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Abstract

Background: The B.1.1.7 SARS-CoV-2 variant results in spike gene target failure (SGTF) in reverse transcription-quantitative polymerase chain reaction (RT-PCR) assays. Few studies have been published on the clinical impact of B.1.1.7/SGTF.

Aims: To assess the incidence of B.1.1.7/SGTF and its associated clinical characteristics among hospitalized COVID-19 patients.

Methods: This observational, single-centre, cohort study was conducted between December 2020 and February 2021 and included 387 hospitalized COVID-19 patients. The Kaplan–Meier

method was used for survival analysis, and logistic regression to identify risk factors associated with B.1.1.7/SGTF.

Results: By February 2021, B.1.1.7/SGTF (88%) dominated the SARS-CoV-2 PCR results in a Lebanese hospital. Of the 387 eligible COVID-19 patients confirmed by SARS-CoV-2 RT-PCR, 154 (40%) were non-SGTF and 233 (60%) were B.1.1.1.7/SGTF; this was associated with a higher mortality rate among female patients [22/51 (43%) vs 7/37 (19%); P = 0.0170]. Among patients in the B.1.1.7/SGTF group, most were aged ≥ 65 years [162/233 (70%) vs 74/154 (48%); P

Conclusion: There was a clear difference between the clinical features associated with B.1.1.7/SGTF and non-SGTF lineages. Tracking viral evolution and its clinical impact is crucial for proper understanding and management of the COVID-19 pandemic.

Keywords: COVID-19, in-hospital mortality, SARS-CoV-2, spike gene target failure, variant B.1.1.7

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Introduction

The highly pathogenic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in Wuhan, China, and constituted a global public health emergency (1,2). Worldwide, reverse transcription-quantitative polymerase chain reaction (RT-PCR) is used to confirm the SARS-CoV-2 infection (3,4). At least 2 SARS-CoV-2 genes are targeted by the majority of the currently available RT-PCR assays. These include the 5′ frameshifted polyprotein

(ORF1a/ORF1ab), nucleocapsid (N), envelope (E), spike (S) and RNA-dependent RNA polymerase (RdRP) genes (5). Multiplex PCR assays that detect several genes offer greater assay sensitivity (6).

The B.1.1.7 SARS-CoV-2 variant was reported on 14 December 2020 in the United Kingdom and is estimated to have emerged in September 2020 (7). It carries a deletion mutation at positions 69 and 70 in the spike protein that increases binding affinity to the angiotensin-converting enzyme 2 (ACE2) receptor (8). It results in S-gene target failure (SGTF) in some RT-PCR assays (9). The spike glycoprotein is an envelope protein that binds with high affinity to mammalian ACE2 (10).

Borges et al. suggested that SGTF or S gene target late detection (SGTL) can constitute a useful surrogate to track the spread of B.1.1.7 (11). Only a few studies have assessed the clinical impact of the B.1.1.7/SGTF (12–14), mostly in community settings (15–18). However, mortality can be more accurately investigated in a study of hospitalized patients. We aimed to assess the association of B.1.1.7/SGTF with clinical characteristics and outcomes of COVID-19 among hospitalized patients. We also aimed to trace the emergence and incidence of B.1.1.7/SGTF in a Lebanese hospital, adding evidence to the natural history of COVID-19. We then identified risk factors associated with the B.1.1.7/SGTF infection.

Methods

Study design

This was an observational, single-centre, prospective, cohort study involving 387 hospitalized COVID-19 patients admitted to Saint George Hospital, Beirut, Lebanon. The institutional review board at Al-Rassoul Hospital approved the study.

Participants and settings

Saint George Hospital is one of 2 Lebanese hospitals dedicated exclusively to treating COVID-19 cases in Lebanon. The cohort included adult COVID-19 patients admitted to the hospital between December 2020 and February 2021. The last included patient was admitted on 28 February 2021 and followed up until the final outcome was known. We excluded patients under 18 years of age, those discharged against medical advice, transferred to other hospitals, probable cases with a negative RT-PCR, and RT-PCR-confirmed cases without an S gene amplification result. Of 387 eligible patients, 154 were identified as non-SGTF and 233 as B.1.1.1.7/SGTF. Patients were followed up until death or hospital discharge after improvement.

Outcomes and variables

The COVID-19 diagnosis was confirmed by a positive RT-PCR result for SARS-CoV-2. The primary outcome was defined as in-hospital mortality associated with COVID-19 by direct cause or contribution. The main explanatory variable for this analysis was the spike gene detection status in the RT-PCR test. The covariates of interest included demographics, symptoms at admission and pre-existing comorbidities. Variables were used in their original scale, and age was categorized into groups aged ≥ 65 and