

# Evaluation of patients with COVID-19 and the United Kingdom mutations in a training and research hospital in Istanbul

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## ABSTRACT

**OBJECTIVE:** This study aims to evaluate the patient clinics by studying Variant of Concern (VOC) Polymerase Chain Reaction (PCR) on conventional PCR-positive samples in a training and research hospital COVID test center in Istanbul.

**METHODS:** The study is a descriptive type and VOC PCR from all samples (from a total of 1300 samples) which detected positive by conventional PCR in a training and research hospital COVID test center between February 2 and 9, 2021. The United Kingdom mutation (VOC 202012/01, B.1.1.7) has been studied. Clinics parameters of the patients were evaluated from Public Health Management System (HSYS) records. The statistical significance was taken as  $p < 0.05$  in the analysis.

**RESULTS:** Within the scope of the research, 1300 PCR-positive COVID-19 patients were evaluated. VOC mutation was positive in 26.1% of all patients (339 persons), and 5.8% of patients (75 persons) were hospitalized. While 3.2% (11 persons) of those with VOC positivity were hospitalized, 6.7% (64 persons) of VOC negatives were hospitalized ( $p = 0.020$ ). About 18.2% of hospitalized VOC positives (two persons) and 23.4% of VOC negatives (15 persons) are in intensive care.

**CONCLUSION:** When VOC mutation was examined in all admitted and hospitalized patients, it was detected that VOC mutation was less frequent in hospitalized patients. No relationship between hospitalization and intensive care stay and VOC mutation was detected. It is recommended to determine with studies the contagiousness of patients with VOC mutations.

*Keywords:* COVID-19; mutation; patients.

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The coronavirus disease 2019 (COVID-19) is caused by SARS-CoV-2, which causes severe acute respiratory syndrome that first appeared in Wuhan, China's Hubei Province, in December 2019. SARS-CoV-2 is an RNA virus that is infectious disease in humans [1].

A total of 113,076,707 confirmed COVID-19 cases and 2,512,272 deaths occurred in the world until February 27, 2021. While there were 28,102,166 confirmed cases and 504,654 deaths in the USA, the country with the highest number of cases, there were 2,683,971 confirmed cases

After we sent our article, WHO named B.1.1.7 United Kingdom mutation as alpha variant.  
<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/Accessed August 22, 2021>.



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and 28,432 deaths in Turkey [2]. When viruses multiply, changes (mutations) occur in the genome, especially in RNA viruses such as SARS-CoV-2 [3]. The alarming (VOC) features of variants of SARS-CoV-2 include as follows; increase in COVID-19 infectiousness or harmful variation, increase in virulence or variation in disease clinic, a decrease in the effectiveness of public health and social measures, or existing diagnoses, vaccines, and treatments [4]. Determining the variants of SARS-CoV-2 and the characteristics of the COVID-19 patients and other patients' clinics, such as hospitalization, intensive care, response to treatment, and infectiousness, will be significant in controlling the pandemic. This study aims to evaluate patient clinics by studying VOC PCR on conventional PCR test with positive samples in COVID test center of a training and research hospital in Istanbul.

## MATERIALS AND METHODS

This research is a descriptive study (retrospective file search). The study was conducted between February 2 and February 9, 2021, in the COVID test center of Istanbul Kanuni Sultan Suleyman Training and Research Hospital with VOC PCR combined with the UK mutation (VOC 202012/01, B.1.1.7) in the samples with positive PCR. The age, gender, and hospitalization status of the patients, whose laboratory samples were examined, were analyzed from the HSYS records. Ethics committee approval of the study was obtained from the Istanbul Kanuni Sultan Suleyman Training and Research Hospital Clinical Research Ethics Committee with the decision number 2021/100. The VOC kit (SARS-CoV-2 + VOC202012/01 RT-qPCR, Bio-Speedy) came from the Ministry of Health.

### Statistical Analysis

The study data were evaluated with SPSS 22.0 program (IBM, Chicago, IL, USA). The descriptive statistics were presented as average±standard deviation, frequency distribution, and percentage. Pearson Chi-square test, Fisher's exact Chi-square test, Mann-Whitney U-test, and binary logistic regression tests were used as statistical methods. The statistical significance was accepted as  $p < 0.05$  in the analysis.

## RESULTS

Within the scope of the research, 1300 PCR-positive COVID-19 patients were evaluated.

### Highlight key points

- Those with positive VOC mutations were detected to have a lower frequency of hospitalization.
- There was no statistically significant difference between VOC mutations according to the gender parameter.
- Statistically significant difference was not found between the VOC mutations according to the final state of the patients.

**TABLE 1.** Distribution of hospitalization status of all PCR-positive patients by mutated (VOC) status

Hospitalization status*	VOC positive n=339 (%)	VOC negative n=961 (%)	Total n=1300 (%)
Hospitalized	3.2	6.7	5.8
Not hospitalized	96.8	93.3	94.2
<b>p=0.020</b>			

\*: Pearson's Chi-square.

In the study, 26.1% (n=339) of all patients were found to be positive and 73.9% (n=961) of all patients were found to be negative for VOC mutation. About 5.8% (n=75) of the patients were hospitalized.

Of all the patients, 3.2% (n=11) with positive VOC mutations and 6.7% (n=64) with negative VOC mutations were hospitalized. Those with positive VOC mutations were detected to have a lower frequency of hospitalization ( $p=0.020$ ) (Table 1).

Of the hospitalized patients, 53.3% were male (n=40) and 46.7% (n=35) were female; their age average is  $61.2 \pm 16.4$ , and the median is 64 (min: 5 and max: 88). About 85.3% (n=64) of the patients were VOC mutation negative and 14.7% (n=11) were VOC mutation positive. About 28.0% (n=21) of the patients were discharged, 48.0% (n=36) were followed up in the ward, 22.7% (n=17) were followed up in the intensive care unit, and 1.3% (n=1) were dead (Table 2).

In the study, 45.5% (n=5) of hospitalized VOC mutation positive patients were male, and 54.7% (n=35) of those VOC mutation negative patients were male. There was no statistically significant difference between VOC mutations according to the gender parameter ( $p=0.571$ ). In the study, while the median age of patients with positive VOC mutation was detected as 57 (min: 29 and max: 80), the median age of patients with negative VOC mutation was 64.5 (min: 5 and max: 88). There was no

**TABLE 2.** Distribution of some characteristics of hospitalized patients

	n=75 (%)
Gender	
Male	53.3
Female	46.7
Age	
Average 61.2±16.4 median 64 (min: 5 and max: 88)	
VOC positivity	
Positive	14.7
Negative	85.3
Last status	
Discharged	28.0
In service	48.0
In intensive care unit	22.7
Ex	1.3

Min: Minimum; Max: Maximum.

statistically significant difference between the VOC mutations according to the age of the patients ( $p=0.177$ ). In the study, 27.3% ( $n=3$ ) of those with positive VOC mutation are discharged, 54.5% ( $n=6$ ) are followed up in the service, and 18.2% ( $n=2$ ) are followed up in the intensive care unit. Of those with negative VOC mutation, 28.1% ( $n=18$ ) were discharged, 46.9% ( $n=30$ ) were followed up in the ward, 23.4% ( $n=15$ ) were followed up in the intensive care unit, and 1.6% ( $n=1$ ) was found to be ex. Statistically significant difference was not found between the VOC mutations according to the final state of the patients ( $p=0.939$ ) (Table 3).

Gender, age, and VOC positivity were included in the logistic regression model as variables that may affect admission to intensive care unit. When analyzed, none of them were found to be statistically significant ( $p=0.525$ ; 0.075, and 0.930, respectively) (Table 4).

## DISCUSSION

In our study, VOC mutation was detected in 26% of COVID-19 PCR-positive patients on February 2–9 in Istanbul. A study conducted in Portugal by Borges et al. [5] estimated that around 8000 (13.3%) of 59,951 confirmed COVID-19 cases in Portugal during the 2<sup>nd</sup> week of 2021 were caused by the VOC 202012/01 variant (B.1.1.7). It was observed that the spike gene target fail-

**TABLE 3.** Distribution of some characteristics of hospitalized patients according to their mutated (VOC) status

	VOC positive n=11 (%)*	VOC negative n=64 (%)*
Gender**		
Male	45.5	54.7
Female	54.5	45.3
	$p=0.571$	
Age***		
	57 (min: 29 and max: 80)	64.5 (min: 5 and max: 88)
	$p=0.177$	
Last status**		
Discharged	27.3	28.1
In service	54.5	46.9
In intensive care unit	18.2	23.4
Ex	–	1.6
	$p=0.939$	

\*: Column percentage; \*\*: Pearson Chi-square; \*\*\*: Mann-Whitney U-test; Min: Minimum; Max: Maximum.

**TABLE 4.** Distribution of intensive care status of hospitalized patients according to some characteristics

	p	OR	95% CI
Gender			
Male		1	
Female	0.525	0.691	0.221–2.160
VOC positivity			
Negative		1	
Positive	0.930	0.927	0.170–5.060
Age	0.075	1.040	0.996–1.085
Constant	0.018	0.030	

OR: Odd ratios; CI: Confidence interval.

ure (SGTF)/spike gene target late amplification (SGTL) rate increased by 70% (63–76%, CI 95%) per week. For the next 4 weeks, it shows that the rate of estimated SGTF/SGTL cases can reach 60% of TaqPath-positive cases by the 5<sup>th</sup> week. A new variant of SARS-CoV-2, also known as VOC-202012/01, classified as B.1.1.7, has been reported to spread rapidly unexpectedly in the United Kingdom [6]. In Turkey and in Istanbul after the date of mutation research of the UK, infectiousness of

COVID-19 England mutations has been reported to increase. In this case, it is an expected situation that the mutant strain, which we determined as 26% after the dates of February 2–9, will become more widespread in Istanbul. In addition to determine the frequency of strain-related hospitalizations and the need for intensive care for those who are hospitalized, this mutant has also been a guide in planning health services.

In the study, it was determined that 5.8% of patients with a positive COVID-19 PCR test result were hospitalized. It was determined that 3.2% of those with positive VOC results and 6.7% of those with negative VOC results were hospitalized. In the study conducted by Davies et al. [7], there was no clear evidence that VOC 202012/01 results in more or less disease severity than pre-existing variants. It is a similar result with our study.

In the study, there was no difference determined between the final state of the hospitalized patients and the VOC mutation. In the study, it was determined that VOC positivity did not affect staying in intensive care unit. The study conducted by Leung et al. [8] shows that 501.Y Variant 2 was estimated to present an R0 1.75 times higher than 501 N.

### Conclusion

It has been determined that patients with VOC mutations have a lower frequency of hospitalization. In our study, it was found that the VOC mutation had no negative effect on the patient's clinic and the hospitalization rates were lower. Although the clinical conditions of patients with mutations do not get worse, the extension of infectiousness will increase the total number of patients, and it may cause an increase in the number of patients who have bad clinical condition.

**Ethics Committee Approval:** The Istanbul Kanuni Sultan Suleyman Training and Research Hospital Clinical Research Ethics Committee granted approval for this study (date: 24.03.2021, number: 100).

**Conflict of Interest:** No conflict of interest was declared by the authors.

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**Authorship Contributions:** Concept – HY, KM; Design – HY, AEG; Supervision – KM, IM; Fundings – SZMK, CK; Materials – SZMK, CK; Data collection and/or processing – HY, MC, CK; Analysis and/or interpretation – MC, IM; Literature review – HY, MC, SZMK, CK, AEG, KM, IM; Writing – HY, MC; Critical review – HY, MC, SZMK, CK, AEG, KM, IM.

### REFERENCES

1. World Health Organization. Clinical management of COVID-19: interim guidance, 27 May 2020. Available at: <https://www.who.int/publications/i/item/WHO-2019-nCoV-clinical-2021-1>. Accessed Jun 22, 2021.
2. World Health Organization. WHO Coronavirus (COVID-19) Dashboard. Available at: <https://covid19.who.int/>. Accessed Feb 28, 2021.
3. Candido DS, Claro IM, de Jesus JG, Souza WM, Moreira FRR, Dellicour S, et al. Evolution and epidemic spread of SARS-CoV-2 in Brazil. *Science*. 2020 Sep 4;369(6508):1255–60. [CrossRef]
4. World Health Organization. COVID-19 Weekly Epidemiological Update 25 February 2021. 2021. Available at: <https://www.who.int/docs/default-source/coronaviruse/situation-reports/20210225-weekly-epi-update-voc-special-edition.pdf>. Accessed Jun 22, 2021.
5. Borges V, Sousa C, Menezes L, Gonçalves AM, Picão M, Almeida JP, et al. Tracking SARS-CoV-2 VOC 202012/01 (lineage B. 1.1.7) dissemination in Portugal: insights from nationwide RT-PCR Spike gene drop out data. Available at: <https://virological.org/t/tracking-sars-cov-2-voc-202012-01-lineage-b-1-1-7-dissemination-in-portugal-insights-from-nationwide-rt-pcr-spike-gene-drop-out-data/600>. Accessed Jun 22, 2021.
6. Kupferschmidt K. Viral evolution may herald new pandemic phase. *Science* 2021;371:108–9. [CrossRef]
7. Davies NG, Abbott S, Barnard RC, Jarvis CI, Kucharski AJ, Munday J, et al. Estimated transmissibility and severity of novel SARS-CoV-2 Variant of Concern 202012/01 in England. *MedRxiv* Dec 26, 2020, doi: 10.1126/science.abg3055. [CrossRef]
8. Leung K, Shum MH, Leung GM, Lam TT, Wu JT. Early transmissibility assessment of the N501Y mutant strains of SARS-CoV-2 in the United Kingdom, October to November 2020. *Euro Surveill* 2021;26:2002106. [CrossRef]