

# Genomic epidemiology on the move

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**This Genome Watch article explores how portable sequencing technology is reshaping the field of genomic epidemiology.**

Portable sequencing technology enables whole-genome sequencing (WGS) to be carried out in real-time and for a low capital investment, providing information and data about infectious disease for epidemiologists and clinicians in a manner that was not possible until recently. A wealth of literature is now available documenting the range of uses to which these portable sequencing devices have already been applied. An important feature from some of these outputs is the ability of portable sequencing technologies to produce good-quality WGS data within remote or resource-limited settings, where non-portable WGS equipment may be unavailable or logistically impractical to use. An early use of the technology was in 2014–2015 as a means of providing real-time genome surveillance data to track the spread of Ebola virus in Liberia<sup>1</sup>. The MinION used to track the patterns of Ebola virus evolution during this outbreak was able to function well while connected only to a laptop and produced results by analysing the DNA through a ‘flow cell’<sup>2</sup>.

One of the most beneficial evolutions of the use of portable sequencing technology in the field is related to investigation of mobility. Two different aspects of this can be demonstrated within the following case studies from

a pandemic and an endemic situation. Analysis of SARS-CoV-2 genomes in Bangladesh, generated by the use of in-country portable sequencing technology, in combination with human mobility data have demonstrated that expansion of the dominant lineages B.1.1.25, B.1.1 and B.1.36 in March 2020 coincided with the mass movement of people around the country<sup>3</sup>. Facebook ‘Data for Good’ and mobile phone operators from three networks provided mobility data that were used to substantiate this theory. This information helped to provide information to policy makers regarding appropriate local control measures in a timely manner.

Portable sequencing technology has also revolutionized the detection and tracing of endemic disease within the field. Rabies, a neglected zoonotic disease, is typically transmitted to humans via a bite from a rabid dog. Control and surveillance programmes are often limited due to lack of adequate funds and resources. Portable sequencing technologies provide a means by which genomes can be sequenced in the field close to source and at a low, and continually decreasing, cost. This has enabled the identification of different rabies virus lineages and some results are suggestive of predominantly enzootic viral transmission cycles in selected study areas<sup>4</sup>. Preliminary results suggest that the combination of these genomic data with traditional epidemiological analysis and contact tracing following the occurrence of an infected bite enables more accurate targeting of control strategies and vaccination programmes<sup>5</sup>. Portable sequencing technology will also enable the timely monitoring of cross-border incursion of the virus, or specific viral lineages, into a country, which is particularly important in light of the current programme to eliminate rabies in dogs globally by 2030. A well-documented challenge with portable genome sequencing is the high rate of errors in homopolymer regions of the genome, when a reference genome is not available. New approaches to de novo assembly of long reads and to correction of errors are now enabling high-quality genome sequences to be generated<sup>6,7</sup>.

We are seeing the anticipated potential for portable sequencing technologies to provide

good-quality genome sequences be realized. The utility of this technology opens up many exciting and varied applications both globally and beyond.

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