ABSTRACT

Background-

Chikungunya fever is an arthropod borne debilitating non-fatal viral fever. It was originally distributed in several parts of Africa, South Asia and Southeast Asia. Chikungunya is an RNA virus. Chikungunya virus is an Arthropod borne virus, which spreads from one person to other person by the bite of vector mosquitoes – Aedes genus (Aedes aegypti and Aedes albopictus). Chikungunya fever presents with High fever, severe joint pain and rashes. The mortality and morbidity of Chikungunya were drastically increased after 2005-06 outbreaks in Indian-ocean islands and India due to mutations and increased host range.

Aim-

To find-out the prevalence of Chikungunya disease, genotype responsible for and mutations in E1 gene and correlation of protein structure, infectivity, virulence and clinical manifestations with observed mutations.

Materials and Methods-

Clinical samples (500 blood samples) were collected from Chikungunya suspected cases from primary health centers, community health centers, taluk hospitals and district hospital of Vijayapura district, Karnataka. Chikungunya IgM antibody ELISA test was performed on all serum samples. Chikungunya IgM antibody positive samples were further tested for Chikungunya RNA by RTPCR test. Molecular characterisation studies like Phylogenetic analysis, mutational analysis, protein modeling and mutations mapping studies were conducted to find-out the genotype prevalent in the area and mutations in E1 gene.

Statistics - Chi square test is done.
Result-

Out of 500 serum samples tested, 33 samples were found positive by Chikungunya IgM antibody ELISA test. Chikungunya RNA was detected in 31 of 33 seropositive samples. The current strains clustered with ECSA genotype and are closely related to Reunion strains. **E1K211E, E1M269V and E1D284E**, three observed amino acid mutations were present in all strains. All the three mutations observed in E1 gene lie in the area of the major secondary structure. Novel mutation E1A226V was absent in current strains.

Conclusion-

We have found that, Chikungunya prevalence in and around the region of Vijayapura district was 6.2% and Statistical analysis concluded that there was no significant difference between suspected and confirmed cases with respect to year, sex, age and taluk. The ECSA strains of current study may have evolved from ECSA Reunion islands strains. From the study, we have concluded that the observed mutations in E1 gene couldn’t alter the protein structure and ECSA strain circulating in Vijayapura district are comparatively less virulent.