Mini Review
Volume 7:6, 2022

Journal of Infectious Diseases and Medicine

ISSN: 2576-1420 Open Access

Epidemiology, Kleihauer and Medicinal Research of Chikungunya Virus Infection

Kobporn Sukphopetch*

Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand

Abstract

From 2018 to 2020, the Chikungunya virus (CHIKV) outbreak re-emerged in Thailand with a report of greater than 10,000 instances up till the give up of 2020. Here, we studied acute CHIKV-infected sufferers who had introduced to the Bangkok Hospital for Tropical Diseases from 2019 to 2020 by using assessing the relationship between viral load, scientific features, and serological profile. The outcomes from our find out about confirmed that viral load was once notably excessive in sufferers with fever, headache, and arthritis. We additionally decided the neutralizing antibody titer in response to the viral load in patients, and our facts aid the proof that an advantageous neutralizing antibody response in opposition to the virus is necessary for manipulate of the viral load. Moreover, the phylogenetic evaluation printed that the CHIKV traces we studied belonged to the East, Central, and Southern African (ECSA) genotype, of the Indian ocean lineage (IOL), and possessed E1-K211E and E1-I317V mutations. Thus, this learn about offers perception for a higher grasp of CHIKV pathogenesis in acute infection, alongside with the genomic range of the modern CHIKV lines circulating in Thailand.

Keywords: Virus • CHIKV • ECSA

Introduction

Chikungunya is are-emerging neglected Tropical complaint that has caused several outbreaks throughout history in multitudinous countries. Chikungunya contagion (CHIKV) is transmitted through the bite of an infected Aedes mosquito either A. albopictus orA. Aegypti. It's known to beget patient arthralgia, which has a significant impact on the case's quality of life and has contributed to the profitable burden of numerous countries over the once decades. CHIKV is believed to have been begun in Africa in 1952 and is widespread in numerous countries, including Asia. CHIKV exists in three different genotypes West African (WA), East/ Central/ South African (ECSA), and Asian. The first reported case of CHIKV infection in Thailand was caused by an Asian genotype in 1953 and spread to numerous regions of the country, especially Southern Thailand, which had a large outbreak in 2008 – 2009 [1].

The outbreak was caused by the ECSA genotype and infected over, 50000 cases. In 2018 – 2020, the infectionre-emerged with a shifted form of the ECSA genotype, known as India Ocean lineage (IOL), which is responsible for utmost cases in Southern Thailand, especially in sightseer magnet spots. These outbreaks came a major contributor to the trip- associated imported CHIKV cases, especially from Thailand to other countries. Clinical instantiations of CHIKV infection are high- grade fever, severe arthralgias, myalgias, maculopapular rash, nausea, puking, and headache during the acute stage. In the habitual stage, regressed symptoms with seditious polyarthritis and neurological complications have been observed in numerous cases. still, CHIKV- convinced habitual arthritis remains inadequately understood and treatment relies solely on the supposition of immunopathogenesis following CHIKV infection [2].

***Address for Correspondence:** Kobporn Sukphopetch, Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; E-mail: Kobpornsukphopetch54@gmail.com*

Date of submission: 01 June, 2022, Manuscript No. jidm-22-72371; **Editor Assigned:** 03 June, 2022, PreQC No. P-72371; **Reviewed:** 17 June, 2022, QC No. Q-72371; **Revised:** 23 June, 2022, Manuscript No. R-72371; **Published:** 29 June, 2022, DOI: 10.37421/2576-1420.2022.7.242

The complaint is frequently underdiagnosed because of the analogous clinical donations to dengue and other aboriginal infections. thus, there's an critical need for an early and accurate opinion of CHIKV for timely treatment and to limit farther transmission of the complaint. presently, there are no specific rectifiers against CHIKV infection, and severe patient symptoms in the habitual stage are set up to be associated with a high viral cargo during the acute period. The relationship between viral cargo and clinical symptoms of CHIKV infection has been proved in a many studies, but the understanding is still limited especially in an aboriginal area similar as Thailand. Hence, we used real- time quantitative RT- PCR to descry and quantify CHIKV viral cargo in the serum samples of suspected CHIKV- infected cases presented at the Sanitarium for Tropical conditions, Mahidol University [3].

The correlation of CHIKV viral cargo with the clinical symptoms and antibody biographies of the cases was further anatomized negativing antibodies against CHIKV have been proposed as one of the factors that are associated with a drop in viral cargo, furnishing protection against habitual arthritis in the future. therefore, this study also investigates the negativing antibody pattern in CHIKV- infected cases and farther supplements it with viral cargo and clinical symptoms. The results from this study will give sapience into clinical incarnation in the correlation between the viral cargo and antibody profile during CHIKV acute infection.

Literature Review

For the quantitative real- time RT- PCR, the RNA from an insulated CHIKV contagion strain TM009 2019 was uprooted using an RNA birth tackle (Bioneer Accuprep viral RNA birth tackle, Daejeon, Korea) according to the manufacturer's protocol. The Nsp1 scrap of CHIKV RNA was amplified using CHIKV forward and reverse manuals. Nsp1 CHIKV cDNA products were also introduced into the pGem- 4z plasmid vector (Promega, Madison, USA) containing a T7 protagonist by restriction enzymes HindIII and Xbal (Promega, Madison, WI, USA) and converted into competent JM109 Escherichia coli. The recombinant plasmids were also uprooted using the Geneaid ™ Midi Plasmid tackle(PI025) (New Taipei City, Taiwan) and were purified with a MEGAquick- spin Plus scrap DNA sanctification tackle(Intron Biotechnology, Gyeonggi- do, Korea). The in vitro recap of the plasmid DNA was performed using the MEGAscript T57 tackle (Invitrogen, Carlsbad, CA, USA), according to the manufacturer's instruction [4].

The synthesized RNA was also purified with the phenol – chloroform

birth system. Purified RNA was quantified by nanodrop (Thermo scientific, Waltham, MA, USA) and the attention, in nanograms, was converted into RNA dupe figures and used as CHIKV RNA standard, ranging from 101 to 1010 clones/ µL. Real- time RT- PCR was performed using serially adulterated RNA norms. The cycle threshold (Ct) values attained were colluded against the log dilution of in vitro transcripted RNA to induce the standard wind. Viral RNA birth from the serum samples was performed using an RNA birth tackle (Bioneer AccuPrep ® viral RNA birth tackle, Daejeon, Korea) according to the manufacturer's instruction. Viral cargo estimation was performed by the TaqMan quantitative real- time RT- PCR system.

Specific manuals and the inquiry targeting 1200 bp region of the Nsp1 gene of CHIKV were used for modification. A 20 µL volume response was subordinated to thermal conditions as follows; activation of rear recap at 50 °C for 15 min, followed by original denaturation at 95 °C for 30 s, 35 cycles of denaturation at 95 °C for 10 s, and annealing at 60 °C for 30s. All of the trials were performed on the CFX96 touch real- time PCR machine (Bio-Rad, Hercules, CA, USA). Cycle threshold (Ct) values were colluded against log dilutions of the RNA generated by in vitro recap for construction of the standard wind. The dupe figures in the serum samples were calculated from the crossroad points on the standard cure. Cases clinical symptoms were collected using case record forms (CRFs) [5-10].

Discussion

Although CHIKV contamination is an rising mosquito-borne virus accountable for outbreak in many countries, the development of extended persistent arthralgia/arthritis in contaminated sufferers continues to continue to be a burden to patients. This caused many scientists now not solely to enhance feasible redress to fight and stop the unfold of disease, however additionally to apprehend the pathogenesis of sickness in development to persistent conditions. Chronic stage CHIKV is described as having chronic signs of arthralgia/arthritis for greater than three months after the preliminary analysis. According to a few prior studies, CHIKV IgM was once detectable in sufferers after 2–3 years and the longest power case of joint ache and stiffness was once located in South African sufferers after three to 5 years of acute contamination. So far, the underlying motive of continual CHIKV arthropathy stays doubtful, and quite a few research have stated the elements that should make a contribution to assisting alleviate persistent arthralgia/arthritis. The important contributors to continual contamination are viral load and person immune responses.

Conclusion

Further research are wished to consider the purposeful function of the E1-I317V mutation in adaptation to the mosquito species. An evolutionary find out about of the CHIKV IOL lineage recommended that E1-A226V mutation was once absent from India after 2014 and a new amino acid substitution of E1-K211E/E2-V264A emerged alongside with an extra mutation of E1-I317V in early 2010, which swiftly unfold to Bangladesh in 2017 and from Bangladesh to Thailand in 2018–2020. Meanwhile, an evaluation of the genetic variety of field-catch A. aegypti mosquitos in endemic areas of Thailand additionally detected the presence of the E1-K211E mutation. This proof helps the concept that the environment friendly transmission of CHIKV in extraordinary vectors performs an imperative function in the evolution of CHIKV over a duration of time. Overall, the outcomes from our find out about exhibit that CHIKV circulating in Bangkok, Thailand, in 2019–2020 belongs to the ECSA genotypes and consists of E1-K211E and E1-I317V mutations.

Acknowledgement

None.

Conflict of Interest

None.

References

1. Staples, J. Erin, Robert F. Breiman and Ann M. Powers. "Chikungunya fever: An epidemiological review of a re-emerging infectious disease." *Clin Infect Dis* 49 (2009): 942-948
2. Mohan, Alladi, D.H.N. Kiran and D. Prabath Kumar. "Epidemiology, clinical manifestations, and diagnosis of Chikungunya fever: lessons learned from the re-emerging epidemic." *Indian J Dermatol* 55 (2010): 54.
3. Thiberville, Simon-Djamel, Nanikaly Moyen and Xavier de Lamballerie. "Chikungunya fever: epidemiology, clinical syndrome, pathogenesis and therapy." *Antiviral Res* 99 (2013): 345-370.
4. Patel, Ashok Kumar, Sushil Kumar Kabra and Pratima Ray et al. "Virus load and clinical features during the acute phase of Chikungunya infection in children." *PLoS One* 14 (2019): e0211036.
5. Zaid, Ali, Patrick Gérardin and Suresh Mahalingam. "Chikungunya arthritis: Implications of acute and chronic inflammation mechanisms on disease management." *Arthritis Rheumatol* 70 (2018): 484-495.
6. Agarwal, Ankita, Ajay Kumar Sharma and Paban Kumar Dash. "Two novel epistatic mutations (E1: K211E and E2: V264A) in structural proteins of Chikungunya virus enhance fitness in Aedes aegypti." *Virology* 497 (2016): 59-68.
7. Tsetsarkin, Konstantin A., Dana L. Vanlandingham, Charles E. McGee and Stephen Higgs. "A single mutation in chikungunya virus affects vector specificity and epidemic potential." *PLOS Pathog* 3 (2007): e201.
8. Khongwichit, Sarawut, Jira Chansaenroj, Thanunrat Thongmeex and Yong Poovorawan, et al. "Large-scale outbreak of Chikungunya virus infection in Thailand, 2018–2019." *PloS one* 16 (2021): e0247314.
9. Rianthavorn, Pornpimol, Kesmanee Prianantathavorn and Yong Poovorawan et al. "An outbreak of chikungunya in southern Thailand from 2008 to 2009 caused by African strains with A226V mutation." *Int J Infect Dis* 14 (2010): e161-e165.
10. Anwar, Saeed, Jarin Taslem Mourosi and Mohammad Jakir Hosen. "Chikungunya outbreak in Bangladesh (2017): Clinical and hematological findings." *PLoS Negl Trop Dis* 14 (2020): e0007466.

How to cite this article: Sukphopetch, Kobporn. "Epidemiology, Kleihauer and Medicinal Research of Chikungunya Virus Infection." J Infect Dis Med 7 (2022): 242.