

A Comparative Study on Pre Epidemic and Post Epidemic ZIKV Strain from Asia, America and Africa

Sabiha Imran* and Garima Ahuja

**Associate Professor, Department of Biotechnology, FET,
Manav Rachna International University, Faridabad, Haryana*

Abstract—Zika infection is a mosquito borne flavivirus that is the concentration of a continuous pandemic and general wellbeing emergency. It is restricted to sporadic cases in Asia and Africa, the development of Zika infection contaminations are portrayed by subclinical or mild flu like illness, severe appearance have been described, including Guillain-Barre disorder in grown-ups and microcephaly in infants destined to infected mothers. Neither a compelling treatment nor an antibody is accessible for Zika virus. Despite developing learning about this virus, questions remain in regards to the virus's vectors and reservoirs, pathogenesis, genetic diversity, and potential synergistic impacts of co-disease with other circling viruses. Less than 20 sporadic instances of human Zika infection (ZIKV) contamination were accounted for in Africa and Asia before 2007, yet vast breakouts including up to 73% of the populaces on the Pacific islands have begun since 2007, and spread to the United States in 2014. We extensively thought about the genome groupings of pre-pestilence and pandemic ZIKV strains with finish genome or finish polyprotein successions accessible in GenBank. Phylogenetic examine uncovered that Southeast Asian ZIKV won't not be the immediate wellspring of South American flare-ups as already guessed. These one of a kind buildups on outside viral proteins are not found in Southeast Asian ZIKV and could be in charge of the progressing flare-up either through a characteristic property of the infection or communications with human insusceptibility.

Over the past half century, a significant number of ZIKV isolates have been obtained sporadically from three continents (Africa, Asia, and America); however, little is known about the genetic variation among these geographically and temporally distinct ZIKVs because of the limited number of fully sequenced ZIKV genomes. Less than 20 sporadic cases of human Zika virus (ZIKV) infection were reported in Africa and Asia before 2007, but large outbreaks involving up to 73% of the populations on the Pacific islands have started since 2007, and spread to the Americas in 2014. Phylogenetic analyses integrating geographical and time factors revealed that South Asian ZIKV might not be the direct source of South American outbreaks as previously speculated. The genome sequences of pre-epidemic and epidemic ZIKV strains with complete genome or complete polyprotein sequences available in GenBank has been comprehensively compared. Besides the reported phylogenetic clustering of the epidemic strains with the Asian lineage, we found that the topology of phylogenetic tree of all coding regions is the same except that of the non-structural 2B (NS2B) coding region. This finding was confirmed by bootscan analysis and multiple sequence alignment. The Genomic and phylogenetic analyses of ZIKV strains of Asian lineages is compared with ZIKV found in America and Africa have been demonstrated in this paper.