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Variants in Africa: Recommendations for Preventing an Enduring Pandemic

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Foreword by Tony Blair

Much of Africa has so far escaped the worst of the Covid-19 pandemic. But that calculus may be changing, due to the spread of new variants – including but not limited to the Delta variant – in a continent where very few people have been vaccinated.

There is now a very real risk that at least some African countries follow the same path taken by India earlier this year. This could have truly devastating consequences, both in terms of increased Covid-19 mortality and the wider impact on overwhelmed health systems. This means there is an urgent need to get vaccine supply to Africa, and Western nations must act now to make this happen.

Many African governments have responded swiftly and effectively to the pandemic. In this latest phase of Covid-19, there is much they can do to protect their people.

Governments must treat new variants as they treated those first cases of Covid-19 by enhancing surveillance and testing, increasing contact tracing and isolating of probable cases, and introducing localised restrictions on movement and other targeted measures to prevent transmission.

As well as looking to increase vaccine supplies beyond the COVAX programme, governments should do everything possible to increase vaccine absorption rates by addressing logistical challenges and vaccine hesitancy, so new stocks can be rolled out efficiently as they arrive.

Gathering and analysing data has always been a critical element in responding to the virus. Joining global platforms of shared data will help surveillance of variants.

Critically, Africa lacks genomic-sequencing capacity. Scaling it up will enable governments to identify the presence of variants and take swift action to prevent their spread. Leaders should prioritise investment in this and consider partnering with existing international initiatives such as the Africa Pathogen Genomics Initiative, which aims to expand next-generation genomic-sequencing tools and expertise across Africa to tackle disease outbreaks more effectively.

Tony Blair
Executive Chairman

Executive Summary

Since the start of the pandemic, recorded Covid-19 cases and deaths have remained low in Africa compared to the rest of the world. Though the continent accounts for 17 per cent of the global population, it has registered just 2.9 per cent of global cases and 3.5 per cent of deaths.¹ Although low testing rates have some impact on reporting, other factors such as swift initial mitigation measures and age demographics have likely played a role in the continent's lower rates of Covid-19 infection. However, as the world has watched a devastating new wave of cases overwhelm India's health-care system, the implications for Africa are particularly alarming.

The emergence of more potent and transmissible "variants" of SARS-CoV-2, a key factor in India's current wave, has put the African continent at high risk of experiencing a new wave that is similar in severity to India's – or worse. (We define "variants" and their different classifications, including "variants of concern", in the next chapter.) Though most vaccines are so far proving effective against the current variants, low vaccination rates in Africa mean a significant majority of the population remains unprotected. This paper outlines the current variant situation across the continent and explores the growing risks. We provide recommendations for how to manage and mitigate the proliferation of variants and set out the other steps governments must urgently take to limit the human, economic and political consequences of an enduring pandemic. Our argument is structured around four main points:

1. **Variants of concern (VOCs), particularly the Delta variant, pose a great risk for Africa.** More transmissible and potent variants threaten to overwhelm the continent's vulnerable health systems. Mutations also increase the likelihood that factors that have so far kept symptomatic cases – and the associated clinical manifestations – relatively low will no longer prove protective. The greatest worry now is the Delta variant, which at 40 to 60 per cent higher infectiousness than the Alpha variant, is the most transmissible to emerge yet.
2. **Vaccines are proving effective in protecting against severe illness, hospitalisation and deaths due to the current variants – but only if people get vaccinated (and with both doses for double-dose regimes).** The current vaccine regimes are so far demonstrating efficacy against the four variants of concern currently in circulation, especially when it comes to preventing severe illness and death. But vaccination rates in Africa are the lowest in the world, and this is mostly attributable to supply shortages, logistical challenges and growing hesitancy among the public. In the absence of effective mass vaccination, governments must take alternative measures to protect their populations, including public-health and social measures (such as mask-wearing) and enhanced surveillance and sequencing to identify the presence of variants and track transmission.
3. **Genomic sequencing and surveillance are critical for tracking and containing variant spread.** They can provide early warning of new variants to allow targeted containment measures, both clinical and

non-clinical. More work needs to be done to expand sequencing and data-sharing capacity globally, but especially in Africa.

4. **Variants pose a threat to Africa that calls for a proactive, coordinated and holistic approach by governments.** By conducting genomic sequencing and contributing to a platform of shared data, African policymakers will be able to stay up-to-date on mutations and variants of SARS-CoV-2 and identify those that are most critical to track at any given time. Governments should be focused on enhancing their genomic-sequencing capacity, expanding their vaccine access from and beyond COVAX, introducing or continuing targeted containment measures and increasing their vaccine absorption rates, i.e. the ability of countries to administer the doses available to them.

We conclude the paper by proposing three key recommendations for African policymakers:

1. Prioritise investments in genomic-sequencing capacity to proactively identify Covid-19 variants and other infectious pathogens and enable early action to prevent the spread of any VOCs.
2. Make use of available data and join global platforms of shared data to ensure adequate surveillance of mutations and up-to-date awareness of those that are most critical to track at any given time, and enforce public-health measures accordingly.
3. Focus on expanding vaccine access beyond COVAX, introducing targeted containment measures and increasing their vaccine absorption rates.

Variants, Particularly Delta, Pose a Great Risk for Africa

The virus SARS-CoV-2 caused an outbreak of viral pneumonia in December 2019 that quickly grew into the global Covid-19 pandemic. Despite efforts to contain it, the virus has infected more than 181 million people and caused nearly 4 million deaths worldwide.²

As a result of its rapid and ongoing spread, SARS-CoV-2 has naturally evolved. Every time the virus replicates, there is an opportunity for genetic mutation. Thousands of mutations have occurred since it began to spread globally. Most of these mutations are inconsequential in that they have not changed the virus's ability to generate infection and disease compared to the original strain. However, a small proportion of mutations – or combinations of mutations – have proved significant because they provide the virus with a selective advantage: increased transmissibility, increased severity, the ability to evade the host immune response and/or the ability to evade countermeasures (such as diagnostics, antivirals and vaccines).

Defining Variants

An interagency group in the US government created a three-tier variant classification system for these consequential mutations, listing the three tiers as Variants of Interest, Variants of Concern and Variants of High Consequence. Variants of Interest (VOIs) are those that are *suspected* to evade the protection conferred by vaccines or to cause more severe disease or are more contagious than the original strain.³ They become Variants of Concern (VOCs) when data confirm that they cause one or more of the outcomes listed above for VOIs. Variants of High Consequence (VHCs) are the last class: **“A variant of high consequence has clear evidence that prevention measures or medical countermeasures (MCMs) have significantly reduced effectiveness relative to previously circulating variants.”**⁴

To date, globally, the WHO has identified seven VOIs, four VOCs and no VHCs. National authorities may decide to designate local variants as of interest or concern. For example, India has designated a new variant, named Delta Plus (AY.1), as a national variant of concern. This variant has been identified in nine other countries and is similar to Delta but has an additional mutation (K417N) that is also found in the Beta and Gamma variants. Preliminary studies from India indicate it may be more transmissible and resistant to monoclonal antibody therapies, but there is not enough data yet for Delta Plus to be distinguished from Delta and labelled as a separate variant of concern globally. As surveillance activities to detect variants, such as genome sequencing (see below), have increased globally, the number of reported VOIs and VOCs has also increased.⁵

The four VOCs as classified by the WHO are Alpha (also known as B.1.1.7, first identified in the UK), Beta (B.1.351, first identified in South Africa), Gamma (P.1, first identified in Brazil) and Delta (B.1.617.2, first identified in India). All four are more transmissible than the original strain. Whether any of the variants are more deadly has yet to be officially confirmed, though evidence suggests that Alpha may be more virulent. Beta and Delta are both reported to decrease the strength of the immune response.⁶

Genome Sequencing Defined

Genome sequencing is a process that involves analysing the letters of a virus's genetic code to track its mutations. Samples of the virus are collected through routine surveillance testing and sent to a laboratory where specialised technicians sequence the virus's DNA. Viral genome data allow researchers and governments to trace the origin of Covid-19 outbreaks in their jurisdiction and pin down the moment when community transmission occurred.⁷ Genome sequencing is a critical tool for identifying Covid-19 variants.

Risks of Variants

The emergence of concerning variants has significant implications for governments. A mutation that makes the virus more transmissible increases the speed at which it spreads among the population, making it more difficult to control, increasing the number of infected individuals at any given time and escalating exposure risk to those who are most vulnerable. Ultimately, this leads to increased hospitalisations, health-system strain and mortality. A mutation that makes the virus more virulent may not necessarily make it more transmissible, but because it increases the severity of symptoms in infected individuals, it also is likely to cause an increase in these three outcomes.

Africa has so far experienced lower clinical manifestations, in terms of hospitalisations and mortality overall, relative to the rest of the world. This can likely be attributed to several factors, including age demographics (less than 6 per cent of the African population is over 60, an increased risk factor for severe illness^{8, 9}). However, every new mutation carries the risk that factors like age will no longer continue to protect the population. Moreover, with each mutation comes the possibility of the emergence of a new VOC that could render existing vaccination, therapeutic or public-health regimes, including diagnostics, less effective. This would not only cause a rise in cases and mortality but also prolong the global pandemic.

The development of variants carries economic and political implications as well. The greater the degree of illness, the less productive the community, not least because of the public-health and social measures that must be implemented in order to gain control of transmission. Government resources will continue to be strained by pressures on health systems and fiscal squeezing. The longer the pandemic lasts, the higher the toll on society – in some cases setting back decades of progress.

VOCs in Africa

Three of the four VOCs – Alpha, Beta and Delta – have been traced across 46 different African countries in total. Alpha has been identified in 36 countries. Beta has been identified in 32 countries. Delta, the most recent VOC to emerge, has been confirmed in 14 African countries so far. Seven countries – Democratic Republic of the Congo (DRC), Ghana, Kenya, Malawi, Mauritania, South Africa and Uganda – have identified the presence of all three variants. ¹⁰

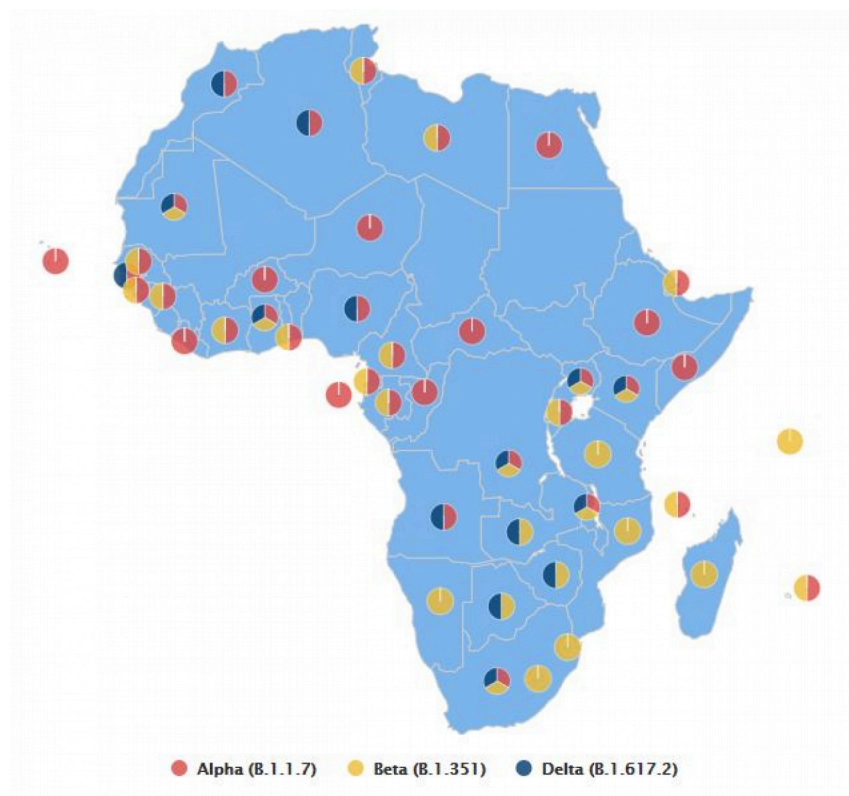
- **Alpha (B.1.1.7):** This variant was initially detected in the UK between late summer and early autumn 2020 and was designated as a VOC in early December 2020. This variant has several mutations of interest, including N501Y, which increases transmissibility. This mutation affects the spike protein that is located on the virus's outer surface. The spike protein enables the virus to link to and enter human cells, causing infection. Research in the UK indicates that the Alpha variant is somewhere between 30 per cent and 50 per cent more transmissible than the original strain. ¹¹ Some UK studies indicate that it is also more likely to lead to hospitalisations and deaths, though its higher virulence has yet to be widely confirmed. ¹² Alpha has no impact on monoclonal antibody treatments and minimal impact on the effectiveness of antibody neutralisation. ¹³
- **Beta (B.1.351):** This variant was detected by South African scientists during the course of routine genome sequencing last October. The variant has spike mutations in common with the Alpha variant, specifically N501Y, but also carries E484K (now also identified in some Alpha lineages) and K417N. At issue is the role of these spike mutations in reducing the potency of neutralising antibodies and the duration of the body's immune response; reinfection is possible for those infected with the original variant of Covid-19. ¹⁴ In total, Beta has eight distinctive mutations in the virus's spike protein. Beta is not considered more virulent than the original strain, but some studies have found that it is 50 per cent more transmissible. ¹⁵ The effectiveness of some monoclonal antibody treatments is significantly reduced against Beta. ¹⁶
- **Delta (B.1.617.2):** This variant was initially detected in India in October 2020 but was not registered as a variant of concern until May 2021. It has several significant genetic alterations, including mutations labelled E484Q, L452R and T478K. The E484Q mutation is similar to the E484K mutation present in the Beta strain, which helps the virus evade the immune response (particularly antibodies). The L452R mutation may also help the virus evade the immune response, particularly immune cells. The T478K mutation alters the spike protein and has been linked to increased transmissibility. Delta is now believed to be 40 to 60 per cent more transmissible than the Alpha variant; it currently constitutes 60 per cent of new cases in the UK. ¹⁷ No studies have yet found Delta to be more virulent than the original strain.

Still, the evidence is not clear as to whether the Delta variant bears the responsibility for the outbreak that has overwhelmed India's health system. Researchers outside India also cite the fact that the Alpha

variant is in wide circulation.¹⁸ However, Delta seems to be behaving differently in that it is affecting younger people, including babies. Population density, multi-generational living groups and poorly ventilated spaces have also fuelled the spread of this more transmissible virus.

The Tony Blair Institute for Global Change recently published a detailed primer on the Covid-19 variants of concern, which provides a deeper dive into the specific mutations of the global VOCs and several VOIs.

Figure 1 – Variants of concern identified per country



Source: WHO weekly epidemiological update on Covid-19, 22 June 2021

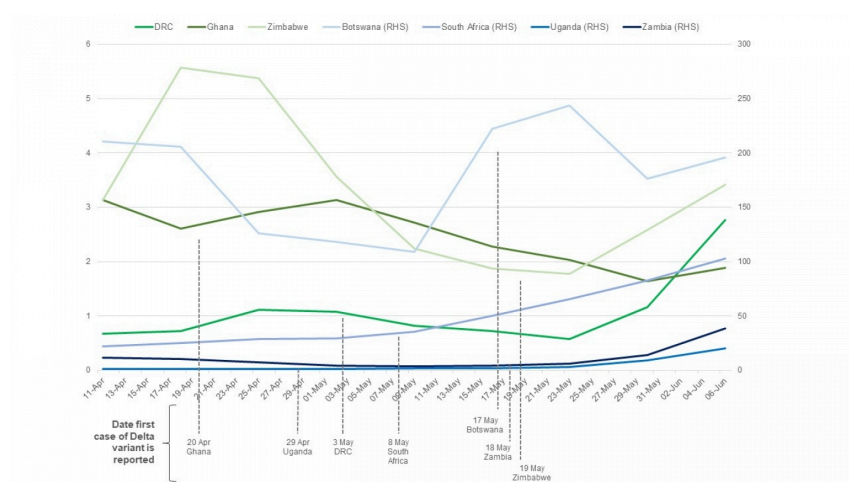
The presence of the Delta variant in Africa is of particular concern given its significantly higher transmissibility, and that it has affected younger populations as well as having a devastating impact on India's health system. In late April, Dr John Nkengasong, director of the Africa Centres for Disease Control and Prevention (Africa CDC), warned that if Africa experienced a surge in cases similar to that seen in India, the continent would be severely overwhelmed due to its more fragile health system – specifically its insufficient number of health-care workers, limited hospital beds and ICU equipment, and low oxygen supplies.¹⁹ In order to prevent surges in transmission caused by new variants, Dr Nkengasong has appealed to the continent to practise public-health and social measures, such as wearing masks and avoiding large gatherings, with increased rigour.

Infections on the Rise

Alarming, new cases in Africa have been increasing for the past six consecutive weeks, with the daily average of new cases more than double that of mid-May. As of 20 June, new infections rose by 31 per cent from the previous week. After several months of stable death rates, mortality jumped by 33 per cent in the same week.²⁰ Daily testing rose by 16 per cent, though average daily tests have been relatively fixed since late May.²¹ It is important to note that Africa's low testing rates mean that actual case numbers are likely higher than reported.

As of 20 June, 27 countries have experienced an increase in cases compared to the previous two weeks, with daily new cases in 18 countries increasing by 20 per cent or more. New exponential growth, particularly when accompanied by an increase in mortality, suggests the presence of a variant. Eleven of the 14 countries that have confirmed the presence of the Delta variant are among the countries experiencing growth: DRC (where daily cases are up 249 per cent compared to the previous two weeks), Zimbabwe (214 per cent), Zambia (119 per cent), Malawi (111 per cent), Kenya (54 per cent), South Africa (50 per cent), Uganda (43 per cent), Gambia (40 per cent), Algeria (9 per cent), Botswana (8 per cent), and Morocco (6 per cent).²² Of these ten, six – Botswana, DRC, South Africa, Uganda, Zambia and Zimbabwe – also experienced an increase in deaths compared to the previous two weeks.

Figure 2 – 14-day rate of new cases and date Delta variant first identified in each country



Source: ECDC data on 14-day notification rate, 7 June 2021. Note: Testing rates impact the number of reported cases. If testing rates are low, number of reported cases is lower than actual number of cases.

An analysis of the 14-day rate of newly reported cases against the timeline of when the Delta variant was first publicly reported in select countries illustrates the challenges in directly attributing surges in Africa to variants. The timing of when the first variant case is officially reported depends on factors beyond the rate of transmission. Low surveillance capacity and limited availability of genome-sequencing resources

impact the speed at which a mutation can be identified. As a result, variant cases are both unidentified and underreported on the continent.

Limited data on the presence and prevalence of strains make it difficult to determine for certain whether case growth is caused by a mutated virus or a reduction in public-health precautions and pandemic fatigue – or both. Many African countries have seen a decrease in adherence to public-health measures, driven partly by relatively lower clinical manifestations and partly by the need to maintain livelihoods after a punishing year for businesses and workers.

Still, the exponential growth in daily case numbers that Africa is currently experiencing is undoubtedly attributable, at least in part, to the presence of a variant other than the original strain. Given the devastation the Delta strain has caused in India, if governments do not take a proactive approach now to reduce transmission rates there is mounting fear that this variant will lead to similar – if not worse – outcomes in Africa.

Vaccines Are Proving Effective in Protecting Against the Current Variants – But Only If People Get Vaccinated

The current vaccine regimes are so far demonstrating efficacy against the four VOCs, especially when it comes to preventing severe illness and death – but only if the full dosage of the vaccine is received. Vaccination rates in Africa are the lowest in the world, mostly due to supply shortages, logistical challenges and hesitancy among the public. Given supply constraints, many countries are currently unable to offer the second jab of a two-dose regime to their health-care workers and highest risk populations. In the absence of mass protection via vaccination, governments must take alternative measures to protect their populations from the spread of variants.

Vaccine Efficacy Against the Variants

Research is ongoing regarding the efficacy of the various vaccines currently in use against the four variants of concern. Preliminary data suggest that the Oxford/AstraZeneca, Pfizer-BioNTech, Moderna, Johnson & Johnson's Janssen (J&J), Sinopharm, SinoVac, Sputnik V, Covaxin and Novavax (not yet on the market) vaccines all maintain a high degree of protection against the Alpha variant.²³

Beta is so far proving to be the most evasive with respect to vaccines. Data indicate that AstraZeneca and Sputnik V may have significantly lowered efficacy against mild-to-moderate illness with this variant, though protection against severe illness likely endures. The J&J vaccine, which was trialled in South Africa, is also less effective against mild and moderate Covid-19 caused by Beta. Evidence indicates that Pfizer and Moderna are still effective, though the efficacy of both is moderately reduced (Pfizer's efficacy, for instance, may be reduced from more than 90 per cent to 72 to 75 per cent). China has released data showing that Sinopharm and SinoVac do trigger an immune response against the Beta variant, though a weaker one than against the original strain.

As the newest VOC, less is known about the impact of Delta on vaccine efficacy. However, based on its specific mutations and early studies, there is an indication that the vaccines are still largely successful against Delta, albeit with slightly reduced efficacy rates. Real-world data from the UK so far show that Pfizer is 88 per cent effective and AstraZeneca is 60 to 67 per cent effective against Delta.²⁴

Figure 3 – Vaccines approved for emergency use and their efficacy against the VOCs

Vaccine (Type)	Approval Status*	Efficacy	Efficacy Against VOCs	Number of Doses	Cold Storage Requirements
Pfizer / Comirnaty (mRNA)	WHO EUL; US FDA; UK MHRA	95% (clinical) 90–91.3% (real world)	Alpha: 87–95% Beta: 72–75% Gamma: Works, minimal loss of neutralisation Delta: 88%, some loss of neutralisation	2 (3 weeks apart)	-20°C transport (5-day lifespan at 2°C to 8°C)
Moderna (mRNA)	WHO EUL; US FDA; UK MHRA	94.1% (clinical) 90% (real world)	Alpha: Works Beta: Works, some loss of neutralisation Gamma: Works, minimal loss of neutralisation Delta: Works, some loss of neutralisation	2 (4 weeks apart)	-20°C transport (30-day lifespan at 2°C to 8°C)

Oxford- AstraZeneca (Viral Vector)	WHO EUL; UK MHRA	76% (clinical US) 67–90% (real world)	Alpha: 66–74% Beta: 10–22% Gamma: Works, minimal loss of neutralisation Delta: 60–67% (UK)	2 (4 to 12 weeks apart)	2°C to 8°C (at least 6-month lifespan)
Johnson & Johnson (Viral Vector)	WHO EUL; US FDA; Endorsed by Africa Regulatory Taskforce	66% (clinical) 72% (real world US) 68% (real world Brazil) 64% (real world South Africa)	Alpha: Works Beta: 64% (82% against severe illness) Gamma: 51% Delta: Unknown	1 (two- dose trial in process)	2°C to 8°C (3-month lifespan; 2-year lifespan if stored at -20°C)
Sinopharm (Inactivated)	WHO EUL	78.1% (clinical); real world data may point to lower efficacy	Alpha: Works Beta: Works, minimal loss of neutralisation Gamma: Unknown Delta: Unknown	2 (3 weeks apart)	2°C to 8°C

SinoVac / CoronaVac (Inactivated)	WHO EUL	50%–83.5% (depending on clinical trial)	Alpha: Works Beta: Works, minimal loss Gamma: 50% Delta: Unknown	2 (2 weeks apart)	2°C to 8°C
Gamaleya / Sputnik V (Viral Vector)	Russia	95% (clinical) 91.6% (real world)	Alpha: Works Beta: Substantial loss of neutralisation Gamma: Unknown Delta: Unknown	2 (3 weeks apart)	Liquid form must be stored at -20°C
Bharat Biotech / Covaxin (Inactivated)	India	78% (clinical); final analysis expected in June	Alpha: Works Beta: Likely works Gamma: Works Delta: Works, some loss of neutralisation**	2 (4 weeks apart)	2°C to 8°C (at least one-week lifespan at room temp)

CanSino / Convidicea (Viral Vector)	China	65.3%	Alpha: Unknown Beta: Unknown Gamma: Unknown Delta: Unknown	1 (6-month booster may be needed)	2°C to 8°C
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Novavax*** (Protein)	Phase 3	96.4% (clinical)	Alpha: 86.3% Beta: 49% Gamma: Unknown Delta: Unknown	2 (3 weeks apart)	2°C to 8°C
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**Emergency use may be authorised in countries not listed.*

***Study did not specify sublineage of B.1.617.*

****Still in Phase 3 trials, not yet approved for emergency use or available on the market.*

All of these findings are based on completion of the required dosage per vaccine, underscoring the importance of not skipping the second dose in two-shot regimes. Where vaccines may lose efficacy against these variants, booster shots or tailored vaccine updates are already in development.

Importantly, in spite of some reduced efficacy in protection against current variants of concern, evidence to date suggests that most of the vaccines are still likely to be effective in preventing severe Covid-19 illness. For example, while the J&J vaccine is 64 per cent effective against mild to moderate disease caused by the Beta variant, it is 82 per cent effective at reducing an individual's risk of hospitalisation and death at least 28 days after vaccination.²⁵ AstraZeneca may only be 60 per cent effective against mild to moderate disease caused by Delta, but it is 92 per cent effective against hospitalisation.²⁶ This is a

critical distinction when evaluating the vaccines, especially in Africa where clinical manifestations of the virus have been lower than the global average. In effect, vaccinating the population with any of the available vaccines would significantly diminish the threat of variants and reduce, if not eliminate, severe and mortal Covid-19 incidence in Africa.

Low Covid-19 Vaccination Rates in Africa

Yet diminishing the spread and threat of variants by way of vaccination in Africa is severely hindered by current vaccine access and administrative challenges. With most countries relying on the COVAX AMC facility for their procurement, the moratorium on exports from the Serum Institute of India (SII), the largest manufacturer of AstraZeneca, has adversely affected COVAX supply; SII had committed to produce as much as 45 per cent of all COVAX vaccines by the end of 2021. As a result, the facility had distributed less than a third of what it was expected to deliver to Africa by the end of May: just 22 million doses had been received of the nearly 75.5 million expected.

Although there is a global shortage of vaccines overall (approximately 9.4 billion doses are estimated to be produced by the end of 2021, while global demand amounts to 11.5 billion doses), supply constraints in Africa are exacerbated by the disproportionate accumulation of vaccines by high-income countries. Nations such as Canada, Switzerland and Israel, for example, have purchase agreements securing enough vaccines for three times their populations while African countries have so far only ordered enough doses to vaccinate 38 per cent of the continent's population.

To complicate matters, vaccine hesitancy in Africa is on the rise. Studies carried out in 2020, before most vaccines were successfully developed, showed that Africans were generally more likely to agree to take vaccines than others. Since then, perceptions on the continent have hardened. In March 2021, the Africa CDC released a study on perceptions and hesitancy in 15 countries. The responses showed a rise in vaccine hesitancy, driven by conspiracy theories and other factors that have taken hold in the face of confusing global regulatory advice on the safety and efficacy of different vaccines.²⁷ Comparatively lower clinical manifestations of Covid-19 in the region compared to the rest of the world have also contributed to high levels of hesitancy: many people do not believe they are at risk of the disease and therefore do not see a need to receive a vaccine.

Together, these factors have led to Africa having the lowest vaccination rates in the world. Africa has administered just 3.1 doses per 100 people, compared to 17 doses per 100 in Oceania, 30 in Asia, 33 in South America, 56 in Europe and 67 in North America.²⁸ Although Africa makes up over 17 per cent of the global population, it has administered only 1.7 per cent of global doses.²⁹ Of those who have received a jab, the majority are still not fully vaccinated, meaning most have not received the second dose of a two-dose regime. Although a first-dose-to-many strategy has been effective against the

original strain of Covid-19, given the emergence of VOCs and the necessity of receiving a full course in order to be adequately protected against them, many in Africa who have received their first jab, particularly health-care workers, remain at risk of exposure to VOCs amid a shortage of sufficient supply to distribute second doses.

In the absence of mass vaccine protection in the immediate term, African governments must look to other measures to restrict the spread of current VOCs and prevent the emergence of future VOCs. Chief among these is the urgent need to enhance surveillance and genome-sequencing capacities in order to rapidly identify the presence and prevalence of variants and stem transmission.

Genomic Sequencing and Surveillance Are Critical for Tracking and Containing Variant Spread

Genomic sequencing can assist in identifying new pathogen variants shortly after they appear and in generating more data to estimate the prevalence of variants in populations, thus ensuring that African policymakers can implement the necessary public-health measures. Governments need to prioritise this approach because by conducting genomic sequencing and joining a platform of globally shared data, African policymakers will be able to stay up-to-date on mutations and those that are most critical to track at any given time. When combined with epidemiological information, genomic sequencing can facilitate linkages during the early detection phase of outbreaks, accurate tracing of transmission chains, precise delineation of the geographical spread of an outbreak and the identification of sources of infection. Timely outbreak detection and removal of sources of infection are critical for enabling African policymakers to prevent the public-health crises that have taken place in other parts of the world.

Capacity for Genomic Sequencing

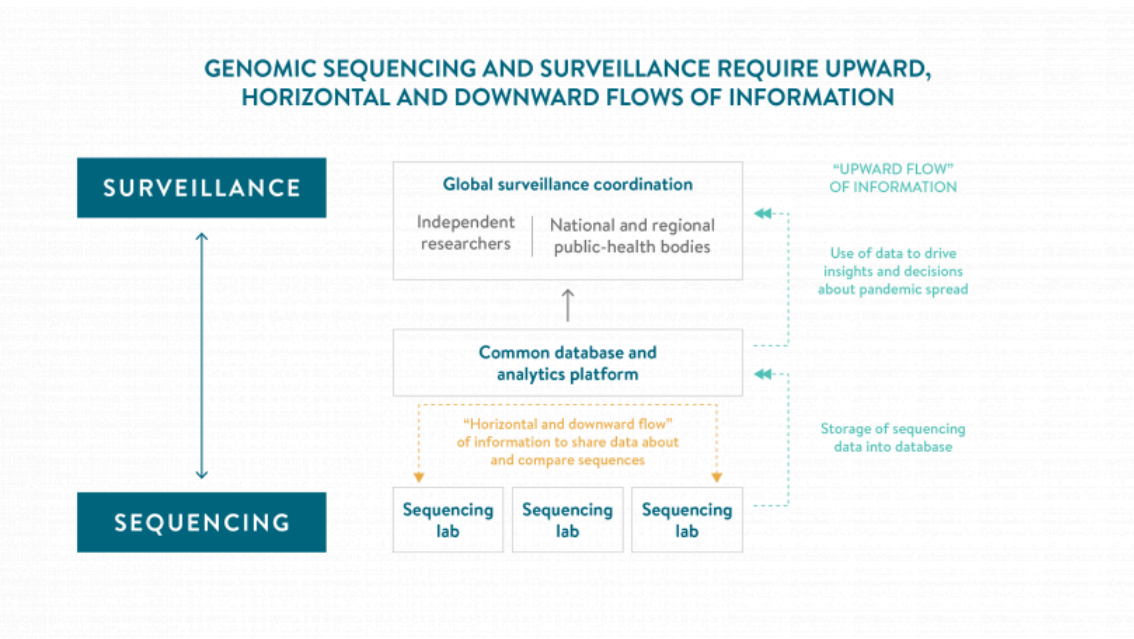
At the beginning of the Covid-19 pandemic, governments across sub-Saharan Africa demonstrated a willingness to undertake testing but were hampered by a lack of test kits. The scientific community has previously developed methods for the rapid, near-sample sequencing of pathogens in multiple outbreak situations including for Zika, Ebola, yellow fever, swine flu and a range of other pathogens. A global effort to sequence and share Covid-19 genomes is crucial for tracking mutations, as well as for investigating viral evolution and transmission dynamics. Genomic surveillance, which refers to the systematic and regular collection of genetically sequenced information, is important for existing outbreak investigation and active surveillance at major hospital health centres. Rapid data-sharing has been key to the public-health response, and researchers all over the world have been sharing sequenced genomes on public databases such as the global sequence repository GISAID, GenBank and elsewhere.

The global pandemic has exposed the weakness of viral genomic-sequencing capacity globally. Of 152 countries for which data are available, 100 had uploaded sequence data to GISAID for less than 1 per cent of their reported cases. A total of 51 of those countries, including India, Indonesia, Russia and Brazil, had uploaded sequences for less than 0.1 per cent of their cases. As of mid-May, ten high-income countries accounted for 82 per cent of the total sequences in GISAID's database.³⁰ In March 2020, the UK government allocated £20 million to launch the Covid-19 Genomics UK Consortium (COG-UK), an initiative to increase the country's capacity to sequence Covid-19 genomes using a network of 12 sequencing centres, with the results informing the development of drugs, vaccines and other

responses. After six months, COG-UK had already sequenced over 61,000 samples (equivalent to 15 per cent of the UK’s cases).

A mere 2 per cent of the 100,000-plus sequenced Covid-19 samples on the global database come from sub-Saharan Africa. This is a key challenge for African policymakers to address because the early detection of variants requires a timely and regular flow of information. Genomic sequencing and surveillance involve both (1) an “upward” flow of information that moves data from individual sequencing labs into databases that allow them to be stored and used for diagnostic, clinical and public-health purposes, and (2) a “horizontal and downward” flow of information that allows for comparison of sequences within and between sovereign sequencing facilities, where it can be linked to patient-identifiable or sensitive data.³¹ In a best-case scenario, these flows of information would be used to guide the global response to the pandemic. They would serve as an early-warning system for how the virus is evolving and how to combat it. However, low sequencing capacity hinders continental and global ability to get ahead of the virus.

Figure 4 – Genomic sequencing and surveillance information flow



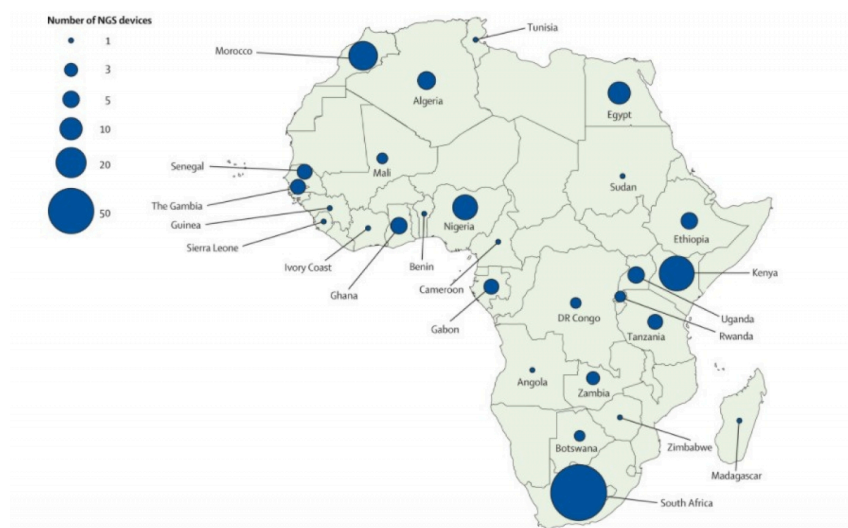
Source: Global Health Security Consortium: Tech Solutions for Global Genomic Sequencing and Surveillance, May 2021

Covid-19 sequencing in Africa is in its infancy stage for investigating variations among countries. The biggest sequencer by far is South Africa, along with Egypt, Kenya and Nigeria. The DRC has contributed the second-most genome sequences in the region; it is speculated that the country’s legacy of foreign interventions from previous Ebola virus outbreaks is the reason for its active participation because it has witnessed the positive outcome of these collaborations. Nigeria’s African Centre of Excellence for

Genomics of Infectious Diseases was the first on the continent to sequence Covid-19, yet its ability to ramp up sequencing has been restricted due to financial limitations. Based on interest and capability, Ghana and Senegal also have the potential to expand their sequencing capacity.

Rapid innovation in sequencing technologies has led to the development of robust next-generation sequencing (NGS) equipment with the capability for high pathogen resolution at increasingly affordable prices. A *Lancet* assessment of sequencing capacity within Africa reveals that capacity is sparse and concentrated in a few countries. Up to 72 per cent of next-generation sequencers are concentrated in five countries: South Africa (38 per cent), Kenya (14 per cent), Nigeria (6 per cent), Morocco (9 per cent) and Egypt (5 per cent). However, most of the capacity in the continent (70 per cent) is found outside of national public-health institutes.³² This highlights the need to create better partnerships with the private sector, academic institutions and networks among countries with varying levels of capacity to even out coverage and ensure equal access. The map below shows the scarce number of NGS devices available across Africa.

Figure 5 – Next-generation sequencing capacity in Africa



Source: *The Lancet: Genomic-informed pathogen surveillance in Africa: opportunities and challenges*, February 2021, [https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(20\)30939-7/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30939-7/fulltext)

Limited capacity for sequencing and surveillance in Africa means that the spread of current variants is not being traced fast enough and the emergence of future variants is likely to go under- or undetected.

Variants Pose a Threat to Africa That Calls for a Proactive, Coordinated and Holistic Approach by Governments

To minimise the human and economic costs of these more dangerous variants, African governments must support efforts to rapidly expand sequencing and data-sharing capacities, immediately implement the public-health and social measures necessary for stemming the spread of current VOCs, and strengthen their vaccination strategies.

African governments should prioritise investments in genomic-sequencing capacity to proactively identify Covid-19 variants and other infectious pathogens and enable early action to prevent the spread of any VOCs.

Sequencing is an expensive process that requires specialised infrastructure and trained individuals. Even when funding is available, getting access to the necessary reagents required to perform the sequencing has been difficult for lower-income countries due to shipment delays that can last for months. Reagents are also more expensive for lower-income countries because wealthier countries buy in bulk, thus driving an increase in prices. Most molecular diagnostic labs with capacity for Covid-19 detection can sequence Covid-19 samples, with the estimated cost of acquiring sequencing instruments and reagents standing at around £21,000 per lab (about £76 per sequenced sample). ³³

There is a need for investment in key high-end technology platforms – or, more specifically, a need for transformational investment to support full genome-sequencing capability in Africa. This capacity-building will be a huge part of the “hardware” required for health systems to be prepared for emerging infectious diseases in our region in the future and for our emergency response during this outbreak.

Enhanced capacity can be achieved by expanding the network of regional sequencing hubs throughout Africa, creating a network of laboratories across the continent with capacity to conduct the necessary tests. However, there are numerous gaps that hinder the smooth flow of this network – from transportation and logistical complications to delays in testing results – that prevent countries from identifying solutions ahead of time. ³⁴ It is therefore necessary to encourage decentralised development of genomic-sequencing capacity at country level that can function in parallel to these regional hubs. Governments need to direct funding towards research and development to enable country-level genomic sequencing, collaborate with countries with advanced genomic-sequencing ability for capacity-building, and establish partnerships with private sector and academic institutions to ensure maximum productivity.

In order to scale up investment, African governments need to explore and partner with existing international initiatives such as the Africa Pathogen Genomics Initiative (Africa PGI). The initiative is a four-year collaboration between the Africa CDC Institute of Pathogen Genomics, the US CDC, the Bill & Melinda Gates Foundation, Microsoft, genomic-sequencing technology company Illumina and UK-based biotechnology company Oxford Nanopore Technologies. Its aim is to expand next-generation genomic-sequencing tools and expertise across Africa that could be used to tackle disease outbreaks more effectively. ³⁵ Africa PGI will equip national public-health institutes and train scientists in Africa to effectively use next-generation sequencing technologies. An African-owned data library and real-time data-sharing platform will be established to support the laboratory network, in alignment with different African Union member states' regulations.

In addition, countries should also consider adding genomic-sequencing capacity as a significant part of their emergency response to Covid, whether dealing with international partners or national financial planning. For example, a key part of the World Bank COVID-19 Emergency Response and Health Systems Preparedness Project, which is implemented in various countries in Africa, involves building in-country genomic-sequencing capacity.

Testing must also be ramped up to a mass scale. Testing is essential not only for gaining control of transmission, but also for ensuring there are diverse samples for sequencing and that there is sufficient surveillance to understand and monitor disease levels. Currently a majority of African countries record much-higher positive test rates than the WHO-recommended threshold of 5 per cent. ³⁶ Governments need to prioritise mass testing because it is an integral part of genomic sequencing and identifying and tracking variants.

Policymakers should use available data and join global platforms of shared data to ensure adequate surveillance of mutations and up-to-date awareness of those that are most critical to track at any given time. Public-health measures should also be taken in response to increased risks indicated by these platforms.

It is critical to complement expansion of on-the-ground genomic-sequencing capabilities with the appropriate technological solutions, financing and governance to ensure that captured sequence data can be used to inform public-health response. This should include capabilities to rapidly upload and process genomic-sequencing data in standardised ways; analyse data to make inferences about variants; and provide ways to use genomic-sequencing data to inform public-health response and R&D for Covid-19 response tools (vaccines, therapeutics and diagnostics). Broader governance measures to create an enabling environment should include common data standards, incentives for data-sharing that respect the needs of individual researchers and sovereign nations, and scientific advisory committees to assess emerging data and issue normative guidance on public-health response.

In the immediate term, policymakers should make use of available data to track the existence and potential spread of new variants. In the absence of genomic sequencing, increased surveillance and effective use of available data on the spread of Covid-19 are vital as new variants emerge. This requires enhanced tracking of transmission rates, hospitalisation rates, mortality rates and test-positivity ratios at regional and local levels, to swiftly identify escalating patterns and send samples to regional hubs. By conducting genomic sequencing and joining a platform of shared data, African policymakers will be able to stay up-to-date on mutations and those that are most critical to track at any given time. The identification of some variants may also be possible through PCR testing, without the need to fully sequence samples. For example, in the UK, researchers have been able to quickly track the transmission of the Delta variant because it has a genomic ‘marker’ that the Alpha variant does not. This marker is known as the “S gene target” and can be found in some PCR test results. A sample that is positive for the S gene target therefore serves as a proxy for the spread of the Delta variant. ³⁷ As new variants emerge and their properties are identified PCR testing may, in certain cases, also be a mechanism for tracking the spread without having to sequence. TBI’s paper on [tech solutions for global genomic sequencing and surveillance](#) provides further details on the critical importance of such a platform. ³⁸

African governments should expand their vaccine access beyond COVAX, introduce targeted containment measures and increase their vaccine absorption rates.

Considering COVAX’s supply shortages, African governments should not rely exclusively on COVAX and should reorient their focus to ramp up efforts for bilateral deals – either with companies directly or with other governments by making use of embassies (such as those of the US, UK, Russia and China) and leveraging diplomatic ties. In addition, reallocation of stockpiles may happen through bilateral arrangements, rather than through COVAX. It is likely those efforts will prioritise countries with clear absorptive capacity. Therefore, it is critical for governments to have a detailed and costed plan for rollout (including a strategy for overcoming vaccine hesitancy) and to make the best use of any limited supply they do have. Where there are deficits in planning or operational support for national vaccine rollouts, now is the time to plan and mobilise this support, alongside the efforts to procure vaccines. African Export-Import (Afrexim) Bank is supporting \$2 billion of initial procurement guarantees and facilitating ease of financing, enabling access to 270 million doses under the African Union’s Covid-19 Vaccine Acquisition Task Team (AVATT) by July or August of this year. To tap into this pool and additional resources governments need to seek assistance from the World Bank, with whom AVATT has a partnership, or explore other funding options.

In the near-term absence of sufficient vaccine supply and uptake, African governments must also continue to rely on other measures to protect their populations. The rapid spread of more transmissible VOCs means there is an urgent need for targeted public-health measures. Governments must treat the new variants as they treated the first cases of Covid-19 by enhancing surveillance and testing, increasing

contact-tracing and isolating of probable cases, and introducing localised restrictions on movement and other targeted measures in order to prevent further local transmission.

Conclusion

The longer the virus is allowed to circulate, the higher the risk that a new mutation will make the virus more contagious, more virulent and/or more evasive of vaccines, treatments or immune responses. This in turn may lead to new, more lethal waves of Covid-19, adding strain to fragile health systems, including increased risk to frontline health-care workers. Africa already has a dearth of doctors and nurses and cannot afford to lose any more. In addition, the continuing preoccupation of health systems with Covid-19 leads to the possible neglect of other essential health services.

Variants that increase transmissibility of the disease also increase the incidence of new mutations, leading to a vicious circle. Adequate public-health measures and vaccines can break the cycle, but they require the trust and compliance of the population. The economic impact of certain public-health measures, such as restrictions on movement, signals that the public can tolerate these control mechanisms only to a certain point. Compromised livelihoods and fatigue will drive noncompliance which, in an under-vaccinated population, will increase transmission. To complicate matters, rising case numbers in spite of vaccination efforts and relatively lower clinical manifestations of Covid impede trust in the vaccines, which is already low in many countries.

If their populations remain under-vaccinated, African countries may be facing the perfect storm as insufficient vaccination rates create breeding grounds for new variants. The proliferation of variants has human, economic and political consequences, not only for Africa but for the world. The longer the pandemic carries on, the more strained government resources will be, aggravating even long-term stability.

To avoid this impending crisis, African governments need to focus on enhancing genomic-sequencing and surveillance capacity to inform public-health measures, expand vaccine access from and beyond COVAX, and increase their vaccine absorption rates.

The leaders of the World Health Organisation, World Bank, International Monetary Fund and World Trade Organisation recently raised the alarm that the emergence and spread of new variants due to inequitable vaccine access would worsen the pandemic and deepen the global economic divide, the impact of which would be felt worldwide.³⁹ To prevent this outcome, they are proposing \$50 billion of funding to globally accelerate vaccination, increase testing, implement therapeutics and public-health measures, and insure against the risks of new variants. Doing so requires sharing technology and rapidly strengthening local capacities for surveillance and viral genomic sequencing. The longer it takes to act, the higher the human and economic cost will be.

Key Recommendations:

We propose that African policymakers should:

1. Prioritise investments in genomic-sequencing capacity to proactively identify Covid-19 variants and other infectious pathogens and enable early action to prevent the spread of any VOCs.
2. Make use of available data and join global platforms of shared data to ensure adequate surveillance of mutations and up-to-date awareness of those that are most critical to track at any given time, and enforce public-health measures accordingly.
3. Focus on expanding vaccine access beyond COVAX, introducing targeted containment measures and increasing their vaccine absorption rates.

Charts created with [Highcharts](#) unless otherwise credited.

Footnotes

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