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Contemporary Issue

Dengue, chikungunya ... and the missing entity – Zika fever: A new emerging threat



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ABSTRACT

Zika virus (ZIKV), a relative newcomer from the flavivirus group that includes dengue, Japanese encepahalitis and yellow fever, is one of the emerging pathogens that is fast transcending geographical boundaries. It is a vector-borne disease transmitted by the same *Aedes aegypti* and *Aedes albopictus*, which cause dengue and chikungunya. In addition to the vector-mediated transmission of Zika fever, probable human-to-human transmission through exchange of body fluids, including sexual and perinatal transmission and through blood transfusion, makes containment of this new entity more challenging. Moreover, a high index of suspicion by an astute physician is necessary for diagnosis of Zika fever in view of the similarity of symptoms with dengue and chikungunya, especially in areas, where these two diseases are already endemic.

Zika, till recently, has had minimal impact, but its true potential is unfolding with increasing detection of congenital malformities, Guillain–Barré syndrome and other neurological and autoimmune syndromes in patients with recent history of ZIKV infection, or when mothers get infected with Zika during first or second trimester of pregnancy. The association, however, needs to be established, nonetheless it is important that we keep a close vigil on this emerging vector borne disease – the 'ZIKA' fever.

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Introduction

Zika fever, an emerging zoonotic disease is caused by Zika virus (ZIKV), a Flavivirus member of the Spondweni serocomplex, which shares limelight with the other well-known members of the Flavivirus family i.e. dengue, yellow fever, West Nile and Japanese encephalitis (Fig. 1).^{1,2} ZIKV is a positive sense single-stranded RNA molecule 10,794 bases long containing a nucleocapsid approximately 25–30 nm in diameter, which is surrounded by a host-membrane derived lipid bilayer that contains envelope proteins E and M and seven

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Fig. 1 – Phylogenetic relationship of Zika virus to other flaviviruses based on nucleic acid sequence of nonstructural viral protein 5.

non-structural proteins; of which NS5 is the largest. The virion is approximately 40 nm in diameter with surface projections that measure roughly 5–10 nm. The surface proteins are arranged in an icosohedral-like symmetry.^{3,4} Zika is one of the emerging arboviral diseases that is transcending geographical boundaries at a very fast rate. The recent reports of Zika activity from across the continents (Fig. 2)⁵ have attracted the attention of public health specialists, as it too is a vector mediated disease transmitted by *Aedes aegypti* and *Aedes albopictus*, the vectors of dengue and chikungunya, which are already on a global rampage. The global predicted distribution of *A. aegypti*, the principal vector of Zika is presented in Fig. 3.⁶ Till date, the *Aedes* species, which have been implicated in the transmission of ZIKV are *A. aegypti*, *A. vitattus*, *A. furcifer*, A. africanus, A. apicoargenteus and A. luteocephalus. However, A. aegypti and A. albopictus are considered to be the major players in the transmission of the virus due to their ubiquitous global presence. The evidence so far implicates monkeys and humans as the sole reservoirs of the disease.^{7–9}

Outbreaks of ZIKV

ZIKV was first described in April 1947, when a sentinel rhesus monkey fell sick in the Zika Forest of Uganda while participating in a jungle Yellow fever research programme of the United States.^{7–9} Report of Human ZIKV was for the first time published in 1964 by a scientist, who described his own Download English Version:

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