

Comparative genomics of Lassa virus strains in West Africa: Insights into viral evolution

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Introduction

Lassa fever, caused by the Lassa virus (LASV), is a viral hemorrhagic fever, and a zoonotic arenavirus endemic in West Africa, with significant public health implications due to its high mortality and frequent outbreaks. While previous studies have characterized LASV lineages, understanding the genetic variability of LASV strains circulating in different ecological settings is crucial to elucidate mechanisms of viral evolution and transmission dynamics. In this study, we performed a comparative genomic analysis of LASV strains from human and rodent hosts collected across multiple West African countries to investigate evolutionary patterns, regional clustering, and signatures of functional divergence.

Methods

Whole-genome sequences (160 complete genomes) of both human and rodent were retrieved considering the NCBI Virus database and the BV-BRC database. They were subjected to high-resolution alignment and variant calling. Phylogenetic analysis and population structure were inferred using MEGA X and IQ-tree tools. Pangenomic mapping and variant annotation were also done to identify lineage-specific insertions.

Results

Phylogenetic analysis delineated strains into well-supported lineage clusters, with distinct genetic signatures corresponding to geographic regions such as Nigeria, Sierra Leone, and Liberia. Notably, strains from Nigeria showed greater intra-lineage diversity, whereas isolates from Sierra Leone exhibited a more conserved genomic profile. Comparative analysis of coding regions revealed mutations predominantly localized in the glycoprotein complex (GPC) and nucleoprotein (NP), with evidence of positive selection in domains associated with host cell entry and innate immune antagonism. Variation in the zinc-binding domain of the NP and fusion loop of GPC may contribute to differences in pathogenicity and immune evasion strategies.

Conclusion

These findings emphasize the genomic plasticity of LASV and its capacity for regional adaptation. The observed heterogeneity may influence the efficacy of diagnostic tools and universal vaccine candidates. Continuous genomic surveillance and comparative analysis are essential to inform regional preparedness strategies of effective medical countermeasures.