Detection of SARS-CoV-2 501Y.V1 and 501Y.V2 variants of concern in samples collected in Nairobi

Key Points
• We sequenced and obtained partial genomes from 4 out of 9 SARS-CoV-2 positive samples collected between 4th and 15th February 2021 and provided by the UN staff clinic in Nairobi, Kenya.
• A total of 3 of the sequenced samples were identified as variants of concern, two were classified as B.1.1.7/501Y.V1 and one was classified as B.1.351/501Y.V2 based on phylogenetic clade assignment and mutation profiling.

Background
To date, three major variants of concern have been described, B.1.1.7/501Y.V1, B.1.351/501Y.V2 and P.1/501Y.V3. Each variant has been detected in more than 23 countries across the globe including several countries in Africa. In Kenya, we have reported detection of B.1.1.7/501Y.V1 and B.1.351/501Y.V2 during local and border point screening.

Findings from sequence data obtained on 5th March 2021
We received 9 samples collected between 4th and 15th February 2021 from the UN Staff clinic in Nairobi Kenya for the purposed of whole genome sequencing. We obtained partial genomes from 4 of the 9 samples. Five of the nine samples failed quality control steps and were not sequenced.

We classified the recovered genome sequences into 3 lineages; B.1.1.7/501Y.V1 (n=1), B.1.351/501Y.V2 (n=2) and B.1.95 (n=1) (Figure 1). Table 1 provides a detailed summary for each sample.

<table>
<thead>
<tr>
<th>Date of Collection</th>
<th>County</th>
<th>Nextstrain Clade</th>
<th>Pango lineage</th>
<th>Cycle threshold (Ct) score</th>
<th>Genome recovered (%)</th>
<th>Gender</th>
<th>Age</th>
</tr>
</thead>
<tbody>
<tr>
<td>04-02-2021</td>
<td>Nairobi</td>
<td>20H/501Y.V2</td>
<td>B.1.351</td>
<td>26.31</td>
<td>96.4</td>
<td>Male</td>
<td></td>
</tr>
<tr>
<td>12-02-2021</td>
<td>Nairobi</td>
<td>20I/501Y.V1</td>
<td>B.1.1.7</td>
<td>36.2</td>
<td>55.4</td>
<td>42</td>
<td></td>
</tr>
<tr>
<td>13-02-2021</td>
<td>Nairobi</td>
<td>20H/501Y.V2</td>
<td>B.1.351</td>
<td>28.0</td>
<td>81.7</td>
<td>Male</td>
<td></td>
</tr>
<tr>
<td>15-02-2021</td>
<td>Nairobi</td>
<td>20A</td>
<td>B.1.95</td>
<td>22.29</td>
<td>95.8</td>
<td>64</td>
<td></td>
</tr>
</tbody>
</table>

Table 1: A basic summary of sequencing results of the 4 samples collected from the UN staff Clinic in Nairobi, Kenya. The samples are sorted by the date of samples collection from top to bottom.

Figure 1. A phylogenetic analysis of four SARS-CoV-2 sequences from samples collected between 4th February 2021 and 15th February 2021 from the UN Staff Clinic in Nairobi, Kenya. The figure shows the relationship between the sequenced genomes (light green markers) and the global variants of concern (501Y.V1 in orange, 501Y.V2 in blue, 501Y.V3 in cyan), non-variants (grey) and previous sequences from western Kenya (grey).
Implications
The detection of the SARS-CoV-2 variants of concern among these samples emphasize the need for enhanced control of SARS-CoV-2 across the region.

Data availability
Whole genome sequence data are available from GISAID database to allow access to the global scientific community.

Acknowledgements:
This work was supported by the National Institute for Health Research (NIHR) (project references 17/63/82 and 16/136/33) using UK aid from the UK Government to support global health research, The UK Foreign, Commonwealth and Development Office and Wellcome Trust (grant# 102975; 220985). The views expressed in this publication are those of the author(s) and not necessarily those of NIHR, the Department of Health and Social Care, Foreign Commonwealth and Development Office, Wellcome Trust or the UK government. In addition, this work was supported by the KEMRI Internal Research Grant (Grant # KEMRI/COV/SPE/012