

# New analysis sheds light on Zika virus evolution and spread

13 October 2016, by Donna Hutchinson

In a study published in *Pathogens and Global Health*, researchers have modelled the evolutionary development and diversity of the Zika virus to better understand how infection spreads between populations and how the virus reacts with the immune system. Such an understanding is essential if an effective vaccine is to be developed.

First found in Uganda in 1947, Zika is the newest discovery among a group of mosquito-transmitted viruses known as flaviviruses. It is an emerging threat in South and Central America and the Caribbean, with the recent Brazilian epidemic resulting in 440,000-1,300,000 cases and spreading to more than thirteen other countries.

While infected people usually show no symptoms, these can include fever, rash, joint pain or conjunctivitis. In addition, the Brazilian outbreak indicated Zika might cause fetal losses in pregnant women or microcephaly in infants born to infected women.

Dr. Silvia Angeletti from the University Campus Bio-Medico, Rome, and colleagues, carried out evolutionary analysis of the virus combined with homology (shared ancestry) modelling and T- and B-cells epitope prediction, which aims to determine how immune system responses cause the virus to react and change.

Their analysis revealed two distinct genotypes of the virus, African and Asiatic, and two separate clades (biological groupings that include a common ancestor and all the descendants of that ancestor). Clade I represented African gene sequences and Clade II, sequences of Asiatic and Brazilian origin.

The Brazilian sequences were found to be closely related to a sequence from French Polynesia. This lends support to the hypothesis that the virus might have been introduced to Brazil during the Va'a World Sprint Canoeing Championship in Rio de

Janeiro in 2014, which included a team from French Polynesia, rather than the World Cup in which no teams from Pacific countries participated.

Among the factors that influence Zika infection, 'antigenic variability' (the way the virus alters its surface proteins to evade the host's immune response) and pre-existing immunity caused by cross-reactions with other viruses might play an important role. Such cross-reactions also make diagnosis of Zika infection unreliable, and could thus facilitate the spread of the virus.

"Understanding the differences and similarities between Zika and other flaviviruses, such as the dengue fever and chikungunya viruses, is essential if effective drugs, vaccines and Zika-specific immunological tests for large population screening are to be designed," the authors say.

**More information:** Silvia Angeletti et al. Phylogenesis and homology modeling in Zika virus epidemic: food for thought, *Pathogens and Global Health* (2016). [DOI: 10.1080/20477724.2016.1235337](https://doi.org/10.1080/20477724.2016.1235337)

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