

Real time outbreak surveillance using genomics now possible in resource-limited conditions

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The lab in Guinea. Credit: European Mobile Lab

New research published in *Nature* has shown how genome sequencing can be rapidly established to monitor outbreaks.

Researchers designed a "[genome sequencing](#) laboratory in a suitcase", employing a novel DNA sequencer, transporting the equipment in less than 50kg of airline luggage. This was initially deployed in Conakry, Guinea in April 2015 where Ebola samples from patients could be sequenced as soon as new cases were diagnosed. This reduced delays shipping to traditional genome laboratories often located on a different continent. The team found that they could generate sequencing [information](#) in as little as 24 hours after receiving a sample, with the sequencing process taking less than an hour.

Genome sequencing in outbreaks is useful to understand how the virus evolves. However, the information must be available quickly in order for this information to guide control efforts. By sequencing 142 samples from Ebola patients in Guinea they were able to provide very detailed information about how cases were related, providing important clues to World Health Organisation epidemiologists battling to halt transmission of the virus.

Co-author of the study Dr Nick Loman, from the Institute of Microbiology and Infection at the University of Birmingham, explained, "Genome sequencing information is valuable for researchers and epidemiologists during an epidemic. Yet, generating such information is a laborious process typically performed in well-equipped laboratories using large, delicate and expensive hardware. Having a portable DNA sequencing system opens up the possibility to do outbreak genome sequencing in real-time, which can directly impact on the response on the ground, as well as providing a wealth of information about pathogen evolution. Crucially we shared our data as it was generated, increasing its use immensely."



The lab in Guinea. Credit: European Mobile Lab

Dr. Jared Simpson from the Ontario Institute for Cancer Research, also a co-author on the study, said, "In this paper we've shown that we can find [single nucleotide polymorphisms](#) (SNPs) at whole genome resolution using portable technology. While sequencing has until now been confined to a lab, this opens up genomic research to far more applications around the world. We look forward to building upon the work done in this study and applying it to other fields, including [cancer research](#)."

The team employed a lightweight MinION DNA sequencer from Oxford Nanopore Technologies. This device weighs less than 100g, is powered

by the USB of a laptop which is currently being used by more than 1,000 researchers worldwide.

Dr Loman worked with an interdisciplinary team based on three continents, including the European Mobile Laboratories, Public Health England and Ontario Institute for Cancer Research. The researchers worked with other diagnostic laboratories and WHO epidemiologists based in Guinea.

The Ebola outbreak in West Africa was the deadliest occurrence of the disease since its discovery in 1976. Since the first confirmed case was recorded on 23 March 2014, over 11,000 people have died as the result of the virus.

The epidemic was officially declared to be over on 14 January 2016. However, just hours later, a new case was confirmed in Sierra Leone. New cases, when sequenced and linked to a database of previous sequences can provide important clues as to their origin. The sequencing laboratory, currently located in Nongo, Guinea, will continue to provide surveillance information until the outbreak is officially declared to be over.

More information: *Nature*, [DOI: 10.1038/nature16996](https://doi.org/10.1038/nature16996)

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