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Zika Virus: An Update on Epidemiology, Pathology, Molecular Biology, and Animal Model

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Abstract

Zika virus (ZIKV) was first described in 1947, and became a health emergency problem in 2016 when its association with fetal microcephaly cases was confirmed by Centers for Disease Control and Prevention (CDC) in the United States. To date, ZIKV infection has been documented in 66 countries. ZIKV is recognized as a neurotropic virus and numerous diseases manifested in multiple neurological disorders have been described, mainly in countries that have been exposed to ZIKV after the 2007 outbreak in the Federated States of Micronesia. The most dramatic consequence of ZIKV infection documented is the abrupt increase in fetal microcephaly cases in Brazil. Here, we present an update of the published research progress in the past few months.

Keywords

Zika virus; epidemiology; pathology; transmission; animal model

INTRODUCTION

Although Zika virus (ZIKV) was described 70 years ago, it only became a public health problem at the end of 2015 when an outbreak in Brazil was associated with a significant increase of microcephaly cases in fetus and newborns. Since then, scientists all over the world are rushing to study the pathogenesis of ZIKV infection and understand the differences of infection between the first described strain African MR766, which only caused some mild symptoms, and the one identified in Asia at the Yap Island of the Federated States of Micronesia in 2007 and later in French Polynesia in 2013, which resembles the one in Brazil. New scientific information about ZIKV is available almost daily. Although a few great reviews have been recently published, important information has been described since then. Here we present an update review with the latest available information. Detailed reviews may be found elsewhere [Lazear and Diamond, 2016; Musso and Gubler, 2016; Petersen et al., 2016; Weaver et al., 2016].

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ZIKV INFECTION IN DIFFERENT GEOGRAPHIC AREAS

ZIKV was first isolated from a monkey in 1947 and then from an *Aedes africanus* in 1948 at the Zika Forest in Uganda [Dick, 1952, 1953; Dick et al., 1952]. The virus was subsequently detected in humans in other areas of Africa, and South and Southeast Asia in the following years [Smithburn, 1952, 1954; Macnamara, 1954; Smithburn et al., 1954a,b]. From 2007 to 2015, the outbreaks of ZIKV infection have been associated with different consequences in each region. In an outbreak in 2007, most of the population of Yap Island were infected by ZIKV but only mild symptoms including fever, headache, and skin rash previously described [Macnamara, 1954] were observed [Duffy et al., 2009]. When the virus reached French Polynesia in 2013 [Cao-Lormeau et al., 2014], there was an increase in cases of Guillain–Barré syndrome, an auto-immune disease that might cause temporary paralysis [Willison et al., 2016]. ZIKV was first detected in Brazil in early 2015. By the end of the year, a dramatic increase in cases of microcephaly in fetus and newborns were reported [Campos et al., 2015; Cardoso et al., 2015; Schuler-Faccini et al., 2016]. In February 2016, the World Health Organization (WHO) declared ZIKV infection as a Public Health Emergency of International Concern [Heymann et al., 2016], and in April 2016, the association between ZIKV infection and microcephaly was confirmed by the United States Centers for Disease Control and Prevention (CDC) [Rasmussen et al., 2016].

Neurological Diseases Associated With ZIKV Infection: Microcephaly

ZIKV has mainly been associated with a number of neurological disorders including Guillain–Barré syndrome [Oehler et al., 2014; Araujo et al., 2016; Cao-Lormeau et al., 2016; Malkki, 2016; Roze et al., 2016; Watrin et al., 2016] and acute disseminated encephalomyelitis (ADEM) [Ferreira, 2016] in adults, and with a drastic increase of microcephaly cases in fetus and newborns [Broutet et al., 2016; Cauchemez et al., 2016; Schuler-Faccini et al., 2016]. Microcephaly is characterized by a decrease in the head circumference of the fetus or baby. In Brazil, the cut off for term newborns is set at 32 cm after December 2015 [Victora et al., 2016]. Before the ZIKV epidemic in Brazil, numerous well-known infectious agents including toxoplasmosis, *Treponema pallidum*, varicella-zoster, parvovirus B19, rubella, cytomegalovirus (CMV), and herpes simplex virus (HSV) infections have been associated with cases of microcephaly [Neu et al., 2015]. ZIKV has now been suggested as a new cause for the outbreak of microcephaly cases in Brazil since October 2015 [Rasmussen et al., 2016]. The raw numbers for microcephaly that are indeed caused by ZIKV but not by aforementioned other etiologies are still controversial. Clinical re-evaluation of the early diagnosed cases and the molecular detection of ZIKV have expressively cut down the initial numbers of cases [Victora et al., 2016] though it remained possible that some of these cases were false negative. However, the number of cases confirmed as microcephaly between the end of 2015 and the beginning of 2016 remains at least five times higher than the number of annual cases reported before 2015 [Victora et al., 2016].

ZIKV was specifically detected in the brain tissue of a fetus with microcephaly, whose mother was probably infected around gestational week 13th in Brazil [Mlakar et al., 2016]. The virus was also identified in the amniotic fluid collected at gestational week 28th in two

other patients, whose babies were diagnosed with microcephaly [Calvet et al., 2016a]. No correlation has been found between the gestational time of infection and the severity of the microcephaly [Brasil et al., 2016]. Besides Brazil, a few other countries have detected ZIKV in fetus/newborn with microcephaly or central nervous system anomalies [Driggers et al., 2016; WHO, 2016]. ZIKV has also been associated with the death of a few patients but none was related to microcephaly [Arzuza-Ortega et al., 2016; Sarmiento-Ospina et al., 2016].

One of the first studies showing ZIKV infection of neurons and astrocytes in mice was published in 1971 [Bell et al., 1971]. ZIKV productive infection of human neural progenitor cells (hNPC) has recently been shown [Tang et al., 2016]. ZIKV-infected hNPC had reduced cellular proliferation as a result of activated caspase-3 and cell cycle arrest [Tang et al., 2016]. In a separate study, it was also reported that ZIKV infection induced cell death in human neural stem cells (hNSC) derived from human induced pluripotent stem cells (hiPSC) [Garcez et al., 2016]. ZIKV-infected hNSCs generated abnormal neurospheres compared with the non-infected hNSCs; and that apoptotic nuclei were detected in the ZIKV-infected neurospheres [Garcez et al., 2016]. Additionally, hiPSC-derived brain organoids exposed to ZIKV had a 40% reduction in the growth area compared with non-exposed ones. These cytopathic effects were not observed with DENV-2 infection [Garcez et al., 2016].

In an elegant study, forebrain organoids from hiPSCs mimicking human cortical development were generated in 3D cell culture using a mini-bioreactor spin Ω [Qian et al., 2016]. Following exposure to ZIKV, there was a decrease in the size of the organoid with a thinner ventricular zone-like layer. An increase in cell death, decrease of neural progenitor cells proliferation, and increase of the lumen size in the ventricular structures were also observed. These observed phenotypes resembled the characteristics of microcephaly [Qian et al., 2016]. A tropism of ZIKV for neural progenitor cells was also observed when different stages of hiPSCs mimicking first and second gestational trimesters were tested. There was an increase in the infected cells indicating productive infection and spread of the virus in the culture. Interestingly, no difference of phenotype between ZIKV strains from African or Asian lineages was observed [Qian et al., 2016]. It is unclear whether the Brazil strain would behave the same as the other lineages. This important model should be valuable for exploring ZIKV infection with close biological relevance, and useful for drug screening [Qian et al., 2016].

It remains unclear how ZIKV is able to cross the placenta barriers. In one study, it was shown that primary human trophoblast (PHT) cells from full-term placentas were resistant to infection of ZIKV when the African and Asian lineage were used. Since PHT cells constitutively release interferon (IFN)-III/IFN λ 1, this might avoid ZIKV infection. Although the mechanism is still unknown, it has been suggested that ZIKV evasion of IFN-III signaling and the placenta barrier bypass might depend on the gestational stage [Bayer et al., 2016]. On the other hand, IgM against ZIKV has been detected in 97% of the cerebrospinal fluid (CSF) samples, and in 90% of the serum from 31 evaluated newborns with microcephaly, indicating that the fetus/newborn might be infected in the central nervous system [Cordeiro et al., 2016].

Structural Characteristics for ZIKV Lineages

Two ZIKV lineages have been described so far, African and Asian. The strains isolated from samples in Brazil between 2015 and 2016 resembled those of Asian strains, particularly the French Polynesia strain [Baronti et al., 2014; Brasil et al., 2016; Faria et al., 2016; Giovanetti et al., 2016]. ZIKV is an arbovirus of the *Flaviviridae* family, *Flavivirus* genus, which also includes Dengue virus (DENV-1 to DENV-4), West Nile virus (WNV), Japanese encephalitis virus (JEV), and Yellow fever virus (YFV) [Musso and Gubler, 2016].

The ZIKV genome consists of one complete open reading frame (ORF) of less than 11 kb, and, as other flaviviruses, encodes three structural proteins: capsid, envelope glycoprotein (E) and membrane (M) or pre-membrane (prM), and seven non-structures proteins: NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5 [Lindenbach and Rice, 2003]. Its recently described 3.8 Å structure has revealed an important difference from those of other flaviviruses in the amino acids around Asn154 in the E protein [Sirohi et al., 2016]. Within this glycoprotein, ZIKV has a glycosylation site at Asn154 [Sirohi et al., 2016] while DENV has two glycosylation sites at Asn67 and Asn153, which influence viral assembly and exit, and infectivity, respectively [Johnson et al., 1994; Mondotte et al., 2007], and WNV has an glycosylation site at Asn154, which has been associated with neurotropism [Beasley et al., 2005]. It is possible that modifications at the glycosylation sites might be associated with the differences of tropism, infectivity, fitness, and pathogenicity among different strains of ZIKV. Some glycosylation sites were absent in a few African strains; however, passage of the virus might have caused the alterations, making it difficult to track when the modifications had occurred in the earlier isolated strains [Wang et al., 2016]. A detailed analysis comparing the available ZIKV isolates showed a 59 amino acid variation between the Asian and African lineages, where around 10% of the variations are located in the prM region [Wang et al., 2016].

Among the NS proteins, NS1, which also contains N-glycosylation sites, is essential for the replication and late infection of flaviviruses [Muller and Young, 2013]. Structural differences in the ZIKV NS1 has been discovered recently revealing different electrostatic potentials among ZIKV, DENV, and WNV, which might help clarify the differences in the pathogenesis among these viruses, as well as among different ZIKV strains [Song et al., 2016]. A mutation region in NS1 was observed in some isolates from Brazil compared with other Asian strains but the biological implication was unclear [Wang et al., 2016]. Another unique characteristic of the ZIKV structure is its stability in a wide range of temperatures ranging from 4 to 40°C [Kostyuchenko et al., 2016].

ZIKV TRANSMISSION

The main route for ZIKV transmission to a human is through a mosquito bite with *Aedes aegypti* and *Aedes albopictus* as the most common vectors. Two different cycles have been described: the first transmission cycle is restricted to non-human primates designated sylvatic; and the second transmission cycle is through the human-mosquito-human cycle (urban cycle) [Petersen et al., 2016; Weaver et al., 2016]. Recently, ZIKV has been detected in marmosets and capuchin-monkeys, most of which have been kept as pets, in Brazil [Favoretto et al., 2016].

Additional transmission routes have recently been described. Following the ZIKV outbreak in South America, autochthonous transmission not facilitated by mosquito has been described in Brazil and Colombia [Zanluca et al., 2015; Camacho et al., 2016] including a person with HIV [Calvet et al., 2016b]. Sexual transmission of ZIKV through vaginal, oral, and anal sex has also been reported and the virus was detected in saliva, urine, and semen samples [D'Ortenzio et al., 2016; Hills et al., 2016; McCarthy, 2016]. In Italy, import of ZIKV from Thailand through sexual transmission was described in a case [Venturi et al., 2016]. Additionally, blood transfusion transmission from an asymptomatic donor was reported in Brazil [Cunha et al., 2016]. Thus, extreme cautions should be taken for women who plan for a pregnancy.

ZIKV RECEPTORS

AXL, a receptor tyrosine kinase, which is also known as ARK, JTK11, or Tyro7, has been described as a main possible receptor for ZIKV entry in hNSCs [Nowakowski et al., 2016]. AXL is highly expressed in human radial glia cells, astrocytes, and endothelial cells [Nowakowski et al., 2016]. ZIKV entry of cells is also mediated by DC-SIGN and Tyro3 [Hamel et al., 2015]. Some cell types such as dermal fibroblasts, epidermal keratinocytes, and dendritic cells were described as permissive to ZIKV infection though the infection might be inhibited by types I and II IFNs [Hamel et al., 2015]. ZIKV infection triggers the innate antiviral response in skin fibroblasts with upregulation of Toll-like receptor 3 (TLR3) transcription but no change of interferon 3 (IRF3) gene expression [Hamel et al., 2015]. Other upregulated genes included retinoic acid-inducible gene 1 (RIG-I), Melanoma Differentiation-Associated protein 5 (MDA5), and Chemokine (C-C Motif) Ligand 5 (CCL5) [Hamel et al., 2015]. Interesting, ZIKV infection also induced an autophagy program, which might promote viral replication in permissive cells [Hamel et al., 2015].

ANIMAL MODELS

A mouse model for ZIKV has recently been reported [Lazear et al., 2016]. In this model, mice lacking IFN- α and - β signaling developed neurological disease and died as a consequence of ZIKV infection. High viral loads in the brain, spinal cord, and testes were detected compared to the wild-type mice. The lethal ZIKV infection was detected in adult mice lacking the capacity to either respond to or induce IFN- α/β (*Ifnar1*^{-/-}, *Irf3*^{-/-} *Irf5*^{-/-} *Irf7*^{-/-} triple knockout), and in AG129 mice (*Ifnar1* and *Ifngr1* deficient) [Lazear et al., 2016]. Although, AG129 mice are deficient in IFN- α , - β , and - γ receptors, the humoral and cellular T cell responses are intact. A separate study also showed a deadly ZIKV infection in young and adult AG129 mice. It was noted that the cytopathic effect was observed in the brain but not in other organs [Aliota et al., 2016].

The importance of developing a valid animal model cannot be denied; however, the results from an animal model may not always be extrapolated to humans, and the correlations of infection in the model and in humans should be carefully analyzed. This is particularly true for ZIKV because the natural reservoirs for the ZIKV are humans, non-human primates and mosquitoes, which makes precise modeling of natural transmission and infection difficult. Furthermore, the anatomy of mouse is quite different from that of human. For example, the

mouse placenta structure is distinct from that of human, thus, limiting the use of a mouse model for studying the infection and transmission of ZIKV across the placenta barriers in human.

PERSPECTIVES AND FUTURE DIRECTIONS

In the early studies with ZIKV following its initial discovery, most of the mice and even some monkeys infected by ZIKV had only mild symptoms. For almost 70 years, ZIKV was not associated with serious health problems in humans until it reached the Pacific Islands and South America. Even in this scenario, Brazil is the only country that is presenting a dramatic number of microcephaly cases despite ZIKV infection has been detected in 66 countries up to this day [WHO, 2016]. While there are differences between the African and Asian lineages, countries impacted by the Asian lineage also have had different outcomes ranging from low fever, Guillain–Barré syndrome to microcephaly. The development of the 3D model mimicking different stages of the central nervous system should help clarify the pathological features manifested in different geographic regions [Qian et al., 2016].

The dramatic differences could be related with the geographic areas affected, which present different climate, temperature, and population. Even inside Brazil, the distribution is also not clear-cut with most of the cases restricted to a limited area in the Northeast region [Faria et al., 2016]. A study showed that both *Aedes aegypti* and *Aedes albopictus* were susceptible to ZIKV infection but they also depended on the mosquito population in each region or country [Chouin-Carneiro et al., 2016]. Importantly, the study indicated that both mosquitoes were not competent vectors as expected. It was pointed out that there was no data available on ZIKV isolated from any *Aedes* mosquitoes from Brazil since the focus had been on humans so far [Chouin-Carneiro et al., 2016].

Another fact that cannot be ignored is the presence of other flaviviruses in the affected regions. Co-infections with DENV and CHIKV have been described in Brazil and New Caledonia [Dupont-Rouzeyrol et al., 2015; Pessoa et al., 2016] but synergetic effect has not been noticed in the patients. However, the idea that a pre-infection with another flavivirus might cause a worsen scenario for ZIKV infection should not be ruled out. A better understanding of the diseases associated with ZIKV will become possible when all the information about the distribution of *Aedes* mosquitoes, the differences in climate and season in the affected regions, geographic distribution [Messina et al., 2016; Rodriguez-Morales et al., 2016], precise mechanism of transmission, functional consequences of genetic variations among different strains, and the gestational stage(s) affected by infection become available.

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