I BEST OF THE WEEK (06 giu – 12 giu 2022)

Q. Wang et al.

SARS-CoV-2 Omicron BA.2.12.1, BA.4, and BA.5 subvariants evolved to extend antibody evasion

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Abstract

The Omicron subvariant BA.2 accounts for a large majority of the SARS-CoV-2 infection worldwide today. However, its recent descendants BA.2.12.1 and BA.4/5 have surged dramatically to become dominant in the United States and South Africa, respectively. That these novel Omicron subvariants carry additional mutations in their spike proteins raises concerns that they may further evade neutralizing antibodies, thereby further compromising the efficacy of our COVID-19 vaccines and therapeutic monoclonals. We now report findings from a systematic antigenic analysis of these surging Omicron subvariants. BA.2.12.1 is only modestly (1.8-fold) more resistant to sera from vaccinated and boosted individuals than BA.2. On the other hand, BA.4/5 is substantially (4.2-fold) more resistant and thus more likely to lead to vaccine breakthrough infections. Mutation at spike residue L452 found in both BA.2.12.1 and BA.4/5 facilitates escape from some antibodies directed to the so-called Class 2 and Class 3 regions of the receptor-binding domain (RBD). The F486V mutation found in BA.4/5 facilitates escape from certain Class 1 and Class 2 antibodies to the RBD but compromises the spike affinity for the cellular receptor ACE2. The R493Q reversion mutation, however, restores receptor affinity and consequently the fitness of BA.4/5. Among therapeutic antibodies authorized for clinical use, only bebtelovimab (LY-COV1404) retains full potency against both BA.2.12.1 and BA.4/5. The Omicron lineage of SARS-CoV-2 continues to evolve, successively yielding subvariants that are not only more transmissible but also more evasive to antibodies.

J.W. Cabore et al.

COVID-19 in the 47 countries of the WHO African region: a modelling analysis of past trends and future patterns

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Abstract

Background COVID-19 has affected the African region in many ways. We aimed to generate robust information on the transmission dynamics of COVID-19 in this region since the beginning of the pandemic and throughout 2022.

Methods For each of the 47 countries of the WHO African region, we consolidated COVID-19 data from reported infections and deaths (from WHO statistics); published literature on socioecological, biophysical, and public health interventions; and immunity status and variants of concern, to build a dynamic and comprehensive picture of COVID-19 burden. The model is consolidated through a partially observed Markov decision process, with a Fourier series to produce observed patterns over time based on the SEIRD (denoting susceptible, exposed, infected, recovered, and dead) modelling framework. The model was set up to run weekly, by country, from the date the first infection was reported in each country until Dec 31, 2021. New variants were introduced into the model based on sequenced data reported by countries. The models were then

extrapolated until the end of 2022 and included three scenarios based on possible new variants with varying transmissibility, severity, or immunogenicity.

Findings Between Jan 1, 2020, and Dec 31, 2021, our model estimates the number of SARS-CoV-2 infections in the African region to be 505·6 million (95% CI 476·0–536·2), inferring that only 1·4% (one in 71) of SARS-CoV-2 infections in the region were reported. Deaths are estimated at 439 500 (95% CI 344 374–574 785), with 35·3% (one in three) of these reported as COVID-19-related deaths. Although the number of infections were similar between 2020 and 2021, 81% of the deaths were in 2021. 52·3% (95% CI 43·5–95·2) of the region's population is estimated to have some SARS-CoV-2 immunity, given vaccination coverage of 14·7% as of Dec 31, 2021. By the end of 2022, we estimate that infections will remain high, at around 166·2 million (95% CI 157·5–174·9) infections, but deaths will substantially reduce to 22 563 (14 970–38 831).

Interpretation The African region is estimated to have had a similar number of COVID-19 infections to that of the rest of the world, but with fewer deaths. Our model suggests that the current approach to SARS-CoV-2 testing is missing most infections. These results are consistent with findings from representative seroprevalence studies. There is, therefore, a need for surveillance of hospitalisations, comorbidities, and the emergence of new variants of concern, and scale-up of representative seroprevalence studies, as core response strategies.