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Popular Article

Japanese encephalitis: an epidemiological paradigm

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Abstract

A Major havoc, flavivirus in the Asia-Pacific region is the Japanese encephalitis virus (JEV). Over two billion individuals are susceptible to infection because they reside in endemic and epidemic regions. The first native human case was recently reported in the African continent, while birds with the infection have been discovered in Europe. JEV might spread to different continents. The worldwide distribution of JEV is covered in the first half of this review along with some recent findings. The effects of JEV on people, including their natural course and immunity, are the main topics of the following sections.

Keywords: Epidemiological studies, blood-brain barrier, transmission, cellular events, Japanese encephalitis virus (JEV), flavivirus, JEV

Introduction

The Japanese encephalitis virus (JEV), a recently identified flavivirus transmitted by mosquitoes, has connections to the virus that causes dengue (DENV), the Western Nile virus (WNV), the Zika virus (ZIKV), or the encephalitis brought on through the tick-borne viral (TBEV). JEV is an encapsulated virus with the virion size of approximately fifty nm, an RNA single-stranded genome that has a positive sense of about 11 kB, and minimal length changes between genotypes, as reported by Lu *et al.* (2017) & Desingu *et al.* in (2017). JEV is the primary cause of encephalitis in humans in the Asia-Pacific region. JEV originated from an African ancestor virus that had long since

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relocated into the Indonesia-Malaysia area, from which it subsequently spread through Asia and all of the way to Australia, consistent with genetic studies (Solomon *et al*.,2003).One serotype and several genotypes have been mapped by serological and genetic investigations across Australia and New Zealand and also in Africa and Europe, demonstrating ongoing changes in the geographic distribution of JEV and JEV adaptation to novel circumstances (Oliveira *et al*., 2018; Samy *et al*.,2018; Fang *et al*.,2019; Gao *et al*.,2019; Garjito *et al*.,2019;Karna *et al*., 2019).While epidemic episodes were reported in temperate and cooler-climate regions, only tropical places have been considered to be endemic. Recently, Angola, Africa, has reported the first indigenous human case outside of Australasia [10], while Italy, Europe, has reported finding JEV in birds. But other transmission cycles and chains have been identified. Wild water and wading birds, especially migratory species including herons, egrets, and ducks, create a natural JEV reservoir. With the possible exception with the Middle East and certain regions of Australia, when the presence with the birds has been established but where no JEV cases have been recorded by Sammy *et al.* (2018) have predicted the geographic spread of egrets throughout the Australasian region, this corresponds well to the observed presence of JEV cases (Gao *et al*.,2019).Therefore, one must take into account that eagles and egrets travel in the summer to the northwestern temperate parts of Eurasia for breeding.

They may also live year-round in the subtropical and less chilly parts of Europe, Africa, and Asia, but they move to the tropics for the winter. Therefore, JEV may move across the ocean out of endemic tropical locations into countries with temperate and tropical climates where JEV may reemerge due to long-distance migratory birds (herons and egrets). Ducks have been found to transmit JEV across seas as well as shorter distances, as was the case in Japan as well as Korea (Simon *et al*.,2017). JEV has been surprisingly discovered in the lymph nodes the birds in Italy, likely as a result of long-distance bird migration between Asia to Europe. However, nothing is known about these species' migratory paths.Future research estimating the propagation of JEV by migrating birds may benefit from technological advances, such as satellite-based tracking, as it has been demonstrated in recent research for the influenza H5N1 virus (Samy *et al*.,2018).

The fact that the infected birds are asymptomatic JEV carriers is crucial (Karna *et al*., 2019). However, more recent research suggests that specific JEV strains can cause illness in newly hatched birds (Oliveira *et al*., 2018). To comprehend the immune chemistry of JEV in various vulnerable birds, more study is required. Bats, in addition to other birds, may serve as natural JEV is a reservoirs and contribute significantly to JEV transmission.Two scenarios are theoretically possible: first, migratory JEV carrying birds may have entered Angola, and second, JEV could have been spread by comparable indigenous mosquitoes. Second, one must take into account the fact that Angola has grown to be China's principal African trading partner, or vice versa. However, only additional cases in the future and related research will shed light on potential infection paths for African patients.

Conclusion

The pathophysiology concentrating on humans and biological pathways that foster JEV infection were covered in the following sections. For the focused development of novel effective anti-viral medicines, a deeper knowledge of infection with JEV at the cellular or system level is necessary.

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