

## Research Article

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# A cross-sectional overview of SARS-CoV-2 genome variations in Turkey

## [Türkiye kaynaklı SARS-CoV-2 genom varyasyonlarının kesitsel değerlendirilmesi]

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### Abstract

**Objectives:** We assessed SARS-CoV-2 genome diversity and probable impact on epidemiology, immune response and clinical disease in Turkey.

**Materials and methods:** Complete genomes and partial Spike (S) sequences were accessed from the Global Initiative on Sharing Avian Influenza Data (GISAID) database. The genomes were analysed for variations and recombinations using appropriate softwares.

**Results:** Four hundred ten complete genomes and 206 S region sequences were included. Overall, 1,200 distinct nucleotide variations were noted. Mean variation count was 14.2 per genome and increased significantly during the course of the pandemic. The most frequent variations were identified as A23403G (D614G; 92.9%), C14408T (P323L, 92.2%), C3037T (89.8%), C241T (83.4%) and GGG28881AAC (RG203KR, 62.6%). The A23403G mutation was the most frequent variation in the S region sequences (99%). Most

genomes (98.3%) belonged in the SARS-CoV-2 haplogroup A. No evidence for recombination was identified in genomes representing sub-haplogroup branches. The variants B.1.1.7, B.1.351 and P.1 were detected, with a statistically-significant time-associated increase in B.1.1.7 prevalence.

**Conclusions:** We described prominent SARS-CoV-2 variations as well as comparisons with global virus diversity. Continuing a molecular surveillance in agreement with local disease epidemiology appears to be crucial, as vaccination and mitigation efforts are ongoing.

**Keywords:** COVID-19; genome; mutation; SARS-CoV-2; Turkey; variant.

### Öz

**Amaç:** Türkiye kaynaklı SARS-CoV-2 genomik dizi çeşitliliğinin ve epidemiyoloji, bağışık yanıt ve hastalık seyri üzerine muhtemel etkili varyasyonların incelenmesi.

**Gereç ve Yöntem:** “Global Initiative on Sharing Avian Influenza Data” (GISAID) veri tabanında yer alan tüm genom ve “Spike” (S) bölgesine ait verilere ulaşılarak uygun yazılımlar yardımıyla varyasyon ve muhtemel rekombinasyonlar araştırıldı.

**Bulgular:** Toplam 410 tam genom ve 206 S bölgesi dizisi incelendi, 1200 farklı nükleotid düzeyinde varyasyon saptandı. Genom başına toplam varyasyon ortalaması 14.2 olarak hesaplandı ve salgının ilerleyişi süresince istatistiksel olarak anlamlı artış izlendi. En sık saptanan varyasyonlar A23403G (D614G; 92.9%), C14408T (P323L, 92.2%), C3037T (89.8%), C241T (83.4%) ve GGG28881AAC (RG203KR, 62.6%) olarak sıralandı. S bölgesi dizilerinde de A23403G, en yaygın varyasyon (%99) şeklinde izlendi. İncelenen genomların sıklıkla (%98.3) SARS-CoV-2 A haplogrubuna ait olduğu görüldü. Alt haplogrubları temsil eden genomlarda yapılan incelemelerde rekombinasyon bulgusu saptanmadı. Çalışma grubunda B.1.1.7, B.1.351 ve

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P.1 varyantları tespit edildi. B.1.1.7 prevalansında izlenen zamanla ilişkili artış, istatistiksel olarak anlamlı bulundu. **Sonuçlar:** Çalışmada ülkemiz kaynaklı SARS-CoV-2 genomlarında belli başlı varyasyonlar belirlenmiş ve küresel virüs çeşitliliği ışığında değerlendirilmiştir. Kontrol ve aşılama çalışmaları ile eşzamanlı olarak önemli varyantların tanımlanabilmesi için, bölgesel epidemiyoloji ile uyumlu moleküler sürveyans çalışmaları sürdürülmelidir.

**Anahtar kelimeler:** COVID-19; genom; mutasyon; SARS-CoV-2; Türkiye; varyant.

## Introduction

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the causative agent of the pandemic of the 21st century, also called as Coronavirus Disease-2019 (COVID-19) [1, 2]. Initially emerging as cases of atypical viral pneumonia in the Wuhan city, Hubei province of China, SARS-CoV-2 have readily spread around the globe, currently affecting millions of people in more than 220 countries. More than a year after its official announcement, the control of the pandemic and mitigating its health, economic and social impact have become the foremost priority in all countries and international organizations.

SARS-CoV-2, classified in the *Betacoronavirus* genus of the family *Coronaviridae*, is an enveloped particle with a positive-stranded RNA as its genome [3]. The viral genome is approximately 29.9 kb in size and flanked by untranslated regions (UTRs) in the 3' and 5' ends. Virus proteins comprising the structural components nucleocapsid (N), envelope (E), membrane (M) and spike (S), as well as several accessory and non-structural proteins (NSPs) are encoded by several open reading frames (ORFs) on the genome [4, 5]. Variations occur spontaneously during SARS-CoV-2 replication but mutation frequency is relatively low compared to other RNA viruses, owing to the activity of nsp14 exoribonuclease [6, 7].

The exploration of SARS-CoV-2 genetic diversity in has been pivotal for control efforts since the beginning of the pandemic. Sequencing of the virus genome has provided critical information for the investigation of origin and spread of the infection as well as development of appropriate diagnostics. It further enables surveillance of virus molecular epidemiology and identification of variants that can undermine mitigation and vaccination efforts [8, 9]. Aided by the widespread availability of next generation sequencing technologies and online sharing of genome information, a significant number of virus genomes originating from several countries affected by the pandemic has now been

available. As the vaccination efforts are spreading in many countries, the monitorization of the virus genetic diversity will continue to be crucial to identify variants with enhanced transmissibility or clinical disease as well as potential escape mutants [9]. In this study, we aimed to evaluate SARS-CoV-2 genomic diversity from Turkey since the emergence of initial cases, to gain insights into origin, patterns of variation and their probable impact on epidemiology.

## Materials and methods

The “Global Initiative on Sharing Avian Influenza Data” (GISAID) [10] database (<https://www.gisaid.org>) was screened for SARS-CoV-2 sequences originating from Turkey and all complete virus genomes dated between 16.03.2020 and 30.01.2021 were accessed (Supplement 1). High quality virus genomes larger than 29,000 nucleotides with less than 1% N content and 0.05% specific amino acid variation were selected. Recurrent submissions and genomes with unverified insertion/deletions were omitted. The SARS-CoV-2 Wuhan-Hu-1 isolate genome sequence (GISAID access: EPI\_ISL\_402125, GenBank access: MN908947.3, NC045512) was used as the reference. Sequences were aligned using MUSCLE within the MSA package (v1.22.0), based on the R platform (v4.0.3, 2020-10-10) [11, 12]. Nucleotide variations were identified by the Sequence Variation (SNP) package in the Virus Pathogen Resource (ViPR) database and further confirmed via MEGAX [13–15]. Probable recombinations were screened using the R8DP, Geneconv, Bootscan, MaxChi, Chimaera, SiScan, 3Seq tools of the RDP4 software in the default settings [16]. A total of 410 genomes were analysed.

To incorporate recent data in the analysis, we further screened spike region sequences uploaded at a later date in the database and accessed a total of 206 non-redundant sequences, collected between 30.04.2020–03.02.2021 but mostly during January 2021 (170/206) (Supplement 1). Descriptive statistics, data distribution and correlations were analysed using Analyse-it v4.20.1 (Analyse-it Software Ltd. Leeds, United Kingdom).

The study and its findings are based on virus genome sequences obtained from online sources and is not related to either human or animal use. Therefore, no institutional ethics board approval was required nor sought. The study was approved by the COVID-19 Scientific Research Evaluation Committee, the Ministry of Health of Turkey (2021-03-22T11\_13\_48).

## Results

Among the 410 SARS-CoV-2 genomes included in the study, 261 (63%) originated from specimens collected during March–June 2020, 27 (6.58%) in July–October 2020 and 122 (29.75%) in December 2020–January 2021. Age, gender, residence and other demographic or clinical features of infected cases were not evaluated due to the lack of sufficient information in the database.

Complete genome sequencing revealed a total of 1,200 different nucleotide variations (Table 1). Majority of the

variations were missense (661/1,200, 55.1%) and silent mutations (441/1,200, 36.7%). The variations were frequently located in ORF1a/1b region (684/1,200, 57%), that encodes for the proteins and cofactors participating in viral replication; as well as in S region (153/1,200, 12.5%), involved in virus attachment on the respiratory epithelium and the main target for neutralizing antibodies (Table 1).

Median variation count per genome was calculated as 12 (mean + standard deviation: 14.2 + 6.5, range: 4–36). Temporal distribution of the total variation count per genome according to sampling date revealed a positive correlation and statistically-significant increase during the course of the pandemic (Figure 1).

Variations frequently-identified in the SARS-CoV-2 genomes were overviewed in Figure 2. Here, the most commonly-observed variations representing 62.2–92.9% of the diversity repertoire resulted in amino acid substitution; whereas silent changes and non-ORF mutations were also noted (Table 2). Among these, the A23403G, C14408T and GGG28881AAC variations stood out, as they are reported to be associated with severe infections requiring hospitalization [8]. Further screening for previously-reported globally-prevalent variations revealed G25563T (ORF3, Q57H) (n=92), C1059T (nsp2, L37F) (n=9), C8782T (n=7) and C17747T (nsp13, P504L) (n=1) in the study groups [8, 17].

We also checked particular mutations, previously-reported to potentially affect predicted T and B cell epitopes in S, N ve M proteins [18]. The most frequent of such mutations is the A23403G, resulting in the D614G substitution, which is also reported to enhance virus infectivity

as well as B cell epitopes in S1 spike region [18, 19] (Table 2). Other include the S region T cell epitope variations C24378T (n=2) ve C24381T (n=2), and N region B cell epitope variations G29383A (n=1) and G29405C (n=2).

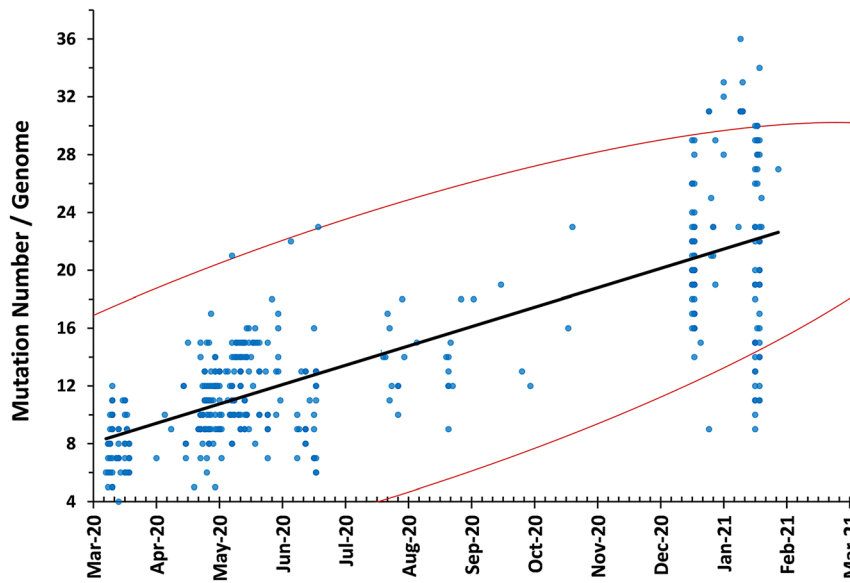
We further evaluated the diversity of the SARS-CoV-2 genomes as previously-described mutation-annotated virus lineages and haplotypes [8]. Majority of the genomes (403/410, 98.3%) were observed to belong in haplogroup A, from which various subhaplogroups were further identified (A2: n=381, 92.9%; A3: n=39, 9.5%; A9: n=29, 7.1%; A12: n=2, 0.5%) (Figure 3). The most frequent subhaplogroup was noted as A2a, that diversifies from A2 by the C14408T variation. Haplogroup B genomes were relatively few (7/410, 1.7%), with subhaplogroups B4 and B4a represented with 8 and 23 genomes, respectively (Figure 3). No evidence of recombination was observed among viruses of the A2a2b2a, A3a1a, A12 and B4a subhaplogroups, representing highly-diversified genomes within the group.

In the spike region dataset, a total of 44 nucleotide variations comprising missense (32/206, 72.7%) and silent (12/206, 29.3%) mutations (Figure 4). The most frequent variation was observed as A23403G (204/206, 99%), similar to the complete genome dataset. Of the virus epitopes located in the spike protein, the C24378T (S939F) variation, affecting predicted T cell epitope was detected in 2 (0.9%) sequences.

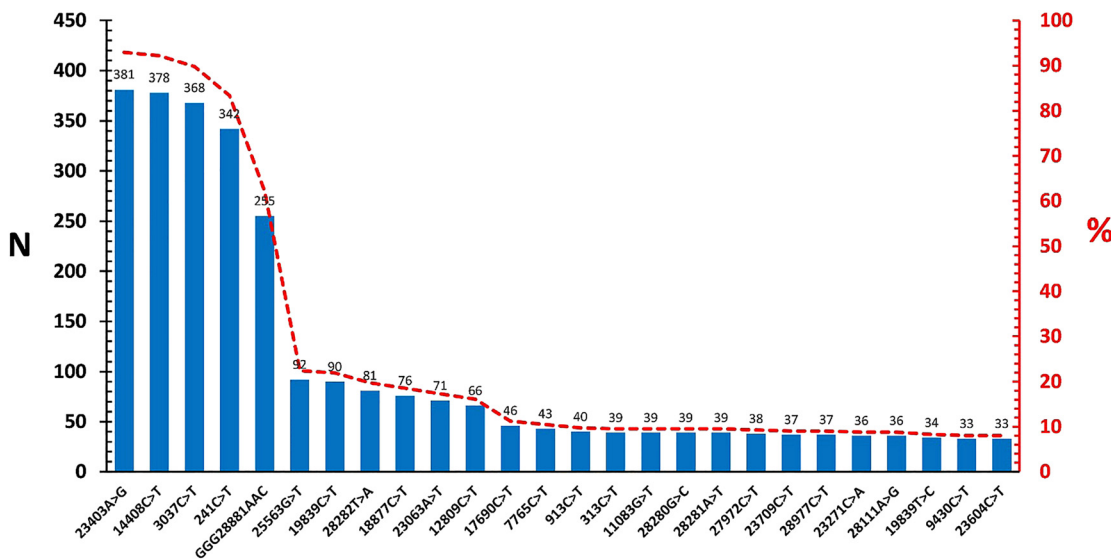
Finally, particular SARS-CoV-2 variants with potential impact on transmission, disease course and immune protection were screened in the study groups [20–22]. These were detected in 30.2% (186/616) of the individual viruses where the B.1.1.7 variant (variant 1 or 501Y.V 1) was noted

**Table 1:** Spatial distribution of the variations observed in SARS-CoV-2 genomes.

Region	Location	Variation type					Total
		Missense mutation	Silent mutation	Nonsense mutation	Deletion	Non-ORF change	
5'UTR	1–258	–	–	–	–	22	22
ORF1a	259–13,476	282	107	1	–	–	390
ORF 1b	13,461–21,548	101	193	–	–	–	294
S	21,556–25,377	102	51	–	–	–	153
ORF3a	25,386–26,213	53	17	–	–	–	70
E	26,238–26,465	2	2	–	–	–	4
M	26,516–27,184	10	19	–	–	–	29
ORF6	27,195–27,380	2	7	–	–	–	9
ORF7a	27,387–27,752	14	8	1	–	–	23
ORF7b	27,749–27,880	4	2	–	–	–	6
ORF8	27,887–28,252	18	5	48	–	–	71
N	28,267–29,526	68	27	1	2	5	103
ORF10	29,551–29,667	5	3	–	–	–	8
3'UTR	29,668–29,868	–	–	–	–	18	18
	<b>Total</b>	<b>661</b>	<b>441</b>	<b>51</b>	<b>2</b>	<b>45</b>	<b>1,200</b>



**Figure 1:** Temporal distribution of the total variation counts in the study. Spearman test was used to calculate correlation coefficient. Red lines indicate 95% confidence intervals. A time-related, statistically-significant increase total variation count per genome was observed ( $r=0.776$ ,  $p<0.001$ ).



**Figure 2:** Distribution of the frequently-observed variations in complete SARS-CoV-2 genome dataset.

as the most frequent (176/186, 94.6%) (Table 3). In the complete genomes, B.1.1.7 and B.1.351 (501Y.variant 2) were relatively scarce, but was significantly-increased in the spike region dataset (chi-square test,  $p<0.001$ ), where B.1.1.28 (variant P.1) also became detectable (Table 3).

## Discussion

In this study, we provide a cross-sectional overview and potential impact of the SARS-CoV-2 genome variations from Turkey. The genomes were accessed from the GISAID

database, originated from specimens collected during a 10-month period in 2020 and 2021. We further included additional S region sequences, submitted after our initial database searches as an update, representing viruses circulating in early 2021. Therefore, the findings are based on these datasets of 410 complete and 206 partial (spike) sequences, being so far the most comprehensive analysis performed in Turkey [23–26].

In the complete SARS-CoV-2 genomes, we identified 1,200 individual nucleotide variations, with a median frequency of 12 (range:4–36) per genome (Table 1). Moreover, the temporal distribution of the variations indicated a

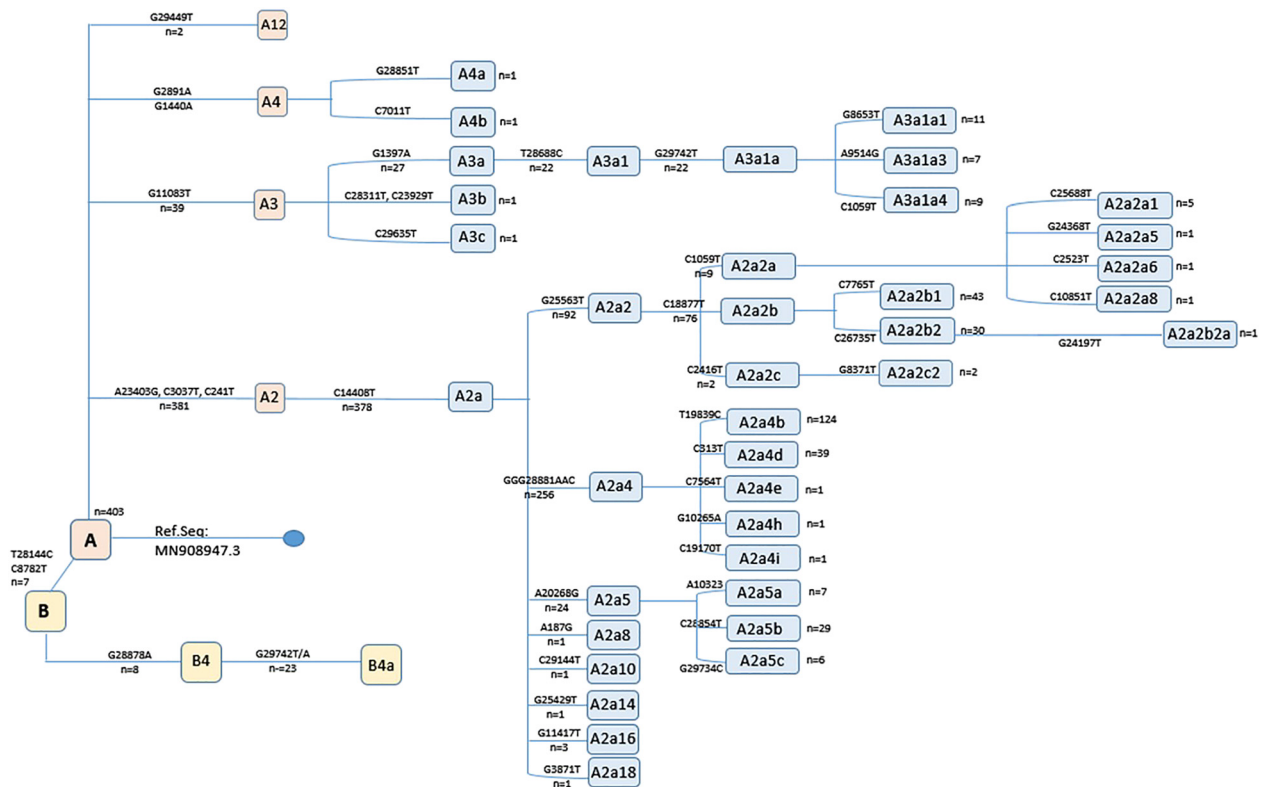
**Table 2:** Common variations and predicted outcomes in SARS-CoV-2 genomes.

Variation	Frequency, n, %	Target region	Outcome
A23403G	381, 92.9	S – spike protein	Amino acid change: D614G
C14408T	378, 92.2	Non-structural protein 12 – RNA-dependent RNA polymerase	Amino acid change: P323L
C3037T	368, 89.8	Non-structural protein 3 – phosphoesterase	Silent
C241T	342, 83.4	5'UTR	Non-ORF
GGG28881AAC	255, 62.6	N – nucleocapsid protein	Amino acid change: RG203KR

statistically-significant accumulation of variations during the 10-month period examined (Figure 1). Comparable findings were reported in globally-distributed virus isolates, with more than 3,000 specific point mutations being detected and an increased frequency of variation during

the course of the pandemic [8]. However, SARS-CoV-2 isolates from Turkey was proposed to exhibit an elevated variation rate in a study focusing on 166 virus genomes accessed during July 2020, where frequently-detected variations C14408T and C18877T, affecting viral polymerase (nsp12) and exoribonuclease (nsp14), respectively; were suggested as a possible precipitating factors [26–29]. These variations were also noted in our study with varying rates (Table 2, Figure 2). In addition, the co-detection of C14408T and A23403G variations were suggested to be associated with increased diversity [27, 28] In parallel with global isolates, the SARS-CoV-2 genome variations in Turkey are mostly missense or silent mutations, frequently involving the enzymes and co-factors, participating in replication in ORF1a/1b or the S regions of the virus genome [8, 17, 27].

In the study, the most frequently-detected variations, namely the A23403G, C14408T and GGG28881AAC mutations resulting in amino acid substitutions in the corresponding virus proteins, were reported in previous analyses from Turkey [23–26]. However, they seem to be positively-selected in the local virus population pool, as their abundance seem to be elevated. For example, the A23403G



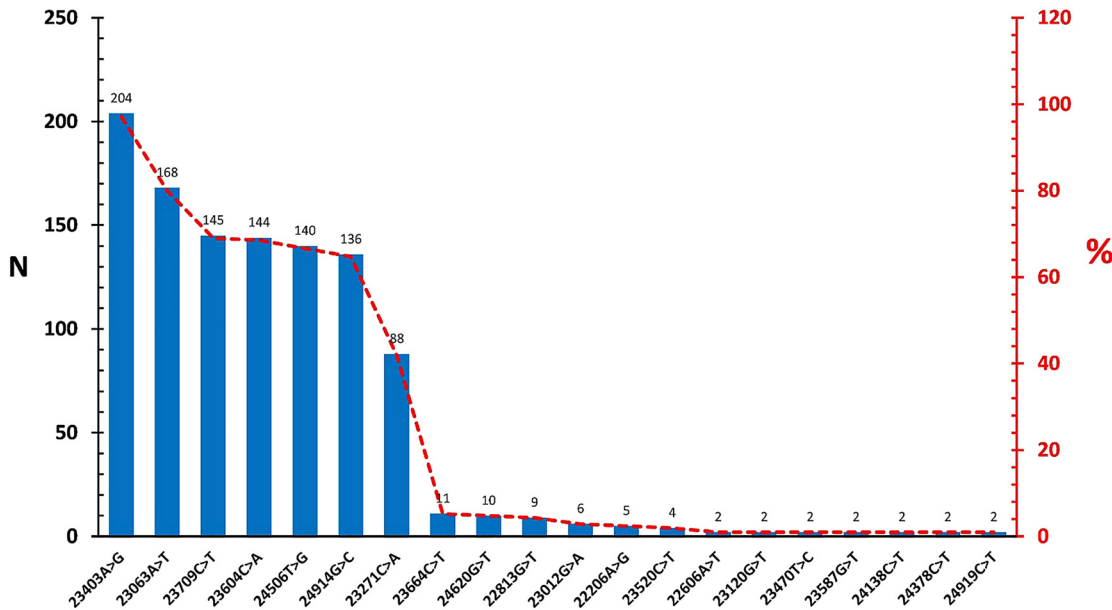


Figure 4: Distribution of the frequently-observed variations in spike region dataset.

variation was reported as low as 56.2% in previous reports, while it is detected in 92.9% of the complete genomes and 99% in S regions in this study (Figure 2, Figure 4). This observation is also evident in global genome data, where viruses with the A23403G and C14408T variations were steadily increased in frequency during the course of the pandemic and have become the majority in late 2020 [8]. The amino acid substitutions occurring as a result of these variations, namely P323L, D614G ve RG203KR, were also associated with a more severe COVID-19 clinical presentation [8]. Moreover, the D614G mutation, a defining component of the variant of concern B.1.1.7, is also likely to affect immune responses to the S protein. In addition to the high frequency of this substitution in the study, we further identified other variations that might affect T and B cell epitopes, albeit with lower rates.

Throughout the pandemic, the availability of virus genome sequences and powerful online tools have enabled a nearly real-time monitorization of SARS-CoV-2 molecular

epidemiology [8, 17]. Previous reports on SARS-CoV-2 genetic diversity have described particular virus lineages and clades, mostly in overall agreement but lacking a uniform nomenclature [8, 30]. The size of accumulating sequence data further warrants more practical approaches to indicate phylogeographic relationships than standard phylogenetic reconstruction. Here, we adopted a previously-reported mutation-annotated reference strategy to describe intraspecific phylogeny of SARS-CoV-2. We observed the majority of the SARS-CoV-2 genomes from Turkey to belong in the haplogroup A (98.3%), with main subhaplotype diversification into A2 (Figure 3). SARS-CoV-2 haplogroup A isolates constitute the ancestral node and predominant clade across the world. They are frequently-represented in isolates from Europe (97%) Africa (93%) and Asia (77%), but relatively scarce in South America (68%) and North America (53%) [8]. Among global haplogroup A subclades, A2 and A2a appears as the majority, with the phylogeographic inferences indicating a European origin. We observed haplogroup B is with a much lower frequency, and B4a subhaplotype representing the majority within this group (Figure 3). Haplogroup B viruses have been identified in all continents, with higher prevalence in North America (47%), South America (32%), Asia and Oceania (23%), with all major and minor subclades present in Asia [8]. The haplotype B viruses were introduced in Turkey likely by travel to endemic regions and further local spread was presumably prevented by isolation. Our analyses employing highly-diversified subclades of each main haplogroup failed to identify any evidence for recombination among local

Table 3: Distribution of the current variants of concern in the study groups.

Variant	Genome (n=410)		S region (n=206)		Total
	n	%	n	%	
B.1.1.7	31	7.6	145	70.4	176
B.1.351	2	0.5	7	3.4	9
P.1	–	–	1	0.5	1
Total	33	–	153	–	186

SARS-CoV-2 genomes. Overall, the findings on virus genome diversity in Turkey suggest several introductions originating from multiple sources and subsequent local adaptation, also noted in previous reports using smaller datasets [23].

The emergence and rapid spread of SARS-CoV-2 variants has raised significant concern, due to their potential for enhanced transmissibility, altered clinical progression and escape from protective immune response induced by previous infection or widely-available vaccines [20, 31]. Also dubbed as the variant of concern (VOC), these viruses exhibit a wide array of amino acid changes accumulated in several regions of the virus genome including the spike protein [20–22]. The rapid spread of particular VOCs in several countries during fall 2020 called for more stringent public health measures as well as targeted monitorization, which is also initiated and currently ongoing in Turkey. We detected three major VOCs in the study group, with increased prevalence of B.1.1.7 and B.1.351 in the recently-dated dataset (Table 3). Moreover, the detection of P.1 in this group suggests not only an elevated prevalence but also a broader repertoire of variants in the population. These findings justify the efforts to identify and monitor known and potentially-emerging virus variants.

Particular limitations of this study need to be addressed. An important issue is the heterogeneity in temporal and spatial distribution of the samples employed for genome sequencing, which suggests a lack of organized sampling strategy for screening. In addition, missing demographic and location data in many instances also prevented further evaluations. Therefore, it is not possible to assess whether the current dataset fully represents the epidemiology and diversity in circulating viruses in Turkey. A continuous and organized surveillance strategy in conjunction with local transmission dynamics and infection epidemiology, will provide a better understanding of the SARS-CoV-2 molecular epidemiology in Turkey.

In conclusion, in this analysis of complete and partial SARS-CoV-2 genome sequences almost covering the first year since emergence, we described main variations associated with epidemiology and immune response, with the observation of increased incidence of VOCs in Turkey. With the ongoing pandemic and accelerated vaccination campaigns, such investigations should be performed periodically for precise screening and coordination of control measures.

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**Competing interests:** The authors declare no actual or potential conflict of interest in relation with the article.

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