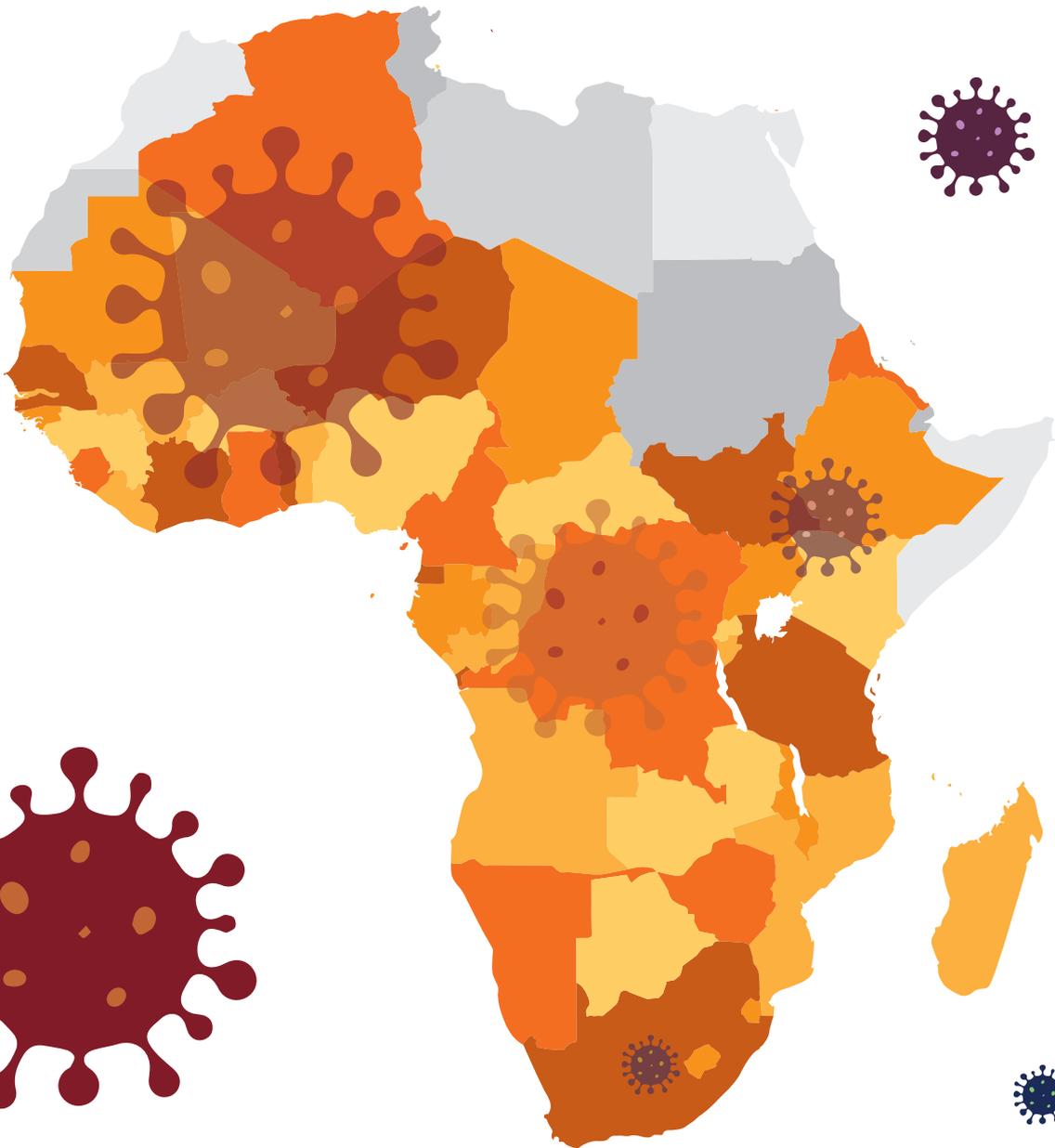
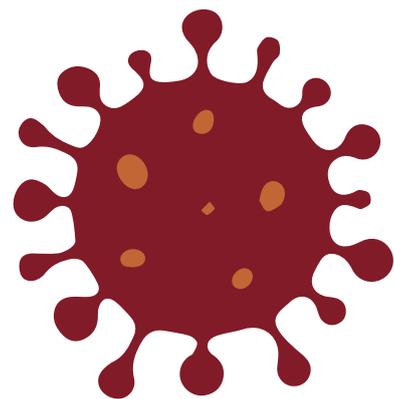


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Building capacity for whole genome sequencing of SARS-COV-2 in East Africa

Building capacity for whole genome sequencing of SARS-COV-2 in East Africa to inform epidemic response preparedness

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There is a credible threat of SARS-CoV-2 in East African countries in the wake of the pandemic. A number of countries in the region, in particular Kenya, have close interactions with China through trade and associated travel. In addition, there has been an increased global spread of the COVID19 (the disease caused by SARS-CoV-2) epidemic over the last few months. Kenya, a lower-middle income country, lacks adequate resources for comprehensive preparedness to counter a large-scale epidemic as has been witnessed in the People's Republic of China. To support the country's epidemic preparations, it is important to setup whole genome sequencing (WGS) using portable technology to support public health control measures. More broadly across the region, the introduction of the virus into East Africa requires understanding of the origins and local spread patterns. This information as previously observed with the Ebola epidemic helps to better target interventions.

The merits of genome sequencing to support epidemiological and evolutionary analysis has already been proven in the current epidemic in China, with WGS providing insights on virus spill-over to the human population, introduction of the virus into new geographical regions, and the mutation rate is providing information on capacity to adapt and to enhance its current human-to-human transmission potential. The Oxford Nanopore Technology (ONT) has been shown to be a cost effective and portable sequencing platform and is an important consideration for Kenya and other East African countries.

At KEMRI-Wellcome Trust Research Programme (KWTRP) we have established a sequencing and bioinformatics network of contacts in East Africa through the NIHR Global Health Research Project GeMVi ('On the application of Genomics and Modelling to the Control of Virus Pathogens in East Africa) linking to Public Health Reference Laboratories in Uganda, Kenya and Tanzania, and, also Rwanda (via involvement with NIHR Global Health Research Tackling Infections to Benefit Africa at the University of Edinburgh (TIBA) and the ARTIC Network), links to similar labs in Rwanda. Furthermore, we are developing or have established a range of WGS protocols for virus pathogens such as measles, influenza and RSV on the ONT MinION platform.

We propose to develop human resource and technical i.e. ability to setup successful portable genomics including the relevant hardware and bioinformatics capacity for genome sequencing of SARS-CoV-2 in Kenya and East Africa in general to support epidemic preparedness. We will equip select National Public Health Laboratories (NPHLs) and provide sequencing kits. The project will enhance our Nanopore WGS capacity at the KWT, support sequencing of up to 50 genome sequences, allow us to support transfer of portable cost-effective genome sequencing methods to public health facilities in the region and enhance an existing network through a collaborator workshop, including facilitated training on handling outbreak pathogens (e.g. SARS-CoV-2) and clinical cases.



Objectives:

We intend to improve on the surveillance and diagnostic capacity for emerging infections with special focus on the SARS-CoV-2 and the associated COVID-19 disease. We are going to achieve this through developing local capacity for portable sequencing within KWT and equipping select NPHLs with portable sequencing devices. We envision that this will boost the region's capacity to respond to infectious diseases emergencies through genomics.

Through TIBA we will establish links with National Institute for Medical Research (NIMR) in Tanzania and with the Rwanda Biomedical Centre and exploit synergy and expertise from shared technical and resource capacity. In addition, and through GeMVi, we are supporting building virus genomics and bioinformatics capacity in East Africa and have established links with Uganda Virus Research Institute (UVRI) and Makerere University in Uganda, Kilimanjaro Christian Research Institute (KCRI) in Tanzania, and the University of Nairobi Institute of Tropical and Infectious Diseases (UNITID) in Kenya.

Already and with our links with TIBA, we are establishing Nanopore technology protocols to support the surveillance of chikungunya virus in Kenya and Sudan, with these capabilities now also extended to Rift Valley Fever virus sequencing in partnership with Kenya's NPHL.

Impact context of the project

1. Establish WGS protocol for SARS-COV-2 at KEMRI-Wellcome using both the ONT MinION and Flongle and supporting VolTRAX to automate sample processing where applicable.
2. Identify partner NPHLs in Rwanda (through TIBA Rwanda) and Tanzania (through NIMR and other contacts at the Ifakara Health Institute) and bring people for training and transfer of the genomic methodologies to their laboratory setup, and finally run a collaborators workshop to bring together stakeholders from the public health facilities and the research institutes to plan and work together.
3. During this workshop (virtual) we will conduct a facilitated training on the handling of SARS-COV-2 specimens (in the lab) and clinical cases (by healthcare workers). This would build on our current experience in clinical management and handling of specimens from patients with respiratory illness in the region.
4. We will conduct follow-up engagement meetings with partners in this project, to discuss outputs, successes and challenges, with support or facilitation from TIBA secretariat. The capacity developed during this project will be of benefit to the regional response to both the SARS-COV-2 outbreak as well as other viral illnesses of public health concern.

