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Covid-19: Africa scrambles to increase genomic testing capacity as variants spread

African countries are struggling to bolster genomic sequencing as SARS-CoV-2 variants spread on the continent, reports **Abdullahi Tsanni**

Abdullahi Tsanni *science journalist*

As the world entered 2021, the covid-19 pandemic began a new phase, one dominated by worries over emerging variants. But the way of detecting these threats has not been standardised—even in the UK, where genomic sequencing is relatively frequent, only 5-10% of covid-19 positive cases were being sequenced at the start of the year.¹

The spotlight on sequencing has highlighted inequalities in global capacity. Many countries in Africa do not perform sequencing themselves, and those that do only do so on a small scale. Genomic sequencing requires expertise, machinery, software, reagents, and funding. Over the past year, as African countries grappled with scaling up basic testing capacity for covid-19, it hasn't been a high priority.

But as variants such as B.1.351—first identified in South Africa and which now accounts for some 90% of the country's covid-19 cases—led to growing concern, there are worries that the lack of sequencing capacity will leave the continent unable to spot and stop variant outbreaks before they fuel a new wave of infections.

Nigeria, the continent's most populous country, has sequenced and shared 0.03% of its reported covid-19 cases (versus, at the time of writing, nearly 2% for the US, 42% for Singapore, and 48% for Australia). As of 14 February 2021, there were around 55 different lineages of SARS-CoV-2 known to be circulating in Nigeria, and changing rapidly.² According to the Nigeria Centre for Disease Control (NCDC), these strains provide evidence of multiple introductions of the virus into the country from different parts of the world and add to proof of community transmission in different parts of Nigeria.

"Genomic sequencing is crucial at this point to understand circulating strains and their impact on vaccine efficacy, disease transmission, and severity," says Christian Happi, director of the African Centre of Excellence for Genomics of Infectious Diseases (ACEGID) in Ede, south west Nigeria. "We need to keep sequencing so that we can see exactly how the virus is mutating and spreading."

ACEGID is a reference laboratory for the joint World Health Organization and Africa Centres for Disease Control and Prevention (Africa CDC) Covid-19 Genomic Sequencing Network. Happi's team sequenced the first coronavirus samples in sub-Saharan Africa within 72 hours of diagnosis and identified two new variants—B.1.5.2.5, first found in Nigeria, and B.1.1.7, first identified in the UK.³

Chikwe Ihekweazu, director general of NCDC, says sequencing has a key role as Nigeria begins vaccination—in March it received 3.9 million doses of the Oxford AstraZeneca vaccine from the Covax initiative. "If the effectiveness of vaccines is affected by the evolution of new variants, we have to be able to detect them. Genomic sequencing, linked to good surveillance data, is one way of doing this," he says. This is especially important in large countries like Nigeria, which sees a lot of movement between regions as well as a high influx of travellers from other countries.

There are only three institutions in Nigeria with the capacity to do genomic sequencing—ACEGID, the NCDC, and the Nigeria Institute for Medical Research—Ihekweazu told *The BMJ*. Genomic surveillance is not something you can set up overnight, he says, it's "resource and knowledge intensive and requires skills such as sequencing, bioinformatics, and data analysis."

Despite financial limitations, ACEGID is sequencing 20% of all SARS-CoV-2 samples in Nigeria to gain insights into the state of the pandemic in the country. Ihekweazu says he expects the three institutions to sequence 100 SARS-CoV-2 positive samples each week and carry out routine analysis of genomic data to support the NCDC's public health response.

Variant spread

There are no SARS-CoV-2 sequences available for about 40% of African countries in GISAID, the global online database of viral sequences. According to the media outlet Devex, South Africa leads the continent with the number of sequences of SARS-CoV-2 contributed—nearly 4000 samples—but has only sequenced about 0.3% of its positive cases.⁴

In April 2021, John Nkengasong, director general of Africa CDC in Addis Ababa, Ethiopia, told *The Lancet Microbe* that it wants African countries to have contributed 50 000 genomic sequences to GISAID by the end of 2021.⁵ The continent, however, contributed only 2435 sequences to the database in February, meaning it would need to produce nearly double that output every month to meet the target.

Mosoka Fallah, director of the National Public Health Institute of Liberia, says the lack of sequencing capacity is, in part, caused by lack of investment in science and research as well as infrastructure for continent-wide genomic testing, "and this is now hurting us." Most of the testing in Africa is not done within communities so the extent to which variants

have spread is unknown, he adds. “It’s a call for Africa to invest in science.”

Some 175 000 new covid-19 cases and more than 6200 deaths were reported in Africa last January while infections rose by 50% on the continent between December 2020 and January 2021.⁶ The B.1.351 variant is powering record case numbers in and around South Africa, including Botswana, Comoros, Ghana, Kenya, and Zambia.

Additionally, Nicksy Gumede-Moeletsi, regional virologist for WHO Africa, told *The BMJ* that more than 25 countries in Africa have reported both B.1.1.7 and B.1.351. Yet many can’t see the extent of the damage as they cannot carry out sequencing.

The concern, says Fallah, is if any of them becomes more transmissible, causes severe disease, or evades immune response—B.1.351 is already known to be better at evading the body’s immune response and is 50% more transmissible compared with the original virus. With B.1.351 and B.1.1.7 already circulating in many African countries, the chances of further viral mutations will increase, posing a threat to vaccine efficacy, just as the worldwide clamour for limited vaccine stocks already looks likely to leave Africa short of doses for several years.

That’s why genomic sequencing is critical for the continent, Fallah says, while emphasising the relation to testing capacity in general. “More variants are emerging, but we don’t know the extent to which these variants exist in Africa. This is just a tip of the iceberg.”

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