



# Sharing outbreak data

Posted at: 03/12/2018

## **Sharing outbreak data-Publishing epidemic data on open access platforms can help countries tackle outbreaks better**

- The recent Zika outbreaks in Rajasthan and Madhya Pradesh are a reminder of how poor Indian authorities are at sharing health data.
- Even though the Indian Council of Medical Research (ICMR) has genetically sequenced Zika viruses from five patients in Rajasthan, it hasn't published these sequences in any open access databases such as GenBank.
- Both daily case counts and genetic sequences of the viruses circulating in India can be extremely useful to epidemiologists studying Zika.
- Daily case counts can show how quickly the virus is spreading.
- Genetic sequences can help us understand from where the virus came to India and for how long it had been circulating in Rajasthan and M.P. before it was detected.
- Using data from previous epidemics, scientists have been able to estimate the rate at which the Zika virus mutates.
- Given how important such data are during epidemics, the World Health Organisation (WHO) released a policy statement in 2016 saying "pathogen genome sequences be made publicly available as rapidly as possible through relevant databases."
- There are reasons why researchers are often reluctant to share genome sequences.
- During the Ebola outbreak, some scientists were worried that they may not be credited for their work if someone else published an analysis based on their sequences, and waited for months before publishing.
- But given the benefits to public health from data-sharing, Indian authorities should do their part too.

The Hindu