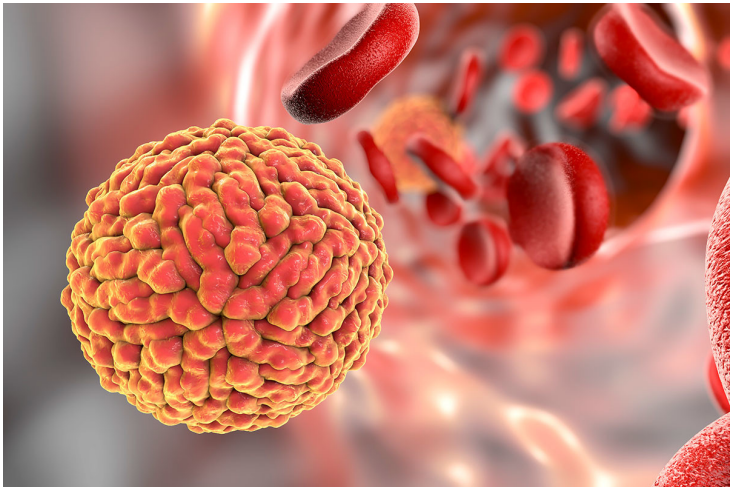


New gene sequencing study unleashes the spread of Zika

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The research led by the Universities of Birmingham and Oxford in partnership with FioCruz Bahia, the University of Sao Paulo with the support of the Brazilian Ministry of Health, has found how Zika spread through space and time. This has provided a new understanding of the disease.

By carrying out genome sequencing to understand the virus' genetic make-up, the team was able to track the spread of the virus across Brazil. The study showed that Zika's establishment within Brazil - and its spread from there to other regions - occurred before Zika transmission in the Americas was first discovered. By revealing this 'hidden' epidemic, the results will help scientists to better understand the link between the Zika epidemic and reports of birth defects and other diseases.

According to a news release by the University of Oxford, the researchers travelled 2,000 km across the northeast Brazil in June last year in a minibus equipped with cutting-edge mobile DNA sequencing capabilities and tested samples from more than 1,300 patients infected with the virus.

During the genome sequencing journey that travelled across Brazil, the researchers used the portable MinION DNA sequencer from the company Oxford Nanopore Technologies, which started as an Oxford University spinout company. The portable device weighs less than 100g and is powered by the USB port of a laptop, so is ideal for cross-country fieldwork.

The project is now expanding to other geographic areas in Brazil, where not only Zika virus but also dengue and chikungunya viruses are being tackled, as well as the very recent ongoing yellow fever epidemics. The threat posed from viruses transmitted by mosquitoes in Brazil is severe and there is a pressing need to better understand their epidemiology in order to prevent their spread.