

Molecular and clinical investigation of *Chikungunya virus* cases in Piauí

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The arboviruses compose the viruses that cause human and animal diseases, transmitted by hematophagous arthropod vectors, distributed in families: *Togaviridae*, *Flaviviridae*, *Bunyaviridae*, *Rhabdoviridae*, *Reoviridae*, and *Orthomyxoviridae*. Among them is the *Togaviridae*, composed of two genera *Rubivirus* and *Alphavirus*, which in the latter contains the *Chikungunya virus* (CHIKV). CHIKV infection can range from asymptomatic to symptomatic cases, in which case symptoms that start milder can evolve into impairments. Moreover, the severity of the condition is related to chronicity since persistent arthralgia after the disease is recurrent in 40-80% of cases. Due to the similarity of symptoms between different arboviruses, especially in the initial phase, it is necessary to differentiate the pathogen. The use of molecular diagnosis can obtain more sensitive and specific results than other techniques, such as serological, which can result in cross-reactions with other endemic viruses that circulate in the area studied. The present study aims to investigate the dynamics of CHIKV circulation and evaluation of the clinical and epidemiological profile of positive cases by molecular and serological methods in the years 2017 to 2020, through serum samples from patients Hospital Estadual Dirceu Arcoverde (HEDA) and Laboratório Central de Saúde Pública do Piauí (LACEN-PI). The viral RNA was extracted following the protocol proposed by the manufacturer and sent for conversion into cDNA by the Reverse Transcriptase technique and subsequent amplification of the material present. To detect the arboviruses studied, protocols that amplify distinct regions of the genes were standardized after tests evaluating different PCR optimization parameters. With the premise of implementing a new methodology in the laboratory, the PCR reaction to detect regions *E1*, *E2*, *nsP2*, and *E2-6K*, and in the RT-qPCR method, the *nsP1* region. For this study, 363 samples were collected, and of these, 230 were submitted to IgM serology and 56 to RT-PCR and RT-qPCR, being positive in 170 and 14, respectively. The sample of chronic patients was predominantly the female gender and age over 49 years, and the main symptoms were stiffness and edema in the peripheral joints. In addition, a case of peripheral polyneuropathy was detected in the upper and lower limbs in an elderly patient with a febrile illness and severe arthralgia diagnosed with the virus. The present study successfully standardized the RT-qPCR technique for the genomic quantification of CHIKV to extend and improve the detection of this virus. Through the study, it was possible to infer the pattern of circulation of CHIKV in Piauí state and outline the epidemiological characteristics of patients who progressed to the chronic phase of the disease.

Palavras-Chaves: *Chikungunya virus*; Molecular diagnosis; Piauí

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