

Whole-genome sequencing of chikungunya virus-infected cases during 2016 in North India



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Abstract

Chikungunya fever is an emerging arboviral disease caused by the chikungunya virus (CHIKV). While many CHIKV infected patients recover after primary illness, others suffer from persistent debilitating arthralgia that can last for months to years. There is an urgent need to understand the epidemiology, pathogenesis and determine the disease burden due to chikungunya. We, therefore, used molecular diagnostic tests for the detection of CHIKV infections at Jamia Hamdard Institute of Medical Sciences (JHIMS) hospital in New Delhi and assessed viral diversity of infecting strains and clinical characteristics associated with chikungunya disease. We enrolled 325 acute febrile patients suspected to have CHIKV infection. All samples were screened by RT-PCR (One-step RT-PCR kit, Qiagen), IgM ELISA (SD Chikungunya IgM ELISA kit). Whole CHIKV genome sequences were carried out for chikungunya RT-PCR positive samples and assessed by phylogenetic analysis. Whole-genome sequence analysis of CHIKV structural and nonstructural gene showed the maximum number of mutations in the structural gene compare to nonstructural gene this is comparable to the prototype ECSA strains, of CHIKV and physiochemical properties of proteins, was also assessed by in silico approach. The study emphasizes the need for continuous surveillance for disease burden using multiple diagnostic tests, characterization, changes in vector-pathogen compatibility and host-pathogen interactivity for the development of suitable vaccine candidates and antivirals.

Biography:

I am Md. Naushad khan doctoral fellow in Department of Biotechnology, School of Chemical and Life Sciences, Jamia Hamdard University, India. I did complete the Master of Philosophy from the Jamia Millia Islamia University, India. Currently, I am publishing the four papers and participate as a speaker in the National and International Conferences. I have experience in research fields since 2011.



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