OPEN ACCESS Freely available online

ISSN: 2329-891X
Journal of
Tropical Diseases &
Public Health

Perspective

Phylogenetic Analysis of Chikungunya Virus in Myeloradiculoneuropathy Cases

Sabino Souza*

Department of Microbiology, University of Kentucky, Lexington, United States of America

DESCRIPTION

Intracellular Chikungunya Virus (CHIKV) is an arthropod-borne alphavirus transmitted primarily by Aedes mosquitoes, particularly *Aedes aegypti* and *Aedes albopictus*. It causes an illness characterized by fever, joint pain, muscle aches and, in some severe cases, neurological complications. While the typical clinical manifestations of Chikungunya are well-known, the virus can also lead to more serious conditions, such as myeloradiculoneuropathy, a disorder affecting the spinal cord and peripheral nerves. This neurological complication has been increasingly reported in outbreaks of CHIKV. Phylogenetic analysis has emerged as a vital tool to understand the evolution, spread and genetic diversity of CHIKV, especially in relation to cases presenting with atypical symptoms like myeloradiculoneuropathy.

When CHIKV explores the importance of phylogenetic analysis in understanding the association between CHIKV and myeloradiculoneuropathy, shedding light on the virus's genetic evolution, strain differences and how these variations might influence the clinical manifestations of the disease. Chikungunya Virus and neurological complications when it was first identified in Tanzania in 1952, and since then, the virus has caused multiple outbreaks across Asia, Africa and the Americas. Although CHIKV is primarily known for its acute febrile illness, recent studies have highlighted an increasing incidence of neurological manifestations during outbreaks. Myeloradiculoneuropathy, characterized by inflammation of the spinal cord, nerve roots and peripheral nerves, is one such severe complication. Patients with this condition may experience motor weakness, sensory abnormalities and paralysis. Neurological manifestations have been more commonly reported in older adults or individuals with pre-existing conditions, but young and healthy individuals can also be affected. The exact pathogenesis behind these neurological symptoms remains unclear, although it is hypothesized that both direct viral invasion and immune-mediated mechanisms could be responsible.

Importance of Phylogenetic analysis is the study of evolutionary relationships between different organisms or, in the case of viruses, between different strains. By analyzing the genetic sequences of CHIKV isolated from patients, researchers can track mutations and determine how the virus has evolved over time. This helps in identifying specific strains or lineages of the virus that might be associated with more severe clinical manifestations, including neurological comp lications like myeloradiculoneuropathy. Phylogenetic analysis is particularly important for understanding the global spread of CHIKV. As the virus moves through different populations and regions, it accumulates mutations. Some of these mutations may affect the virus's ability to infect human cells or evade the immune system, potentially leading to differences in disease severity. By comparing the genetic sequences of CHIKV from different outbreaks, researchers can identify common mutations associated with severe disease outcomes, such as neurological involvement.

Genetic variability of CHIKV exists as a single-stranded RNA virus with a high mutation rate, which is typical for RNA viruses. Three major lineages of CHIKV have been identified the West African lineage, the East/Central/South African (ECSA) lineage, and the Asian lineage. These lineages are characterized by specific mutations in the viral genome, which can influence the virus's behavior, including its virulence, transmissibility and ability to cause complications like myeloradiculoneuropathy. The ECSA lineage has been particularly associated with outbreaks in India, where neurological complications have been reported. Mutations in the Envelope Protein (E1) and other structural and non-structural genes are thought to contribute to the virus's ability to cause more severe symptoms. Phylogenetic studies have shown that certain mutations may increase the virus's fitness, making it more efficient at infecting human hosts and potentially more neurotropic, or capable of infecting nerve tissues.

Phylogenetic findings in myeloradiculoneuropathy cases several studies have employed phylogenetic analysis to investigate CHIKV strains involved in cases of myeloradiculoneuropathy. In one study conducted during an outbreak in India, CHIKV strains isolated from patients with neurological symptoms, including myeloradiculoneuropathy, were compared to strains

Correspondence to: Sabino Souza, Department of Microbiology, University of Kentucky, Lexington, United States of America, E-mail: souza_s@email.com

Received: 26-Aug-2024, Manuscript No. JTD-24-27208; **Editor assigned:** 30-Aug-2024, PreQC No. J JTD-24-27208 (PQ); **Reviewed:** 13-Sep-2024, QC No. JTD-24-27208; **Revised:** 20-Sep-2024, Manuscript No. JTD-24-27208 (R); **Published:** 27-Sep-2024, DOI: 10.35241/2329-891X.24.12.449

Citation: Souza S (2024). Phylogenetic Analysis of Chikungunya Virus in Myeloradiculoneuropathy Cases. J Trop Dis. 12:449

from patients with typical symptoms. The analysis revealed that the strains associated with neurological complications belonged to the ECSA lineage and harbored specific mutations in the E1 gene that were absent in strains from non-neurological cases. These findings suggest that certain viral genotypes or mutations may predispose patients to developing neurological symptoms. It is possible that these mutations enhance the virus's ability to invade the central nervous system or trigger an exaggerated immune response, leading to inflammation of the spinal cord and peripheral nerves. Another study examined CHIKV strains from a large outbreak in the Americas and found that strains from patients with neurological symptoms were closely related to Asian lineage strains that had recently been introduced into the region. This highlights the importance of phylogenetic surveillance in tracking the spread of CHIKV and identifying mutations that may lead to more severe disease outcomes.

Understanding the phylogenetic relationships between different CHIKV strains has important public health implications. By identifying specific mutations associated with severe disease outcomes, such as myeloradiculoneuropathy, public health officials can prioritize monitoring and control efforts in regions where these mutations are circulating. This can help in preventing the spread of more virulent strains and in implementing targeted interventions to reduce the burden of severe disease. Phylogenetic analysis can guide vaccine development. Current vaccines under development are based on CHIKV strains from different lineages and understanding the genetic variability of the virus can help ensure that vaccines are effective against a broad range of strains, including those associated with neurological complications. Research can be focus on expanding phylogenetic studies to include a wider range of CHIKV strains, especially those isolated from patients with neurological symptoms.