

# Real-time sharing of Zika genomes—the race against a virus

October 5 2016, by Bronwyn Macinnis

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As the global health emergency caused by the Zika outbreak continues, the virus underlying it remains a mystery, with devastating consequences still being identified. More than a year after Zika became widespread in the Americas, scientists have yet to fully unravel its trajectory across the continents, the scale and impact of disease risk, or how the virus might be defeated.

Given the pressing need to better understand this growing public health threat, researchers at the Broad Institute, Massachusetts Institute of Technology, and Harvard University, in partnership with colleagues at Florida Gulf Coast University, The Scripps Research Institute, the Oswaldo Cruz Foundation (known as Fiocruz) in Rio de Janeiro, the National Autonomous University of Honduras, and others, are working together to bring the power of genomics to bear on the Zika outbreak.

Today this partnership is releasing 33 Zika virus genome sequences obtained directly from patients or mosquitoes in the affected regions across the outbreak. The [genome data](#), together with related information about the samples, are being made freely available to the global scientific community to speed Zika research worldwide. The data are currently available as consensus sequences on the open-access viral genomics community website [Virological.org](#), and will soon be deposited on NCBI GenBank.

The data offer a window into the genetic underpinnings of the Zika virus as it circulates across the hemisphere. The researchers hope it may also

harbor important clues that could aid in understanding how the virus spreads and causes disease, and improving diagnostics and therapies to control it.

## **Share and share alike**

From the outset, the investigators involved in this project agreed that the Zika sequences should be shared openly as soon as they were generated and verified.

"With people's health on the line, it is essential to make new information public as soon as possible," says Pardis Sabeti, a leader in the Infectious Disease and Microbiome Program at the Broad Institute. "We hope that this contribution will help fill gaps in our understanding of this devastating virus and help create tools to defeat it."

Often in outbreaks, sharing of scientific data—including genome sequences—is delayed until after researchers have conducted their own in-depth analysis and published a manuscript describing their work. Sadly, this means that important insights that could come only from pooling data across multiple groups are often not identified until it is too late to impact the course of the outbreak.

Instead, this Zika genome effort is modeled on the experience of Sabeti and her team during the Ebola outbreak of 2014. Already on the ground in Sierra Leone researching Lassa fever, Sabeti's lab and partners in West Africa were able to collect patient samples when the outbreak began, analyze the genomes, and immediately release the information. Their data, combined with data shared by other groups with a similar approach, provided key insights into the evolution and transmission of Ebola and helped inform the development of better Ebola diagnostics.

Their work also demonstrated the feasibility and value of sharing

genomic data in real time, while an outbreak is in progress (Yozwiak et al, Nature 2014). It's a model that the team, together with their international partners, is now committed to applying to help combat Zika.

Today's release includes 33 near-complete Zika genome assemblies sequenced directly from infected patient and mosquito samples. The samples were collected between March and September 2016 as part of long-term clinical studies led by collaborating investigators: In Brazil, Dr. Fernando Bozza's team from Fiocruz and D'or Institute is investigating infections by mosquito-transmitted viruses such as dengue, chikungunya, and Zika within the urban environment of Rio de Janeiro. In Honduras, Ivette Lorenzana leads the national reference laboratory and with her team studies clinical correlates of viral infections. In Florida, Sharon Isern and Scott Michael are investigating Zika molecular epidemiology, immunology, and therapeutic development. At MIT, Irene Bosch and Lee Gehrke, whose strong research network in South and Central America helped seed this partnership, are developing rapid diagnostics for Zika and other arboviruses. The teams are now working together to analyse and publish findings from their genome data.

## **The Zika challenge**

While the Zika epidemic has been unfolding for nearly a year, much of the genetic information generated to date has been either incomplete (describing only small regions of the genome) or obtained from "cultured" virus samples, which may lead to artifacts in the data. Consequently, fundamental questions about Zika that could be addressed with better genetic data—for example, questions related to viral diversity, evolution, transmission patterns, and pathogenesis—remain poorly understood.

The shortage of genomic data has been due, in part, to the fact that Zika

virus has been particularly difficult to sequence, as virus levels within patients tend to be low and transient.

The Broad's Viral Genomics Group, under Sabeti's direction, has brought to bear its extensive experience developing robust laboratory and computational approaches for sequencing viruses such as Lassa, Ebola, and chikungunya, directly from clinical samples. In addition to releasing the Zika data, the group is working to optimize and share robust protocols and guidelines for clinical Zika sequencing.

The Zika genomes were isolated from serum, urine, and/or plasma collected from infected patients and from Zika-positive mosquito pools and were sequenced on the Illumina MiSeq or HiSeq platform at the Broad. At least 70 percent of the genome is covered in all 33 samples, and at least 95 percent in 22 samples.

"This collaboration represents a transnational effort to better comprehend molecular epidemiology of Zika virus," says Thiago Moreno L. Souza from Fiocruz. "Collaborators shared their unique resources and expertise—samples, protocols, insights—to help understand and fight Zika. Sharing the data widely for the same end goal is an obvious extension of that ethos."

The Sabeti Lab is continuing to work in collaboration with partners from across the Zika outbreak—in South America and in the US—with the common goals of quickly advancing our understanding of this mysterious virus, and building better tools to beat it.

Provided by Broad Institute of MIT and Harvard

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