SARS-CoV-2 Delta Variant Predominant at a Tertiary-Care Hospital in Saudi Arabia

Fatimah Alhamlan (✉ falhamlan@kfshrc.edu.sa)

King Faisal Specialist Hospital and Research Centre

Ahmed Al-Qahtani

King Faisal Specialist Hospital & Research Centre

Dalia Obeid

King Faisal Specialist Hospital and Research Centre

Suliman Aljumaah

King Faisal Specialist Hospital and Research Centre

Salem Alghamdi

King Faisal Specialist Hospital and Research Centre

KHALED ALNAFEE

King Faisal Specialist Hospital and Research Centre <https://orcid.org/0000-0001-6407-9713>

Madain Alsanea

King Faisal Specialist Hospital and Research Centre

Basma Alahideb

King Faisal Specialist Hospital and Research Centre

Shuruq Almutairi

King Faisal Specialist Hospital and Research Centre

Feda Alsuwairi

King Faisal Specialist Hospital and Research Centre

Maha Al-Abdulkarim

King Faisal Specialist Hospital and Research Centre

Mohamed Asiri

King Faisal Specialist Hospital and Research Centre

Jalwa Alkahtani

King Faisal Specialist Hospital and Research Centre

Sara Altamimi

King Faisal Specialist Hospital and Research Centre

Maysoon Mutabagani

Department of Pathology and Laboratory Medicine, King Faisal Specialist Hospital and Research Center

Sahar Althawadi

Department of Pathology and Laboratory Medicine, King Faisal Specialist Hospital and Research Center

Reem Almaghrabi

Article

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Abstract

Despite the effectiveness of the Pfizer-BioNTech and Oxford-AstraZeneca vaccines against SARS-CoV-2, the delta (B.1.617.2) variant of concern (VOC) has spread globally, and breakthrough infections have been reported. We identified the circulating variants and effectiveness of those vaccines between April and June 2021 at a tertiary-care hospital in Saudi Arabia. Among 320 patients with confirmed COVID-19 (mean age, 39 years; 53.6% male), 70.6% received a one-dose vaccination; 15.1% received two-dose vaccinations; 14.3% were unvaccinated; 64.9% received Oxford-AstraZeneca; and 32.5% received Pfizer-BioNTech. Most breakthrough cases involving VOCs (71%) occurred among patients who received a one-dose Oxford-AstraZeneca vaccination, and most patients with breakthrough disease were infected with the delta variant. Among all VOCs and non-VOCs, the delta variant was most frequently detected and was associated with young age (20–49 years), males, symptoms, and low cycle threshold value. These findings indicate an increased rate of transmission for the delta variant in this cohort.

Introduction

A novel corona virus emerged in Wuhan, China, in December 2019—later named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)—but human-to-human transmission gained a foothold worldwide [1]. Vaccination programs started in most countries, leading to global numbers of cases and deaths decreasing during the month of June 2021, with just over 2.5 million new cases weekly and more than 64,000 deaths. After detecting the SARS-CoV-2 delta variant (B.1.617.2) in the United Kingdom in April 2021, Public Health England announced 3 July 2021 that this was now the dominant variant in the UK [2], accounting for approximately 99% of sequenced and 97% of genotyped cases from 27 June to 3 July 2021. The World Health Organization (WHO) reported the week of 13 July 2021 that the variant had been detected in more than 111 countries [3]. The number of new cases reported to WHO globally from the 5th through the 11th of July 2021 was nearly 3 million, a 10% increase compared with the previous week, with reported deaths of more than 55,000, a 3% increase [3]. The cumulative number of SARS-CoV-2 infections reported globally is more than 186 million, with the number of deaths due to COVID-19 exceeding 4 million. Mortality continues to remain high, with more than 9000 deaths reported each day.

As of July 2021, four variants of concern (VOCs) and nine variants under investigation had been announced by the health authorities worldwide, including WHO, Public Health England, and the U.S. Centers for Disease Control and Prevention. The VOCs included alpha (B.1.1.7), beta (B.1.351), gamma (P.1), and delta (B.1.617.2) [3]. According to WHO, by July 2021, the alpha variant had been reported in 178 countries, beta in 123 countries, gamma in 75 countries, and delta in 111 countries [3].

In Saudi Arabia, the first COVID-19 case was reported 2 March 2020—a Saudi national who had returned to the country from Iran [4]. As of 19 July 2021, there had been 507,000 confirmed COVID-19 cases, 10,805 active cases, 488,000 recovered cases, and 8048 deaths attributed to COVID-19 in Saudi Arabia [5]. As of 18 July 2021, 22.6 million total doses of vaccine had been given, with 4.2 million (12.3%) fully vaccinated individuals (ages 12 years or older). The first two vaccines approved in the country were the

Pfizer-BioNTech and Oxford-AstraZeneca vaccines. They were granted approval by the Saudi Food and Drug Authority in December 2020. The Johnson and Johnson and the Moderna vaccines were approved in July 2021.

King Faisal Specialist Hospital and Research Centre (KFSHRC) is a tertiary-referral hospital in Saudi Arabia, providing specialized care for patients with cancer and transplantation and for immunocompromised patients as well as offering other medical specialties. However, because there has been increasing concern over the protection the approved vaccines are able to provide and the evasion mechanisms used by the VOCs, KFSHRC is conducting epidemiologic and genomic surveillance to monitor the circulating VOCs and to report vaccine effectiveness. This report is, to our knowledge, the first from Saudi Arabia to show evidence of an increased transmission of the SARS-CoV-2 delta variant and increasing rates of vaccine breakthrough infections.

Results And Discussion

We obtained 320 COVID-19–positive samples from April through June 2021. The mean (standard deviation) age of patients in this cohort was 39 (13.7) years, and 53.6% were males. Overall, 70.6% of the cohort received one dose of vaccine, whereas only 15.1% received two doses, and 14.3% receive no vaccination. The most commonly received vaccines were Oxford-AstraZeneca (64.9%) followed by Pfizer-BioNTech (32.5%). In total, 8 patients in our cohort were admitted to the intensive care unit (ICU): 87.5% were infected with non-VOCs and 12.5% with the beta variant; 75% were male; 75% were 40 years or older and 100% were Saudi. All patients admitted to the ICU had comorbidities, which worsen the effects of their infection (**Table 1**). In addition, they were all unvaccinated indicating that the administered vaccines in this cohort remained effective in preventing ICU admission.

The variants were detected, sequenced, and sorted into four groups depending on their mutation profile: VOCs alpha, beta, delta, and non-VOCs that belonged to none of these variants. Of 320 samples with viral genomes sequenced in the Department of Infection and Immunity at KFSHRC, the delta VOC (40.9% of samples) displaced the beta (15.9% of samples) and alpha (11.6% of samples) VOCs as being the most frequently detected in patient samples in fewer than 6 weeks. The timeline for the percentage of all samples with each detected variant is shown in **Figure 1**. The samples containing the alpha, beta, and delta VOCs contained the reported major mutations. The major mutations detected in samples with the alpha variant included 69del, 70del, 144del, N501Y, A570D, P681H, T716I, and S982A; three samples contained B.1.1.7 +E484K mutations. Samples infected with the beta VOC also contained D80A, E484K, A570D, and P681H mutations. The gamma variant was not detected in our samples. The major mutations in samples with the delta variant included G142D, L452R, T478K, P681R, and D950N.

The first appearance of the delta variant in KFSHRC was detected in an individual coming from India in early May 2021. **Figure 2** shows the frequency distribution of the detected VOCs with time from April through June 2021. From May through June, the delta variant was the predominant VOC. This finding is consistent with reported transmission rates from other countries, including the UK [2] and France, which reported a rapid spread of the delta variant in some French regions in June 2021 [6]. WHO recently reported that the delta variant shows higher transmissibility than all other VOCs identified to date. This increased transmissibility—which may be due to the relaxation of precaution measures, vaccine inequity, or increased social activity worldwide—means that the delta variant is likely to become the dominant variant globally in the coming months.

Limitations exist in the epidemiologic surveillance and genomic sequencing of VOCs in many parts of the world because not every country has the capability and facilities necessary for timely reporting of the circulating VOCs [3]. Thus, the present study assessed whether there was an association between the current VOCs detected at a tertiary-referral hospital and selected demographic or clinical characteristics of patients with confirmed infections (**Table 1**). We found significant sex differences, with higher numbers of male patients infected primarily with either the delta or non-VOC variants, whereas female patients were infected primarily with the alpha variant. A significant association was also detected between age groups and the variants. The delta variant was the most common variant observed in younger age groups (ages 20-49 years). Moreover, our results showed that most of the patients infected with the delta variant were symptomatic (39%) while only 3% were asymptomatic; however, there was no ICU admission associated with delta variant infection. Several factors may have contributed to this observation, including the vaccination rate being higher in populations of older individuals, an active social life among younger people who may or may not follow recommended health precautions, or the virus being more infectious in younger individuals. Further studies are needed to explore these possibilities.

The alpha variant became less circulated with time in our cohort, a finding in agreement with those in the UK, France, and the GISAID surveillance database during the same time frame [2, 7, 8]. On 11 May 2021, WHO designated delta a VOC owing to evidence of increased transmissibility. The increase in the effective reproduction number compared with the alpha variant is estimated to be 55% (95% CI: 43%–68%). [3] Given its increase in transmissibility, the delta variant is expected to rapidly outcompete other variants and become the dominant variant during the coming months [8].

Having all eligible individuals in Saudi Arabia fully vaccinated with two doses each was a challenge owing to limited supplies, which led to the postponement of second vaccinations for most individuals. For a few patients who received two doses (N=42), we found that those with infection most often carried the beta variant (30.9%) followed by the delta variant (28.6%). For patients who received one dose of a

vaccine (N=197), the majority of infected individuals carried the delta variant (55.8%), followed by non-VOCs (26.9%). For patients who received no vaccination, most were infected with non-VOCs. We found a significant association between the variant detected and the number of vaccinations received ($P < 0.001$) (**Figure 3**). We also found a significant association between variant and vaccination type, with individuals receiving either the Pfizer-BioNTech or the Oxford-AstraZeneca vaccine most commonly infected with the delta variant followed by infection with non-VOCs. The post vaccination period was also associated with variant type. Our results showed that most breakthrough disease with VOCs occurred among individuals who had received only one dose of the Oxford-AstraZeneca vaccine (71%), and most of those infections were with the delta variant. These results are in agreement with a publication released by Public Health England on 22 May 2021 indicating that one dose of either Pfizer-BioNTech or Oxford-AstraZeneca was only 33% effective against symptomatic disease from the delta variant, whereas they were 50% effective against the alpha variant [9]. Public Health England reported in its 18th technical report that the Pfizer-BioNTech and Oxford-AstraZeneca vaccines were 96% and 92% effective against hospitalization after two doses, respectively [2].

Several studies have investigated the neutralization of the VOCs. Planas et al. isolated the delta variant from a traveler returning from India [10]. This research team compared the sensitivity between the delta variant and other viral strains to monoclonal antibodies and to antibodies present in sera from individuals who were convalescent from COVID-19 or who were vaccine recipients. The delta variant was resistant to neutralization by some anti-N-terminal domain and anti-receptor binding domain (RBD) monoclonal antibodies, indicating immune evasion to antibodies targeting non-RBD and RBD spike epitopes. When the sera from individuals who had received one dose of Pfizer-BioNTech or Oxford-AstraZeneca vaccines was assessed, the team found that these vaccines barely inhibited the delta variant [10]. Wall et al. [11] assessed vaccine-induced neutralizing antibody escape by the delta variant and compared the activity to previous strains with existing estimates for population-based vaccine efficacy. For single-dose recipients, neutralizing antibody titers were significantly lower against the beta and delta VOCs relative to the alpha VOC, suggesting that although a single dose may provide considerably more protection than no vaccination, single-dose recipients are likely to be less protected against these SARS-CoV-2 variants [11]. A study in Israel assessed the delta variant and other VOCs that are spreading in Europe [14]. Microneutralization assays with sera obtained from 36 health care workers (31 women) after receipt of the Pfizer-BioNTech vaccine showed a significant reduction in neutralizing titers of beta, gamma, and delta compared with the original virus. The reduction for the alpha variant was not significant. Despite being lower, the remaining neutralization capacity conferred by the Pfizer-BioNTech vaccine against the delta variant and other VOCs is likely protective [14]. Overall, there is a pressing need to increase vaccine supply and coverage to enable all countries to protect their population with two doses.

In Saudi Arabia, administration of the second vaccine dose was suspended late January 2021 owing to limited supplies and the desire to vaccinate as many individuals as possible with the first dose. However, wherever travel restrictions were lifted in the country in May 2021, the number of COVID-19 cases increased. This surge prompted the implementation of additional social gathering guidelines and restrictions, especially for mass and entertainment gatherings. In May, efforts resumed for second vaccinations for individuals 60 years and older and in June 2021, the Saudi Food and Drug Authority approved the vaccination of children (12-16 years old). Later, second vaccinations were offered to individuals 50 years or older and to all health care workers. In July, all age groups were invited to receive a second vaccination. Given all the aforementioned challenges in the country, the numbers of fully vaccinated individuals, type of vaccination, and effective dose observation assessed in this study were limited.

A summary of the number and percentage of variants detected by patient vaccination status, including the number, type, and schedule of vaccination received, are given in **Table 2**. Significant associations were found for the variants detected with the number of vaccinations received, the type of vaccinations received, and the time of infection post vaccination. For patients who received two doses, the most commonly detected variants were beta followed by delta. For patients who received one dose of the vaccine, the majority of detected variants were delta followed by non-VOC. For patients who didn't receive vaccinations, most of the samples were non-VOC. Demographic and clinical characteristics of vaccinated individuals by number of vaccinations received and days after vaccine receipt are reported in **Table 3**. For vaccine type, individuals who were infected more than 14 days after receipt of the first dose had primarily received the Oxford-AstraZeneca vaccine, whereas individuals who were infected more than 14 days after the second dose had primarily received the Pfizer-BioNTech vaccine. The distributions of the frequency of each variant detected by vaccine type, number of vaccinations, and days since vaccine receipt, from 15 April to 30 June 2021, are shown in **Figure 3**. Although evidence of the efficacy and effectiveness of the current vaccines against emerging variants remains limited, recent published reports indicate that full vaccination (2 doses) provides high levels of protection against hospitalization and death for infections with the current VOCs. Notably, the vaccines do not prevent infection but rather prevent disease severity and death. It is critical to communicate this information to the public to encourage individuals to continue following precaution measures to break the infection chain and not allow the virus to replicate and circulate. "Anti-vax" sentiments or vaccine hesitancy may be contributing to new surges and emergence of new variants. Indeed, England's former Secretary of State for Health and Social Care, Matt Hancock, suggested that the high rates of infection and hospital admissions for people with COVID-19 infected with the delta variant are due to vaccine hesitancy [12].

In the present study, we used the RT-PCR cycle threshold (Ct) value as an indicator of viral load and increased transmissibility. Our results indicated that the Ct value differed by VOC infections, with the

lowest Ct values detected for the delta variant (mean Ct, 23) **Figure 4**. Because delta is a new emerging variant, researchers around the world are engaged in ongoing discussions about the low Ct values observed worldwide for the delta variant. One of the largest studies that analyzed 88,375 Ct values from variant-specific RT-PCR tests performed between 26 January and 13 March 2021, found that samples with the alpha, beta, and gamma VOCs exhibited significantly lower Ct values than the wild-type virus [13]. However, more studies are needed to support our observations with delta low Ct value. In addition, our results indicated that non-VOC Ct value was lower than beta and alpha. Overall, our results showing a rapid increase in the number of individuals infected with the delta variant rather than with the alpha or beta variant suggest a competitive advantage for the delta variant in our cohort. Further studies on a larger sample size is needed.

In conclusion, we conducted this study when we noticed a sharp increase in the occurrence of the delta variant in our community. This work provides the first report, to our knowledge, to document the increased frequency and dominance of delta variant at a tertiary-referral hospital in Saudi Arabia. The reported observations indicated a high transmissibility rate of the delta variant compared with the other circulating VOCs in our population, including the alpha and beta variants. These data will inform policymakers about the effectiveness of the Pfizer-BioNTech and Oxford-AstraZeneca vaccines, the breakthrough rates as the delta variant dominates and the importance of accelerating the second dose coverage to combat the spread of delta. Our findings underscore the importance of maintaining vigilance, conducting surveillance, and sequencing patient samples to monitor emerging variants.

Methods

Ethical considerations

This study was performed in compliance with all applicable national and international ethical guidelines for conducting research on human participants, including in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki). The institutional review board at KFSHRC approved this study (IRB #2200009) and granted a waiver for the requirement of obtaining informed consent owing to the use of deidentified samples.

Collection of samples and of clinical and demographic data

Samples were collected from 320 patients with confirmed COVID-19 (positive PCR test results) using a nasopharyngeal swab and then coded by the Microbiology Section of the Pathology and Laboratory Medicine Department at KFSHRC. The use of an unambiguous patient identification code enabled identification of all data reported for each patient without breaking patient privacy or confidentiality. Clinical and demographic electronic medical records from 18 May to 30 June 2021 were obtained from the Infection Control and Hospital Epidemiology Department at KFSHRC. Variables assessed included

demographic characteristics, virus exposure (travel history and human and animal contact), vaccination history, comorbidities, signs and symptoms, laboratory reports and ICU admission.

Sequencing

Nasal swab samples (200 µL) underwent total nucleic acid extraction using MagMAX™ Viral/Pathogen II (MVP II) Nucleic Acid Isolation Kit (ThermoFisher Scientific, USA). The viral load was estimated based on the Ct value of the N, ORF, and S genes using TaqPath™ COVID-19 CE-IVD RT-PCR Kits (ThermoFisher Scientific, USA) by following the manufacturer's instructions. All samples positive for SARS-CoV-2 were converted to cDNA using SuperScript™ IV VILO™ Master Mix (ThermoFisher Scientific, USA). The cDNAs were amplified using the Ion AmpliSeq™ SARS-CoV-2 Insight Research Assay as indicated by the manufacturer's instructions. Amplified products were ligated with unique barcode adaptors using the Ion Xpress Barcode Adaptors 1-16 kit (ThermoFisher Scientific, USA) and purified with 1.5× volume of Agencourt AMPure XP Reagent (Beckman Coulter, USA). Final library concentrations were measured using the Ion library TaqMan™ quantification kit (ThermoFisher Scientific, USA). Libraries were normalized to 33 pM using nuclease-free water, and up to 16 libraries were equally pooled for further processing. Pooled libraries were used as a template input for emulsion PCR and enrichment of template-positive particles using the Ion Chef automated system with the Ion 510 & Ion 520 & Ion 530 Kit-Chef kit (ThermoFisher Scientific, USA) according to the manufacturer's instructions. Enriched template-positive ion sphere particles were loaded onto an Ion 530 chip (ThermoFisher Scientific, USA), and sequencing was performed with Ion GeneStudio (ThermoFisher Scientific, USA) using Ion S5 sequencing solutions from the Ion 510 & Ion 520 & Ion 530 Kit-Chef kit. The obtained data were primarily processed (base calling, base quality recalibration, alignment, assembly, and variant calling) with Torrent Suite Server, version 5.12 (ThermoFisher Scientific, USA). De novo assembly of the contigs was performed using the assembly Trinity plugin (v1.2.1), and consensus sequences of each sample were generated using the IRMA plugin (v1.2.1). Variant call files were analyzed on the COVID19AnnotateSnpEff plugin to identify and annotate variants with public and private databases. In addition, in-house SARS-CoV-2 spike gene sequencing protocol to identify variants of concern using sanger sequencing was used in this study to overcome the shortage of whole genome sequencing supplies. Protocol and primers are available on request.

Statistical analysis

All collected data were stored and analyzed using SAS, version 9.4, software and Prism, version 9.0 (GraphPad). Inferential and descriptive statistics were conducted to study clinical variables. Analysis of variance or t tests were used to assess continuous variables, and χ^2 tests were used to assess categorical variables. All reported P-values were two-tailed and were considered to be statistically significant at <0.05.

Declarations

Data availability

Data will be available following article publication. SARS-CoV-2 whole genome sequences will be uploaded to the GISAID database and will be available on request.

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Author contributions

F-Alhamlan designed the study, wrote the initial draft of the manuscript, and provided data acquisition, analysis and interpretation. AA and DO helped in the study design and statistical analysis. S-Aljumaa, S-Alghamdi, KA, S-Almutairi, and JA comprise the infection control team who helped in tracing, testing, and reporting. MAlsanea, BA, F-Alsuwairi, M-AlAbdulkarim, M-Asiri and S-Altamimi provided technical support and conducted sequencing. MM, S-Althawadi, RA reviewed medical records and helped in clinical data interpretation. All authors assisted in writing and reviewing the manuscript and read and approved the final manuscript.

Ethics declarations

This study was approved by the Research Ethics Committee at King Faisal Specialist Hospital and Research Centre (RAC# 2200009). All samples were coded to maintain patient privacy and confidentiality.

Competing interests

Authors have no competing interests to disclose.

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Tables

Table 1. Demographic and clinical characteristics of 320 patients with confirmed COVID-19 at King Faisal Specialist Hospital and Research Center, by variant.

<i>Characteristic</i>	<i>Variant, No. (%) of 321 infected samples</i>				<i>X², P-Value</i>
	<i>Alpha (N=37)</i>	<i>Beta (N=51)</i>	<i>Delta (N=131)</i>	<i>Non-VOC (N=101)</i>	
Sex					
Male	14 (4.4)	22 (6.9)	83 (26.0)	52 (26.0)	11.1 (0.014) *
Female	23 (7.2)	29 (9.1)	48 (15.1)	48 (15.1)	
Age Group, years					
0-19	2 (1.0)	6 (1.9)	1 (0.31)	1 (0.31)	56.3 (<0.001) *
20-29	11 (3.5)	13 (4.1)	19 (5.9)	17 (5.3)	
30-39	11 (3.5)	8 (4.1)	59 (18.5)	29 (9.1)	
40-49	2 (0.6)	10 (3.1)	38 (11.9)	21 (6.6)	
50-59	7 (2.1)	15 (4.7)	11 (3.5)	19 (5.9)	
60-69	2 (0.6)	5 (1.6)	3 (0.94)	7 (2.2)	
70-102	2 (0.6)	1 (0.31)	0	6 (1.9)	
Nationality					
Saudi	21 (6.6)	31 (9.8)	26 (8.2)	69 (21.8)	63.9 (<0.0001) *
Non-Saudi	16 (5.1)	20 (6.3)	104 (32.8)	30 (9.5)	
Symptomatic					
Yes	25	40	72	48 (24.6)	2.9 (0.400)

	(12.8)	(20.5)	(36.9)		
No	2 (1)	1 (0.5)	6 (3.1)	1 (0.5)	
Intensive Care Unit Admittance					17.3 (0.006) *
Yes	0	1 (0.5)	0	7 (3.5)	
No	28 (14.3)	39 (19.9)	78 (39.8)	43 (21.9)	
Comorbidity					
Yes	4 (5.2)	7 (9.1)	2 (2.6)	17 (22.1)	5.9 (0.110)
No	15 (19.5)	15 (19.5)	2 (2.6)	15 (19.5)	

VOC indicates variant of concern; * Denotes statistical significance at $P < 0.05$.

Table 2. Patient vaccination status by detected variant.

Variable	Variant, No. (%) of infected samples				χ^2 , P-Value
	<i>Alpha</i> (N=37)	<i>Beta</i> (N=51)	<i>Delta</i> (N=131)	<i>Non-VOC</i> (N=101)	
No. of Vaccines received					
Two doses	10 (3.6)	13 (4.7)	12 (4.3)	7 (2.5)	51 (<0.0001) *
One dose	11 (3.9)	23 (8.3)	110 (39.6)	53 (19.1)	
No vaccine	9 (3.2)	7 (2.5)	4 (1.4)	19 (6.8)	
Type of Vaccine					
Pfizer-BioNTech	3 (1.1)	14 (4.9)	36 (12.8)	23 (8.2)	26.7 (0.0002) *
Oxford-AstraZeneca	15 (5.3)	21 (7.5)	82 (29.2)	35(12.5)	
NA	10(3.6)	9 (3.2)	9(3.2)	24(8.5)	
Time After Vaccination					
<14 days since the first dose	1 (0.3)	0	8 (2.5)	2 (0.6)	54 (<0.0001) *
>14 days since the first dose	15 (4.7)	30 (9.4)	103 (32.2)	53 (16.6)	
<14 days since the second dose	3 (0.9)	1 (0.3)	4 (1.3)	1 (0.3)	
>14 days since the second dose	1 (0.3)	4 (1.3)	4 (1.3)	2 (0.6)	
NA	17 (5.3)	16 (5)	12 (3.8)	43 (13.4)	

NA indicates data not available, and it is not included in the data statistics. * Denotes statistical significance at $P < 0.05$.

Table 3. Demographic and clinical characteristics of vaccinated individuals by number of vaccinations received and days after vaccine receipt.

<i>Characteristic</i>	<i>No. (%) of patients</i>				<i>X², P-Value</i>
	<i>After First Dose</i>		<i>After Second Dose</i>		
	<14 days	>14 days	<14 days	>14 days	
Sex					
Female	5 (2.2)	83 (35.9)	6(2.6)	3 (1.3)	4.7 (0.19)
Male	6 (2.6)	118 (51.1)	6 (2.6)	8 (3.5)	
Age Group, years					
0-19	0	0	0	0	35.2 (<0.0001)*
20-29	3 (0.9)	45 (14.1)	2 (0.6)	1 (0.3)	
30-39	6 (1.9)	78 (24.5)	2 (0.6)	1 (0.3)	
40-49	2 (0.6)	55 (17.2)	2 (0.6)	6 (1.9)	
50-59	0	22 (6.9)	2 (0.6)	2 (0.6)	
60-69	0	0	3 (0.9)	1 (0.3)	
70-102	0	0	0	0	
Nationality					
Saudi	2 (0.9)	65 (28.3)	4 (1.7)	6 (2.6)	3.9 (0.37)
Non-Saudi	9 (3.9)	135 (58.3)	5 (2.2)	5 (2.2)	
Symptomatic					
Yes	8 (5.4)	114 (75.5)	5 (3.4)	10 (6.7)	1.1 (0.97)
No	1 (0.7)	8 (3.4)	0	1 (0.7)	
NA	0	2 (1.3)	0	0	
Type of Vaccine					
Pfizer-BioNTech	8 (2.6)	58 (18.7)	0	9 (2.9)	98.5 (<0.0001)*
Oxford-AstraZeneca	3 (0.97)	142 (45.8)	6 (1.9)	2 (0.7)	
NA	0	0	3 (0.97)	0	

NA indicates data not available, and it is not included in the data statistics. * Denotes statistical significance at $P < 0.05$.

Figures

Figure 1

Percentage of sequenced samples with variants of concern (VOCs) detected from 15 April to 30 June. The delta variant was first detected in early-May and continued to be the highest percentage of the VOCs in June, replacing the alpha and beta variants.

Figure 2

Frequency of variants of concern (VOCs) detected in sequenced samples from 15 April to 30 June 2021. The delta variant was detected in early-May and continued to be the most common variant detected in June.

Figure 3

Frequency of variants of concern (VOCs) by vaccine type, number of vaccinations, and days since vaccine receipt, from 15 April to 30 June 2021. A) Patients infected ≤ 14 days after receiving the first vaccine by vaccine type and variant detected. B) Patients infected > 14 days after receiving the first vaccine by vaccine type and variant detected. C) Patients infected ≤ 14 days after receiving the second vaccine by vaccine type and variant detected. D) Patients infected > 14 days after receiving the second vaccine by vaccine type and variant detected.

Figure 4

Distribution of patient sample Ct values by variant of concern. The upper and lower limits of the error bars represent 95% confidence intervals. The delta variant has the lowest mean Ct value (Ct = 23).