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Editorial

Zoonotic Virus Genetic Description in the Central African Republic Virus for Use as a Systems Integration When Trying to Test for Persons Infected and Stomach Flu in Food and Water

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Abstract

Chikungunya virus (CHIKV) is an alphavirus spread by mosquito bites. Over the last decade, the virus has undergone mutations that increase its transmissibility by the Aedes albopictus vector, resulting in massive outbreaks in the Indian Ocean, Asia, and Central Africa. The recent introduction of competent A. albopictus vectors into the Central African Republic (CAR) raises the possibility of a Chikungunya fever (CHIKF) epidemic in this region. We conducted this study to assess the genetic diversity and background of CHIKV strains isolated in the CAR between 1975 and 1984, as well as to estimate the ability of local strains to adapt to A. albopictus. Our findings suggest that local CHIKV strains have a genetic background compatible with rapid adaptation to A. albopictus, as previously suggested. Other Central African countries have reported similar findings (Allen B et al ., 2017).

In order to prevent or anticipate the emergence of a massive CHIKF epidemic in the CAR, intensive surveillance of human and vector populations is required. Noroviruses (NoV GI and NoV GII) and the hepatitis A virus (HAV) are frequently involved in foodborne infections around the world. They are primarily transmitted through fecal-oral contact, direct person-to-person contact, or the consumption of contaminated water and foods. Detection methods in food virology are currently based on identifying viral genomes using real-time reverse transcriptase PCR (RT-qPCR). As described in ISO/TS 15216-1 and ISO/TS 15216-2, one of the general requirements for detecting these viruses in food is the use of a process control virus to monitor the quality of the entire viral extraction procedure. In 2013, the 15216-2 standards were published. The chosen process control virus should have similar morphological and physicochemical properties to the screened pathogenic virus, allowing it to provide comparable extraction efficiency. The purpose of this study was to determine which virus, murine norovirus (MNV-1) or Mengovirus, should be used for process control when testing for the presence of HAV, NoV GI and NoV GII in bottled water, lettuce, and semi-dried tomatoes(Arrowsmith Jet al .,2011). HAV, NoV GI, or NoV GII were added to food samples alone or in combination with MNV-1 or Mengovirus. Using a multiple comparison procedure, the recovery rates of each pathogenic virus were compared to those of both process control viruses. Regardless of the process control virus, neither influenced pathogenic virus recovery.

DESCRIPTION

(Asher M et al., 2011) Chikungunya virus (CHIKV), which was first isolated from human serum during an epidemic in Tanzania in 1953, is an arbovirus of the genus Alphavirus (Togaviridae family). It causes Chikungunya fever (CHIKF) in humans, an acute fever characterised by arthralgia and myalgia that can progress to chronic arthropathy. CHIKV is found in tropical Africa and Asia, where it is transmitted to vertebrate hosts via mosquito bites of the Aedes genus. Two distinct ecological transmission cycles have been documented. (Batagelj V et al.,2017) Sylvan mosquitoes,

primarily Aedes furcifer, Aedes taylori, Aedes africanus, and Aedes luteocephalus, serve as vectors in an enzootic cycle described in West Africa in forested habitats. Nonhuman primates are the most likely reservoirs and amplification hosts, with human cases appearing infrequently. (Bettini E et al., 2016) In Asia, CHIKV has a primarily urban epidemic cycle, primarily involving the anthropophilic vectors Aedes aegypti and Aedes albopictus, with humans serving as its only amplification host. CHIKF was previously described primarily in rural Sub-Saharan Africa and urban Southeast Asia. (Boulesteix AL et al., 2015) Since 2005, however, (Cordero OX et al., 2016).) massive epidemics have indicated the virus's emergence or re-emergence in the Indian Ocean, including the island of La Réunion, in India, in urban areas of Central Africa, the Caribbean, South America, (Harrison et al., 2007) and even Europe. Except in some areas of India and Southeast Asia, where Aedes aegypti was identified as the main vector, Aedes albopictus (Imrie et al ., 1991) was the main vector in almost all of these outbreaks. A. albopictus, a mosquito native to Asian forests, has spread to the United States(Jackson et al., 2019).

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