Prevalence, Spread and Mutation of SARS-CoV-2 Variants in COVID-19 Testing in Salvador, Brazil

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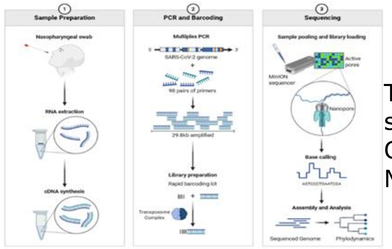
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BACKGROUND

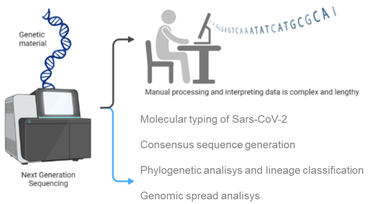
COVID-19 case and death data reflect the global impact of the circulation of the SARS-CoV-2 virus, triggering mutations and giving rise to variants that, in turn, can increase these numbers. Genomic sequencing is essential to identify the genomic characteristics of strains, facilitating the tracking of their spread. This analysis is necessary for creating public health strategies that can mitigate new infections and the effects of the pandemic. The study aims to investigate the prevalence and genomic spread of SARS-CoV-2 variants in a survey of the expansion of COVID-19 testing, quarantine, and telemonitoring (TQT-C19) strategies in Salvador, Brazil.

METHODS

177 samples collected between July 2022 and April 2023 from users of 17 Primary Health Care (PHC) units in Salvador-BA



The samples were sequenced with Oxford Nanopore MinION technology



Analyzed by bioinformatics for variant typing and analysis of genomic dispersion

RESULTS

The population profile was:

- 68.9% female
- 50.6% up to 39 years old
- 66.5% public transport
- 66.5% no comorbidities
- 41.5% mild symptoms
- 40.6% second dose of vaccine

Identifying **specific mutations** associated with **vaccination status** and the detailed phylogeographic analysis of lineages present in Salvador is crucial for anticipating challenges to vaccine efficacy and developing more effective control strategies.

The most prevalent Omicron subvariants were types B (13.39%), BA (66.96%), and BQ (12.5%). However, other variants (A, BF, and XBB) were also identified (Fig. 1).

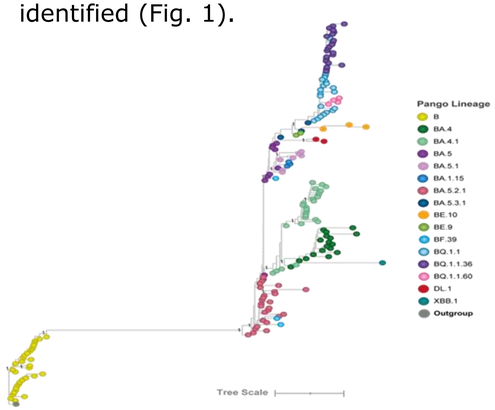


Fig. 1: Phylogenetic tree of SARS-CoV-2 variants identified in patients from Salvador between July and November 2022

Figure 2A highlights the routes of SARS-CoV-2 dispersal, where lines connecting colored dots represent the virus's dispersal trajectories. Figure 2B reveals a high frequency of transitions within this cluster, suggesting intense mutation or exchange activity within this group.

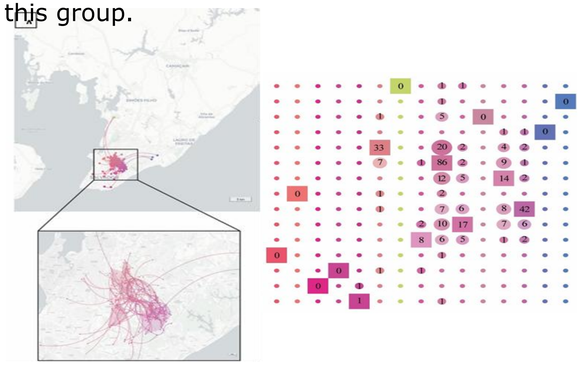


Fig 2. A. Phylogeographic Dispersion Analysis. B. Transition Matrix of Phylogenetic Clusters

Our findings suggest a heterogeneous spread of SARS-CoV-2 in Salvador, with certain lineages showing rapid expansion in specific areas (Fig. 3). Phylogeographic analysis indicates that the virus's spread is complex and influenced by multiple epidemiological and social factors, highlighting the need for continuous monitoring and an adaptive control strategy (Fig. 4).

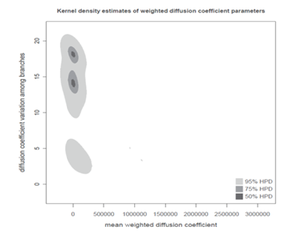


Fig 3. Kernel Density Estimates of the Weighted Diffusion Coefficient Parameters

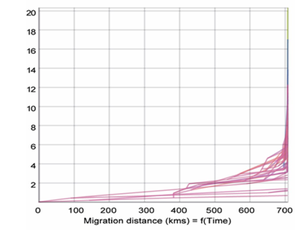


Fig. 4. Temporal Dynamics of Migration Distance

The analysis of SARS-CoV-2 samples collected revealed distinct mutation patterns in the spike protein correlated with the individual's vaccination status. The results indicate that vaccinated patients who received different vaccines showed specific and consistent mutations in a particular region of the spike protein. In contrast, unvaccinated patients exhibited different mutations in the distinct areas of the spike protein (Fig. 5).

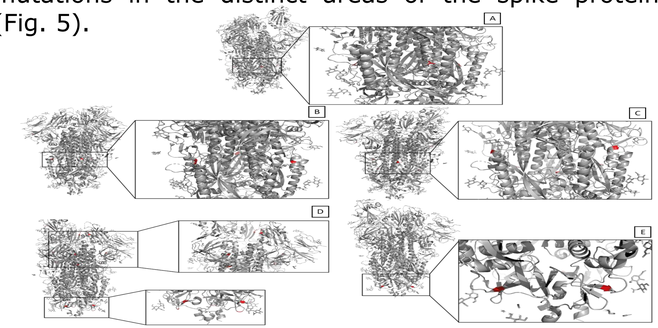


Fig 5. Spike Protein Mutations. Three-dimensional structure of the SARS-CoV-2 spike protein highlighting mutations in red, identified in the genomes of individuals: A - unvaccinated with the first and second doses; B - vaccinated with AstraZeneca for the first and second doses; C - vaccinated with Coronavac for the first and second doses; D - vaccinated with Pfizer for the first and second doses; E - vaccinated with Jansen for the first and second doses. The enlarged regions show specific mutations in the subunits of the spike protein.

CONCLUSIONS

These results are essential to guiding strategy regarding implementing measures to control and prevent viral spread and directing the development of more effective vaccines against circulating variants.

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