Preparing for the next Ebola outbreak: in-country genomic capacity in Africa

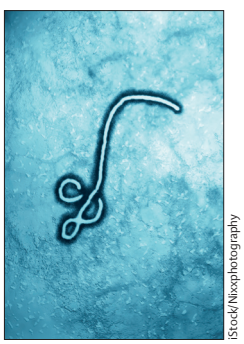
The resurgence of Ebola virus disease (EVD) in Équateur province in the Democratic Republic of the Congo in May 2018, is an important reminder of the difficulties of predicting when and where the next outbreak will occur. The subsequent July 2018 outbreak of EVD in the Democratic Republic of the Congo has affected about 1000 people and the outbreak has the highest case fatality rate (62%) for EVD to date.[1] Conflict, insecurity, poverty, mistrust, poor health systems, and other factors have been implicated in sustaining the outbreak. The response to the July 2018 EVD outbreak in North Kivu Province has highlighted the positive impact of lessons learnt during the 2013–16 EVD outbreak in west Africa. These lessons included real-time genomic analysis of viruses and the use of different countermeasures during the outbreak response,[2] strong collaborations between countries of the northern hemisphere and southern hemisphere and between countries within the southern hemisphere and rooted investment for research capacity building to address disease outbreaks,[3] and timely and committed responses from WHO and other health development agencies.[4]

In the *Lancet Infectious Diseases*, Placide Mbala-Kingebeni and colleagues[2] demonstrated how in-country genomics capacity has been integrated in the current EVD outbreak response in North Kivu Province of the Democratic Republic of the Congo. The authors report the use of genomics tools for assessment of medical countermeasures such as diagnostics and therapeutics deployed during the outbreak. Mbala-Kingebeni and colleagues used real-time genomic viral sequencing to demonstrate that the virus strain identified in the North Kivu and Ituri Provinces is different from the strain identified in the previous May 2018 EVD outbreak in Équateur Province. The authors used the Nextera Flex method for viral genome enrichment, developed by Illumina Technologies (San Diego, CA, USA), to shorten the time between blood sample collection and generation of whole viral genome sequences from 72 to 28 h. They also identified a small number of mismatches and mutations in targeted areas of some PCR tests available for field deployment; however, none of these mismatches affected the performance of the PCR tests. The authors' assessment of the binding capacity of the monoclonal antibodies Zmapp and mAb114—deployed as therapeutics during the previous outbreak—to the new strain of the Ebola virus identified in Ituri Province, showed that the changes in the newly identified Ituri strain did not affect their binding capacity. These findings were translated into actionable information and used by stakeholders for evidenced-based interventions in the outbreak response.

The approach used by these authors,[2] confirms and reinforces the notion that proactive, real-time genomic viral sequencing and surveillance of human populations represents a simple and cost-effective method of mitigating outbreaks in countries and locations that are most at risk of infectious disease outbreaks. For example, researchers at the African Center of Excellence for Genomics of Infectious Diseases (Redeemer's University, Ede, Nigeria) have used real-time next-generation sequencing technology to minimise public concerns regarding the surge in Lassa fever[5] and yellow fever[6] cases during the 2018 outbreaks in Nigeria, and successfully guided outbreak responses in the country.

To prepare for the next EVD outbreak, we advocate the establishment of national and regional hubs of excellence in infectious diseases genomics in regions with a high risk of outbreaks, where untargeted metagenomic sequencing analysis would be done. Thus, providing a potential one-step solution for outbreak pathogen detection of both known and novel pathogens would replace the need for multiple individual pathogen assays.[7] Although the main advantage of metagenomic sequencing is that it does not require a priori knowledge of the pathogen, specialised laboratory equipment and highly complex bioinformatic tools are required, which are expensive. Rapid identification of viruses will only be achieved if novel genomic technologies and the people trained to use them are available in many of the resource-limited regions of Africa where the risk of outbreaks is high.

The establishment of the African Center of Excellence for Genomics of Infectious Diseases as a regional hub of genomics excellence for infectious diseases by the National Institutes of Health (H3 Africa Consortium)



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and the World Bank (through the African Center of Excellence project) has demonstrated capabilities for in-country real-time surveillance and tracking of infectious agents during outbreaks.[5,6,8]

Previous reports[2,5,6,9] from many parts of Africa indicate that long-term capacity building, continued technology transfer among partners, deep rooted investments[3] in in-country real-time genomics surveillance, and the integration of such capacity into the established but siloed pathogen-specific diagnostic platforms in Africa are needed for quick response in outbreaks.

Additionally, improved trust and transparency through immediate public sharing of data, resources and samples if feasible, and strong partnerships with local communities, will help prevent the next major Ebola outbreak on the continent.

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Point-of-care tests to reduce the burden of sexually transmitted infections


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WHO recommends syndromic management of sexually transmitted infections in patients attending health-care facilities in resource-limited settings where laboratory services are limited. With a syndromic approach, care providers treat all the common causes of a presenting syndrome, and provide counselling, condom promotion, and contact tracing. Syndromic management has been successfully rolled out to primary health care in many countries, and has been shown to reduce the prevalence of sexually transmitted infections and HIV.[1]

Limitations of syndromic management include its lack of specificity, leading to overtreatment in many cases, and its inability to identify asymptomatic infections. WHO algorithms work reasonably well for the management of urethral discharge in men and for patients with genital ulcers, but the algorithm for vaginal discharge is neither sensitive nor specific. In *The Lancet Infectious Diseases*, the women's improvement of sexual and reproductive health (WISH) study by Janneke van de Wijgert and colleagues[2] compared the performance of point-of-care testing in the WISH algorithm with that of syndromic management in the WHO algorithm and gold standard testing. 705 women in Kigali, Rwanda were enrolled in the study and completed a study visit in which they were interviewed and asked about current urogenital symptoms. Next, the WISH algorithms were implemented; patients had rapid point-of-care tests for bacterial vaginosis,