POST-VACCINATION SARS-COV-2 INFECTIONS AMONG VACCINATED INDIVIDUALS TESTED AT THE UNAM MOLECULAR DIAGNOSTIC LABORATORY, JUNE 2021- MAY 2022

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ABSTRACT

Background: Coronavirus disease 2019 (COVID-19) is a respiratory disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). To curb the disease, COVID-19 vaccines were rolled out. However, because vaccines are not 100% protective against the virus, post-vaccination SARS-CoV-2 infections (PVSI) do occur. Thus, the study aimed to analyze the occurrence of post-vaccination SARS-CoV-2 infections among vaccinated individuals tested at the UNAM Molecular Diagnostic Laboratory (UNAM-MDL) from June 2021 to May 2022.

Methods: We conducted a retrospective cohort study of SARS-CoV-2 immunized individuals tested at the laboratory between June 2021 and May 2022. COVID-19 Case Investigation Forms (CIFs) were reviewed, and data from 5389 individuals were collected based on inclusion and exclusion criteria. Using Statistical Package for the Social Sciences (SPSS) v.26, descriptive and inferential analysis was performed; this included logistic regression, Kaplan-Meier survival curve, 95% confidence interval, and p-value < 0.05 statistical significance. The study was conducted in compliance with ethical principles.

Results: The post-vaccination SARS-CoV-2 infection rate among vaccinated individuals was 99.8 per 1,000 population with a median age of 40 years and a mortality rate of 1.1 per 1,000. The majority of individuals in the study were males, with 4016 (74.5%). Most individuals were vaccinated with Sinopharm 2399 (44.5%), asymptomatic and had no comorbidities. Only 10 (2%) had sequenced data of the SARS-CoV-2 variants with three variants: Beta, Delta and Omicron. PVSI were characterized as early post-vaccination 52 (9.7%), partially vaccinated 201(39%) and fully vaccinated 276 (51.3%). The survival distribution in the study was statistically significant ($p < 0.05$). Age, number of doses and sex were shown to be significant factors associated with PVSI.

Conclusion: The study showed that PVSI occurred mostly among fully vaccinated individuals, although without complications. Although the study's goal was to further knowledge of SARS-CoV-2 infections following immunization, the significance of maintaining high vaccination rates in Namibia is highlighted by our results. To protect against severe COVID-19, it is critical to raise community health awareness and actively encourage public vaccination uptake.

Keywords: COVID-19, vaccination, variants, post-vaccination infections, Namibia.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS AND ACRONYMS

CDC	Centers for Disease Control and Prevention
CIFs	Case Investigation Forms
COVID-19	Coronavirus 2019
FDA	Food and Drug Administration
HCoVs	Human Coronaviruses
HCW/P	Healthcare Worker/ Practitioner/Professional
MERS-CoV	Middle Eastern Respiratory Syndrome Coronavirus
MoHSS	Ministry of Health and Social Services
PVSI/C	Post-vaccination SARS-CoV-2 Infection/ Case
RT-PCR	Reverse Transcriptase Polymerase Chain Reaction
SARS-CoV	Severe Acute Respiratory Syndrome Coronavirus
SARS-CoV-2	Severe Acute Respiratory Syndrome Coronavirus 2
SITREP	Situational Report
SPSS	Statistical Package for Social Sciences
UNAM-MDL	University of Namibia Molecular Diagnostic Laboratory
VBM	Variants Being Monitored
VOHC	Variants of High Consequence
VOC	Variants of Concern
VOI	Variants of Interest
WGS	Whole Genome Sequencing
WHO	World Health Organization

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Thank you all so much, May God bless you all.

DEDICATION

This thesis is dedicated to God my strength and source of wisdom, knowledge and understanding. I also dedicate this work to my family, who have been my pillar from the very beginning of this journey and to my sister, my greatest support system and hype man. The enormous influence you have had on my life is demonstrated by this commitment. It serves as both a little mark of my appreciation and a tribute to your significant achievements. I want you to know that I will always be grateful to you and that your efforts have not gone forgotten or unappreciated. This is also dedicated to my aunty, my second mother; Aunty Onye, may her soul rest in peace.

DECLARATIONS

I Nkemdilim V. Ndozi-Okia, hereby declare that this study is a true reflection of my research and that this work, or part thereof has not been, submitted for a degree in any other institution of higher education.

I Nkemdilim V. Ndozi-Okia, grant the University of Namibia the right to reproduce this thesis in whole or in part, in any manner or format, which the University of Namibia may deem fit, for any person or institution requiring it for study and research; provided that the University of Namibia shall waive this right if the whole thesis is being published in a manner satisfactory to the University.

Nkemdilim V. Ndozi-Okia	[signature]	April 2024
Name of Student	Signature	Date

CHAPTER 1: INTRODUCTION TO THE STUDY

1.1 INTRODUCTION

This chapter presents the background of the study, the problem statement, the aim of the study, specific objectives, the significance of the study, and the definition of critical concepts.

1.2 BACKGROUND OF THE STUDY

Coronavirus disease 2019 (COVID-19) is a novel pandemic that is a respiratory disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). SARS-CoV-2 can spread through both direct means (droplet and human-to-human transmission, through coughing and sneezing) and indirect contact (contaminated objects) (1). COVID-19 symptoms commonly recognized are fever, dry cough, myalgia, and shortness of breath (2). To mitigate the spread and impact of SAR-CoV-2, prevention strategies have been implemented. These strategies can be broadly categorized into non-pharmaceutical interventions (NPIs) and pharmaceutical interventions. The NPIs approaches include quarantine, social distancing, the use of face masks, washing of hands, and the use of hand sanitizer (3–5). Meanwhile, pharmaceutical interventions include vaccination administration, antiviral medications, antibody testing and the use of antiseptics and disinfectants (5).

On March 11th, 2020, the World Health Organization (WHO) declared COVID-19 a global pandemic (6). Namibia reported its first case of COVID-19 on the 13th of March 2020, which were imported cases (7). Globally, more than 772 million cases have been confirmed with COVID-19, and over 6.9 million have died as of 19th November 2023 (8,9). Africa has a cumulative total of over 9.5 million (1%) cases and over 175 thousand (3%) deaths (9). A cumulative total of 172 208 COVID-19 confirmed cases and 4104 deaths have been reported in Namibia as of 03rd December 2023 (10).

As part of global efforts to curb the spread of COVID-19, vaccines have been developed and distributed to multiple countries over a short period. Namibia commenced its vaccination program in March 2021 (11). As of 03rd December 2023, 598 552 of the total targeted population (1 779 271) have been vaccinated with the first dose, while 519 712 (29.2 %) are fully vaccinated (10).

Early studies and clinical trials have indicated that COVID-19 vaccines protect people against severe illness (12). Subsequently, if the body is later exposed to those disease-causing microorganisms after vaccination, it is ready to kill them immediately, preventing illness (13). However, because COVID-19 vaccines are not 100% protective, post-vaccination SARS-CoV-2 infections (PVSI) may occur (14). Post-vaccination SARS-CoV-2 infections comparing multiple vaccines in one population analysis are limited (15). Although research suggests that COVID-19 vaccines protect against severe illness and hospitalization, post-vaccination SARS-CoV-2 infection can occur because they are not 100% effective (16).

The Centers for Disease Control and Prevention (CDC) continuously gathers information and data on vaccine breakthroughs and continues to aggressively study vaccine safety and effectiveness against new and emerging variations of COVID-19 (16). Thus, to investigate SARS-CoV-2 infections among fully vaccinated persons and monitor trends in case characteristics and SARS-CoV-2 variants identified from persons with these infections (17). Studies on post-vaccination SARS-CoV-2 infections among healthcare workers, skilled nursing facility residents, and staff members have been conducted in the United States (18–

20). Additionally, studies were conducted in this regard in other countries, such as Israel and the United Kingdom (15,21). However, none has been conducted in Namibia.

Secondly, concerns regarding the emergence of SARS-CoV-2 variants, including those first identified in the United Kingdom (Alpha), South Africa (Beta), Brazil (Gamma), California (Epsilon), India (Delta), and recently identified in South Africa and Botswana (Omicron) have dampened hopes for a quick end to COVID-19 pandemic through vaccination (18). During the third and fourth wave of COVID-19 (June and December 2021, respectively), an observation of the presence of COVID-19 has been reported among individuals who have received one or both vaccine doses tested at the UNAM Molecular Diagnostic Laboratory (UNAM-MDL). However, there is no data to substantiate this. Subsequently, the increase in the number of COVID-19 cases due to the emergence of the new variants also shows some increase in post-vaccination infections. Although a few studies on PVSI globally exist, none have been conducted in Namibia.

1.3 STATEMENT OF PROBLEM

In Namibia, the emergence of Post-vaccination SARS-CoV-2 Cases (PVSCs) has raised concerns, as fully vaccinated individuals have been reported to contract COVID-19 (13,15,20). Despite the high level of vaccination efficacy, nothing is known about the prevalence of post-vaccination infections among the fully vaccinated population in Namibia. The available statistics on COVID-19 in the country primarily focus on new infections and re-infections, with no information on post-vaccination infections (SITREP No. 992) (22). As of July 9th, 2023, the cumulative total of re-infections was recorded at 3279, but the statistics on post-vaccination infections remain scarce.

The absence of comprehensive data on post-vaccination infections may have created blind spots in assessing the true impact of the virus, particularly in the context of circulating variants. Furthermore, vaccine hesitancy may be influenced by the lack of knowledge about post-vaccination infections. To address these gaps, this study aimed to provide a thorough analysis of post-vaccination infections, focusing on individuals who tested for SARS-CoV-2 through laboratory-confirmed PCR tests after receiving at least one dose of a SARS-CoV-2 vaccine.

Given that other countries have conducted studies on post-vaccination infections, the lack of equivalent research in Namibia emphasizes the importance of this investigation. The study intended to shed information on the efficiency of SARS-CoV-2 vaccinations in the face of emerging variants. Breakthrough infections have been observed despite the high level of vaccine efficacy, warranting a closer examination of the characteristics of these infections and the variants responsible.

Understanding SARS-CoV-2 breakthrough infections is crucial for improving public health strategies, particularly during vaccination campaigns. With an emphasis on the Khomas Region, this study aimed to provide valuable insights into the patterns of post-vaccination infections in Namibia. Additionally, this study aimed to inform evidence-based decision-making, mitigate vaccine hesitancy, and enhance the overall effectiveness of the country's COVID-19 response, while providing insights into patterns and variations linked to breakthrough infections. In summary, the study addressed the urgent problem of post-vaccination SARS-CoV-2 cases in Namibia, highlighting the necessity of thorough data on breakthrough infections to comprehend their impact and public health implications.

1.4 THE AIM OF THE STUDY

This study aimed to analyze the occurrence of post-vaccination SARS-COV-2 infections among vaccinated individuals tested at the UNAM Molecular Diagnostic Laboratory (UNAM-MDL) from June 2021 to May 2022.

1.5 OBJECTIVES OF THE STUDY

The objectives of the study were:

- To determine post-vaccination SARS-CoV-2 infection rate among vaccinated individuals tested at the UNAM-MDL from June 2021 to May 2022.
- To determine the variants causing these infections and characterize post-vaccination SARS-CoV-2 infections among vaccinated individuals tested at the UNAM-MDL from June 2021 to May 2022.
- To determine the factors associated with post-vaccination SARS-CoV-2 infections among vaccinated individuals tested at the UNAM-MDL from June 2021 to May 2022.

1.6 HYPOTHESIS

These hypotheses serve as a base for assessing the study's objectives, allowing statistical analysis to determine the significance of observed patterns in post-vaccination SARS-CoV-2 infections, and influencing factors in the analyzed group. There is no significant association between demographic factors and the occurrence of post-vaccination SARS-CoV-2 infections among individuals tested at the UNAM-MDL from June 2021 to May 2022.

1.7 SIGNIFICANCE OF THE STUDY

The rationale for this study is based on the critical need to address the existing gaps in understanding post-vaccination infections of COVID-19 in Namibia and globally. The significance of this research lies in its potential to significantly contribute to the global knowledge base on COVID-19 infections, particularly in terms of emerging variants and vaccination efficacy.

As the COVID-19 pandemic continues to pose a substantial worldwide public health threat vaccination campaigns have emerged as an essential strategy for mitigating its serious health effects. However, since the end of 2020, vaccination coverage has increased globally, raising questions about the efficacy of vaccinations, especially concerning newly developing variations like delta and omicron. The uncertainty has thus prompted reluctance to receive vaccinations, emphasizing the pressing need for thorough research on post-vaccination infections.

The reason for this study is to fill a gap in the post-vaccination literature on COVID-19, particularly in the Namibian context. The research seeks to provide significant insight into the occurrence of COVID-19 post-vaccination by analyzing instances of Post-vaccination SARS-CoV-2 cases (PVSCs) and describing breakthrough infections. These findings will not only contribute to knowledge of the disease but also guide Namibia's public health initiatives.

Furthermore, the study's significance is highlighted by the potential to inform the Ministry of Health and Social Services (Epidemiology division) and other stakeholders about post-vaccination infections in Namibia. The research findings will enhance our knowledge of the disease, guide evidence-based decision-making, and assist in the implementation of public health strategies to counter emerging variants of COVID-19, as the world scientific community continues to struggle with the virus's evolving nature.

1.8 DEFINITION OF KEY CONCEPTS

COVID-19 - when the SARS-CoV-2 virus infects people and results in illness. Coronavirus disease is abbreviated as COVID. Although the pandemic began in 2020, the sickness was initially discovered in 2019, as indicated by the number “19” (23)

Post-vaccination SARS-CoV-2 infection – is the detection of SARS-CoV-2 RNA or antigen in a respiratory specimen collected from a person 14 days or more after receiving prescribed vaccine doses (17,21).

Vaccine Breakthrough infection - is when one contracts a virus, bacteria, or other germs after vaccination (24).

Variants - A variant has one or more mutations distinguishing it from other SARS-CoV-2 virus variants.

1.9 CHAPTER LAYOUT

This thesis was presented in the following chapters:

Chapter 1: This chapter comprises the introduction and background of the study. The rationale for the researcher to conduct the study, as well as the objectives and significance of the study, are covered in this chapter.

Chapter 2: This chapter covers the literature review.

Chapter 3: In this chapter, the research methodology, which includes the research design, is described, data collection methods, the procedure followed, and ethical considerations.

Chapter 4: In this chapter, the results are presented.

Chapter 5. In this chapter, the findings of the study are discussed. Various similar findings by other researchers are compared in this chapter, as literature is integrated into the discussions to serve as additional evidence to the findings.

Chapter 6. The study's conclusions, recommendations, and limitations are also found in this study.

1.10 SUMMARY

This chapter provided introductory information, background, location of the study, and why the study was conducted. What coronavirus is, a picture of the global and local public health impact of coronavirus was given. The study's aim, significance, and objectives, as well as the outline of all the study chapters, were covered in this chapter.

CHAPTER 2: LITERATURE REVIEW

2.1 INTRODUCTION

Many complex challenges, such as new illnesses, confront the globe that no single discipline, institution, or country can address alone. Thus, this chapter provides an overview of the literature relevant to the field of study. A literature review aims to provide foundation knowledge on a topic. It establishes existing knowledge and ideas that other researchers have done on a particular topic and identifies methods relevant to the study under consideration. The literature review of this study focused on the epidemiology of COVID-19, transmission, prevention, treatment, and vaccination, as well as on post-vaccination SARS-CoV-2 infection studies.

2.2 CORONAVIRUS EPIDEMIOLOGY

Coronaviruses are enveloped viruses with a sizeable plus-strand RNA genome that belongs to the Coronaviridae family (25). The Coronaviridae family comprises two subfamilies: Coronavirinae and Torovirinae (26). The subfamily Coronavirinae is divided into four genera: Alphacoronavirus (α), Betacoronavirus (β), Gammacoronavirus (γ), and Deltacoronavirus (δ) (27). The genus Alphacoronavirus includes viruses previously in group 1. In contrast, Betacoronavirus includes viruses previously in group 2, most notably severe acute respiratory syndrome coronavirus (SARS-CoV), Middle Eastern respiratory syndrome coronavirus (MERS-CoV), Gammacoronavirus which includes viruses previously in group 3, and Deltacoronavirus includes several newly described avian and swine viruses (27).

Generally, α and β infect mammals and humans, whereas γ and δ genera mainly infect birds (28). Coronaviruses, specifically the genus Betacoronavirus in the family Coronaviridae, are a subset of respiratory viruses that offer a constant pandemic threat (29). Coronaviruses are not novel infectious pathogens. In 1937, the first coronavirus was isolated from chickens, whereas human coronaviruses were initially first identified in the mid-1960s (28).

Human coronaviruses (HCoVs), including SARS-CoV and MERS-CoV, are zoonotic pathogens originating in wild animals (30). Coronaviruses have an enormous RNA genome and cause a diverse range of multisystem diseases in birds and mammals, including upper respiratory infections in chickens, enteritis in pigs and cows, and potentially fatal human respiratory disease (31).

Coronavirinae members are widely distributed among mammals, causing only minor respiratory or gastrointestinal illnesses (26). Only seven human coronaviruses have been identified so far, which include human coronavirus 229E (HCoV-229E), OC43 (HCoV-OC43), NL63 (HCoV-NL63), HKU1 (HCoV-HKU1), SARS-CoV, and MERS-CoV as well as SARS-CoV-2 (28). Several viruses are responsible for common colds and self-limiting upper respiratory infections (31).

Additionally, at least three have caused widespread fatal outbreaks, including the highly pathogenic severe acute respiratory syndrome coronavirus (SARS-CoV), Middle Eastern respiratory syndrome coronavirus (MERS-CoV), and, most recently, SARS-CoV-2 (31). Figure 2.1 below shows animals being the origin of human coronaviruses and how these viruses are transmitted to humans (32).

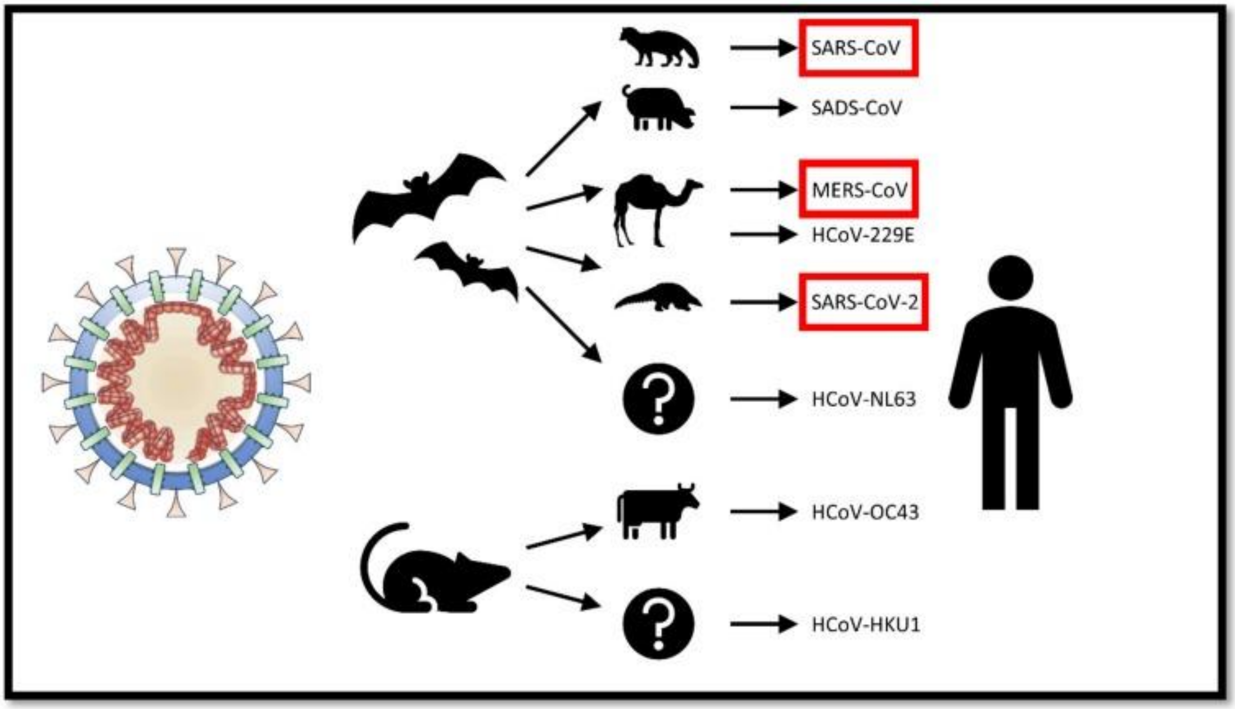

Figure 2.1: Prospective animal origins of coronaviruses transmitted to humans (32).

Human coronaviruses have animal origins. The SARS-CoV and MERS-CoV were spread from bats to people by dromedary camels and civet cats, respectively. Pangolins illegally sold in Chinese markets were likely how the 2019 SARS-CoV-2 virus infected people (33,34).

2.2.1 SARS-CoV

Severe acute respiratory syndrome (SARS) is caused by coronavirus infection, SARS-associated coronavirus (SARS-CoV) (35). SARS originated in Southern China in late 2002-2023 and caused an outbreak linked to infection with a new CoV (SARS-CoV). The outbreak was spread globally and transmitted by unsuspecting travellers (36). SARS typically begins with flu-like symptoms, such as fever, chills, muscle aches, headache, and sometimes diarrhoea (36).

The disease had high mortality (10%) and morbidity (35). The SARS-CoV outbreak was contained through quarantine (37). Like all RNA viruses, SARS-CoV replication is associated with genomic and antigenic variation (38). Therefore, the outbreak heightened curiosity about CoV replication, distribution, evolution, transmission, and pathogenesis (26).

2.2.2 MERS-CoV

Another coronavirus (unrelated to SARS-CoV) was isolated in 2014 in connection with a severe respiratory disease outbreak in the Middle East. MERS is a viral respiratory disease caused by the Middle East respiratory syndrome coronavirus (MERS-CoV), discovered in Saudi Arabia in 2012 (39). MERS-CoV is a zoonotic virus which spreads from animals to humans (40).

The clinical spectrum of MERS-CoV infection varies from asymptomatic to mild respiratory symptoms, severe acute respiratory illness, and death (39). Symptoms of MERS include fever, cough, and shortness of breath (41). Pneumonia is a common illness; however, MERS patients may not constantly develop it (41). About 35-40 % of MERS cases reported to WHO have led to fatalities (39). This virus is still causing sporadic cases of severe respiratory illness (26).

2.2.3 SARS-CoV-2

SARS-CoV-2 is the seventh member of the coronavirus family that can infect humans, following the emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) (28). On January 30, 2020, the World Health Organization declared the novel coronavirus pneumonia epidemic caused by SARS-CoV-2 a public health emergency of international concern, and on March 11, 2020, it was declared a global pandemic (42,43).

Coronavirus disease 2019 (COVID-19) was named after the new coronavirus disease caused by SARS-CoV-2 and was discovered in Wuhan, China, in December 2019 (44). It is very contagious and has spread rapidly over the world. It is called COVID-19 because it was discovered in 2019, and SARS-CoV-2 due to its similarities to SARS-CoV of 2003. More than 70% genetic similarity exists between the coronavirus SARS-CoV-2, which caused COVID-19 and SARS-CoV-1, the cause of the SARS outbreak in 2003 (45).

SARS-CoV-2 is round or oval in shape, with a diameter of 60–140 nm and a crown-shaped appearance under electron microscopy (28). The SARS-CoV-2 protein-coding genes share a sequence with SARS-CoV and MERS-CoV that is 79.5% and 51% identical, respectively (1). The coronavirus genome encodes five protein structures: the spike (S), membrane (M), envelope (E) glycoproteins, hemagglutinin esterase (HE), and nucleocapsid (N) (46). Figure 2. 2 shows the genome of the coronavirus.

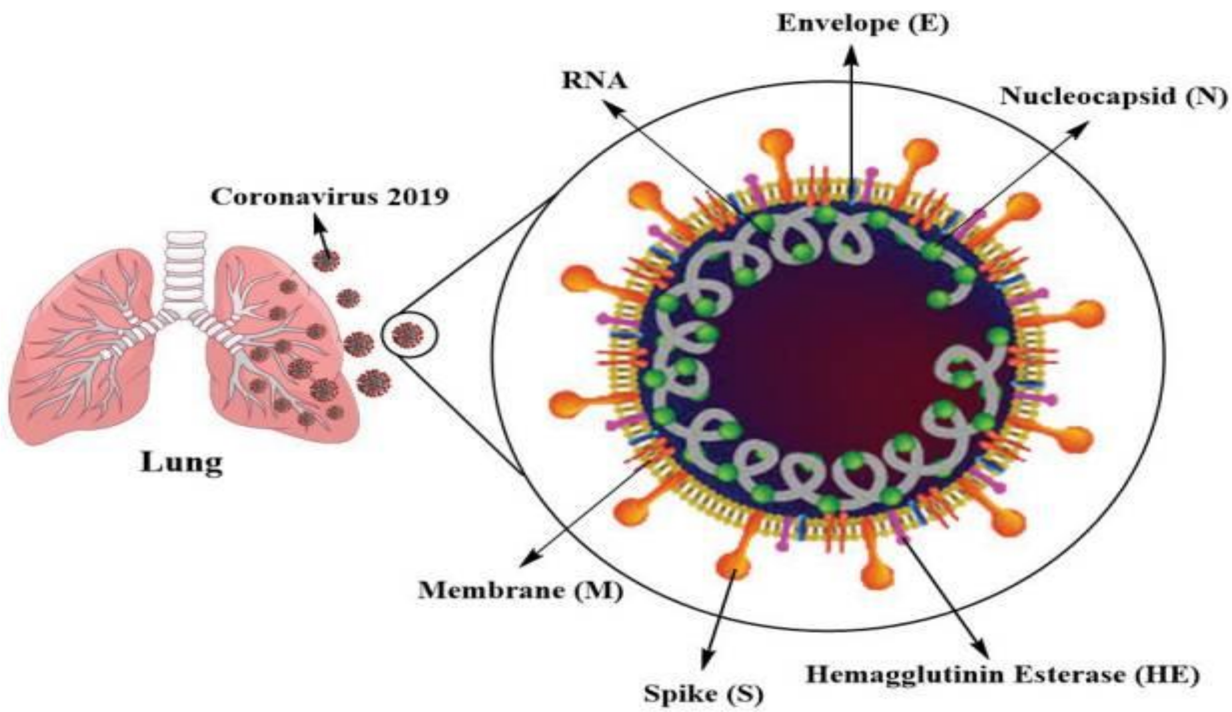

Figure 2. 2: The coronavirus genome with protein structure (46).

2.3 CLINICAL PRESENTATION

The most commonly recognized symptoms are fever, dry cough, sore throat and shortness of breath (1,7,44,47). Although around 20–25% of patients with MERS-CoV or SARS-CoV infection had diarrhoea, COVID-19 patients rarely exhibit gastrointestinal symptoms (1). Other symptoms may include confusion, chest pain, vomiting, headache, and nausea (48). The estimated range for SARS-CoV-2 infection is 14 days (32).

2.4 TRANSMISSION

SARS-CoV-2 can spread directly (through droplets and human-to-human transmission) as well as indirectly (through touch) (contaminated objects and airborne contagion) (1). The human pulmonary system is prone to infections caused by contact-based inoculation of infectious material in droplets through the eyes, nose, or mouth, as well as airborne transmission (29). Although it had been suggested that the COVID-19 patients in China may have eaten infected animals or may have visited a seafood market, it was discovered that human-to-human transmission of the virus was also possible through coughing, sneezing, and the spread of respiratory droplets or aerosols into the upper respiratory tract and lungs through inhalation (1).

COVID-19 can be contracted if a person comes into direct contact with mucous membranes such as the eyes, nose, or mouth after touching a surface contaminated with SARS-CoV-2 (49). Both symptomatic and asymptomatic individuals can also spread SARS-CoV-2. The reported contagion rates from a symptomatic infection vary depending on location and the effectiveness of infection control measures (1). The spread of SARS-CoV-2 from asymptomatic people (or people in the incubation period) has also been reported (1,49). As a result, improvements in rapid and sensitive diagnostic methods for detecting infected individuals are necessary.

2.5 DIAGNOSIS

The standard test to diagnose acute COVID-19 is reverse transcriptase polymerase chain reaction (RT-PCR) (50). Real-time RT-PCR is commonly used in diagnostic virology. The test is performed using nasopharyngeal swab samples. SARS-CoV-2 identification relies on virus blood culture and high-throughput whole genome sequencing (46). In a public health emergency, competent diagnostic laboratories can rely on this dependable technology (RT-PCR) to integrate new diagnostic tests into their routine services before pre-formulated assays become available (51).

2.6 VARIANTS

Viruses like SARS-CoV-2 evolve as changes in the genetic code (caused by genetic mutations or viral recombination) occur during genome replication (52). A viral genome (genetic code) variant contains one or more mutations. A variant has one or more mutations distinguishing it from other SARS-CoV-2 virus variants (52). A lineage is a group of viruses with a common ancestor (52). SARS-CoV-2 has several lineages, all of which cause the disease. COVID-19 Variants are classified as variants of interest (VOI), variants of concern (VOC), variants of high consequence (VOHC), and variants being monitored (VBM). Currently, variants of concern or the monitored variants include but are not limited to Table 2. 1 (52).

Table 2. 1: *Lists of Variants and Pango lineage of SARS-CoV-2.*

WHO Label	**Pango lineage**
Alpha	B.1.1.7 and Q lineages
Beta	B.1.351 and descendent lineages
Gamma	P.1 and descendent lineages
Delta	B.1.617.2 and descendant lineages

Epsilon	B.1.427 and B.1.429
Kappa	B.1.617.1
Omicron	B.1.1.529 and descendant lineages

2.7 TREATMENT

According to the WHO, prevention, transmission control, isolation, education, and treatment of afflicted individuals are essential for managing contagious diseases like COVID-19 (43). There is no specific treatment for COVID-19. Patients with COVID-19 infection are primarily treated symptomatically (1).

2.8 PREVENTION

These prevention strategies can be broadly categorized into non-pharmaceutical interventions (NPIs) and pharmaceutical interventions. These methods reduce transmission from both inhalations of the virus and deposition of the virus on exposed mucous membranes (1).

2.8.1 NON-PHARMACEUTICAL INTERVENTION

The NPIs recommended methods that have been demonstrated to be effective in preventing the transmission of SARS-CoV-2. NPIs are divided into personal, community and environmental. NPIs include (3–5): Physical distancing, and maintaining a safe distance from others to reduce transmission of the virus. Using face masks, and wearing a face mask indoors or particularly in crowded settings to prevent respiratory droplets spread. Washing of hands, and the use of hand sanitizer. Adequate ventilation in indoor spaces, avoiding crowded spaces and quarantine of individuals who may have been exposed to the virus, while isolating those confirmed positive to prevent further spread. Practising good hygiene and keeping the environment clean is also essential in curbing the spread of the virus.

2.8.2 PHARMACEUTICAL INTERVENTION

Pharmaceutical interventions include administering vaccines to individuals to provide immunity against COVID-19. Antiviral medications to treat those with severe COVID-19 symptoms. Antibody testing to identify individuals who may have developed SARS-CoV-2 immunity before vaccination or after and use of antiseptic and disinfectants (5).

2.8.3 VACCINATION

Vaccination is a simple, safe, and efficient technique to protect one from deadly diseases before infection. It strengthens the immune system by utilizing the body's defences to create resistance to specific pathogens (13). The induction of protective immunity in a large enough proportion of the population may be required for disease control or elimination. Immunization regimens that induce long-term immunity are the best way to do this (53). In many parts of the world, significant immunization efforts started employing newly authorized vaccines against SARS-CoV-2(54).

In addition to the preventive measures implemented, such as remaining at least one meter away from others, covering a cough or sneeze with the elbow, constant washing of hands, and wearing a mask to curb the spread of COVID-19, vaccines were developed at an incredible speed. Several safe and effective vaccines are available to protect people from becoming very ill or dying due to COVID-19 (55).

WHO has assessed that the following vaccinations against COVID-19 have passed the relevant safety and effectiveness requirements as of June 03, 2021: AstraZeneca/Oxford vaccine, Johnson and Johnson, Moderna, Pfizer, Sinopharm, Sinovac, and COVAXIN (55,56). The vaccines currently administered in Namibia include Sinopharm. AstraZeneca, Johnson and Johnson, Pfizer, and Sputnik V (22). In Namibia, all the currently available vaccines are administered to people 18 years and older. In comparison, those 12 to 17 years are only administered Pfizer, and no vaccine is available for those younger than 12 (22).

As mass vaccination campaigns are ongoing globally, randomized clinical studies using vaccinations demonstrated efficacies of 94 percent (%) to 95% in preventing COVID-19 (54). In order studies, the vaccinations showed 52 % to 95% effectiveness against symptomatic illness in clinical trials 14 days after the first dose, and 7 days after the second dose, 95% efficacy was achieved (18). Conversely, breakthrough infections are bound to happen because no vaccine is perfectly adequate.

2.9 POST-VACCINATION INFECTIONS

Post-vaccination SARS-CoV-2 infection, also known as a breakthrough infection, is the detection of SARS-CoV-2 RNA or antigen in a respiratory specimen collected from a person either 14 days or more after receiving all prescribed doses of a Food and Drug Administration (FDA) approved COVID-19 vaccine (17). Breakthrough infections can occur mainly among older, immunocompromised people with specific comorbidities (16). When a vaccinated host is exposed to an infectious person, whether a breakthrough infection occurs relies on whether the immune response present during exposure is sufficient to abort or quickly control the infection (16). COVID-19 can be transmitted by people who have been infected but were vaccinated (16).

Though no comprehensive theory focuses only on post-vaccination infections, concepts from immunology, virology, and vaccine research inform our knowledge of these infections. The conceptual framework for post-vaccination SARS-CoV-2 infection to guide this study literature review is outlined in Figure 2. 3 as follows:

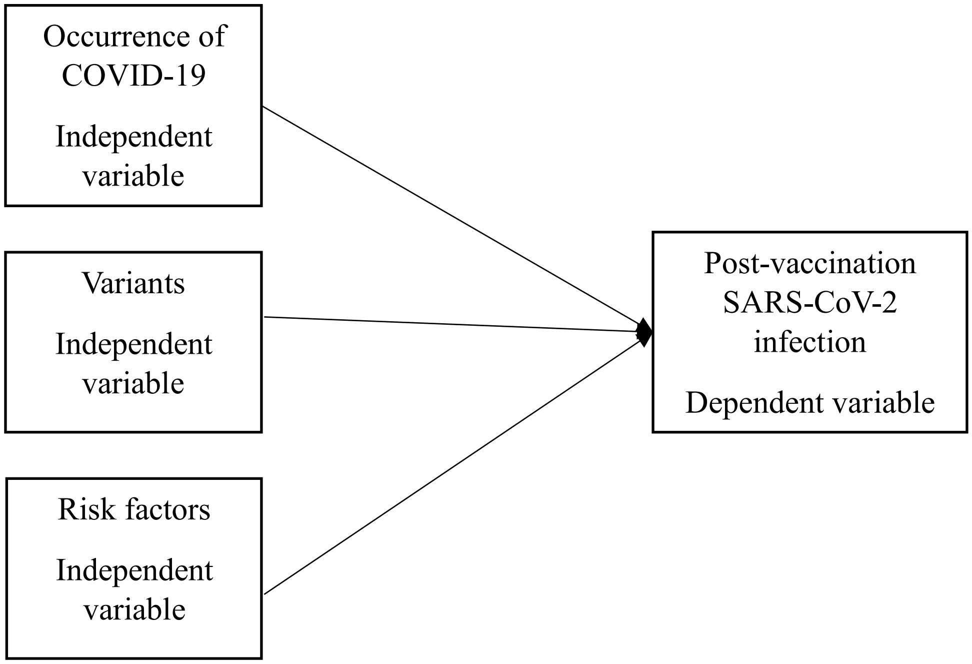

Figure 2. 3: Conceptual framework for this study's literature review

A study by Nisha B et al. (57) determined the incidence/rate of post-vaccination infections among healthcare workers (HCWs) and the contributing factors. The study showed that the incidence of postvaccination was 66.5 per 1000 HCWs, and partial vaccination status was one of the determinants of postvaccination.

Butt et al (58), a study that describes the rate of SARS-CoV-2 breakthrough infection in persons who have been fully vaccinated found that a low rate of infection was among those who were fully vaccinated and age associated with confirmed infections.

A retrospective cohort study conducted among healthcare professionals (HCPs) vaccinated against COVID-19 by Perrella et al (59), prospectively assessed the occurrence of post-vaccination infections. The study found that only 1% of HCPs tested positive, and that HCPs had a lower risk of contracting COVID-19 after receiving at least one vaccine dose, the risk also decreased with age.

Jacobson et al. (18), a study that aimed to define and characterize post-vaccine SARS-CoV-2 infections in HCP as well as determine the role of variants causing PVSCs, found that Post-vaccination SARS-CoV-2 infections occurred in <1% of vaccinated HCP, with cases defined as either unvaccinated, partially, or fully vaccinated. This study suggested that continued post-vaccine cases with variant surveillance are imperative to anticipate and control future surges of infections.

Other studies on post-vaccine infections have been conducted in Europe, America, and Asia; however, these studies were mostly limited to healthcare workers, skilled nursing facilities, gold miners, app users, etc. (15,19–21,60). None has been conducted in Africa, Namibia, or at a COVID-19 testing facility.

Another study by Kustin et al. (61) matched case-control showed that vaccine breakthrough infections occurred within two specific periods with an increased proportion of variants of concerns. People fully vaccinated with Pfizer (BNT162b2) had a higher proportion of Beta (B.1.351) variant 7-14 days after the second dose. Furthermore, a higher proportion of the B.1.1.7 (Alpha) variant was found among those partially vaccinated 14 days after the first dose and 6 days after the second.

An exploratory retrospective case-control study by Peter et al. (62) aimed to determine the risk factors (demographic and clinical) associated with SARS-CoV-2 breakthrough infections in fully vaccinated individuals and compare patient characteristics in breakthrough infections caused by Alpha and Delta variants. This study found that breakthrough infections are rare and occur early after vaccination, with more than 50% of cases within 70 to 80 days post-full vaccination. Patient characteristics showed a median age of 45 years (ranging between 32 and 64 years), and females (52.6%) had slightly more breakthrough infections than males. The study also found that breakthrough infection was common in people vaccinated with the Pfizer/BioNTech vaccine, individuals with chronic disease, or healthcare workers.

The same study by Butt et al (58), found relatively few factors associated with infection after vaccination, which included increasing age, and increased risk of infection. Increasing age is a well-recognized risk factor for SARS-CoV-2 infection and it is also associated with more severe disease and poorer clinical outcomes.

Meanwhile, a report on the COVID-19 vaccine breakthrough reported by the CDC United States in May 2021 (17) showed that about 10 262 SARS-CoV-2 vaccine breakthrough infections were reported by 46 states, which were only 0.01% of the confirmed cases (approximately 101 million) as at that time. Among these cases, 6,446 (63%) occurred in females; the median patient age was 58. Among these cases, 356 (64%) SARS-CoV-2 variants of concern were identified, including Alpha (B.1.1.7-199; 56%), Epsilon (B.1.427/B.1.429-(28; 8%), (88; 25%) respectively), Gamma (P.1 (28; 8%), and Beta (B.1.351-13; 4%).

However, there was a limitation in this report: the breakthrough infections were likely to be a significant undercount of all SARS-CoV-2 infections among people who have been fully vaccinated, and it was based on only the facilities that reported breakthrough infections as the national surveillance system relied on passive and voluntary reporting. Therefore, this study would be the first of its kind in Namibia, conducted at a COVID-19 testing facility, and will include other individuals who are not just healthcare workers but random persons who were tested for COVID-19.

2.10 SUMMARY

This chapter gave an overview of coronaviruses, epidemiology, transmission, prevention, diagnosis, and variants. It also discussed vaccination and post-vaccination infections, highlighting this study's importance.

CHAPTER 3: METHODOLOGY

3.1 INTRODUCTION

This chapter outlines the research design and methodology employed to achieve the study's objectives. It includes the research design, study population, inclusion and exclusion criteria, sampling method, data collection, reliability, validity, and data analysis. Additionally, in this chapter, ethical considerations and the rights of the participants are also discussed.

3.2 RESEARCH METHOD AND DESIGN

This is a retrospective cohort study design. In a retrospective cohort study, the exposure and outcomes have already happened (63). This cohort study investigated the reason behind SARS-CoV-2 infections among individuals tested between June 2021- May 2022. The exposure factor is vaccination against SARS-CoV-2;(exposure categories; early vaccinated, partially vaccinated, fully vaccinated). The exposure variable is used to assess the vaccination of study participants and to compare the risk of SARS-CoV-2 infection among different vaccination groups. The Outcome is the occurrence of post-vaccination infections, the outcome measures the effectiveness of the vaccine in preventing SARS-CoV-2 and assesses whether there are differences in infection rates or severity among different vaccination groups the outcome is COVID-19. Data was collected from UNAM-MDL records and reviewed.

3.3 STUDY SETTING

The study was conducted at the Molecular Diagnostic Laboratory of the University of Namibia located in Windhoek, Namibia's capital city, located in the central part of the country, approximately 645 square kilometres in size, in the Khomas region. The region consists of only one (1) district (Windhoek District) with numerous private facilities and two (2) major referral hospitals. Additionally, the region includes one (1) health centre, ten (10) urban clinics, two (2) rural clinics, one hundred ninety-nine (199) outreach points, and numerous laboratories. According to the 2011 Population and Housing Census (64), Windhoek has a population of 325 858, with a growth rate of 3.5% and a gender distribution of 50%. The laboratory was established during the COVID-19 pandemic and tests for COVID-19, as well as one of two laboratories in Namibia that sequences SARS-CoV-2 variants.

3.4 STUDY POPULATION

The population for the current study was 9,261 immunized individuals tested at the UNAM Molecular Diagnostic Laboratory (UNAM-MDL) from June 2021 until May 2022 who had their COVID-19 documents (case investigation forms) reviewed during that time frame. The study cohort was divided into two groups; Group A and Group B.

Group A: Individuals infected after COVID-19 vaccination named "COVID-19 Positive".

Group B: Individuals uninfected after COVID-19 vaccination named "COVID-19 Negative.

Case definition:

SARS-CoV-2 immunized individuals – are any persons who have received any of the recommended vaccinations for COVID-19 (65,66). For this study cohort, SARS-CoV-2 immunized individuals are defined as documentations of any persons who have received at least one dose of any COVID-19 recommended vaccinations.

RT-PCR test– reverse transcriptase polymerase chain reaction is the gold standard (laboratory confirmation) for COVID diagnosis (50). The study cohort was selected based on the standard RT-PCR test.

Confirmed case – is a person with a positive RT-PCR SARS-CoV-2 infection regardless of clinical signs and symptoms (7). This is also referred to as "COVID-19 Positives" (Group A).

Negative case – is a negative RT-PCR test. These are the "COVID-19 Negatives" (Group B).

3.4.1 INCLUSION CRITERIA

This study included all vaccinated individuals for SARS-CoV-2 with or without COVID-19 by RT-PCR tested between June 2021 and May 2022. Documents with detailed information such as vaccine status, type, date of vaccination, and number of doses were eligible and included in the study.

3.4.2 EXCLUSION CRITERIA

These were documents of unvaccinated individuals, documents of vaccinated individuals without/unknown vaccination status, and incomplete forms (e.g., missing vaccine type, dose, date).

Figure 3.1 below illustrates the flow of the inclusion and exclusion criteria of the study and how the documents reviewed were sampled.

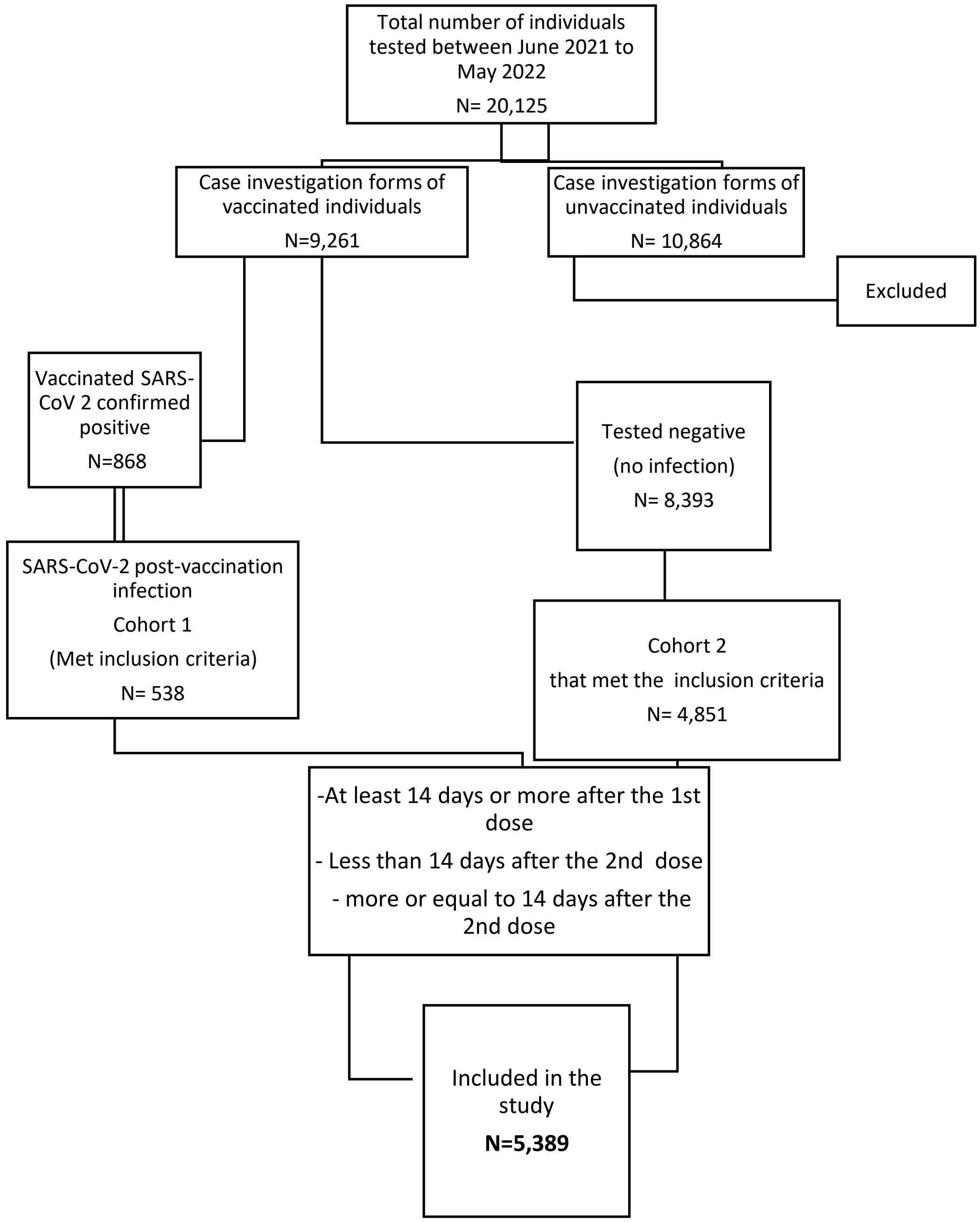

Figure 3.1*:* The flow diagram summarizes the study population and sampling strategy.

3.5 SAMPLE AND SAMPLING METHOD

To determine the estimated sample size for this study with a known population size of 9,261, the sample size formula for a known population was used (67,68).

$$n = \frac{N \times Z^2 \times p(1-p)}{(N-1)d^2 + Z^2 \times p(1-p)}$$

Where:

N = 9621 (population size)

Z = z-score corresponding to the desired level of confidence (1.96 at 95% confidence level)

p = population proportion (set conservatively at 0.5, it should provide the maximum sample size)

d = desired margin of error (5% = 0.05)

Hence, the sample size calculated was:

$$n = \frac{9261 \times (1.96)^2 \times 0.5(1-0.5)}{(9261-1) \times (0.05)^2 + 1.96^2 \times 0.5(1-0.5)}$$

$$n = \frac{9261 \times 3.8416 \times 0.25}{9260 \times 0.0025 + 3.8416 \times 0.25}$$

$$n = \frac{8894.26}{23.15 + 0.9604}$$

$$n = \frac{8894.26}{24.1104}$$

n = 368.90

n ≈ 369

The estimated sample size for the study was approximately 369. However, to improve the study's statistical power, the researcher increased the sample size. All the cases that fulfilled the inclusion criteria were included in the study. The study utilized a cohort of SARS-CoV-2 vaccinated individuals tested at the UNAM-MDL from June 2021 to May 2022 which amounted to a 5,389 study sample size. The sample size was increased by 54% to improve the study's statistical power using simple random sampling.

3.6 DATA COLLECTION PROCEDURE

3.6.1 DATA COLLECTION INSTRUMENTS

The researcher developed a data collection tool based on the Namibian COVID-19 case investigation forms and referred other studies (18,54,59,69) for comprehensive guidance for conducting post-vaccination infection study. The tool was developed to collect data on the following variables: age, sex, vaccine date, types, doses, signs and symptoms, comorbidities, the reason for testing, region, previous COVID-19 positive test, and variants.

3.6.2 DATA COLLECTION METHOD

Case investigation forms containing immunization data gathered between June 2021 and May 2022 from the laboratory were reviewed for consideration for the study. The forms were assessed for inclusion, and only those that met the study criteria were considered for data extraction. Data such as; age, sex, vaccine date, types, doses, signs and symptoms, comorbidities, the reason for testing, region, previous COVID-19 positive test, and variants, and variables information were extracted for the study data collection tool. Data was collected by the researcher and three student data clerks in the laboratory while maintaining confidentiality. Positive samples with cycle threshold (Ct) values ≤ 30 with already sequenced data were used to determine the variants. Whole-

Genome Sequencing (WGS) was done with the residual RNA extract available using iseq100, Artic protocol (Artic v3 kit). An Excel spreadsheet was used as the data-capturing tool.

3.7 DATA ANALYSIS

Statistical analysis was performed using Statistical Package for the Social Sciences (SPSS) (version 26). Descriptive and inferential statistics were used in the analysis of data. Descriptive statistics were used to cross-tabulate different variables. The distribution of variables was displayed using frequencies and percentages. For inferential statistics, multivariate binary logistic regression analysis was used to explore variables independently associated with post-vaccine infections at a 95% confidence interval and p-value < 0.05 statistical significance. The Kaplan-Meier survival curve was used to analyze time to event and compare the two groups of subjects.

3.8 RELIABILITY AND VALIDITY

3.8.1 RELIABILITY

The reliability of an instrument is the constancy of its measurements (70). It is the degree to which a measurement or experiment produces the same results when repeated (71). Using the Ministry of Health and Social Services COVID-19 data collection tool (Case Investigation Forms), a data-capturing tool was created. The algorithm for selecting study participants was circulated for expert input and also tested using pilot testing which was done to determine the consistency and accuracy of the tools. The pilot was conducted by sharing the data capturing tool with a few data clerks with samples of information to be collected to determine if the results obtained were similar and if there were any issues or if the tool required any adjustments. The tool was adjusted according to feedback received from experts and data clerks. The consistency of the results demonstrated that the tool was dependable and produced repeatable measurements.

3.8.2 VALIDITY

Validity is typically defined as the extent to which an instrument measures what it is intended to measure (70). In this study, validity was achieved by cross-checking, inspecting, and scrutinizing the information entered in the extraction tool to ensure that the data collected were accurate, relevant, and complete. The tool was pretested by the researcher with the minimum sample size to confirm whether it could collect data to meet the study objectives.

3.9 ETHICAL CONSIDERATION

Ethical clearance was obtained from the University of Namibia research committee and permission from the Ministry of Health and Social Services was granted to review CIFs. Permission to undertake the study at the laboratory was requested from the UNAM molecular diagnostic laboratory. Following all appropriate research reporting guidelines and ethical principles.

3.9.1 RESPECT FOR PERSONS (Informed Consent)

To recognize people as autonomous beings with the ability to make their own decisions is necessary (72). People with restricted autonomy should be given extra safety, even if it means keeping them away from potentially harmful activities. The type of possible injury and the chance of benefit would determine how much protection would be provided. To implement this principle, subjects must go through an informed consent process wherein they are given all the information (in an understandable format) required to enable them to decide whether or not to voluntarily participate in a study (72). Hence for this study, a request for a waiver of informed consent was required as this is a retrospective study.

3.9.2 BENEFICENCE

Action taken for the benefit of others is referred to as beneficence (73). This necessitates a comparison of prospective risks (potential harm) to anticipated benefits (promotion of health, well-being, or welfare) (72). Researchers must design procedures that optimize the advantages and minimize any potential risks associated with their work. The general public must also be aware of the potential advantages and disadvantages of novel medical, psychological, and social processes and procedures (72). To ensure the well-being of subjects, risks and benefits were assessed by the study design and methods; hence, only relevant data and methods to obtain answers were collected and analyzed.

3.9.3 CONFIDENTIALITY AND ANONYMITY

Ethical principles like confidentiality and anonymity are meant to safeguard human subjects' privacy when gathering, examining, and disseminating data (74). The term "confidentiality" describes how to extract or change any identifying or personally identifiable information that participants have given from the data (74). By contrast, anonymity describes the process of gathering data devoid of any personally identifiable information. In quantitative research, anonymity is typically preserved (74). For privacy compliance, personally identifiable data were anonymized so that they were not linked to other data by anyone else, and each participant was assigned a unique identifier.

3.9.4 PRINCIPLES OF JUSTICE

This principle promotes equitable treatment of all parties and an equitable division of the risks and rewards associated with the research (72). It prohibits taking advantage of those who are susceptible to manipulation due to their circumstances, such as the economically underprivileged or those with low cognitive function. Additionally, the researcher must confirm that the volunteer recruiting process is impartial and fair and that the possible subject pool is suitable for the study (72). The case investigation forms for those vaccinated individuals were selected because they met the requirements for the study, not merely because they were available.

3.10 SUMMARY

This chapter highlighted the research methodology used for the study. The relevant aspects of the study design, study population, sampling method, data collection, and data analysis were explained. Also discussed were the ethical considerations to ensure validity and reliability.

CHAPTER 4: RESULTS

4.1 INTRODUCTION

This section will present, examine, and interpret results using the research approach and data collection process described in the previous chapter. The case investigation forms of vaccinated COVID-19 patients tested at the laboratory between June 2021 and May 2022 served as the foundation for this research. Based on literature that was tailored to the study, the researcher created a checklist. The COVID-19 case investigation forms were used to guide the development of the checklist, which was created to gather information on age, sex, vaccination date, type, dose, signs and symptoms, comorbidities, the purpose of testing, region, prior COVID-19 positive test, and variants. This chapter presents the research findings of the study. The analysis was aimed at obtaining information to provide answers to the research objectives.

4.2 OBJECTIVE 1

The study included 5389 vaccinated individuals tested at UNAM-MDL between June 2021 and May 2022. Demographic characteristics (Table 4.1), showed that about 4851 (90%) tested negative for COVID-19, whereas 538 (10%) tested positive for the disease. The mean age was 40 years (14-89 years old), and the logistic regression analysis indicated that the odds associated with age and being COVID-19 positive was Exp(B)= 1.008, with a p-value of 0.065 which was not statistically significant. Furthermore, the mean number of days of infection after vaccination was 109 days.

Table 4.1: Demographics characteristics of vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory, June 2021 – May 2022.

VARIABLES	Group A N(%)	Group B N(%)	TOTAL N(%)	P-VALUE
Total	538 (10.0)	4851 (90.0)	5389	
Gender				
Male	307 (7.6)	3079 (92.4)	4016 (74.5)	<0.001
Female	231 (16.8)40	1142 (83.2)	1373 (25.5)	
Age (years), mean (SD)	41.3 (13)	40.9 (9.9)	40.5 (10.2)	0.065
Age groups				
≤ 19	7 (25.9)	20 (74.1)	27 (0.5)	0.701
20-29	101 (14.8)	580 (85.2)	681 (12.6)	0.010
30-39	157 (8.2)	1749 (91.8)	1906 (35.4)	<0.001
40-49	139 (8.0)	1593 (92.0)	1732 (32.1)	<0.001
50-59	89 (10.5)	755 (89.5)	844 (15.7)	<0.001
60 Above	45 (22.6)	154 (77.4)	199 (3.7)	<0.001
Reason for testing				
General	67 (5.2)	1228 (94.8)	1295 (24)	0.461
Deceased	1 (16.7)	5 (83.3)	6 (0.1)	.
Health Worker	35 (45.5)	42 (54.5)	77 (1.4)	<0.001
Hospitalization	17 (43.6)	22 (56.4)	39 (0.7)	<0.001
Travel	31 (6.3)	462 (93.7)	493 (9.1)	<0.001
Quarantine	140 (5.4)	2447 (94.6)	2587 (48.0)	0.531
Active Case Search	60 (41.4)	85 (58.6)	145 (2.7)	<0.001
Contact	69 (42.6)	93 (57.4)	162 (3.0)	<0.001
Expanded Target Testing	29 (7.3)	379 (92.7)	399 (7.4)	0.620
Suspected new case	82 (45.8)	97 (54.2)	179 (3.3)	<0.001
Suspected re-infection	3 (42.9)	4 (57.1)	7 (0.1)	<0.001

Table 4.1 showed that the post-vaccination cohort was predominantly male at 4016 (75%) with an attack rate of 7.6%, while females were 1373 (25.5%), with an attack rate of 16.8%, gender was found to be statistically significant with a p-value < 0.001. Males had a PVSI rate of 57.1/100 compared to females (42.9/100). Similarly, age groups had a p-value <0.001 with a Chi-Square (χ^2) of 74.9. Most PVSIs were among those aged between 30 (35.4%) and 49 (32.1%) years old with a p-value < 0.001.

The laboratory tested patients from all 14 regions in Namibia with the highest number of patients tested from Khomas, with 4138 (76.8%), while Kavango West had the least, with two (0.04%).

Among the cohort studied, 1453 (27%) had prior documentation of SARS-CoV-2 infections either before or after receiving their vaccinations and reported experiencing newly developing symptoms at the time of their positive post-vaccination test. The reason for testing was mostly for quarantine 2587 (48%), while deceased was the least 6 (0.1%) giving a mortality rate of 1.1 per 1000 vaccinated population.

Table 4. 2 outlines the distribution of the most common comorbidities among the two groups with the p-values indicating the significance of the association between each comorbidity and the groups. Although most individuals tested had no comorbidities 4608 (85.5%), those with comorbidities were 781 (14.5%) with $\chi^2 = 22.89$ ($p<0.001$), the p-value which is less than 0.05 and considered to be statistically significant.

Notably, there was more than one comorbidity per individual. Hypertension had the highest number, with 465 (37.5%), followed by cardiovascular disease with 268 (21.6%), and diabetes mellitus with 163 (13.2%). Other comorbidities experienced included cancer, glaucoma, epilepsy, allergies, and hypothyroidism. Between the groups, hypertension, HIV and cardiovascular disease had p-values < 0.05 which were considered statistically significant compared to the other comorbid with p-values > 0.05.

Table 4. 2: Comorbidities among vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory, June 2021-May 2022.

Comorbidities N(%)	**Group A 195 (15)**	**Group B 1044 (84.2)**	**Total 1239 (23)**	**P-value**
Hypertension	78 (40.0)	387 (37.1)	465 (37.5)	<0.001
Diabetes Mellitus	21 (10.7)	142 (13.6)	163 (13.2)	0.331
Obesity	6 (3.1)	53 (5.1)	59 (4.7)	0.748
HIV	13 (6.7)	41 (3.9)	54 (4.4)	0.003
Cholesterol	7 (3.6)	62 (5.9)	69 (5.5)	0.793
Asthma	7 (3.6)	49 (4.7)	56 (4.5)	0.657
Cardiovascular disease	47 (24.1)	221 (21.2)	268 (21.6)	<0.001
Others	16 (8.2)	89 (8.5)	105 (8.5)	0.696

The post-vaccination infection rate was 99.8 per 1,000 vaccinated population. The distribution of COVID-19 results among the study cohort by type of vaccine and doses including the p-values indicating the significance of association is presented in Table 4. 3. Moreover, most were vaccinated with Sinopharm 2399 (44.5%) doses, while Sputnik was the least with 2 (0.1%) doses. The post-vaccination infection rate varied by the COVID-19 vaccine received. The highest PSVI rate occurred among Sinopharm vaccine recipients (44.4 per 100), followed by AstraZeneca at 34.8. Comparing the proportion of the two groups, only Pfizer showed a statistically significant (p=0.05) difference, while, none of the other vaccines individually showed a statistically significant (p>0.05) difference.

Each individual in the study received at least one dose of vaccine, Table 4. 3 shows the number of doses by the two groups. Majority had received two doses 3265 (60.6%), while only 353 (6.6%)

had received three (booster) doses. The first dose had a PVSI rate of 13.7/100, while the second and third doses had 8.1 and 7.9/100 respectively. Similarly, there was no significant difference (p> 0.05) in the proportion of group A compared to group B among those who received at least one dose.

Table 4. 3: Number of doses according to vaccine types among the vaccinated cohort.

Variables **N (%)**	**Positive** **538 (10)**	**Negative** **4851 (90)**	**Total** **5389**	**P-value**
Type of vaccine				
AstraZeneca	187 (34.8)	1669 (34.4)	1856 (34.4)	0.122
Johnson & Johnson	84 (15.6)	613 (12.6)	697 (12.9)	0.161
Moderna	1(0.19)	4 (0.08)	5 (0.09)	0.442
Pfizer	23 (4.3)	379 (7.8)	402 (7.45)	0.050
Sinopharm	239 (44.4)	2160 (44.5)	2399 (44.5)	0.120
Sinovac (CoronaVac)	3 (0.6)	25 (0.5)	28 (0.5)	0.169
Sputnik	1 (0.19)	1(0.02)	2 (0.04)	-
Number of Doses				
One dose	243 (13.7)	1528 (86.3)	1771 (32.9)	0.427
Two dose	267 (8.2)	2998 (91.8)	3265 (60.5)	0.851
Booster dose	28 (7.9)	325 (92.1)	353 (6.6)	0.171

Furthermore, most individuals tested were asymptomatic 4634 (86.0%); however, this does not mean that being asymptomatic means no signs or symptoms. Figure 4.1 below shows the common symptoms among the study participants. Individuals experienced more than one sign and symptom; the majority had cough 494 (26.1%), sore throat 300 (15.9%), while other symptoms

362 (19.2%) included but not limited to running nose, headache, chest and back pains, dizziness etc., giving a statistically significant p-value<0.001, and Exp (14.6, 95%CI 11.9-17.7).

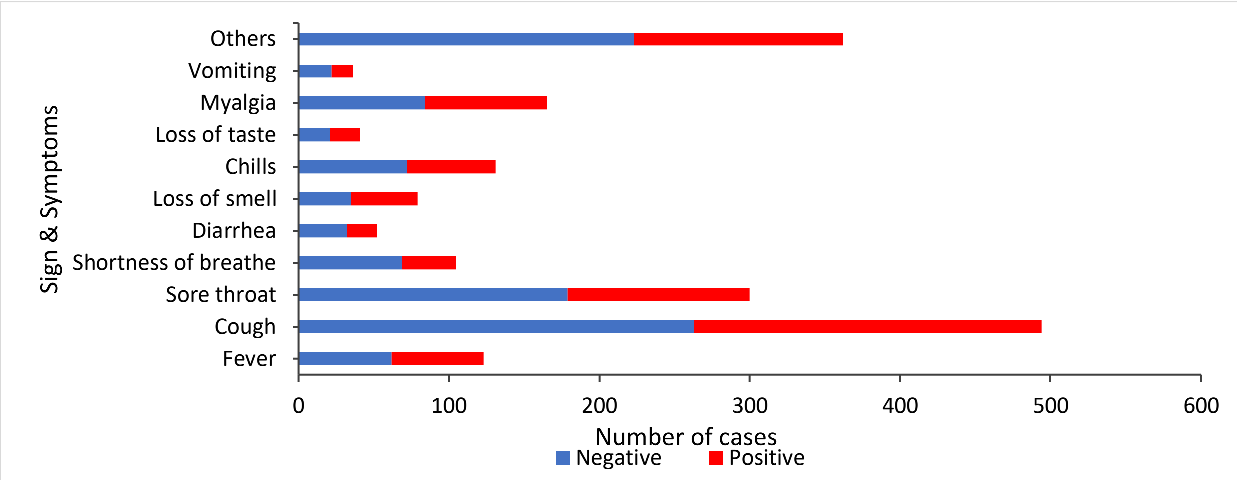

Figure 4.1:Signs & symptoms among vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory, June 2021-May 2022

4.3 OBJECTIVE 2

Figure 4. 2 below shows, that the three dormant variants were Beta, Delta, and Omicron. Among the COVID-19 positive cases, only 10 (1%) had variants sequenced during the study period. Omicron was the variant with the most sequenced 7 (70%). As variants have lineages, the lineages of the three variants were determined of which AY.4 was found for delta, B.1.351 for Beta and BA.1, 2 and 4 for Omicron.

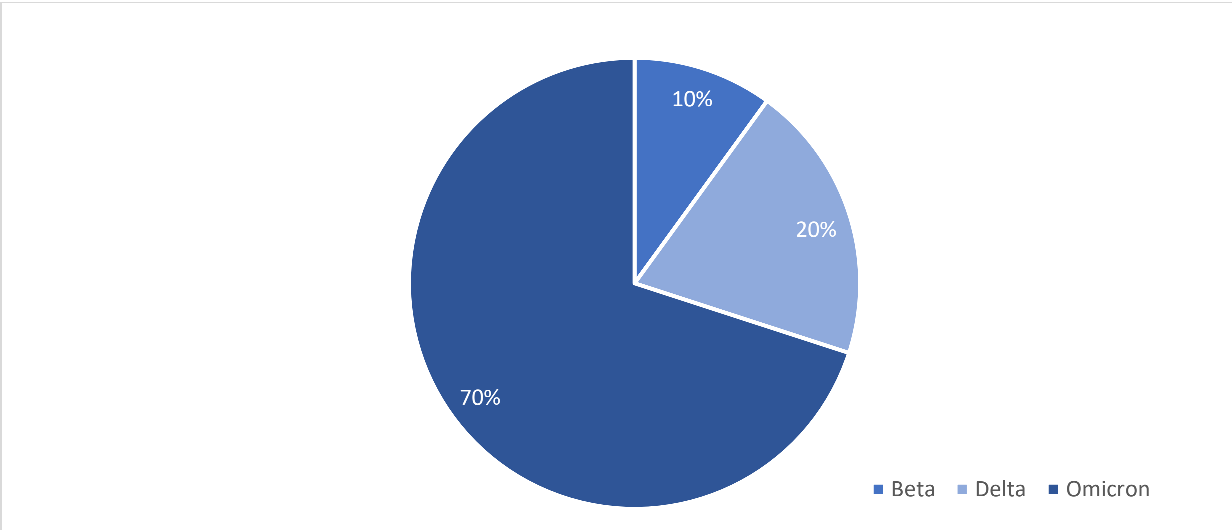

Figure 4. 2: Variants of vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory, June 2021-May 2022.

Subsequently, the characterization of post-vaccination was categorized into three: early post-vaccination, which was a positive test ≤ days after one (1st) dose, while partially vaccinated (positive test > 14 days after the first dose and ≤ 14 days after the second dose), and fully vaccinated (positive test > 14 days after a second dose or three doses) as shown in Figure 4. 3.

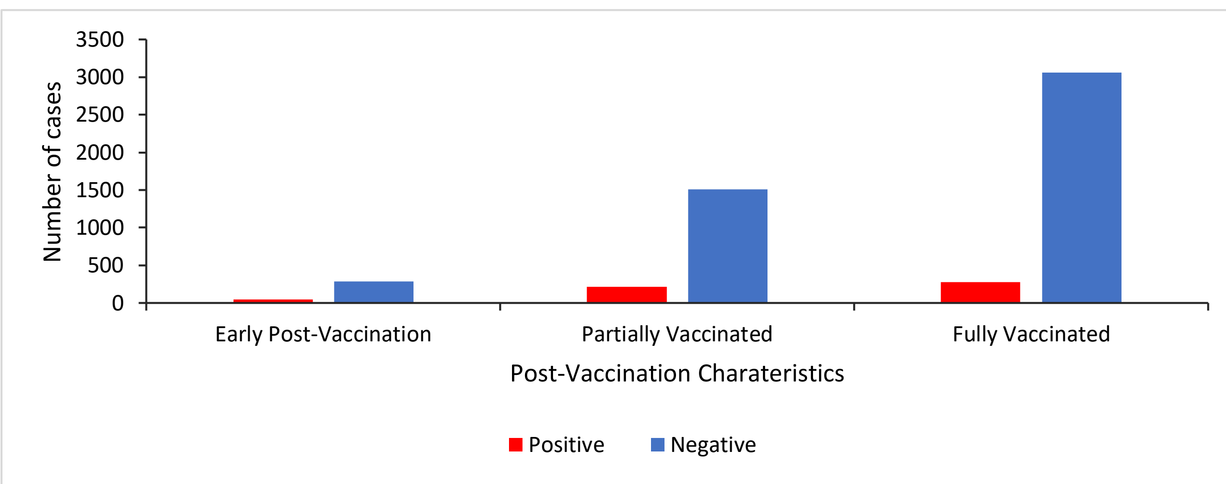

Figure 4. 3:Characteristics of Post Vaccination Infection among vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory June 2021-May 2022.

The majority of (n = 276, 51.3%) PVSIs occurred when fully vaccinated, while (n = 210, 39.0%) occurred when partially vaccinated, and (n=52, 9.7%) occurred early post-vaccination, Table 4.4 with only 17 (3.2%) requiring hospitalization. PVSI gave a Chi-Square (χ^2) = 2.852, p-value = 0.240, which is not statistically significant.

At least 100 (18.6%) of PVSIs received their vaccines between October 2020 and May 2021, with the most significant number in May with 55 (55%).

Notably, most positive tests in PVSIs occurred in December 2021; however, most were fully vaccinated, meaning ≥ 14 days from their second to their third vaccine dose, especially among those who had received the Sinopharm vaccine. Nevertheless, few cases occurred ≤ 14 days (on days 7 and 14) after vaccination, mainly among those who had received Sinopharm and AstraZeneca.

Table 4.4 below shows the post-vaccination characteristics based on age, sex, variants and lineages. The findings are highlighted in the table, showing that being fully vaccinated was dominant in the study.

Table 4.4: Post Vaccination Infection characteristics among vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory June 2021-May 2022.

Variable	**Total n = 538**	**Early Post Vaccination n = 52**	**Partially Vaccinated n = 210**	**Fully Vaccinated n = 276**
Age, mean (SD), years	41.2 (12.9)	42.5 (13.5)	43.2 (15.3)	39.6 (10.6)
Sex				
Female	231 (42.9%)	26 (50.0%)	96 (45.7%)	109 (39.5%)
Male	307 (57.1%)	26 (50.0%)	114 (54.3%)	167 (60.5%)
Variants[a]				
Beta	1 (0.2%)	0 (0.0%)	1 (0.5%)	0 (0.0%)
Delta	2 (0.4%)	0 (0.0%)	1 (0.5%)	1 (0.4%)
Omicron	7 (1.3%)	0 (0.0%)	1 (0.5%)	6 (2.2%)
PANGO lineage[b]				
AY.4	1 (0.2%)	0 (0.0%)	1 (0.5%)	0 (0.0%)
BA.1	1 (0.2%)	0 (0.0%)	1 (0.5%)	0 (0.0%)
B.1.351	1 (0.2%)	0 (0.0%)	1 (0.5%)	0 (0.0%)
B.1.617.2-like	1 (0.2%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
BA.1.18	2 (0.4%)	0 (0.0%)	0 (0.0%)	2 (0.7%)
BA.2	2 (0.4%)	0 (0.0%)	0 (0.0%)	2 (0.7%)
BA.4	2 (0.4%)	0 (0.0%)	0 (0.0%)	2 (0.7%)
No VoC/I	528 (98.1%)	52 (100%)	207 (98.6%)	269 (97.5%)

Abbreviation: SD, standard deviation
[a]Among the samples already sequenced in the laboratory only 10 in the study sample were sequenced, hence the result.
[b]PANGO lineage as determined by next-generation sequencing (NGS) was available for n= 10 samples according to the variants sequenced.

The Kaplan-Meier survival curve compared the two subjects based on the post-vaccination characteristics; see Figure 4. 4 below. The plot (Figure 4. 4) showed that when fully vaccinated, the chances of survival are higher than those partially vaccinated or early post-vaccination.

It was found that being early vaccinated was associated with a decrease of 0.023 in log odds of getting COVID-19, but it was not statistically significant (p=0.898) (95% CI, 69.2%-138.2%). Similarly, being partially vaccinated was associated with a decrease of log (OR)= 0.424, (95% CI, 38.9%-110.2%), although it is not statistically significant at the standard $p< 0.05$ ($p = 0.111$), there may be a trend implying an effect.

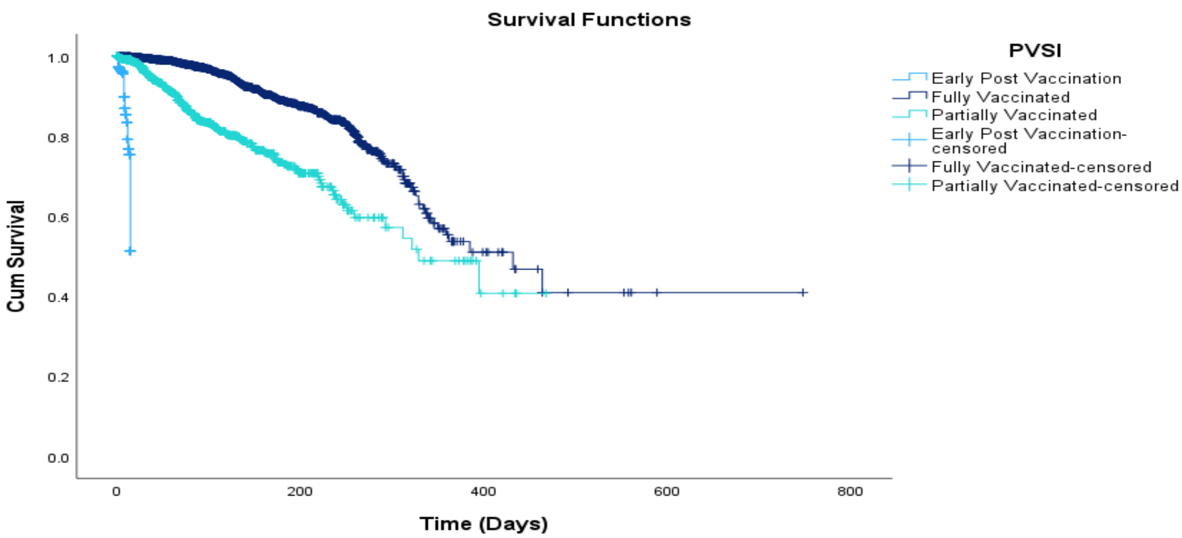

Figure 4. 4: Kaplan-Meier survival curve of post-vaccination infections among those vaccinated at UNAM-MDL June 2021-May 2022.

The Cox Regression function was applied to deliver more accurate estimates of survival probabilities and cumulative hazard than the Kaplan-Meier calculation, assuming that the assumptions of Cox regression were met. Cox regression, often known as proportional hazards regression, examines how different variables affect how long an event takes to occur. Analysis showed that 89.2% of the cases censored resulted in negative after vaccination, and 10.0% resulted in the event (positive).

4.4 OBJECTIVE 3

The first step in figuring out the causes of post-vaccination SARS-CoV-2 infections in those who had received vaccinations was to comprehend and interpret the findings from the plot of cumulative survival functions for the various groups (Early vaccinated, partially vaccinated, and fully vaccinated).

A multivariable logistic regression analysis was performed to explore variables that were independently associated with PVSIs.

Table 4. 5 below breaks down the different variables that may be associated with PVSI, segmented by age groups, number of doses, reason for testing, symptomatic, and comorbidities among the three post-vaccination categories. A multivariable logistic regression analysis was performed to explore variables that were independently associated with PVSIs.

Table 4. 5: Factors associated with post-vaccination infection among vaccinated individuals tested at UNAM Molecular Diagnostic Laboratory June 2021-May 2022.

Variable	**Total n = 538**	**Early Post Vaccination n = 52**	**Partially Vaccinated n = 210**	**Fully Vaccinated n = 276**	**OR**	**95% CI**	**p-value**
Age group	n (%)						
≤ 19	7 (1.3)	1 (1.9)	4 (1.9)	2 (0.7)	1.036	0.351-3.053	0.949
20-29	101 (18.8)	9 (17.3)	42 (20)	50 (18.1)	1.028	0.643-1.644	0.907
30-39	157 (29.2)	12 (23.1)	51 (24.3)	94 (34.1)	1.253	0.803-1.956	0.321
40-49	139 (25.8)	12 (23.1)	48 (22.9)	79 (28.6)	1.297	0.830-2.026	0.253
50-59	89 (16.5)	9 (17.3)	36 (13.0)	44 (15.9)	1.097	0.685-1.758	0.700
60 Above	45 (8.4)	3 (5.8)	32 (15.2)	10 (3.6)	.	.	.
Doses							
First dose	243 (45.2%)	46 (88.5%)	197 (93.8%)	0 (0.0%)	0.728	0.475-1.116	0.145
Second dose	267 (49.6%)	0 (0.0%)	16 (7.6%)	251 (90.9%)	0.966	0.635-1.470	0.872
Third dose	28 (5.2%)	0 (0.0%)	0 (0.0%)	28 (10.1%)	0.874	0.721-1.059	0.170
Reason for testing							
Hospitalization	17 (3.2%)	5 (9.6%)	11 (5.2%)	1 (0.4%)	0.67	0.032-0.140	<0.001
Health Worker	35 (6.5%)	2 (3.8%)	14 (6.7%)	19 (6.9%)	0.61	0.034-0.109	<0.001
Deceased	5 (0.9%)	0 (0.0%)	4 (1.9%)	1 (0.4%)	-	-	-
Suspected Re-infection	3 (0.6%)	0 (0.0%)	2 (0.4%)	1 (0.4%)	0.62	0.13-0.291	<0.001
Symptomatic	318 (59.1%)	28 (53.8)	133 (63.3%)	157 (56.9)	15.02 7	12.244-18.443	<0.001
Comorbidities	117 (21.7%)	8 (15.4%)	54 (25.7%)	55 (19.9%)	0.866	0.671-1.118	0.270

Comorbidities represent the simultaneous presence of two or more diseases in a patient. Among group A, 117 (50.4%) were post-vaccination infections. (Figure 4. 5) shows the common comorbidities among post-vaccination SARS-CoV-2 infections, displaying underlying diseases such as hypertension, diabetes mellitus, obesity, HIV, cholesterol, asthma, cardiovascular disease and others (which include allergies, cancer, pregnancy, etc.).

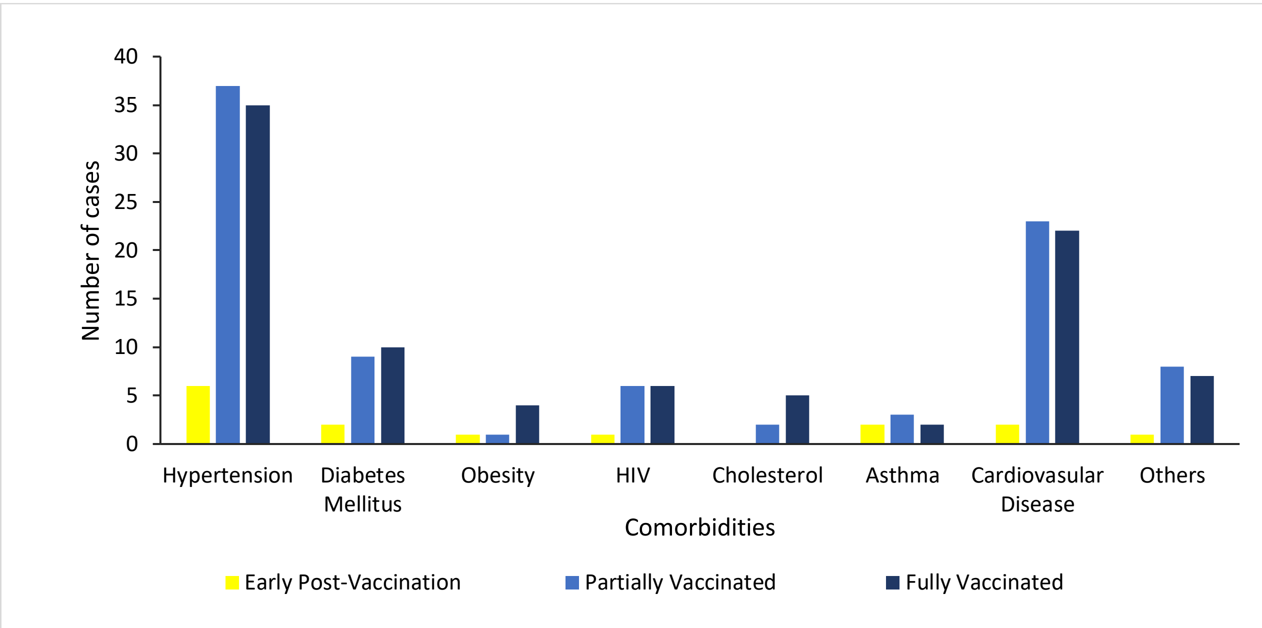

Figure 4. 5: Categorized Post-vaccination infection by comorbidities tested at UNAM-MDL June 2021-May 2022.

The leading comorbidity was hypertension (66.7%) with a statistically significant odds ratio of the outcome (Exp(B) = 1.476, p = 0.043) (95%CI,101.2%-215.4%), followed by cardiovascular diseases (40.2%), and obesity being the least (5.1%), these variables p-value was >0.005, which did not show a significant impact on the odds, unlike HIV with a significantly higher odds ratio (Exp(B) = 2.533, p = 0.004), (95% CI, 135.4%-473.9%). HIV was shown to be statistically significant with a p-value <0.05.

The variants were associated with the number of doses by the vaccine type administered, which can be seen in the graph below (Figure 4.6). The figure showed that the most sequenced cases had at least two doses of Sinopharm. In this study, the variants were not associated with variables such as age, gender, or symptomatic infection.

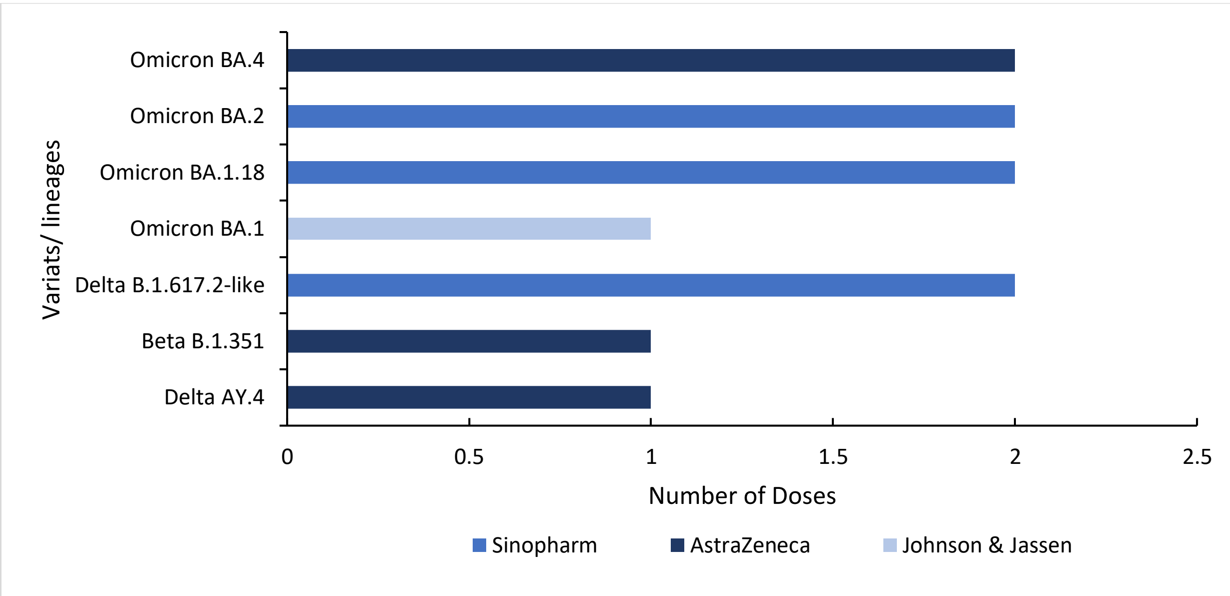

Figure 4.6: Variants/ lineages according to the vaccine type and number of doses sequenced at the UNAM-MDL, June 2021-May 2022.

The logistic regression analysis found that for each additional dose received, there was a decrease in the odds of the outcome Exp (B) = 0.628 (95% CI, 53.6% –73.7%), p<0.001. Therefore, the odds of a patient having all three doses and getting immune to the virus were just 0.628. While the probabilities of the result increase by a factor of 1.009 for each unit increase in age (p=0.045, Exp (B) = 1.009) (95% CI, 100.2%-101.9%). Furthermore, the gender coefficient (-0.898) indicates that being in the reference gender group (as opposed to the omitted category) reduces the probability of the outcome by 0.407 (p 0.001, Exp(B) = 0.407, 95% CI, 33.9%-49.0%).

4.5 SUMMARY

This chapter summarized the study's findings. Results were displayed in the form of tables and figures. The results were further addressed in the subsequent chapter, their reasons, justifications, and references to relevant literature.

CHAPTER 5: DISCUSSION

5.1 INTRODUCTION

In this chapter, the study's findings were discussed, making inferences to the study's objectives. Literature is also integrated into the discussion to compare the study findings with those of other researchers, and it will also serve as additional evidence to the findings. Similarly, the researcher's reflective thoughts were also presented.

5.2 POST-VACCINATION INFECTION RATE

In this cohort, data was presented on 5389 vaccinated individuals with/without test-confirmed SAR-CoV-2 infections. An inverse relationship was observed between age and the risk of post-vaccination. Similar to early studies, it was found that middle-aged were primarily dominant in post-vaccination infections (18,75) the observed mean age was 40, and the statistical significance $p < 0.001$ which may indicate a greater occurrence or increased susceptibility within this age group. This may be due to several factors such as immunological response variability; as people become older, their immune systems may change. While vaccinations are generally effective across all age groups, immune response efficacy may vary with age, potentially affecting vaccine effectiveness in some middle-aged people.

Behavioral factors; even after vaccination, middle-aged adults often participate in habits or employment that enhance their exposure risk. They are more active in particular environments or occupations that enhance their chances of coming into contact with the disease (76). Another factor could be the duration after vaccination, whereby the period after vaccination may have an impact on immunity levels, if vaccinated earlier in the rollout, their immunity may have diminished relative to those newly vaccinated or receiving booster doses (59,77,78). Additionally, the emerging viral strains may represent a threat to vaccination efficacy. Some variations may be able to bypass vaccine-induced immunity, affecting various age groups differently (79).

Compared to females, males were more dominant in our study; conversely, females were most affected, with an attack rate of 16.8%. Although men were more prevalent in the study population, females had a higher attack rate, which indicates the proportion of individuals who got infected within a particular period. Despite their lower numbers, females may have been more vulnerable to infection due to a variety of causes such as biological characteristics, underlying health issues, or unique exposure patterns. However, male persons had a higher infection rate compared to females, these findings are different from that of (59), where females had a higher infection rate.

Overall, the post-vaccination infection rate was 99.8 per 1000 vaccinated people over a year, meaning that within a population of 1000 vaccinated individuals, approximately 99.8 cases of COVID-19 had been diagnosed or occurred within the study period. This rate can offer a snapshot of the disease's prevalence and impact within the community and this could have been influenced by the variations in vaccine efficacy against new variants or declining immunity over time may contribute to post-vaccination infections. This result was similar to that of Butt et al (58), that found a low rate of infection among those who were fully vaccinated and age to be associated with confirmed infection.

Subsequently, the general frequency and transmission rates of the virus in the population can have an influence on the infection rate among vaccinated persons. The amount of time since immunization may also alter susceptibility to infection. Additionally, immunity may also diminish over time, especially if booster doses are not administered. In terms of comorbidities, hypertension, HIV, and cardiovascular disease showed significant associations with the groups studied. Though Group B tends to have higher counts for hypertension, HIV, and cardiovascular disease.

Conversely, diabetes mellitus, obesity, cholesterol issues, asthma, and other comorbidities do not show significant differences in prevalence between the two groups. A study by Alsofayan et al (80) observed hypertension and diabetes mellitus among COVID-19 positive cases.

The PVSI rate varied by the vaccine type received, with Sinopharm having the highest compared to the other vaccines, however, there was no statistically significant difference, compared to Pfizer which had a statistically significant difference among the two groups. The efficacy of different vaccines against particular variations varies. A study by AlQahtani et al (78) found that Sinopharm had a higher risk of PVSI; the performance of the Pfizer/BioNtech vaccine was found to be superior to the Sinopharm vaccine, with the latter associated with a higher risk for post-vaccination infections. Compared to other vaccines, Sinopharm might exhibit lower effectiveness against specific variants, especially when considering its higher uptake rate relative to other vaccines (78).

Likewise, Khomas region had the highest number of tests and cases; notably, it was one of the epicentres of COVID-19. The mortality rate was 1.1 per 1,000 vaccinated persons, which showed that COVID-19 deaths were rare in this vaccinated population. Various factors, such as age distribution, comorbidities, prevalent diseases and other demographic and environmental factors, may have influenced the rate (54,75,81,82). Additionally, a considerable proportion of the cohort had a history of SARS-CoV-2 infection either before or after their vaccinations. Despite being vaccinated, these individuals developed new symptoms when testing positive for COVID-19 post-vaccination. This highlights the possibility of experiencing COVID-19 symptoms even after vaccination, particularly among those with a history of prior infection.

The overall population surveyed experienced symptoms such as cough, sore throat, runny nose, headache, chest and back aches, and dizziness, among others. These symptoms were also observed in another study (80). This proportion was found to be statistically significant (p-value less than

0.001), and the odds of experiencing these symptoms were approximately 14.6 times higher compared to those who did not report these symptoms.

5.3 COVID-19 VARIANTS AND PVSI CHARACTERIZATION

Notably, despite widespread community disease, it was discovered that SARS-CoV-2 infection following vaccination is rare (18). A new variant, Omicron (Pango lineage B.1.1.529), was established and was immediately categorized as VOC in November 2021 (83). The Delta variant (Pango lineage B.1.617.2) from VOI became a VOC in May 2021 until June 2022. The only VOCs currently considered by WHO (until August 2022) were the BA.2, BA.4, and BA.5 Omicron sub-lineages (83).

Delta and Omicron variations circulated simultaneously from November through December of 2021. In January 2022, Omicron became the dominant variant, and sub-lineages have been found. These results from previous studies (62) are consistent with the results in this study, which also found that the two dormant variations are Omicron and Delta. Likewise, most cases occurred in December 2021 due to the peak of cases worldwide during that time.

Unfortunately, only a few variants were sequenced during the study period and among the study samples, as the laboratory caters for SARS-CoV-2 sequencing nationwide. Hence, it does not sequence all the samples explicitly tested in the laboratory but also that of other laboratories or institutions nationwide, thus, the meagre number of variants in this study.

The study-found that PVSIs were most common among those fully vaccinated more than 14 days after the second dose when complete immunity is expected or has developed. It is unknown if these individuals were exposed before or after their dose. Not surprisingly, the majority did not require hospitalization. These results align with real-world reports on vaccine effectiveness >14 days after the first and second doses, especially in preventing severe diseases, emphasizing the need to take strict precautions until complete protection is reached (18,84,85).

Based on studies (85), before the broad transmission of the SARS-CoV-2 Delta variant, investigations have shown that symptomatic COVID-19 needing hospitalization and emergency treatment was uncommon in those who had received all recommended vaccinations. Across every sex, race, ethnicity, and age group examined, the incidence among fully immunized individuals was around three times lower than that among unvaccinated individuals during the period of Delta predominance. Additionally, those who had received the entire vaccination course and had SARS-CoV-2 infection were less likely to have a favourable outcome than unvaccinated patients. However, this study focused primarily on vaccinated individuals.

Fully immunized individuals had a decreased crude risk of death. Besides, a more significant proportion had no underlying medical conditions. These results are congruent with those of another recently released study on COVID-19 incidence during Delta circulation, which showed that vaccination is protective against severe illness from COVID-19 (85). Similar to other studies, our study intended to answer the question about variations of concern in breakthrough infections, that specific variants of concern were more prevalent in infections, in contrast to another report that was not intended to answer this question (21).

The Kaplan-Meier survival curve showed that when fully vaccinated, the chances of survival are higher than those partially vaccinated or early post-vaccination. It appeared that the fully vaccinated group had a much higher cumulative survival proportion than the two other groups, which do not appear to differ significantly. Compared to the other interventions, it would appear that the three dosages considerably lengthen the period until people contract SARS-CoV-2 infections. Corroborating our findings, Perrella et al (59) prospectively assessed the occurrence of post-vaccination infections among healthcare professionals. The number of individuals free of SARS-CoV-2 infections at the end of the research (90%) does not appear to differ significantly across the intervention groups when looking at the curves' last cumulative survival proportion.

Early post-vaccination, partially vaccinated, and fully vaccinated individuals' survival distributions were compared using a log-rank test to see if there were any differences at the UNAM Molecular Diagnostic facility. The three therapies' survival distributions differed statistically considerably from one another. The result is statistically significant in this study since $p < 0.001$. That is, the survival distributions are different in the population.

5.3 FACTORS ASSOCIATED WITH PVSI

Notably, according to the results the distribution of infection across the different age categories, based on the odds ratio (OR) and p-values > 0.05 there doesn't seem to be a significant difference in infection rate between the age groups. In comparison to individuals who got their second or third dosage, those who received their first dose had a lower risk of infection. However, only the difference between the first and second dosage groups approaches significance ($p = 0.145$). These findings are similar to that of Hall et al (79).

When compared to other reasons for testing, those who were examined because of suspected reinfection or hospitalization appeared to have greater odds ratios of infection (p-values < 0.001). Individuals who are hospitalized, for example, have a higher risk of infection than those who are not similar findings were found in (86). Partially vaccinated individuals required hospitalization, however, it was not severe. Additionally, compared to those who don't exhibit any symptoms, those with symptoms have a considerably increased chance of contracting an infection (p 0.001).

The likelihood of infection appears to be unaffected by the presence of comorbidities ($p = 0.270$). Whereas some factors (such as reasons for testing and symptomatic status) appear to be considerably related to the likelihood of infection, others (such as age groups, dosages, and comorbidities) do not appear to be statistically significant.

The results implied that hypertension, cardiovascular disease and diabetes were some of the factors that contributed most as compared to other diseases to the post-vaccination SARS-CoV-2 infections among vaccinated individuals tested at the UNAM Molecular Diagnostic laboratory. This could be because these are chronic conditions which are associated with systemic inflammation and have the potential to damage vital organs, these conditions can overall increase the risk of post-vaccination infection. These findings are similar to those of (69), as the most common comorbidities found were hypertension, cardiovascular disease and diabetes.

Among those with comorbidities, hypertension and HIV have significant associations with the infection, indicating that those with these conditions have a greater risk of getting COVID-19 compared to those without these conditions. These conditions can make infections more likely since they frequently coexist with other medical issues (87). Hypertension or cardiovascular disease and HIV, for example, might cause secondary consequences that weaken general health and immunological function (88). Additionally, the medications administered, and some drugs used to treat these conditions may affect the immune system or interact with the vaccination, reducing its efficacy (88). Conversely, the other medical conditions examined in this model, on the other hand, did not reveal statistically significant relationships with the result.

As seen in the results, there is a decreased likelihood or reduced odds of being immunized after receiving three vaccine doses. The probability of testing positive for COVID-19 drops by around 37.2% as the number of doses rises. Some research shows that further doses or boosters may give enhanced protection against new forms of the virus, decreasing the chance of infection even more (59,89). Likewise, an individual's immune system is strengthened, which may improve its capacity to identify and eliminate the infection. Moreover, an Israeli and Italian study (59,86) confirmed these findings, that additional doses are effective in decreasing COVID-19 positivity, and severity. It can also be noted that the probability of COVID-19 positives rises by roughly 1.1% with each year of age this is correlated with findings by (59,86).

To summarize, the results of this research indicate that age and the number of vaccination doses received are significant predictors associated with PVSI. Age raises the probability of PVSI somewhat each year, however, the number of doses decreases the odds of PVSI as the number of doses increases. Other studies that have investigated factors that influence PVSI rates and the effectiveness of vaccines in various populations that support this study include (12,14).

5.4 SUMMARY

This chapter highlighted and covered the study’s findings while using literature references. The study showed that the survival distributions are different in the population. The next chapter concludes the study and makes recommendations based on its findings.

CHAPTER 6: CONCLUSION, LIMITATIONS AND RECOMMENDATIONS

6.1 INTRODUCTION

This chapter provides the conclusion and recommendations on post-vaccination SARS-CoV-2 infections occurrence among vaccinated individuals tested at the UNAM Molecular Diagnostic Laboratory, June 2021- May 2022. Chapter 1 introduced the research study by highlighting the background of the study and research questions. The second chapter reviewed literature from various contemporary authors on the object of inquiry post-vaccination SARS-CoV-2 infection among vaccinated individuals, while the third chapter outlined the research methodology used in data gathering. The previous chapter looked at the presentation and analysis of research findings. This section looks at the summary conclusions of the study, limitations, and recommendations based on evidence from the study.

6.2 SUMMARY

This study aimed to analyze the occurrence of post-vaccination SARS-COV-2 infections among vaccinated individuals tested at the UNAM Molecular Diagnostic Laboratory from June 2021 to May 2022. The study reviewed literature from various contemporary scholars using a thematic approach. The research design was a retrospective cohort study of SARS-CoV-2 immunized individuals tested between June 2021 and May 2022. Statistical analysis was performed using Statistical Package for the Social Sciences (SPSS) (version 26). Descriptive and inferential statistics were used in the analysis of data. The following are the conclusions:

6.3 CONCLUSION

A low rate of PVSI was found, suggesting that vaccination is effective in reducing the risk of infection. Within this vaccinated cohort, incidence varied by COVID-19 vaccine product received. According to the research findings, the two dormant variants were Omicron and Delta. No other variants of concern were found. This highlighted the ongoing threat of emerging variants and the signifance of continuous surveillance and responds to VoCs.

From the survival functions it appeared that the fully vaccinated group has a much higher cumulative survival proportion than the other two groups, which do not appear to differ significantly (although the partially vaccinated seems to have a slight survival advantage; specifically, fewer participants were not immune to SARS-CoV-2). Compared to the other interventions, it would appeared that the three dosages considerably lengthened the period until people contracted SARS-CoV-2 infections highlighting the potential benefits of booster doses in enhancing immunity and lowering the risk of breakthrough infections.

Partially vaccinated and fully vaccinated individuals' survival distributions differed statistically considerably from one another. Age, number of doses, and sex were identified as significant factors associated with post-vaccination SARS-CoV-2 infections among this vaccinated cohort. Based on the study findings, we can therefore reject the hypothesis, and conclude that there is a significant association between demographics and post-vaccination infection.

6.2 LIMITATIONS

The findings in this report had several limitations. Firstly, a case investigation form (CIF), one of the forms used for COVID-19 sample testing documentation, collects patient information. Since vaccination uptake started, the form has been changed to reflect vaccination status. Because it was impossible to track the vaccination status of individuals who may have been immunized and tested during the study period, using outdated case investigation forms (CIFs) was a restriction. Therefore, the study did not include the older CIF versions.

Secondly, problems with these forms' incompleteness exist, as some of them lack crucial details (such as the number of doses or the type and date of the vaccine) or contain erroneous information. Therefore, incomplete forms were also excluded or not considered in the study. It is possible that individuals with positive SARS-CoV-2 antigen tests or other test results at home, school, or the place of employment were overlooked, and details concerning earlier SARS-CoV-2 infections were not gathered. Additionally, not all positive cases in the study were sequenced, as the laboratory does random sequencing of cases from different laboratories nationwide. Hence, not all the samples in the study were sequenced, and the testing materials were quite costly. Lastly, since the laboratory gives each individual a new lab ID, some tested patients were duplicated, although from different dates; however, it was considered a new entry.

6.3 RECOMMENDATIONS

Although the study aimed to add knowledge to existing studies on PVSIs in the Namibia context, based on the findings found that low infection rates associated with vaccination, circulating variants influence infection and, demographic factors associated with infection. We recommend that the country maintains high vaccination coverage to protect the public from severe COVID-19, including illness and hospitalization brought on by the Delta/Omicron variants, these data support recommendations for COVID-19 immunization, including additional booster doses. To improve the outcomes of SARS-CoV-2 and vaccination hesitancy among the general population, we recommend that key stakeholders involved in vaccination service delivery in Namibia the following:

- Ministry of Health and Social Services: should consider targeted vaccination campaigns to ensure high vaccination coverage across all age groups, and tailor vaccination strategies to prioritize individuals at higher risk of PVSI, those with comorbidities with an emphasis on reaching vulnerable populations and underserved communities. Improve data collection and analysis systems to track vaccination coverage, adverse events following immunization (AEFI), and the prevalence of COVID-19 variants. Continuous variant surveillance to prevent potential infection peaks. This data could be used to inform vaccination strategies and policy decisions. MoHSS should invest in healthcare workers' training and capacity building to ensure they are equipped with the knowledge and skills necessary to effectively administer vaccines and address community concerns.

- Health workers: should maintain a constant state of readiness for the COVID-19 vaccine by conducting education and communication campaigns that accurately convey the vaccine's benefits, safety, and significance in halting the spread of the disease to the community. Offer individualized counselling to individuals considering vaccination, address their concerns, respond to any inquiries and reassure them about the benefits of vaccination. As well as continuous monitoring of any adverse events following immunization (AEFI) and promptly reporting any suspected cases to the appropriate persons for investigation and follow-up.
- Civil Society Organization: Collaboration between MoHSS and CSOs to mobilize communities and raise awareness about the importance of vaccination, emphasizing how immunization protects against severe COVID-19 and prevents the spread of the virus. Collaboration should tackle vaccine hesitancy and misinformation by disseminating correct information, encouraging vaccine confidence, and addressing community concerns. Advocate for policies and resources to support vaccination initiatives, such as funding for vaccine procurement, distribution, and public education campaigns.

- Community-Based Agents: with the assistance of community-based agents conduct door-to-door outreach and education campaigns to encourage immunization and address local concerns. Provide support services, such as assistance with appointment scheduling, transportation to vaccination sites, and language interpretation. Provide feedback channels to address community concerns related to vaccinations, while ensuring the community views and voices are heard and considered in decision-making process.
- Lastly, studies comparing non-vaccinated and vaccinated could be conducted as well.

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APPENDICES

ANNEUXURE A: ETHICAL CLEARANCE FROM UNAM

UNAM
UNIVERSITY OF NAMIBIA

ETHICAL CLEARANCE CERTIFICATE

Ethical Clearance Reference Number: DEC OSH 0037 **Date: 06/12/ 2022**

This Ethical Clearance Certificate is issued by the University of Namibia Ethics Committee (REC) in accordance with the University of Namibia's Research Ethics Policy and Guidelines. Ethical approval is given in respect of undertakings contained in the Research Project outlined below. This Certificate isissued on the recommendations of the ethical evaluation done by the ethics committee.

Title of Project: POST-VACCINATION SARS-COV-2 INFECTIONS INCIDENCE AMONG VACCINATED INDIVIDUALS TESTED AT THE UNAM MOLECULAR DIAGNOSTIC LABORATORY, JUNE 2021- MAY 2022

Principal researcher: NKEMDILIM VICKY NDOZI-OKIA

Staff Number/ Student number: 201406781

Remarks: Low Risk Approved with corrections

Centre for Research Services

Take note of the following:

1. Any significant changes in the conditions or undertakings outlined in the approved Proposal must be communicated to the ethics committee. An application to make amendments may be necessary.
2. Any breaches of ethical undertakings or practices that have an impact on ethical conduct of the research must be reported to the ethics committee
3. The Principal Researcher must report issues of ethical compliance to the ethics committee (through the Chairperson) at the end of the Project or as may be requested by the ethics committee
4. The ethics committee retains the right to:
   i) Withdraw or amend this Ethical Clearance if any unethical practices (as outlined in the Research Ethics Policy) have been detected or suspected,
   ii) Request for an ethical compliance report at any point during the course of the research.

The ethics committee wishes you the best in your research.

____

Prof Hans J Amukugo (Oshakati Campus Chairperson Decentralized Ethics Committee)

____

Prof. Davis Mumbengegwi (Head, Multidisciplinary Research)

ANNEUXURE B: RESEARCH PERMISSION LETTER FROM MoHSS

REPUBLIC OF NAMIBIA

MINISTRY OF HEALTH AND SOCIAL SERVICES

OFFICE OF THE EXECUTIVE DIRECTOR

Ministerial Building
Harvey Street
Private Bag 13198, Windhoek

Tel: No: 061 -203 2507
Fax No: 061-222 558
Andreas.Shipanga@mhss.gov.na

Ref: 22/4/2/3
Enquiries: Mr. A. Shipanga

Date: 15 February 2023

Mr. Nkemdilim V. Ndozi-Okia
PO Box 21724
Windhoek

Dear Mr. Ndozi-Okia

Re: *Post-Vaccination SARS-COV-2 Infections incidence among vaccinated individuals tested at the UNAM Molecular Diagnostic Laboratory, June 2021-May 2022.*

1. Reference is made to your application to conduct the above-mentioned study.
2. The proposal has been evaluated and found to have merit.
3. **Kindly be informed that permission to conduct the study has been granted under the following conditions:**
   3.1 The data to be collected must only be used for operational purpose;
   3.2 No other data should be collected other than the data stated in the proposal;
   3.3 Stipulated ethical considerations in the protocol related to the protection of Human Subjects should be observed and adhered to, any violation thereof will lead to termination of the study at any stage;
   3.4 A quarterly report to be submitted to the Ministry's Research Unit;
   3.5 Preliminary findings to be submitted upon completion of the study;
   3.6 Final report to be submitted upon completion of the study;
   3.7 Separate permission should be sought from the Ministry for the publication of the findings.
4. All the cost implications that will result from this study will be the responsibility of the applicant and **not** of the MoHSS.

Yours sincerely,

BEN NANGOMBE
EXECUTIVE DIRECTOR

EXECUTIVE DIRECTOR
MINISTRY OF HEALTH AND SOCIAL SERVICES

All official correspondence must be addressed to the Executive Director.

My NAMIBIA

ANNEXURE C: DATA COLLECTION TOOL

Data extraction tool for the post-vaccination SARS-COV-2 Infections among vaccinated individuals tested at the UNAM Molecular Diagnostic Laboratory, June 2021-May 2022

Part A	
Case no.	
Test date:	
Result:	
Previously tested positive:	
Vaccine Name:	
Last date of vaccination:	
Number of Doses	Single-dose ☐ 1st dose ☐ 2nd doses ☐ 3rd dose ☐
Part B	
Date of Birth: **Age:** **Region:**	**Sex**: Male ☐ Female ☐ **Nationality:**
Part C - Reason for COVID testing	
Category of test	Suspected new case ☐ Quarantine ☐ Travel ☐ Hospital admission ☐ Contact tracing ☐ Retest ☐ Healthcare worker ☐
Part D	

Symptomatic:	Fever ☐ Cough ☐ Sore throat ☐ Shortness of breath ☐ Diarrhea ☐ Loss of smell ☐ Loss of taste ☐ Vomiting ☐ Myalgia/body pains ☐ Chills ☐ Others ☐ Specify:
Part E	
Comorbidities/ underlying factors	Obesity ☐ Tuberculosis ☐ Chronic kidney disease ☐ Diabetes ☐ Cardiovascular disease ☐ Pregnancy ☐ HIV ☐ COPD ☐ Asthma ☐ Chronic liver disease ☐

ANNEXURE D: COVID-19 CASE INVESTIGATION FORM

COVID -19 Case Investigation Form

Ministry of Health and Social Services, Namibia.

Contact information: Tel: (+264) 61 203 2211/2630/2631 : Hotline: 0800100100

Laboratory Number

EPID Number

REASONS FOR COVID-19 TESTING

URGENT/PRIORITY

☐ HOSPITALIZED PATIENT (SYMPTOMATIC) ☐ HEALTH WORKER (SYMPTOMATIC) ☐ TRAVEL (MEDICAL REASONS)

☐ TRUCK DRIVER (CROSS BORDER) ☐ HOSPITAL ADMISSION PRE-OP ☐ DECEASED

ROUTINE

☐ SUSPECTED NEW CASE ☐ CONTACT ☐ ACTIVE CASE SEARCH ☐ EXPANDED TARGET TESTING ☐ TRAVEL (NON-MEDICAL) ☐ CONFIRMATORY PCR TEST ☐ SUSPECTED

SPECIMEN TYPE

☐ Nasopharyngeal swab ☐ Sputum ☐ Oropharyngeal swab ☐ Saliva ☐ other (specify) ______

TEST

☐ PCR ☐ Antigen RDT ☐ Multiplex PCR

Specimen Collection Date | Date received at Laboratory | Date of last positive result if suspected reinfection

Laboratory results: Positive ☐ Negative ☐ Indeterminate ☐ Invalid (Repeat test) ☐ Rejected ☐ Reason for rejection ______

Date of result

PATIENT DETAILS

Full Name | ID/Passport #

DOB | Age | Sex M ☐ F ☐

Current Address | Nationality

Residential Address

Patient's contact number/s

Occupation

Name of the employer/ place of employment if self employed

Date of consultation/admission

DOCTOR/HEALTH CARE PROVIDER'S DETAILS

Full | Contact

Email Address

Facility Name

Region | District

NEXT OF KIN CONTACT DETAILS

Full Name | Relationship to the patient

Contact Number

SIGNS AND SYMPTOMS (tick all that apply)

Symptomatic Yes/No If Yes ☐ Fever (≥38 °C) ☐ Sore throat ☐ Diarrhea ☐ Loss of smell ☐ Chills ☐ Cough ☐ Shortness of breath ☐ Myalgia/body pains ☐ Vomiting

☐ Loss of taste ☐ Other (specify if other) ______ Date of symptom onset: ____/____/____

*Physical contact with a known COVID-19 case Yes ☐ No ☐ If yes indicate name and surname (If Known) ______

Unknown ☐

*Travel from countries, or other areas in Namibia where there is known COVID-19 community transmission Yes ☐ No ☐

Country	Region	City/Town	Date of departure (travel to area)	Date of return (travel from area)

VACCINATION STATUS

Is the patient vaccinated? Yes ☐ No ☐ Name of Vaccine: ______

Number of Doses: ☐ single dose vaccine ☐ 1st Dose ☐ 2nd Dose ☐ 3rd Dose ☐ Unknown Date of last vaccination:

MEDICAL HISTORY / CO-MORBIDITIES

Obesity ☐ Tuberculosis ☐ Chronic Kidney Disease ☐ Diabetes Mellitus ☐ Cardiovascular disease including Hypertension ☐ Pregnancy ☐ HIV ☐ Asthma ☐ Chronic Liver Disease ☐ COPD/Chronic Pulmonary disease ☐ Others ☐ (specify) ______

Previously tested positive for COVID-19 ? Yes ☐ No ☐ If Yes add Date of confirmation: ____/____/____

Presence of clinical or radiological pneumonia Yes ☐ No ☐ *Were chest X rays (CXR) done: Y ☐ N ☐ CXR Findings: ______

Presence of clinical or radiological acute respiratory distress syndrome (ARDS) Yes ☐ No ☐

Presence of another diagnosis/etiology for their respiratory illness Yes ☐ (specify) ______ No ☐ Unknown ☐

TREATMENT / MANAGEMENT

Patient Hospitalised: Yes ☐ No ☐ Unknown ☐ Admitted to ICU: Yes ☐ No ☐ Unknown ☐ Ventilation: Yes ☐ No ☐ Uknown ☐ On ECMO: Yes ☐ No ☐ Uknown ☐ Transferred ☐ Name of transferred facility ______

Referred ☐ Referral facility ______ Discharged ☐ Discharge date: ____/____/____

PATIENT OUTCOME

Active☐ Recovered ☐ Recovery date: ______ Died ☐ Date of death: ______

Form completed by (Name & Signature) | Contact details (Tel or Cell No) | Unit/Department