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Molecular characterization of Lassa virus (glycoprotein complex gene) in febrile patients in Plateau State, Nigeria

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Introduction

The prevalence of Lassa fever has continued to rise over the years, with over 33 years of national outbreaks and more than 18 years of Lassa fever outbreaks in Plateau State since the detection of the index case in Nigeria in 1969. Plateau state is one of the states with significant increased number of Lassa fever outbreaks in the country. This study aimed at characterising the molecular phenotypes of Lassa virus in febrile patients.

Methods

A cross-sectional study was carried out. Using a simple random sampling technique, a total of 240 blood samples were collected from febrile patients (≥38◦C) in the selected Hospitals within the three zones in Plateau State. Structured questionnaires were administered to the Patients at the point of sample collection to obtain information on various potential risk factors associated with Lassa virus infection. One-step conventional RT-PCR was used to screen the samples. Positive PCR products were sequenced using the Sanger sequencing platform. The data were analysed using SPSS version 20.0, FinchTV software version 1.4.0 and MEGA X.

Results

Of the 240 febrile patients, 9 (3.75%) had Lassa virus; 8 (10.0%) were from the Plateau North zone, 1(1.2%) from the Plateau South, and 0(0%) from the Plateau Central. All eight (8) sequences that passed quality check in this study clustered phylogenetically with Lassa virus strains under lineage III previously known to circulate around Northern Nigeria.

Conclusion

This study highlights the presence of Lassa fever among febrile patients who might not typically be screened for the disease, as they do not meet the standard case definition for suspected Lassa fever. This shows that routine diagnosis for Lassa fever is urgently needed in areas with high Lassa fever transmission rates. Surveillance for Lassa fever among febrile Patients in Plateau State should be a priority.