

## Sero-molecular and vector surveillance of Lassa, Dengue, and Yellow fever viruses in Oyo State, Nigeria: A One Health approach

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### Introduction

The world continues to face recurrent epidemics driven by arboviral and zoonotic pathogens, posing significant threats to global health. In Nigeria, underdiagnosis and misdiagnosis of viral haemorrhagic fevers (VHFs) are common due to weak surveillance systems, limited laboratory capacity, and poor health seeking behaviour. This study assessed the public health burden, vector abundance and climatic influences of Lassa fever virus (LASV), Dengue fever virus (DENV) and Yellow fever virus (YFV) infections in Oyo State, Nigeria.

### Methods

A cross-sectional study was conducted from January 2022 to April 2023. Blood samples from 289 febrile humans were screened for LASV, DENV, and YFV using RT qPCR and serological assays, including IgM/IgG ELISA and lateral flow immunoassay kits. A total of 1,015 *Aedes* mosquitoes were trapped using Biogent Sentinel trap from 10 high risk LGAs, preserved in RNA Shield, and tested for YFV and DENV using RT

qPCR. Additionally, 30 rats were trapped in Iwajowa LGA following LASV confirmation, preserved and tested for LASV via RT PCR. Meteorological data were obtained from the Nigerian Meteorological Agency. Data were analyzed using descriptive statistics and multivariate models to explore associations between, infection, climate and vector dynamics

### Results

LASV IgM and IgG seroprevalence were 9.7% and 10.7%, respectively. DENV IgM and IgG seroprevalence were 6.6% and 37.7%. One individual tested positive for both LASV and DENV. Three LASV cases were confirmed by RT PCR in humans; no YFV or DENV RNA was detected in human or mosquito samples. Rodent samples tested negative for LASV. *Aedes aegypti* was the dominant species (79.5%) followed by *Aedes albopictus* and *Aedes simpsoni* with seasonal population variations linked to climate patterns.

## **Conclusion**

The findings confirm ongoing LASV and DENV transmission and highlight the risk of arboviral outbreaks due to high vector abundance. Strengthened surveillance, accurate differential diagnosis and integrated vector control are urgently needed to mitigate potential outbreaks.