End-to-end surveillance systems in Kenya supports ongoing SARS-CoV-2 variant surveillance and global health security

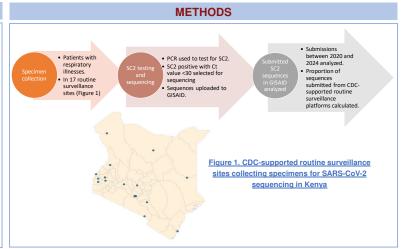
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Routine surveillance platforms play a vital role in supporting SARS-CoV-2 genome surveillance

BACKGROUND

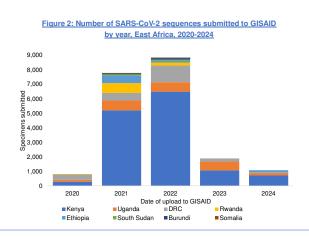
- · New SARS-CoV-2 variants can:
 - lead to evasion of prior immunity causing ongoing health impacts globally.
 - potentially affect the diagnosis or management of SARS-CoV-2.
- Online repository of SARS-CoV-2 genome sequences are an important tool for variant surveillance.
- However, uploaded SARS-CoV-2 sequences dropped dramatically after the WHO ended the COVID-19 public health emergency in mid-2023.

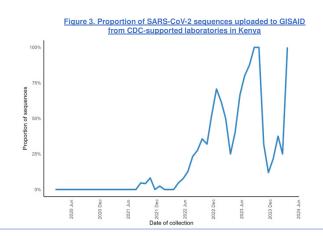
Would routine surveillance platforms provide an alternative source for SARS-CoV-2 genome surveillance?



RESULTS

- Most SARS-CoV-2 genomes from East Africa in GISAID originate from Kenya (Figure 2). However, the total number of genomes submitted into GISAID
 declined substantially in 2023 and 2024 compared to 2022.
- From 2020 to July 2024, there were 13,668 SARS-CoV-2 genomes uploaded from Kenya (annual range: 149 [2024] 7,262 [2022]).
- CDC-supported KEMRI laboratories submitted 721 (5.3%) sequences. However, these laboratories submitted a greater proportion of sequences to GISAID in 2023 and 2024 (Figure 3).
- In total, 690 (95.7%) of genomes submitted by CDC-supported KEMRI laboratories originated from specimens collected at routine surveillance sites.





CONCLUSIONS

- Although the proportion of genomes uploaded by CDC-supported KEMRI laboratories was low, this surveillance system continue to be one of the few
 providing genomic information on circulating SARS-CoV-2 in Kenya, highlighting the role that routine surveillance systems that monitor common syndromes
 like respiratory illnesses and test for common pathogens like SARS-CoV-2 play towards health security assets globally.
- Improving global capacity for SARS-CoV-2 genomic surveillance through end-to-end surveillance programs like the one described could improve identification
 of clinically significant variants, strengthen disease surveillance and improvement of vaccines.





