GENOMIC SURVEILLANCE OF SARS-CoV-2 REVEALS SEVERITY OF DELTA VARIANT IN CAMEROON

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BACKGROUND

At the global level, the dynamics of the COVID-19 pandemic have been driven by several epidemiological waves, determined by the emergence of new SARS-CoV-2 variants from the original viral lineage from Wuhan, China. While the SARS-CoV-2 dynamic has been described globally, there is a lack of data from Sub-Saharan African.

METHODS

•A laboratory-based survey was conducted within the framework of the national public health emergency operational Centre for COVID-19 in Cameroon, from March 1, 2020 to March 30, 2022, through an assessment of the evolutionary patterns of SARS-CoV-2 lineages across the four COVID-19 waves in the country.

• Data on full-length sequencing from all four sequencing laboratories were consecutively entered into the GISAID platform. These data were downloaded, and the molecular phylogeny of the SARS-CoV-2 sequences was performed using Nexstrain.

•The Mann–Whitney U test was used to calculate the correlation between the duration of each outbreak and the number of confirmed cases and between hospitalised cases and CFR, with a p value <0.05 considered statistically significant.

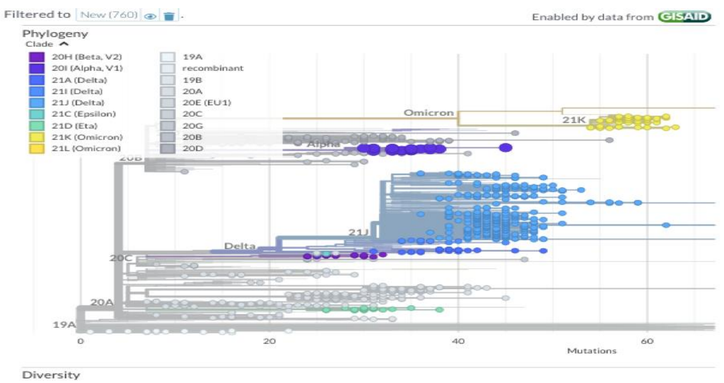


Figure 1: Phylogenetic tree of SARS-COV-2 lineages when using whole-genome sequences

RESULTS

• A total of 3,881 samples were successfully processed, of which 38.9% (n=1,509) using PCR mutation assay, 41.5% (n=1,612) using targeted sequencing, and 19.6% (n=760) using whole-genome sequencing. The mean age of the study population was 36 years (min–max: 2–86), and 45% were within the age range 26–45. Regarding gender distribution, 50.9% were male, and 49.1% were female.

• Phylogenetic analysis of the 760 whole-genome sequences generated from March 2020 to March 2022 revealed that the greater proportion of SARS-CoV-2 circulating in Cameroon belonged to the viral sub-lineages of the original strain from Wuhan (74%), 15% Delta variant, 6% Omicron variant, 3% Alpha variant and 2% Beta variant (Figure 1).

• The pandemic was driven by SARS-CoV-2 lineages of origin in Wave 1 (16 weeks, 2.3% CFR), the Alpha and Beta variants in Wave 2 (21 weeks, 1.6% CFR), Delta variants in Wave 3 (11 weeks, 2.0% CFR), and Omicron variants in Wave 4 (8 weeks, 0.73% CFR), with a declining trend over time (p=0.01208) (Figure 2).

• Across the four waves, there was an overall declining trend in the duration per wave (mean duration: 14 weeks) and the number of confirmed cases per wave (mean value: 25,444) from Wave 1 to Wave 4. These trends showed a significant correlation between the wave duration and the number of confirmed cases (z score= -2.50672; p=0.01208), indicating that the dynamics of SARS-CoV-2 variants were not the primary drivers of the number of cases observed per wave. Hence, the extent of viral transmission was mainly driven by the outbreak duration (Figure 3).

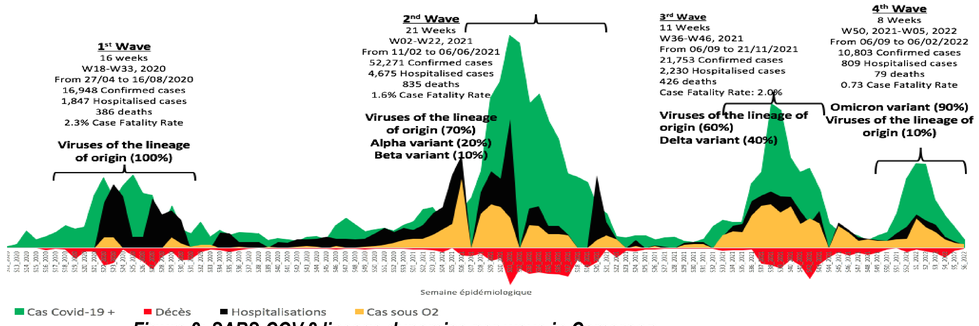


Figure 2: SARS-COV-2 lineage dynamics per wave in Cameroon

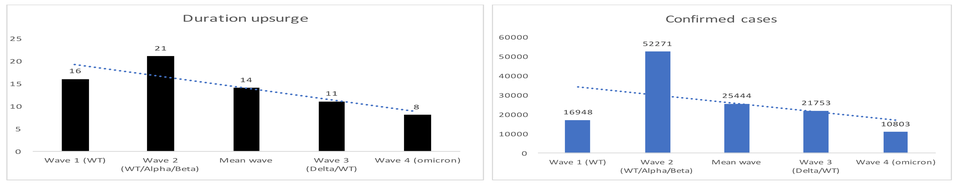


Figure 3: Correlation analysis between the wave length and the number of confirmed cases following variant dynamics

CONCLUSIONS

• In a nutshell, the SARS-CoV-2 epidemic in Cameroon appears to have been driven by the SARS-CoV-2 lineage of origin in Wave 1, the co-introduction of the Alpha and Beta variants in Wave 2, the Delta variant in Wave 3, and the Omicron variant in Wave 4, with an overall declining trend in the wave duration, confirmed cases and hospitalisations over time.

•While viral clades did not seem to affect transmission, the SARS-CoV-2 lineage of origin and the Delta variant appeared to be the drivers of COVID-19 severity in Cameroon.

ADDITIONAL KEY INFORMATION

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