

Leveraging in-silico surveillance and AI-powered modelling of West African arenavirus genomic data for early Lassa fever outbreak prediction

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Introduction

Lassa Fever continues to pose a significant public health burden in West Africa, particularly in regions such as Nigeria, Sierra Leone, Ghana, and Guinea-Bissau, where surveillance gap hinders timely epidemic response. This study proposes a digital innovation framework that integrates bioinformatics, artificial intelligence (AI), and Mobile health platforms to enhance outbreak predictions and epidemic intelligence.

Methods

Utilising curated genomic datasets from the NCBI Virus Database and analysing Lassa mammarenavirus isolates across human and rodent reservoirs. Key accessions included NC_004297(Josiah, Sierra Leone), MK345515.1(AV, Nigeria), MH979661.1(NL-1072H, Nigeria), MH979663.1(NL-1087H, Ghana), and MH979662.1(NL-1079H, Guinea Bisau). Using tools such as MAFFT for multiple sequence alignment and Nextstrain's augur and auspice pipelines, we mapped phylogenetic relationships and inferred regional viral evolution patterns. To support predictive analytics, we trained machine learning models, including Random Forest and Long Short-Term Memory (LSTM) algorithms, using genomic features and outbreak

metadata. The pipeline was implemented in Python, leveraging libraries such as scikit-learn, TensorFlow, and Pandas.

Results

Results showed that high-risk genomic signatures and emerging variants could be linked to geographic clusters ahead of confirmed outbreak reports.

Conclusion

Proposing a regionally integrated West African Lassa Virus Gene Bank Interface to unify in-silicon surveillance with mobile case reporting platforms, enabling frontline health actors to receive early alerts and deploy countermeasures efficiently. This AI-enabled genomic surveillance model demonstrates the viability of low-cost, scalable epidemic control in resource-limited settings and offers a transferable framework for emerging infectious diseases across Africa.