



#### Ministry of Higher Education and Scientific Research University of Babylon College of Pharmacy

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## Statistical study for number of vaccinated persons in the province of Babylon

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### **Dedication**

To express my gratitude to those who supported and	1
encouraged me, I dedicate this research	

..... My Family

..... My Relatives

..... My Friends

#### **Acknowledgment**

If we were to properly acknowledge all the people who supported us, we would exhaust all the ink and paper on this planet. So, gentle reader, if we have omitted a deserving name, know that it was not our gratitude that was limited, but our page count. We owe a great debt to our supervisor (**Dr. Roqaya Monther Jaleel**)

, this research would be nothing without her support and guidance. Her clear and deep understanding of everything related to this research, as well as her ability to cut straight to the heart of a problem, will always stand before us as unforgettable lessons.

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#### **Abstract**

The novel coronavirus disease 2019 (COVID-19) outbreak started in early December 2019 in the capital city of Wuhan, Hubei province, People's Republic of China, and caused a global pandemic. This study is performed to show the Importance Health Complications of COVID19 Infection. Data were collated from the health center (Al-Qadih Health Center)

About Pfizer vaccine and Sinopharm vaccine the result from January to April (2022) which included details of all patients who took the vaccine throughout the city of Hilla. Results shows percentage of female who given the vaccine was 63%, while the male was 37%, which means that woman were more likely to take the vaccine. About Sinopharm vaccine, results show it was specific for patients from 18 to 50 years, but it is limited use because vaccinated people get infected again even after taking the vaccine.

The results of the present study showed significant differences in age groups , previous infection and chronic disease at p<0.0001 in participate whom take pifizer vaccine while we showed no significant differences in age groups , previous infection and chronic disease in participate whom take **Sino pharm** vaccine .

في أوائل ديسمبر (COVID-19) بدأ تفشي مرض فيروس كورونا الجديد ٢٠١٩ في أوائل ديسمبر (COVID-19) بدأ تفشي مرض فيروس كورونا الشعبية ، وتسبب في جائحة عالمي. تم إجراء هذه الدراسة لإظهار أهمية المضاعفات الصحية لعدوى .(تم جمع البيانات من المركز الصحي (مركز القاضي الصحي الصحي .

حول لقاح فايزر ولقاح سينوفارم النتيجة من كانون الثاني (يناير) إلى نيسان (أبريل) ( ٢٠٢٢) والتي تضمنت تفاصيل جميع المرضى الذين أخذوا اللقاح في جميع أنحاء مدينة الحلة. تظهر النتائج أن نسبة الإناث اللاتي تلقين التطعيم كانت ٦٣٪، بينما كان الذكور ٣٧٪، مما يعني أن المرأة كانت أكثر عرضة لتلقي التطعيم. حول لقاح ، تظهر النتائج أنه كان مخصصًا للمرضى من ١٨ إلى ٥٠ عامًا ، Sinopharm لكنه محدود الاستخدام لأن الأشخاص الذين تم تطعيمهم يصابون بالعدوى مرة أخرى . حتى بعد أخذ اللقاح

## **Introduction**

Coronaviruses are important human and animal pathogens. At the end of 2019, a novel coronavirus was identified as the cause of a cluster of pneumonia cases in Wuhan, a city in the Hubei Province of China. It rapidly spread, resulting in an epidemic throughout China, followed by a global pandemic. In February 2020, the

World Health Organization designated the disease COVID-19, which stands for coronavirus disease 2019. The virus that causes COVID-19 is designated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2); previously, it was referred to as 2019-nCoV [1].

COVID-19 infections lead to shortages healthcare workers due to isolation and treatment quarantining of contacts, hospitalization, periods, mortality and the prolonged period from COVID-19. Countries such as the United Kingdom, USA, France, Italy and South Africa reported significant numbers of healthcare workers infections and deaths during the early waves of the pandemic, resulting in a significant strain on human resources. Earlier COVID-19 deaths, which mainly occurred in older age groups above 50 years of age,

sometimes resulted in the loss of significantly experienced healthcare workers, who act as pillars for teaching and providing mentorship to younger healthcare workers [2].

Mortality has been widely used as an outcome in epidemiological studies and randomized controlled trials for patients with COVID-19 but fails to capture the immediate short-term health issues faced by survivors, including in-hospital complications and functional outcomes. In patients with COVID-19 undergoing surgery, high rates of post procedural mortality and complications have been noted, but systematic characterization of hospitalized patients with COVID-19 is lacking [3]. In other non-SARS-CoV-2 viral illnesses, for example influenza, short term complications such as myocardial infarction, acute kidney injury, and stroke are common and can cause greater morbidity than the initial infection itself. Understanding which patients develop short term complications might also allow clinicians and researchers to develop care pathways and interventions to mitigate the impact of complications [4].

Since first reported, there has been a vast amount of social media patient groups, polls, comments, and scientific articles aiming to describe the chronicity of COVID-19. In parallel, hundreds of scientific publications, including cohorts studying specific effects of the disease and lists of case reports, have been described. However, a broad overview of all the possible

longstanding effects of COVID-19 is still needed. Therefore, this research aims to give an overview of COVID-19 and its complications.

# Section one Theoretical Part

### 1. Virology

Coronaviruses are enveloped positive-stranded RNA viruses. Full-genome sequencing and phylogenic analysis

indicated that the coronavirus that causes COVID-19 is a beta coronavirus in the same subgenus as the severe acute respiratory syndrome (SARS) virus (as well as several bat coronaviruses), but in a different clade. The Coronavirus Study Group of the International Committee on Taxonomy of Viruses has proposed that this virus be designated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The Middle East respiratory syndrome (MERS) virus, another beta coronavirus, appears more distantly related. The closest RNA sequence similarity is to two bat coronaviruses, and it appears likely that bats are the primary source; whether COVID-19 virus is transmitted directly from bats or through some other mechanism (eg, through an intermediate host) is unknown [5,6]. The host receptor for SARS-CoV-2 cell entry is the same as for SARS-CoV, the angiotensin-converting enzyme 2 (ACE2). SARS-CoV-2 binds to ACE2 through the receptorbinding domain of its spike protein. The cellular protease TMPRSS2 also appears important for SARS-CoV-2 cell entry [7].

#### 1.1 Variants of concern

Like other viruses, SARS-CoV-2 evolves over time. Most mutations in the SARS-CoV-2 genome have no impact on viral function. Certain variants have garnered widespread attention because of their rapid emergence within populations and evidence for transmission or clinical implications; these are considered variants of concern. Each variant has several designations based on distinct the nomenclature by phylogenetic used classification systems; the World Health Organization (WHO) has also designated labels for notable variants based on the Greek alphabet [8].

Early in the pandemic, a study that monitored amino acid changes in the spike protein of SARS-CoV-2 included in a large sequence database identified a D614G (glycine for aspartic acid) substitution that became the dominant polymorphism globally over time. In animal and in vitro bearing G614 the polymorphism studies, viruses demonstrate higher levels of infectious virus in the respiratory tract, enhanced binding to ACE-2, and increased replication and transmissibility compared with the D614 polymorphism. The G614 variant does not be associated with a higher risk appear

hospitalization or to impact anti-spike antibody binding [9]. It is now present in most circulating SARS-CoV-2 lineages, including the variants of concern listed below.

#### 1.1.1 Delta

This lineage was first identified in India in December 2020 and had since been the most prevalent variant worldwide until emergence of the Omicron variant. The Delta variant is highly transmissible, more so than Alpha (B.1.1.7), which was more transmissible than previously circulating SARS-CoV-2 lineages. In reports from the United Kingdom, the proportion of SARS-CoV-2 infections caused by Delta rose as that caused by Alpha declined, and the secondary household infection rate associated with Delta infection was 13.6 percent compared with 9.0 percent for Alpha. In another report of a small outbreak in the United States, the household attack rate associated with the Delta variant 53%. The underlying mechanism for the increased transmissibility is uncertain. Data, some unpublished, suggest that upper respiratory viral RNA levels are higher at diagnosis and remain higher for longer with Delta variant compared with wild-type virus [10, 11].

#### 1.1.2 Omicron

This variant was first reported from Botswana and very soon thereafter from South Africa on 24 November 2021. It is quickly spreading across the world. The World Health Organization (WHO) declared Omicron to be a COVID-19 variant of concern based on preliminary evidence that it spreads quickly. he severity associated with Omicron is still unknown, but early reports indicate mild disease, at least in the younger population. Experts around the world are monitoring it closely to see if it is more likely to lead to severe illness compared to earlier variants. The Omicron variant, which is a derivative of the Pango lineage B.1.1.529, exhibiting a variation in the 21 amino acid pertaining to the spike protein with the majority residing in the receptor binding domain (RBD) (residues 319-541) compared with the original strain [12, 13].

#### 1.1.3 Alpha

This variant was first identified in the United Kingdom in late 2020 and was temporally associated with an increase in regional infections. This variant contains

more than a dozen mutations compared with other circulating strains, with several within the spike protein. It subsequently became the predominant variant in many countries, including the United States, until the emergence of the Delta variant (B.1.617.2), after which it declined in prevalence globally [14, 15].

#### 1.1.4 Beta

also known as 20H/501Y.V2, This variant, first documented in South Africa in May 2020, the Beta variant was linked with increases in hospitalizations and deaths during that country's second wave was. It is phylogenetically distinct from B.1.1.7 but shares several spike protein mutations. Surveillance data in South Africa indicate that this variant rapidly became the dominant strain there, suggesting that it also has the potential for increased transmissibility. Although it was subsequently identified in other countries, including the United States, it has since declined in prevalence globally, including in South Africa. This lineage contained a mutation in the spike protein, E484K, which has the potential to impact immunity from prior infection or vaccination, and several studies have suggested that convalescent and post-vaccination plasma do not neutralize viral constructs with Beta spike protein as well as those with wild-type spike protein [16, 17].

#### 1.1.5 Gamma

Gamma coronavirus (Gamma-CoV) is one of the four genera of coronaviruses. It is in the subfamily Orthocoronavirinae of the family Coronaviridae. They are enveloped, positivesense, single-stranded RNA viruses of zoonotic origin. Coronaviruses infect both animals and humans. While the alpha and beta genera are derived from the bat gene pool, the gamma and delta genera are derived from the avian and pig gene pools. Gamma-CoV also known as coronavirus group 3 are the avian coronaviruses. This variant was first identified in Japan in four travelers from Brazil and was later reported to account for 42 percent of 31 sequenced specimens in the Amazonas state of Brazil in December 2020. It was subsequently identified in other countries, including the United States, but has since declined in prevalence globally. It has several mutations, including three in the spike protein receptorbinding domain, N501Y, E484K, and K417T, which

raise concern about the potential for increased transmissibility and an impact on immunity [18, 19].

#### 2. Complication

Many people across the world have been hospitalized with COVID-19 following SARS-CoV-2 infection. Evidence has established that these patients have high mortality rates (26%), and up to 17% of patients admitted to hospital will require ventilator support and critical care. Several case reports, cross sectional studies, and case control studies have described the presence of nonrespiratory complications in those with COVID-19 and suggest that these are likely to be associated [20]. Understanding the possible poor outcomes complications of COVID-19 is important for patient management and provision in health care systems. For patients, information around in hospital complication rates are important for decision making about treatment, long term planning, possible resumption of normal activity and, more recently, vaccination. For health care systems, these data are vital to inform immediate (allocation preparedness of measures equipment, and staffing) and also for long term planning

of health care delivery to a population that might have incurred additional morbidity due to COVID-19. A substantial proportion of patients with COVID-19 go on to develop critical illness and require organ support. It is widely recognized that survival following critical illness is accompanied by a substantial burden of additional physical and mental health morbidity that cannot be measured by mortality outcomes [21].

As the duration of the pandemic extends and the number of patients who have recovered increases, many authors have been asking what chronic alterations COVID-19 might cause in this population. Cases of patients with persistent symptoms like dyspnea, fatigue, coughing, chest pain, myalgia and arthralgia have been reported in the literature, even among patients whose acute phase of the disease was mild. Other symptoms that have been include depression, reported cognitive disorders, headache and palpitations. The frequency with which these symptoms persist has not yet been well established, but some studies have shown that it may be high among patients who have recovered from COVID-19.

# Section two Practical Part

In this part of the study, the methodology used and the results obtained is presented.

#### 1. Methodology

The methodology used to perform this study is described in the following sections.

#### 1.2 Data Collection

Data were collated from the health center (<u>Al-Qadih</u> <u>Health Center</u>) about Pfizer vaccine and Sinopharm vaccin which include details of the study sample about the number of people those had took these vaccines in this center according to the gender, age, chronic diseases and previous infected of the virus.

#### 1.3 Materials

Data that we collected, put it in tables show study sample of Pfizer vaccine and sinopharm vaccine.

Table n.1 and n.2 show the study number according to the gender, age, chronic disease previous infection and

the number of dose they took . In theses table 'results shows percentage of female was 63% and percentage of male was 37% . Table n.3 and n.4 shows the study number according to the sinopharm vaccine . number of people they took sinopharm vaccine was little compared to Pfizer vaccine because it specific to certain group (From 18 to 50 years )

#### 2. Results

Table 1: :Study sample of pfizer vaccine representing the number of forms according to gender , age, chronic diseases

Variables	Frequency	Percentage (%)			
Gender					
men	150	(37%)			
women	256	(63%)			
Age groups					
18 years	150	(37%)			
18-50 years	150	(37%)			
Over 50 years	106	(26%)			
Chronic disease					
yes	100	(24.6%)			
No	306	(63.4%)			
Previous infection					
yes	200	(49%)			
no	206	(51%)			

Table 2: Variables associated with pfizer vaccines

Variables	First dose	Second	Third dose	P value	
		dose			
Gender		•			
men	50	40	60		
women	100	60	94	0.47	
Age groups	Age groups				
18 years	70	70	10		
18-50 years	60	60	30	<0.0001*	
Over 50	50	15	41		
Chronic disease					
yes	25	25	50		
No	150	100	56	<0.001*	

Previous infection				
yes	100	50	50	
No	75	70	16	0.001*

Table 3: Study sample of sinopharm vaccine representing the number of forms according to gender , age, chronic diseases

Variables	Frequency	Percentage (%)			
Gender					
men	7	(41%)			
women	10	(59%)			
Age groups					
18 years	3	(18%)			
18-50 years	7	(41%)			
Over 50 years	7	(41%)			
Chronic disease					
yes	4	(23.5%)			
No	13	(76.5%)			
Previous infection					
yes	12	(70.5%)			
no	5	(29.5%)			

**Table 4: Variables associated with Sinopharm vaccines** 

Variables	First dose	Second	Third dose	P value		
		dose				
Gender		·	·	•		
men	3	2	2			
women	3	5	2	0.67		
Age groups	Age groups					
18 years	1	1	1			
18-50 years	2	2	3	0.78		
Over 50	1	3	3			
Chronic disease						
yes	2	1	1			
No	6	6	1	0,57		

Previous infection				
yes	4	4	4	
No	3	1	1	0.59

#### **Discussion**

Vaccination is an effective way to curtail the burden of COVID-19 in which success depends on a high acceptance of the vaccine. However, addressing concerns among vaccine-hesitant individuals is essential to avoid failure of the immunisation programme. This study sought to assess the concerns and acceptance rates regarding the COVID-19 vaccine among Iraqi people(WHO,2021).

Vaccination is recognised as an effective way to reduce and eliminate the burden of COVID-19. However, the success of a vaccination programme depends on the willingness of the population to be vaccinated (Chakraborty etal,2020).

Public confidence in vaccination to prevent infection may be affected by perceived risks associated with vaccination. This was reflected in the hesitant group, in which 95.8% reported a fear of vaccine side effects as a reason for their refusal. With the COVID-19 vaccine and ongoing trials, the most common side effects reported were pain at the injection site, tiredness, headache, muscle pain, chills, joint pain, and fever, which typically would last for several days [WHO,2021]. These side effects were noted more common after the second dose on vaccine trials. Although severe side effects, such as anaphylaxis, may occur, these are rare [CDC,2021]. However, the risks of contracting COVID-19 infection, which may lead to severe complications, outweigh the risks of getting the vaccine.

Although the acceptance of the COVID-19 vaccine in this study was relatively high, the actual willingness to vaccinate will only be known once the vaccine arrives in iraq. As for now, the measures to prevent infection via wearing face masks, physical distancing, proper handwashing and avoidance of crowded and small confined spaces must be emphasised at all times.

#### References

- [1] World Health Organization. Director-General's remarks at the media briefing on 2019-nCoV on 11 February 2020.
- [2] Chitungo, I.; Dzobo, M.; Hlongwa, M.; Dzinamarira, T. COVID-19: Unpacking the low number of cases in Africa. Public Health Pract. 2020, 1, 100038
- [3] Nepogodiev D, Bhangu A, Glasbey JC. Mortality and pulmonary complications in patients undergoing surgery with perioperative SARS-CoV-2 infection: an international cohort study. Lancet 2020; 396: 27–38.
- [4] Paterson RW, Brown RL, Benjamin L. The emerging spectrum of COVID-19 neurology: clinical, radiological and laboratory findings. Brain 2020; 143: 3104–20.
- [5] Lu R, Zhao X, Li J. Genomic characterization and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet 2020; 395:565.
- [6] Perlman S. Another Decade, Another Coronavirus. N Engl J Med 2020; 382:760.

- [7] Hoffmann M, Kleine-Weber H, Schroeder S. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. Cell 2020; 181:271.
- [8] https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ (Accessed on Feb. 07, 2022).
- [9] Korber B, Fischer WM, Gnanakaran S. Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus. Cell 2020; 182:812
- [10] Klumpp-Thomas C, Kalish H, Hicks J. Effect of D614G Spike

  Variant on Immunoglobulin G, M, or A Spike Seroassay

  Performance. J Infect Dis 2021; 223:802.
- [11] Ong SWX, Chiew CJ, Ang LW. Clinical and virological features of SARS-CoV-2 variants of concern: a retrospective cohort study comparing B.1.1.7 (Alpha), B.1.315 (Beta), and B.1.617.2 (Delta). Clin Infect Dis 2021.
- [12] Mannar, D.; Saville, J.W.; Zhu, X.; Srivastava, S.S.; Berezuk, A.M.; Tuttle, K.S.; Marquez, A.C.; Sekirov, I.; Subramaniam, S. SARS-CoV-2 Omicron variant: Antibody evasion and cryo-EM structure of spike protein-ACE2 complex. Science 2022.
- [13] Kumar, S.; Thambiraja, T.S.; Karuppanan, K.; Subramaniam, G. Omicron and Delta variant of SARS-CoV-2: A comparative computational study of spike protein. J. Med. Virol. 2021.
- [14] <u>Davies NG</u>, <u>Jarvis CI</u>, <u>CMMID COVID-19 Working Group</u>. <u>Increased mortality in community-tested cases of SARS-CoV-2</u> lineage B.1.1.7. Nature 2021; 593:270.
- [15] Frampton D, Rampling T, Cross A. 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. Lancet Infect Dis 2021; 21:1246.

- [16] Greaney AJ, Loes AN, Crawford KHD. Comprehensive mapping of mutations in the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human plasma antibodies. Cell Host Microbe 2021; 29:463.
- [17] Xie X, Liu Y, Liu J. Neutralization of SARS-CoV-2 spike 69/70 deletion, E484K and N501Y variants by BNT162b2 vaccine-elicited sera. Nat Med 2021; 27:620.
- [18] Faria NR, Mellan TA, Whittaker C. Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. Science 2021; 372:815.
- [19] Stringhini S, Wisniak A, Piumatti G. Seroprevalence of anti-SARS-CoV-2 IgG antibodies in Geneva, Switzerland (SEROCoV-POP): a population-based study. Lancet 2020; 396:313. Han, Y.; Yang, H. The transmission and diagnosis of 2019 novel coronavirus infection disease (COVID-19): A Chinese perspective. J. Med. Virol. 2020.
- [20] Spagnuolo, G.; De Vito, D.; Rengo, S.; Tatullo, M. COVID-19 outbreak: An overview on dentistry. Int. J. 2020.
- [21] Van Doremalen, N.; Bushmaker, T.; Morris, D.H.; Holbrook, M.G.; Gamble, A.; Williamson, B.N.; Tamin, A.; Harcourt, J.L.; Thornburg, N.J.; Gerber, S.I. Aerosol and surface stability of SARS-CoV-2 as compared with SARS-CoV-1. N. Engl. J. Med. 2020
  - World Health Organization. WHO Coronavirus Disease (COVID-19)
     Dashboard. Available from: <a href="https://covid19.who.int/?gclid=EAIaIQobChMI2\_CM6eDZ6">https://covid19.who.int/?gclid=EAIaIQobChMI2\_CM6eDZ6</a>
     gIVghh9Ch3nDQm1EAAYASAAEgLqwPD\_BwE. Accessed 15 Feb 2021.

- Chakraborty C, Sharma A, Bhattacharya M, Sharma G, Lee SS.
   The 2019 novel coronavirus disease (COVID-19) pandemic: a zoonotic prospective. Asian Pac J Trop Med. 2020;13(6):242–6. <a href="https://doi.org/10.4103/1995-7645.281613">https://doi.org/10.4103/1995-7645.281613</a>.
- World Health Organization. Status of COVID-19 Vaccines within WHO EUL/PQ evaluation process.
   2021.Availablefrom: <a href="https://extranet.who.int/pqweb/sites/default/files/documents/Status\_COVID\_VAX\_20Jan2021\_v2.pdf">https://extranet.who.int/pqweb/sites/default/files/documents/Status\_COVID\_VAX\_20Jan2021\_v2.pdf</a>. Accessed 23 Jan 2021.
- Centers for Disease Control and Prevention. What to Expect after Getting a COVID-19 Vaccine. 2021.