



The Threat of Marburg Virus Disease in West Africa: Implications for Public Health Control in Nigeria

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Marburg virus disease (MVD) is a rare but severe haemorrhagic fever caused by Marburg virus (MARV), a filamentous, non-segmented, single-stranded negative-sense RNA virus which together with Ebola virus (EBOV) are the sole members of the genus Filovirus in the family Filoviridae¹. MARV was first discovered during epidemics in Marburg and Frankfurt, Germany, and in Belgrade, Serbia's capital city in 1967 and its source was traced to African green monkeys imported from Uganda^{2,3}. Despite the significant threat that MARV poses to human and animal health, virulent and pathogenic factors are not completely understood⁴. All six strains of MARV (Musoke, Ratayczak, Popp, Voegelé, Ozolin and Marburg Ravn) are known to be highly pathogenic⁵. The case fatality rate (CFR) varied between 23-90% in past epidemics depending on the virus strain and early diagnosis.

MARV is transmitted to humans through close contact with an infected animal, person or material contaminated with the virus. Human-to-human transmission occurs through direct contact with infected person's blood, secretions, body fluids or contaminated fomites⁶. Available evidence indicates that MARV is transmitted to human population from contact with the Egyptian fruit bat (*Rousettus aegyptiacus*) that resides in the caves and mines of forest communities or consumption of bush meat⁷. The epidemic potential of MARV is limited by the rapid onset of disease and the fact that the virus rarely spreads from person to person through respiratory droplets unlike the respiratory viruses, especially SARS-CoV-2. Perhaps, this could be the reason why the virus rarely spreads beyond family members and healthcare workers. Nevertheless, they are capable of causing global health concern because of their potential for introductions into non-endemic countries through international travel and trade just like the 2022 monkeypox outbreak have taught us⁸.

In the early course of the disease, the symptoms of MVD are clinically indistinguishable from several other tropical febrile illnesses such as malaria, typhoid fever, leptospirosis, and other viral haemorrhagic fevers due to similarities in their clinical presentation¹. This could potentially pose a diagnostic challenge for the frontline physician coupled with the attendant limitation in the molecular detection of the pathogen. The clinical spectrum of MVD involves an initial presentation of fever, severe malaise, severe headache, and chills which are followed by a non-itchy rash that is typically found on the chest, back, and abdomen on the 2nd to 7th day of onset of symptoms. Abdominal pain, nausea, vomiting, and watery diarrhoea may begin on the third day. Severe cases may be worsened by the appearance of yellowness of the eyes, bleeding tendencies, hypotension, multiorgan failure, and death⁹. MARV is detectable up to 12 months in the semen and other body fluids of survivors¹. This has also been reported among Ebola survivors and in the 2022 Monkeypox outbreak with implications for sexual transmission. MVD has no specific treatment or vaccine and relies on early institution of supportive measures such as rehydration with oral or intravenous fluids to improve survival⁶.

Prior to the 2021 outbreak in Guinea when MVD was reported in West Africa for the first time, MVD have been essentially confined to East Africa centered almost exclusively within 500 miles of Lake Victoria where the disease is known to be endemic¹⁰. However, the epidemiology of MVD is changing with the geographical extension of the natural reservoir hosts beyond East and Central Africa into West Africa as discovered by scientists in 2020¹¹. On July 17, 2022, the World Health Organization (WHO) announced an outbreak of MVD in Ghana with three confirmed cases from the same household in the Ashanti region and a 67% CFR¹². Interestingly, both index cases from the outbreaks in





Guinea and Ghana were young male farmers highlighting the vulnerability of this occupation to the virus¹³. Genetic sequencing results indicated that the MARV genomes from Ghana are related to the sequence from the 2021 outbreak and overall, group with sequences obtained from bats in Sierra Leone and an outbreak that occurred in Angola in 2004-2005¹². Given the fruit bat's expanding distribution across Africa, the occurrence of more epidemics appears inevitable. This is concerning for West Africa, a region that is already burdened by fragile health systems, weak public health infrastructure and repeated outbreaks of infectious diseases of high priority. Therefore, there is need for global, regional and national collaboration in the areas of research to better understand the transmission and epidemiology of MVD, and to consider as a priority, the need to develop medical countermeasures.

The recent MVD outbreak in Ghana is a warning to Nigeria given the high rates of cross-border travel often for trade and employment; and the country's huge population. From the lessons learnt from the COVID-19 pandemic, a disease threat anywhere is a disease threat everywhere¹⁴. Thus, the need for Nigeria to strengthen her epidemic preparedness and outbreak response by expanding the diagnostic capabilities of the existing molecular laboratories to detect MARV and other high consequence infectious diseases. To ensure that communities are carried along, health education, risk communication and community engagement should be implemented. In spite of the global decrease in COVID-19 incidence and severity, the use of generic public health measures that might have beneficial effects in the prevention of other emerging and re-emerging infectious diseases including MARV should be sustained particularly among frontline healthcare workers and other high-risk groups. The adoption of One Health approach involving human health experts, animal health experts, environmental scientists, and social scientists during this era of multiple epidemics by zoonotic pathogens is of utmost importance.

Authors' contribution

CAO conceptualized and planned the original manuscript, CAO and ARO prepared the manuscript. Both authors proofread and approval of the final manuscript.

Conflict of Interest

There was no conflict of interest.

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References

1. World Health Organization. Marburg virus disease. <https://www.who.int/health-topics/marburg-virus-disease>. (Accessed August 4, 2022).
2. Ristanovic ES, Kokoskov NS, Crozier I, Kuhn JH, Gligic AS. A Forgotten Episode of Marburg Virus Disease: Belgrade, Yugoslavia, 1967. *Microbiol Mol Biol Rev.* 2020;84:e00095-19. (Accessed October 5, 2022).
3. Wirsiy FS, Ako-Arrey DE, Nkfusai CN, Yeika EV, Bain LE. Marburg virus disease outbreak in Guinea: a SPIN framework of its transmission and control measures for an exemplary response pattern in West Africa. *Pan Afr Med J.* 2021;40:143.
4. Abir MH, Rahman T, Das A, Etu SN, Nafiz IH, Rakib A, *et al.* Pathogenicity and virulence of Marburg virus. *Virulence.* 2022;13:609–33..
5. European Centre for Disease Prevention and Control. Factsheet about Marburg virus disease. <https://www.ecdc.europa.eu/en/infectious-disease-topics/z-disease-list/ebola-virus-disease/facts/factsheet-about-marburg-virus> (Accessed October 4, 2022).
6. Centers for Disease Control and Prevention. About Marburg virus disease | Marburg (Marburg Virus Disease) | . 2021. <https://www.cdc.gov/vhf/marburg/about.html> (Accessed August 4, 2022).
7. Kajihara M, Hang'ombe BM, Changula K, Harima H, Isono M, Okuya K *et al.* Marburgvirus in Egyptian Fruit Bats, Zambia - *Emerg Infect Dis* 2019; 25(8): 1577 - 1580.
8. Mekibib B, Ariën KK. Aerosol Transmission of Filoviruses. *Viruses.* 2016;8(5):148. Available from: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4885103/>. (Accessed October 5, 2022).
9. Mehedi M, Groseth A, Feldmann H, Ebihara H. Clinical aspects of Marburg hemorrhagic fever. *Future Virol.* 2011;6(9):1091–106.
10. Tower JS, Khristova ML, Sealy TK, Vincent MJ, Erickson BR, Bawiec DA *et al.* Marburgvirus Genomics and Association with a Large Hemorrhagic Fever Outbreak in Angola | *Journal of Virology.* 2006;6497-6516.
11. Lawrence JA, UI Rasool MH, Parikh C, Chowdhury S, Sueldo A. Emergence of Marburg Virus Disease in West Africa amid COVID-19 and Ebola: Efforts, Challenges, and Recommendations to Prevent the Next Public Health Crisis. *J Infect Dis Epidemiol.* 2022;8:259. doi.org/10.23937/2474-3658/1510259
12. World Health Organization. Marburg virus disease - Ghana. Available from: <https://www.who.int/emergencies/disease-outbreak-news/item/2022-> (Accessed August 4, 2022)



13. World Health Organization. Marburg virus disease - Guinea. Available from: <https://www.who.int/emergencies/disease-outbreak-news/item/marburg-virus-disease-guinea> (Accessed October 3, 2022).
14. Centers for Disease Control and Prevention. Infectious Diseases Travel Fast and Far. 2022. Available from: <https://www.cdc.gov/globalhealth/security/ghsa5year/cdc-5-years-ghsa.html> (Accessed October 4, 2022).