

# Ebola Virus Ecology

Renuka Jyothi. S

Assistant professor, Department of Life Science,  
School of Sciences, B-II, Jain (Deemed to be University), JC Road, Bangalore-560027  
Email Id: j.renuka@jainuniversity.ac.in

**ABSTRACT:** *Ebola virus has made considerable improvement in knowledge of molecular biology and pathogenesis of Ebola since it was first identified more than 30 years ago. Nevertheless, while attempts are made to react to these concerns, the forms in which Ebola virus is maintained and spread in nature remain unknown. Recent research has shown that bats that play a function as a reservoir, but it is not known if other animals are still involved or the manner in which they are transferred to humans or apes. There have been two contradictory theories on Ebola: one regarding local long-lasting survival in a mysterious, barely reached source and another about recent virus emergence and lateral dissemination by susceptible citizens. Nonetheless it is desperately required to obtain a clearer understanding of Ebola's nature ecology, owing to the growing occurrence of outbreaks of human filoviruses and the enormity of the epidemic in already vulnerable broad ape communities.*

**KEYWORDS-** *Bats, Ebola virus, Filo virus, RNA*

## INTRODUCTION

To date, four Ebola virus (EBOV), three of which coexist in the African co-circulation, have been described: Zaire (ZEBOV), Sudan (SEBOV) and Ivory Coast (ICEBOV). Among such animals, the viral haemorrhagic fever (VHF) inducing viral fatality risk among up to 90%, for which no licensed therapeutics or vaccinations is currently available, has become extremely pathogenic to both human and non-human primates[1]. In tandem with other relative non-specific early symptoms, patients grow a temperature of  $> 38.5$  8C rapidly after 4-10 days of incubation. Such a rash develops in the neck and the shoulders of 50 percent of patients, which and the majority of patients show some signs of impaired coagulation; Significant bleeding, however, is uncommon, primarily limited to the GMT. In severe circumstances there is a death of multi-organ collapse and shock 6 to 16 days after initiation of symptom. The identification is often overlooked early in the development of the illness because of the similarity with other diseases in these areas. Case events are also identified even when anti-malarial and/or antibiotic therapy is not treated and also even when such diseases are impacted by health care professionals[2], [3]. Filovirus outbreaks from infectious areas of Africa have steadily occurred in recent years, and EBOV has become a worldwide public health issue alongside their potential to reach non-endemic countries through foreign travel and their potential to use them as a biosphere. In addition to the relevance of EBOV infection to human wellbeing, the tremendous impact on already endangered large ape communities were recently discovered and attempts to consider EBOV ecology in nature revived[4], [5]. Here, in specific when it applies to transmissions of EBOV in nature, this paper look at the two theories to clarify the mechanism of outbreaks of EBOV and the latest discovery of a probable reservoir[6], [7].

### 1. Epidemiology:

Seventeen haemorrhagic epidemiologic epidemiology (EHF), all within 108 of the equator, have occurred in Africa since it was identified in 1976. Despite the first recorded outbreaks in the Democratic Republic (DRC) and Sudan respectively in 1976, only a single case of retrospective evaluation (DRC 1977) and a minor epidemic (Sudan 1979) were registered for a sustained time. Numerous outbreaks were recorded in the years from 1994 to 1997 and again from 2000 to 2005. Interestingly, with the exception of the two outbreaks in 1976 and 1995 in DRC, all reported ZEBOV outbreaks seem to be associated with the region near the border of Gabon and the Republic of the Congo (RC), the latest of which took place in 2005 at Etoumbi and Mbomo in RC. By contrast, all SEBOV outbreaks reported to date have occurred either in Sudan or in neighbouring Uganda, and only two isolated human cases of ICEBOV have been reported in Ivory Coast and Liberia. A total of 1860 cases of EHF, resulting in 1296 deaths have been recorded to date. Different outbreaks of local chimpanzees and gorillas, contributing to catastrophic losses for communities, were recorded both in this Ivory Coast and more recent outbreaks in Gabon and RC.

## 2. *In Search of a Reservoir for Ebola Virus:*

Scientists have speculated for several years, that EBOV will survive or seldom exist in the resistant areas of a typical zoonotic reservoir. As a consequence of a serious disease close to that of person, apes lead to the infection of EBOV, these animals are not known to be a classic reservoir. Consequently, intense attempts were made to locate the natural reservoir after identification of EBOV in 1976 and again after 1994 on Ivory Coast, as well as the 1995 epidemic in the DRC. ZEBOV RNA is suggested in the CRR and proposed to be classified as reservoir habitats for mice, rats and shrews of the rodents (muridae and soricidae). While it may have an effect on human communities by near approximation of contaminated rodents and shrew organisms, as stated in the case of Lassa Virus, such findings were not confirmed by an alternate approach or certain study groups (e.g. serology, identification of antigens or isolation of the virus).

## 3. *The Case for Bats as the Reservoir:*

A new study of small vertebrates collected in Gabon / RC between the 2001 and 2003 ZEBOV outbreaks has confirmed that three fruit bats (*Hypsignathus monstrosus*, *Epomops franqueti* and *Myonycteris torquata*) had asymptomatic infections. ZEBOV RNA in some liver and spleen samples are observed in this research, while other animals identified EBOV-specific antibodies in a serum, which may suggest the recent infection and non-detectable immune responses of the earlier animal's community. Such results confirm early observations that suggest proliferation and dissemination of EBOV elevated titres in fruit and insectivorous bats that have been experimentally contaminated in the event of disease. The high headers seen in the experimental model pose concerns, however, as to why virus isolation from all of the naturally infected bat species has not been accomplished, especially as virus isolation for filoviruses from the clinical material is usually simple. One hypothesis was that in such naturally infected animals the viral titres might be very small (compatible with the requirement for the RT-PCR buried in the nucleic acid unique to ZEBOV), and that a particular physiologically or atmospheric stimulation might be required to induce infection with the virus. Bats have long been believed to play a possible function as a vector of filovirus infection based on the clear epidemiological association between infection and areas where bats are active. In addition, during 1998 outbreak in the Durba-Watsa area of the DRC, this link became especially evident for the Marburg Virus (MARV), when exposures to an abandoned gold mine had recorded frequent introductions over a span of almost 2 years. Although more laboratory and environmental work is also required, bat species may also appear to be a reservoir for ZEBOV and probably for other filoviruses. More recently, Leroy and colleagues supported a bat reservoir further by showing the existence in the outbreak of epidemic and non-epidemic regions of ZEBOV-specific IgG anticuerpos in five percent of the same three species (*H. monstrosus*, *E. franqueti* and *M. torquata*) which indicated that this virus was circulating in both areas. In comparison, the incidence in all areas since the epidemic decreased to 1%. In general, ZEBOV may also appear in all of Central Africa's wooded countries and could increase and decrease based on far-reaching unidentified movements. Possible causes of waxing and declining disease-related die-offs, decreased fertility in the species involved and/or declining prevalence of the antibodies attributable to fertility is suggested for bat community. While this finding could not be omitted as a consequence of the epizootic wave moving across each study area at that period, the lack of any signs of EBOV in South Gabon, which was situated in the non-epidemic control areas, renders this impossible. Ultimately, these findings often indicate that unrecognized outbreaks in other areas of central Africa that are not considered to be infected by EBOV may occur, summarizing the notion that human and animal mortality outbreaks might not necessarily be accurate measures of the virus existence throughout the area.

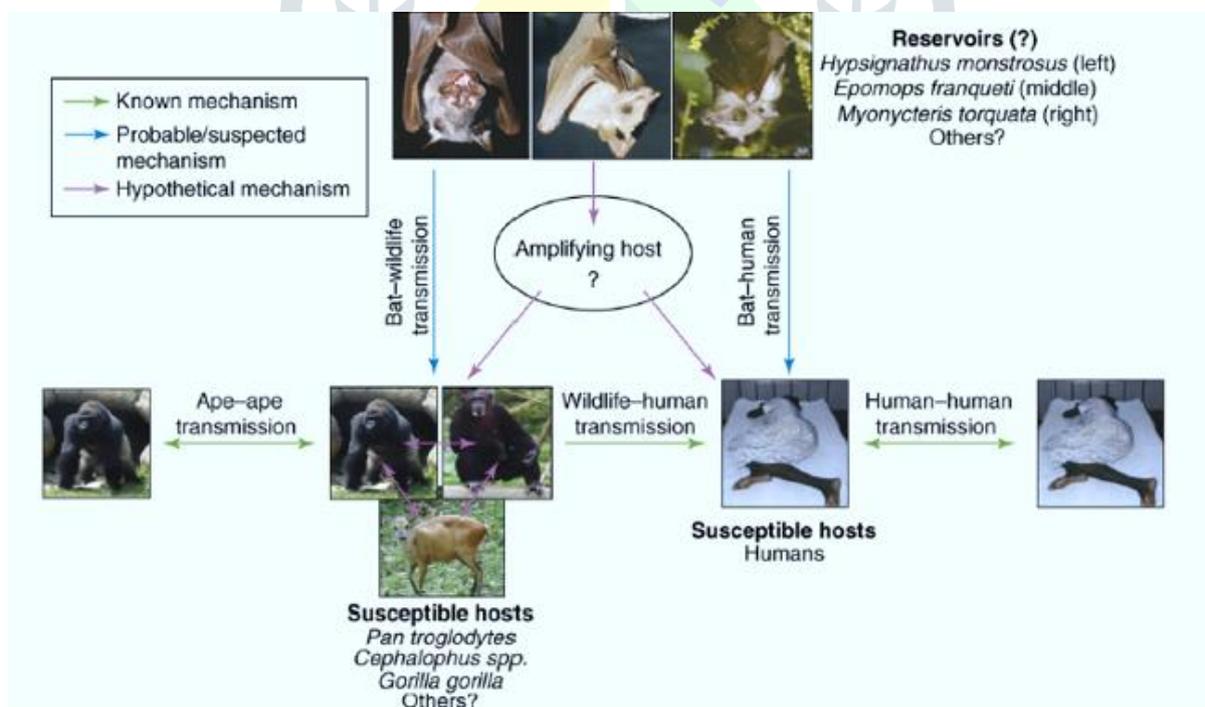
## 4. *The Search Continues:*

Although recent, exciting research on the position of bats in EBOV transmission, other reservoirs and/or possible amplifiers should also be taken into account. This has also been demonstrated by ecological modelling in view of the distinctive geographical areas inhabited by filoviruses. This analysis indicates that EBOV is confined to tropical rain forests in central and West Africa while the associated MARV exists in the drier regions in central and eastern Africa. This bioinformatics method demonstrates that African filoviruses have varying geogram ranges. Across the basis of this study, ZEBOV and ICEBOV were both expected to inhabit a region separate from SEBOV. This, inter alia, is the deeper association between ZEBOV and ICEBOV in which the SEBOV and Reston Ebolavirus (REBOV) come together in a different branch. That is important. This can also be confirmed by the fact that SEBOV human outbreaks have happened during rainy months, compared to ZEBOV and ICEBOV for which humans outbreaks are mostly correlated with diminishing or low precipitation times. Since such human outbreaks are always accompanied by an animal epidemic, recent animal morbidity and mortality tracking information has also been published Connected to the dry season ZEBOV outbreak in Gabon. The statistics from Bermejo et al. suggest that the ZEBOV epizootics in Lossi Sanctuary were found in June

between 2002 and 2003, which is the end of the wet season and the beginning of the dry season. This is compatible with the estimates from this article. Differences in the seasonality of the outbreaks of filoviruses could then indicate that these two ecologically distinct niches may require different reservoir ecosystems and/or dynamics of transmission. For the geographical conditions correlated with the outbreak sites identified for growing filovirus in the field of selection of the candidate reservoir species in-niche, such models are now being used. Interesting enough, many animal types, including a types already mentioned, E, as possible reservoirs are bats. Although further work would be required to show the validity of such forecasts, at least they offer a theoretical foundation for more study.

##### 5. Mechanism of Ebola Virus Transmission in Nature:

When humans are sick, it is apparent that subsequent transmission of EBOV is maintained independently, primarily because of direct interaction with the blood of victims, their secretions or tissues. While the source of the index case infection was not confirmed in many outbreaks, several have recorded interaction with animal species considered to be EBOV-susceptible (i.e. gorillas, chimpanzees and duikers). However, 14 of the 34 animal carcasses in an EHF research sample (10 gorillas, 3 chimpanzees and 1 duiker) showed favourable results on EBOV. What is unknown, though, is how Ebola is spread in the early stages to humans, non-human primate and /or some other vulnerable animal organisms. Despite the restricted field of filoviruses and the massive attempts in the last three decades to locate a storehouse, it would seem possible that wherever the storehouse, it is seldom identified, or transmitted under some circumstances or controlled by it. The bats have a part in promoting viral propagation and then in other responsive hosts in the form of a reservoir for EBOV, it would be necessary to analyse the function of seasonal, environmental or temporal physiological (e.g., pregnancy or other stress) influences. Increased mortality among fragile big apes, due to EBOV infection, is previously observed in the late rainy season and/or in the early dry season. Therefore, it was commonly believed that such seasonal shifts may contribute to closer contact between various animals as they compete during these periods for restricted food supply. The dry season, though, in general is a period of high fruit production in Gabon between November and February, indicating that enhanced contact between the organisms involved during food and/or altered dietary choice could even have a function in spill over during that period. More shifts in the immune system of reservoir bat plants have also been postulated to play a role in the dissemination of these cycles as a consequence of tension either due to food scarcity or due to dietary disparities and/or physiological changes such as pregnancy. Figure 1 is showing the mechanism of Ebola virus transmission in nature.



**Figure 1: Mechanism of Ebola Virus Transmission in Nature**

##### 6. Transmission Among Susceptible Hosts:

Currently there are two theories to understand filovirus transmission among sensitive hosts. The first suggests that the virus has been retained in endogenous areas of a reservoir host in other traditional viral zoonotic infections, and its episodic appearance is attributed to unusual interaction of the reservoir(s) with human or non-

human primates. Nevertheless, an additional dissemination method was suggested, whereby, more recently, the virus was introduced into susceptible communities and transmitted waves via an unknown reservoir host at each outbreak location. Walsh and colleagues were the first research to propose wavelike distribution of ZEBOV. Phylogenetic studies dependent on glycoprotein indicate, first, that all strains of ZEBOV are originated from the near relative of an initial strain in the year 1976 that was slightly north-west of the Yambuku area of the Democratic Republic of the Republic of DRC about 1973. Based on these results, ZEBOV outbreaks have been shown to be spreading either on the front of an advanced wave or in a sequence of hops into new areas. More recently, researcher verified this result by analysing the viral polymerase (L) gene partial sequences. They traced the ancestry of all ZEBOV samples identified as a consequence of cumulative mutations in recent years, and noticed that both human and bat virus samples from 2001 to 2003 might have originated as a result of a very low genetic bottleneck in 1999. Three theories were also suggested to clarify these observations. Next, in 1999, the infectious bat population was incredibly limited and the virus lines were confined to one or loosely related stream. Second, by 1999, other contaminated bats may have carried ZEBOV into the local bat community. The third hypothesis in contrast to the second was the introduction of ZEBOV to the bat colonies in Gabon, and in the RC at the same period as ZEBOV influenced other fauna and humans. Moreover, although these results suggest that ZEBOV has recently been transmitted to Gabon and the RC, they also illustrate the various mechanisms of dissemination that seem to underlie SEBOV's spread, which in the past 30 years has tended to trigger intermittent outbreaks in a limited geographical region, without any indications of outward spread.

### 7. *Identifying Risk Factors for Infection:*

Where there is knowledge, it has frequently been observed that filovirus index patients are typically persons whose work takes them into woods, caves and mines, particularly hunters who have been exposed to infected wildlife. Although the function of direct human bat infection in initiation of outbreaks remains uncertain, studies of human behaviour as a predictor for EBOV seropositivity in Cameroon have also related an increased risk for EBOV infection with bat ingestion and logging activity. Yet since certain index events have also had other sources (i.e. interaction with contaminated animal carcasses) leading to contamination, the magnitude of such behaviours is not apparent or whether geographical variations impact local risk factors. Numerous sero-epidemiological studies that indicate elevated rates of seroprevalence in many African countries where significant disease is missing confuses the interpretation of natural transmission. While this evidence has also been used to indicate that EBOV could be prevalent in several places around Africa, they can also imply a co-circulation of human antigenically cross-reactive yet non-pathogenic EBOVs, other associated disease pathogens and tolerance mechanisms currently not known of human beings given the widespread combination of EBOV infection with high fatality levels. Previous research (especially those before 1995), used serological detection methods that were prone to cross-reactivity, should therefore be verified in these populations by modern, more accurate methods until concrete conclusions can be made. EBOV infection in these populations.

## CONCLUSION

The successful trapping expeditions were not rendered without any hint of the existence of the EBOV natural reservoir owing to the species complexity found in these habitats, the remoteness of the areas concerned and the insufficient funds required for such ventures. This paper is already close to recognizing the biology of EBOV in nature with the latest discovery of successful reservoir candidates. The first compelling proof for a repository is that both nucleic acids and anticuerpos are found in many animals, while virus separation from such organisms is also a definitive indication of infection. This discovery is also compatible with a few historical findings that connect EBOV outbreaks with seasonal trends and cave and mining exploration. Nevertheless, it cannot be eliminated the chance of certain reservoirs or also amplification hosts. Therefore, it remains to be seen precisely how EBOV is preserved in nature. Apparently there are two examples, one in which the virus persists over a long period of time in the reservoir species and is episodically detected in regions with sufficient conditions, and a second in which the virus is only distributed recently across adjacent vulnerabilities. There is both genetic and epidemiological evidence, and thus the reality will anywhere between these two hypotheses be present. The final description of the organisms participating in the reservoir should help explain the function of each of these various transmitting methods. Over the long run, the increased understanding of filo virus ecology will bring strong promise for approaches for the prevention and treatment, and in the future, action through preparation, of filo virus outbreaks in human or animal populations. The goal now is to consider the contribution that different virus and host factors bring to the frequency of EBOV outbreaks, along with environmental and human and animal behaviour. In particular, laboratory trials to establish persistence and factors which promote viral replication in the reservoir and subsequent dissemination to other host species must be undertaken. More research

into the behavioural evolution of both possible reservoir and vulnerable animal hosts would also be desperately required for the safeguarding or future estimation of large ape populations.

#### REFERENCES

- [1] WHO, "Statement on Ebola in the Democratic Republic of the Congo," 2018.
- [2] P. T. J. Johnson, J. C. De Roode, and A. Fenton, "Why infectious disease research needs community ecology," *Science*. 2015, doi: 10.1126/science.1259504.
- [3] D. G. Bausch and L. Schwarz, "Outbreak of Ebola Virus Disease in Guinea: Where Ecology Meets Economy," *PLoS Neglected Tropical Diseases*. 2014, doi: 10.1371/journal.pntd.0003056.
- [4] P. Lawrence, N. Danet, O. Reynard, V. Volchkova, and V. Volchkov, "Human transmission of Ebola virus," *Current Opinion in Virology*. 2017, doi: 10.1016/j.coviro.2016.11.013.
- [5] J. C. Saiz, Á. Vázquez-Calvo, A. B. Blázquez, T. Merino-Ramos, E. Escribano-Romero, and M. A. Martín-Acebes, "Zika virus: The latest newcomer," *Frontiers in Microbiology*. 2016, doi: 10.3389/fmicb.2016.00496.
- [6] J. Emanuel, A. Marzi, and H. Feldmann, "Filoviruses: Ecology, Molecular Biology, and Evolution," in *Advances in Virus Research*, 2018.
- [7] A. Caron, M. Bourgarel, J. Cappelle, F. Liégeois, H. M. De Nys, and F. Roger, "Ebola virus maintenance: if not (Only) bats, what else?," *Viruses*, 2018, doi: 10.3390/v10100549.

