain many of these outbreaks. Vaccination of susceptible population, particularly the veterinarians, cavers, bat ecologists and other laboratory workers who work with bats can be considered as an effective strategy for the prevention and control, especially in the case of Lyssa viral infections. But it is pertinent to note that the use of vaccines may not be a viable solution in these cases. Hence, the strategical prevention and control measures ideally centers around devising techniques and methodologies to minimise the contact between susceptible population and the source of infection.

## SUMMARY

Despite their positive role in ecosystem, bats have also been incriminated for the emergence of numerous deadly zoonotic viruses, which alienates us from them. Being a ubiquitous species with varying levels of adaptive responses, the complete elimination of the human and bat interaction is unavoidable. Thus, enhanced surveillance and monitoring of bat population dynamics and possible human interactions at the regional, national and international levels through collaboration between different sectors involving health workers, veterinarians, forest officials and ecologists are of paramount importance. This helps in making crucial decisions to effectively combat and mitigate the emergence and spillover of a number of zoonotic pathogens as envisaged in the “One Health, One Welfare” policy.

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