

KENYA MEDICAL RESEARCH INSTITUTE



In Search of Better Health

EVIDENCE BRIEF

**Detection of multiple SARS-CoV-2
variants of concern (VOC) in
Nairobi and household genomic
epidemiology of SARS-CoV-2
in Kilifi, Kenya**

KEY MESSAGES

1. **The sudden surge in COVID-19 cases was associated with the detection of circulating Variants of Concerns (VOCs) which increased transmissibility.**
2. **Alpha, Beta and Delta variants were the main VOCs circulating in Kenya during the study period.**

BACKGROUND

Coronavirus Disease of 2019 (COVID-19), a highly transmissible respiratory disease caused by the novel severe acute respiratory syndrome coronavirus type 2 (SARS-CoV-2), was officially declared a pandemic on 11 March 2020 by the World Health Organization (WHO) ¹. In Kenya, the first case of COVID-19 was detected on 13 March 2020 according to the Ministry of Health (MoH). To date, there have been more than 620 million cases with more than 6.5 million people succumbing to the disease globally. In Kenya there have been more than 338,390 cases and 5,690 deaths associated with COVID-19 .

Changes in the genetic properties of the SARS-CoV-2 virus may affect how easily it spreads, the associated disease severity, the performance of vaccines, therapeutic medicines, diagnostic tools, as well as other public health and social measures. In late 2020, the emergence of variants that posed a risk to global public health prompted the characterization of specific Variants of Interest (VOIs) and Variants of Concern (VOCs).

The WHO has defined VoCs as variants that lead to increased transmissibility or detrimental change to COVID-19 epidemiology or decrease the effectiveness of existing health and social measures available for diagnostics, vaccines and therapeutics. VoIs, on the other hand, have been defined as variants with genetic changes that are predicted or known to affect virus characteristics such as transmissibility, disease severity, immune escape, diagnostic or therapeutic escape. Additionally, they have been identified to cause significant community transmission or multiple COVID-19 clusters, in multiple countries with increasing relative prevalence alongside increasing number of cases over time, or other apparent epidemiological impacts to suggest an emerging risk to global public health. VOCs and VOIs have been associated with increased transmissibility of the SARS-CoV-2 leading to an increase in the number of cases worldwide.

The global genomic surveillance of SARS-CoV-2 was useful in the identification of emerging VoCs and associated mutations that impacted virus transmissibility, disease severity, vaccine efficacy, and clinical case management ². Among the VoCs that had a global impact were B.1.1.7 (Alpha) first identified in United Kingdom in September 2020, B.1.351 (Beta) first reported in South Africa in December 2020, B.1.525 (Eta) first identified in the UK and Nigeria in December of 2020, B.1.617.1 (Delta) first identified in India in October 2020, P.1 (or B.1.1.28.1, Gamma) first reported in Brazil in January 2021, and B.1.1.529 (Omicron) first reported in South Africa in November 2021 ^{3 4 5 6} and retroactively detected in samples in the US and other countries around the same time ⁷. Reports from a study to investigate the effect of SARS-CoV-2 Alpha variant in a community cluster concluded that as compared to non-VOCs, the Alpha variant exhibited high transmissibility in a community cluster.

OBJECTIVES

1. To investigate the determinants of the sudden surge in the number of reported COVID-19 cases and deaths in Nairobi
2. To describe the molecular epidemiology of SARS-CoV-2 in rural households using whole genome sequencing

POPULATION TARGET

The population for the two abstracts reviewed was patients who had a positive diagnosis of SARS-CoV-2.

METHODS

We reviewed two abstracts presented in the 12th KEMRI Health and Scientific Conference (KASH). All the abstracts presented in this evidence brief had patients with SARS-CoV-2 infection as the population of interest. All the studies represented here employed Real Time PCR and Whole Genome Sequencing to characterize the variants of interest and concern in the samples analyzed.

RESULTS

The abstracts specifically gave evidence on SARS-CoV-2 Variants of Interest (VOIs) and Variants of concern (VOCs). The issues highlighted by the abstracts included increased transmissibility of the virus as a result of the variants as well as transmission of SARS-CoV-2 within and between households. The results for these studies are represented in Table 1 below.

Abstract Title	Study county	Reporting Period	Variant Prevalence		
			Alpha	Beta	Delta
Household genomic epidemiology of SARS-CoV-2 in rural coastal Kenya	Kilifi	December 2020-September 2021	45.4%	13.6%	40.9%
Detection of multiple SARS-CoV-2 variants of concern (VOC) in Nairobi, Kenya between March 2021 and July 2021.	Nairobi	March-July 2021	62.7%	35.8%	1.5%

Table 1: Variant prevalence from the two studies reviewed.

FINDINGS FROM ABSTRACTS

The findings from the reviewed abstracts are represented in Table 2 below.

Author (s)	Abstract Title	Key issues	Recommendation
Charles Agoti, 2022	Household genomic epidemiology of SARS-CoV-2 in rural coastal Kenya	-Interhousehold transmission events were recorded as evidenced by Genomic data -All recorded genomes were classified within lineages of known variants of concern; Alpha (n=60), Beta (n=18), Delta (n=54)	-There was evidence of circulation of Variants of Concern in Nairobi -Transmission of SARS-CoV-2 within and between households was common in rural Kenya.
Silvanos Opanda et al, 2022	Detection of multiple SARS-CoV-2 variants of concern (VOC) in Nairobi, Kenya between March 2021 and July 2021.	-Kenyan viruses were genetically similar to those that circulated in other regions -Detection of multiple lineages of SARS-CoV-2 in Kenya.	-Variants associated with increased spread and community transmission of these viruses among the population.

Table 2: Key issues and recommendations from the abstracts under review.

DISCUSSION

In the abstracts that were reviewed, the dominant variants were Alpha, Beta and Variants which corresponded to reports presented in global publications. Previous studies conducted on the ins and outs of SARS-CoV-2 variants of Concern, demonstrated that emerging VOCs exhibit greater transmissibility, cause more disease and are better able to escape immunity and have been reported to have higher mortality than the original Wuhan strain⁸

The studies in this review also indicate that the variants Alpha, Beta, Gamma and Delta were the most common in the Kenyan regions of Coastal Kenya and Nairobi. This corroborates reports from other studies in the African region which have reported presence of these three major Variants of Concern with the inclusion of the Omicron Variant which was reported outside the reporting periods of the studies under review³.

RECOMMENDATIONS

The major recommendations from the abstracts under review in this brief include the following;

- Genomic data can be used as a tool to calculate the attack rates for different diseases in the community.
- To monitor the causes for an increase in the number of cases of COVID-19, genomic surveillance tools in the form of Whole Genome Sequencing play a vital role.

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