

MOLECULAR DIAGNOSTIC AND EVOLUTIONARY HISTORY OF ZIKA VIRUS IN BRAZIL, IN THE LATIN AMERICAN OUTBREAK THROUGH GENOMICS METHODS

Marta Giovanetti^{1,2}, [Jaqueline Goes de Jesus](#)², Maricelia Maia de Lima³, Joshua Quick⁴, Nuno Rodrigues Faria⁵, Erenilde Marques de Cerqueira³, Nick Loman⁴, Luiz Carlos Junior Alcantara^{6,7}

¹Department of Biology, University of Rome Tor Vergata, Rome, Italy, ²Laboratory of Hematology, Genetics and Computational Biology, Instituto Gonçalo Moniz, Salvador, Bahia, Brazil, ³Departamento De Saude, Universidade Estadual De Feira De Santana, Feira De Santana, Brazil, ⁴Institute for Microbiology and Infection, University of Birmingham, Birmingham, UK, ⁵Department of Zoology, University of Oxford, Oxford, UK, ⁶Instituto Gonçalo Moniz, Fundação Oswaldo Cruz, Salvador, Brazil, ⁷Depto. De Biologia, Universidade Estadual De Feira De Santana, Feira De Santana, Brazil

Background: Zika virus (ZIKV) has caused an estimated number of >40 million cases in Brazil and is now considered a Public Health Emergency of International Concern. Despite its associations with microcephaly, its disease severity and its recent Pan-American spread, complete genome sequences of the ZIKV of the current epidemic in Brazil are still very limited.

Findings: Through the diagnosis by RT-qPCR, 108 clinical specimens from Feira de Santana, the second largest city of Bahia state in Brazil, and 72 from Manaus the Amazon's largest city in the North of Brazil, including microcephaly cases have been tested. We found 10 samples from Feira de Santana and 3 from Manaus positive for the presence of ZIKV with an average Ct value of 33,71 (minimum 24.72 - 42.7 maximum). Phylogenetic analysis of the new complete genome sequences generated by Minion showed that all new sequences belonged to the Asian genotype. ZIKV genomes from Brazil appear phylogenetically interspersed with those from other South American and Caribbean countries. The sequences from the Manaus were dated back in the tree in April 2014 prior to the first detection of ZIKV in Brazil. If the ZIKV epidemic in Brazil did indeed arise from a single introduction then the virus must have circulated in the country for at least 12 months prior to the first case being reported in May 2015.

Conclusion: Considering the small number of ZIKV complete genomes available worldwide the analysis carried out, may contribute substantially to obtain large number of complete genomes that will provide information regarding the entrance of the virus in Brazil, the transmission route, genetic variability, pathogenesis, viral evolution, the dispersion and adaptation, and generate data for the development of molecular tests and more effective drugs and/or vaccines.