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Using genomics to improve preparedness and response of future epidemics or pandemics in Africa



Emerging infectious diseases, such as COVID-19¹ and Ebola virus disease,² pose a major threat to public health. Despite the presence of Ebola virus disease in central and west Africa for several years,² many African countries are yet to fully utilise genomics in public health. This situation is highlighted by the current COVID-19 pandemic caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).¹ By Oct 5, 2020, 9 months into the COVID-19 pandemic, 2980 SARS-CoV-2 genomes sampled from patients with COVID-19, from 21 of 54 African countries, had been deposited in the GISAID database. Most of the African SARS-CoV-2 genomes are from South Africa (n=1409), The Gambia (360), Democratic Republic of the Congo (346), Kenya (290), Egypt (152), Senegal (136), Nigeria (87), Ghana (53), and Morocco (48). Although the number of genomes sampled from Africa is slightly higher than that from South America (n=1988), the breadth of sampling is much higher in Asia (n=9874), Oceania (n=12 313), North America (n=34 670), and Europe (n=75 670). The absence of genomic data from most African countries shows that the benefits of these data for public health threats are yet to be fully achieved for preparedness and response to emerging infectious diseases.

As seen during the early stages of the COVID-19 pandemic, sequencing of samples from patients with respiratory diseases of unknown cause not only identified SARS-CoV-2 as the causative pathogen and its zoonotic origin but also facilitated development of molecular assays for diagnosis to inform treatment and infection control.¹ Genomic data also provide sufficient resolution for monitoring local transmission and for inferring routes and times of importation of viruses between countries.^{3,4} This inference is crucial for SARS-CoV-2, particularly in African settings where delays in testing were notable but serosurveys (eg, in Malawi and Kenya) showed high exposure to the virus,⁵ suggesting that importation occurred earlier than expected. Furthermore, genomic surveillance of evolving viruses (including SARS-CoV-2) in Africa could inform rational design of specific and sensitive molecular assays to guide treatment and prevention and to monitor viral adaptations favouring pathogenicity and transmissibility.⁶ Crucially, genomic

data inform design of life-saving vaccines, which are vital, particularly when no effective treatments are available.⁷ Applications for genomic data are not restricted to investigating known outbreaks or epidemics.⁸ Metagenomics and transcriptomics could be used to diagnose infections of unknown cause potentially causing undetected outbreaks in Africa, as seen with the neuroinvasive meningitis Chikungunya virus outbreak in Bangladesh.⁹ Because the viral repertoire is geographically diverse¹⁰ and the origin of the next deadly virus is unknown, genomics could lead to proactive epidemic intelligence—eg, early identification of novel viruses with potential to spill over into the human population in Africa, therefore, informing evidence-based preparedness and control for future epidemics.

Some success of local sequencing of SARS-CoV-2 strains in Africa,⁴ and the joint initiative by WHO and Africa Centres for Disease Control and Prevention (CDC) to scale-up sequencing of SARS-CoV-2 strains across Africa, supports the need for integration of genomics into public health in Africa. However, substantial investment in research infrastructure and capacity development by African governments will be needed to achieve the benefits of genomics. If local institutions doing genomics research are well supported locally, these institutions could act as focal points for research into future epidemics or pandemics and into infection control, including assay development, diagnosis, and surveillance. To ensure swift responses during epidemics, governments should formulate clear guidelines to facilitate sample and data sharing, to avoid delays or failure to sequence SARS-CoV-2 samples, as seen in some African countries during the COVID-19 pandemic. It is imperative that African leaders who implement government policy and lead academic and public health institutions promote the application and integration of genomics into public health, because the success and sustainability of such initiatives requires appropriate support by African governments.

We uphold the efforts by the Africa CDC and WHO to build and strengthen genomic-based surveillance systems, reinforce collaborative networks, and develop the capacity of African researchers in genomics to enhance understanding of the ongoing COVID-19 pandemic

For more on the GISAID database see <https://www.gisaid.org>

For more on the WHO and Africa CDC joint initiative see <https://www.afro.who.int/news/covid-19-genome-sequencing-laboratory-network-launches-africa>

in Africa. We urge for sustenance and scale-up of such innovative initiatives beyond the current pandemic to augment traditional approaches for preparing and controlling future epidemics, the occurrence of which seems inevitable in the light of ongoing changes in climate, biodiversity, and human behaviour. Considering the highest burden of endemic infectious disease globally is in Africa, integration of genomics into public health could save lives on the continent and abroad.

There is no more pertinent time than now for African countries to strengthen epidemic intelligence systems for emerging infectious disease threats of local and international origin. This needed action includes integration of genomics into public health systems to improve preparedness and control of future outbreaks that, compared with the Ebola virus disease epidemic and COVID-19 pandemic, might hit harder in Africa. Without adequate and proactive preparation, mortality projections for the COVID-19 pandemic in Africa, which universally pointed towards an insurmountable death toll thousands-fold higher than seen to date, could unfortunately lead to huge loss of life and undermine economic prosperity of the African continent.

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- 1 Wu F, Zhao S, Yu B, et al. A new coronavirus associated with human respiratory disease in China. *Nature* 2020; **579**: 265–69.
- 2 Gire SK, Goba A, Andersen KG, et al. Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. *Science* 2014; **345**: 1369–72.
- 3 Worobey M, Pekar J, Larsen BB, et al. The emergence of SARS-CoV-2 in Europe and North America. *Science* 2020; published online Sept 10. <https://doi.org/10.1126/science.abc8169>.
- 4 Giandhari J, Pillay S, Wilkinson E, et al. Early transmission of SARS-CoV-2 in South Africa: an epidemiological and phylogenetic report. *medRxiv* 2020; published online May 30. <https://doi.org/10.1101/2020.05.29.20116376> (preprint).
- 5 Chibwana MG, Jere KC, Kamng'ona R, et al. High SARS-CoV-2 seroprevalence in health care workers but relatively low numbers of deaths in urban Malawi [version 1; peer review: awaiting peer review]. *Wellcome Open Res* 2020; **5**: 199.
- 6 Volz EM, Hill V, McCrone JT, et al. Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity. *medRxiv* 2020; published online Sept 1. <https://doi.org/10.1101/2020.07.31.20166082> (preprint).
- 7 Zhu F-C, Li Y-H, Guan X-H, et al. Safety, tolerability, and immunogenicity of a recombinant adenovirus type-5 vectored COVID-19 vaccine: a dose-escalation, open-label, non-randomised, first-in-human trial. *Lancet* 2020; **395**: 1845–54.
- 8 Kress WJ, Mazet JAK, Hebert PDN. Intercepting pandemics through genomics. *Proc Natl Acad Sci USA* 2020; **117**: 13852.
- 9 Saha S, Ramesh A, Kalantar K, et al. Unbiased metagenomic sequencing for pediatric meningitis in Bangladesh reveals neuroinvasive Chikungunya virus outbreak and other unrealized pathogens. *mBio* 2019; **10**: e02877-19.
- 10 Shi M, Lin XD, Tian JH, et al. Redefining the invertebrate RNA virosphere. *Nature* 2016; **540**: 539–43.