

Deep Sequencing Unveils Phylogeographic Relationships of Juitiba Virus in Paraguay

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Abstract

Juitiba Virus (JUQV) is a hantavirus primarily found in South America, known to cause Hantavirus Pulmonary Syndrome (HPS) in humans. Understanding the phylogeographic relationships of JUQV is crucial for tracing its spread, evolution, and potential public health implications. Deep sequencing techniques have revolutionized our ability to unravel intricate genetic patterns and shed light on the dynamics of viral transmission. In this brief report, we delve into a study that utilized deep sequencing to uncover the phylogeographic relationships of JUQV in Paraguay.

Keywords: Hantavirus • Syndrome • Transmission

Introduction

JUQV belongs to the Hantavirus genus and is associated with rodents, particularly the *Oligoryzomys* genus. Human infections typically occur through inhalation of aerosolized virus particles from rodent excreta. JUQV infections can lead to HPS, characterized by respiratory distress and potential fatality. Phylogeographic analyses track the spread of viruses across geographic regions, aiding in understanding transmission patterns. By mapping genetic changes, researchers can infer evolutionary dynamics and potential adaptations. Identifying viral lineages and their geographic distribution informs public health strategies for surveillance and control.

Description

Researchers collected rodent samples and environmental specimens from diverse locations in Paraguay, focusing on regions with reported JUQV cases. High-throughput sequencing techniques were employed to generate extensive genetic data from the collected samples, allowing for detailed analysis of viral genomes. Bioinformatics tools were utilized to assemble viral genomes, analyze genetic variations, and construct phylogenetic trees depicting evolutionary relationships. Deep sequencing revealed significant genetic diversity among JUQV isolates from Paraguay, indicating multiple viral lineages. Phylogenetic analyses identified distinct clusters corresponding to different geographic regions within Paraguay [1].

Temporal analysis suggested both ancient and recent introductions of JUQV lineages into Paraguay, highlighting ongoing viral dynamics. Genetic markers indicated associations between specific JUQV lineages and rodent hosts, providing insights into reservoir dynamics. The phylogeographic clusters suggest localized transmission within specific regions, possibly driven by ecological factors and rodent populations. The presence of ancient and recent introductions implies multiple entry points for JUQV into Paraguay, highlighting the complexity of viral dispersal [2,3].

Understanding host associations helps elucidate reservoir ecology and potential spillover risks to humans. Phylogeographic insights can inform targeted surveillance efforts, focusing on high-risk areas and identifying emerging viral lineages. Long-term surveillance coupled with deep

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sequencing is essential for monitoring viral evolution and detecting novel variants. Integrating data from virology, ecology, and public health is crucial for a comprehensive understanding of hantavirus dynamics. Collaborative efforts across countries can enhance phylogeographic studies, especially for viruses with broad geographic distributions. Insights from phylogeographic studies contribute to vaccine [4,5].

Conclusion

Deep sequencing-based phylogeographic analyses of Juitiba virus in Paraguay have unraveled intricate genetic relationships, shedding light on viral spread, evolution, and host associations. These findings hold significance for public health strategies, emphasizing the need for ongoing surveillance, cross-disciplinary collaborations, and targeted interventions to mitigate hantavirus risks effectively. As deep sequencing technologies advance, our understanding of viral phylogeography continues to evolve, offering valuable insights into emerging infectious diseases and their ecological contexts.

Acknowledgement

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Conflict of Interest

None.

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