

# SARS-CoV-2 Introduction and Lineage Dynamics in Cameroon: Evidence from the Genomic Surveillance Network

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# PLAN

- BACKGROUND & RATIONALE
- OBJECTIVES
- METHODS
- RESULTS AND DISCUSSION
- CONCLUSION & RECOMMENDATIONS

# BACKGROUND & RATIONALE

- Cameroon: first COVID-19 case detected on March 6, 2020;
- Epidemiology of COVID-19: four different waves until mid 2022;
- Outbreak dynamics: may differ in magnitude, number of cases, hospitalisations and deaths across country;
- Research question: What are the implications of SARS-CoV-2 variants on the features of COVID-19 pandemic at country-level?

# STUDY OBJECTIVES

## **General objective:**

To study the introduction and dynamics of SARS-CoV-2 lineages and their potential effects on transmission and disease severity following the various epidemiological waves registered in Cameroon.

## **Specific objectives:**

1. To design and set-up a SARS-CoV-2 genomic surveillance network in Cameroon;
2. To study the diversity of SARS-CoV-2 lineages in Cameroon using whole-genome sequencing;
3. To study the effects of viral lineages on COVID-19 outcomes.

# METHODS (1/2)

## Study design

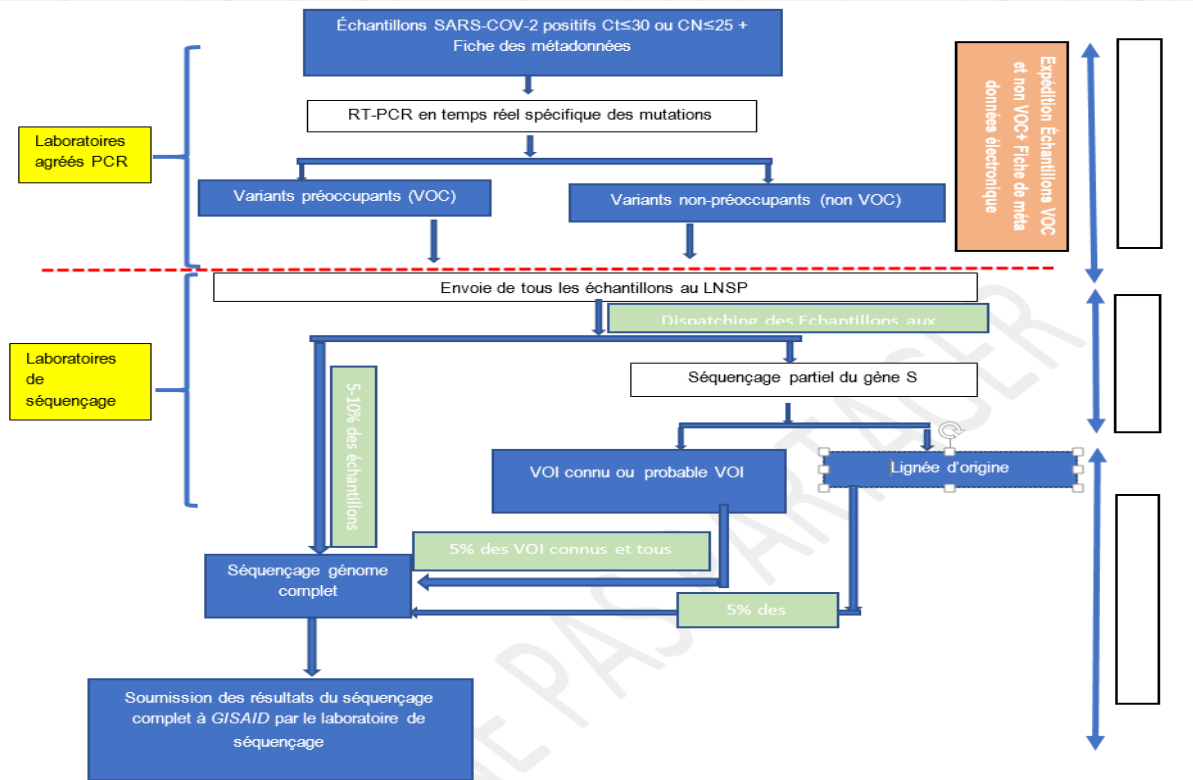
- A laboratory-based survey within the national public health emergency operational framework for COVID-19 in Cameroon, from March 1, 2020 to March 30, 2022,
- An assessment of the national capacity for SARS-CoV-2 genomic surveillance and the evolutionary patterns of SARS-CoV-2 lineages across the four COVID-19 waves in the country.

## Evaluation of the SARS-CoV-2 genomic surveillance network capacity

- (1) the number of frameworks for genomic sequencing,
- (2) the number of national strategies for SARS-CoV-2 genomic surveillance,
- (3) the number of laboratories with COVID-19 molecular testing capacity;
- (4) the number of laboratories with the capacity for variant screening using PCR point mutation assay,
- (5) the number of laboratories with SARS-CoV-2 sequencing capacity,
- (6) The number of samples processed for SARS-CoV-2 genomic surveillance.

# METHODS (2/2)

## Procedures for SARS-CoV-2 genomic surveillance



### Data analysis

- Full-length sequencing from all four sequencing laboratories consecutively entered into the GISAID platform;
- Molecular phylogeny of the SARS-CoV-2 sequences performed using Nexstrain

### Ethical considerations

- Ministry of Public Health (368/NS/ /SG/CCOU SP/CSO).



# RESULTS AND DISCUSSION (1/4)

## I- Outcomes of the SARS-CoV-2 genomic surveillance network in Cameroon

N°	Key indicators	March 2020, (n)	March 2022 (n)	Specific comments
i.	Number of frameworks for the genomic surveillance platform	0	1	Strong governmental engagement (ministerial decision, April 12, 2021)
ii.	Number of national strategies for SARS-CoV-2 genomic surveillance	0	2	The first plan has been revised as per changes in the pandemic.
iii.	Number of laboratories with the capacity for COVID-19 molecular testing	1	45	24 public laboratories and 21 private laboratories
iv.	Number of laboratories with the capacity for variant screening by PCR point mutation assay	0	16	These are laboratories with open real-time PCR systems for SARS-CoV-2
v.	Number of laboratories with the capacity/network for SARS-CoV-2 sequencing	0	6	5 public labs and 1 private lab (performing targeted and/or whole-genome sequencing)
vi.	PCR-positive samples successfully processed for SARS-CoV-2 genomic surveillance	0	3,881	1,509 PCR-mutation assays, 1,612 targeted sequencing, 760 whole-genome sequencing



# RESULTS AND DISCUSSION (2/4)



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## II- Diversity of SARS-CoV-2 lineage from whole-genome sequencing

### Study population

- 760 individual samples from Cameroon residents were enrolled in this study;
- Based on the quality of the whole-genome sequences of SARS-CoV-2 that were deposited in GISAID between March 2021 and March 2022.

### Distribution according to regional residence

Region	Number	Percentage
Adamawa	17	2.2%
Centre	373	49.1%
East	45	5.9%
Far-North	11	1.4%
Littoral	142	18.7%
North	27	3.6%
West	44	5.8%
South	25	3.3%
South-West	76	10.0%
Total	760	100.0%





# RESULTS AND DISCUSSION (3/4)

## Overall distribution of SARS-COV-2 VOCs

- 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 (Among 760 individuals).

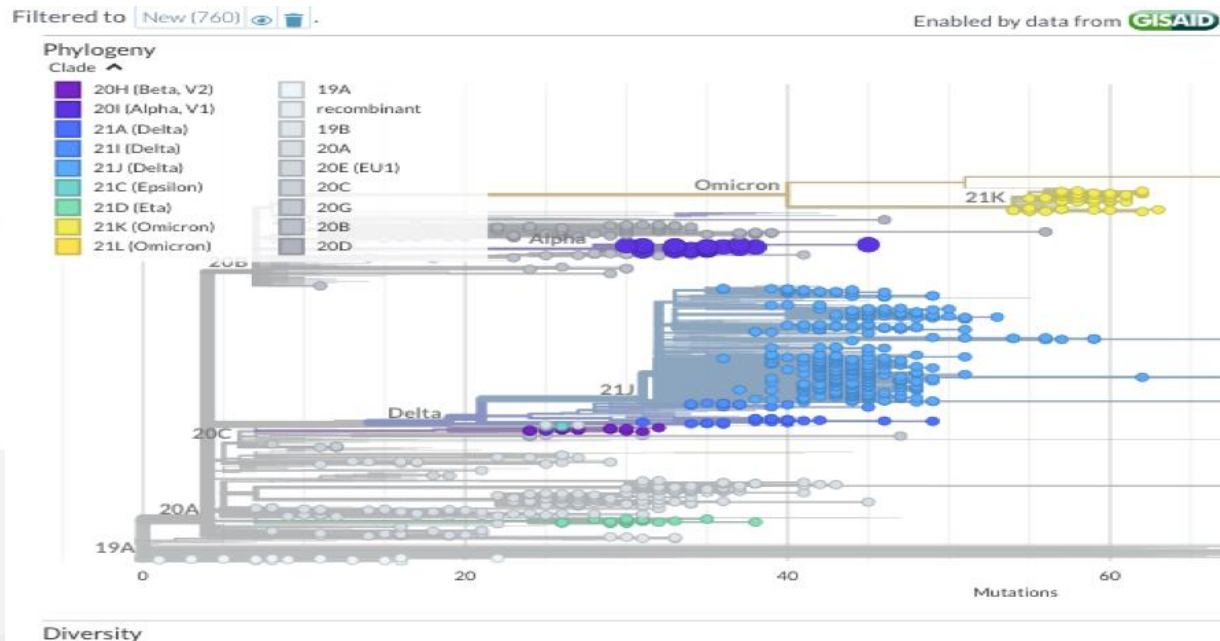


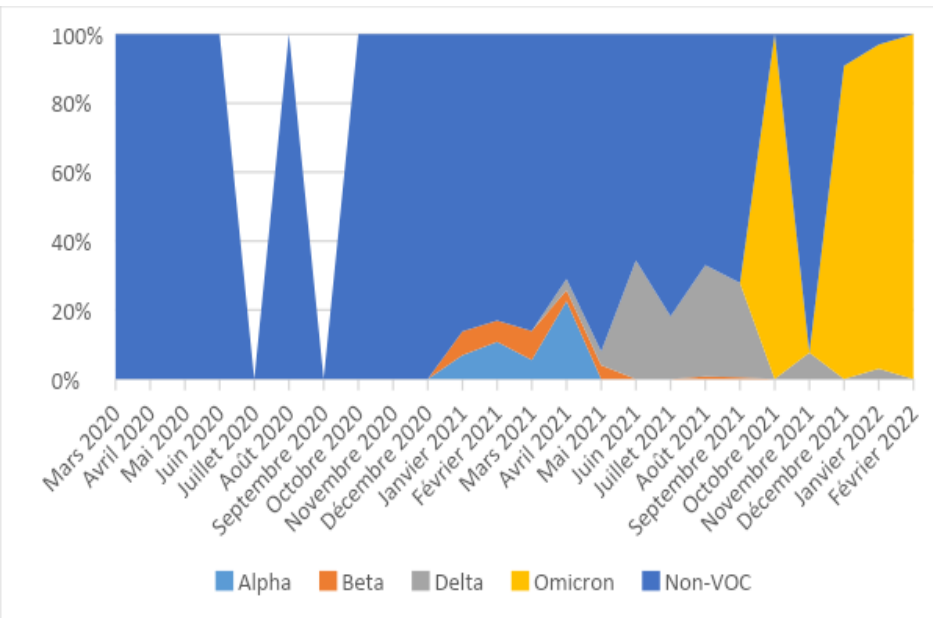
Figure Phylogenetic tree of SARS-COV-2 lineages when using whole-genome sequences



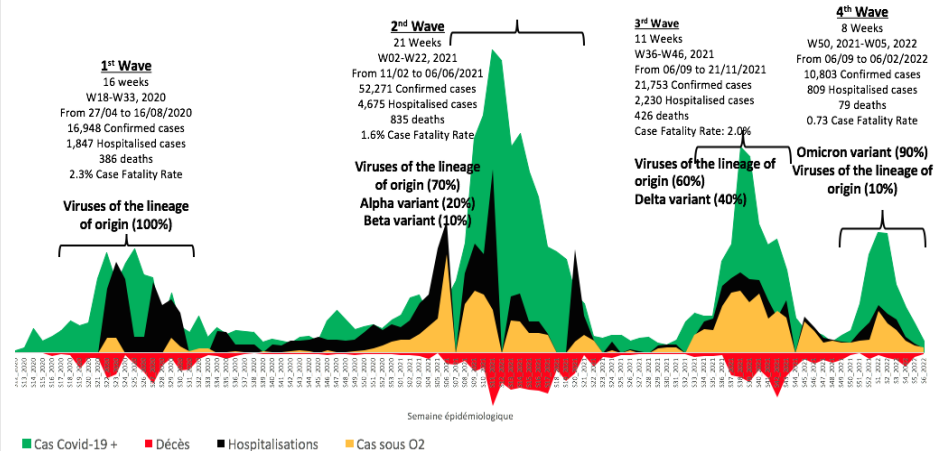
# RESULTS AND DISCUSSION (4/4)

## III. Dynamics of SARS-CoV-2 lineages over time

### Evolutionary trends of SARS-CoV-2 lineages per month



### SARS-COV-2 lineage dynamics per wave in Cameroon





# CONCLUSION & RECOMMENDATIONS



- **Established genomic surveillance framework in Cameroon:** 6 sequencing laboratory, with the identification of four VOCs were identified by whole genome sequencing (Alpha, Beta, Delta, and Omicron);
- **SARS-CoV-2 epidemic in Cameroon:** driven by the viral 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, hospitalisations, and CFR over time;
- **Effect of viral clades:** while transmissibility seems similar, SARS-CoV-2 lineage of origin and the Delta variant appeared to be the drivers of COVID-19 severity in Cameroon.



# REMERCIEMENTS / ACKNOWLEDGEMENT



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