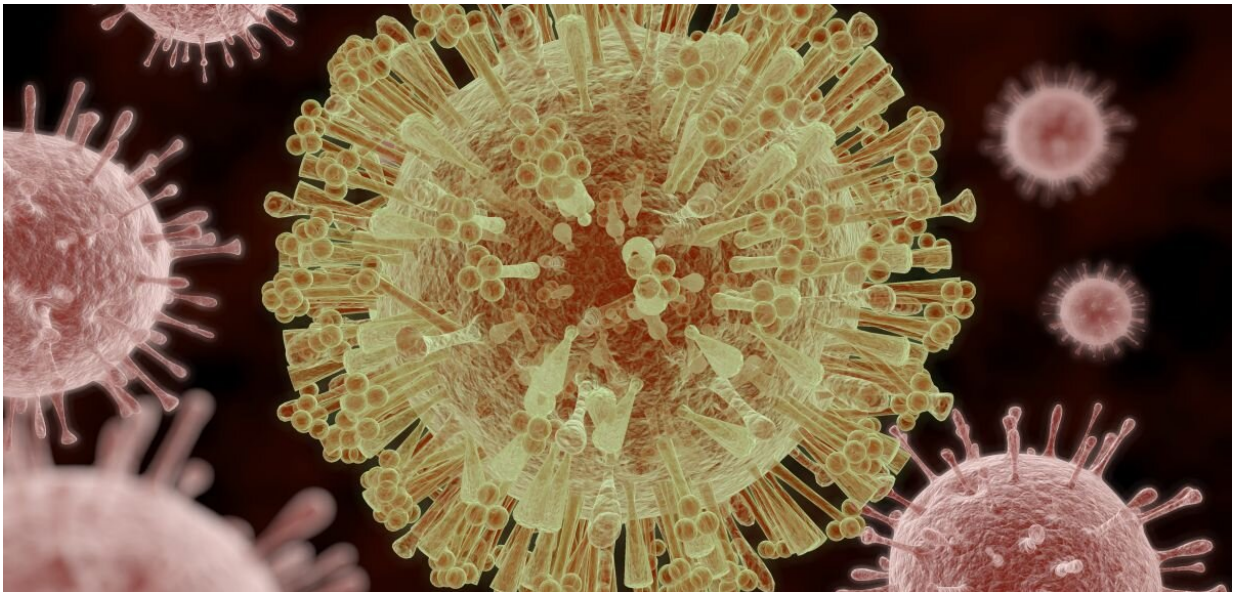


The Zika virus discovered on the African continent

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Credit: University of Oxford

Researchers from the University of Oxford teamed up with the Angolan Ministry of Health to study the introduction and circulation of the Asian genotype of Zika virus in Angola, southwestern Africa. The Asian genotype caused the 2015-16 epidemic of microcephaly and other birth defects in the Americas.

Their findings are published today in *The Lancet Infectious Diseases*.

In 2017 Angola started reporting cases of microcephaly in newborns. Until that point only the African genotype of Zika was known to circulate in Africa.

Researchers from Oxford's Department of Zoology and the Instituto Nacional de Investigação em Saúde in Luanda, followed up on reports of microcephaly cases in Angola, which they suspected could be caused by Zika virus infection in pregnancy. They carried out molecular testing and genome sequencing to understand the virus's genetic history and its epidemiology in this ground-breaking genomic detective work. This is the first time that complete virus genomes have been generated on-site in Angola.

They found that:

- The Asian genotype of Zika virus had been circulating in Angola since at least 2016.
- The strains circulating there were most likely to be introduced from Brazil.
- The virus migration route reflects the large number of travellers flying between Angola and Brazil.
- The Asian genotype of Zika virus is likely linked to an upsurge in microcephaly cases in Angola.

Lead author, Dr. Nuno Faria, said: "Zika virus has been circulating in Africa for centuries. It can be classified in two virus lineages, named as African lineage, restricted to the African continent, and the Asian lineage, responsible for the large epidemics of Zika and associated microcephaly in the Americas. Up until now only the African lineage had been detected in Africa. Back in 2017 Angola started reporting several cases of microcephaly in newborns.

"By carrying our molecular testing and genome sequencing to understand

the virus genetic make-up and its epidemiology, we found that the Asian lineage was introduced from Brazil into Angola in 2016, probably by a traveller infected with Zika. This virus then led to the recent upsurge in microcephaly cases in the country. Our study highlights the need of increased surveillance in areas that are connected by travellers to regions where Zika and other mosquito-borne viruses circulate."

The [international collaboration](#) coordinated by scientists from Oxford University and the Ministry of Health in Angola, together with the Ministry of Health in Portugal and several research institutes in Brazil, used the latest handheld portable sequencing technologies to investigate the epidemiology of Zika virus in Africa.

First author of the study, Dr. Sarah Hill, said: "During 2017, Angola began reporting an increased number of babies born with suspected microcephaly. Detailed investigation into two mothers and their infants showed that the mothers had antibodies to Zika virus, and that their infants had brain abnormalities consistent with congenital Zika syndrome.

"We searched for Zika virus in patients presenting with symptoms compatible with Zika infection in Angola. Zika virus infection often does not cause symptoms, so we also screened hundreds of asymptomatic patients for the virus. We only detected Zika virus in a total of five patients, but by using viral genome sequences to reconstruct the outbreak we showed that Zika virus likely circulated in Angola for over 17 months. Therefore, the true scale of the outbreak in Angola was likely larger than the small number of identified cases would suggest. Our work involves an international collaboration between research groups from four continents."

The research coupled scientific detective work in challenging conditions with the latest, agile technology.

Dr. Joana Afonso, director of the Public Health Laboratory, Ministry of Health in Angola, co-lead author of the study, said: "Techniques such as on-site portable DNA sequencing and computational analysis, linked with traditional molecular diagnostics, allowed us to get a better understanding of the virus epidemiology and its link with microcephaly in our country. Bringing rapid genomic sequencing tools to Angola is empowering local academics and is helping us to improve early detection of future virus threats. Ultimately, fostering scientific innovation and research in Angola will help to improve the health of our country."

Dr. Jocelyne Vasconcelos, said: "We still need to conduct additional studies to investigate what was the fraction of the population exposed to Zika and other viruses transmitted by mosquitoes." Dr. Zoraima Neto, concluded, "We are now working on expanding genomic surveillance to dengue, chikungunya and yellow fever and other neglected viral infectious diseases."

Dr. Eve Lackritz, Zika Task Force Lead from World Health Organization, said: "Use of viral sequence analysis is a powerful tool for tracking the global spread of Zika and other viruses of epidemic potential. These results are significant in that they demonstrated the introduction of the Asian genotype into continental Africa, demonstrating the ongoing spread of Zika virus worldwide and our continued need to remain vigilant to Zika [virus](#) infection and its impact on pregnant women and infants."

More information: Sarah C Hill et al. Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation, *The Lancet Infectious Diseases* (2019). [DOI: 10.1016/S1473-3099\(19\)30293-2](https://doi.org/10.1016/S1473-3099(19)30293-2)

Provided by University of Oxford

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