SHARING OUTBREAK DATA

Relevant for: Health, Education & Human Resources | Topic: Health & Sanitation and related issues

The recent Zika outbreaks in Rajasthan and Madhya Pradesh are a reminder of how poor Indian authorities are at sharing health data. Neither Rajasthan, which saw 154 cases, nor M.P., which saw 127, published the day-wise numbers of confirmed infections. Meanwhile, 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. So, by comparing genome sequences from multiple patients, they can estimate when these viruses diverged from their most recent common ancestor, giving an idea of when the virus entered India. If this date is much earlier than the date of the first detected case (September in Rajasthan), that would mean a larger number of patients were infected, which in turn could help customise our outbreak response.

However, ICMR has only announced that the Rajasthan Zika strain is genetically close to the Brazilian strain (suggesting that the virus came from Latin America), and that it does not have certain mutations. "Genetically close" is a broad term, and without the sequence information, other researchers cannot independently interpret and validate ICMR's claims. ICMR says it has submitted the data to a peer-reviewed journal for publication, but publication in journals takes longer than publication in an open access database.

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." West Africa's 2013 Ebola virus outbreak and Latin America's 2015 Zika outbreak showed how useful such proactive sharing can be — during the Ebola epidemic, around 80% of the epidemiological modelling studies used only open data, according to a 2016 *PLOS Medicine* paper.

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. Such concerns are valid, and the WHO says it is important to address this. But given the benefits to public health from data-sharing, Indian authorities should do their part too.

The writer is Senior Assistant Editor with The Hindu in Bengaluru

The government's maternity benefit programme must be implemented better and comply with the Food Security Act

Our existing notification subscribers need to choose this option to keep getting the alerts.