The Need for Continuous Genomic Surveillance for Early Diagnosis of Novel Virus Infection

Letter to Editor

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DEAR EDITOR:

All viruses mutate as they spread and replicate in a population. DNA viruses like monkey pox viruses mutate slower than RNA viruses like COVID-19 and influenza. All minor changes and mutation do not cause disease, but the recent COVID-19 pandemic and Monkey pox epidemic, currently affecting more than 30 000 cases worldwide as of and causing epidemics, demonstrate the need for rapid diagnosis, continuous surveillance, and real-time tracking of infectious disease (Kugelman et al., 2014; Centers for Disease Control and Prevention, 2022). Despite the knowledge acquired from previous outbreaks, such as severe acute respiratory syndrome (SARS) epidemic in 2002–2003 and the influenza pandemic in 2009, novel and mutated emerging and reemerging diseases tend to surprise and overwhelm the global health response. Global public health surveillance system has evolved to meet the changing needs, yet we continue to underestimate our vulnerability to both emerging and reemerging viruses. In recent times, there is a gap in the existing infectious disease surveillance system, especially when a novel virus extends to a large geographical area (Gardy and Loman, 2018).

Genomic surveillance is a consistent accumulation of genomic sequences to identify the variant of the infection. Effective surveillance does not require all samples to be sequenced; collecting enough samples from a representative population helps in identifying new variants and monitoring trends of the disease. Uses of genomic surveillance are monitoring changes in genetic code, spread of variants, and geographical isolation of variants. Collectively, it helps to understand how different variants affect public health (Kugelman *et al.*, 2014; Gardy and Loman, 2018; Centers for Disease Control and Prevention, 2022). Globally, the WHO's Global Influenza Surveillance and Response System (GISRS), which was formed in 1952, was used for conducting surveillance and for alerting any novel influenza and other respiratory viruses. In India, during the COVID-19 pandemic, the Indian SARS-CoV-2 Genomics Consortium (INSACOG) was built up to extend Entire Genome Sequencing of SARS-CoV-2 over the country, helping our understanding of how the infection spreads and evolves. Three strategies were used for genomic surveillance, which focused on international travelers, sentinel surveillance in the community, and event-based surveillance in special case scenarios (Ministry of Health and Family Welfare, 2021; Bellizzi, et al., 2022).

Among these three strategies followed by India during the pandemic, genomic surveillance of international travelers should be made mandatory for all passengers both in and out of the country with proper reporting system; this prevents rapid spread of any novel infection, early diagnosis, and proper isolation of infected. Other two strategies such as sentinel surveillance and eventbased surveillance should be complimentary services with all these three strategies acting synergistically to prevent rise of a new pandemic and to prevent rapid spread of any novel viral infection. Testing international travelers, both departure and arrival, helps in tackling the problem more effectively. Quarantine and isolation facilities should be available near both air and sea ports. In international borders where road transport are common, quarantine and isolation facilities should be properly setup to tackle this problem.

CONFLICT OF INTEREST

There are no conflicts of interest.

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