**ISSN: 0067-2904**

# Clinical Characteristics of the SARS-CoV-2 Alpha, Delta, Delta plus and Omicron Variants *versus* the Wild Type in Iraqi Patients

**Khadija Th. Salah*, Hula Y. Fadhil**
*Department of Biology, College of Science, University of Baghdad, Baghdad, Iraq*

Received: 2/8/2022 Accepted: 27/9/2022 Published: 30/9/2023

**Abstract:**

Coronavirus disease 2019 (COVID-19) is caused by severe acute respiratory syndrome called coronavirus 2 (SARS-CoV-2). Due to its concerning rate of transmission and intensity, coronavirus was classified as a pandemic on March 11, 2020. With the continuous evolution of the viral genome and mutations that may alter infectivity, disease severity or interactions with host immunity, SARS-CoV-2 has evolved into many variants: Alpha (B.1.1.7 lineage), Delta (B.1.617.2 lineage), Delta plus (B.1.617.2.1), Omicron (B.1.1.529 lineage) and other variants. Thus, this study aimed to find and provide database for local clinical characteristics of different variants of SARS-COV-2 and severity of infection with viral load compared with the wild type. A total of 247 nasal swabs were collected from COVID-19 positive patients between March 2021 to March 2022. Specimens were tested by using real time reverse transcriptase polymerase chain reaction rRT-PCR assay to confirm the infection after RNA extraction by specialized kits. Results showed Alpha, Delta, Delta plus and Omicron variants presence in local population at the same time of their global spread at high rates with different cases of severity. The finding showed increase in severity with Alpha 79/87 (90%), wild type 26/32 (81%) (with 3 mortality cases), Delta/ Delta plus 68/84 (80%) and Kappa only one case. Also, Alpha along with the wild type was more associated to severe and critical cases, while mild to moderate group appeared with Omicron variant (32/43 (74%)). In addition, there was an increase in the severity among older patients (>40) and in men more than the women. Results indicate that although the wild type was no less dangerous or severe than Alpha or other variants, but with continuous appearence of new variants led to its reduced prevalence. In conclusion, findings demonstrated that most of the severe and critical cases had infection with Alpha, wild type than Delta or Delta plus variants. Whereas mild to moderate cases occurred in Omicron variants.

**Keywords**: SARS-CoV-2 Variants, SGTF assay, RT-PCR, N501Y mutation.

# الخصائص السريرية لمتغيرات SARS-CoV-2
# الفا، بيتا، دلتا بلس و اوميكرون بالمقارنة مع النمط البري

**خديجة صلاح* ، حلا يونس فاضل**
قسم علوم الحياة، كلية العلوم، جامعة بغداد، بغداد، العراق

*Emails: khadijath.salama@gmail.com

**الخلاصة :**

مرض فيروس كورونا COVID−19 و الذي يسببه متلازمة الجهاز التنفسي الحادة الشديدة فيروس كورونا SARS−COV−2. وصف بأنه جائحة في 11 مارس2020 بسبب مستويات الانتشار والخطورة المقلقة لمرض فيروس كورونا COVID−19. مع التطور المستمر للجينوم الفيروسي والطفرات التي قد تغير شدة العدوى وانتقال المرض أو التفاعلات مع مناعة المضيف، SARS−CoV−2 طور العديد من المتغيرات:( Alpha (B.1.1.7) , (B.1.617.2) Delta , (B.1.617.2.1) Delta plus و( B.1.1.529) Omicron ومتغيرات أخرى. تشير الأدلة إلى ان متغيراتSARS−CoV−2 ذات خصائص مميزة سريرية مثل (الشدة ودرجة العدوى) عند مقارنتها مع النمط البري. تهدف هذه الدراسة إلى إيجاد الصفات السريرية المحلية مع المتغيرات المختلفة لفيروس كورونا ( SARS−COV−2 ) وشدة الإصابة بالحمل الفيروسي وبالمقارنة مع النوع البري wild type و تزويد قاعدة بيانات للمرضى العراقيين المصابين بفايروس كورونا و تحديد المتغايرات و شدة خطورتها. جمعت 247 مسحة أنف من أفراد مصابين بفيرسCOVID−19 في الفترة من مارس 2021 إلى مارس 2022. تم اختبار العينات باستخدام اختبار تفاعل البوليميراز المتسلسل للنسخة العكسية في الوقت الفعلي ( RT−PCR ) لتأكيد العدوى بعد استخراج الحمض النووي الريبي بواسطة مجموعة خاصة.. أظهرت النتائج وجود متغيرات ( Alpha, Delta, Delta plus, Omicron) مع وجود (Wild type) في مجتمعنا في نفس الوقت من انتشارها العالمي بمعدلات عالية مع حالات مختلفة من الشدة. و أكدت النتائج زيادة في الخطورة مع(% 90) 79/87 Alpha,(81%) 26/32 Wild type,68/84 (80%Delta, Delta plus ) ،هذا للمجموعة الحرجة مع (3 حالات وفيات) مصابة (Wild type). بينما تظهر مجموعة خفيفة إلى معتدلة مع32/43 Omicron (74%) ، و سجلت حالة واحدة مصابة بمتغاير Kappa . بالإضافة إلى زيادة الشدة لدى المرضى الأكبر سنًا (> 40) وعند الرجال أكثر من النساء. في الختام ، أظهر الاكتشاف معظم حالات الإصابة الشديدة والحرجة بنوع (ألفا ، وايلد ، ثم دلتا ، ودلتا بلس) من المتغيرات بينما تحدث الحالة الخفيفة إلى المتوسطة في متغيرات أوميكرون. بالإضافة إلى ذلك تشير النتائج إلى أن النوع البري ليس أقل خطورة أو شدة من النوع ألفا أو المتغيرات الأخرى ، ولكن مع الظهور المستمر للمتغيرات يؤدي إلى تقليل ظهور النوع البري.

## 1. Introduction

The severe acute respiratory syndrome coronavirus (SARS-CoV-2) pandemic, which began almost two years ago, was still going strong coronavirus disease (COVID-19) when this study was being conducted. The virus disrupted the global economy, impeded free travel, affected millions of individuals and put a strain on medical personnel, leaving them emotionally vulnerable and physically and psychologically exhausted. [1]**.** Symptoms of pneumonia, such as fever, coughing, shortness of breath, sputum production, and myalgia or weariness, have mostly been observed in patients with the new SARS-CoV-2 infection [2]. Since alterations in the genetic code (genetic mutations) take place during genome replication, viruses like SARS-CoV-2 continue to develop. A lineage is a collection of genetically distinct viral strains that have a common ancestor. A variety of the SARS-CoV-2 viruses contain one or more mutations that set it apart from other variants [3]**.** With the continued emergence of multiple variants, the Center for Disease Control and Prevention and the World Health Organization have separately developed a mechanism for classifying the newly emerging SARS-CoV-2 variations into variants of interest (VOIs) and variants of concern (VOCs). The spike protein in the alpha version (B.1.1.7) carries a number of significant alterations. A mutation, N501Y, increases the spike protein's ability to connect to cellular receptors and making the virus more infectious. Additionally, it has the P681H mutation, although whose function is unknown, but has repeatedly appeared spontaneously, and the D614G mutation, which is likely to improve viral replication. The E484K mutation in an extra Alpha form, which may aid the virus in escaping the body's immune systems by avoiding neutralizing antibodies produced by vaccination or prior infection, is being closely watched by the WHO [4]. According to the estimates, B.1.1.7 strain of SARS-CoV-2 first circulated in England in September 2020 and has since then

overtaken all other variants [5]. Many spike mutations have happened to Delta (B.1.617.2) genome, namely: T19R, G142D, del157/158, L452R, T478K, D614G, P681R and D950N. At the end of 2020, India was the first country to report Delta variant which has since spread around the world. [6]. There were significantly more high-prevalence mutations (20%) in the Delta Plus variation (B.1.617.2.1) than in the Delta variant. Spike's signature mutations (G142D, A222V, and T95I) were present in the Delta Plus variation at a higher rate than the Delta variant. Spike's K417N, V70F and W258L mutations were all found solely in the Delta Plus variant. With a frequency of about 58%, A1146T, a novel mutation in ORF1a, was found to be present solely in the Delta Plus variation. Additionally, the prevalence of five important mutations (T95I, A222V, G142D, R158G and K417N) was considerably higher in the Delta Plus variant compared to the Delta variant**.** Delta plus variant was first reported in India in March, 2021. Omicron (B.1.1.529) variant, a recently discovered highly mutated virus strain, was categorized as a VOC by the WHO on November 26, 2021 [7]. With over 50 mutations in its genome, Omicron is the most mutated SARS-CoV-2 variant. It is of special interest and worry since 26–32 of these changes have been reported in the viral spike (S) protein region, and 15 of them are in the receptor-binding domain (RBD) [8]. The spike (S) protein of Omicron has about 30 mutations, some of which are shared by the VOCs Alpha (del69/70, P681H), Beta (K417N, N501Y) and Delta (G142D, T478K). The del69/70 mutation is one of these mutations that is anticipated to or is known to have an effect on immune escape or transmissibility [9]. The Kappa (B.1.617.1) variant, which was originally identified in India in December 2021 and is categorized by the WHO and the CDC as a VOI, has important mutations ((T95I), G142D, E154K, L452R, E484Q, D614G, P681R and Q1071H) [4]. Because a little research had already been done on SARS-CoV-2 variants among Iraqi patients, this research aimed to offer regional information and understand the difference of clinical characters between different SARS-CoV-2 variants.

## 2. Materials and Methods

### *2.1. Study participants*

A total of 247 COVID-19 patients' respiratory nasal swabs were selected randomly from Baghdad Central Public Health Laboratory (CPHL) during the period from March 2021 to March 2022 for testing SARS-CoV-2 and its variants. Iraq's Department of Biology, College of Science, University of Baghdad and Ministry of Health and Environment Ethics Committee (Ref: CSEC/0921/0046) approved the study protocols. Written consent was obtained from all participants for collection of nasal swabs. Following WHO guidelines and the physician's diagnosis, cases were categorized by the COVID-19 infection as mild-moderate, severe and critical. Ages of patients ranging from 17 to 68 year olds, included 172 males and 74 females, excluding the vaccinated patients. The collected nasal swabs were placed in screw-capped containers with VTM (viral transport medium) to preserve viral vitality while being transported. These swabs were kept at -70˚C until the extraction of viral RNA experiment.

### *2.2. Molecular assay*

#### *2.2.1. Viral RNA extraction*

All specimens were extracted by special laboratory kit (AddPrep Viral Nucleic Acid Extraction Kit, Add bio, Korea) and according to the manufacturer's instructions. The viral RNA was stored at –70˚C until SARS-CoV-2 was tested by real time reverse transcriptase polymerase chain reaction (rRT-PCR).

*2.2.2. Real time reverse transcriptase polymerase chain reaction assay*

The 10µl of extracted RNA was tested using real-time reverse transcriptase PCR analysis utilizing a specialized SARS-COV-2 detection kit (AccuPower® SARS-CoV-2 Multiplex RT-PCR Kit, Bioneer, Korea). The RT step activation at 50˚C for 15min, pre-denaturation 95 ˚C for 5min, followed by denaturation 95˚C for 5sec, then annealing and extension 57˚C for 30sec. The cases that were less than 37 cycle number and were hence rendered as positive diagnostic.

*2.2.3. SARS-COV2 variants detection*

All 247 samples tested positive for SARS-CoV-2 variants with special kit (AccuPowerSARS-CoV-2 Variant RT-PCR Kit ID2). This kit was used to detect variant target genes (**N501Y, Hv69/70DEL, E484Q, P681R, L452R)** which occur in **Alpha, Delta or Delta plus and Kappa** respectively. This kit contains oligo mix (TaqMan) probe, enzyme mix and controls. After entering the plate into the real-time PCR thermal cycler (ABI 7500 fast), the following amplification was performed: RT activation step at 50°C for 15min, pre-denaturation at 95°C for 5min, followed by 45 cycles at 95°C and 57°C for 35sec.

*2.2.4. Detection for Omicron variant*

For Omicron detection (TaqPATH COVID-19 CE-IVD RT-PCR Kit, ThermoFisher, Germany) was used by (S gen target failure) assay (as a proxy for the omicron variant). The plate was put into a real-time PCR thermal cycler (ABI 7500 fast) and the amplification was performed as follows: UNG incubation at 25°C for 2 minutes, reverse transcription at 53°C for 10 minutes, activation at 95°C for 2 minutes, denaturation at 95°C for 3 seconds and anneal/extension at 60°C for 30 seconds.

*2.2.5. Statistical analysis*

Data was entered, managed and analyzed using the statistical package IBM SPSS Statistics 25.0 (Armonk, NY: IBM Corp.). GraphPad Prism version 8.0.0 was used to perform these analysis. Continuous variables were first checked with normality test to describe the median with interquartile range for not being normally distributed. Mann-Whitney U and Kruskal-Wallis tests were used to assess significant differences between medians. The categorical variables were presented as number and percentage and were analyzed to compare the frequency using the two-tailed Fisher exact or Pearson Chi-square tests. Statistical significance was defined as a probability ($p$) value 0.05.

## 3. Results and Discussion

*3.1. Baseline features of the patients*

A total of 247 cases with 172 males (69.6%) and 75 females (30.4%) were enrolled in this study. All patients were diagnosed with COVID-19 using PCR technique with mild to moderate, severe and critical disease according to the WHO criteria for classification of disease severity. As indicated in Table 1, statistical analysis revealed significant ($p < 0.001$) differences between COVID-19 patients according to age group, with the median age of 52 [IQR: 45-57] years being substantially higher than 33 [IQR: 26-38] years. According to the findings, we were able to conclude that older patients were more likely to contract COVID-19. These findings are supported by other studies which indicate a positive relationship between age and COVID-19 infection. This disorder was brought on by changes in the immune system's quantity or quality which has an impact on how immune cells and mediators react in peripheral tissues. These changes regulate not just infection susceptibility but also disease progression, potential clinical risk [10]. In another local study the findings revealed that out of 31 critical cases, 7 death cases of over 50 years old patients were recorded. Aging is usually accompanied with comorbidities and a decrease in the immune system function. Although males exceeded females

in illness (172 vs. 69.6%), females outnumbered males (75 vs. 30.4%). As the male to female infection ratio was larger in many nations and there was a correlation between sex and illness outcome, men were more impacted than women [11]. These disparities may be due to hormonal influences on the immunological response as well as higher levels of ACE2 and TMPRSS2 in males. High severity and fatality rates of COVID-19 that are seen in males may potentially be a result of behavioral differences among men. Smokers and patients with comorbidities linked to COVID-19 are more likely to be men. As shown in Table 1, the Ct value between 11- 20 cycle had a higher percentage (59.1%) than those of Ct value between 21-36 which was 40.9%. Many clinical studies proved that low Ct indicates a high concentration of genetic material which is often associated with a greater risk of infection. As it demonstrates a low concentration of viral genetic material, a high Ct value suggests a lesser likelihood of disease development [12]. Table 1 shows that 74.4 % of patients being in severe and critical groups which indicates severity increase with emersion of different variants. Different studies provide evidence that the mutations in variants allow SARS-CoV-2 to be more successful in evading the immune system, even in people who have already been exposed to it or had a full vaccination [13]. Furthermore, the researcher noticed rapid evolution of SARS-CoV-2 mutations during this outbreak. The emergence of immune escape is also linked to several of these mutations. SARS-CoV-2 variants are now the predominant strains in a number of geographical areas. Some of these mutations have been linked to SARS-CoV-2 immunological escape or partial vaccination escape. The RBD (receptor-binding-domain), linked to immune escape, has two mutations: K417N/T and E484K. D614G, another mutation in the S-glycoprotein area has been linked to immunological evasion. At the time of our study, prevalence of Alpha variant was highest (n=87) which was followed by Delta, Delta plus (n=84) and Omicron (n=43), and last but not least wild type (n=32). This data has been supported by many studies [14, 15]. Also a local study done in March of this year found prevalence of Alpha and Beta variants [16].

**Table 1:** Baseline characteristics of patients with SARS-CoV-2 infection.

| Characteristics | | SARS-CoV-2 Cases; n = 247 | *p*-value |
|---|---|---|---|
| **Age; year** | ≤ 40 | 33 (26 – 38) n= 92 | **< 0.001** |
| | > 40 | 52 (45 – 57) n= 155 | |
| **Gender** | Male | 172 (69.6) | **< 0.001** |
| | Female | 75 (30.4) | |
| **Ct Threshold Values** | 11 - 20 | 146 (59.1) | **< 0.01** |
| | 21 - 36 | 101 (40.9) | |
| **Severity Group** | Mild-moderate | 63 (25.5) | **< 0.001** |
| | severe | 112 (45.3) | |
| | *Critical | 72 (29.1) | |
| **SARS-CoV-2 Variants** | Wild type | 32 (13.0) | **< 0.001** |
| | Alpha | 87 (35.2) | |
| | Delta or Delta plus | 84 (34.0) | |
| | Omicron | 43 (17.4) | |
| | Kappa | 1 (0.4) | |

Values of age are given as median with interquartile range (continues variables) or number and percentage (categorical variables);*: included three of death cases; *p*: Mann-Whitney U test probability When comparing continuous variables, to compare categorical variables, used the two-tailed Fisher exact test or the Pearson Chi-square test.

*3.2. Variants of SARS-CoV-2 infection*

Table 2 it shows that 63% of infections were related with people >40. A previous research has also shown that the age of patients has a significant impact on the severity and prognosis of COVID-19. This may be related to immune senescence and cellular senescence where two aging-related immune processes that can decrease immunological responses to SARS-CoV-2 and escalate systemic inflammation, as a result of cell cycle arrest that cannot be reversed [17]. Table 2 clarifies results which indicate that Alpha and Delta, Delta plus (68%) were with Ct value ranging between 11-20 while (17%) of wild type with Ct value ranging between 11-20. In addition, at the time of this study, as shown in Table 2, the results proved that the highest prevalence of severe and critical patients fell in Alpha (n=79) and Delta, Delta Plus (n=68) then in Wild type (n=26), while mild to moderate patients had Omicron (n=32), and there were highly significant ($p < 0.001$) differences between SARS-COV2 variants. Results summation indicate that Alpha and Delta, Delta Plus had more severe and high transmission than wild type. Reports have proved that Alpha variant is 50% more transmissible than the prior strains, whereas the Delta variant is up to 60% more transmissible [18]. Numerous investigations have supported that Alpha causes severe outcomes. According to this investigation, which describes the features of SARS-CoV-2 VOC infections in seven EU/EEA countries, older patients who were infected with Alpha variants were at higher risk of hospitalization and ICU admissions. Similar to this, Germany observed an increase in hospitalization among middle-aged patients infected with Alpha variant. There was no evidence that the Alpha had a greater case of fatality than the wild type [19]. While another study documented that compared to the wild type virus, Alpha was linked with 73% greater risks of all-cause mortality and 62% higher risks of hospital admissions [20]. It should be advantageous for the interaction with ACE2 to have N501Y substitution in this area of the interface. Previous research indicates that the Alpha strain of UK should have a stronger affinity for ACE2 which would increase its transmissibility, and perhaps even its pathogenicity. A high transmission rate of South African Alpha variant may be because of the N501Y replacement and/or replacements in areas that are not directly adjacent to the Spike-ACE2 interface [21]. However, three significant S mutations in the Delta variant, L452R, T478K and P681R, provide tolerance to certain neutralizing monoclonal antibodies and may increase transmission [22]. These mutations impair the antibodies ability to attach to the RBD spike while giving viral resistance to neutralizing monoclonal antibodies [23]. For mild to moderate patients with Omicron, early research indicates that Omicron may spread more swiftly than other variants and may be less severe than the Delta variant [24]. The report demonstrates that patients with the Omicron variant infection have a lower probability of getting serious illness and dying than those with the Delta variant [25]. Summary of the current studies suggest that variants Alpha and Delta or Delta Plus were more severe and highly transmissible and could even lead to death more than the wild type. In this study, three patients infected with the wild type died and all of them were with chronic diseases linked with aging such as cardiovascular disease, renal failure, NHL, etc. These comorbidities have been linked to an increased risk of morbidity and mortality as well as an increased risk of developing COVID-19 and disease severity [26]. According to a local study, these comorbidities can increase the viral load in COVID-19 infected patients. Diabetes and hypertension are risk factors for the condition [27]. By the time other VOC emerged, the wild type had already started to deteriorate as a result of the non-pharmaceutical interventions (NPI) [28].

**Table 2:** Frequencies of SARS-CoV-2 infection and variants stratified to patient ages, gender, severity and Ct threshold values.

| Characteristic; n = 247 | | Wild type | Variant of SARS-CoV-2 | | | | Total | *p*-value |
|---|---|---|---|---|---|---|---|---|
| | | | Alpha (B.1.1.7) | Delta (B.1.617.2) or Delta plus (AY.1) | Kappa (B.1.617.1) | Omicron (B.1.1.529) | | |
| **Age; year** | ≤ 40 | 9 | 33 | 33 | 1 | 16 | 92 | < **0.001** |
| | > 40 | 23 | 54 | 51 | 0 | 27 | 155 | < **0.001** |
| ***p*-value** | | < 0.05 | < 0.05 | *p* = 0.05 | -- | *p* = 0.09 | | |
| **Gender** | Male | 23 | 66 | 60 | 0 | 23 | 172 | < **0.001** |
| | Female | 9 | 21 | 24 | 1 | 20 | 75 | < **0.01** |
| ***p*-value** | | < 0.05 | < **0.001** | < **0.001** | -- | *p* =0.65 | | |
| **Ct Threshold Values** | 11 - 20 | **25** | **49** | **51** | 1 | 20 | 146 | < **0.001** |
| | 21 - 36 | 7 | 38 | 33 | 0 | 23 | 101 | < **0.001** |
| ***p*-value** | | < **0.01** | *p* = 0.24 | *p* = 0.05 | -- | *p* =0.65 | | |
| **Severity Group** | Mild-moderate | 6 | 8 | 16 | 1 | **32** | 63 | < **0.001** |
| | severe | **15** | **49** | **37** | 0 | 11 | 112 | < **0.001** |
| | Critical (dead) | **8 (3)** | **30** (0) | **31 (0)** | **0** | **0** (0) | 72 (3) | < **0.001** |
| ***p*-value** | | *p* =0.15 | < **0.001** | < **0.05** | -- | < **0.01** | | |

; *p*: two-tailed Fisher exact test or Pearson Chi-square test probability to compare frequency in categorical variables.

*3.3. Correlation of CT value with age groups, severity, and SARS-CoV-2 variants.*

The results obtained from Figure 1 show that Ct value with age and severity group had non-significant differences at $p$ =0.74 and $p$ =0.21 respectively, which means that there is no correlation between Ct value and age. However, the results revealed that there was a significant difference between median of Ct value and SARS-CoV-2 variants at $p$ <0.05. Analysis showed lowest Ct value were found in wild type and then Alpha and Delta. This indicates that not only wild type is as severe as Alpha, it can also cause serious diseases with high viral load. According to a Chinese study, severe infections have higher viral loads (lower Ct values) with longer virus persistence [29] [30]. Moreover, most severe and critical cases (74.5%) included in the study, fall within the Ct value range of 10-20., These findings proved that lower Ct value cases had higher viral load and were more severe and had critical illness. While mild / moderate cases (25%) had Ct values falling within 21-36 range, which means that it had lower viral load and develops less severe illness.

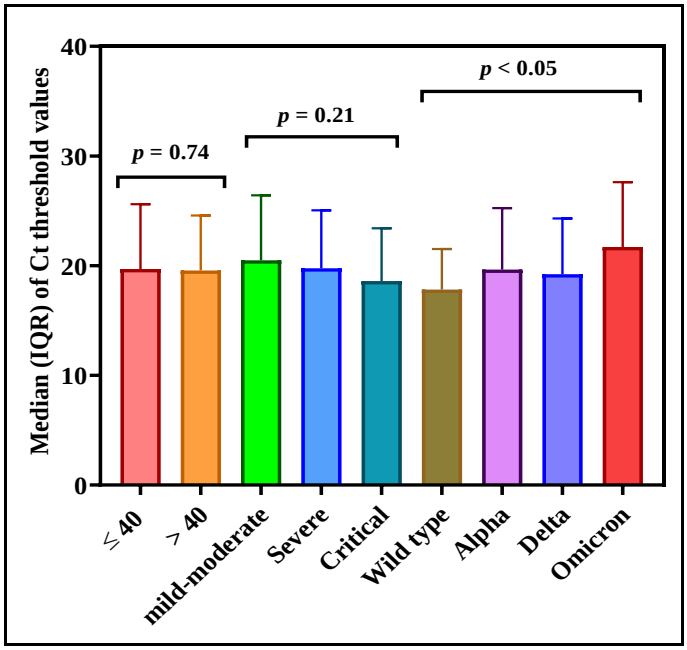


**Figure 1:** Median of Ct threshold values stratified to age groups, severity, and SARS-CoV-2 variants among patients. *p*: Mann-Whitney *U* test and Kruskal-Wallis test probability were used to assess significant differences between medians.

*3.4. Age distribution to gender and disease severity*

Figure 2 box plot shows that age median had highly significant relation with severity ($p$ <0.0001) meaning that there is correlation between age and severity. Highest median of age [53 IQR (44-56)] was recorded in critical cases of patients which indicated that older patients (>40) may have severe infection. This also proved by a previous study [10]. Since aging is usually accompanied with comorbidities, there is a decrease in the immune system functions [27]. In addition, older patients may have an immune signature characterized by the suppression of T-cell responses and deregulation of innate immunity. which isthen followed by median age of [43 IQR (34-52)] in severe cases and finally median age of [39 IQR (35-46)] in mild to moderate illness.

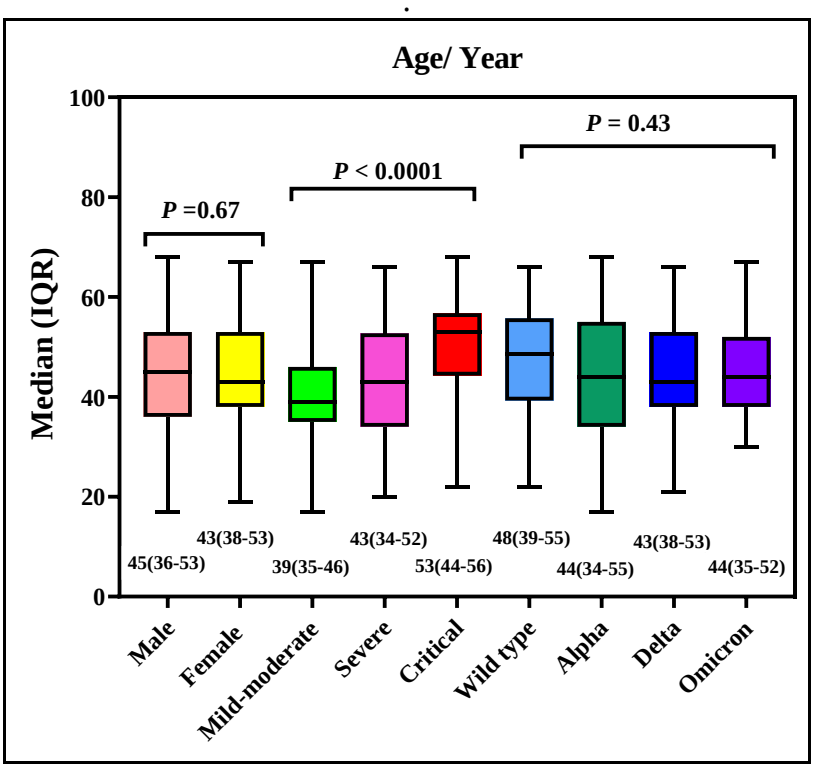


**Figure 2:** Box plot of age (median and interquartile range) in COVID-19 patients according to gender, disease severity and SARS-CoV-2 variants. *p*: Kruskal-Wallis test and Mann-Whitney *U* test probability was used to assess significant differences between medians.

## Conclusion

Older aged patients and males are more susceptible to severe illness of SARS-CoV-2. Most of Ct value ranges between 11-20 cycle have been linked with higher viral load. Critical and severe cases are found mostly with Alpha and Delta/Delta plus variants when compared with the wild type. On the other hand, Omicron variant spreads more speedily but causes less severe infections. Concluding that most mild/moderate cases were infected with Omicron.

## Acknowledgments

The authors thank the medical staff at the Central Public Health Laboratory (CPHL) / Molecular biology department in Baghdad for their kind cooperation.

## References

**[1]** E. Kutscher, "Preparing for Omicron as a covid veteran," *BMJ*, p. 375:n 3021, 2021. doi:10.1136/bmj.n3021

**[2]** Ch. Huang *et al* ., "Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China," *The Lancet*, vol. 395, no. 10223, pp. 497-506, 2020. DOI:https://doi.org/10.1016/S0140-6736(20)30183-5

**[3]** C. f. D. C. a. Prevention, "Centers for Disease Control and Prevention," 26 April 2022. [Online]. Available: https://www.cdc.gov/coronavirus/2019-ncov/variants/about-variants.html.

**[4]** M. Cascella *et al.*, "Features, Evaluation, and Treatment of Coronavirus (COVID-19)", StatPearls [Internet], 2022. Available from: https://www.ncbi.nlm.nih.gov/books/NBK554776/

**[5]** L. Geddes, "From Alpha to Omicron: Everything you need to know about SARS-CoV-2 variants of concern," 6 December 2021. [Online]. Available: https://www.gavi.org/vaccineswork/alpha-omicron-everything-you-need-know-about-coronavirus-variants-concern.

**[6]** Y. Zhan, H. Yin, and J. Yin1, "B.1.617.2 (Delta) Variant of SARS-CoV-2: features, transmission and potential strategies," *international journal of biological sciences,* vol. 18, no. 5, pp. 1844-1851, 2022. doi: 10.7150/ijbs.66881.

**[7]** S. Kannan, *et al.,* "Evolutionary analysis of the Delta and Delta Plus variants of the SARS-CoV-2 viruses," *Journal of Autoimmunity,* vol. 124, no. 102715, 2021. doi: 10.1016/j.jaut.2021.102715.

**[8]** R. Khandia *et al*., "Emergence of SARS-CoV-2 Omicron (B.1.1.529) variant, salient features, high global health concerns and strategies to counter it amid ongoing COVID-19 pandemic," *Environmental Research,* vol. 209, no. 112816, 2022. DOI: 10.1016/j.envres.2022.112816

**[9]** K. Subramoney *et al*., "Identification of SARS-CoV-2 Omicron variant using spike gene target failure and genotyping assays, Gauteng, South Africa, 2021," *Journal of Medical Virology,* vol. 94, no. 8, p. 3676–3684, 2022. doi: 10.1002/jmv.27797.

**[10]** V. Bajaj *et al*,. "Aging, Immunity, and COVID-19: How Age Influences the Host Immune Response to Coronavirus Infections?," *Frontiers in Physiology,* vol. 11, no. 571416, pp. 1-23, 2021. DOI: 10.3389/fphys.2020.571416

**[11]** G. Sharma, A.Volgman, E. Michos, "Sex Differences in Mortality From COVID-19 Pandemic: Are Men Vulnerable and Women Protected?," *JACC: Case Reports,* vol. 2, no. 9, pp. 1407-1410., 2020. DOI: 10.1016/j.jaccas.2020.04.027.

**[12]** S. Rao *et al*., "A Systematic Review of the Clinical Utility of Cycle Threshold Values in the Context of COVID-19," *Springer Link,* vol. 9, no. 3, pp. 573-586., 2020. DOI: 10.1007/s40121-020-00324-3.

**[13]** A. Souza *et al*.,"Severe Acute Respiratory Syndrome Coronavirus 2 Variants of Concern: A Perspective for Emerging More Transmissible and Vaccine-Resistant Strains," *Virsues,* vol. 14, no. 4, p. 827, 2022. Availlable: https://doi.org/10.3390/v14040827

**[14]** S.Buchan *et al*., "Increased Household Secondary Attacks Rates With Variant of Concern Severe Acute Respiratory Syndrome Coronavirus 2 Index Cases," *Clinical Infectious Diseases,* vol. 74, no. 4, pp. 703-706, 2022. Available: https://doi.org/10.1093/cid/ciab496

**[15]** H. Tegally *et al.,* "Emergence of a SARS-CoV-2 variant of concern with mutations in spike glycoprotei," *Nature,* vol. 592, no. 7854, 2021. DOI:10.1038/s41586-021-03402-9

**[16]** Th. Abdul Hussein, H. Fadhil "Analysis of mutations in conserved and susceptible region across the whole genome sequencing analysis for SARS-CoV-2 in Iraqi patients," *Iraqi Journal of Science,* vol. 63, no. 7, pp. 3487-3496, 2022.

**[17]** D. Zhou, M. Borsa , A. Simon, "Hallmarks and detection techniques of cellular senescence and cellular ageing in immune cells," *Aging Cell,* vol. 20, no. 2, 2021. DOI: 10.1111/acel.13316.

**[18]** D. Duong, "Alpha, Beta, Delta, Gamma: What's important to know about SARS-CoV-2 variants of concern?," *Canadian Medical Association Journal,* vol. 193, no. 27, pp. E1059-E1060, 2021. doi: 10.1503/cmaj.1095949

**[19]** D. Frampton *et al*., "Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study," *The Lancet,* vol. 21, no. 9, pp. 1246-1256, 2021. DOI:https://doi.org/10.1016/S1473-3099(21)00170-5

**[20]** D. Grint *et al*., "Severity of SARS-CoV-2 alpha variant (B.1.1.7) in England," *Clinical Infectious Diseases,* vol. ciab754, 2021. https://doi.org/10.1093/cid/ciab754

**[21]** B. Villoutreix *et al.,* "In Silico Investigation of the New UK (B.1.1.7) and South African (501Y.V2) SARS-CoV-2 Variants with a Focus at the ACE2–Spike RBD Interface," *International Journal of Molecular Sciences,* vol. 22, no. 4, p. 1695, 2021. doi: 10.3390/ijms22041695.

**[22]** Q. Li *et al.,* "The Impact of Mutations in SARS-CoV-2 Spike on Viral Infectivity and Antigenicity," *Cell Press journal,* vol. 182, no. 5, pp. 1284-1294.e9, 2020. doi: 10.1016/j.cell.2020.07.012

**[23]** S.Cherian *et al.,* "SARS-CoV-2 Spike Mutations, L452R, T478K, E484Q and P681R, in the Second Wave of COVID-19 in Maharashtra, India," *Microorganisms,* vol. 9, no. 7, p. 1542, 2021. DOI: 10.3390/microorganisms9071542

**[24]** UNICEF, "What we know about the Omicron variant, What is Omicron and what precautions should you take to protect your family?," 18 January 2022. [Online]. Available: https://www.unicef.org/iraq/stories/what-we-know-about-omicron-variant .

**[25]** W. H. Organization, "Severity of disease associated with Omicron variant as compared with Delta variant in hospitalized patients with suspected or confirmed SARS-CoV-2 infection," World Health Organization., 2022. Available: https://www.who.int/publications/i/item/9789240051829

**[26]** B. Almeida-Pititto *et al.*, "Severity and mortality of COVID 19 in patients with diabetes, hypertension and cardiovascular disease: a meta-analysis," *Diabetol Metab Syndr,* vol. 12, no. 1, pp. 1-12, 2020. DOI: https://doi.org/10.1186/s13098-020-00586-4

**[27]** Z.. Mahmood, H. Fadhil, and A. Adʹhiah, "Estimation of Hematological Parameters of Disease Severity in Iraqi Patients with COVID-19," *Iraqi Journal of Science,* vol. 62, no. 10, pp. 3487-3496, 2021.

**[28]** A. Layton, M. Sadria, "Understanding the dynamics of SARS-CoV-2 variants of concern in Ontario, Canada: a modeling study," *Scientific Reports,* vol. 12, no. 1, p. 2114, 2022. DOI https://doi.org/10.1038/s41598-022-06159-x.

**[29]** F. Fang, S. Naccache, A. Greninger, "The Laboratory Diagnosis of Coronavirus Disease 2019-Frequently Asked Questions," *Clinical Infectious Diseases,* vol. 71, no. 11, pp. 2996-3001, 2020. DOI: 10.1093/cid/ciaa742

**[30]** T. Xu *et al.*, "Clinical features and dynamics of viral load in imported and non-imported patients with COVID-19," *International Journal of Infectious Diseases,* vol. 94, pp. 68-71, 2020. DOI: 10.1016/j.ijid.2020.03.022.