Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern

Less than 5% (23 815 of 537 360) of public SARS-CoV-2 genomes are from low-income and middle-income countries, where 80% of the world's population resides and has been similarly affected by COVID-19. The recent, worldwide spread of variants of concern has highlighted the need for global vigilance. Prospective surveillance of SARS-CoV-2 by genome sequencing in Zimbabwe between December, 2020, and January, 2021 (the period of the so-called second wave), has identified that variants with concerning mutations are prevalent in sequenced samples. In December, 2020, 95 (89%) of 107 sequenced cases contained mutations of concern, rising to 102 (98%) of 104 in January, 2021. The identified variants included the previously reported B.1.351 (501Y.V2) and A.23.1 variants, along with a novel variant under investigation (C.2).[1–3] The B.1.1.7, B.1.525, P.1, and P.2 and variants were not identified in Zimbabwe. Variants with concerning mutations have all replaced previously identified lineages in Zimbabwe (appendix).[4]

Firstly, the B.1.351 variant of concern, originally identified in South Africa,[2] accounted for 74 (69%) of 107 sequenced cases in December, 2020, and 99 (95%) of 104 sequenced cases in January, 2021. The population structure was consistent with multiple separate introductions. Zimbabwe is the second country other than South Africa to report B.1.351 as the dominant variant to date.[5] As in other countries, this variant has been associated with increased transmissibility, resulting in overwhelmed health-care systems and in higher mortality than the first wave (appendix). Secondly, the A.23.1 variant of concern, first reported in Uganda,[1] was observed in 3 (3%) of 107 sequenced cases in December, but was not observed in 104 sequenced cases in January. Thirdly, a variant designated C.2 and containing a spike protein mutation (N501T) that was previously reported in another lineage of SARS-CoV-2 found in mink was present in Zimbabwe in both December, 2020, and January, 2021. N501T is thought to improve ACE2 receptor binding in mink.[3] A mutation in the same location, N501Y, is associated with increased transmissibility in humans. In December, 2020, 18 (15%) of 117 of cases were found to be of the C.2 variant, whereas in January, 2021, this number fell to 3 (3%) of 104. Phylogenetic analysis of international genomes of the C.2 variant indicated that they were interspersed with C.2 genomes from Zimbabwean cases, indicating that Zimbabwe was a possible source. In conclusion, variants with concerning mutations identified in December, 2020, and January, 2021, have replaced previously identified lineages in Zimbabwe.[4] This observation highlights the importance of global surveillance by whole-genome sequencing of SARS-CoV-2 to identify sources and transmission routes, and to provide supporting evidence for policy decisions.

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See **Online** for appendix