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SARS-CoV-2 Evolution, Reinfection and Sustained Viremia in Cancer Patients

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BACKGROUND

- Several studies with longitudinal follow-up on SARS-CoV-2 infection have been reported.
- Most cases of sustained viremia in immunocompromised subjects is associated to viral persistence;
- However, reinfection can not be ruled out.

In this study we employed genomic epidemiology methods to untangle cases of persistent or repeated infections in a cohort of cancer patients from Instituto Nacional do Cancer (INCA), Brazil, early in the COVID-19 pandemic.

METHODS

Twenty-six cancer patients followed at Brazilian National Cancer Institute (INCA), Rio de Janeiro, Brazil, with more than one SARS-CoV-2 RT-PCR-positive test from April to August 2020 were included.

Viral nucleic acid was isolated from naso- and oropharyngeal SARS-CoV-2$^+$ swabs

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Complete viral genomes were amplified using ARTIC-network v.3 primers

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Sequencing was performed in a MiSeq platform

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Viral genome were assembled and consensus extracted using Geneious R11

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Maximum-likelihood tree was inferred using IQ-Tree2 with the 20 most similar sequences to each consensus

Confirmed persistence	Plausible persistence	Confirmed reinfection	Plausible reinfection
• Cluster with >70% support • Exclusive mutations	• Cluster with <70% support • No exclusive mutations • Includes Sequences with no phylogenetic resolution	• Distinct clades with > 70% support • Each clade has exclusive mutations	• Distinct clades with at least one with > 70% support • Each clade has exclusive mutations

RESULTS



Figure 1. Maximum likelihood phylogenetic reconstruction of SARS-CoV-2 complete genomes. Genomes generated in this study and the 20 most similar sequences identified using Audacity were used in this analysis. Sequences characterized herein are colored according to the classification: **confirmed persistence** are in green, **plausible persistence** in blue, **confirmed reinfection** in yellow and **plausible reinfection** in pink.

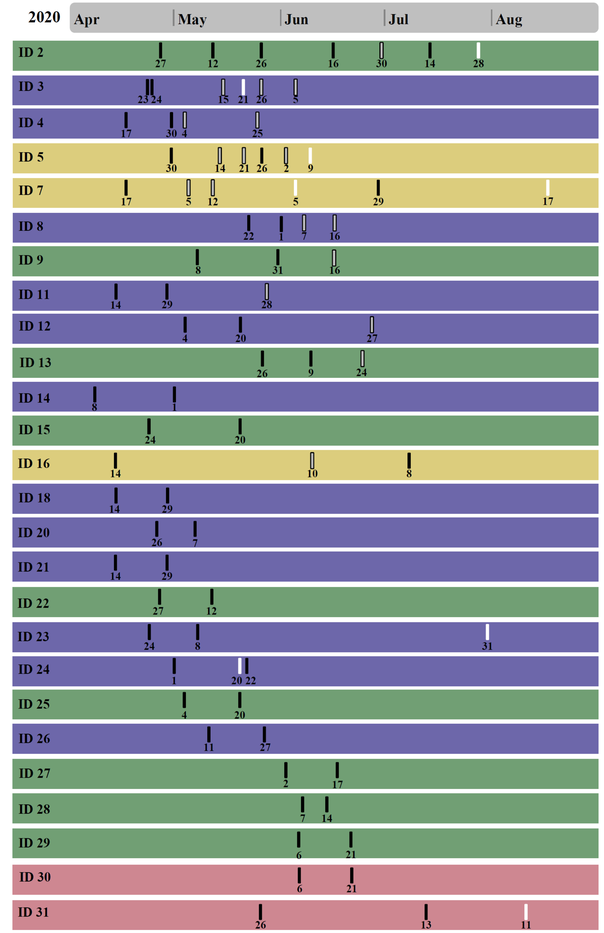


Figure 2. Timeline for SARS-CoV-2 RT-qPCR tests of patients included in the study. Black bars represent RT-qPCR-positive samples that were sequenced, gray bars show positive samples not sequenced and white bars show RT-qPCR-negative samples. Cases classified as SARS-CoV-2 confirmed persistence are in green, plausible persistence in blue, confirmed reinfection in yellow and plausible reinfection in pink.

CONCLUSIONS

Herein, we describe 26 different cases of SARS-CoV-2 infections in cancer patients with multiple longitudinal samples analyzed and described the different scenarios of sustained viremia.

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