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ZIKA VIRUS: AN EMERGING THREAT TO HUMAN LIVES

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ABSTRACT

Zika infection is a mosquito borne flavivirus that is the concentration of a continuous pandemic and general wellbeing emergency.It is restricted to sporadic cases in Asia and Africa, the development of Zika infection contaminations are portrayed by subclinical or mild flu like illness, severe appearance have been described, including Guillain-Barre disorder in grown-ups and microcephaly in infants destined to infected mothers. Neither a compelling treatment nor an antibody is accessible for Zika virus.despite developing learning about this virus, questions remain in regards to the virus's vectors and reservoirs, pathogenesis, genetic diversity and potential synergistic impacts of co-disease with other circling viruses. Less than 20 sporadic instances of human Zika infection (ZIKV) contamination were accounted for in Africa and Asia before 2007, yet vast breakouts including up to 73% of the populaces on the Pacific islands have begun since 2007 and spread to the Unites states in 2014. We extensively thought about the genome groupings of pre-pestilence and pandemic ZIKV strains with finish genome or finish polyprotein successions accessible in GenBank. Phylogenetic examine uncovered that Southeast Asian ZIKV won't not be the immediate wellspring of South American flare-ups as already guessed. These one of a kind buildups on outside viral proteins are not found in Southeast Asian ZIKV and could be in charge of the progressing flare-up either through a characteristic property of the infection or communications with human unsusceptibility.

KEYWORDS: Zika virus, infection, pathogen, immunity, chemotherapy.

INTRODUCTION

Zika virus infection is an emerging disease caused by Zika virus (ZIKV), a mosquito-borne arbovirus of growing public health importance.[1] It belongs to the family Flaviviridae, genus Flavivirus, with little genomic divergence from other viruses of the same genus[2] The first formal description of Zika virus was published in 1952,[3] and for much of the following 60 years, interest in this virus was confined to a few specialised researchers. On 1st February 2016, the disease has been declared as a ‘Public Health Emergency of International Concern[4] by the World Health Organization (WHO). Zika virus infection has recently been demonstrated as a global threat, changing its manifestations from an endemic mild disease to an epidemic severe one.[5] The virus was first isolated from a rhesus monkey in Zika forest of Uganda in 1947 and then from mosquitoes (i.e. Aedes africanus) in the same forest in 1948 and from humans in Nigeria in 1954.[6] For about 60 years after its first isolation,[3] the Zika virus (ZIKV) infection has been considered responsible for an extremely rare exotic disease of poor clinical relevance and limited public health importance. However, since the virus spread to the Pacific islands and the South America, causing an unprecedented epidemic, it has received the attention of the scientific community along with public opinion.[7] Zika virus is a growing concern – it is endemic in parts of Africa, has been reported in South East Asia and is becoming established in the Americas and Caribbean. Since its detection in Brazil in 2015, it has emerged as a major public health challenge in the Americas. As of 16 June 2016,[8] 60 countries and territories report continuing mosquito-borne transmission of which:

- 46 countries are experiencing a first outbreak of Zika virus since 2015, with no previous evidence of circulation, and with ongoing transmission by mosquitos.
- 14 countries have reported evidence of Zika virus transmission between 2007 and 2014, with ongoing transmission.

Serological studies and isolation of ZIKV strains have subsequently demonstrated that the virus has a wide geographical distribution, including eastern and western Africa, south and south-east Asia and Micronesia.[9] Also, the alarming scale of the current outbreak and the potential for autochthonous transmission of this virus in North America and elsewhere3,4,14 have heightened awareness of this emerging mosquito-transmitted disease.[10-12] As the epidemic expands its range, increasing numbers of travellers are transporting Zika virus to distant regions across the world.[13] If competent mosquito vectors become infected from these travellers in areas where environmental conditions are conducive to the virus’s spread, new epidemics could occur, subject to the presence of an immunologically susceptible human population.[14]

TIMELINE OF ZIKA VIRUS

The following timeline charts the origin and spread of the Zika virus from its discovery in Uganda nearly 70 years ago:

Year	**Discovery**
1947	Scientists researching yellow fever in Uganda's Zika Forest isolate the virus in samples taken from a rhesus monkey
1948	Virus recovered from Aedes africanus mosquito in the Zika forest
1952	First human cases detected in Uganda and Tanzania
1954	Virus found in young girl in Nigeria
1960s-1980s	Zika detected in mosquitoes and monkeys in band of countries stretching across equatorial Africa
1969-1983	Zika is found in equatorial Asia, including India, Indonesia, Malaysia and Pankistan
2007	Zika spreads from Africa and Asia to cause the first large outbreak in the Pacific island of Yap
2012	Two distinct lineages of the virus, African and Asian, are identified by researchers
2013-2014	Zika outbreaks in French Polynesia, Easter Island, the Cook Islands and New Caledonia. Retrospective analysis shows possible link to birth defects and severe neurological complications in babies in French Polynesia
March 2, 2015	Brazil reports an illness characterized by skin rash in northeastern states
April 29, 2015	Brazilian samples test positive for Zika
July 17, 2015	Brazil reports detection of neurological disorders in newborns associated with a history of infection
October 5, 2015	Cape Verde reports cases of illness with skin rash
October 22, 2015	Colombia confirms cases of Zika
October 30, 2015	Brazil reports unusual increase in cases of microcephaly - abnormally small heads - among newborns
November 11,2015	Brazil declares a national public health emergency
November 2015-January 2016	Cases reported in Suriname, Panama, El Salvador, Mexico, Guatemala, Paraguay, Venezuela, French Guiana, Martinique, Puerto Rico, Guyana, Ecuador, Barbados, Bolivia, Dominican Republic, Nicaragua, Curacao, Jamaica
February 1, 2016	World Health Organization declares a public health emergency of international concern

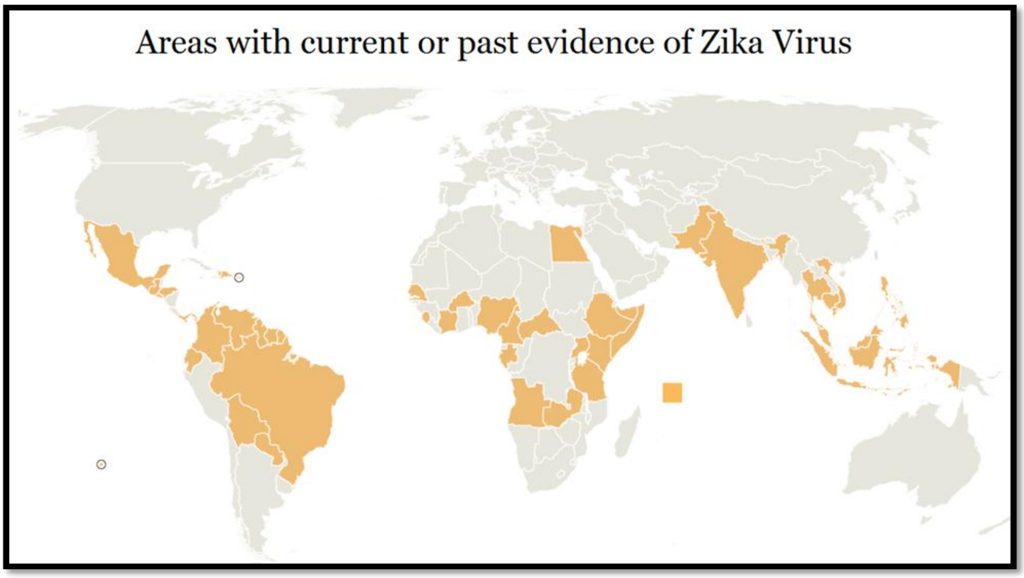
EPIDEMIOLOGY OF ZIKA VIRUS

Zika virus was first discovered in Uganda in 1947 in rhesus monkeys and was subsequently identified in humans in 1952. Since then, outbreaks have occurred in Africa, the Americas, Asia and the Pacific. The first large outbreak, with 185 confirmed cases, was reported on the island of Yap (Federated States of Micronesia) in 2007. Another large outbreak was seen in French Polynesia from 2013 to 2014. In the current South American outbreak, the first reports of locally transmitted infection came from Brazil in May 2015 and the country is currently experiencing the largest epidemic ever recorded with 497,593 to 1,482,701 suspected cases reported by the Brazilian health authorities. There are 3174 cases and 38 deaths from microcephaly in Brazil as of 21 October 2015. There has been total death of 152 as of 21 October 2015 in the world. By the beginning of February 2016, local transmission had been reported in 26 countries/territories in the Americas. After Brazil, Colombia reported the largest number of cases (20,297 as of 23 January 2016) since October 2015. There is also an ongoing outbreak in Cabo Verde, West Africa (7081 cases as of 17 January 2016) which started in October 2015. Cases in returning travellers have now been reported in other countries including the US, UK, Australia and China.

Affected Countries

Barbados, Bolivia, Brazil, Colombia, the Dominican Republic, Ecuador, El Salvador, French Guiana, Guatemala, Guadeloupe, Guyana, Haiti, Honduras, Martinique, Mexico, Panama, Paraguay, Puerto Rico, Saint Martin, Suriname and Venezuela.

Countries and territories with active Zika virus transmission as of Jan 2016.

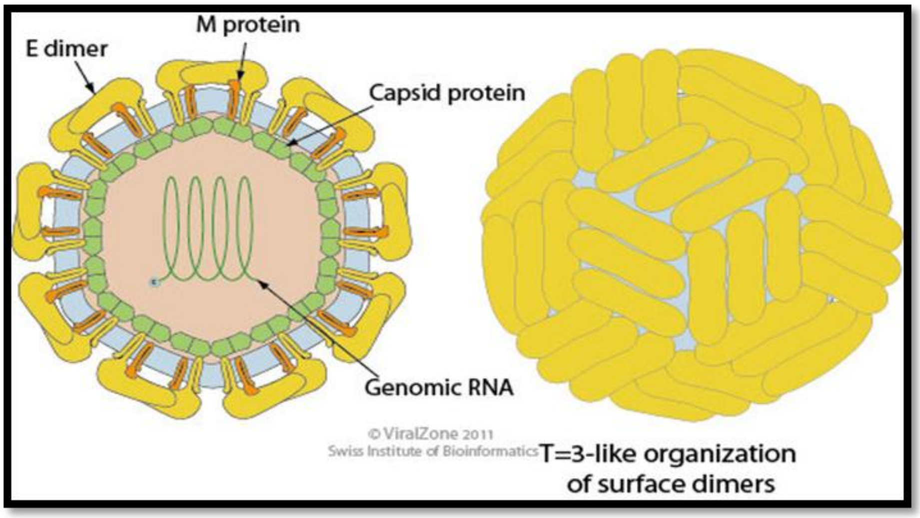


Source: CDC

Since November, Brazil has seen nearly 4,000 cases of microcephaly in babies born to women who were infected with Zika during their pregnancies.

STRUCTURE OF ZIKA VIRUS

- The virion is approximately 40 nm in diameter with surface projections that measure roughly 5-10 nm.
- Nucleocapsid is 25-30 nm in diameter surrounded by a host-membrane derived lipid bilayer.
- Enveloped
- Icosahedral
- Contains envelope proteins E and M



Group: Group IV ((+) ssRNA)

Family: Flaviviridae

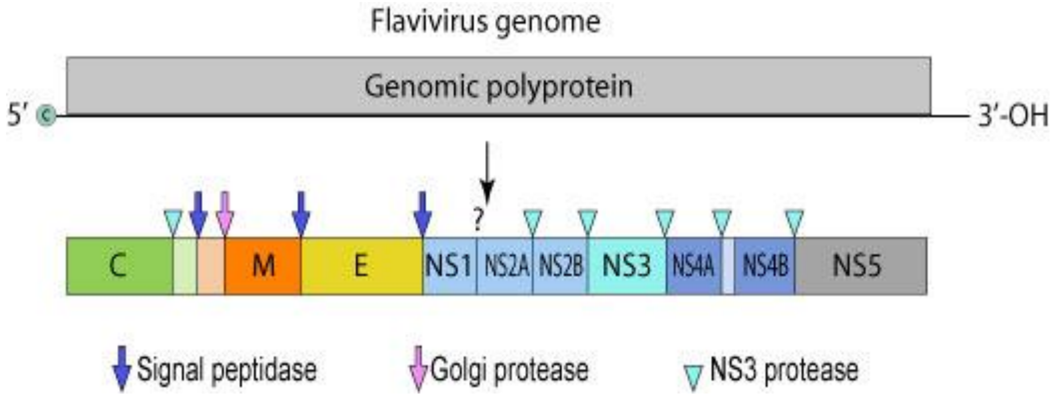
Genus: Flavivirus

Species: Zika virus

The ZIKV genome consists of a single-stranded positive sense RNA molecule with 10794 kb of length with 2 flanking non-coding regions (5′ and 3′ NCR) and a single long open reading frame encoding a polyprotein: 5′-C-prM-E-NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5-3′, that is cleaved into capsid (C), precursor of membrane (prM), envelope (E) and seven non-structural proteins (NS). The E protein (≈53 kDa) is the major virion surface protein. E is involved in various aspects of the viral cycle, mediating binding and membrane fusion. The NS5 protein (≈103 kDa) is the largest viral protein whose C-terminal portion has RNA-dependent RNA polymerase (RdRP) activity and the N-terminus is involved in RNA capping by virtue of its processing due to methyl transferase activity. The 3′NCR of the ZIKV genome contains about 428 nucleotides, including 27 folding patterns that may be involved in the recognition by cellular or viral factors, translation, genome stabilization, RNA packaging, or cyclization. Although diverse studies have contributed greatly to our understanding of the evolutionary biology of flaviviruses in general, few studies have addressed ZIKV evolutionary biology. Those studies report three main ZIKV lineages, one from Asia and two from Africa. Aiming to fill this gap and gain better insights ZIKV molecular evolution in the 20th century, we investigated 43 ZIKV strains, sampled from 1947 to 2007 in Africa and Asia, to describe phylogenetic relationships, selective influences, recombination events, phylodynamics, phylogeography, host correlations with viral lineages and glycosylation patterns.

GENOME OF ZIKV

The Zika virus is a positive sense single-stranded RNA molecule 10794 bases long with two non-coding regions flanking regions known as the 5' NCR and the 3' NCR. The open reading frame of the Zika virus reads as follows: 5′-C-prM-E-NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5-3′ and codes for a polyprotein that is subsequently cleaved into capsid (C), precursor membrane (perm), envelope (E) and non-structural proteins (NS). The E protein composes the majority of the virion surface and is involved with aspects of replication, such as host cell binding and membrane fusion. NS1, NS3 and NS5 are large, highly-conserved proteins while the NS2A, NS2B, NS4A and NS4B proteins are smaller, hydrophobic proteins. Located in the 3' NCR is 428 nucleotides that may play a part in the translation, RNA packaging, cyclization, genome stabilization and recognition. The 3' NCR forms a loop structure and the 5' NCR allows translation via a methylated nucleotide cap or a genome-linked protein.



TRANSMISSION

Zika virus is transmitted to people through the bite of an infected mosquito from the*Aedes* genus, mainly *Aedes aegypti* in tropical regions. This is the same mosquito that transmits dengue, Chikungunya and yellow fever. However, sexual transmission of Zika virus has been described in 2 cases and the presence of the Zika virus in semen in 1 additional case. There has been one report of possible spread of the virus through blood transfusion and one report of possible spread of the virus through sexual contact. In 2015, Zika virus RNA was detected in the amniotic fluid of two fetuses, indicating that it had crossed the placenta and could cause a mother-to-child infection. The Asian tiger mosquito, *Aedes albopictus*, is also known to transmit the virus, but it is not clear how efficiently. To date, there are no reports of infants getting the Zika virus through breastfeeding.

PREVENTION

The epidemiological and clinical experience obtained during the current outbreak makes the development of a ZIKV vaccine a global health priority.[16] Currently there is no drug or vaccines available for Zika virus Infection. There are reports of an Indian Biotech company which is ready with two candidate vaccines for ZIKV infection to be tested in preclinical stages. Hence the prevention of this disease becomes the most crucial method to control the outbreak and its spread.[17] Also, protecting against mosquito bites is the primary method of prevention. The achievement of a ZIKV vaccine for humans requires a better insight into ZIKV immunology and mechanisms of immune protection. For example, the development of a live-attenuated vaccine is inadvisable until the link between GBS and ZIKV will be elucidated and additional complications related to pre-existing flavivirus exposure should be deeply probed in order to develop an efficient and safe vaccine.[18]

CONCLUSION

It is observed that there occurs regional differences exist in the transmission of Zika virus in different parts of the world. Zika virus infection is considered as a global threat, changing its manifestations from an endemic mild disease to an epidemic severe one, associated with certain neurological complications, such as microcephaly and Guillain-Barré syndrome. Taking into consideration the climate change and its consequences on global ecology, the fact that the majority of the human population lives in areas infested by mosquitoes of the *Aedes* genus, as well as the effects of globalization and increased air travel in the spread of infectious diseases, the potential of a ZIKV pandemic is of immense concern. Molecular and serological methods have been successfully established for the laboratory diagnosis of the disease; however, since in most cases there are no typical clinical symptoms or laboratory findings, ZIKV disease may be misdiagnosed or confused with other flaviviral diseases.

Thus, more effective vector control and surveillance measures are required along with the development of effective drugs and vaccines for controlling the infection.

Complications: Guillain-Barre syndrome

During the current outbreak in South America, an increased incidence of Guillain-Barre syndrome (GBS) has been reported. An increased incidence was also reported in a previous large outbreak in French Polynesia in 2013 and 2014. According to WHO, available data are insufficient to interpret the observed differences in GBS incidence globally and among states in Brazil. Case-control studies are ongoing. The CDC is working with Brazil to investigate the association.

Complications: pregnancy-related

The WHO Emergency Committee has agreed that a causal relationship between Zika virus infection during pregnancy and microcephaly in the baby is strongly suspected; however, this is yet to be proven.

Zika virus infection has been confirmed in several infants with microcephaly from Brazil. The time frame and geographical location of reports of infants with microcephaly coincides with the outbreak of Zika virus infection in Brazil. The baseline prevalence of congenital microcephaly is difficult to determine because of under-reporting and the inconsistency of clinical criteria used to define microcephaly. Although population-based estimates of congenital microcephaly in Brazil vary, the number of infants with microcephaly currently being reported in Brazil is greater than would be expected. The Ministry of Health reported 4783 cases of microcephaly between October 2015 and 30 January 2016, including 76 deaths. The incidence is usually significantly lower; between 2001 and 2014, 163 cases were reported nationwide per year. Authorities in Brazil are currently investigating the 4783 reported cases.

Brain abnormalities reported in infants with microcephaly and laboratory-confirmed congenital Zika infection includes microcephaly and disrupted brain growth. Some infants with possible Zika virus infection have been found to have intracranial calcifications and abnormal eye findings. It is not known if Zika virus infection caused any of these abnormalities and long-term sequelae are not yet clear.

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