

Circulation of Lassa virus in multimammate rats in Northern Côte d'Ivoire

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Introduction

Lassa fever is a viral haemorrhagic illness endemic to West Africa, caused by Lassa virus (LASV), a zoonotic pathogen primarily maintained by *Mastomys natalensis*, a rodent widely distributed across Sub-Saharan Africa. While Lassa fever has been reported in countries such as Benin, Ghana, Guinea, Liberia, Mali, Sierra Leone, and Nigeria, genome sequences of LASV are not available from all regions. The virus may also be circulating undetected in countries with limited surveillance and diagnostic capabilities, including Côte d'Ivoire.

Methods

In a previous investigation, we detected LASV RNA in *M. natalensis* specimens collected in rural settlements in northern Côte d'Ivoire near the border with Mali. Building on these findings, we conducted an extended rodent sampling campaign in the same region from Korhogo to the border of Mali. Lung samples were screened for LASV, and positive samples were subjected to whole-genome sequencing for genetic characterization.

Results

We report the genomic characterization of thirteen LASV strains isolated from *M. natalensis* captured in northern Côte d'Ivoire. Phylogenetic analysis confirmed the presence of two genetically distinct LASV lineages, suggesting local viral evolution and sustained, previously undetected circulation in the region.

Conclusion

Our findings provide the first genomic data of LASV from Côte d'Ivoire and highlight the importance of continued and expanded surveillance in both rodent reservoirs and human populations. Enhanced genomic monitoring across West Africa is essential to elucidate the evolutionary dynamics, geographic spread, and potential public health threat posed by Lassa.