

Short Communication

Zika virus, American lineage?

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The Zika virus belonging to group IV of the Baltimore viral classification, which encompasses it as a positive single-stranded RNA virus, is a member of the Flaviviridae family and genus Flavivirus, was isolated for the first time in 1947, from a Rhesus macaque in the Zika forests, in Uganda. In 1968 he was isolated for the first time in humans from a sample from Nigeria and there was evidence of distribution by Africa and some cases in Asia as well as Oceania. In such reports, an acute febrile syndrome was observed, accompanied by conjunctivitis, rash, arthralgia and rarely bleeding tendency. He was credited with a benign course without major complications. No mortality was commented. Among its vectors that include nematopores dipterans of the Culicidae Family, stand out *Aedes Africanus*, *Aedes Opok*, *Aedes Vittatus* and *Aedes Luteocephalus*.^{1,2,3}

From the 60s, until 2007 the reports were isolated, however in that year there was an outbreak in some islands of Micronesia (Oceania) mainly in the Island of Gabon and Yap and later in French Polynesia in 2013, where it was reported an increase in the incidence of cases and highlighting that acute clinical neurological syndromes mainly Guillain Barre syndrome were added to the clinical picture. This constituted the beginning of the American colonization. The vectors shown in these outbreaks were from the *Aedes* genus, such as *A. Hensilii* and *A. Polynesiensis*.^{2,4}

In 2014, the first case was reported in Chile, beginning the American colonization, with wide distribution in South America, that through vectors other than *Aedes* but of the Culicidae family, such as *Culex*, *Anopheles*, *Mansonia*, *Haemagogus*, among others, combined with *A. Aegypti* and *A. albopictus* viral dissemination could be faster and more effective, later colonizing Central America and North America and exporting cases to Europe and China (cases imported from inhabitants who had traveled to America and it is believed, others transmitted by vectors such as *A. Koreicus* and *A. Japonicus*).

The American invasion was characterized by a large increase in the incidence of cases of Guillain Barre Syndrome that culminated in demonstrating viral neurotropism, as well as the affectation demonstrated by vertical transmission, initially cataloged as microcephaly however currently characterized as Congenital Zika Syndrome, which it encompasses a variety of malformations to important organs, which demonstrate an established fetal neurotropism and teratogenicity. In the same way, he highlighted in this American raid the routes of transmission, such as labor, vertical, transfusion, sexual, and more worrisome, the transmission from person to person without a necessary vector, having reported so far 13 cases of this situation. Similarly, in America if mortality associated with Zika has been reported.

So far and according to the figures presented by the World Health Organization in its last report of August 2017, it mentions 20 deaths by Zika (without taking into account deaths by Guillain Barré), 3,539 cases of Congenital Syndrome Associated with Zika and 1,003,509 cumulative cases of Zika in the period from 2015 to 2017.^{1,2,4,5,6}

The viral lineage is believed to begin in Africa with two branches, a West African lineage (Nigerian cluster), and another from East Africa (MR766 prototype group), subsequently a third lineage, called the Asian lineage, has been added. The theory postulates that the lineage originated in East Africa and subsequently migrated to West Africa and Asia, approximately 50-100 years ago. The first phylogenetic analyzes of the virus in Brazil show that the virus is closely related to that found in French Polynesia, from the Asian Lineage. Genome sequencing in isolated viruses in Guatemala and Puerto Rico demonstrates that the isolated virus in these countries is closely related to those found in Brazil and French Polynesia, that is, Asian Lineage.

Currently, genetic sequences of the virus have been characterized in several countries (2015-2016), the sequences of: Brazil, Colombia, Suriname, Venezuela, Guatemala, Puerto Rico, Mexico, Martinique, Haiti, the United States of America, among others being relevant. Other genetic sequencing in countries such as China and Italy (2016) stand out, which are similarly cases from the Asian Lineage derived from America, and that speak of the extent of colonization that encompassed all of America and once again extended to Asia (with different viral genomes having relation to the Americans) and to Europe.^{7,8,9,10,11}

During the genetic analyzes, mutations were detected that could explain, in part, the characteristics of the Zika virus throughout the Americas, the total being 1,030 mutations throughout the genome, of which 202 are non-synonymous mutations (changes in the sequence of amino acids) and 32 mutations are in the 5' and 3' regions (which regulate viral replication and gene expression), such mutations give the new mutant virus greater pathogenicity and virulence, as well as adaptability to the environment, the host and other vectors, which can be related to what was previously commented, where the Zika virus in America, had a totally different behaviour than previously observed, with greater transmission capacity even without needing a specific vector (person to person), use of vectors other than the Aedes genus , a clinical picture with non-febrile and asymptomatic cases (carriers), presence of neurotropism and teratogenicity, and mortality demonstrated, on the other hand it has stimulated the investigation of its pathogenesis, diagnosis and treatment; We believe that at some point a lineage different from that of Africa and Asia could be developed, more aggressive, more virulent and more pathogenic, that confers greater morbidity and mortality, such as the one we saw and will continue to see in America, and which has now moved again towards Africa (Cape Verde, Zika virus Asian-American lineage) and Asia as a vicious circle, with documented cases in China, Japan and Korea, as well as in Europe, with cases in Spain, France and Italy, after the American wave, in where the virus has practically completed a circumnavigation throughout the land; Some authors call it the Asia-Pacific-America Lineage, however, it is in America where the manifestations changed markedly in every way, so it could be an American Lineage, descendant of the Asian.^{3,8,9,10.}

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