



Viral Diversity in African Mammals and its Role in the Wild Meat Supply Chain

Elysia Drakemore*

Department of Public Health, The University of British Columbia, Canada

INTRODUCTION

The wild meat trade in Africa has long been a significant aspect of local and regional economies, but it has also raised important concerns regarding public health and biodiversity. In recent years, increasing attention has been given to the potential for zoonotic diseases-those that jump from animals to humans-emerging from this trade. African mammals, many of which are hunted for bush meat, harbor a wide diversity of viruses, some of which have the potential to spill over into human populations, posing significant public health risks. A growing body of research has sought to investigate the viruses present in African mammals, focusing on those involved in the wild meat supply chain.

DESCRIPTION

The viruses detected in these animals range from well-known pathogens to more obscure or novel viruses, underscoring the risks associated with the trade in bush meat. Many of the mammals involved in the wild meat supply chain, such as primates, rodents, bats, and antelopes, serve as hosts for a broad range of viruses, including those belonging to families such as Filoviridae, Paramyxoviridae, and Flaviviridae, among others. These families include some of the most notorious pathogens in human history, such as the Ebola virus, which is transmitted by fruit bats and primates, and the Marburg virus, which also belongs to the Filoviridae family. Both of these viruses are associated with high mortality rates in humans and are of particular concern due to their potential for rapid spread in regions with limited healthcare infrastructure. Bats, in particular, are known to harbor a wide variety of viruses without necessarily being affected by them. These viruses include coronaviruses, filoviruses, and lyssaviruses, which are of great concern due to their ability to spill over into human

populations. The role of bats in transmitting these viruses to humans through direct contact, consumption, or exposure to bodily fluids such as saliva, urine, or feces, has been highlighted in numerous studies. Given the importance of bats in the African wild meat trade, especially in regions where they are hunted for food, there is a heightened risk of zoonotic disease transmission, particularly in rural communities where bush meat consumption is common. Rodents, which are widely hunted for bush meat in many African countries, also harbor a variety of viruses, many of which have the potential to infect humans. These include hantaviruses, which can cause severe respiratory disease, and arenaviruses, which are known to cause hemorrhagic fevers in humans. Though rodent-borne viruses are less often associated with outbreaks than those from primates or bats, their widespread presence in the wild meat supply chain further highlights the complexity of viral diversity in African mammals. Moreover, the hunting and processing of these animals in unregulated environments increases the risk of exposure to these viruses. The diversity of viruses detected in African mammals involved in the wild meat supply chain emphasizes the need for better surveillance and control measures to reduce the risk of zoonotic spillover. The detection of viruses in these animals does not necessarily imply that they will immediately cause an outbreak in humans, but it underscores the latent threat that exists due to the close interaction between humans and wildlife in the context of bush meat consumption. A better understanding of the viral diversity present in these animals is critical for predicting and preventing potential zoonotic disease outbreaks. Surveillance efforts need to focus not only on the animals themselves but also on the environments in which they are hunted, processed, and consumed. Strengthening regulations around the trade and consumption of bush meat, improving public health education, and enhancing disease monitoring systems are crucial steps in mitigating the risks associated with zoonotic viruses [1-4].

Received:	30-October-2024	Manuscript No:	IPJIDT-25-22117
Editor assigned:	01-November-2024	PreQC No:	IPJIDT-25-22117 (PQ)
Reviewed:	15-November-2024	QC No:	IPJIDT-25-22117
Revised:	20-November-2024	Manuscript No:	IPJIDT-25-22117 (R)
Published:	27-November-2024	DOI:	10.36648/2472-1093-10.11.110

Corresponding author Elysia Drakemore, Department of Public Health, The University of British Columbia, Canada, E-mail: ElysiaDrakemore9054@yahoo.com

Citation Drakemore E (2024) Viral Diversity in African Mammals and its Role in the Wild Meat Supply Chain. J Infect Dis Treat. 10:110.

Copyright © 2024 Drakemore E. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

CONCLUSION

In conclusion, the wide diversity of viruses detected in African mammals involved in the wild meat supply chain presents a significant public health concern. These viruses, which range from well-known pathogens like Ebola and HIV to lesser-known but equally dangerous viruses, highlight the risk of zoonotic diseases spilling over into human populations. With the increasing demand for bush meat in many African communities, the potential for viral transmission is ever-present, making it essential to implement better surveillance, regulation, and education to reduce the risks associated with the trade in wild meat.

ACKNOWLEDGEMENT

None.

CONFLICT OF INTEREST

The author declares there is no conflict of interest in publishing

this article.

REFERENCES

1. Gaudin T, Emry R, Wible J (2009) The phylogeny of living and extinct pangolins (Mammalia, Pholidota) and associated taxa: A morphology based analysis. *J Mamm Evol* 16:235-305.
2. Heled J, Drummond AJ (2010) Bayesian inference of species trees from multilocus data. *Mol Biol Evol* 27:570-580.
3. Jaclin D (2016) Poached lives, traded forms: Engaging with animal trafficking around the globe. *Soc Sci Inf* 55:400-425.
4. Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol* 33:1870-1874.