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Age, Race/Hispanic Origin, and COVID-19 Mortality Among Sickle Cell Disease Patients in the United States

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Walden University
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Abstract

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by

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MD, Windsor University School of Medicine, 2008

Dissertation Submitted in Partial Fulfillment

of the Requirements for the Degree of

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Public Health

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Abstract

The COVID-19 pandemic remains a global health challenge, with 6.7 million deaths worldwide as of January 2023. It has illuminated the health iniquities in underserved communities and populations like those with sickle cell disease (SCD). Researchers have associated the COVID-19 outcome among SCD patients in other regions of the globe. The purpose of this retrospective cross-sectional observational study was to investigate the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in the United States from January 2020 to March 2021. The Krieger ecosocial theory of disease distribution framed the study. Data were drawn from an existing Centers for Disease Control and Prevention provisional SCD death data set (N = 140). The binary logistic regression analysis result showed a statistically significant relationship between age and race/Hispanic origin and COVID-19 mortality. The variability between ages was 42.9%; race/Hispanic origin was 29.9%; and age and race/Hispanic origin were the highest, with 62.4% dying from COVID-19. Non-Hispanic Black patients were 9.6 times more likely to die overall but those aged 60+ were 17.5 times more likely to die from COVID-19 than the reference groups (0–19-year-old and other race). This study can benefit the research community, public health workers, medical professionals, and policymakers to understand better and influence policy on developing and prioritizing age- and race-tailored preventive protocols and medical care. They may minimize pain and suffering while mitigating mortality from COVID-19 and other unforeseen future pandemics within the SCD community at home and abroad and positively effect social change.

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Dedication

I am dedicating this dissertation to my wonderful parents and only sister Susan Ndula (all of late); without their unconditional love, their utmost sacrifices, and their blessings, I would not have inculcated the virtues, especially those of patience, respect, and tenacity, to get to this level. Moreover, I dedicate this work to my beautiful, lovely, and talented wife, Charlotte. She has persevered and stood by my side to ensure that everyone in the house was comfortable and that I met deadlines. My daughter, Giovanna-Michelle, and my son, Giani-Joel, have also been extremely supportive and understanding throughout the process, for which I remain grateful. Finally, I thank God and all my loved ones who fervently pray for my dream to come to fruition.

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Chapter 1: Introduction to the Study

Sickle cell disease (SCD) is one of the many serious heterozygous hemoglobinopathies and sickle cell disorders with insufficient public health, medical, and policymakers' attention. SCD remains an inherited blood disease and an invisible global health problem that has disproportionately affected individuals of African descent in the continent of Africa but also affects those living elsewhere (Aiko et al., 2018; Mburu & Odame, 2019; Panepinto et al., 2020). Although SCD is most common among people from sub-Sahara Africa, SCD consists of different genotypes (Hemoglobin [Hgb] SS disease, Hbg SC disease, Hgb S beta + thalassemia, and Hgb S beta zero thalassemia) that are prevalent and affect people from Latin America; Saudi Arabia; India; the Mediterranean, and Europe (Guarda et al., 2020; Panepinto et al., 2020). The disease comes with many health complications and is not limited to a particular geographical region. Public health agencies, medical professionals, and policymakers should pay more attention to this disease that comes with comorbidities and premature death when compared with those without the disease (Lee et al., 2019; Lubeck et al., 2021; Mburu & Odame, 2019; Panepinto et al., 2020).

SCD is an underappreciated global health problem affecting millions of people worldwide. According to Clift et al. (2021), an estimated 8 million to 12 million persons globally have the disease, with approximately 15,000 in the United Kingdom and 100,000 in the Unites States with the disease. Additionally, more than 300,000 babies are delivered annually with the disease in Africa, per Mburu and Odame (2019). Of the 1% of children diagnosed with SCD, 50% to 90% died before 5 years of age (Uyoga et al.,

2019). However, when compared to the general population, persons with SCD and a weak immune system, short life span, and coronavirus disease 2019 (COVID-19) suffered from the severest form of the viral infection (Mburu & Odame, 2019; Panepinto et al., 2020; U.S. Department of Health and Human Services [USDHHS], 2020). This global health issue has a high prevalence that warrants measures like any other disease, with the COVID-19 pandemic exacerbating SCD and increasing incidence, hospitalizations, and death (Clift et al., 2021; Panepinto et al., 2020). Policymakers and decision-makers need to investigate ways to prioritize this disease that causes not only physical but also psychological trauma to those with the disease and their caregivers (Aiko et al., 2018; Buscetta et al., 2022; Madani et al., 2018; Tezol & Unal, 2021; Vinkers et al., 2020).

Background

SCD is not only a medical condition that affects those with the disease, but the patients are at high risk for many comorbidities and respiratory infections. The disease affects the physical and psychological well-being of the sick and their families and also the social and economic aspects of their communities (Aiko et al., 2018; Buscetta et al., 2022; Madani et al., 2018; Tezol & Unal, 2021; Vinkers et al., 2020). Panepinto et al. (2020) noted that persons with SCD are immunocompromised and have a higher risk of respiratory infections, especially those of viral origin, than the normal population showing that SCD patients were likely to be infected with the influenza virus. The novel coronavirus is a viral infection transmitted via the respiratory route, like the influenza

virus, rendering patients with SCD vulnerable during the COVID-19 pandemic (Buscetta et al., 2022; Minniti et al., 2021; Teulier et al., 2021; Tonen-Wolyec et al., 2020).

Unlike bacterial outbreaks, viral outbreaks are more common and have been responsible for causing pandemics. Viruses have been known to cause contagious and deathly respiratory infections, such as severe acute respiratory syndrome (SARS; Fauci et al., 2020). In late 2019, the novel coronavirus that was isolated and identified as Coronavirus 2 (COV-2) was structurally a SARS-associated coronavirus (SARS-COV-2) and responsible for causing COVID-19 (Fauci et al., 2020; Kim & Bostwick, 2020; Menapace & Thein, 2020; Panepinto et al., 2020; Tezol & Unal, 2021; Tonen-Wolyec et al., 2020). In late January 2020, the director general of the World Health Organization (WHO, 2020) declared the novel viral outbreak a public health emergency of international concern (Buscetta et al., 2022). Because of the high transmission rate from person to person of COVID-19, the pandemic has been a global burden (WHO, 2020, 2021). The pandemic has not only affected individuals from all walks of life but has adversely affected vulnerable communities, especially people with SCD (Buscetta et al., 2022; Fauci et al., 2020; Mburu & Odame, 2019; Panepinto et al., 2020; Tonen-Wolyec et al., 2020; Vinkers et al., 2020).

Although SCD patients can be found in Africa, globalization and transportation have made it a global medical condition, especially in the United States, having one of the largest communities of patients (CDC, 2020b; Sotomayor & Barrero, 2020; USDHHS, 2020). Of the estimated 100,000 U.S. persons with SCD, most were Black (*OR* = 1/365), but Hispanic-American people were also affected (*OR* = 1/16,300)

(Panepinto et al., 2020). Of these, an estimated 37% of adults and 40% of youths with SCD suffer from the painful crisis every day, leading to functional disabilities (physical, social, and educational) and an overall low quality of life when compared to those without SCD (Kim & Bostwick, 2020; Panepinto et al., 2020). The United States has been reported to have the highest prevalence of persons with SCD in the Western world (CDC, 2020b; Clift et al., 2021; USDHHS, 2020). The multiple comorbidities associated with the disease and the high prevalence made a good recipe for increased risk of cases and mortality due to the U.S. COVID-19 pandemic (USDHHS, 2020; WHO, 2021).

The incidence and mortality in the United States due to COVID-19 are unmatched by other nations (Gelfand et al., 2021; WHO, 2021). Ortaliza et al. (2021) noted that COVID-19 was the number one leading cause of U.S. deaths in late 2020 and the early months of 2021, surpassing coronary heart disease and cancer in that same period. Globally, as of October 1, 2021, the United States contributed to 18.4% of the world's COVID-19 cases and 14.4% of deaths and demonstrated a racial and ethnic disparity in both COVID-19 infections and SCD (Gelfand et al., 2021; Hsu et al., 2020; Kim & Bostwick, 2020; Panepinto et al., 2020; WHO, 2021). This pandemic has affected individuals and their communities on a large scale. However, it has disproportionately affected the underserved and those with underlying and compromised immunity, such as those in the SCD community (Moore et al., 2020; Panepinto et al., 2020; USDHHS, 2020).

The compromised immunity of SCD arises from having hemoglobinopathy and other comorbidities (Minniti et al., 2021; Panepinto et al., 2020; Teulier et al., 2021). For

instance, having a normal and functional spleen is vital and dictates the morbidity and mortality of persons with SCD (Hoss et al., 2019). Splenic injury due to acute splenic sequestration (ASS) is a common medical condition that causes functional asplenia. It weakens the immune function of those with SCD and renders them susceptible to many diseases and aplastic crises (Hoss et al., 2019; Hsu et al., 2020; Parminder et al., 2017). Moreover, Teulier et al. (2021) and Tonen-Wolyec et al. (2020) elaborated on how SCD, older age, and comorbid diseases (e.g., cardiovascular disease, chronic lung disease, diabetes, or cancer) were risk factors related to fatal complications among patients infected by SARS-COV-2. These factors would increase acute respiratory distress syndromes, systemic vasculopathy, and a high risk of thrombosis.

Additionally, SCD expresses many debilitating signs and symptoms, including severe anemia, acute and chronic pain, fatigue, shortness of breath, painful crises, clubbing, leg ulcers, stroke, chronic renal disease, and pulmonary hypertension with end-organ and tissue damage (Aiko et al., 2018; Menapace & Thein, 2020; Nardo-Marino et al., 2017; Panepinto et al., 2020; Teulier et al., 2021; Tonen-Wolyec et al., 2020; Telfer, 2019; Tezol & Unal, 2021). Although the signs and symptoms of SCD are sometimes identical to and are exacerbated by COVID-19, prompt testing and treatment are warranted. When ignored, the concurrent infection of SCD and COVID-19 may lead to increased hospitalizations and even death (Clift et al., 2021; Minniti et al., 2021; Panepinto et al., 2020; Telfer, 2019; USDHHS, 2020). All these comorbidities of individuals with SCD infected with COVID-19 increases pain and suffering, resulting in higher hospital visits and death and causing strain on the healthcare system during the

COVID-19 pandemic (Clift et al., 2021; Fauci et al., 2020; Hsu et al., 2020; Redaelli et al., 2021; Vinkers et al., 2020).

Moreover, it has been well documented that persons with a hemoglobinopathy such as SCD are commonly infected by viral respiratory infections, such as the influenza virus (Panepinto et al., 2020; USDHHS, 2020). However, as noted and elaborated by AbdulRahman et al. (2020), the novel COVID-19 does change the configuration of blood by forming a complex with a 1-beta chain of Hgb, thereby changing the shape and making it dysfunctional, resulting in decreased heme oxygen-carrying capacity. COVID-19 has been shown to affect the Hgb beta chain, the same mutated chain among people with SCD (AbdulRahman et al., 2020). Genetic susceptibility increases the risk of coronavirus infection in SCD communities. The similar physiopathology of the mutated genes between both diseases (SCD and COVID-19) rendered those with SCD more vulnerable to contracting COVID-19 infection. Therefore, individuals with both illnesses suffered from unfavorable health outcomes, creating a disparity between those with and without SCD in the communities (Panepinto et al., 2020; USDHHS, 2020).

During the early stages of the COVID-19 outbreak in the United States, the disparities and inequities with the pandemic were not well understood. Research indicated that only adults and senior citizens in nursing home settings were affected and had the worse outcome of the outbreak (Ceglie et al., 2019; Fauci et al., 2020; Gebhard et al., 2020; Hussain et al., 2020; Kim & Bostwick, 2020; Menapace & Thein, 2020; Panepinto et al., 2020; Redaelli et al., 2021; Teulier et al., 2021; Wenham et al., 2020). However, as of December 30, 2020, the Centers for Disease Control and Prevention

(CDC, 2020a, 2020b) revised their information on COVID-19 in children (0 to 17 years), stipulating how incidence, severity, hospitalization, and even death were on the rise. The increase in hospitalization and severity of COVID-19 in children was a breakthrough, as this age group was not considered when the pandemic started. Children with genetic diseases, such as SCD, may be at high risk; thus, healthcare providers should pay a high degree of concern to this population for suspicious COVID-19 infection (CDC, 2020a).

Moreover, with the advancement in research on this pandemic, many studies have found different associations and outcomes on the pandemic in different parts of the globe (AbdulRahman et al., 2020; Ceglie et al., 2019; Clift et al., 2021; Gebhard et al., 2020; Kim & Bostwick, 2020; Menapace & Thein, 2020; Panepinto et al., 2020; Tonen-Wolyec et al., 2020; Wenham et al., 2020). Some race and sex differences in the susceptibility to COVID-19 among people with SCD have been studied in different regions of the world. However, to my knowledge, no studies have explored the association between race/Hispanic origin, age difference, and COVID-19 mortality among those with SCD in the United States.

The information above should help public health, medical professionals, policymakers, and decision-makers identify and provide comparative age- and race/Hispanic-origin-specific COVID-19 mortality rates between persons with SCD and those without SCD. Understanding the rates will help direct and prioritize meaningful community-level interventions to identify and minimize racial disparity, hospitalizations, and death properly from the COVID-19 pandemic in persons with SCD in the United

States. For this study, I used a quantitative approach in which a nonparametric binary logistic regression test was used in the data analysis.

Problem Statement

Although infectious disease outbreaks have threatened U.S. society today, genetic disease transmission among humankind has continued for centuries (Fauci et al., 2020; Houwing et al., 2019). Globalization, transportation, lack of sanitation, the ambiguous nature of the disease, and lack of adequate public health preparedness have helped in fueling those diseases which are easily transmittable (Fauci et al., 2020; Gebhard et al., 2020; Gelfand et al., 2021; Shrestha et al., 2020; Sigler et al., 2021). The dynamic nature of the population with the sociocultural and racial interaction had facilitated the propagation of diseases across the globe. The ease of travel from one part of the continent to another has created a global village that enhanced the spread of genetic and communicable diseases within 24 hours (Fauci et al., 2020; Pronk & Faghy, 2022; Sohrabi et al., 2020).

Any infectious agents have the potential to cause disease outbreaks; historically, viral agents have been responsible for causing pandemics, especially those that affect the respiratory system (Fauci et al., 2020; Sohrabi et al., 2020). As Gebhard et al. (2020) noted, the outbreak of the acute respiratory illness that started in Wuhan, China, and was identified as SARS-CoV-2 (COVID-19) in 2019 had traveled across continents to 196 countries and was declared by the WHO as a pandemic accounting for 2 million cases and over 130,000 deaths globally as of April 2020 (Introduction, para. 1). Gelfand et al. (2021) also indicated how the pandemic from the epicenter of Wuhan had crossed the

planet; as of October 2020, 39 million cases and over 1 million deaths were reported worldwide (Introduction, para. 1). Viral outbreaks are dangerous and highly transmissible.

COVID-19 does not discriminate against whom it affects; however, people with other medical conditions and weak immune systems are more prone to contracting the disease (CDC, 2020a, 2020b; Panepinto et al., 2020; USDHHS, 2020). According to Panepinto et al. (2020), CDC (2020a, 2020b), and Mucalo et al. (2021), people with compromised immune systems and other underlying medical conditions had a high chance of getting and suffering from a severe form of COVID-19 infection. Immune-challenged people are at high risk of many other illnesses (Mucalo et al., 2021; USDHHS, 2020). This significant finding showed that those more susceptible to the pandemic included patients with hypertension, obesity, diabetes, cancer, and blood diseases such as SCD (CDC, 2020a, 2020b; Mucalo et al., 2021).

SCD is a hereditary hematologic medical condition and public health issue. This hemoglobinopathy disproportionately affects underserved communities and people of color and may be exacerbated by the COVID-19 pandemic (Mburu & Odame, 2019; Minniti et al., 2021; Panepinto et al., 2020). This finding indicated that disparaged communities inhabited by persons with many underlying medical conditions and people of color bore most of the brunt and remained disproportionately affected by COVID-19 (Mucalo et al., 2021; Panepinto et al., 2020; USDHHS, 2020).

SCD remained a serious genetic medical condition and an underappreciated global health problem that affected tens of millions of people worldwide in underserved

communities. Persons concurrently affected by SCD and COVID-19 had the worst health outcomes and even death (Mucalo et al., 2021; Panepinto et al., 2020). However, there was a gap in the literature examining the relationship between age, race/Hispanic origin, and mortality of COVID among SCD patients in the United States.

Although genetic disorders, especially hemoglobinopathies such as SCD, have been around for centuries, the novel coronavirus was just discovered in 2019, resulting in a serious global health crisis (Buscetta et al., 2022; CDC, 2020b; Pronk & Faghy, 2022; USDHHS, 2020; WHO, 2021). Although sex, gender difference, and response to COVID-19 among people with SCD has been studied in different regions of the world, to my knowledge, no studies have explored the association between age, race/Hispanic origin difference, and COVID-19 mortality among those with SCD in the United States (AbdulRahman et al., 2020; Ambrosino et al., 2020; Ceglie et al., 2019; Clift et al., 2021; Gebhard et al., 2020; Kim & Bostwick, 2020; Menapace & Thein, 2020; Panepinto et al., 2020; Tonen-Wolyec et al., 2020; Wenham et al., 2020). Panepinto et al. (2020) and Payne et al. (2020) also indicated that the age, sex, and race data mortality rate of patients with SCD from COVID-19 was lacking. Therefore, exploring the above association in this research would help prioritize the SCD populations to many available preventive strategies during this and subsequent unforeseen pandemic. Understanding those associations would improve health outcomes minimize death, and facilitate positive social change (Panepinto et al., 2020).

Purpose of the Study

The purpose of this retrospective cross-sectional observational study was to investigate the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in the United States. COVID-19 infection among persons with SCD could result in serious complications, morbidities, and death compared to the general population (Mucalo et al., 2021). Mucalo et al. (2021) noted that children and adults with SCD and comorbidities had severe cases of COVID-19 infection. Additionally, the case-series findings by Panepinto et al. (2020) found that mortality due to COVID-19 was observed among those with severe and mild-to-moderate SCD genotypes and those with mild-to-moderate severity of COVID-19. Ortaliza et al. (2021) and Payne et al. (2020) stated that COVID-19 was the number one leading cause of death in late 2020 and early 2021, surpassing coronary heart disease and cancer in that same period. Historically cancer and heart disease have always been the leading cause of death in the United States, but COVID-19 death was number one on the list. Ortaliza et al. and Payne et al. also indicated that the excess death was not only observed in the general population, but sickle cell registries also demonstrated excess death among patients with SCD.

Moreover, since the pandemic started, there has been an ongoing collection of data, and most data up to date are not completed (Panepinto et al., 2020). Due to the lack of relevant age, race/Hispanic origin, sex, and empirical SCD and COVID-19 data to help assess the severity and mortality of COVID-19 in persons with SCD in the United States, Panepinto et al. (2020) and Payne et al. (2020) were not confident whether the increased

COVID-19 infection rate was due to the COVID-19 pandemic's influence in exacerbating preexisting SCD concurrent conditions. To my knowledge, no such study had been done in the United States; hence, further study was needed to investigate the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in the United States. Therefore, getting access to and analyzing the variables would help prioritize intervention by public health and policymakers and decision-makers to improve health and health outcomes in the SCD population.

However, this study's independent and dependent variables (DV) were categorical. Although the independent variable (IV) of age was ordinal, race/Hispanic origin was measured as a nominal variable; on the other hand, the DV of COVID-19 death was measured as a binomial variable (see Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Salazar et al., 2015).

Research Questions/Hypotheses

Research Question 1

What is the relationship between age and mortality from COVID-19 among persons with SCD in the United States?

$H_0$1. There is no relationship between age and mortality from COVID-19 among persons with SCD in the United States.

H_a1. There is a relationship between age and mortality from COVID-19 among persons with SCD in the United States.

Research Question 2

What is the relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States?

$H_0$2. There is no relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States.

H_a2. There is a relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States.

Research Question 3

What is the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States?

$H_0$3. There is no relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

H_a3. There is a relationship between age and race/Hispanic origin in mortality from COVID-19 among persons with SCD in the United States.

Theoretical Framework

In the social sciences, although many theories are readily available to be used in a research study, it is essential to employ the most appropriate theory that will link the study. Krieger's (2020) ecosocial theory was the theory of choice in this study. This theory of disease distribution has been widely used in the field of public health, especially in the discipline of Epidemiology. However, the application of this theory focusing on this topic has not been mentioned or used in research in the SCD population thus far. It is fundamental for understanding the epidemiology of diseases and how they

could change due to changes in conditions (e.g., civil unrest, mass migration, natural disasters, and global climate change; Krieger, 2000, 2020). Therefore, considering the burden of COVID-19 on those with SCD and the general population in the United States, the ecosocial theory would help illuminate the underlying health disparities during the pandemic. This integrative theory shows all the different social determinants that influenced the spread of COVID-19 in the United States from the social, racial, ecological, biological, and political perspectives.

Public health sectors of the different states, in close collaboration with federal programs such as the Behavioral Risk Factor Surveillance System, National Health and Nutrition Examination Survey, and the Census, monitor the health of U.S. citizens. Those governmental agencies collected data on health indicators like infant mortality rate, life expectancy, and various social determinants of health (SDH), including a person's age, race/Hispanic origin, sex, where a person lived, environment, socioeconomic status, and social injustice (Hahn et al., 2018; Kim & Bostwick, 2020; Krieger, 2020; Smedley et al., 2003). The political atmosphere also impacted health and health outcomes (Gelfand et al., 2021; Hahn et al., 2018; Krieger, 2020). The COVID-19 pandemic has been challenging and has impacted every aspect in both the private and public sectors in the United States and the entire globe (Fauci et al., 2020; Gebhard et al., 2020; Minniti et al., 2021; Panepinto et al., 2020). Moreover, despite the advancement in technology, medicine, and public health systems in the United States, politics, racial, and social inequalities have fueled the COVID-19 pandemic. This issue led the United States to claim the highest rate of COVID-19 cases and death of any nation, overwhelming and challenging the country's

public health sectors, research, and medical communities (Fauci et al., 2020; Robertson, 2021; WHO, 2021).

The social, political, and ecological construct of a community or a nation has a pivotal role in dictating the health and health outcome of the population. According to Carter-Smith (2021), social epidemiology is the study that illuminates how "the role of politic, social, environmental, and institutional factors played on the overall health of individuals and the population" (p. 20). Further, from social epidemiology stems the ecosocial theory, which explains the social iniquities of health and determinants of disease distribution in the population by merging social and biological concepts with historic and ecological viewpoints (Carter-Smith, 2021; Krieger, 2000, 2020). The effect of the pandemic not only on the general population but also on the underserved and disparaged ecosocial theory would better explain communities. The theory gave a better understanding of the various inequalities and inequities of health to underserved communities, especially persons with SCD that are disproportionately impacted by the COVID-19 pandemic in the United States.

Compared to other nations during this pandemic, the various social and ecological factors helped in the propagation and spread of the pandemic in the United States (Gelfand et al., 2021; Robertson, 2021; Yam et al., 2020). The ecosocial theory would help the vulnerable community, especially those with SCD, to understand not only the science but also the political and social influence of the spread of COVID-19 and develop protective measures by following public health recommendations of wearing a mask, social distancing, hand washing, the appropriate time to seek medical care and get

vaccinated and boosted (Fauci et al., 2020; Gelfand et al., 2021; Krieger, 2000). Moreover, the above theory would help policymakers, public health and medical practitioners, the SCD community, and the different stakeholders to get a better understanding of the epidemiology, social and political implications of both diseases (SCD and COVID-19) and develop tailored age- and race/Hispanic-origin-specific guidelines and preventive interventions for proper mitigation of the COVID-19 pandemic in the United States (Fauci et al., 2020; Gelfand et al., 2021; Hsu et al., 2020; Krieger, 2000, 2020; Panepinto et al., 2020; Robertson, 2021; Tonen-Wolyec et al., 2020). Although it was evident that the pandemic had affected the U.S. general population, the underserved communities, especially persons with SCD, bore much of the brunt (Panepinto et al., 2020; Tonen-Wolyec et al., 2020).

Researchers have documented how stress is associated with exacerbating acute and chronic diseases, especially among the vulnerable population (Vinkers et al., 2020). SCD remained a stressful medical condition for those with the disease and their families, while the public panicked from the COVID-19 pandemic as the social isolation; government-mandated orders; the politicization of the pandemic; and economic, racial, and health disparities all caused enormous stress for the SCD community (Buscetta et al., 2022; Panepinto et al., 2020; Vinkers et al., 2020). All those mentioned above created the various racial, social, and health iniquities, especially in U.S. vulnerable populations, which would be best articulated with Krieger's (2000, 2020) ecosocial theory (Gelfand et al., 2021). The theory would help better understand all the factors that had fueled the pandemic and illuminate the various health iniquities in the United States. Applying this

theory would also direct and facilitate good health policies. Leaders of such policies may employ meaningful preventive measures necessary for protecting subgroups or communities of persons with SCD. Such leaders may help prevent further crises, hospitalizations, and deaths from the pandemic.

Nature of the Study

I addressed the research question and the timeframe of this quantitative study by aligning it with the most appropriate study design and method for analysis. In this study, the specific research design included a retrospective cross-sectional survey of COVID-19 mortality among persons with SCD examined in a single period from January 2020 to March 2021 (Aschengrau & Seage, 2020; Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Rudestam & Newton, 2015; Salazar et al., 2015). Employing the correct study design in this study gave a clear picture of the mortality rate of patients with SCD from COVID-19 during the pandemic. This study helped show the age and race/Hispanic origin of U.S. COVID-19 mortality rates among SCD patients during the study.

Additionally, I answered the research questions based on having the correct measurements of the variables in the study. As described by Frankfort-Nachmias and Leon-Guerrero (2018) and Gerstman (2015), having the correct measurement of the study variables would help select the most appropriate statistical test for analysis and be vital in coming up with the correct findings of the study. In this study, both the independents and the DVs were categorical. The IVs consisted of two independent categorical variables, with the following nominal variables: race/Hispanic origin (1 = non-Hispanic Black, 2 =

non-Hispanic White, and 3 = Other [includes but is not limited to Hispanic, non-Hispanic Asian, Non-Hispanic American Indian, non-Hispanic Native Hawaiian, people of multiple races and those with unknown race or Hispanic origin]) and an ordinal variable age-groups (1 = 0–19, 2 = 20–39, 3 = 40–59, and 4 = 60+). The binomial DV was for COVID-19 mortality (1 = death from COVID-19 and 0 = not death from COVID-19) among persons with SCD. This quantitative analysis answered whether there was a relationship between age and race/Hispanic origin in COVID-19 mortality among persons with SCD in the United States when the appropriate statistical test was employed.

Although parametric and nonparametric statistical tests were used to answer the research questions, it was paramount to link the measurement of the variables in the study with the best statistical test for inquiry. I set criteria that allowed the test to be used. For instance, multiple regression, linear regression, chi-square, or Fisher Exact Test was used to investigate the association between categorical variables (Blatyta et al., 2020; Brandão et al., 2018; Díaz de Neira et al., 2021; Fan et al., 2021). However, considering the levels of measurements of both the categorical IVs with two or more groups and a binary DV, the association between the variables was investigated by using a binomial logistic regression as the statistical test to answer my research questions (e.g., Creswell & Creswell, 2018; Díaz de Neira et al., 2021; Fan et al., 2021; Frankfort-Nachmias & Leon-Guerrero, 2018; Laerd Statistics, 2018; Tzeng et al., 2021). Moreover, a binary logistic regression was used as the most appropriate test for this study, but various criteria had to be met. Hence, meeting the criteria was an impetus for employing the test statistic for the analysis of the study.

The two IVs were grouped and categorical in this study, while the DV was binary. As defined by Laerd Statistics (2018), "a binomial logistic binomial which is also popularly known as logistic regression and must have a dependent variable that is dichotomous with one or more independent variable that was categorical or continuous level of measurement" (p. 20). The author also described how logistic regression helped to predict the probability that an observation fell into one of two categories of a dichotomous DV. However, many assumptions had to be met for this statistical test. There had to be independent observations due to the nominal and ordinal levels of measurement, the two independent categorical grouping of the IVs, and the DV's dichotomous nature. Also, there must be linearity between the DV. Both IVs would meet when the DV was continuous, and satisfying the assumptions enabled binary logistic regression as the most appropriate statistical test for analysis (see Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Laerd Statistics, 2018; Salazar et al., 2015). Therefore, the nature of this study was quantitative with a binomial logistic regression design. This method and design were consistent with understanding the association between age, race, and COVID-19 mortality in persons with SCD in the United States. The race/Hispanic origin and age difference in the COVID-19 mortality rate of those with SCD would be the primary concern to be examined in this study. This quantitative analysis should answer the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD.

Definitions

Age: COVID-19 does not discriminate against whom it affects (CDC, 2020a, 2020b; USDHHS, 2020). In this study, the chronological age from 0 to 60+ of persons with SCD infected and died from the pandemic in all 50 states, including Washington, DC, was a categorical variable coded into four different age groups.

COVID-19 mortality: To date, the COVID-19 pandemic is the deathliest global health crisis that has killed not only people in the general population but has also disproportionately killed the immunocompromised, such as persons with SCD (CDC, 2020a, 2020b; Panepinto et al., 2020; Tonen-Wolyec et al., 2020). In this study, COVID-19 mortality was the binary DV, where persons with SCD who died from COVID were coded as 1, while those who did not die from COVID-19 were coded as 0.

Gene: A gene is a protein of DNA responsible for a person's genetic makeup (CDC, 2020a).

Gene mutation: According to USDHHS (2020), a gene mutation is a permanent alteration in a normal DNA's shape and function, which may lead to not only diseases such as SCD but also cancer.

Globalization: This term is the interaction and interexchange of ideas from the socioeconomic to political level from the individual to organizational of one country with others globally through transportation (Sotomayor & Barrero, 2020). This phenomenon has been observed to facilitate the spread of hereditary and emergent diseases from one part of the globe, from human-to-human, animal-to-human interactions, and vice versa (Fauci et al., 2020; Sotomayor & Barrero, 2020).

Hemoglobinopathy: This term refers to any red blood disorder that results in an abnormality in the structure or production of the red blood cell, thereby interfering with cell and organ function in the body (CDC, 2020a). According to the CDC (2020a), hemoglobinopathies, such as SCD and thalassemia, are genetically transmitted generationally.

Orphan disease: This term refers to rare diseases affecting fewer than 200,000 people or being ignored (Lee et al., 2019). Certain diseases, be they chronic or acute, have caught the attention of policymakers, public health officials, and medical research institute leaders. Funders want to sponsor research and invest in developing new pharmacotherapy for those diseases because of financial gains. Although this information was true for rare diseases like cystic fibrosis, Lee et al. (2019) found the reverse true with SCD, making SCD an orphan disease with no return on investment.

Race/Hispanic origin: As with age, the pandemic affected people from all racial and ethnic groups (CDC, 2020a, 2020b; USDHHS, 2020). However, in this study, the provisional data set used race/Hispanic origin as an independent variable further divided into three categorical groups: non-Hispanic Black, non-Hispanic White, and Other (as reflected in the code book). Moreover, although non-Hispanic Black and non-Hispanic White were self-explanatory, the other was broad and was not defined in the data set code book. However, after emailing the originators of the data set to clarify “other,” I got a reply after a couple of days. According to the email correspondence from the National Center for Health Statistics (NCHS) and the CDC, the Mortality Statistics Branch in the Division of Vital Statistics,

> The "Other" category in the "Race or Hispanic origin" column is a residual that counts decedents from all other race and Hispanic origin groups not shown specifically on the table. The "Other" category includes (but is not limited to) Hispanic, Non-Hispanic Asian, Non-Hispanic American Indian, Non-Hispanic Native Hawaiian, people of multiple races, and those with unknown race or Hispanic origin.

SCD: This disorder is one of the sickle cell disorders caused by a mutation of a change that results in the change of the shape of red blood cells from oval to sickle shape, causing morbidities and even mortality (CDC, 2020a, 2020b; Mucalo et al., 2021; Telfer, 2019; Teulier et al., 2021; USDHHS, 2020). In this study, the target population was U.S. SCD patients who were infected and died from COVID-19.

SCD community: This community consists of all stakeholders, such as public health and medical professionals (e.g., public health specialists, doctors, nurses, pharmacists, social workers, therapists, and faith-based societies), parents, caregivers, and individuals with SCD (CDC, 2020a; Lee et al., 2019).

Severe acute respiratory syndrome (SARS): This term refers to an acute injury of the respiratory system, especially the lungs, from infections such as the COVID-19 virus. It can lead to lung damage and death due to the deprivation of oxygen from the bad lung to other organs of the body (Mucalo et al., 2021; Teulier et al., 2021).

Vaso-occlusive crisis (VOC): VOC is a disabling, painful crisis mostly experienced by SCD patients. It results from the occlusion of microvascular vessels,

leading to extreme and generalized painful crises, chest pain, end-organ damage, stroke, and even death (Telfer, 2019; Teulier et al., 2021).

Assumptions

SCD is a complicated genetic disease with many commodities and mortality (Mucalo et al., 2021; Panepinto et al., 2020; USDHHS, 2020). However, with the high incidence and mortality of COVID-19 and the 100,000 U.S. children and adults living with SCD, it was assumed that there would be increased incidence, hospitalization, and death from the pandemic among those with SCD in the United States (USDHHS, 2020; WHO, 2021). It was also assumed that the deaths of those with SCD from the pandemic might have been underrepresented as possible death at the beginning of the pandemic. These deaths might have been missed or not registered as COVID, a misrepresentation that the person died from SCD complications or other unknown causes. For instance, the SECURE-SCD Registry Surveillance Epidemiology of COVID-19 Under Research Exclusion collected data on those with SCD infected with COVID-19 (updated March 2022). The registry showed a global mortality rate of just 19, while the CDC's (2020a) provisional data demonstrated much higher mortality in the United States alone (Panepinto et al., 2020).

It was assumed that this quantitative cross-sectional design was appropriate to get a valid result during the time of the study retrospectively from January 2020 to March 2021. Additionally, it was assumed that the variables would be correctly measured and coded to facilitate the employment of the most appropriate statistical test of binary logistic regression. This test was assumed in alignment with the methodology to realize a

valid and reliable result from the study (Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Laerd Statistics, 2018).

Lastly, considering the U.S. pandemic's social, political, and negative economic impact, it was assumed that Krieger's ecosocial theory would be linked to this study. I assumed it would reveal the various health and racial iniquities responsible for the propagation of the pandemic, especially in vulnerable populations like those with SCD in the United States (Gelfand et al., 2021; Krieger, 2000, 2012, 2014, 2020).

Scope and Delimitations

SCD is a silent global health issue that warrants attention for those with the disease; their families and communities bear much of the burden. The COVID-19 pandemic is the worst infectious disease outbreak that has impacted individuals and their communities globally (Buscetta et al., 2022; Fauci et al., 2020; Sohrabi et al., 2020; Vinkers et al., 2020). Panepinto et al. (2020), Payne et al. (2020), and Clift et al. (2021) discussed how persons with SCD were disproportionately affected by COVID-19 and were more likely not to only suffer from the severe form of COVID-19 and be hospitalized but also have a high risk of dying when compared to the general population. Although SCD and COVID-19 are global health issues and many research studies have been done in other nations, I focused on persons with SCD in all 50 U.S. states, including the District of Columbia. I studied those infected and who had died of COVID-19, as recorded in the CDC registry, excluding those with SCD abroad and those with sickle cell trait. Although relevant data on SCD and COVID-19 on age, sex, and race/Hispanic origin mortality rate were lacking, I attempted to find an association between age,

race/Hispanic origin, and COVID-19 mortality among those with SCD in the United States. I used the CDC provisional mortality data set, specifically for SCD patients who died from COVID-19. Moreover, I increased the validity and reliability because the mortality data were gathered rigorously from all 50 U.S. states, including the District of Columbia. I did so to ensure the generalizability of the study as a measure to improve health outcomes in this population and positively impact social change.

Limitations

SCD patients are at increased risk and are disproportionately affected by the COVID-19 pandemic (Panepinto et al., 2020; USDHHS, 2020). Compared to the morbidity and mortality of the SCD population before the pandemic, global findings from the registry demonstrated an increase in hospitalization and death, resulting in excess death during the pandemic (Clift et al., 2021; Payne et al., 2020). However, this cross-sectional study explored the relationship between age, race, and mortality due to COVID-19 in U.S. persons with SCD. Thus, some limitations might have affected the internal and external validity of the study. The first limitation of this study was the cross-sectional study design causing temporality, for it did not tell if the exposure or the disease came first, which might have led to bias in the result of the research (Aschengrau & Seage, 2020, p. 161). Although other designs, like a longitudinal study, could have been employed, a cross-sectional study design was ideal for this research.

The ICD 10 CODES and Cause of Mortality Registry were used to select patients who died due to the pandemic; however, during the early stages of the pandemic, it would have been difficult to assess if deaths were due to other SCD complications, such

as heart and other respiratory diseases than COVID-19. Research at the beginning of the pandemic stipulated that only older adults were prone to and succumbed to COVID-19 and neglected that children with an underlying medical condition, such as those with SCD, could also contract COVID-19 and eventually die from it, which led to an underestimation of the mortality rate as the second limitation (Tzeng et al., 2021). The third limitation stemmed from not considering those with SCD who died and were unregistered and accounted for gave an underestimation of the mortality rate. All the limitations above skewed the study, possibly causing misclassification and selection bias.

In quantitative studies, having a large sample size is vital to ensure the validity and generalizability of the study. According to Aschengrau and Seage (2020), Creswell and Creswell (2018), and Salazar et al. (2015), an appropriate sample size would dictate the power and effect of a study. The fourth limitation of this study was the small sample size, which may affect the generalizability of the study. To minimize the sample size limitation and to increase the reliability and validity of this study, random sampling, age, and race/Hispanic origin stratification was addressed.

The last limitation of this study stemmed from how the variable race/Hispanic origin in the data set was coded in the code book. Although the race/Hispanic origin subcategory of non-Hispanic Black and non-Hispanic White was self-explanatory in the code book, the data set did not clearly define the category “other.” As discussed above, I contacted the owner of the data set to clarify what “other” consisted of and got a response via email on the coding of “other,” which was broad but understandable.

Significance of the Study

The racial tension and the various SDH existing in U.S. society have helped fuel poor health and health outcomes, especially in underserved communities (Kim & Bostwick, 2020; Moore et al., 2020; Smedley et al., 2003). This study is significant in that various SDH that exist, such as socioeconomic challenges and injustice, access to health information, and health care in U.S. society, have significantly contributed to rendering some subgroups, especially people of color, more vulnerable to suffering from many adverse health and health outcomes (Fauci et al., 2020; Mburu & Odame, 2019; Menapace & Thein, 2020; Moore et al., 2020; Panepinto et al., 2020; Smedley et al., 2003; Tezol & Unal, 2021; Tonen-Wolyec et al., 2020). Kim and Bostwick (2020) and Moore et al. (2020) documented that people of color, such as the Blacks and Latinos subgroup, would suffer more from most communicable and noncommunicable diseases. This finding may show how those in poor communities, such as African Americans and Hispanics in impoverished communities with a lot of SDH, are prone to having poorer prognoses than their White counterparts (Kim & Bostwick, 2020; Krieger, 2020; Moore et al., 2020; Panepinto et al., 2020; Smedley et al., 2003).

Moreover, SCD is not an isolated hereditary medical condition, for it is found among other racial groups in other parts of the globe but is more prevalent among individuals of Black ancestry (Lee et al., 2019; Panepinto et al., 2020). Although African Americans have been disproportionately affected by SCD, African Americans with SCD are highly susceptible to COVID-19 and to the worst health complications and even death when affected (Clift et al., 2021; Lubeck et al., 2019; Moore et al., 2020; Panepinto et al.,

2020; Teulier et al., 2021). The various SDH in the communities and the comorbidities faced by persons with SCD made an excellent recipe for getting infected by COVID-19. Hence, being an African American with SCD in an underserved community compounded their already compromised status for a severe COVID-19 outcome and eventually death from it when infected by the virus.

Furthermore, the COVID-19 pandemic has negatively impacted individuals, families, and all the social, medical, public health, and economic institutions globally (Béné et al., 2021; Buscetta et al., 2022; Davvetas et al., 2022; Fauci et al., 2020; Pronk & Faghy, 2022; Vinkers et al., 2020). The enormous public health, healthcare access, and socioeconomic challenges of SCD and COVID-19 were not limited to the African Americans communities in developing nations in sub-Saharan Africa but also in the United States, Europe, the Middle East, and China (AbdulRahman et al., 2020; Beerkens et al., 2020; Gebhard et al., 2020; Panepinto et al., 2020; Smedley et al., 2003; Teulier et al., 2021; Tonen-Wolyec et al., 2020). However, though universal, the SCD and COVID-19 challenges have been pronounced in the United States (AbdulRahman et al., 2020; Mucalo et al., 2021; Panepinto et al., 2020; Payne et al., 2022). This dilemma might be a reason that the Unites States bore much of the burden of the pandemic and persons with SCD compared with other Western nations (Clift et al., 2021; Fauci et al., 2020; Gelfand et al., 2021).

SCD remains a complex genetic disease of global health attention that badly needs more research, specialized medical professionals, and much sensitization and education to the public (Lubeck et al., 2019; Mburu & Odame, 2019; Telfer, 2019; Uyoga

et al., 2019). SCD is a preexisting condition documented as a reason for increased cases, morbidity, and mortality from COVID-19 and therefore warrants measures that would better serve communities with a high prevalence of SCD (AbdulRahman et al., 2020; Gebhard et al., 2020; Mburu & Odame, 2019; Moore et al., 2020; Panepinto et al., 2020; Tonen-Wolyec et al., 2020). Although many treatments and therapeutic protocols are available to manage the SCD crisis, medical advances in research, such as blood infusions, bone marrow, and stem cell transplants, and genomic engineering (e.g., the RNA-guided Cas9 nuclease from the microbial clustered regularly interspaced short palindromic repeats [CRISPR]), may cure many genetic diseases, such as SCD (CRISPR Therapeutics, 2021; Telfer, 2019). Gene therapy, if utilized appropriately, may become the solution for most genetic diseases, such as SCD. Genomic engineering should be encouraged as it would address the aforementioned and cure and alleviate the pain, suffering, and health disparities among the SCD community.

During the early phases of the pandemic, an elderly adult with pre-existing conditions was universally documented to be the most vulnerable to contracting and dying from the COVID-19 infection. However, more research has demonstrated that different age groups can be infected by the COVID-19 virus resulting in different severity and even death (Hsu et al., 2020; Kim & Bostwick, 2020; Lubeck et al., 2019; Mburu & Odame, 2019; Moore et al., 2020; Nardo-Marino et al., 2017; Panepinto et al., 2020; Tonen-Wolyec et al., 2020). Studying the complications of COVID-19 outcomes on persons with SCD while researching race and age differences in the mortality of CVID-19 infection among persons with SCD would help shed light for medical and public

health professionals to understand better, develop, and implement race/Hispanic origin and age-appropriate treatment and preventive measures (Aiko et al., 2018; Ceglie et al., 2019; Isa et al., 2020; Panepinto et al., 2020; Tonen-Wolyec et al., 2020; Veselka et al., 2018).

The results of this research may effect positive social change. It may help prioritize age- and race-specific interventions. Such interventions may minimize incidents and hospitalizations while decreasing mortality and improving health outcomes of persons with SCD and their communities. These actions will help during this deadly COVID-19 pandemic and any other unforeseen pandemic of this magnitude.

Summary

SCD has remained an underappreciated hereditary disease that is a global health issue, especially in the United States (CDC, 2020a; Houwing et al., 2019; Lee et al., 2019; Panepinto et al., 2020; Uyoga et al., 2019). This disease has affected individuals of African descent in Africa and elsewhere (Aiko et al., 2018; Mburu & Odame, 2019; Panepinto et al., 2020). The disease came with many health complications and was not limited to a particular geographical region (Mburu & Odame, 2019; Minniti et al., 2021; Panepinto et al., 2020). Public health agencies, medical professionals, and policymakers had to pay more attention to this disease that came with comorbidities and premature deaths (Clift et al., 2021; Minniti et al., 2021; Mucalo et al., 2021; Panepinto et al., 2020; Teulier et al., 2021). According to Clift et al. (2021), an estimated 8 million to 12 million persons globally had the disease with approximately 15,000 in the United Kingdom and 100,000 in the Unites States with SCD.

Moreover, researchers have documented that persons with a hemoglobinopathy such as SCD are commonly infected by viral respiratory infections from the influenza virus (Beerkens et al., 2020; Mucalo et al., 2021; Panepinto et al., 2020; USDHHS, 2020). However, AbdulRahman et al. (2020) noted that the novel COVID-19 changed the configuration of blood by forming a complex with a 1-beta chain of Hgb, thereby changing the shape and making it dysfunctional. This issue resulted in decreased heme oxygen-carrying capacity. COVID-19 was shown to affect the Hgb beta chain, the same mutated chain among people with SCD. Genetic susceptibility increases the risk of coronavirus infection in SCD communities. The similar physiopathology of the mutated genes between both diseases (SCD and COVID-19) rendered those with SCD more vulnerable to contracting COVID-19 infection. Therefore, individuals with both illnesses suffered from unfavorable health outcomes, creating a disparity between those with and without SCD in the communities (Mucalo et al., 2021; Panepinto et al., 2020; USDHHS, 2020).

In this research, I explored the relationship between age, race/Hispanic origin, AND COVID-19 mortality among people with SCD in the United States Both the independent and the DVs were categorical. Although the IV (i.e., age) was ordinal, race/Hispanic origin was measured as a nominal variable. The DV of COVID-19 death was measured as a binary variable. I found the most appropriate statistical test for analysis was the binary logistic regression based on researchers' suggestions (e.g., Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Salazar et al., 2015).

The cross-sectional nature of this study showed temporality, misclassification of COVID-19 death due to underestimation as relevant data were lacking, and the lack of appropriate sample size all hindered the validity and reliability of the study. However, random sampling and appropriate sample size will increase the power and effect of the study and positively impact social change. Finally, this chapter ended with definitions of some keywords in the study, assumptions, delimitations, and limitations. Analyzing relevant scholarly articles concerning this subject matter is the focus for Chapter 2. Chapter 2 contains the literature review and synthesis of the study broken into different subsections. The chapter begins with an introduction, followed by a discussion of the literature search strategy and the study's theoretical foundation. The literature review of the key variables (i.e., the epidemiology and pathophysiology of SCD and COVID-19, sex and COVID-19, race/Hispanic origin, and COVID-19, SCD and COVID-19, and age and COVID-19) is then discussed in detail. Chapter 2 ends with the summary and transitions to Chapter 3.

Chapter 2: Literature Review

Although the ambiguous nature of infectious disease outbreaks is a threat to society today, genetic disease transmission amongst humankind has been going on for centuries (Fauci et al., 2020). As noted by Fauci et al., Shrestha et al. (2020), and Sigler et al. (2021), emergent and hereditary diseases are found even in remote regions of the globe. The dynamic nature of the population with the sociocultural and racial interaction has facilitated the propagation of diseases across the globe. Although globalization and transportation have improved the livelihood of humans, it has also been responsible for turning endemics into pandemics. It also encouraged social mélange between races and cultures that had spread genetic diseases such as SCD and many emergent infectious diseases from one continent to other parts of the globe (Fauci et al., 2020; Shrestha et al., 2020; Sigler et al., 2021).

Although any infectious agent has the potential to cause disease outbreaks, historically, viral agents have been responsible for causing pandemics, especially those that affect the respiratory system (Fauci et al., 2020). As Gebhard et al. (2020) noted, the outbreak of the acute respiratory illness that started in Wuhan, China, and was identified as SARS-CoV-2 (COVID-19) in 2019 had traveled across continents to 196 countries and was declared by WHO as a pandemic and accounted for 2 million cases and over 130,000 deaths globally as of April 2020 (Introduction, para. 1). Gelfand et al. (2021) also indicated how the pandemic from the epicenter of Wuhan had crossed the planet. As of Oct 2020, 39 million cases and over 1 million deaths were reported worldwide (Introduction, para. 1). This disease is rapidly transmissible and has quickly changed

from a simple outbreak into a pandemic. The global distribution of this infectious disease and the lethality from the respiratory presentation of the disease was a cause for concern by the public and medical health community (CDC, 2020a, 2020b).

COVID-19 did not discriminate against those it affected; however, people with other medical conditions and weak immune systems were more prone to contracting the disease (CDC, 2020a, 2020b; WHO, 2020). According to Panepinto et al. (2020), CDC (2020a, 2020b), and Mucalo et al. (2021), people with compromised immune systems and other underlying medical conditions had a high chance of getting and suffering from a severe form of COVID-19 infection. This significant finding showed that those more susceptible to the pandemic included patients with hypertension, obesity, diabetes, cancer, and blood diseases like SCD. The authors above identified that although the pandemic can negatively impact the health of any person, SCD patients remained at a higher risk of contracting COVID-19 infection.

SCD remains a serious hereditary hematologic medical condition and public health issue that is underappreciated globally and in the United States, making it an orphan disease (CDC, 2020a, 2020b; Houwing et al., 2019; Lee et al., 2019). This hemoglobinopathy has disproportionately affected underserved communities and people of color; it may also be exacerbated by the COVID-19 pandemic (Mburu & Odame, 2019; Minniti et al., 2021; Panepinto et al., 2020). The various SDH in those poor communities may have contributed to the health inequalities associated with the COVID-19 pandemic. This finding indicated that disadvantaged communities inhabited by

persons with many underlying medical conditions and people of color bore most of the brunt and remained disproportionately affected by COVID-19.

SCD is an immunocompromised illness with many comorbidities of which patients with SCD remain at high risk of developing the severe form of COVID-19 infection (Minniti et al., 2021; Mucalo et al., 2021; Panepinto et al., 2020). Moreover, those concurrently affected by SCD and COVID-19 developed the severe form, with the worst health outcomes, such as death, from the pandemic (Ambrosino et al., 2020; Ceglie et al., 2019; Fauci et al., 2020; Gebhard et al., 2020; Kim & Bostwick, 2020; Minniti et al., 2021; Panepinto et al., 2020; Payne et al., 2022; Redaelli et al., 2021; Teulier et al., 2021). Having SCD and contracting COVID-19 is not a favorable health combination. Understanding the medical ramification of patients with SCD and infected with COVID-19 warrants research, policymakers' involvement, public health attention, and sex-specific interventions. The goal should be to minimize health disparities and improve health outcomes by prioritizing treatment for persons with SCD. The purpose of this retrospective cross-sectional study observational study was to investigate the relationship between age, race/ethnicity, and COVID-19 mortality among persons with SCD in the United States. I used the CDC provisional mortality data set to explore the relationship between the IV and the DV in this study.

COVID-19 infection among persons with SCD can result in serious complications, morbidities, and death. Mucalo et al. (2021) noted that children and adult patients with SCD with comorbidities had severe cases of COVID-19 infection. Additionally, the case-series findings by Panepinto et al. (2020) found that mortality due

to COVID-19 was observed among those with severe and mild-to-moderate SCD genotypes and those with mild-to-moderate severity of COVID-19. Due to the lack of relevant age, race/Hispanic origin, and sex-specific data, empirical SCD and COVID-19 data were needed to help assess the severity of COVID-19 on persons with SCD in the United States. Thus, Panepinto et al. (2020) and Payne et al. (2020) were unconfident whether the increased COVID-19 infection rate was due to the COVID-19 pandemic's influence in exacerbating preexisting SCD concurrent conditions. Despite the health complications and death from the pandemic among those with SCD, there remains a lack of relevant data. Little or no association between different variables and COVID-19 has been determined since the pandemic started in 2019; however, there remains an ongoing collection of data, and most up-to-date data are incomplete. Hence, more data and research are needed to investigate whether age and race/Hispanic origin influence the mortality rate from COVID-19 in U.S. persons with SCD.

In this study, both IVs were categorical, and DVs were scale variables. Although the IV of age was measured as an ordinal variable, race/Hispanic origin was measured as nominal. Both IVs were categorically grouped. On the other hand, the DV of COVID-19 death among those with SCD was measured as a binary variable.

In this chapter, I explore the association between age, race/Hispanic origin, and COVID-19 mortality among SCD in the United States. I provide a thorough review of existing literature on the association of my research question. I begin with a detailed account of the various strategies employed to search the literature. Next, the theoretical framework for the study is elaborated in this chapter. I then provide a synopsis of the

current literature on the various variables and investigate their associations in the study. A summary of the main findings of the literature review is discussed before transitioning to Chapter 3.

Literature Search Strategy

Selected articles relating to SCD, COVID-19 alone, SCD and COVID-19, age, race or Hispanic origin, race and Hispanic origin, sex, and gender differences in the susceptibility, severity, and COVID-19 outcome and mortality between persons with SCD and persons without the disease were searched from accessible databases. Search engines, such as PubMed (National Library of Medicine) and SAGE Journals, and current peer-reviewed articles were comprehensively searched for by using Walden University's (n.d.-a, n.d.-b, n.d.-c) electronic database. I also conducted a multidatabase search that included ProQuest and internationally recognized public health websites like those of the CDC, USDHHS, SECURE-SCD registry, and WHO.

The keywords and terms searched included *sickle cell disease*; *the age, race/Hispanic origin, sex, and gender difference in sickle anemia*; *sickle cell anemia crisis*; *sickle cell anemia in Sub-Saharan Africa (SSA)*; *sickle cell disease in the United States*; *COVID-19 and SCD*; *the impact of COVID-19 on persons with SCD in the United States and other regions of the globe*; *sickle cell and comorbidities*; *sickle cell disease genotypes, race, and health in the United States*; *COVID-19 and race/Hispanic origin in the United States*; *race and SCD, age, and COVID-19*; and *SCD and death due COVID-19*. I found 150 plus articles, which I narrowed to the recent ones from 2018 to 2022,

except for seminal articles published in 1994, 2001, and 2003. These seminal articles were original and classic materials with vital contributions worth inclusion in this study.

Theoretical Foundation

A society's socioeconomic and political constructs can dictate the health indicators such as the infant mortality rate, life expectancy, and the general health and health outcome of its citizens (Wilkinson & Pickett, 2010). According to Wilkinson and Pickett, poor health outcomes and social problems are more common in unequal countries and are fueled by political or economic changes and vice versa. The various SDH and the genetic makeup of an individual, a person's age, race/Hispanic origin, sex, where a person lives, their environment, socioeconomic status, and the social injustice and the political state of the country are determinant factors in dictating their general wellbeing and health outcomes (Gelfand et al., 2021; Hahn et al., 2018; Kim & Bostwick, 2020; Krieger, 2001; Smedley et al., 2003). Smedley et al. (2003) and Gelfand et al. (2021) stated that social injustice, poor public health systems, and governance were strong predictors of health disparities. The pandemic had created widespread confusion due to misinformation from public health and media, distrust in politician and scientist recommendations, economic hardship, social isolation, and poor health policies on mitigation, all from the political influence in scientific decision-making in the United States (Lebedeva, 2022; Moore et al., 2020; Peng, 2022).

The social and political implications of COVID-19 have greatly contributed to the disparities associated with the general population and SCD communities due to the pandemic. Thus, it is worth exploring the above determinants and perspectives.

Moreover, Smedley et al. (2003) and Gelfand et al. (2021) articulated how, despite the U.S. advancement in technology, medicine, and public health systems, the politics of COVID-19, racial issues, and social inequalities damaged public confidence in mitigation strategies. These issues worsened the pandemic, causing the highest rates of cases, hospitalizations, and deaths for minorities. These issues overwhelmed and challenged the public health sectors, research, and medical community globally, particularly in the United States.

In the world of social science research, various theories have contributed significantly to gathering knowledge and better understanding people's perceptions of the world. Additionally, theoretical and conceptual frameworks play a vital role in social epidemiology and have been typically used to seek and understand social inequities of health and the etiology and distribution of diseases (Chijioke et al., 2021; Krieger, 2020).

In this research, although other theories such as Simon's (1952) theory of interaction could have been used, doing so would not have accurately addressed the social and political impact of the impact on COVID-19 infection on the SCD community in the United States. Homan's theory of interaction might explain why one would expect the IVs to influence the DVS, but it would not appropriately link theory and method in this research (see Creswell & Creswell, 2018; Salazar et al., 2015; Warner, 2013). Furthermore, I could also have employed the health belief model of self-efficacy. According to Glanz et al. (2015), self-efficacy was applied to many domains of health behavior and adopted for use in other theories, such as the health belief model. The major appeal of self-efficacy in health behavior was that it was a modifiable factor with which

one could intervene. Sources of self-efficacy include personal experiences, persuasion, and vicarious experiences learned from observing others or modeling. The health belief model would play a great role in encouraging those with SCD not only to follow science and get vaccinated but also to maintain social distancing, wear a mask, and wash their hands regularly as a measure to protect themselves and others as well, but this model would not address the social inequities of the pandemic on patients with SCD like the ecosocial theory of disease distribution would.

In social epidemiology, the ecosocial theory has helped address the various social inequities of health and the etiology and distribution of diseases. The theory has also played a vital role in answering questions on "who" and "what" caused the health disparities and distribution of diseases in a population that helped to elucidate the interplay between societal and biological influences of diseases (Krieger, 2001). As Krieger (2001) noted, social epidemiology was first noticed in the mid-20th century, around 1950. Krieger stated, "It is the study of social factors in the etiology of disease" (para. 20). Krieger further elaborated that social epidemiology illuminated how "the role of politics, social, environmental, and institutional factors play on the overall health of individuals and the population" (para. 20). Social epidemiology is made up of three theoretical frameworks which include: psychosocial theory, social production of disease and or the political economy of health, and ecosocial theory and related multilevel framework.

Although all three theories were geared to explain social disparities in health in the population, it was vital to know the most appropriate framework for the current study.

With that in mind, I used the ecosocial approach without the multilevel framework to explain the population's social iniquities of health and determinants of disease distribution (see Krieger, 2001). This approach merged social and biological concepts with historic and ecological viewpoints (Krieger, 2001); thus, it was the most appropriate theory for this study. Social epidemiologist Krieger introduced the ecosocial theory and gained recognition in 1994. Krieger's (1994) ecosocial theory of disease distribution was widely used in public health, especially in epidemiology. It is fundamental for understanding the epidemiology of diseases and how they can change due to changes in conditions (e.g., civil unrest, mass migration, natural disasters, and global climate change; Krieger, 1994, 2000, 2001, 2020). Therefore, considering the burden of COVID-19 on those with SCD and the U.S. population, the ecosocial theory was an integrative theory that touched on all the different social determinants that had influenced the spread of COVID-19. These determinants ranged from social, racial, ecological, biological, and political perspectives.

Many researchers have successfully used the ecosocial theory to link research, theory, and method. Although not specifically stated as the framework employed in their studies, Moore et al. (2020) and Panepinto et al. (2020) discussed how the various SDH and racial injustices had created COVID-19 disparity among people of color in underserved communities, especially in U.S. COVID-19 hotspots. In addition to the social and ecological disparities, there exist the biological disposition of persons with SCD. All the above determinants put the patients at higher risk of getting the severe form

of COVID-19 and succumbing to the complications of SCD as well (Minniti et al., 2021; Mucalo et al., 2021; Panepinto et al., 2020).

There was social and political pressure at a global scale on how to address the pandemic properly (Gelfand et al., 2021; Kim & Bostwick, 2020; Robertson, 2021; Vinkers et al., 2020; Yam et al., 2020). Moreover, the politicization of the COVID-19 pandemic in the United States and the psychological trauma on SCD patients and their families could be analyzed using the psychosocial and social production and the political economy of health theoretical frameworks. However, the genetic predisposition of patients with SCD to many comorbidities and severe COVID-19 infection, in addition to the degree of spread of the COVID-19 pandemic due to globalization, transportation, and social interactions between persons worldwide, warranted the employment of the ecosocial theory (e.g., Fauci et al., 2020; Gelfand et al., 2021; Krieger, 2001; Mucalo et al., 2021; WHO, 2021). Krieger (2001) supported the biological and societal influence of the theory by emphasizing how the ecosocial theory was aimed to

> foster analysis of current and changing population patterns of health, disease, and well-being in relation to *each* level of biological, ecological, and social organization (e.g., cell, organ, organism/ individual, family, community, population, society, ecosystem) as manifested at *each* and every scale, whether relatively small and fast (e.g., enzyme catalysis) or relatively large and slow (e.g., infection and renewal of the pool of susceptible for a specified infectious disease). (para. 21)

This theory was efficiently helpful for use in this research. Krieger (2001) narrated how the ecosocial theory would help the vulnerable community, especially those with SCD, to understand the science of the spread of COVID-19. Leaders may develop protective measures by following public health recommendations of wearing a mask, social distancing, hand washing, knowing the appropriate time to seek medical care, and getting vaccinated to prevent morbidity and more mortality from the pandemic. Thus, employing the above theory was appropriate in linking theory and method while answering the research questions of the current study.

The theory will help public health and medical practitioners better understand the epidemiology of both diseases (SCD and COVID-19). They may develop tailored guidelines and preventive interventions to mitigate the COVID-19 pandemic properly in the United States (Fauci et al., 2020; Gelfand et al., 2021; Krieger, 2001; Panepinto et al., 2020; Tonen-Wolyec et al., 2020). The appropriateness of the ecosocial theory in this research was paramount. All the measures discussed by the authors were not only pivotal to protect subgroups or communities of persons with SCD and others but were also helpful to facilitate and prevent further crises, hospitalizations, and deaths from the pandemic by the general population (Fauci et al., 2020; Gelfand et al., 2021; Krieger, 2001).

Literature Review Related to Key Variables

Epidemiology and Pathophysiology of SCD and COVID-19

SCD is a group of hereditary blood disorders that includes sickle cell anemia and thalassemia. SCD is a hemoglobinopathy that affects the Hgb protein due to a missense

mutation of the beta globin chain in Chromosome 11, where the amino acid valine is replaced by glutamic acid leading to many health complications and even death (Panepinto et al., 2020; USDHHS, 2020). The disease has many genotypes and affects people from different races in different regions of the globe. The defective gene is transmitted from parents to their offspring from birth. It may be of generational inheritance if proper education, detection through screening, and prevention of the disease are not ensured.

The physiological change of the red blood cell is responsible for the pathology presented by patients suffering from SCD. The mutated gene causes polymerization and transforms the blood cell from an oval to a half-moon or sickle shape. This issue makes them stick together and interferes with transporting oxygen-rich blood to many organs in the body, thereby causing many health complications and decreasing life expectancy for those with SCD (Beerkens et al., 2020; Lubeck et al., 2019; Madani et al., 2018; Menapace & Thein, 2020; Telfer, 2019; Tezol & Unal, 2021; USDHHS, 2020). The sickling of the red blood cell that interferes with carrying oxygen-rich blood to vital organs in the body has contributed to many health issues, including the death of those with the disease (Lee et al., 2019; USDHHS, 2020).

SCD is an unrecognized health problem affecting people in many parts of the world and needs global health attention. As Lee et al. (2019) posited, SCD is an orphan disease compared to other chronic diseases. Additionally, Mburu and Odame (2019) articulated how SCD has remained a silent global health crisis that requires global awareness of SCD and therapeutic protocols. Such protocols would decrease morbidity

and mortality, especially among SCD children. Though not symptomatic in the first year of life, this disease continues to cause enormous pain, suffering, and death from many comorbidities. Although the disease has a high incidence and prevalence in the continent of Africa, it is also prevalent in other countries across the globe among people that are not of African descent (Lee et al., 2019; Mburu & Odame, 2019).

Additionally, SCD is not limited to a particular race, ethnicity, or geographic region (Lee et al., 2019). Guarda et al. (2020) and Panepinto et al. (2020) reiterated that although SCD was most common among people of African descent in sub-Saharan Africa, the disease is also prevalent and affects people from Latin America; Saudi Arabia; India; the Mediterranean, and Europe as well. However, SCD is more prominent in countries or communities with a high Black population. Therefore, countries in North America, such as the United States, with a large SCD community of about 100,000 SCD patients, need inferential data on age, race, sex, and genotype for research that will influence meaningful social change in those communities.

SCD has also negatively impacted the physical and psychological well-being of those with the disease, their families, and their communities' social and economic aspects (Béné et al., 2021; Buscetta et al., 2022; Davvetas et al., 2022; Vinkers et al., 2020). Aiko et al. (2018) examined the various social factors associated with SCD, such as stigma, lack of support systems, poverty, despair, and hope. The perspectives of parents with children with SCD in Africa who migrated to North America are sought. Data were collected and analyzed using semistructured interviews. Aiko et al. showed that parents still carried vivid memories of SCD in Africa, bringing back psychological and emotional

stress in caring for their children. The psychological challenges faced by parents and family having a child or sibling with SCD seems a universal phenomenon. The authors requested future studies to show whether a clear understanding from an immigrant parent's perspective would be essential in addressing the medical complexities of SCD by healthcare providers in North America compared with those in Africa.

SCD consists of different genotypes, including Hgb SS disease, Hgb SC disease, Hgb S beta + thalassemia, and Hgb S beta zero thalassemia (Panepinto et al., 2020; USDHHS, 2020). Although these different genotypes are considered sickle cell disorders, they have different severity in the manifestation of the diseases. The incidence and the prevalence of the different genotypes vary by race, geographical region, and the severity and clinical symptom depending on the genotype of the individual with the disease. Panepinto et al. discussed how the most common of them is the heterozygote form HgbSS, which causes many comorbidities and presents many sickle cell crisis episodes compared to the other genotypes. It is most prevalent among Black people.

SCD is a serious inherited medical condition that comes with many comorbidities. According to Telfer (2019), SCD comes with many debilitating medical conditions, including severe anemia, acute and chronic pain, fatigue, shortness of breath, painful crises, clubbing, leg ulcers, stroke, chronic renal disease, pulmonary hypertension, and cardiac problems with end-organ and tissue damage. The other health issues arising from SCD alone made it a serious medical and public health issue. All the health issues leading to the medical complications of SCD constituted the underlying medical conditions and comorbidities, rendering them weaker immunity than those without SCD.

SCD patients are prone to many painful crises and respiratory infections. The genetic mutation and the configuration of the RBC of persons with SCD make them immunocompromised and susceptible to many painful crises, especially from acute chest pain syndrome, VOC, and viral influenzas-like illnesses targeting their respiratory system (Panepinto et al., 2020; Telfer, 2019). Therefore, persons with SCD were at high risk during the COVID-19 pandemic (USDHHS, 2020). The weak immune status of those with the disease raised considerable health concerns during any outbreak, especially contagious respiratory infections such as those viral outbreaks of the SARS family, like COVID-19 (Panepinto et al., 2020; Payne et al., 2022; USDHHS, 2020).

The COVID-19 infection affects the respiratory system and causes other health complications and death. Like many pandemics, it has been fueled by globalization and transportation to other parts of the globe from the epicenter of Wuhan, China. Ambrosino et al. (2020) elaborated on how the COVID-19 pandemic was the worst global public health crisis when compared to other coronavirus diseases such as SARS (2002 and 2003) and Middle East Respiratory Syndrome (MERS; 2012). Despite the various treatment, preventive strategies, and the rapid development and availability of vaccines with high efficacy to all, however, up to date, COVID-19 remains a global threat to humankind. The ease of transmissibility of the virus from person to person, especially those with preexisting medical conditions, made the infectious disease agent an excellent recipe to travel across continents and causing a pandemic.

Although the pandemic does not discriminate against those it affects, some communities, age groups, and races were affected more than the general population (Kim

& Bostwick, 2020; Moore et al., 2020). According to Panepinto et al. (2020) and USDHHS (2020), patients with underlined medical conditions and weak immune systems are most vulnerable to being infected with COVID-19 and have the worst health outcome. Panepinto et al. and USDHHS indicated that persons with SCD constituted a high-risk population because of their immune status and were disproportionately affected by the COVID-19 pandemic. The SCD community is at a disadvantage during this pandemic. Although people with the disease have a higher risk factor for contracting COVID-19 infection, not much public health attention has been geared to the enormous morbidity and mortality of this community from the present pandemic in the United States

SCD affects tens of millions of people worldwide. According to Clift et al. (2021), approximately 8 million to 12 million persons globally have SCD. Mburu and Odame (2019) stated that more than 300,000 babies were delivered annually with the disease in Africa. As the CDC (2020b) and USDHHS (2020) noted, SCD is a global health concern and affects 100,000 Americans. In the United States, Black (*OR* = 1/365) and Hispanic Americans (*OR* = 1/16,300) were affected by SCD, as reported by Panepinto et al. (2020). Compared to other Western nations, like the United Kingdom, the United States has the highest population with the disease. This high number of U.S. patients with the disease indicated the prevalence of SCD in the country's diverse and dynamic population, which made a good study on the impact of the pandemic.

Moreover, the COVID-19 pandemic has been medically, physically, emotionally, and economically devastating to individuals and their communities worldwide. However,

when comparing the COVID-19 cases and mortality to other countries around the globe, the United States contributes to 18.4 % of cases and 14.4% of death and demonstrates a racial/ ethnic and sex disparity of both COVID-19 infections and SCD (Fan et al., 2021; Gelfand et al., 2021; Hsu et al., 2020; Kim & Bostwick, 2020; Panepinto et al., 2020; WHO, 2021). The shutdown of the communities due to COVID-19 impacted every individual and every country in one way or another. The medical, emotional, and economic upheavals and share number of cases and deaths due to the pandemic in communities such as SCD in all 50 states in the United States showed COVID-19 outcomes on persons with SCD.

Although COVID-19 has not only affected individuals, their families, and entire communities by disrupting their way of life, it has also affected the medical and public health sectors, and relevant data are scarce in the United States. On the one hand, Moore et al. (2020) illustrated how mortality data disaggregated by race/Hispanic origin were not sufficient to generate reliable estimates of COVID-19 infection in the United States. On the other hand, Ambrosino et al. (2020) and Payne et al. (2020) also identified a sex/gender difference in COVID-19 infection. Further, they explained how research trials had provided COVID-19 outcomes on both men and women. However, age, race/Hispanic origin, gender-specific, and mortality rate research approaches to the analyses of outcome data were absent. Although ongoing studies and data collection are conducted, most current COVID-19 trials take a sex-blind and age-blind approach to the analyses of outcome data. Therefore, obtaining and analyzing relevant data with available variables will better show the association between COVID-19 and SCD in this research.

Race and COVID-19

Historically, in the United States, racial tension, political divides, and mistrust of the political and medical institutions have created a huge disparity in access to health care for the minority population in the country (Hahn et al., 2018; Krieger, 2020). People of color have been known to suffer from any imaginable disease and to experience the worst health outcome from those diseases compared to other racial groups due to social injustice (Krieger, 2020; Smedley et al., 2003; Wilkinson & Pickett, 2010). According to Smedley et al. (2003), "race remained a significant predictor of the quality of health care received" (p. 20). There is an existing mistrust of the medical and research institution by the U.S. minority population (Kim & Bostwick, 2020; Moore et al., 2020; Smedley et al., 2003). This social injustice has created a significant gap in research participation and access to health and mental care, thereby creating iniquities in the health outcomes of the minority population (Krieger, 2020; Smedley et al., 2003; Wilkinson & Pickett, 2010).

The racial disparity in health in the United States was evident from the incidence and mortality during this pandemic (Kim & Bostwick, 2020; Moore et al., 2020). The racial health disparity has been illuminated due to the COVID-19 pandemic in which there is a gap in the existing knowledge of health inequities and the race/ethnicity disparity of the COVID-19 pandemic in underrepresented U.S. communities of color (Kim & Bostwick, 2020; Moore et al., 2020; Panepinto et al., 2020). Moore et al. (2020) investigated whether persons of color were more prone to be affected by COVID-19 and experience a difference in health outcomes than other racial groups by examining county-level disparities among underrepresented racial/ethnic groups in counties identified as

hotspots. Moore et al. noted that African Americans and Hispanics/Latinos were identified as living in hotspots and were disproportionately affected by COVID-19.

Additionally, Hsu et al. (2020) conducted a cohort study at a medical center in Boston, Massachusetts. The study assessed the effect of race/ethnicity, pre-existing medical conditions, hospitalization, and other social factors (e.g., homelessness) that could contribute to severe COVID-19 infection to show how the COVID-19 pandemic could strain the healthcare system in an urban region. The authors deduced that persons of color were more likely to become infected with and experience more severe COVID-19-associated illness and hospitalization. They also would have a higher risk of death from the infection, significantly straining the healthcare system.

Although the pandemic does not discriminate against whom it affects, some communities, especially the disenfranchised counties, suffered much of the burden. In the United States, COVID-19 national and state policies and mitigation recommendations have greatly impacted the Black community's sociocultural and economic aspects (Moore et al., 2020). According to Moore et al., 205 counties in 33 states were identified as hotspots; among these counties, race was reported for ≥ 50% of cumulative cases in 79 (38.5%) counties in 22 states; 96.2% of these counties had disparities in COVID-19 cases in one or more underrepresented racial/ethnic groups. The racial/ethnic disparities in underserved counties and communities during the pandemic were alarming. Nevertheless, the authors acknowledged that the county-level mortality data disaggregated by race/ethnicity were insufficient to generate reliable U.S. estimates. The researchers proposed, "As more complete data are made available in the future, county-level analyses

examining disparities in mortality might be possible" (Moore et al., 2020, Discussion, para. 2). Therefore, researchers have shown the need for relevant race/ethnicity and age-stratified mortality data on the general population and those with suppressed immunity, such as SCD, to explore COVID-19 disparities in the United States.

SCD and COVID-19

SCD is a genetic blood disorder that causes many health complications. Those medical conditions can lead to significant morbidity, mortality for those with the disease, and profound psychological and economic distress to families and the community (Aiko et al., 2018). Conversely, COVID-19 did not discriminate against whom it affects (USDHHS, 2020); however, Fauci et al. (2020) stated that the disease was more common and deathly among immunocompromised people. Those with SCD have many health and psychological issues that adversely affect their overall health and quality of life. Additionally, the weak immune system stems from preexisting chronic medical conditions, such as cancer, diabetes, COPD, cardiopulmonary diseases, and SCD (Panepinto et al., 2020; USDHHS, 2020).

SCD remained one a serious hemoglobinopathy (CDC, 2020b). The genetic predisposition and the immunocompromised nature of persons with SCD made them susceptible to many painful crises and infections, especially respiratory infections caused by influenza and SARS, such as COVID-19 (Clift et al., 2021; Panepinto et al., 2020; Payne et al., 2022; USDHHS, 2020). A study in the United Kingdom demonstrated that those with SCD were almost 4 times at risk of being hospitalized and 2.5 times at risk of dying from COVID-19 compared to the general population (Clift et al., 2021). Although

Clift et al. provided a wealth of relevant information to my research about the mortality rate of COVID-19 in persons with SCD, they did not show the relationship between age, race, and COVID-19 mortality among U.S. patients with SCD.

Additionally, AbdulRahman et al. (2020) conducted a cross-sectional study in Bahrain. The study described the pathophysiology and similarity between COVID-19 infection and the mutated gene responsible for causing SCD. The authors investigated if COVID-19 caused an increase in the severity of SCD in the Bahraini population. Findings showed no difference in the infection rate, clinical course, and viral clearance between SCD patients with COVID-19 to those without SCD. Although the infection rate of COVID-19 among people with SCD did not differ from that of the general population, the sample size (n = 6) was too small to yield statistically significant results, thereby adversely affecting the reliability and validity of the study. Nonetheless, the study constituted a base to compare results with other studies seeking similar relationships. Even though the study did not show higher susceptibility of SCD patients to COVID-19 infection, it was useful in comparing results from similar studies in other regions of the globe, especially in the United States, where the SCD population and the COVID-19 infection rate was very high; and where African Americans remained disproportionately affected. Persons with SCD constituted the high-risk population and were disproportionately affected by the COVID-19 pandemic, possibly resulting in a high fatality U.S. rate. Both diseases came with significant morbidities and mortality. The authors identified that those with SCD who became infected by COVID-19 had a severe form of the disease to which many succumbed, but data were lacking. The association

between age, race-specific, and COVID-19 research had not been explored in the United States.

Age and COVID-19

Globally, age susceptibility to COVID-19 was not well understood during the start of the COVID-19 pandemic (Hussain et al., 2020). Older adults were known to contract the disease faster, suffer from the severe form of the virus, and eventually die from it more when compared to children (Hussain et al., 2020). However, with advancements in research on this variable, COVID-19 did not discriminate by age for children, as they also became infected by the virus, suffered from severe disease, and could eventually die from it (Clift et al., 2021; Panepinto et al., 2020). Moreover, Payne et al. (2020) and Panepinto et al. noticed the high number of emergency room visits, hospitalization, and death of children and adults with SCD from COVID-19 from different registries, such as the SECURE-SCD Registry. This finding indicated that any age could be affected by the virus. The authors reiterated that although any age group could be affected by this pandemic, age-specific fatality data were lacking for those with SCD in the United States. Nevertheless, with much COVID-19 data now available, Guarino et al. (2022) and Payne et al. (2022) found that although SCD patients of any age had a high potential of hospitalization and dying from COVID-19 infection, most patients who died were adults, with a sharp increase of death among those greater or equal to 60 years .

Summary

Globalization and transportation have facilitated the spread of both communicable and noncommunicable diseases. Although SCD is the most common genetic disease affecting people of African descent, SCD affects tens of millions worldwide. Guarda et al. (2020) and Panepinto et al. (2020) stated that the disease was also prevalent in and affected people from Latin America, Saudi Arabia, India, the Mediterranean, and Europe with different genotypes of the disease.

Due to the comorbidities associated with SCD, the CDC (2020b) and USDHHS (2020) discussed how SCD was a global health concern. SCD affects 100,000 Americans (USDHHS, 2020). In the United States, Black (*OR* = 1/365) and Hispanic Americans (*OR* = 1/16,300) were affected by SCD, as shown by Panepinto et al. (2020).

Additionally, though the COVID-19 pandemic affected almost every part of the globe, conversely, compared to other countries, identified U.S. cases and deaths from the pandemic remained the highest, contributing to 18.4% of cases and 14.4% deaths. The virus demonstrated a racial, ethnic, and sex disparity for both COVID-19 infections and SCD (Fan et al., 2021; Gelfand et al., 2021; Hsu et al., 2020; Kim & Bostwick, 2020; Panepinto et al., 2020; WHO, 2021). Studies have shown that COVID-19 ranked number one for U.S. mortality rates. The risk of hospitalization and death from the pandemic surpassed that of heart disease and cancer, and those with suppressed immunity were more susceptible to COVID-19.

Panepinto et al. (2020) and USDHHS (2020) stated that persons with SCD had a weak immune system and were more susceptible to viral influenzas-like illnesses

targeting their respiratory systems; thus, they were a high-risk population and were disproportionately affected by the COVID-19 pandemic. The cross-sectional study by Panepinto et al. showed how U.S. African Americans were disproportionately affected by COVID-19. Of the 178 persons with SCD in the United States who participated in the study, 122 (69%) were hospitalized, and 13 (7%) died due to COVID-19. However, data were lacking to assess whether the findings above were due partly to the impact of COVID-19 exacerbating pre-existing cardiac or SCD concurrent conditions. Also, data were not aggregated to show the severity and outcome of COVID-19 and SCD concurrently during the peak of the U.S. pandemic. Moreover, Guarino et al. (2022) and Payne et al. (2022) found that although SCD patients of any age had a high potential of hospitalization and dying from COVID-19 infection, most patients who died were adults who showed a sharp increase in death among those greater or equal to 60 years.

In social epidemiology, theory plays a vital role as it helps researchers analyze the societal and biological perspective of disease distribution in a population. The psychosocial and social production and the political economy of health theoretical frameworks could help answer who and what was responsible for disease distribution and social inequality of health (Krieger, 2001). However, the genetic predisposition of patients with SCD to many comorbidities made a good recipe for contracting COVID-19 (Mucalo et al., 2021; Panepinto et al., 2020; USDHHS, 2020). SCD patients would have a severe COVID-19 infection and die from complications. All these issues are amplified by the various SDH contributing to propagating the COVID-19 pandemic among the U.S. SCD community, as best explained by the ecosocial theory (Krieger, 2012, 2020).

In Chapter 3, I introduce to the research method and then discuss the research design and rational, the methodology, the data analysis plan, and threats to validity. Finally, I provide a detailed summary presented before transitioning to Chapter 4.

Chapter 3: Research Method

The purpose of this retrospective cross-sectional study observational study was to investigate the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in the United States. COVID-19 infection among patients with SCD could result in serious complications, morbidities, and mortality compared to the general population (Clift et al., 2021; Mucalo et al., 2021; Panepinto et al., 2020). Mucalo et al. noted that children and adult patients with SCD with other comorbidities had severe COVID-19 infection. Additionally, in a case-series study, Panepinto et al. observed mortality due to COVID-19 among those with severe and mild-to-moderate SCD genotypes and those with mild-to-moderate severity of COVID-19. Historically, other coronaviruses have not been as contagious, with cancer and heart disease remaining the leading cause of U.S. deaths. However, according to Ortaliza et al. (2021) and Payne et al. (2020), COVID-19 surpassed both coronary heart disease and cancer as the leading cause of death in late 2020 and the early months of 2021. The authors also indicated that the excess death was not only observed in the general population, but sickle cell registries also demonstrated excess death among patients with SCD during the pandemic.

Moreover, since the pandemic started, data collection has been incomplete (Moore et al., 2020). Due to the lack of relevant age, race, sex, and empirical SCD and COVID-19 data to help assess the severity and mortality of COVID-19 in persons with SCD in the United States, Panepinto et al. (2020) and Payne et al. (2020) were not confident about whether the increased COVID-19 infection rate was due to the COVID-19 pandemic's influence on exacerbating pre-existing SCD concurrent conditions. To my

knowledge, no such study had been done in the United States; hence, further study was needed to show the relationship between age, race/Hispanic origin, and mortality rate of U.S. patients with SCD infected with COVID-19. Therefore, accessing and analyzing the variables will help prioritize intervention by public health and policy decision-makers to improve health and health outcomes in the SCD population.

Research Design and Rationale

The specific research design included a cross-sectional design on COVID-19 mortality among persons with SCD examined in a single period from January 2020 to March 2021 to address the research questions in this quantitative study. Moreover, although the pandemic started in late 2019, the collection of reliable mortality data was still ongoing (Soldi et al., 2021). The high incidence and mortality during the different waves in the United States were within the timeframe as aforementioned (Soldi et al., 2021). The cross-sectional research design was employed to determine the relationship between the variables and answer the research questions and hypotheses.

Making sure the variables in the study were correctly measured and knowing the type of study were essential in linking the research design to the most appropriate method and statistical test for the research. In this study, both the independent and DVs were categorical. The IV of age was ordinal. Race/Hispanic origin was measured as a nominal variable, and the DV of COVID-19 mortality was binary and measured as a nominal variable, as suggested by researchers (e.g., Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Rudestam & Newton, 2015; Salazar et al., 2015). Getting a clear understanding of the measurements of the variables in this

study was vital. The correct measurement of the variables not only helps in the employment of the most appropriate statistical test that answers the research question but also linked the method to the study design that will yield valid and reliable results that are inferential (Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015).

In public health research, many research designs are fundamental in ensuring the correct alignment between a study's method and research design. As mentioned previously, in this research, I chose a cross-sectional research design. Aschengrau and Seage (2020) defined this design as the following: "Cross-sectional studies examine the relationship between the exposure and disease prevalence in a defined population at a single point in time" (p. 161). Additionally, when compared to other observational research designs, the cross-sectional study had some strengths in that whenever a sample of the general population was studied, the results would be generalizable; they were also cost-effective because the research could be carried out in such a short period (e.g., Aschengrau & Seage, 2020; Creswell & Creswell, 2018).

Moreover, the design had some limitations as it assessed for temporality, for it does not tell if the exposure or the disease comes first, which might lead to bias in the result of the research (e.g., Aschengrau & Seage, 2020; Creswell & Creswell, 2018). Furthermore, an observational research method was warranted to answer the research questions above. Other designs, such as the experimental study, and observational studies, such as case-control, case-series, and ecological study, like the longitudinal study, might have been employed. However, because of the snapshot of the period of this

study, a cross-sectional study design was ideal for this research (e.g., Aschengrau & Seage, 2020; Creswell & Creswell, 2018; Salazar et al., 2015).

Due to the benefits of a cross-sectional study, it has been widely used in research to help facilitate health promotion. It enabled data collection on the health condition at one point. Salazar et al. (2015) indicated how

> the association and differences between variables in a cross-sectional study could be variables such as those from a person's race or ethnicity, sex/gender, age, socioeconomic level, or exposure to a certain health risk; phenomena could include prevalence of various health-related conditions, treatments, services, or other outcomes and the factors associated with such outcomes. (p. 20)

However, this design can measure only differences between people, subjects, or phenomena rather than any change; it efficiently establishes the relationships and differences between variables. Aschengrau and Seage (2020) noted that getting the correct measurement of the variables in the research questions and employing the most appropriate statistical tests were essential. Because of the levels of measurement between the two IVs and the DVs, a nonparametric statistical test was used to demonstrate the relationship between the categorical DVs and IVs with the various confounders or modifiers that might exist.

In this study, the variables consisted of two IVs, with categorical grouping with the following nominal variables: race/Hispanic origin made up of three groups (i.e., 1 = *non-Hispanic Black*; 2 = *non-Hispanic White*; and 3 = *Other* [includes but is not limited to Hispanic, non-Hispanic Asian, non-Hispanic American Indian, non-Hispanic Native

Hawaiian, people of multiple races and those with unknown race or Hispanic origin]). The ordinal variable age-groups included four groups (i.e., 1 = 0–19, 2 = 20–39, 3 = 40–59, and 4 = 60+). The categorical binary DV consisted of the number of COVID-19 deaths (1 = *death from COVID-19* and 0 = *not death from COVID-19*) among persons with SCD. This quantitative analysis should answer the relationship between ages, races/Hispanic origin, and mortality rates from COVID-19 among persons with SCD in the United States

Therefore, considering the measurement of the categorical IVs and DV, the association between the variables was investigated using a quantitative method. This method was the most appropriate for providing an idea about the two factors' interactions and the binary nature of the DV; thus, it helped show the most appropriate statistical test to answer my research questions adequately (Creswell & Creswell, 2018; Frankfort-Nachmias & Leon-Guerrero, 2018; Gerstman, 2015; Laerd Statistics, 2018; Warner, 2013). The nominal and ordinal levels of measurement, the two independent categorical grouping of the IVs, and the binary nature of the DV met the assumptions to employ the binary logistic regression as the most appropriate statistical test for analysis. Therefore, the nature of this study was quantitative, with a binary logistic regression design consistent with understanding the association between age, race, and COVID-19 deaths among patients with SCD in the United States.

The unit of analysis in this study was the individuals with SCD who died from COVID-19 in the United States. The ages and racial differences in the COVID-19 mortality rates of those with SCD were the primary concern of this study. The COVID-19

deaths of SCD were examined between age groups and races. This quantitative analysis was used to show if there was an association between having SCD and subsequent dying from COVID-19, as well as if there was an age and racial difference in the COVID-19 mortality rates among persons with SCD in all 50 U.S. states, including the District of Columbia.

Methodology

This Methodology section includes subsections on the population studied, inclusion and exclusion criteria, sampling procedures and sample size, recruitment of participants, and the procedure for access to archival data.

Population

Due to the influence of globalization, SCD and the COVID-19 pandemic are medical conditions that are not limited to a geographical region but affect people and their families worldwide (Mburu & Odame, 2019; Uyoga et al., 2019; WHO, 2021). As stated by Mburu and Odame and Uyoga et al., tens of millions of people have and live with SCD globally. Panepinto et al. (2020) stated that an estimated 100,000 of those with SCD were in the United States and were disproportionately affected by the COVID-19 pandemic. Furthermore, participants of this study represented persons from both sexes, all ages, and races/ethnicities from different geographical locations with different SCD genotypes. Though COVID-19 did not discriminate against whom it infected, people with SCD were more prone to contract and die from the infection than the general population (Clift et al., 2021; Panepinto et al., 2020; Uyoga et al., 2019).

Moreover, Clift et al. (2021) and WHO (2021) stated that the United States had the highest number of deaths from the pandemic and the highest number of SCD patients in the Western world. The pandemic does not select a particular age to affect it because SCD is a chronic hereditary medical condition that affects those with the disease from birth to death. Therefore, the study's target population was persons < 19 years with SCD from who were affected and eventually died from COVID-19 in all 50 U.S. states, including the District of Columbia.

Sampling and Sampling Procedures

A researcher may struggle to visit every household, hospital, and community to collect the necessary data to conduct a study (see Creswell & Creswell, 2018; Salazar et al., 2015). Therefore, using the correct study design, sample technique, and appropriate sample size for the target population was vital (Aschengrau & Seage, 2020; Creswell & Creswell, 2018; Salazar et al., 2015). Salazar et al. stipulated that one of the essential aspects of any study was not only to represent the target population study fairly, but the sampling of the target population must be performed in a manner that will help minimize bias. In this cross-sectional study, probability sampling, or random sampling, was employed to minimize selection bias and yield high generalizability compared to a nonprobability sampling method. Furthermore, Salazar et al. justified the use of a random sampling method in cross-sectional studies: "To make valid inferences using a cross-sectional design, it was extremely important that the results generalize to the larger population; Therefore, the sample selected should be a random sample if possible and of sufficient size" (p. 20). Knowing how to recruit participants and minimize bias in a study

is a vital aspect of research. Although random sampling will minimize bias and guarantee the inference of a study, having the correct sample size remains equally essential (Ellis, 2015; Salazar et al., 2015).

Inclusion Criteria

Respondents who met the following conditions were qualified to participate in the study:

- They were within the age group (0–60+), as stipulated by the data set in 2022.
- They were patients with SCD in 2022.
- COVID-19 infected them during the study in 2022.
- They resided in the United States and died from COVID-19 during the time of research from January 2020 to March 2021, as stipulated by the data set.

Exclusion Criteria

Participants were unqualified for the study based on the following exclusion criteria:

- They had sickle cell trait.
- They did not reside in the United States.
- Individuals with SCD with more comorbidities can die from other underlying medical conditions and not from COVID-19 infection (Telfer, 2019; WHO, 2020, 2021); thus, I excluded those not infected with SCD who had died from COVID-19 (see Mucalo et al., 2021; Panepinto et al., 2020).

Sample Size

The correct sample size remains vital when carrying out any research study, for it indicates the maximum or the minimum number of participants needed to ensure statistical power and generalizability by calculating the required sample size. As narrated by Salazar et al. (2015) and Ellis (2015), analyzing a study's sample size was necessary as it indicates whether a study is statistically significant or not statistically significant when inferring results from the general population. The sample size is directly proportional to statistical power. At the same time, it is indirectly proportional to a study's effect size. Salazar et al. and Ellis stated that having an appropriate larger sample size guaranteed identifying the variables (internal validity) in the study while aiding the generalizability, inference from the population (external validity), and replicability of the study.

It is sometimes challenging to calculate and get the recommended sample size of a study. G*Power and the event per variable have been used to calculate the sample size, especially when using logistic regression (Bujang et al., 2018). However, this study calculated the sample size using G*Power analysis. As noted by Ellis (2015) and Wagner (2016), G*Power should be used to generate the sample size of a study. This study used G*Power as the most appropriate statistical analysis to give the current study the most precise effect size and statistical significance or power.

Although the statistical power was geared toward generating the real probability of the effect of a study, the power dictated the level of Type II error. According to Burkholder et al. (2016) and Ellis (2015), a study must be prudent in setting the statistical

power because it signifies how accurately the sample size will produce the most desirable effect. This process enabled the realization of the precise association of the variables, thereby decreasing the Type II error of the study.

When employing a power analysis, it was essential to have an accurate statistical power that would maximize the effect of a study. As Salazar et al. (2015) noted, the most appropriate statistical power is warranted to obtain a meaningful statistical effect of a research study. Although different levels of statistical power can be used in a study, I used a power set at 0.8. According to Ellis (2015), higher power is vital to reduce Type II errors. It ensures a meaningful effect from the sample size selected. When power was set at 0.8, the desired effect of this study was attainable 80% of the time during the study. Moreover, the effect size is the calculated mean difference divided by the standard deviation. It has a value that ranges from 0 to 1, where 0 indicates no effect, and 1 identifies that a statistically meaningful association exists between the variables in the study (Ellis, 2015). In this study, the odds ratio, denoted the effect size, was calculated in G*Power as 2.33.

As narrated by Salazar et al. (2015) and Frankfort-Nachmias and Leon-Guerrero (2018), a researcher must be cognizant of the most appropriate sample size to generate the most meaningful effect of the study. Frankfort-Nachmias and Leon-Guerrero also stated,

> A power analysis remained a very important step to undertake before you start your experiment as it will determine how large a sample size is needed to adequately ensure that your statistical tests are accurate and valid and also the

> likelihood that your statistical tests would detect effects of a research for a given effect size. (p. 20)

Salazar et al. (2015) reiterated that some studies using randomized control trials might need a large resource to implement that would involve time and money to show an effect if one truly existed. Conversely, if the sample size was too small, the trial would lack precision and would have been all for naught. Therefore, it was essential to use power analysis to calculate the most appropriate sample size to yield the most meaningful effect and save time and resources.

Additionally, alpha levels play a pivotal role when carrying out a study, for it increases the probability of a Type I error, which is the probability of the population having different mean levels when the mean difference does not exist. Moreover, Ellis (2015) elaborated that alpha levels could range from 0.01 to 0.05, but the level of 0.05 was frequently used in research. An alpha level of 0.05 can show a 5% chance that a researcher will reject the null when, in fact, it should not be so (Ellis, 2015). Moreover, the benefit of using the alpha level at .05 in research is that there is relatively minimal risk of making a Type I error when the alpha is not so small that researchers greatly increase their risk of not rejecting the null when they actually should (a Type II error; Aschengrau & Seage, 2020; Ellis, 2015; Salazar et al., 2015). In setting an alpha, researchers should remain aware of the risk of rejecting the null erroneously and not rejecting it when they should. Therefore, the alpha level was set at the .05 level in this research.

Researchers have learned to minimize errors and increase the precision of their estimates around the population mean by developing an approximate required size of a study sample to be significant. Frankfort-Nachmias and Leon-Guerrero (2018) stated,

> As a general rule of thumb, researchers have used a minimum sample size (*N*) to ascertain a normal distribution and hence inference to the general population. For example, when *N* in any study is greater or equal to 50, we can be certain that, the sampling distribution of the mean will be approximately normal regardless of the shape of the distribution. (p. 20)

Additionally, the authors discussed that researchers have assumed that some samples in a study might be "more tightly clustered with *N* to be as small as 30 for the population distribution to approximate normality where the confidence intervals will be narrower and more precise" (Frankfort-Nachmias & Leon-Guerrero, 2018, p. 20). Moreover, G*Power was employed at a power of 0.80, an alpha level of 0.05, and a high effect size (odds ratio) of 2.33. It calculated minimum sample size needed in this study was 190.

In this study, the calculated sample size of 190 was not met, for the study had a sample size of 140, which may affect the study by increasing Type II error and decreasing the study's validity and reliability. However, considering that the sample size of this study of 140 was greater than the minimum sample size (*N*) of 50 required in quantitative studies, Frankfort-Nachmias and Leon-Guerrero (2018) indicated that a sample size of greater or equal to 50 would be sufficient to ascertain a normal distribution and inference. Frankfort-Nachmias & Leon-Guerrero also discussed that it was important

to reduce the limitation of not having the appropriate sample size in a study, and one of the methods to minimize Type II error was to employ the most appropriate statistical test for a study. Therefore, although a calculated sample size of 190 was needed, the sample size of 140 (greater than 50) was sufficient for the study to decrease the Type II error and demonstrate a statistically meaningful result when using the binary logistic regression as a statistical test for analysis.

Procedures for Recruitment, Participation, and Data Collection

I did not collect primary data, so secondary analysis archival data (SAAD) were requested from a publicly accessible database from the CDC. The data set was the SCD Provisional Death Count from COVID-19 and SCD death due to underlying conditions, with data collection from 2019 through 2021. Moreover, although I focused on analyzing SCD patients who died from COVID-19, in this study, only patients who met the inclusion criteria and resided in the United States were selected as participants.

To answer my research questions, I used deidentified secondary data to gather the specific data points containing both the independents categorical groupings and the dependent categorical binomial variables. The data were collected from a publicly accessible CDC Internet site. As stated earlier, I used a power analysis, specifically G*Power, to determine the appropriate sample size, effect size, and other parameters for this study.

I sent an email to the CDC requesting them to deidentify data on SCD and COVID-19 and received a positive reply. The SCD and COVID-19 mortality provisional publicly accessible data set with the IVs of age and race and the DV of COVID-19

mortality was made available to me. Though one of the limitations of the publicly available data might be that the variables of interest might not be available, all the variables of my study were in the data set. Also, the data might not have been properly coded and cleaned; thus, some cleaning and other manipulations were required for proper analysis to answer the research questions. The CDC rigorously recruited participants using the survey and collected relevant data from electronic medical records using International Classification of Disease (ICD 10) codes for SCD patients who died from COVID-19. They also provided data from death certificates from vital records in all 50 U.S. states. The CDC provisional data set was coded and de-identified to ensure good ethical research practice. However, the research limitation was that the deaths in the data from COVID-19 might not represent all persons with SCD in the United States, possibly leading to a systematic selection bias affecting the study sample's representativeness, as suggested by researchers (Aschengrau & Seage, 2020; Panepinto et al., 2020).

Additionally, there might also be a misclassification bias. This bias might have resulted from some SCD patients dying from complications and comorbidities other than COVID-19 infection but being recorded as having died due to the pandemic. However, SCD death from underlying and multiple conditions not from COVID-19 were identified in the data set, thereby decreasing the chance of a misclassification bias that might have reduced the reliability and validity of the study.

Data Analysis Plan

Researchers use statistical methods to analyze the relationship between different variables (Ellis, 2015). It is also worthwhile knowing the program in which the test will

be performed for analyses to understand the type of statistical test most suitable for this study. With that in mind, although there exists much statistical software that can be used for this study. The IBM software, Statistical Package for the Social Sciences (SPSS), was used with the most appropriate statistical test in analyzing and finding the association between the IVs and DVs of the study (see Frankfort-Nachmias & Leon-Guerrero, 2018; Wagner, 2016). The following research questions represented the basis for data analysis and collection:

Research Question 1

What is the relationship between age AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$1. There is no relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

H_a1. There is a relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

Research Question 2

What is the relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$2. There is no relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

H_a2. There is a relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

Research Question 3

What is the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States?

$H_0$3. There is no relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

H_a3. There is a relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

Statistical Tests

Furthermore, although many statistical tests can be used to explore the associations between the dependent and IV of a study, using the most appropriate test was essential. Although other statistical tests were used to explore the relationship between variables (e.g., Aschengrau & Seage, 2020; Osborne, 2015; Szumilas, 2010; Wagner, 2016), logistic regression was employed in this study to predict the odds, conditional odds, and odds ratio. This process was made significant by using a categorical dependent dichotomous variable to predict the outcome of the IVs (Aschengrau & Seage, 2020; Osborne, 2015; Szumilas, 2010; Wagner, 2016). In this study, the nature of the two grouped categorical IVs and the dichotomous DV met the assumptions of a binary logistic regression to be employed as the statistical test of choice. Using the most appropriate statistical test facilitated a valid result and inference of the study.

Missing Data

When performing secondary analyses of extensive surveys, it was important to familiarize oneself with, clean, and address missing data in the data set. However, depending on the percentage of cases with missing observations, the researcher must use appropriate techniques to handle those cases with missing data to reduce bias and reach valid conclusions for the target population (Langkamp et al., 2010). Many techniques exist to handle missing data, including multistage sampling schemes, such as listwise or pairwise deletion, imputation (single or multiple imputations), and the reweighing technique (Langkamp et al., 2010). Of the many techniques, the reweighing technique was used during the analysis in this research.

Employing the weight technique was the most efficient for this study. With the said approach, the missing data were addressed by attaching weights to each subject included in the analysis to represent subjects who were excluded due to missing data (see Fink, 2013; Langkamp et al., 2010). This technique was the most appropriate because it gave a sense of equal selection of cases. The statistical weights of individuals with missing or incomplete records were redistributed to individuals with similar demographic characteristics who had complete information. Weighing the missing data helped increase rigor by minimizing selection bias, ensuring this study's generalizability, validity, and reliability.

Threats to Validity

External and Internal Validity

Compared to many decades ago, health outcomes and life expectancy have increased globally and were credited to research. However, to ensure that public health research studies are of sound quality design and methods, the findings must not only describe accurately or reflect the phenomenon under investigation, but they should also be replicable (see Burkholder et al., 2016). Burkholder et al. defined external validity as "the extent to which findings of a study hold across context" (p. 20). In other words, the study's findings must be generalizable to different populations and settings; any deflection would constitute a threat. This study aimed to make it generalized in the U.S. SCD community. However, the study would not be generalizable to other settings outside the United States with a low rate of COVID-19 infection, and the timing of the study was a potential threat to external validity.

In research, it is good to carry out a study that not only has a relationship between variables but can also be repeatedly done and yield the same result. Burkholder et al. (2016) described how internal validity was the degree to which the result of research could establish if the relationship between the independent and the DVs exists and can be replicated. The claims are supported by another experiment and demonstrate causal inferences. Additionally, Fink (2013) stated, "Internal validity in reference to whether an experimental program makes a difference and whether there is sufficient evidence to support the claim" (p. 20). Many studies were shown using different experiments to deduce that persons with SCD were disproportionately affected by the COVID-19

pandemic, producing a high degree of internal validity; nevertheless, the authors noted that selection bias remained one of the threats to internal validity (Burkholder et al., 2016; Fink, 2013). However, this threat was mitigated as random sampling rather than a purposeful selection was performed on SCD patients who died from COVID-19 in all 50 states, including the District of Columbia, from death registries and ICD codes during the primary data collection process for the secondary data set of this study.

The researcher must validate internal and external validity in any research. Fink (2013) concluded, “External validity is solely dependent upon internal validity in a study” (p. 20). This finding implies that researchers must be prudent when generalizing research findings to other populations and settings. In most research, findings may be skewed unless researchers remain cognizant that the findings are due to the program or other factors, such as confounding variables.

Ethical Procedures

When researching humans, it is vital to have an independent review committee review your research for its adherence to ethical standards and to ensure that informed consent is obtained before initiating any research (Ellis, 2015). Although not all studies may require written informed consent agreements, a researcher does not make this determination independently. All studies should be reviewed regardless of whether the researcher believes their study may lack the potential to harm human subjects (Rudestam & Newton, 2015). For instance, Rudestam and Newton discussed how some methodologies that did not require informed consent included secondary data analyses,

archival research, and the systematic observation of publicly observable data. However, the data set for this research was publicly available.

Though informed consent was not needed for SAAD, ethical concerns, confidentiality, and proper coding of the SAAD for any study in this institution had to be reviewed and approved by the institutional review board (IRB) at Walden University (n.d.-a, n.d.-b, n.d.-c) before conducting the study (e.g., Rudestam & Newton, 2015; Smith et al., 2011). Therefore, even though a secondary publicly available data set was used for this research, IRB approval (No. 08-22-22-0832066) was required and was granted before proceeding with the analysis. I also ensured that the individual's data were deidentified, coded appropriately, and double-locked in a password-accessible safe box in a locked drawer. This drawer was in my office and accessible only to me. I will destroy the data 5 years after the research to safeguard respondents' identities and dignity for good public health research practice.

Summary

The purpose of this retrospective cross-sectional study observational study was to investigate the relationship between age, race/ethnicity, and COVID-19 mortality among persons with SCD in the United States. Thus, the specific research design included a cross-sectional design to research COVID-19 deaths among persons with SCD examined in a single period from January 2020 to March 2021.

Due to the influence of globalization, SCD and the COVID-19 pandemic are both medical conditions unlimited to a specific geographical region, influencing people and their families worldwide. Participants of this study represented persons from both sexes,

all ages, and races/ethnicities and were included from different geographical locations with different SCD genotypes; however, the target population of the study was persons with SCD from less than 5 years to 60 plus years of age who were affected by and died from COVID-19 in all 50 U.S. states, including the District of Columbia. Parameters were used that included and excluded participants from this study.

This study requested SAAD from public databases, such as CDC (2020a), the American Society of Hematology, and the Secure-SCD Registry, Surveillance Epidemiology of Coronavirus (COVID-19) Under Research Exclusion. This registry had the latest SCD and COVID-19 global registry. However, the provisional death data set from CDC for patients with SCD who died from COVID-19 was used for this research.

The employment of the G*Power analysis calculated the sample size in this study. As noted by Ellis (2015), G*Power is used to generate the sample size of a study and dictates the most appropriate statistical analysis to give a precise effect size and statistical significance or power. When G*Power had a power of 0.80, an alpha level of 0.05, and a high effect size of 2.33, the minimum sample size needed for this study was 190. Although the calculated minimum sample size of 190 was not met, however, because the sample size of this study was greater than 50, therefore the sample size of 140 would demonstrate a statistically meaningful result when using the statistical test of binary logistic regression for analysis (Frankfort-Nachmias & Leon-Guerrero, 2018, p. 20).

SPSS was the program used to employ the most appropriate statistical test of binary logistic regression in analyzing and finding the association between the IVs and DVs of the study (Frankfort-Nachmias & Leon-Guerrero, 2018; Wagner, 2016). The

researcher must validate internal and external validity in any research (Fink, 2013). This study aimed to make the findings generalizable to the U.S. SCD community; however, the study would not be generalizable to other settings outside the United States with low rates of COVID-19 infections. The timing of the study represented a potential threat to external validity.

Publicly available data were collected from the CDC, and IRB clearance was sought to ensure the data set was free from any unethical practices for which IRB approval was granted. The SAAD obtained for this research had all the variables already coded; however, prudence was taken to refamiliarize oneself with the data set, change the age and race/Hispanic origin groupings to individualized entries, and verify data with the code book. The goal was to ensure that the coded variables had the appropriate numerical values attached, with no missing data, as a measure of cleaning and expanding the data set for efficient analysis.

Although many techniques are available to address missing data in research, in this study, the reweighting technique was the most appropriate (see Langkamp et al., 2010). Expanding the data by changing the grouping of the IVs to individualized codes and weighing the missing data were essential for analyzing data in SPSS while eliminating bias. The goal was to ensure this study's generalizability, validity, and reliability.

Finally, though informed consent was not needed for SAAD; however, due to ethical concerns, the IRB at Walden University (n.d.-a, n.d.-b, n.d.-c) reviewed confidentiality and proper coding of the SAAD for this study before I continued with my

study (see Rudestam & Newton, 2015). I ensured that the individual's data were deidentified, coded appropriately, and double-locked. Only I could access the data, with plans to destroy all data 5 years after the research to safeguard respondents' identities. After the IRB approved the study, I downloaded the data and wrote Chapter 4. Chapter 4 contains the collection, analysis, and results of the data of this study.

Chapter 4: Results

Introduction

I conducted a retrospective cross-sectional study investigating the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in all 50 U.S. states, including the District of Columbia, from January 2020 to March 2021. The study was guided by the following three research questions and hypotheses:

Research Question 1

What is the relationship between age AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$1. There is no relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

H_a1. There is a relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

Research Question 2

What is the relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$2. There is no relationship between race/ Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

H_a2. There is a relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

Research Question 3

What is the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States?

$H_0$3. There is no relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

H_a3. There is a relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

This chapter begins with an explanation of the secondary data set's data collection and source. Next, the descriptive statistics of all persons with SCD who have died of COVID-19 and other conditions during the study's timeframe are analyzed. The assumptions of the model are explained. Furthermore, the results and findings are presented following the above-mentioned specific research questions. Finally, I summarize the findings and the statistical test employed to answer the various research questions.

Data Collection

I did not collect primary data from the CDC in 2022. Instead, I used secondary data previously deidentified by the CDC to gather the specific data points containing both the independent categorical groupings and the dependent categorical binomial variable. The data were collected from a publicly accessible CDC Provisional SCD and COVID-19 death data set from 2019 to 2021. As stated earlier, a power analysis, specifically G*Power, was employed to determine the appropriate sample size, effect size, and other parameters for the study. Although the required minimum calculated sample size of 190

was not met, quantitative studies with a sample size of more than or equal to 50 were said to produce meaningful results equally. Therefore, the sample size of 140 in this study was sufficient to ensure inference to the general population.

Results

Descriptive Statistics

Table 1 shows that from 2020 to 2021, 1,814 respondents with SCD died during the study period. The information includes a breakdown of the circumstances of the respondents' deaths. However, the statistics of the entire study were based on the 140 patients with SCD affected by COVID-19 from January 2020 to March 2021 (see Table 1).

Table 1

Sickle Cell Disease Death Trend From 2020 to 2021

Period	Total sickle cell disease (SCD) underlying	Total SCD multi	Total number of deaths from SCD and COVID-19 recorded	Total number of patients with SCD who had COVID-19 but did not die because of COVID-19
2020	531	1023	86	37
2021	43	77	14	3
Total	574	1,100	100	40

Demographic Information of Eligible Death Cases

Among the 140 individuals with SCD affected by COVID-19, 100 SCD patients died from COVID-19 from January 2020 to March 2021; of those who died, 99 (70.7%) were non-Hispanic Black people, and 14 (10.0%) were non-Hispanic White people. Moreover, 27 (19.3%) were of other races/Hispanic origins (see Table 2).

Table 2

Distribution of Death Cases by Race/Hispanic Origin

Race/Hispanic origin	Frequency	Percentage
Non-Hispanic Black	99	70.7
Non-Hispanic White	14	10.0
Other	27	19.3
Total	140	100

Table 3 provides a breakdown of the ages of the 140 individuals with SCD affected by COVID-19 who died from January 2020 to March 2021.

Table 3

Distribution of Cases by Age Group

Age group	Frequency	Percentage
0-19	21	15.0
20-39	38	27.1
40-59	43	30.7
60+	38	27.1
Total	140	100

Underlying Assumptions of the Model

The statistical test for this analysis was the binary logistic regression which was interpreted based on regression coefficient (*B*), standard error of *B* (*SEB*), standardized beta, the *t*-test *p* values associated with the regression coefficient, as well as their 95% confidence intervals. However, before the regression was computed, the data were not paired. All the IVs, such as age and race/Hispanic origin, were checked to ensure that there are not highly correlated, and this was done using a bivariate. The Spearman's rho test showed a low correlation between the predictor variables (.144). The Spearman's rho test was preferred over the Pearson test because the data were not normally distributed.

Outliers

The variables were also checked to eliminate outliers, namely extremely high or low cases; however, the probability results computed using Mahal Distance showed no outliers that could seriously affect the study's findings. The selected cases were above 60%, and the nonsignificant *p* value of the Hosmer and Lemeshow Test, a statistical test for goodness of fit for the logistic regression model, indicated that the observed event rates matched the expected event rates in subgroups of the model population.

Collapsing of Data for Age Group

The original data for the age group were in seven categories, with some cells having just five persons. Therefore, because of binary logistic regression, the age group was further categorized into seven groups of four. Additionally, the original data's three categories of race/Hispanic origin were not further manipulated but numerically coded. The goal was to ensure that each group was well-fitted into the model and to obtain a more accurate result.

Linearity and Heteroscedasticity Assumption

Linearity is also one of the basic assumptions of the logistic regression model, where the DV should have a linear relationship with one or more predictor variables. Linearity and heteroscedasticity refer to the model's errors and fit. Again, the non-significant *p*-value of the Hosmer and Lemeshow Test implied that the error term had a constant variance. The low pairwise correlation value between the predictors of the IV in the model < 0.7 also showed no multicollinearity between age and race.

Test of Normality Assumption

The reason for using Spearman's rho test to check whether the predictors of the IVs were not highly correlated was because the test of normality assumption showed that the data significantly deviated from the normal distribution pattern. In other words, the data were not normally distributed. I relied on the Kolmogorov-Smirnov (K-S) test results because the sample was above 30 (see Table 4).

Table 4

Tests of Normality

Variables	Kolmogorov-Smirnov [a]		
	Statistic	*df*	*p*
Race/Hispanic Origin	.425	140	.000
Age Group	.235	140	.000
SCD and COVID-19	.450	140	.000

[a] Lilliefors Significance Correction.

As depicted in Table 4, the *p* value for race, age, SCD, and COVID-19 was less than .001. This finding indicated that the data did not significantly deviate from the normal distribution pattern. However, it should be noted that logistic regression, by design, overcomes many of the restrictive assumptions of linear regression.

Research Question 1

Research Question 1 was the following: What is the relationship between age AND mortality from COVID-19 among persons with SCD in the United States? This research question showed the relationship between age and mortality from COVID-19 among persons with SCD in the United States. The null hypothesis was rejected: There is no relationship between age and mortality from COVID-19 among persons with SCD in the United States. Thus, the alternative hypothesis was supported: There is a relationship

between age and mortality from COVID-19 among persons with SCD in the United States. In the regression analysis, the predicted probability was for members to die from COVID-19. Table 5 shows the results.

Table 5

Relationship Between Age Group and COVID-19 Mortality Among Persons With Sickle Cell Disease

Age	B (*SE*)	Wald	Sig.	Exp(B) (*OR*)	95% CI for EXP(B)	
					Lower	Upper
0-19 (reference category)						
20-39	1.245 (.499)***	6.222	$p = .013$	3.474	1.306	9.243
40-59	1.820 (.532)***	11.704	$p = .001$	6.174	2.176	17.517
60+	2.862 (.729)***	15.425	$p < .001$	17.499	4.195	73.002
Constant	.540 (.231)***	5.450	$p = .020$	1.715		
Nagelkerke R^2	.429					

Note. *B* stands for statistics coefficient b; SEB = standard error of *B* in the analysis; *** is $p < .001$; ** is $p < .01$, and * is $p < .05$. The *R* square in this model is .429.

The results were computed using the binary logistic regression model to determine the relationship between age and mortality from COVID-19 among persons with SCD in the United States (see Table 5). Statistics showed that the predictor variable, age, was found as significantly associated with COVID-19 mortality among U.S. persons with SCD, with the unstandardized beta weight for the predictor variable ($B = .540$, $SE = .231$, Wald statistics = 5.450, $p < .020$). The total variability explained by age concerning COVID-19 mortality was 42.9% (Nagelkerke $R^2 = .429$). In other words, age accounted for 42.9% of COVID-19 deaths among SCD patients. It demonstrated a proportional relationship between an increase in age and mortality during this study, with older U.S. persons having the highest death rate than young persons. Figure 1 graphically displays the predicted probability of a member dying of COVID-19 based on age.

Figure 1

Graphical Display of Predicted Probability for Members to Die From COVID-19 by Age

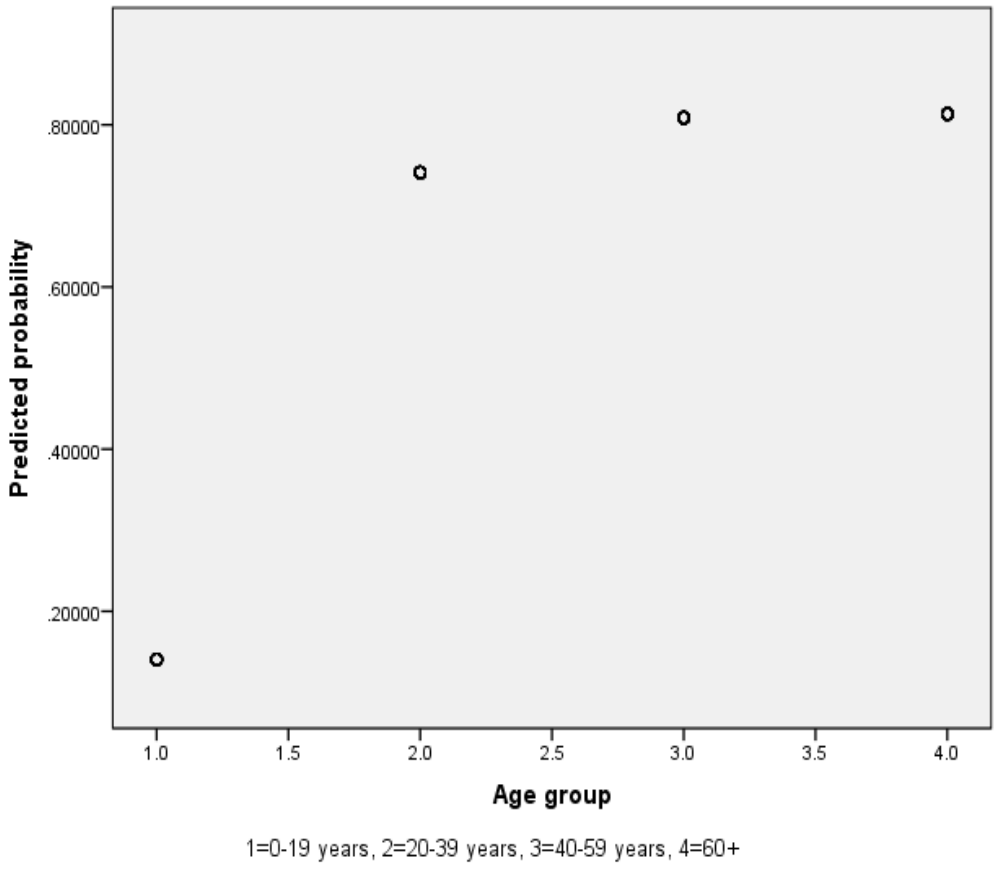


Figure 1 shows that COVID-19 mortality among U.S. persons with SCD was found to increase with age for persons with SCD aged 60+ and die more from COVID-19, followed by those aged 40 to 59 and 20 to 39 years. Only some aged 0 to 19 years were observed to die from COVID-19. Table 6 further presents the percentages of COVID-19 mortality from U.S. persons with SCD by age for better understanding.

Table 6

Distribution of Mortality Rate Among Sickle Cell Disease Persons by Age Group

	SCD and COVID-19		
Age group	Not died of COVID-19 *n* (%)	Died of COVID-19 *n* (%)	Total
0-19	20 (95.2%)	1 (4.8%)	21
20-39	9 (23.7%)	29 (76.3%)	38
40-59	6 (14.0%)	37 (84.0%)	43
60+	5 (13.2%)	33 (86.8%)	38
Total	40 (28.6%)	100 (71.4%)	140

Note. Fisher's Exact Test value = 55.104 and $p < .001$.

Statistically, using percentages with the aid of a cross-tabulation technique, findings in Table 6 show that the COVID-19 mortality rate for persons with SCD significantly increased with age. Between the age group 0 to 19 years, a COVID-19 mortality rate was observed at only 4.8%; within 20 to 39 years of age, the mortality rate was 76.3%, which steadily increased to 84.0% for persons aged 40 to 59. Of persons aged 60 years and above, 86.8% of them died from COVID-19. Therefore, the null hypothesis was rejected: there is no relationship between age and mortality from COVID-19 among persons with SCD in the United States. A statistically significant relationship between age and COVID-19 mortality was realized during the analysis.

Research Question 2

Research Question 2 was the following: What is the relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States? The purpose of this question was to determine the relationship between race and mortality from COVID-19 among persons with SCD in the United States. The null hypothesis indicated that no relationship existed between race/Hispanic origin and

mortality from COVID-19 among persons with SCD in the United States. The alternative hypothesis stated that a relationship existed between race/Hispanic origin AND mortality from COVID-19 among patients with SCD in the United States. In the regression analysis, the predicted probability was for members to die from COVID-19. Table 7 shows the results.

Table 7

Relationship Between Race/Hispanic Origin and COVID-19 Mortality From Persons With Sickle Cell Disease

					95% CI for EXP(B)	
Race/Hispanic origin	B (*SE*)	Wald	Sig.	Exp(B) (*OR*)	Lower	Upper
Other (reference category)						
non-Hispanic Black	2.259 (.477)***	22.403	$p < .001$	9.577	3.758	24.409
non-Hispanic White	-.182 (.671)	.074	$p = .786$	.833	.224	3.103
Constant	-.405 (.373)	1.184	$p = .277$	.667		

Note. *B* stands for statistics coefficient *b;* SEB = Standard Error of *B* in the analysis; *** is $p < .001$, ** is $p < .01$, and * is $p < .05$.; the Nagelkerke *R* square in this model is .299.

The results depicted in Table 7 were computed using the binary logistic regression model to determine if there was a relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States. The statistics revealed that the predictor variable race/Hispanic origin was significantly associated with COVID-19 mortality, $p < .001$. Race/Hispanic origin was found to explain a total variability of 29.9% (Nagelkerke *R*-Square = .299) of the outcome variable (Die of COVID-19). Race/Hispanic origin accounted for approximately 30% of COVID-19 deaths in U.S. patients with SCD. Figure 2 displays the predicted probability of a member dying of COVID-19 based on race/Hispanic origin.

Figure 2

Graphical Display of Predicted Probability for Member to Die From COVID-19 by Race/Hispanic Origin

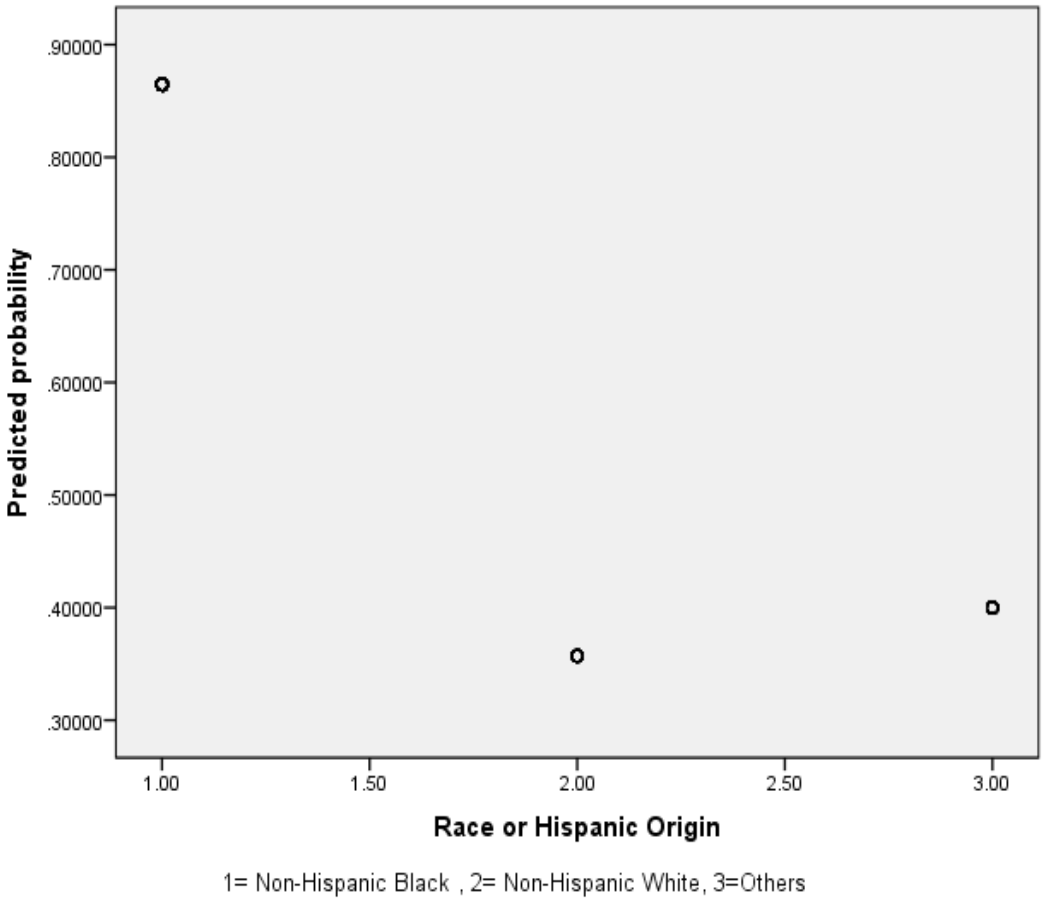


Figure 2 shows that non-Hispanic Black people (n = 3) have a predicted probability of a member dying from COVID-19 far more than non-Hispanic White people and others. Table 8 also presents the percentages of COVID-19 mortality from U.S. persons with SCD by race/Hispanic origin for a better understanding.

Table 8

Distribution of COVID-19 Mortality From Persons With Sickle Cell Disease by Race/Hispanic Origin

	SCD and COVID-19		
Race/Hispanic origin	Not died of COVID-19 *n* (%)	Died of COVID-19 *n* (%)	Total
Non-Hispanic Black	13 (13.5%)	83 (86.5%)	96
Non-Hispanic White	9 (64.3%)	5 (35.7%)	14
Other	18 (60.0%)	12 (40.0%)	30
Total	40 (28.6%)	100 (71.4%)	140

Note. Fisher's Exact Test = 32.537 and $p = .001$.

The statistics in Table 8 reveal that COVID-19 mortality was 86.5% among non-Hispanic Black, which was more than two times higher compared to COVID-19 mortality from non-Hispanic White people at 35.7% and others at 40.0% (p-value < .001). Therefore, the null hypothesis was rejected: there is no relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States. The alternative hypothesis indicating that such a relationship existed was not rejected.

Research Question 3

Research Question 3 was the following: What is the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States? This research question was used to show the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States. The null hypothesis stated that there was no relationship between age and race with mortality from COVID-19 among persons with SCD. The alternative hypothesis reiterated a relationship between age and race/Hispanic origin and mortality

from COVID-19 among persons with SCD in the United States. In the regression analysis, the predicted probability was for members to die from COVID-19. Table 9 shows the results.

Table 9

Relationship Between Age Group and Race/Hispanic Origin With COVID-19 Mortality Among Persons With Sickle Cell Disease

Variable	B (*SE*)	Wald	sig.	Exp (B) (*OR*)	95% CI for EXP(B) Lower	Upper
0-19 (Reference category)						
20-39	1.198 (.519)**	5.329	$p = .021$	3.314	1.198	9.165
40-59	1.500 (.535)***	7.845	$p = .005$	4.480	1.569	12.795
60+	2.921 (.774)***	15.437	$p < .001$	18.564	4.323	79.717
Other (reference category)						
Non-Hispanic Black	1.837 (.472)***	15.149	$p < .001$	6.278	2.489	15.832
Non-Hispanic White	-.401 (.719)	.311	$p = .577$	.670	.164	2.740
Constant	-.113 (.273)	.170	$p = .681$	.894		
Nagelkerke R^2	.624					

Note. *B* stands for statistics coefficient b; SEB = Standard Error of *B* in the analysis; *** is $p < .001$, ** is $p < .01$, and * is $p < .05$; Nagelkerke R^2 in this model is .624.

The results depicted in Table 9 were computed using the binary logistic regression model to investigate if there is a relationship between age and race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States. The statistics showed that the predictor variables, age and race/Hispanic origin, significantly interacted to contribute to the model with the unstandardized beta weight for the predictor's variable (B = -.113, SE = .273, Wald statistics = .170, p = .681). The estimated odds ratio obtained between race/Hispanic origin and age showed that persons aged 60+ were observed to die more from COVID-19, *Exp* (*B*) = 18.564, 95% CI (4.323, 79.717), than those in the

reference group (0 to 19 years) at a significant level of $p < .001$. Further, non-Hispanic Black was observed to die more than those in the reference group (Others) [*Exp* (B) = 6.278, 95% CI (2.489, 15.832) at a significant level of 0.000. The relationship between both age and race/Hispanic origin explained a total variability of 62.4% (Nagelkerke *R*-Square = .624) of the outcome variable, meaning that both age and race/Hispanic origin account for 62.4% of COVID-19 deaths among SCD patients, particularly the age groups from 20-39, 40-59 and those 60+ and the race of non-Hispanic Black in the United States.

Table 10 also presents, in percentages, the COVID-19 mortality from persons with SCD in the United States by age group when controlled by race/Hispanic origin for better understanding among lay people.

Table 10

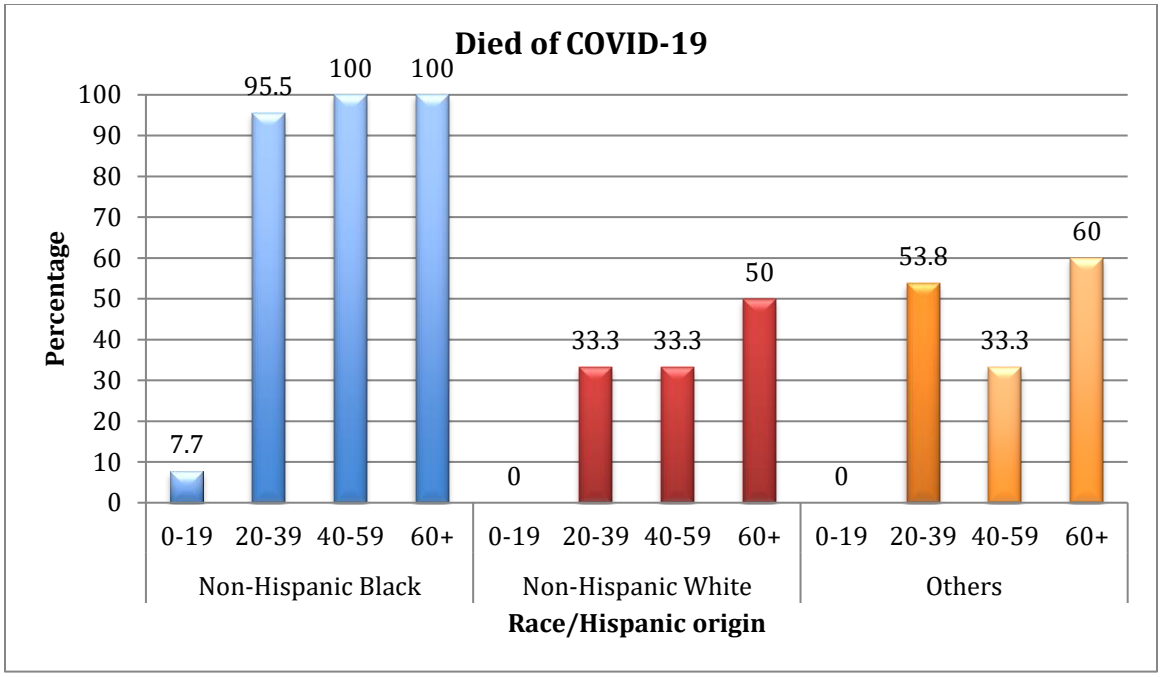
Distribution of COVID-19 Mortality by Race/Hispanic Origin and Age Group

Race or Hispanic Origin	Age group		SCD and COVID–19		Total	Fisher Exact test
			Not died of COVID–19	Died of COVID–19		
Non–Hispanic Black	0–19	*n*	12	1	13	Test value = 53.563 $p < .001$
		%	92.3%	7.7%		
	20–39	*n*	1	21	22	
		%	4.5%	95.5%		
	40–59	*n*	0	34	34	
		%	0.0%	100.0%		
	60+	*n*	0	27	27	
		%	0.0%	100.0%		
	Total	*n*	13	83	96	
		%	13.5%	86.5%		
Non–Hispanic White	0–19	*n*	2	0	2	Test value = 1.676 $p = .865$
		%	100.0%	0.0%		
	20–39	*n*	2	1	3	
		%	66.7%	33.3%		
	40–59	*n*	2	1	3	
		%	66.7%	33.3%		
	60+	*n*	3	3	6	
		%	50.0%	50.0%		
	Total	*n*	9	5	14	
		%	64.3%	35.7%		
Others	0–19	*n*	6	0	6	Test value = 6.045 $p = .117$
		%	100.0%	0.0%		
	20–39	*n*	6	7	13	
		%	46.2%	53.8%		
	40–59	*n*	4	2	6	
		%	66.7%	33.3%		
	60+	*n*	2	3	5	
		%	40.0%	60.0%		
	Total	*n*	18	12	30	
		%	60.0%	40.0%		

Figure 3 shows that non-Hispanic Black persons aged 20 to 39, 40 to 59, and 60+ died more from COVID-19 at almost the same rate but far more than the non-Hispanic White and Others. In non-Hispanic White people and others, persons aged 20 to 39, 40 to 59, and 60+ did not die from COVID-19 compared to non-Hispanic Black people (see Table 10).

Figure 3

Distribution of COVID-19 Mortality by Race/Hispanic Origin and Age Group



The results in Table 10 and Figure 7 revealed that when COVID-19 mortality from persons with SCD was distributed by age group versus race/Hispanic origin, non-Hispanic Black people with SCD within the age group of 20 to 39 years, 40 to 59 years, and 60+ years of almost equal proportions died of COVID-19; however, this trend was not observed with non-Hispanic White people and others. The proportion of Hispanic Black people aged 20 to 39, 40 to 59, and 60+ who died of COVID-19 were more than two times higher for persons aged 60+ as with non-Hispanic White people. Finally, based on others, the proportion of non-Hispanic Black people aged 40 to 59 who died from COVID-19 was more than two times higher compared to those who died of COVID-19 among others and almost two times as with persons aged 60+.

Summary

In summary, the results showed a statistically significant relationship between age and mortality from COVID-19 among persons with SCD in the United States ($p < .001$). The estimated odds ratio for persons age 60+ that die from COVID-19 is [*Exp* (B) = 17.499, 95% CI 4.195, 73.002) which is significant at the .000 level compared to the reference group. Also, for persons aged 40-59, the estimated odds ratio for those who die of COVID-19 is *Exp* (B) = 6.174, 95% CI (2.176, 17.517), which was significant at the .001 level when compared to those in the reference group. Finally, for persons aged 20 to 39, the estimated odd ratio for those who die of COVID-19 is *Exp* (B) = 3.474, 95% CI (1.306, 9.243), which was significant at a level of $p < .013$. The total variability explained by age concerning COVID-19 mortality was 42.9% (Nagelkerke *R*-Square = .429). Age accounted for 45.5% of COVID-19 deaths among SCD patients, and older U.S. patients died more than the reference group during the timeframe of this study.

Furthermore, the results showed a statistically significant relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States ($p < .001$). The estimated odds ratio showed that non-Hispanic Black die more from COVID-19, *Exp* (B) = 9.577, 95% CI (3.758, 24.409), than those in the reference group (Others) at a significant level of 0.000, and non-Hispanic White were observed to die less than those in the reference group (Others), *Exp* (B) = .833, 95% CI (.244, 3.103), at a significant level of 0.000. Race/Hispanic origin was found to explain a total variability of 29.9% (Nagelkerke *R*-Square = .299) of the outcome variable (Die of COVID-19). Race/Hispanic origin accounted for approximately 30% of COVID-19

patients with SCD, and non-Hispanic Black people were more than twice as likely to die than non-Hispanic White people and the reference group during the study.

The results also showed a significant relationship between age and race/Hispanic origin with mortality ($p < .001$). The estimated odds ratio obtained between race/Hispanic origin and age showed that persons aged 60+ were observed to die more from COVID-19, *Exp* (B) = 18.564, 95% CI (4.323, 79.717), than those in the reference group (0 to 19 years) at a significant level of 0.000. Also, persons aged 40-59 years were observed to die more from COVID-19, *Exp* (B) = 4.480, 95% CI (1.569, 12.795), than those in the reference group (0 to 19 years) at a significant level of 0.005. Finally, persons aged 20 to 39 years were also observed to die more from COVID-19, *Exp* (B) = .3.314, 95% CI (1.198, 9.165), than those in the reference group (0 to 19 years) at a significant level of .021, < 0.05.

Based on race/Hispanic origin, non-Hispanic Black was observed to die more than those in the reference group (Others), *Exp* (B) = 6.278, 95% CI (2.489, 15.832), at a significant level of 0.000, and non-Hispanic White were observed to die less from COVID-19, *Exp* (B) = .670, 95% CI .164, 2.740), than those in the reference group, although not significant (lower bond less than 1 and $p = .577$). More so, the relationship between both age and race explained a total variability of 62.4% (Nagelkerke *R*-Square = .624) of the outcome variable, meaning that both age and race/Hispanic origin accounted for 62.4% COVID-19 deaths among SCD patients, particularly the age groups from 20 to 39, 40 to 59, and 60+ for the race of non-Hispanic Black in the United States. Both age

and race accounted for the highest variability (42.4%) of COVID-19 deaths than age (45.5%) and race (~30%) alone among SCD patients in the United States.

In Chapter 5, I provide interpretations of the findings, limitations of the study, and recommendations for future research and practice. The implications for social change are presented, followed by a thoughtful discussion and conclusion.

Chapter 5: Discussion, Conclusions, and Recommendations

I conducted a retrospective cross-sectional study. I presented findings from data collected from the field to investigate the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in all 50 U.S. states, including the District of Columbia, from January 2020 to March 2021. The study was guided by three specific research questions and their hypotheses.

Research Question 1

What is the relationship between age AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$1. There is no relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

H_a1. There is a relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

Research Question 2

What is the relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$2. There is no relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

H_a2. There is a relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

Research Question 3

What is the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States?

$H_0$3. There is no relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

H_a3. There is a relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

In this chapter, I discuss the findings following the specific research questions stated in chapter one, and a review of related literature and theories supports the results. The results indicated a significant relationship between age and mortality from COVID-19 among persons with SCD in the United States (B = .540, SE = .231, Wald statistics = 5.450, p = .020 < .05). Furthermore, the results revealed that beta standardized coefficient is not significantly different from zero (B = -.405, Wald = 1.184, p = .277). However, the estimated odds ratio showed that non-Hispanic Black die more from COVID-19, *Exp* (B) = 9.577, 95% CI (3.758, 24.409), than those in the reference group (Others) at a significant level of 0.000. Finally, the results demonstrated a significant relationship between age and race with mortality from COVID-19 among patients ages 20 to 39, 40 to 59, and 60+ and non-Hispanic Blacks compared to the reference groups.

In this chapter, I provide an in-depth interpretation of the results of this study. I also discuss the limitations of the study. I offer recommendations for future studies and practice, consider the implications of this research, and provide a conclusion to the study.

Interpretation of the Findings

I investigated the relationship between age, race/Hispanic origin, and COVID-19 mortality among persons with SCD in all 50 U.S. states, including the District of Columbia, from January 2020 to March 2021. I used existing data compiled by the CDC on SCD and death from COVID-19. I traced the relationship between age, race/Hispanic origin, and mortality from COVID-19 among U.S. persons with SCD. The design was intended to show the correlation between age, race, and mortality from COVID-19 among sickle cell persons. I used the binary logistic regression using the Wald forward and stepwise method of the binary logistic regression model to analyze and answer the research questions

Research Question 1

What is the relationship between age AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$1. There is no relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

H_a1. There is a relationship between age AND mortality from COVID-19 among persons with SCD in the United States.

From the perspective of age and COVID-19, research had shown that older adults were especially known to contract the disease faster, suffer from the severe form, and eventually die from it compared to children (Hussain et al., 2020). However, with advancements in research on this variable, COVID-19 did not discriminate the age of an individual for children as well as adults were infected by the virus, suffered from severe

disease, and could eventually die from it (Clift et al., 2021; Panepinto et al., 2020). Moreover, Payne et al. (2020) and Panepinto et al. noticed the high number of emergency room visits, hospitalizations, and deaths of children and adults with SCD from COVID-19 from different registries, such as the SECURE-SCD Registry. This finding indicated that any age could be affected by the virus. Moreover, according to Payne et al. (2022) and Hussain et al., the COVID-19 pandemic did not cause excess death among persons with SCD compared to years before the pandemic. However, most deaths recorded were among patients 25 to 59, with the sharpest death among those 60+, thus indicating that older persons with SCD died far more from COVID-19 than children.

Moreover, when assessing the relationship between age and COVID-19 deaths in the United States, the first research question, the results showed a highly significant relationship between age and mortality from COVID-19 among persons with SCD (p = .020 < .05).The estimated odds ratio for respondents aged 60+ showed that they died more from COVID-19 than those in the reference group (0 to 19) at a significance level of .000, *Exp* (B) = 17.499, 95% CI (4.195, 73.002). Additionally, persons aged 40 to 59, *Exp* (*B*) = 6.174, 95% CI (2.176, 17.517.488), were observed to die more from COVID-19 than those in the reference group (0 to 19) at a significance level of .000. More so, persons aged 20 to 39, *Exp* (*B*) =3.474, 95% CI (1.306, 9.243), were significant at a level of p < .013. They were observed to die more from COVID-19 than in the reference group (0 to 19 years of age). Furthermore, the Nagelkerke *R*-square showed that age accounted for 42.9% of COVID-19 deaths among SCD patients. This study demonstrated a proportional relationship between increases in age and mortality from COVID-19 during

the timeframe of this study but also confirmed existing literature. It confirmed how adults, especially older adults SCD patients, had recorded the highest death rates over young patients during the pandemic in the United States (Hussain et al., 2020; Payne et al., 2022).

Research Question 2

What is the relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States?

$H_0$2. There is no relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

H_a2. There is a relationship between race/Hispanic origin AND mortality from COVID-19 among persons with SCD in the United States.

SCD affects tens of millions of people worldwide. According to Clift et al. (2021), approximately 8 million to 12 million persons globally have SCD. Per Mburu and Odame (2019), more than 300,000 babies are delivered annually with the disease in Africa. As the CDC (2020b) and USDHHS (2020) noted, SCD is a global health concern and affects 100,000 Americans. In the United States, Black (*OR* = 1/365) and Hispanic Americans (*OR* = 1/16,300) are affected by SCD, as per Panepinto et al. (2020). Compared to other Western nations, like the United Kingdom, the United States has the highest population with the disease (Clift et al., 2021; Panepinto et al., 2020). This high number of U.S. patients with the disease indicates the prevalence of SCD in the country's diverse and dynamic population, which makes a good study on the impact of the pandemic. Kim and Bostwick (2020) and Moore et al. (2020) noted that U.S. underserved

communities were mostly people of color and disproportionately affected by the pandemic, suffering the worst health outcomes. Guarino et al. (2022), Panepinto et al. (2020), and USDHHS (2020) further discussed the racial disparity of the pandemic among U.S. SCD patients, where non-Hispanic Black was more likely to bear the burden of the pandemic and subsequently die for it that non-Hispanic White and other counterparts.

Additionally, in this study, answering the second research question required determining whether there was a relationship between race/Hispanic origin and COVID-19 mortality among persons with sickle cell. The test statistics showed a statistically significant relationship between race/non-Hispanic origin and mortality from COVID-19 among U.S. persons with SCD. The estimated odds ratio showed that non-Hispanic Black people died more from COVID-19, *Exp* (*B*) = 9.577, 95% CI (3.758, 24.409), than non-Hispanic White and others. Race/Hispanic origin accounted for 29.9% of COVID-19 deaths of U.S. patients with SCD, whereas non-Hispanic Black people had the highest deaths and were 9.577 times more likely to die. Non-Hispanic White people were 16.7 times more likely to survive than the reference group (other) during the study. This study did not only identify the disparity of health and health outcome among non-Hispanic Black in the United States during the pandemic but also confirmed existing literature on the burden of excess deaths from the COVID-19 pandemic among non-Hispanic Black patients with SCD in the United States.

Research Question 3

What is the relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States?

$H_0$3. There is no relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

H_a3. There is a relationship between age and race/Hispanic origin with mortality from COVID-19 among persons with SCD in the United States.

Historically, in the United States, racial tension, political divides, and mistrust of the political and medical institutions have created a huge disparity in access to health care for the minority population in the country (Hahn et al., 2018; Krieger, 2020). People of color have been known to suffer from any imaginable disease and to experience the worst health outcome from those diseases compared to other racial groups due to social injustice (Krieger, 2020; Smedley et al., 2003; Wilkinson & Pickett, 2010). As Smedley et al. stated, "Race and ethnicity remain significant predictors of the quality of health care received" (p. 20). More so, globally, age susceptibility to COVID-19 was not well understood during the start of the COVID-19 pandemic (Hussain et al., 2020). Moreover, as discussed by Clift et al. (2021) and Panepinto et al. (2020), more research on this variable has demonstrated that COVID-19 did not discriminate by age for children, as they also became infected by the virus suffered from severe disease and could eventually die from the pandemic.

However, in answering the third research question, the findings showed a significant relationship between age and race/Hispanic origin with mortality. It was

observed that non-Hispanic Black people with SCD within the age group of 20 to 39 years, 40 to 59 years, and 60+ years of almost equal proportions died of COVID-19; this trend was not observed with non-Hispanic White people and others. The proportion of non-Hispanic Black SCD patients aged 20 to 39, 40 to 59, and 60+ who died of COVID-19 were more than two times higher for persons aged 60+ as with non-Hispanic White SCD patients. Finally, based on others, the proportion of non-Hispanic Black people aged 40 to 59 who died from COVID-19 was more than two times higher than those who died of COVID-19, among others.

Furthermore, the estimated odds ratio between race/Hispanic origin and age showed that persons aged 60+ were observed to die more from COVID-19, *Exp* (*B*) = 18.564, 95% CI (4.323, 79.717), followed by persons aged 40 to 59 years *Exp* (*B*) = 4.480, 95% CI (1.569, 12.795), and persons aged 20 to 39 years, *Exp* (*B*) = 3.314, 95% CI (1.198, 9.165), than those in the reference group (0 to 19 years) Moreover, based on race/Hispanic origin, non-Hispanic Black people were observed to die more, *Exp* (B) = 6.278, 95% CI (2.489, 15.832), while non-Hispanic White people were observed to die less than those in the reference group (others), *Exp* (B) = .670, 95% CI (.164, 2.740). The relationship between age and race/Hispanic origin accounted for 62.4% of COVID-19 deaths among U.S. SCD, the highest variability compared to age and race/Hispanic origin, with 42.9% and 29.9%, respectively. Although many studies have discussed the effect and mortality due to the pandemic among SCD in the United States and abroad, existing literature from Guarino et al. (2022), Panepinto et al. (2020), Payne et al. (2022), and the USDHHS (2020) demonstrated and confirmed the high mortality among older

adults than younger age groups and non-Hispanic Black than non-Hispanic White and other SCD patients. Furthermore, the difference in the variability of the variables in this research, especially that of both race/Hispanic origin and age with the highest variability, has expanded knowledge in research that not only age or race/Hispanic origin but also both race/Hispanic origin and age should be considered by policymakers and decision-makers, public health workers, and health care professionals when developing health policies and preventive protocols in the SCD community.

Moreover, social injustice, racial tension, and political divides have created a gap in research participation and access to health and mental care, thereby creating iniquities in the health outcomes of the minority population (Krieger, 2020; Smedley et al., 2003; Wilkinson & Pickett, 2010). The racial disparity in health in the United States is evident from the incidence and mortality during this pandemic (Kim & Bostwick, 2020; Moore et al., 2020). The racial health disparity has been illuminated due to the COVID-19 pandemic in which there is a gap in the existing knowledge of health inequities and the racial disparity of the COVID-19 pandemic in the underrepresented communities of color in the United States (Kim & Bostwick, 2020; Moore et al., 2020; Panepinto et al., 2020). Although the pandemic does not discriminate in whom it affects, some communities, especially the disenfranchised counties, bear much of the burden. In the United States, COVID-19 national and state policies and mitigation recommendations have greatly impacted the Black community's sociocultural and economic aspects (Moore et al., 2020).

SCD is a genetic blood disorder that causes many health complications. Those medical conditions can lead to significant morbidity, mortality for those with the disease, and profound psychological and economic distress to families and the community (Aiko et al., 2018). COVID-19 does not discriminate against whom it affects (USDHHS, 2020); however, Fauci et al. (2020) stated that the disease was more common and deathly among those who were immunocompromised, such as patients with SCD. This finding may account for why biologically, adults and older persons than younger ones with SCD and socially, why non-Hispanic Black than non-Hispanic White and others from my study died more from COVID-19 Persons with SCD have many health and psychological issues that adversely affect their overall health and quality of life. More so, the findings of this study were also analyzed and interpreted in the context of the theoretical framework that was employed in this study.

COVID-19 is a respiratory infection that disproportionately affected not only people of adult age groups and those who are immunocompromised but also demonstrated a racial disparity (Kim & Bostwick, 2020; Moore et al., 2020). SCD, on the other hand, is the most common hematologic genetic and immunocompromised disease that affects people of all ages and does not only come with many comorbidities and results in increased hospitalization and mortality, especially when infected with COVID-19 but shows a racial disparity, particularly among non-Hispanic black (Clift et al., 2021; Panepinto et al., 2020). Findings confirmed that older and non-Hispanic Black patients were more likely to die from COVID-19 infection during the pandemic than younger SCD patients. The distribution of both diseases and disparity in mortality that existed in

the United States could be explained by employing the biological and social perspectives of the ecosocial theory of disease distribution (Kim & Bostwick, 2020; Krieger, 2020; Moore et al., 2020; Panepinto et al., 2020). The biological perspective explained the susceptibility and mortality from COVID-19 due to the immunocompromised nature of older SCD patients; on the other hand, the social perspective of the ecosocial theory explained the various SDH in the United States that had helped in fueling the health disparity and illuminated COVID-19 mortality rates, especially of non-Hispanic Black due to racial and social discrimination (Gebhard et al., 2020; Gelfand et al., 2021, 2020; Guarino et al.,2022; Kim & Bostwick, 2020; Krieger, 2020; Moore et al., 2020; Panepinto et al., 2020).

Limitations of the Study

Those with SCD, because of their immunocompromised status, are at increased risk and are disproportionately affected by the COVID-19 pandemic (Panepinto et al., 2020; USDHHS, 2020). However, compared to the morbidity and mortality of the SCD population before the pandemic, findings and the global registry demonstrated an increase in hospitalization and death, resulting in excess death during the pandemic (Clift et al., 2021; Payne et al., 2020). This cross-sectional study explored the relationship between age, race/Hispanic origin, and mortality due to COVID-19 in persons with SCD in the United States. However, some limitations could affect the internal and external validity of the study.

In this observational study, the first limitation of temporality came from the cross-sectional study design. This design would not show if the exposure or the disease came

first and did not give an association between cause and effect, possibly leading to bias in the results (Aschengrau & Seage, 2020, p. 161). Although other designs, such as a longitudinal study, could have been employed, a cross-sectional study design was ideal in this research as it provided a snapshot of the exact period of the study.

The ICD 10 CODES and Cause of Mortality Registry were used to select patients who died due to the pandemic; however, during the early stages of the pandemic, it would be difficult to assess if death was due to other SCD complications, such as heart and another respiratory disease, than COVID-19, thereby missing most of the COVID-19 death. Additionally, although researchers at the beginning of the pandemic stipulated that only older adults were prone to COVID-19, they neglected that children with underlying medical conditions, such as SCD, could also contract COVID-19 and eventually die from it. This study showed that though most deaths were older, some children still died, leading to underestimating the mortality rates (Tzeng et al., 2021). This issue represented a second limitation. Moreover, not considering those with SCD who died and were not registered and accounted for will also give an underestimation of the mortality rate and is the third limitation. These issues might have skewed the study's results, causing misclassification and selection bias.

Large sample size in quantitative research was vital to ensure the validity and generalizability of the study. According to Aschengrau and Seage (2020), Creswell and Creswell (2018), and Salazar et al. (2015), appropriate sample sizes would dictate the power and effect of a study. The fourth limitation of this study was the small sample size, which might affect the generalizability of the study. From G*Power calculation, a sample

size of 190 respondents was required for maximum effect, however, although 1,814 SCD patients died during the study period from January 2020 to March 2021, only 140 respondents had COVID-19, and 100 died from COVID-19. Forty died from other complications, hence not reaching the minimum sample size per calculated G*Power. Therefore, in ensuring that an appropriate sample size would offset this limitation, random sampling, age, and race/Hispanic origin stratification were done in this cross-sectional study. The most appropriate statistical test of binary logistic regression was also employed during the analysis to help decrease those limitations. Thus, these processes should increase the reliability and validity of this study.

This pandemic did disrupt the lives and livelihoods of countries and people globally (Béné et al., 2021; Buscetta et al., 2022; Davvetas et al., 2022; Fauci et al., 2020; Gelfand et al., 2021; Pronk & Faghy, 2022; Vinkers et al., 2020; WHO, 2021). However, it hit the most developed nations, especially the United States (Clift et al., 2021; Fauci et al.,2020; Gelfand et al., 2021; Panepinto et al., 2020). The United States has the highest number of cases and death and the highest population of SCD patients in the Western world (Clift et al., 2021; Fauci et al., 2020; Gebhard et al., 2020; Gelfand et al., 2020, 2021; Panepinto et al., 2020; Teulier et al., 2021; Tonen-Wolyec et al., 2020). AbdulRahman et al. (2020), Clift et al., and Panepinto et al. discussed how the United States had the highest population of SCD patients of more than 100,000, while the U.K and Bahrain had just 15,000 and 6,933, respectively. Additionally, the United States had the highest cases and mortality from COVID-19 among SCD patients. For example, according to AbdulRahman et al., although the CDC provisional mortality data set

showed 140 cases and 100 deaths, studies from a country like Bahrain with less COVID-19 burden showed six cases with no deaths from the pandemic. Therefore, compared to countries with a lesser burden with this pandemic and with fewer SCD patients, this study cannot be replicated and generalized, thereby decreasing the reliability of the study and creating the fifth limitation.

The last limitation resulted from how the race/Hispanic variable was operationalized in the study. Although the category of non-Hispanic Black and non-Hispanic White was easily understood, the category of "other," as stated in the data set, was too broad, consisting of many subcategories. This issue made it difficult to ascertain properly and identify the death rate of different races/Hispanic origins in the subcategory "other," hence decreasing the reliability of the study.

Recommendations

Since the beginning of this pandemic, many studies have investigated the relationship between COVID-19 and SCD in many regions of the globe; however, to my knowledge, no study has yet explored the relationship between age, race, and the mortality of COVID-19 among U.S. patients with SCD. The findings answered my research questions and rejected the null hypotheses in favor of the alternative hypotheses that there was not only a relationship between age and race but also a relationship between both age and race with COVID-19 mortality among U.S. patients with SCD; however, recommendations for future research and practice are warranted.

Recommendations for Future Research

Although the findings of this study all showed a statistically significant relationship between age, race/Hispanic origin, and COVID-19 mortality in U.S. persons with SCD, future research studies, such as longitudinal studies and bigger sample size, are needed to explore the relationship between the variables of this study properly. Additionally, a wealth of information about the sex difference in mortality from COVID-19 in persons with SCD is valuable in this research; therefore, further research is recommended to explore the relationship between sex and COVID-19 mortality in the United States.

Recommendations for Practice

SCD remains a complex and debilitating inherited genetic orphan disease that comes with not only physical and psychological pain and suffering to the patients and their families and leads to a decreased quality of life, but it is also stigmatized by the public and even some medical personnel (Lubeck et al., 2019; Mburu & Odame, 2019; Telfer, 2019; Uyoga et al., 2019). Therefore, for future practice, I recommend that public health professionals develop awareness programs to properly sensitize the public about SCD. Due to the lack of medical professionals, more medical doctors and nurses should be trained on how to properly manage the care of this vulnerable population, especially during a pandemic. Lastly, although many prevention and treatment modalities are readily available for COVID-19, few treatments, such as bone marrow transplants, are available for those with SCD. Hence, for future practice, genomic engineering should be

encouraged as it will address, cure, and alleviate the pain, suffering, and health disparities among the SCD community in the United States and globally.

Implications

Positive Social Implications

According to Kim and Bostwick (2020) and Moore et al. (2020), people of color, such as the Blacks and Latinos subgroup, have been documented to suffer more from most communicable and noncommunicable diseases, especially among the elderly population. This study is significant as various SDH exist, such as socioeconomic challenges and social injustice, access to health information, and health care in U.S. societies today. These have significantly contributed to rendering some subgroups, especially people of color, more vulnerable to suffering from many adverse health and health outcomes and prognoses than their White counterparts (Fauci et al., 2020; Mburu & Odame, 2019; Menapace & Thein, 2020; Moore et al., 2020; Panepinto et al., 2020; Smedley et al., 2003; Tezol & Unal, 2021; Tonen-Wolyec et al., 2020). Moreover, this health inequality has been specially illuminated in the United States as disproportionately affecting poor communities, such as African Americans and Hispanics, who reside in impoverished communities with a lot of SDH. They are prone to having poorer prognoses with genetic diseases, such as SCD (Kim & Bostwick, 2020; Krieger, 2020; Moore et al., 2020; Panepinto et al., 2020; Smedley et al., 2003).

SCD remains an orphan and neglected hereditary medical disease affecting many racial groups in other parts of the globe (Lee et al., 2019; Panepinto et al., 2020). This disease requires global health attention, more research, specialized medical professionals,

and much sensitization and education to the public (Lubeck et al., 2019; Mburu & Odame, 2019; Telfer, 2019; Uyoga et al., 2019). Guarino et al. (2022), Panepinto et al. (2020), and Clift et al. (2021) also noted that people of color with SCD who became infected with COVID-19 had a severe form of the disease and a high case fatality rate. The various SDH in the communities and the comorbidities faced by persons with SCD make an excellent recipe for contracting COVID-19. Hence, African Americans with SCD in an underserved community subsequently compound their already compromised statuses for a severe COVID-19 outcome, eventually dying from it when infected by the virus.

Furthermore, the COVID-19 pandemic has negatively impacted individuals; families; and all the social, medical, public health, and economic institutions globally (Béné et al., 2021; Buscetta et al., 2022; Davvetas et al., 2022; Fauci et al., 2020; Pronk & Faghy, 2022; Vinkers et al., 2020). The enormous public health, healthcare access, and socioeconomic challenges of SCD and COVID-19 are not limited to communities in sub-Saharan Africa, Europe, the Middle East, and China but are amplified in the United States (AbdulRahman et al., 2020; Beerkens et al., 2020; Gebhard et al., 2020; Panepinto et al., 2020; Smedley et al., 2003; Teulier et al., 2021; Tonen-Wolyec et al., 2020). This dilemma may result in the United States bearing much of the burden of the pandemic and persons with SCD compared with other Western nations (Clift et al., 2021; Fauci et al., 2020; Gelfand et al., 2021).

Moreover, during the early phases of the pandemic, studies have shown that elderly adults with preexisting conditions were universally documented to be the most

vulnerable to contracting and dying from the COVID-19 infection. However, more research has demonstrated that different age groups can be infected by the COVID-19 virus resulting in different severity and even dying from it (Hsu et al., 2020; Kim & Bostwick, 2020; Lubeck et al., 2019; Mburu & Odame, 2019; Moore et al., 2020; Nardo-Marino et al., 2017; Panepinto et al., 2020; Tonen-Wolyec et al., 2020). However, studying the complications of COVID-19 outcome on persons with SCD while researching race/Hispanic origin and age differences in the mortality of COVID-19 infection among persons with SCD helped shed light on how the SCD community can manage the dual disease in the United States at the national level, and for medical and public health professionals to better understand, develop, and implement race/Hispanic origin and age-appropriate treatment and preventive measures at the community and individual levels (Aiko et al., 2018; Ceglie et al., 2019; Isa et al., 2020; Panepinto et al., 2020; Tonen-Wolyec et al., 2020; Veselka et al., 2018).

This study not only supports the various research findings of the existence of a correlation between age and race/Hispanic origin, especially older age and African Americans with COVID-19 but demonstrates that there is a statistically significant relationship between age and race/Hispanic origin with COVID-19 mortality among patients with SCD in all 50 U.S. states, including the District of Columbia. The relationship was more significant among non-Hispanic Black than Hispanics and non-Hispanic White and statistically significant among those aged 20 to 39, 40 to 59, and 60+ than younger age group 0 to 19.

The findings of this research may cause positive social change at the individual, community, and societal levels by helping to develop and prioritize age and race/Hispanic-origin-specific interventions. Specific interventions may minimize incidents, hospitalizations, and mortality rates while improving the overall health and health outcomes of persons with SCD and their communities during this deadly COVID-19 pandemic. It may provide information for another unforeseen pandemic of this magnitude in the United States and other regions of the globe.

Methodological, Theoretical, and Empirical Implications

Racial tension, political divides, global warming, globalization, and the various SDH in our society have added to poor health outcomes, especially in underserved communities (Kim & Bostwick, 2020; Moore et al., 2020; Smedley et al., 2003). This study is significant. Various SDHs exist, such as socioeconomic challenges, social injustice, and a lack of access to health information and health care in U.S. societies. These issues have significantly contributed to rendering some subgroups, especially people of color more vulnerable to suffering from many adverse outcomes with a prognosis than their White counterparts (Fauci et al., 2020; Mburu & Odame, 2019; Menapace & Thein, 2020; Moore et al., 2020; Panepinto et al., 2020; Smedley et al., 2003; Tezol & Unal, 2021; Tonen-Wolyec et al., 2020).

Additionally, Carter-Smith (2021) elaborated on how “the role of politic, social, environmental, and institutional factors plays on the overall health of individuals and the population” (p. 20). In this study, the Krieger (2000, 2020) ecosocial theory explains the social iniquities of health and determinants of disease distribution in the population by

merging social and biological concepts with historic and ecological viewpoints used in linking the methodology of this study (Carter-Smith, 2021). The effect of the pandemic has not only devastated the general population but has also disproportionately affected the underserved and vulnerable communities and will be better explained by the socioecological theory and a cross-section study design.

This study was a retrospective observational cross-sectional study design. The secondary data were from the CDC's provisional mortality rates for COVID-19 on SCD patients in all 50 U.S. states. These data were used to find a relationship between age, race, and COVID-19 mortality among patients with SCD in the United States from January 2020 to March 2021. The ecosocial theory was employed to direct and explain findings. The theory is an integrative theory that shows all the different social determinants that influence the spread of COVID-19 in the United States from the social, racial, ecological, biological, and political perspectives (Krieger, 2000, 2020). The theory does not only explain how a single agent (COVID-19) will interact with genetics (SCD) but also explains how social, political, and ecological environments bring about inequity in health and the distribution of disease in society (Krieger, 2000, 2020).

The result of this study demonstrated a strong statistically significant association not only between age and race but also between both age and race and mortality from COVID-19 among SCD patients in the United States. To my knowledge, no study has explored this relationship in the United States before; however, this result increases the knowledge base for stakeholders, practitioners, and policymakers. They may find the

findings beneficial for program design and implementing age- and race-specific care that will bring about positive societal changes.

Conclusion

I conducted a retrospective cross-sectional study investigating the relationship between age, race/Hispanic origin, and COVID-19 mortality among SCD patients in all 50 U.S. states, including the District of Columbia. I used secondary data for the analysis. Data for the SCD and COVID-19 mortality were obtained from the CDC website. The data were publicly accessible, and no formal user agreement was necessitated. The ecosocial theory was used to direct the methodology and explain this study's findings. The theory was used because of the inequality in the distribution of COVID-19 and deaths due to the pandemic among persons with SCD in the United States. SPSS was employed to analyze the data using the backward binary logistic regression method.

The result showed that the predictor variable of age was found to be significantly associated with COVID-19 mortality among U.S. persons with SCD. The estimated odds ratio for respondents age 60+, *Exp* (*B*) = 17.499, 95% CI (4.195, 73.002), showed that persons aged 60+ died more and were 17.499 times more likely to die from COVID-19 than those in the reference group (0 to 19) at a significance level of $p < .001$. Additionally, persons aged 40 to 59, *Exp* (*B*) = 6.174, 95% CI (2.176, 17.517), were observed to die 6.174 times more from COVID-19 than those in the reference group (0 to 19) at a significance level of $p = .001$. Patients aged 20 to 39, *Exp* (*B*) = 3.474, 95% CI (1.306, 9.243), were also observed to die 3.474 times more but had a 99.2% from COVID-19 than those in the reference group (0 to 19 years of age) at a significance level

of $p = 0.013$. The total variability explained by age concerning COVID-19 mortality was 42.9% (Nagelkerke *R*-Square = .455). Age accounted for 42.9% of COVID-19 deaths among SCD patients. During this study, a proportional relationship between increases in age and mortality was demonstrated in the United States, with older patients recording the highest death rates over young patients with SCD and vice versa. The results of this study also confirmed existing literature regarding how adults, especially older adults SCD patients, had recorded the highest death rates over young patients during the pandemic in the United States (see Hussain et al., 2020; Payne et al., 2022).

Moreover, there is a statistically significant relationship between race/Hispanic origin and mortality from COVID-19 among persons with SCD in the United States. The estimated odds ratio showed that non-Hispanic Black died more from COVID-19, *Exp* (*B*) = 9.577, 95% CI (3.758, 24.409), and were 55.7 times more likely to die during the study period than those in the reference group (other) at a significance level of $p < .001$. Moreover, non-Hispanic White people were observed to die less and were 16.7 times more likely to survive COVID-19 than those in the reference group (other), *Exp* (*B*) = .833, 95% CI (.244, 3.103), but not significant $p > 0.05$ and lower point less than 1. Race/Hispanic origin was found to explain a total variability of 29.9% (Nagelkerke *R*-Square = .299) of the outcome variable (Die of COVID-19). Race/Hispanic origin accounted for approximately 30% of COVID-19 deaths, and non-Hispanic Black people died more than twice as non-Hispanic White people and others, with the highest odds of death. They were 9.577 times more likely to die, while non-Hispanic White people were 16.7 times more likely to survive than other races during the study. This study did not

only identify the disparity of health and health outcome among non-Hispanic Black in the United States during the pandemic, but also confirmed existing literature on the burden of excess death from the COVID-19 pandemic among non-Hispanic Black patients with SCD in the United States, as posited by Guarino et al. (2022), Panepinto et al. (2020), and Payne et al. (2022).

Lastly, the results demonstrated a significant relationship between age and race/Hispanic origin with mortality from COVID-19. The estimated odds ratio obtained between race and age showed that persons aged 60+ were observed to die more from COVID-19, *Exp* (*B*) = 18.564, 95% CI (4.323, 79.717), than those in the reference group (0 to 19 years) at a significance level of 0.000. Additionally, while persons aged 40 to 59 years were observed to die more from COVID-19, *Exp* (*B*) = 4.480, 95% CI (1.569, 12.795), at a significance level of 0.005, persons aged 20 to 39 years were observed to die more from COVID-19, *Exp* (*B*) = 3.314, 95% CI (1.198, 9.165), than those in the reference group (0 to 19 years) at a significance level of 0.021. Further, based on race/Hispanic origin, non-Hispanic Black people were observed to die more than those in the reference group (other), *Exp* (B) = 6.273, 95% CI (2.489, 15.832), at a significance level of .001; however, non-Hispanic White people were observed to die less than those in the reference group (others), *Exp* (*B*) = .670, 95% CI (..164, 2.740, 2.658), at a non-significance level of *p* = .577. The relationship between both age and race/Hispanic origin explained a total variability of 62.4% (Nagelkerke *R*-Square = .624) of the outcome variable, meaning that both age and race/Hispanic origin accounted for the highest (62.4%) COVID-19 deaths over age (42.9%) and race/Hispanic origin (~30%)

alone among U.S. SCD patients. The results confirmed existing literature on the crucial role of age and race/Hispanic origin in SCD patients' mortality during the pandemic in the United States (Guarino et al., 2022; Panepinto et al., 2020; Payne et al., 2022; USDHHS, 2020).

The COVID-19 pandemic has not only negatively impacted the lives, livelihood, and the economy of individuals and countries globally but has also overwhelmed the public health and health care systems, causing more than 6.7 million deaths (Béné et al., 2021; Buscetta et al., 2022; Fauci et al., 2020; Panepinto et al., 2020; Payne et al., 2022; USDHHS, 2020; WHO, 2021). On the other hand, SCD remains an inherited genetic orphan medical condition that not only negatively affects the physical and psychological well-being of those with the disease, their families, and their communities' social and economic aspects but also comes with many comorbidities and even death. (Béné et al., 2021; Buscetta et al., 2022; Davvetas et al., 2022; Guarino et al., 2022; Vinkers et al., 2020). It has been well-documented that people with SCD are more susceptible to contracting a respiratory infection and are also at an increased risk of becoming infected by and dying from COVID-19 (Payne et al., 2022). The United States is credited for having the highest number of cases and deaths from the pandemic and a high population of people with SCD (Clift et al., 2021; WHO, 2021). Additionally, the pandemic has disproportionately affected people in underserved communities and the immunocompromised, especially those with SCD in the United States (Guarino et al., 2022; Panepinto et al., 2020; Payne et al., 2022; USDHHS, 2020). According to Payne et

al. (2022), the health disparity and the challenges faced by a person with SCD during the pandemic were attributed to

> socioeconomic and health care challenges such as low educational attainment, employment, other disabling SCD complications, lack of health care providers with expertise in SCD care and treatment; and both structural and interpersonal racism in the health care system that had further complicated efforts to prevent or access timely care for respiratory infections, including COVID-19 illness. (p. 20)

Findings of published case series and a registry-based study, such as the SECURE-SCD registry, provided empirical evidence that SCD patients infected with COVID-19 suffered from worse outcomes and had a high hospitalization and fatality rate. However, the finding of this study showed that age or race/Hispanic origin had not only a statistically significant relationship with COVID-19 mortality, but age and race/Hispanic origin also had a higher variability with COVID-19 mortality among U.S. persons with SCD. The results of this study provide a knowledge base that can influence policy creation and decision-making that may foster positive social change among the SCD community in the United States. Moreover, the findings of this study may prompt not only public health professionals to develop programs to create more awareness about SCD and prevention from COVID-19 but also medical practitioners to get the proper training to provide age- and race-specific interventions. They can also encourage pharmaceuticals and genomic engineering to develop novel treatments for the targeted population and public agencies to develop a good surveillance system to properly monitor and promptly mitigate epidemics from becoming a pandemic. Moreover, the development

of age and race/Hispanic-origin-specific interventions and protocols may minimize incidents, hospitalizations, morbidity, and mortality rates while improving the overall health and health outcomes of persons with SCD and their communities during this deadly COVID-19 pandemic. The results of this study may provide information to use in the SCD community in another unforeseen pandemic of this magnitude in the United States and other regions of the globe and positively influence social change.

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Appendix: Analysis Output

Descriptive Statistics

Race or Hispanic Origin

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Others	30	21.4	21.4	21.4
	non-Hispanic White	14	10.0	10.0	31.4
	non-Hispanic Black	96	68.6	68.6	100.0
	Total	140	100.0	100.0	

Age group

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	0-19	21	15.0	15.0	15.0
	20-39	38	27.1	27.1	42.1
	40-59	43	30.7	30.7	72.9
	60+	38	27.1	27.1	100.0
	Total	140	100.0	100.0	

SCD and COVID-19

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Not died of COVID-19	40	28.6	28.6	28.6
	Died of COVID-19	100	71.4	71.4	100.0
	Total	140	100.0	100.0	

Cross-Tabulation: Race and COVID-19 Mortality

Crosstab

			SCD and COVID-19		
			Not died of COVID-19	Died of COVID-19	Total
Race or Hispanic Origin	Others	Count	18	12	30
		% within Race or Hispanic Origin	60.0%	40.0%	100.0%
	non-Hispanic White	Count	9	5	14
		% within Race or Hispanic Origin	64.3%	35.7%	100.0%
	non-Hispanic Black	Count	13	83	96
		% within Race or Hispanic Origin	13.5%	86.5%	100.0%
Total		Count	40	100	140
		% within Race or Hispanic Origin	28.6%	71.4%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	33.896[a]	2	.000
Likelihood Ratio	32.747	2	.000
Linear-by-Linear Association	29.182	1	.000
N of Valid Cases	140		

a. 1 cells (16.7%) have expected count less than 5. The minimum expected count is 4.00.

Age and COVID-19 Mortality

Age group * SCD and COVID-19 Crosstabulation

			SCD and COVID-19		
			Not died of COVID-19	Died of COVID-19	Total
Age group	0-19	Count	20	1	21
		% within Age group	95.2%	4.8%	100.0%
	20-39	Count	9	29	38
		% within Age group	23.7%	76.3%	100.0%
	40-59	Count	6	37	43
		% within Age group	14.0%	86.0%	100.0%
	60+	Count	5	33	38
		% within Age group	13.2%	86.8%	100.0%
Total		Count	40	100	140
		% within Age group	28.6%	71.4%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)
Pearson Chi-Square	55.104[a]	3	.000
Likelihood Ratio	53.525	3	.000
Linear-by-Linear Association	33.798	1	.000
N of Valid Cases	140		

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 6.00.

Age, Race, and COVID-19 Mortality

Age Group * SCD and COVID-19 * Race or Hispanic Origin Crosstabulation

Race or Hispanic Origin				SCD and COVID-19: Not died of COVID-19	SCD and COVID-19: Died of COVID-19	Total
Others	Age Group	< 5 years	Count	1	0	1
			% within Age Group	100.0%	0.0%	100.0%
		5-14 years	Count	2	0	2
			% within Age Group	100.0%	0.0%	100.0%
		15-19 years	Count	3	0	3
			% within Age Group	100.0%	0.0%	100.0%
		20-24 years	Count	4	1	5
			% within Age Group	80.0%	20.0%	100.0%
		25-39 years	Count	2	6	8
			% within Age Group	25.0%	75.0%	100.0%
		40-59 years	Count	4	2	6
			% within Age Group	66.7%	33.3%	100.0%
		60+	Count	2	3	5
			% within Age Group	40.0%	60.0%	100.0%
	Total		Count	18	12	30
			% within Age Group	60.0%	40.0%	100.0%
non-Hispanic White	Age Group	5-14 years	Count	2	0	2
			% within Age Group	100.0%	0.0%	100.0%
		25-39 years	Count	2	1	3
			% within Age Group	66.7%	33.3%	100.0%
		40-59 years	Count	2	1	3
			% within Age Group	66.7%	33.3%	100.0%
		60+	Count	3	3	6
			% within Age Group	50.0%	50.0%	100.0%
	Total		Count	9	5	14
			% within Age Group	64.3%	35.7%	100.0%
non-Hispanic Black	Age Group	< 5 years	Count	4	0	4
			% within Age Group	100.0%	0.0%	100.0%
		5-14 years	Count	4	1	5
			% within Age Group	80.0%	20.0%	100.0%
		15-19 years	Count	4	0	4
			% within Age Group	100.0%	0.0%	100.0%
		20-24 years	Count	1	5	6
			% within Age Group	16.7%	83.3%	100.0%
		25-39 years	Count	0	16	16
			% within Age Group	0.0%	100.0%	100.0%
		40-59 years	Count	0	34	34
			% within Age Group	0.0%	100.0%	100.0%
		60+	Count	0	27	27
			% within Age Group	0.0%	100.0%	100.0%
	Total		Count	13	83	96
			% within Age Group	13.5%	86.5%	100.0%
Total	Age Group	< 5 years	Count	5	0	5
			% within Age Group	100.0%	0.0%	100.0%

	5-14 years	Count	8	1	9
		% within Age Group	88.9%	11.1%	100.0%
	15-19 years	Count	7	0	7
		% within Age Group	100.0%	0.0%	100.0%
	20-24 years	Count	5	6	11
		% within Age Group	45.5%	54.5%	100.0%
	25-39 years	Count	4	23	27
		% within Age Group	14.8%	85.2%	100.0%
	40-59 years	Count	6	37	43
		% within Age Group	14.0%	86.0%	100.0%
	60+	Count	5	33	38
		% within Age Group	13.2%	86.8%	100.0%
Total		Count	40	100	140
		% within Age Group	28.6%	71.4%	100.0%

Chi-Square Tests

Race or Hispanic Origin		Value	df	Asymptotic Significance (2-sided)
Others	Pearson Chi-Square	9.861[b]	6	.131
	Likelihood Ratio	12.011	6	.062
	Linear-by-Linear Association	4.283	1	.038
	N of Valid Cases	30		
non-Hispanic White	Pearson Chi-Square	1.659[c]	3	.646
	Likelihood Ratio	2.293	3	.514
	Linear-by-Linear Association	1.478	1	.224
	N of Valid Cases	14		
non-Hispanic Black	Pearson Chi-Square	82.049[d]	6	.000
	Likelihood Ratio	65.728	6	.000
	Linear-by-Linear Association	61.085	1	.000
	N of Valid Cases	96		
Total	Pearson Chi-Square	59.011[a]	6	.000
	Likelihood Ratio	59.079	6	.000
	Linear-by-Linear Association	46.846	1	.000
	N of Valid Cases	140		

Note. 5 cells (35.7%) have expected count less than 5. The minimum expected count is 1.43; 14 cells (100.0%) have expected count less than 5. The minimum expected count is .40; 8 cells (100.0%) have expected count less than 5. The minimum expected count is .71; and 10 cells (71.4%) have expected count less than 5. The minimum expected count is .54

Binary Logistic Regression Output: Race and COVID-19 Mortality

Case Processing Summary

Unweighted Cases[a]		N	Percent
Selected Cases	Included in Analysis	140	100.0
	Missing Cases	0	.0
	Total	140	100.0
Unselected Cases		0	.0
Total		140	100.0

Note. If weight is in effect, see classification table for the total number of cases.

Dependent Variable Encoding

Original Value	Internal Value
Not died of COVID-19	0
Died of COVID-19	1

Categorical Variables Codings

			Parameter coding	
		Frequency	(1)	(2)
Race or Hispanic Origin	Others	96	1.000	.000
	non-Hispanic White	14	.000	1.000
	non-Hispanic Black	30	.000	.000

Iteration History

			Coefficients
Iteration		-2 Log likelihood	Constant
Step 0	1	167.616	.857
	2	167.515	.916
	3	167.515	.916

Note. Constant is included in the model; Initial -2 Log Likelihood: 167.515; Estimation terminated at iteration number 3 because parameter estimates changed by less than .001.

Classification Table[a,b]

			Predicted		
			SCD and COVID-19		
	Observed		Not died of COVID-19	Died of COVID-19	Percentage correct
Step 0	SCD and COVID-19	Not died of COVID-19	0	40	.0
		Died of COVID-19	0	100	100.0
	Overall Percentage				71.4

Note. Constant is included in the model; the cut value is .050

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 0	Constant	.916	.187	23.988	1	.000	2.500

Variables not in the Equation

			Score	df	Sig.
Step 0	Variables	Race	33.896	2	.000
		Race(1)	33.810	1	.000
		Race(2)	9.722	1	.002
	Overall Statistics		33.896	2	.000

Iteration History[a,b,c,d]

Iteration		-2 Log likelihood	Coefficients		
			Constant	Race(1)	Race(2)
Step 1	1	136.703	-.400	1.858	-.171
	2	134.794	-.405	2.212	-.182
	3	134.769	-.405	2.259	-.182
	4	134.769	-.405	2.259	-.182

Note. Method: Forward Stepwise (Wald); constant is included in the model; initial -2 Log Likelihood: 167.515; estimation terminated at iteration number 4 because parameter estimates changed by less than .001.

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	32.747	2	.000
	Block	32.747	2	.000
	Model	32.747	2	.000

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	134.769[a]	.209	.299

Note. Estimation terminated at iteration number 4 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	.000	1	1.000

Contingency Table for Hosmer and Lemeshow Test

		SCD and COVID-19 = Not died of COVID-19		SCD and COVID-19 = Died of COVID-19		
		Observed	Expected	Observed	Expected	Total
Step 1	1	9	9.000	5	5.000	14
	2	18	18.000	12	12.000	30
	3	13	13.000	83	83.000	96

Classification Table[a]

			Predicted		
			SCD and COVID-19		
	Observed		Not died of COVID-19	Died of COVID-19	Percentage Correct
Step 1	SCD and COVID-19	Not died of COVID-19	0	40	.0
		Died of COVID-19	0	100	100.0
	Overall Percentage				71.4

Note. The cut value is .050

Variables in the Equation

								95% C.I.for EXP(B)	
		B	S.E.	Wald	df	Sig.	Exp(B)	Lower	Upper
Step 1[a]	Race			29.059	2	.000			
	Race(1)	2.259	.477	22.403	1	.000	9.577	3.758	24.409
	Race(2)	-.182	.671	.074	1	.786	.833	.224	3.103
	Constant	-.405	.373	1.184	1	.277	.667		

Note. Variable(s) entered on step 1: Race.

```
            Step number: 1

            Observed Groups and Predicted Probabilities

     160 +                                                                                                    +
         I                                                                                                    I
         I                                                                                                    I
F        I                                                                                                    I
R    120 +                                                                                                    +
E        I                                                                                                    I
Q        I                                                                                      D             I
U        I                                                                                      D             I
E     80 +                                                                                      D             +
N        I                                                                                      D             I
C        I                                                                                      D             I
Y        I                                                                                      D             I
      40 +                                                                                      D             +
         I                                        D                                             D             I
         I                                        N                                             D             I
         I                                   N    N                                             N             I
Predicted ---------+---------+---------+---------+---------+---------+---------+---------+---------+----------
  Prob:   0        .1        .2        .3        .4        .5        .6        .7        .8        .9         1
  Group:  NDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

          Predicted Probability is of Membership for Died of COVID-19
          The Cut Value is .01
          Symbols: N - Not died of COVID-19
                   D - Died of COVID-19
          Each Symbol Represents 10 Cases.
```

Predicted Probability for Member to Die of COVID-19 by Race

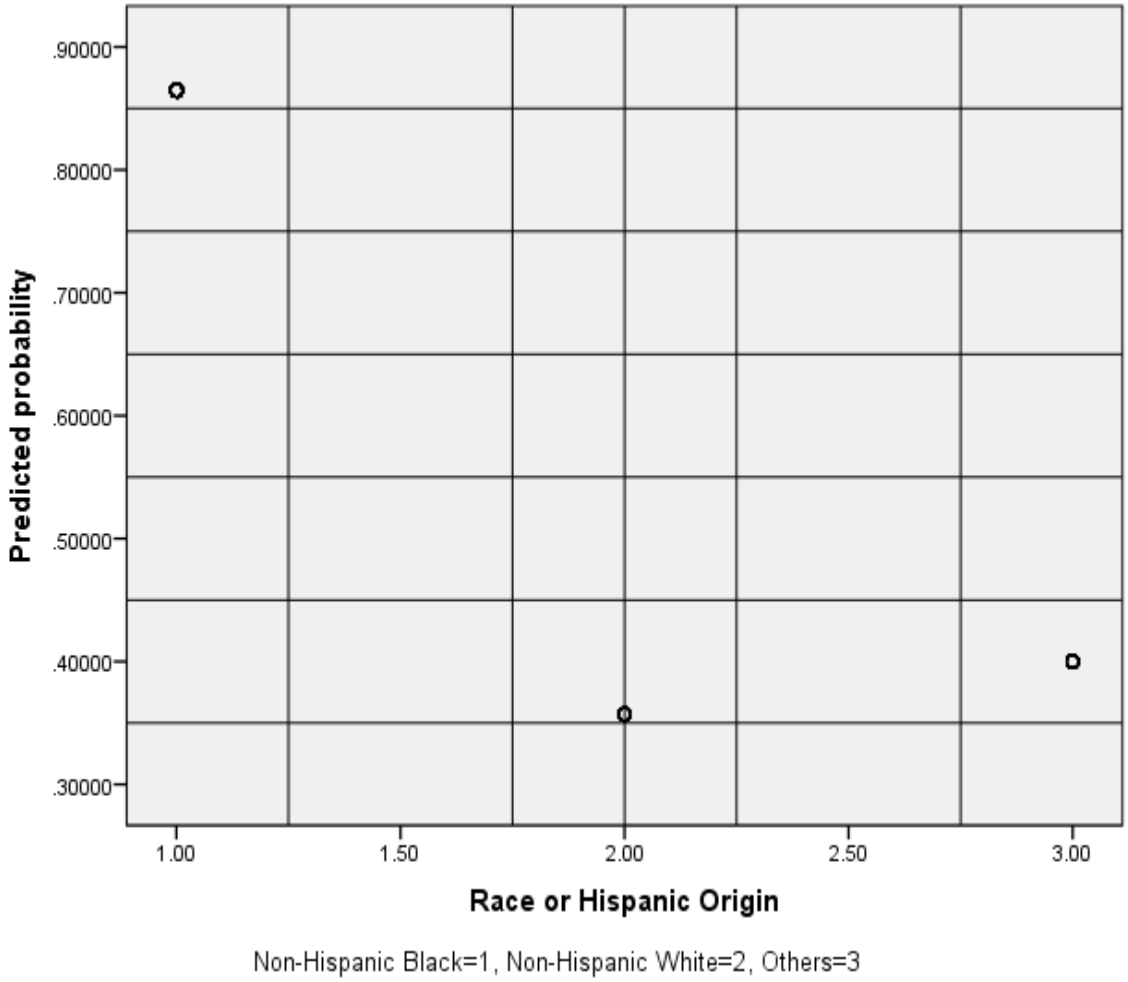
Casewise List						
Cases	Race	Observed	Predicted	Predicted Group	Temporary Variable	
		SCD and COVID-19			Resid	ZResid
1	Non - Hispanic Black	N**	.865	D	-.865	-2.527
2	Non - Hispanic Black	N**	.865	D	-.865	-2.527
3	Non - Hispanic Black	N**	.865	D	-.865	-2.527
4	Non - Hispanic Black	N**	.865	D	-.865	-2.527
5	Non - Hispanic Black	N**	.865	D	-.865	-2.527
6	Non - Hispanic Black	N**	.865	D	-.865	-2.527
7	Non - Hispanic Black	N**	.865	D	-.865	-2.527
8	Non - Hispanic Black	N**	.865	D	-.865	-2.527
9	Non - Hispanic Black	N**	.865	D	-.865	-2.527
10	Non - Hispanic Black	D	.865	D	.135	.396
11	Non - Hispanic Black	D	.865	D	.135	.396
12	Non - Hispanic Black	D	.865	D	.135	.396
13	Non - Hispanic Black	D	.865	D	.135	.396
14	Non - Hispanic Black	D	.865	D	.135	.396
15	Non - Hispanic Black	D	.865	D	.135	.396
16	Non - Hispanic Black	D	.865	D	.135	.396
17	Non - Hispanic Black	D	.865	D	.135	.396
18	Non - Hispanic Black	D	.865	D	.135	.396
19	Non - Hispanic Black	D	.865	D	.135	.396
20	Non - Hispanic Black	D	.865	D	.135	.396
21	Non - Hispanic Black	D	.865	D	.135	.396
22	Non - Hispanic Black	D	.865	D	.135	.396
23	Non - Hispanic Black	D	.865	D	.135	.396
24	Non - Hispanic Black	D	.865	D	.135	.396
25	Non - Hispanic Black	D	.865	D	.135	.396
26	Non - Hispanic Black	D	.865	D	.135	.396
27	Non - Hispanic Black	D	.865	D	.135	.396
28	Non - Hispanic Black	D	.865	D	.135	.396
29	Non - Hispanic Black	D	.865	D	.135	.396
30	Non - Hispanic Black	D	.865	D	.135	.396
31	Non - Hispanic Black	D	.865	D	.135	.396
32	Non - Hispanic Black	D	.865	D	.135	.396
33	Non - Hispanic Black	D	.865	D	.135	.396
34	Non - Hispanic Black	D	.865	D	.135	.396
35	Non - Hispanic Black	D	.865	D	.135	.396
36	Non - Hispanic Black	D	.865	D	.135	.396
37	Non - Hispanic Black	D	.865	D	.135	.396
38	Non - Hispanic Black	D	.865	D	.135	.396
39	Non - Hispanic Black	D	.865	D	.135	.396
40	Non - Hispanic Black	D	.865	D	.135	.396
41	Non - Hispanic Black	D	.865	D	.135	.396

42	Non - Hispanic Black	D	.865	D	.135	.396
43	Non - Hispanic Black	D	.865	D	.135	.396
44	Non - Hispanic Black	D	.865	D	.135	.396
45	Non - Hispanic Black	D	.865	D	.135	.396
46	Non - Hispanic Black	D	.865	D	.135	.396
47	Non - Hispanic Black	D	.865	D	.135	.396
48	Non - Hispanic Black	D	.865	D	.135	.396
49	Non - Hispanic Black	D	.865	D	.135	.396
50	Non - Hispanic Black	D	.865	D	.135	.396
51	Non - Hispanic Black	D	.865	D	.135	.396
52	Non - Hispanic Black	D	.865	D	.135	.396
53	Non - Hispanic Black	D	.865	D	.135	.396
54	Non - Hispanic Black	D	.865	D	.135	.396
55	Non - Hispanic Black	D	.865	D	.135	.396
56	Non - Hispanic Black	D	.865	D	.135	.396
57	Non - Hispanic Black	D	.865	D	.135	.396
58	Non - Hispanic Black	D	.865	D	.135	.396
59	Non - Hispanic Black	D	.865	D	.135	.396
60	Non - Hispanic Black	D	.865	D	.135	.396
61	Non - Hispanic Black	D	.865	D	.135	.396
62	Non - Hispanic Black	D	.865	D	.135	.396
63	Non - Hispanic Black	D	.865	D	.135	.396
64	Non - Hispanic Black	D	.865	D	.135	.396
65	Non - Hispanic Black	N**	.865	D	-.865	-2.527
66	Non - Hispanic Black	D	.865	D	.135	.396
67	Non - Hispanic Black	N**	.865	D	-.865	-2.527
68	Non - Hispanic Black	N**	.865	D	-.865	-2.527
69	Non - Hispanic Black	N**	.865	D	-.865	-2.527
70	Non - Hispanic Black	D	.865	D	.135	.396
71	Non - Hispanic Black	D	.865	D	.135	.396
72	Non - Hispanic Black	D	.865	D	.135	.396
73	Non - Hispanic Black	D	.865	D	.135	.396
74	Non - Hispanic Black	D	.865	D	.135	.396
75	Non - Hispanic Black	D	.865	D	.135	.396
76	Non - Hispanic Black	D	.865	D	.135	.396
77	Non - Hispanic Black	D	.865	D	.135	.396
78	Non - Hispanic Black	D	.865	D	.135	.396
79	Non - Hispanic Black	D	.865	D	.135	.396
80	Non - Hispanic Black	D	.865	D	.135	.396
81	Non - Hispanic Black	D	.865	D	.135	.396
82	Non - Hispanic Black	D	.865	D	.135	.396
83	Non - Hispanic Black	D	.865	D	.135	.396
84	Non - Hispanic Black	D	.865	D	.135	.396
85	Non - Hispanic Black	D	.865	D	.135	.396
86	Non - Hispanic Black	D	.865	D	.135	.396
87	Non - Hispanic Black	D	.865	D	.135	.396
88	Non - Hispanic Black	D	.865	D	.135	.396
89	Non - Hispanic Black	D	.865	D	.135	.396

90	Non - Hispanic Black	D	.865	D	.135	.396
91	Non - Hispanic Black	D	.865	D	.135	.396
92	Non - Hispanic Black	D	.865	D	.135	.396
93	Non - Hispanic Black	D	.865	D	.135	.396
94	Non - Hispanic Black	D	.865	D	.135	.396
95	Non - Hispanic Black	D	.865	D	.135	.396
96	Non - Hispanic Black	D	.865	D	.135	.396
97	Non - Hispanic White	N**	.357	D	-.357	-.745
98	Non - Hispanic White	N**	.357	D	-.357	-.745
99	Non - Hispanic White	D	.357	D	.643	1.342
100	Non - Hispanic White	N**	.357	D	-.357	-.745
101	Non - Hispanic White	N**	.357	D	-.357	-.745
102	Non - Hispanic White	D	.357	D	.643	1.342
103	Non - Hispanic White	N**	.357	D	-.357	-.745
104	Non - Hispanic White	N**	.357	D	-.357	-.745
105	Non - Hispanic White	N**	.357	D	-.357	-.745
106	Non - Hispanic White	N**	.357	D	-.357	-.745
107	Non - Hispanic White	N**	.357	D	-.357	-.745
108	Non - Hispanic White	D	.357	D	.643	1.342
109	Non - Hispanic White	D	.357	D	.643	1.342
110	Non - Hispanic White	D	.357	D	.643	1.342
111	Other	N**	.400	D	-.400	-.816
112	Other	N**	.400	D	-.400	-.816
113	Other	N**	.400	D	-.400	-.816
114	Other	N**	.400	D	-.400	-.816
115	Other	N**	.400	D	-.400	-.816
116	Other	N**	.400	D	-.400	-.816
117	Other	N**	.400	D	-.400	-.816
118	Other	N**	.400	D	-.400	-.816
119	Other	D	.400	D	.600	1.225
120	Other	D	.400	D	.600	1.225
121	Other	D	.400	D	.600	1.225
122	Other	D	.400	D	.600	1.225
123	Other	N**	.400	D	-.400	-.816
124	Other	D	.400	D	.600	1.225
125	Other	D	.400	D	.600	1.225
126	Other	D	.400	D	.600	1.225
127	Other	N**	.400	D	-.400	-.816
128	Other	N**	.400	D	-.400	-.816
129	Other	D	.400	D	.600	1.225
130	Other	D	.400	D	.600	1.225
131	Other	N**	.400	D	-.400	-.816
132	Other	N**	.400	D	-.400	-.816
133	Other	N**	.400	D	-.400	-.816
134	Other	N**	.400	D	-.400	-.816
135	Other	N**	.400	D	-.400	-.816
136	Other	N**	.400	D	-.400	-.816
137	Other	N**	.400	D	-.400	-.816

138	Other	D	.400	D	.600	1.225
139	Other	D	.400	D	.600	1.225
140	Other	D	.400	D	.600	1.225
a. S = Selected, U = Unselected cases, and ** = Misclassified cases.						

Note. Predicted probability is of membership for died of COVID-19; the cut value is .01; symbols: N - Not died of COVID-19, D - Died of COVID-19; each symbol represents 10 cases



Age and COVID-19 Mortality

Block 1: Method = Forward Stepwise (Wald)

Case Processing Summary

Unweighted Cases[a]		N	Percent
Selected Cases	Included in Analysis	140	100.0
	Missing Cases	0	.0
	Total	140	100.0
Unselected Cases		0	.0
Total		140	100.0

Note. If weight is in effect, see classification table for the total number of cases.

Dependent Variable Encoding

Original Value	Internal Value
Not died of COVID-19	0
Died of COVID-19	1

Categorical Variables Codings

		Frequency	Parameter coding (1)	(2)	(3)
Age group	0-19	21	1.000	.000	.000
	20-39	38	.000	1.000	.000
	40-59	43	.000	.000	1.000
	60+	38	.000	.000	.000

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	53.525	3	.000
	Block	53.525	3	.000
	Model	53.525	3	.000

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	117.659[a]	.300	.429

Note. Estimation terminated at iteration number 1 because maximum iterations has been reached. Final solution cannot be found.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	.000	2	1.000

Contingency Table for Hosmer and Lemeshow Test

		SCD and COVID-19 = Not died of COVID-19		SCD and COVID-19 = Died of COVID-19		
		Observed	Expected	Observed	Expected	Total
Step 1	1	20	20.000	1	1.000	21
	2	9	9.000	29	29.000	38
	3	6	6.000	37	37.000	43
	4	5	5.000	33	33.000	38

Classification Table[a]

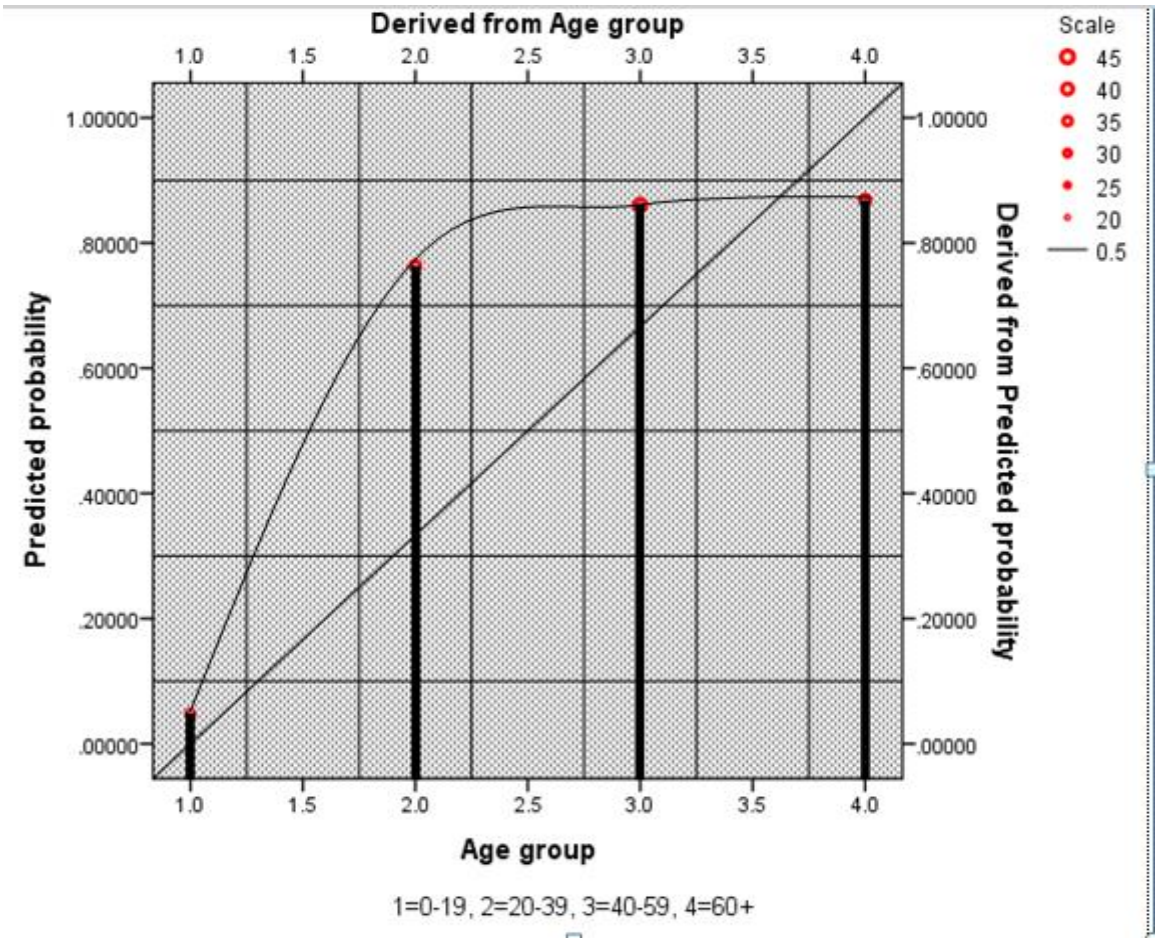
			Predicted		
			SCD and COVID-19		
	Observed		Not died of COVID-19	Died of COVID-19	Percentage Correct
Step 1	SCD and COVID-19	Not died of COVID-19	0	40	.0
		Died of COVID-19	0	100	100.0
	Overall Percentage				71.4

Note. The cut value is .001

Variables in the Equation

								95% C.I.for EXP(B)	
		B	S.E.	Wald	df	Sig.	Exp(B)	Lower	Upper
Step 1[a]	Age			22.600	3	.000			
	Age(1)	2.862	.729	15.425	1	.000	17.499	4.195	73.002
	Age(2)	1.820	.532	11.704	1	.001	6.174	2.176	17.517
	Age(3)	1.245	.499	6.222	1	.013	3.474	1.306	9.243
	Constant	.540	.231	5.450	1	.020	1.715		

Note. Variable(s) entered on step 1: Age.


Derived from Age group
Scale
45
40
35
30
25
20
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
1.00000
.80000
.60000
.40000
.20000
.00000
Predicted probability
Derived from Predicted probability
Age group
1=0-19, 2=20-39, 3=40-59, 4=60+

```
             Step number: 1

             Observed Groups and Predicted Probabilities

     160 +                                                                                                    +
         I                                                                                                    I
         I                                                                                                    I
F        I                                                                                                    I
R    120 +                                                                                                    +
E        I                                                                                                    I
Q        I                                                                                                    I
U        I                                                                                                    I
E     80 +                                                                                      D             +
N        I                                                                                      D             I
C        I                                                                                      D             I
Y        I                                                                                      D             I
      40 +                                                                            D         D             +
         I                                                                            D         D             I
         I    N                                                                       D         D             I
         I    N                                                                       N         N             I
Predicted ---------+---------+---------+---------+---------+---------+---------+---------+---------+----------
  Prob:   0       .1        .2        .3        .4        .5        .6        .7        .8        .9         1
  Group:  DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

          Predicted Probability is of Membership for Died of COVID-19
          The Cut Value is .00
          Symbols: N - Not died of COVID-19
                   D - Died of COVID-19
          Each Symbol Represents 10 Cases.
```

Predicted Probability for Member to Die of COVID-19 by Age

Case	Age group	Observed: SCD and COVID-19	Predicted	Predicted Group	Temporary Variable: Resid	Temporary Variable: ZResid
1	0-19	N**	.048	D	-.048	-.224
2	0-19	N**	.048	D	-.048	-.224
3	0-19	N**	.048	D	-.048	-.224
4	0-19	N**	.048	D	-.048	-.224
5	0-19	N**	.048	D	-.048	-.224
6	0-19	N**	.048	D	-.048	-.224
7	0-19	D	.048	D	.952	4.472
8	0-19	N**	.048	D	-.048	-.224
9	0-19	N**	.048	D	-.048	-.224
10	0-19	N**	.048	D	-.048	-.224
11	0-19	N**	.048	D	-.048	-.224
12	0-19	N**	.048	D	-.048	-.224
13	0-19	N**	.048	D	-.048	-.224
14	0-19	N**	.048	D	-.048	-.224
15	0-19	N**	.048	D	-.048	-.224
16	0-19	N**	.048	D	-.048	-.224
17	0-19	N**	.048	D	-.048	-.224
18	0-19	N**	.048	D	-.048	-.224
19	0-19	N**	.048	D	-.048	-.224
20	0-19	N**	.048	D	-.048	-.224
21	0-19	N**	.048	D	-.048	-.224
22	20-39	N**	.763	D	-.763	-1.795
23	20-39	D	.763	D	.237	.557
24	20-39	D	.763	D	.237	.557
25	20-39	D	.763	D	.237	.557
26	20-39	D	.763	D	.237	.557
27	20-39	D	.763	D	.237	.557
28	20-39	N**	.763	D	-.763	-1.795
29	20-39	N**	.763	D	-.763	-1.795
30	20-39	N**	.763	D	-.763	-1.795
31	20-39	N**	.763	D	-.763	-1.795
32	20-39	D	.763	D	.237	.557
33	20-39	D	.763	D	.237	.557
34	20-39	D	.763	D	.237	.557
35	20-39	D	.763	D	.237	.557
36	20-39	D	.763	D	.237	.557
37	20-39	D	.763	D	.237	.557
38	20-39	D	.763	D	.237	.557
39	20-39	D	.763	D	.237	.557
40	20-39	D	.763	D	.237	.557
41	20-39	D	.763	D	.237	.557
42	20-39	D	.763	D	.237	.557
43	20-39	D	.763	D	.237	.557
44	20-39	D	.763	D	.237	.557
45	20-39	D	.763	D	.237	.557
46	20-39	D	.763	D	.237	.557
47	20-39	D	.763	D	.237	.557
48	20-39	D	.763	D	.237	.557
49	20-39	N**	.763	D	-.763	-1.795

50	20-39	N**	.763	D	-.763	-1.795
51	20-39	D	.763	D	.237	.557
52	20-39	D	.763	D	.237	.557
53	20-39	D	.763	D	.237	.557
54	20-39	D	.763	D	.237	.557
55	20-39	N**	.763	D	-.763	-1.795
56	20-39	D	.763	D	.237	.557
57	20-39	D	.763	D	.237	.557
58	20-39	D	.763	D	.237	.557
59	20-39	N**	.763	D	-.763	-1.795
60	40-59	D	.860	D	.140	.403
61	40-59	D	.860	D	.140	.403
62	40-59	D	.860	D	.140	.403
63	40-59	D	.860	D	.140	.403
64	40-59	D	.860	D	.140	.403
65	40-59	D	.860	D	.140	.403
66	40-59	D	.860	D	.140	.403
67	40-59	D	.860	D	.140	.403
68	40-59	D	.860	D	.140	.403
69	40-59	D	.860	D	.140	.403
70	40-59	D	.860	D	.140	.403
71	40-59	D	.860	D	.140	.403
72	40-59	D	.860	D	.140	.403
73	40-59	D	.860	D	.140	.403
74	40-59	D	.860	D	.140	.403
75	40-59	D	.860	D	.140	.403
76	40-59	D	.860	D	.140	.403
77	40-59	D	.860	D	.140	.403
78	40-59	D	.860	D	.140	.403
79	40-59	D	.860	D	.140	.403
80	40-59	D	.860	D	.140	.403
81	40-59	D	.860	D	.140	.403
82	40-59	D	.860	D	.140	.403
83	40-59	D	.860	D	.140	.403
84	40-59	D	.860	D	.140	.403
85	40-59	D	.860	D	.140	.403
86	40-59	D	.860	D	.140	.403
87	40-59	D	.860	D	.140	.403
88	40-59	D	.860	D	.140	.403
89	40-59	D	.860	D	.140	.403
90	40-59	D	.860	D	.140	.403
91	40-59	D	.860	D	.140	.403
92	40-59	D	.860	D	.140	.403
93	40-59	D	.860	D	.140	.403
94	40-59	N**	.860	D	-.860	-2.483
95	40-59	N**	.860	D	-.860	-2.483
96	40-59	D	.860	D	.140	.403
97	40-59	N**	.860	D	-.860	-2.483
98	40-59	D	.860	D	.140	.403
99	40-59	D	.860	D	.140	.403
100	40-59	N**	.860	D	-.860	-2.483
101	40-59	N**	.860	D	-.860	-2.483
102	40-59	N**	.860	D	-.860	-2.483
103	60+	D	.868	D	.132	.389
104	60+	D	.868	D	.132	.389

105	60+	D	.868	D	.132	.389
106	60+	D	.868	D	.132	.389
107	60+	D	.868	D	.132	.389
108	60+	D	.868	D	.132	.389
109	60+	D	.868	D	.132	.389
110	60+	D	.868	D	.132	.389
111	60+	D	.868	D	.132	.389
112	60+	D	.868	D	.132	.389
113	60+	D	.868	D	.132	.389
114	60+	D	.868	D	.132	.389
115	60+	D	.868	D	.132	.389
116	60+	D	.868	D	.132	.389
117	60+	D	.868	D	.132	.389
118	60+	D	.868	D	.132	.389
119	60+	D	.868	D	.132	.389
120	60+	D	.868	D	.132	.389
121	60+	D	.868	D	.132	.389
122	60+	D	.868	D	.132	.389
123	60+	D	.868	D	.132	.389
124	60+	D	.868	D	.132	.389
125	60+	D	.868	D	.132	.389
126	60+	D	.868	D	.132	.389
127	60+	D	.868	D	.132	.389
128	60+	D	.868	D	.132	.389
129	60+	D	.868	D	.132	.389
130	60+	N**	.868	D	-.868	-2.569
131	60+	N**	.868	D	-.868	-2.569
132	60+	N**	.868	D	-.868	-2.569
133	60+	D	.868	D	.132	.389
134	60+	D	.868	D	.132	.389
135	60+	D	.868	D	.132	.389
136	60+	N**	.868	D	-.868	-2.569
137	60+	N**	.868	D	-.868	-2.569
138	60+	D	.868	D	.132	.389
139	60+	D	.868	D	.132	.389
140	60+	D	.868	D	.132	.389

Note. S = Selected, U = Unselected cases, and ** = Misclassified cases; predicted probability is of membership for died of COVID-19; the cut value is .01; symbols: N – Not died of COVID-10, D – Died of COVID-19; each symbol represents 10 cases

Age, Race, and COVID-19 Mortality

Case Processing Summary

Unweighted Cases[a]		N	Percent
Selected Cases	Included in Analysis	140	100.0
	Missing Cases	0	.0
	Total	140	100.0
Unselected Cases		0	.0
Total		140	100.0

Note. If weight is in effect, see classification table for the total number of cases.

Dependent Variable Encoding

Original Value	Internal Value
Not died of COVID-19	0
Died of COVID-19	1

Categorical Variables Codings

			Parameter coding		
		Frequency	(1)	(2)	(3)
Age group	0-19	21	1.000	.000	.000
	20-39	38	.000	1.000	.000
	40-59	43	.000	.000	1.000
	60+	38	.000	.000	.000
Race or Hispanic Origin	Others	96	1.000	.000	
	non-Hispanic White	14	.000	1.000	
	non-Hispanic Black	30	.000	.000	

Classification Table[a,b]

			Predicted		
			SCD and COVID-19		
	Observed		Not died of COVID-19	Died of COVID-19	Percentage Correct
Step 0	SCD and COVID-19	Not died of COVID-19	0	40	.0
		Died of COVID-19	0	100	100.0
	Overall Percentage				71.4

Note. Constant is included in the model; the cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 0	Constant	.857	.185	21.515	1	.000	2.356

Variables not in the Equation

			Score	df	Sig.
Step 0	Variables	Age	55.070	3	.000
		Age(1)	21.671	1	.000
		Age(2)	13.280	1	.000
		Age(3)	5.998	1	.014
		Race	35.993	2	.000
		Race(1)	2.031	1	.154
		Race(2)	35.802	1	.000
	Overall Statistics		85.505	5	.000

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	80.128	5	.000
	Block	80.027	5	.000
	Model	80.027	5	.000

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	87.488[a]	.435	.624

Note. Estimation terminated at iteration number 1 because maximum iterations has been reached. Final solution cannot be found.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	3.967	6	.091

Contingency Table for Hosmer and Lemeshow Test

		SCD and COVID-19 = Not died of COVID-19		SCD and COVID-19 = Died of COVID-19		
		Observed	Expected	Observed	Expected	Total
Step 1	1	8	7.572	0	.428	8
	2	12	9.869	1	3.131	13
	3	7	6.405	5	5.595	12
	4	6	6.056	7	6.944	13
	5	6	4.774	5	6.226	11
	6	1	3.193	21	18.807	22
	7	0	4.772	34	29.228	34
	8	0	3.188	27	23.812	27

Classification Table[a]

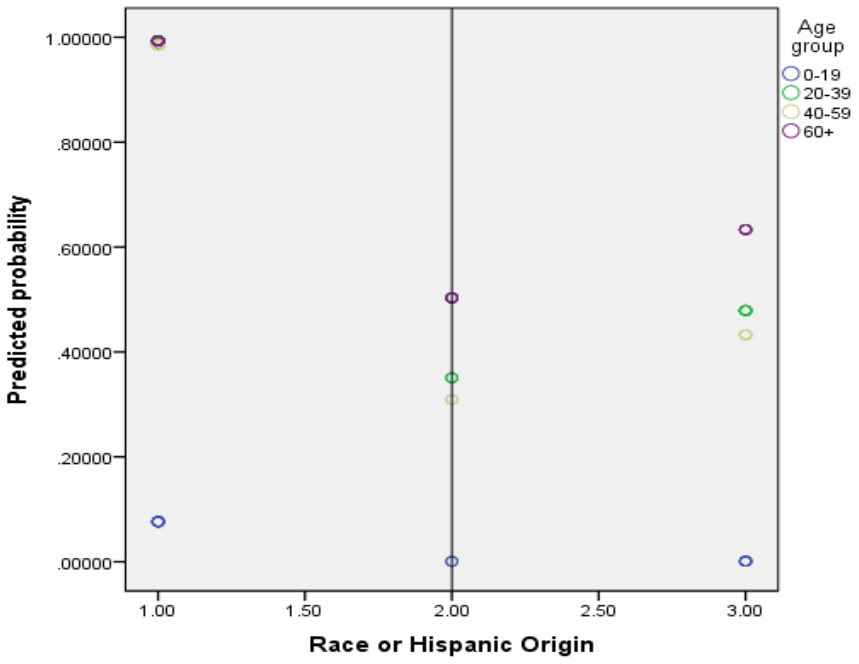
			Predicted		
			SCD and COVID-19		
	Observed		Not died of COVID-19	Died of COVID-19	Percentage Correct
Step 1	SCD and COVID-19	Not died of COVID-19	27	13	67.5
		Died of COVID-19	6	94	94.0
	Overall Percentage				86.4

Note. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I.for EXP(B)	
								Lower	Upper
Step 1[a]	Age			20.881	3	.000			
	Age(1)	2.921	.744	15.437	1	.000	18.564	4.323	79.717
	Age(2)	1.500	.535	7.845	1	.005	4.480	1.569	12.795
	Age(3)	1.198	.519	5.329	1	.021	3.314	1.198	9.165
	Race			15.331	2	.000			
	Race(2)	-.401	.719	.311	1	.577	.670	.164	2.740
	Race(1)	1.837	.472	15.149	1	.000	6.278	2.489	15.832
	Constant	-.113	.273	.170	1	.681	.894		

Note. Variable(s) entered on step 1: Age, Race.



1= Non-Hispanic Black, 2= Non-Hispanic White, 3=Others

Case Processing Summary

Race or Hispanic Origin		Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Others	Age group * SCD and COVID-19	30	100.0%	0	0.0%	30	100.0%
non-Hispanic White	Age group * SCD and COVID-19	14	100.0%	0	0.0%	14	100.0%
non-Hispanic Black	Age group * SCD and COVID-19	96	100.0%	0	0.0%	96	100.0%

Age group * SCD and COVID-19 Crosstabulation

Race or Hispanic Origin				SCD and COVID-19		Total
				Not died of COVID-19	Died of COVID-19	
Others	Age group	0-19	Count	6	0	6
			% within Age group	100.0%	0.0%	100.0%
		20-39	Count	6	7	13
			% within Age group	46.2%	53.8%	100.0%
		40-59	Count	4	2	6
			% within Age group	66.7%	33.3%	100.0%
		60+	Count	2	3	5
			% within Age group	40.0%	60.0%	100.0%
	Total		Count	18	12	30
			% within Age group	60.0%	40.0%	100.0%
non-Hispanic White	Age group	0-19	Count	2	0	2
			% within Age group	100.0%	0.0%	100.0%
		20-39	Count	2	1	3
			% within Age group	66.7%	33.3%	100.0%
		40-59	Count	2	1	3
			% within Age group	66.7%	33.3%	100.0%
		60+	Count	3	3	6
			% within Age group	50.0%	50.0%	100.0%
	Total		Count	9	5	14
			% within Age group	64.3%	35.7%	100.0%
non-Hispanic Black	Age group	0-19	Count	12	1	13
			% within Age group	92.3%	7.7%	100.0%
		20-39	Count	1	21	22
			% within Age group	4.5%	95.5%	100.0%
		40-59	Count	0	34	34
			% within Age group	0.0%	100.0%	100.0%
		60+	Count	0	27	27
			% within Age group	0.0%	100.0%	100.0%
	Total		Count	13	83	96
			% within Age group	13.5%	86.5%	100.0%

Chi-Square Tests

Race or Hispanic Origin		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)
Others	Pearson Chi-Square	5.983[a]	3	.112	.131
	Likelihood Ratio	8.068	3	.045	.086
	Fisher's Exact Test	6.045			.117
	Linear-by-Linear Association	2.248[b]	1	.134	.191
	N of Valid Cases	30			
non-Hispanic White	Pearson Chi-Square	1.659[c]	3	.646	.865
	Likelihood Ratio	2.293	3	.514	.865
	Fisher's Exact Test	1.676			.865
	Linear-by-Linear Association	1.327[d]	1	.249	.344
	N of Valid Cases	14			
non-Hispanic Black	Pearson Chi-Square	79.963[e]	3	.000	.000
	Likelihood Ratio	60.952	3	.000	.000
	Fisher's Exact Test	53.563			.000
	Linear-by-Linear Association	43.039[f]	1	.000	.000
	N of Valid Cases	96			

Note. 6 cells (75.0%) have expected count less than 5. The minimum expected count is 2.00; the standardized statistic is 1.499; 8 cells (100.0%) have expected count less than 5. The minimum expected count is .71; the standardized statistic is 1.152; 4 cells (50.0%) have expected count less than 5. The minimum expected count is 1.76; the standardized statistic is 6.560

```
              Step number: 1

              Observed Groups and Predicted Probabilities

      80 +                                                                                                    +
         I                                                                                                    I
         I                                                                                                    I
F        I                                                                                                    I
R     60 +                                                                                                    +
E        I                                                                                                    I
Q        I                                                                                                    I
U        I                                                                                                   DI
E     40 +                                                                                                   D+
N        I                                                                                                  DDI
C        I                                                                                                  DDI
Y        I                                                                                                  DDI
      20 +                                                                                                  DD+
         IN                                                                                                 DDI
         IN                                                                    D                            DDI
         IN        N         N    D                  N  N   D               D  D                      D     DDI
Predicted ---------+---------+---------+---------+---------+---------+---------+---------+---------+----------
  Prob:   0       .1        .2        .3                  .5        .6        .7        .8        .9         1
  Group:  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN           NNNNNDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

          Predicted Probability is of Membership for Died of COVID-19
          The Cut Value is .50
          Symbols: N - Not died of COVID-19
                   D - Died of COVID-19
          Each Symbol Represents 5 Cases.
```