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Association Between Diabetes Mellitus, Hypertension, Obesity, and Diagnosis of COVID-19 in Puerto Rico

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This is to certify that the doctoral study by

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has been found to be complete and satisfactory in all respects,
and that any and all revisions required by
the review committee have been made.

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Walden University
2025

Abstract

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MPH, Walden University, 2019

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Doctoral Study Submitted in Partial Fulfillment

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Abstract

The population of Puerto Rico has been heavily affected by chronic diseases; however, data remains limited on the influence of diabetes mellitus (DM), hypertension, and obesity on the probability of COVID-19 diagnosis. The purpose of this quantitative study was to evaluate the association between non-communicable diseases that included DM, obesity, hypertension, and COVID-19 diagnosis, controlling for age and sex and person exposure in Puerto Rico. The sample consisted of 1,463 participants who underwent a polymerase chain reaction (PCR) test for COVID-19 from April 1, 2020, to March 31, 2021. Results from adjusted multivariable logistic regression analyses established that obesity $OR = 1.64$, 95% CI [1.23, 2.20], $p < .001$, and hypertension $OR = 1.60$, 95% CI [1.14, 2.26], $p = .007$ were significantly associated with higher odds of COVID-19 diagnosis, whereas DM was not, $OR = 1.08$, 95% CI [0.71, 1.63], $p = .730$. Overall, obesity and hypertension were identified as independent predictors of COVID-19 Diagnosis, while DM showed no significant association. The positive social change impact of these findings could lead to better understanding of how existing chronic diseases in Puerto Rico may influence predisposition to COVID-19, assisting to effective disease prevention and treatment efforts on the island.

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Dedication

To my beloved spouse and dear family members, your unwavering love, patience, and encouragement have been the foundation of my strength. Thank you for believing in me, even during the most challenging moments. This accomplishment belongs to all of us, as much as it belongs to me.

Acknowledgments

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Section 1: Foundation of the Study and Literature Review

The focus of this study was to evaluate the association between chronic diseases and risk factors that included diabetes mellitus, hypertension, and obesity with COVID-19 diagnosed patients in Puerto Rico. The study's main goal was to obtain a better understanding of whether such predictors could affect the probability of the population being diagnosed with COVID-19 infection. Considering that the targeted population is heavily affected by chronic diseases, and their risk factors, it was crucial to evaluate how they behaved and affected the population when impacted by major public health crises and novel infectious diseases like COVID-19. Such understanding would help create more targeted interventions focusing on risk groups suffering from diabetes, hypertension, and obesity. As a result, when the population is exposed to similar scenarios or public health emergencies, it could help guide more efficient and timely public health intervention. Helping protect the population at greater risk of infection may reduce the burden and adverse health effects such groups could experience.

Background

On December 31, 2019, a cluster of atypical interstitial pneumonia cases of unknown origin was discovered in Wuhan, Hubei province, China. An alert was issued by the Wuhan Municipal Health Commission, which led to the deployment of a rapid response team by the Chinese Center for Disease Control and Prevention (China CDC), which notified the World Health Organization (CDC, 2020b; WHO, n.d). The cluster of cases was epidemiologically linked to the Huana Seafood Wholesale Market (Ciottia et al., 2020). On January 7, 2020, the causative agent or pathogen was identified as a novel coronavirus, named 2019-nCoV, which was different from both SARS-CoV and MERS-CoV (CDC, 2020b). At the time of this study, a total of 103,801,821 cases, 1,121,512 deaths, and 6,049,231 total admissions had been reported (CDC, 2023b). The territory of Puerto Rico had reported 1,104,605 cases of COVID-19, with an average of 286 cases reported daily. Not only did COVID-19 significantly impact health and mortality worldwide, but it also placed a lot of stress on the health care system and the economy. Regarding populations or groups at risk, in Puerto Rico, COVID-19 for 2020 was considered the fourth leading cause of death, with a reported mortality rate of 27.3 individuals for every 100,000 people. For 2019, Puerto Rico's hypertension rate had been reported as the highest prevalence of all chronic diseases on the island, at 36.1%. In a similar way, for 2020, diabetes mellitus was reported the third highest prevalence among chronic diseases, with 13.3% among the population. However, risk factors that could contribute to both chronic disease and worse health outcomes indicated that obesity was the leading modifiable risk factor, with 66.9% of the population suffering from it (Cabrera, Felici, Diaz, & Martinez, 2023).

For the year 2020 in Puerto Rico, five of the leading causes of death on the island were related to chronic diseases, which represented 59.1% of all deaths. In the United States, 6 of every 10 individuals lived with at least one chronic disease, compared to Puerto Rico where the prevalence of a person having at least one chronic disease was 47% for 2020. Considering the burden that chronic diseases like hypertension, diabetes, obesity, and COVID-19 had on the population in Puerto Rico, obtaining a better understanding of how chronic disease could affect the population prevalence of COVID-

19 was seen as a great opportunity to target and identify groups that could be considered at greater risk when the next public health emergency came.

Problem Statement

The situation that prompted to search the literature was that chronic disease continued to be one of the leading causes of death in Puerto Rico. Around 58% of the island's population suffered from at least one chronic disease. Not only did the population suffer from chronic disease, but many were overweight and obese, putting them at increased risk of worse health outcomes. Based on data provided by the Behavioral Risk Factor Surveillance System (BRFSS), in Puerto Rico in 2019, hypertension was reported to have the highest prevalence at 36.1%, and for 2020, diabetes mellitus (DM) reported the third highest prevalence at 13.3% among the population (Cabrera, Felici, Diaz, & Martinez, 2023). Risk factors such as obesity, which contributed to worsening prognosis and health issues, reported a prevalence of 66.9% among the population. Five of the six leading causes of death on the island were related to chronic diseases, contributing to 59.1% of the deaths reported that year. COVID-19 was a significant public health emergency that significantly impacted the economy, the healthcare system, and the entire population's health worldwide. COVID-19 presented many challenges to the general population. However, groups suffering from chronic diseases were at greater risk of developing health complications and worsening prognosis when infected with COVID-19. For example, in 2020, in Puerto Rico, COVID-19 was the fourth leading cause of death, with 42.8 deaths for every 100,000 inhabitants on the island. For this reason, it was of great importance to obtain a better understanding of the impact of risk factors and non-communicable diseases that affected mortality rates on the population's prevalence of being diagnosed with COVID-19.

Hispanics were the third group with the highest rates of obesity and Puerto Rico was the second-largest Hispanic subgroup in the United States and the most affected by diabetes mellitus (Johnson et al., 2017). There was limited data on how risk factors and non-communicable diseases that contributed to mortality rates on the island could affect the probability of being diagnosed with COVID-19. Some of the risk factors and chronic non-communicable diseases included obesity, diabetes, and hypertension.

Purpose of the Study

The purpose of this quantitative study was to evaluate the association between risk factors and non-communicable diseases that included DM, obesity, hypertension, and COVID-19 diagnosis, controlling for age and sex and person exposure in Puerto Rico.

Research Questions and Hypothesis

RQ1: What is the association between diabetes mellitus (DM) and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

H_o1: There is no significant association between DM and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure.

H_a1: There is a significant association between DM and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure.

RQ2: What is the association between obesity and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

H_o2: There is no significant association between obesity and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure

H_a2: There is a significant association between obesity and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure.

RQ3: What is the association between hypertension and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

H_o3: There is no significant association between hypertension and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure

H_a3: There is a significant association between hypertension and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure

RQ4: What is the association of (DM, obesity and hypertension) and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

H_o4: There is a negative predictive value of (DM, obesity and hypertension) in patients with COVID-19 diagnosis while controlling for age, sex, and person exposure

H_a4: There is a positive predictive value of DM, obesity and hypertension) in patients with COVID-19 diagnosis while controlling for age, sex, and person exposure

Theoretical Framework

The epidemiological triangle model was used to evaluate the interaction between the external agent being COVID-19 and the host being the population in Puerto Rico and the environment that might be having an impact, which for this study was how risk factors that include DM, obesity, and hypertension are affecting the predisposition for patients to be diagnosed with COVID-19. In this model, diseases are a result of the interaction between the agent and the susceptibility of the host in an environment that supports transmission of the agent.

For the selected theory/model, patients with DM are considered more susceptible to infections, which can include respiratory tract infections. For example, patients with diabetes mellitus usually present with higher amounts of adipose tissue, which can increase chronic inflammation and oxidative stress in the body, negatively impacting the patient's glycemic profile (Stoian et al.,2020). That said the model allowed me to evaluate how risk factors (obesity, hypertension and DM) that impact mortality rates in Puerto Rico, could be affecting their predisposition for being diagnosed with COVID-19. As a result, the model allowed to evaluate the interaction between environment (risk factors) could be affecting the probability of the host for being diagnosed with the agent (COVID-19).

Nature of the Study

To address the research questions in this quantitative study, the specific research design included a secondary analysis from the epidemiologic and clinical features of COVID-19 of the Puerto Rico Community Engagement Alliance (PR-CEAL) database.

The design of the study was a secondary data analysis from data collected based on a cross-sectional design to explore the association between risk factors (obesity, DM, hypertension) and a diagnosis of COVID-19, while controlling for age, sex, and person exposure in the Puerto Rican population.

Literature Review Related to Key Variables and/or Concepts

The keywords and databases searched included COVID-19, Puerto Rico, Diabetes Mellitus and COVID-19, Hispanic, Comorbidities, Risk factors, Hypertension, and Obesity. Most of the searches were performed using Google Scholar. In addition to Google Scholar, a second search engine, the Walden Library, was used. Databases from which papers were extracted included Science Direct, British Medical Journal (BMJ), Lancet, Wiley, and Sage. For supportive references, some government agencies like the Centers for Disease Control and Prevention (CDC), National Institutes of Health (NIH), and Department of Health and Human Services (HHS) were utilized. Most of the references and sources used were from 2019 to 2023. However, given that there was limited data for the key variables used in the Puerto Rican population, there were also sources from 2010 to 2018.

On December 31, 2019, a cluster of atypical interstitial pneumonia cases of unknown origin was discovered in Wuhan, Hubei province, China. An alert was issued by the Wuhan Municipal Health Commission, which led to the deployment of a rapid response team by the Chinese Center for Disease Control and Prevention (China CDC). This team notified the World Health Organization (CDC, 2020b; WHO). The cluster of cases was epidemiologically linked to the Huanan Seafood Wholesale Market (Ciottia et al., 2020). On January 7, 2020, the causative agent or pathogen was identified as a novel coronavirus, named 2019-nCoV, which was different from both SARS-CoV and MERS-CoV (CDC, 2020b). As a result, social containment measures, including mask mandates, isolation, quarantine, and travel restrictions, were adopted worldwide. Such measures forced healthcare systems and providers to reorganize their strategies and interventions to cope with and tackle the growing public health emergency. At the time of this report, there were more than 676 million cases of COVID-19 diagnosed worldwide and more than 6 million deaths globally (JHUM, 2023). Genome analysis of COVID-19 exposed its differences from previous coronaviruses: COVID-19 presented an optimal affinity for angiotensin-converting enzyme 2 (ACE2) receptors and a polybasic cleavage site at the S1/S2 spike junction that determined infectivity and host range (Andersen, et al., 2020;JHUM, 2023).

SARS-COV2

Epidemiology of COVID-19 in the United States and in Puerto Rico

Understanding the epidemiological aspects of COVID-19 that determined its transmission dynamics and symptomatology was crucial for public health intervention. The clinical presentation of COVID-19 diagnosed patients included symptoms like fever, cough, shortness of breath, fatigue, myalgia, headache, loss of taste and smell, sore throat, congestion, and gastrointestinal symptoms such as vomiting, diarrhea, and abdominal pain (CDC, 2022g; Ciottia, et al., 2020). A systematic review and meta-analysis demonstrated a pooled mean incubation period of 6.5 days from exposure to the onset of symptoms (Alene, et al., 2021). The COVID-19 mode of transmission was through exposure to respiratory fluids. Such exposure occurred in three principal ways: 1) inhalation of droplets and aerosol, 2) deposition of respiratory droplets on mucous membranes, and 3) touching mucous membranes after being in contact with surfaces contaminated with viral particles (CDC, 2021a).

Comparing COVID-19 to other viruses like Influenza (flu), it can be said that both are contagious respiratory illnesses. However, COVID-19 can spread more easily and can cause more severe illness in some people while also being able to present symptoms and be contagious for longer periods (CDC, 2022i). In terms of complication, Influenza secondary bacterial infections are more common when compared to COVID-19; however, COVID-19 has additional complications that include blood clots in the veins and arteries of the lungs, heart, leg, brain and multisystem inflammatory syndrome (MIS-C) in children. Overall, it is difficult to differentiate COVID-19 from flu based on symptomatology alone, since they both have similar symptoms. To achieve so, a laboratory diagnostic test is needed for early detection and to reduce the risk of health complications from hospitalizations and possible co-infections from both diseases.

At the time of this study in the United States, there had been a total of 103,801,821 cases reported, 1,121,512 deaths and 6,049,231 total admissions. The territory of Puerto Rico has reported a total of 1,104,605 cases of COVID-19, with an average case reported daily of 286. Age remains the strongest risk factor for severe COVID-19. Data suggest that compared with age group of 18-29, the risk of death is 25 times higher 50-64 years, 60 times higher in groups 65-74 years, 140 times higher in groups aged 75-84 and 340 times higher in those that are 85 years and older

(CDC,2023a). In the younger population, studies have shown that children tend to have similar or higher rates of infection; however, they experience increased rates of asymptomatic patients or reduced severity of symptoms (CDC, 2023c;Dawood, et al., 2021; Laws, et al., 2021). In addition to age, immunocompromised or weakened immune systems are also more likely to become infected with COVID-19 and express symptoms for more extended periods (CDC, 2023d). Factors such as older age and cardiovascular can increase the risk of infection in the general population. However, immunocompromised patients can have an increased risk for traditional risk factors, thus having higher hospitalization rates, complications and death (NIH, 2023b).

Current Diagnostic Protocol for COVID-19

Current COVID-19 diagnostic protocol includes tests looking for current viral infection with SARS-CoV-2 by sampling specimens from a patient's nose or mouth. Two main types of viral testing for COVID-19 diagnosis include nucleic acid amplification tests (NAATs), a type of Reverse transcriptase polymerase chain reaction (RT-PCR) and antigen. The RT-PCR test collects fluid samples by inserting a long nasopharyngeal swap into the nostril and collecting fluid from the back of the nose (Mayo Clinic, 2022). RT-PCR tests are the most reliable for asymptomatic patients since they can detect viral DNA particles up to 90 days after infection (CDC, 2022f). Antigen testing has the capacity to detect specific proteins of the viral capsid and sample is obtained using a long nasal swap (Mayo Clinic, 2022). Antigen tests are less reliable than RT-PCR, especially in asymptomatic patients. Although the antigen test is used for diagnosis, a negative test result does not rule out infection, for such reason it is recommended to use RT-PCR to confirm the antigen test result (CDC, 2022f). Comparing the time needed to obtain a diagnosis for each test. RT-PCR diagnostic test can provide results from 1 to 3 days or longer, depending if the sample is sent outside the lab on which the sample was taken. The antigen diagnostic test can provide results within 15 to 30 minutes after sample collection.

COVID-19 Prevention Measures

The primary mode of transmission for COVID-19, which is through exposure to respiratory fluids carrying viral particles and that during the early stages of the pandemic, there were no treatment or vaccine available for control measures. Most of the prevention strategies consisted of using masks consistently in order to reduce the risk of inhaling viral particles and reduce of infecting others (Christie, et al., 2021). Additional measures included physical distancing, isolation of diagnosed patients, quarantine for contacts, proper handwashing techniques and regular cleaning/disinfection of contaminated surfaces to avoid infection through contaminated fomites. Although there are different strategies for COVID-19 prevention, no single strategy alone could be used effectively. Studies have shown that the effectiveness of quarantine is very high for people who were exposed to COVID-19; however, such strategy effectiveness increases when implemented with additional prevention strategies that include isolation, contact tracing and travel restrictions (Girum et al., 2020). Screening and contact tracing are considered powerful tools for COVID-19 prevention. However, unless the level of coverage for both measures is high, prevention through isolation of COVID-19 alone is limited (Girum et al., 2020). Different strategies must be implemented to obtain the benefits and reduce the weaknesses that each can present individually.

During June and July of 2021, COVID-19 diagnosis surged approximately 300% nationwide, followed by increased hospitalization rates and deaths because of the rapid spreading of a highly transmissible variant B.1.617.2 (Delta) (Christie, et al., 2021). In response, the prevention strategy focused on vaccination. At that time, the United States had three authorized vaccines: Pfizer-BioNTech, Moderna and Janssen (Johnson & Johnson). Vaccination offers high levels of protection for severe illness and death with against circulating COVID-19 variants. One challenge for using vaccination as a prevention strategy is that although available nationwide, vaccine uptake could be affected personal beliefs, cultural values, political factors and factors related to health (CDC, 2022a). As a result, it is crucial to build vaccine confidence in the population, thus creating trust and reducing misinformation that could affect their decision-making process.

Possible Moderating Factors Associated With COVID-19

Diabetes Mellitus (DM)

Diabetes is a chronic health disease that impacts how a person turns food into energy. From a medical perspective, DM is considered a series of metabolic conditions associated with hyperglycemia and caused by partial or insulin insufficiency (Egan & Dinneen, 2018). The mechanism the body uses to turn food into energy is by breaking it down into sugar that is released into the bloodstream. As a result of such an increase in blood sugar, the body's pancreas releases insulin which allows blood sugar to be stored as energy within the cell. Diabetes happens when the body cannot produce enough insulin or cannot use it as it should (CDC, 2022d). Hyperglycemia in diabetes is thought to hurt the immune response as a result of failing to control the spread of invading pathogens in diabetic population (Berbudi, et., 2020). For example, studies have shown that patients with diabetes have an increased risk of lower respiratory tract infection, tuberculosis, pneumonia and urinary tract infections (Berbudi, et., 2020).

The most common types of DM are type 1 and type 2. In a patient with type 1 diabetes, the beta cell of their pancreas are not able to produce insulin, as a result of its immune system mounting an autoimmune inflammatory response against the cells responsible for producing insulin (Berbudi, et., 2020) (Egan & Dinneen, 2018). When it comes to type 2 diabetes, it is considered a metabolic disorder that it associated with a dysfunction of the Beta cells of pancreas or a variation of degrees of insufficient insulin action (Berbudi, et., 2020;Egan & Dinneen, 2018).

Epidemiology of Diabetes Mellitus in the United States and in Puerto Rico

In 2019 there were a total of 28.7 million people of all ages diagnosed with diabetes, which is equivalent to 8.7% of the entire United States population (NIH, 2023a). Of the 28.7 million diagnosed patient, 28.5 million were adults with ages 18 and older and 283,000 were children and adolescents. Although 8.7% of the US population is diagnosed with diabetes, there are 96 million people aged 18 years and older with prediabetes, around 38% of the US adult population (CDC, 2022c). Regarding the prevalence of diabetes by race/ethnicity groups, Mexican reported the highest prevalence with 14.4 %, followed by Puerto Rican with 12.4% (CDC, 2022e). Overall, in the United

Stated adult population aged 20 and older, the prevalence of diagnosed diabetes increased from 6.3% in 2004 to 8.4% in 2019.

In 2021, it was estimated that in Puerto Rico a total of 456,640 for 16.8% of the adult population lived with diabetes, this means that 1 in every 6 adults currently has diabetes (PRDH, 2021). Compared to the United States for the year of 2020, Puerto Rico has an age-adjusted prevalence of 14.4%, while the United States has 11.1%. In terms of mortality for 2020, diabetes was considered the third leading cause of death, representing 60 adults for every 100,000 habitants (PRDH, 2021). For both Puerto Rico and the United States, from 2011 to 2021 the age-adjusted prevalence has increased from 13.7% to 14.4% in Puerto Rico and from 8.9% to 11.1% in the United States. In Puerto Rico, the age group most affected was 65 years and older, responsible for 35% for diagnosis in 2021. Risk factors associated with the disease, obesity and overweight were number one with 82.9%, followed by physical inactivity with 56.9% and smoking with 7.6%.

Current Diagnostic Protocol for Diabetes Mellitus

Currently, there are different tests used for diabetes mellitus diagnosis and each of them needs to be repeated on different days to obtain a complete diagnosis. Some of this test can include:

A1C or HbA1c Test. AIC can be used to diagnose both prediabetes and diabetes by providing a bigger picture of a person’s average blood glucose levels in the past two to three months. When sugar enters the bloodstream after a person consumes a meal, it attaches to the hemoglobin protein in a red blood cell (ADA, n.d.) As a result, the A1C test helps measure the percentage of red blood cells with the hemoglobin protein coated with sugar. As a result, the higher a person has their sugar levels, the greater the chance of developing complications related to diabetes (CDC, 2022h).

Fasting Plasma Glucose (FPG). FPG measures a person's fasting blood sugar levels. When fasting, a person must perform the blood test after at least 8 hours without consuming food except for water (ADA, n.d.). FPG level less than 100 mg/dL is considered normal, 100 to 125 mg/dL is considered prediabetes and 126 mg/dl or higher is indicative of diabetes (CDC, 2022h).

Oral Glucose Tolerance Test (OGTT). OGTT is used to obtain a better understanding of how well a person's body processes sugar. The OGTT measures a person's blood sugar level before and two hours after consuming a special drink that contains glucose. Similarly, to the other tests, the fasting plasma glucose levels must be measured before this test begins. After the person has consumed the sugary drink, the blood glucose levels are measured 1 hour, 2 hours and possibly 3 hours afterward (CDC, 2022h). From the blood sugar levels obtained a measure of 140 mg/dl or less is considered normal, 140 to 199 mg/dl is prediabetes and 200 mg/dl or higher is considered diabetes (ADA, n.d.).

Obesity

Obesity is considered a chronic disease that is affecting adults and children worldwide. Obesity can predispose a person to develop different health issues, meaning that it can be considered a risk factor for different chronic diseases, including cardiovascular, heart disease and stroke (WHO, 2023). Obesity can also be associated with different types of cancer, including endometrial, breast, ovarian, kidney and colon

(WHO, 2023). As a disease the biology of obesity compromises impaired host immunity, chronic inflammation, and blood clotting tendency, that have been well-documented to aggravate COVID-19 infections (Manca et al., 2021). During the H1N1 2009 pandemic, as a risk factor, obesity was associated with complications in the intensive care unit, prolonged hospital stays, prolonged ventilation, deaths and the likelihood of developing community-acquired pneumonia (Morgan et al., 2019).

Epidemiology of Obesity in Puerto Rico and USA

Obesity has become a significant concern for public health professionals in the United States. According to the World Health Organization, obesity has reached global epidemic proportion, with the United States ranking with one of the highest prevalence rates compared to other countries (Forrest et al., 2017). From 1999-2017 the obesity prevalence in the United States increased from 30.5% to 41.9%, by which severe obesity also increased from 4.7% to 9.2% during the same period (CDC, 2022b). Hispanic are the largest minority group in the United States, comprising 17.4% (55.4 million) of the entire USA population and expected to increase to 28.9% (119 million) by 2060 (Mondragon et al., 2016). Hispanics are disproportionally affected by the condition of daily life structural and social factors, including macroeconomics, cultural values, income, and education, better known as social determinants of health (SDH). As a result, such differences in SDH can impact health by engaging in behavioral risk factors like poor diets and sedentary lifestyles, promoting obesity (Mondragon et al., 2016).

Puerto Ricans represent the second largest Hispanic subgroup with 10.1% in the USA. As a result, Puerto Ricans have a higher obesity prevalence rate when compared to the USA general population. In 2021 the obesity prevalence on the island was 66.4% and increased to 66.9% (1,778,464 individuals in 2019 (Cabrera, Felici, Diaz, & Martinez, 2023)Not only is the Puerto Rican population the second largest group within the Hispanic community, but they also present higher rates of diagnosed diabetes (13.8%) when compared to more studied Hispanics of Mexican ancestry (13.3%), while at the same time experiencing considerable health disparities that include obesity (Johnson et al.,2017).

The COVID-19 pandemic impacted different surveillance data collecting efforts that included obesity, diabetes and COVID-19. The National Health and Nutrition Examination Survey (NHANES) which combines in-person interviews with standardized physical examinations and laboratory testing, was halted during March 2020 due to the COVID-19 pandemic. Such impact prevented collection of a nationally representative sample during the planned 2019-2020 data collection, (Stierman, et al., 2021)., Data from the 2017-March 2020 pre-pandemic survey showed an increase in the prevalence for children and adolescents aged 2-19 years (12.7% 2-5 years, 20.7% 6-11 and 22.2% for 12-19) been the highest among the Hispanic groups (Stierman, et al., 2021). For adults, there was no difference in the obesity prevalence rate (39.8% 20-29, 44.3% 40-59 and 41.5% 60>). As a disease, obesity is characterized by body fat accumulation, leading to an increased risk of cardiovascular disease, type 2 diabetes, hypertension, depression, and respiratory problems (Alberca, et al., 2020). Overweight can result from excessive consumption of ultra-processed food, which can translate to a high salt diet linked to reduced expression of Angiotensin Converting Enzyme 2 (ACE2) in the kidneys, which has been associated with greater severity of COVID-19 infection (Alberca, et al., 2020).

Current Diagnostic Protocol for Obesity

The most common way to determine if a person is overweight or obese is by calculating a person's body mass index (BMI), which is considered an estimate of the body fat that compares to a person's weight and height (NIH, 2021). In addition to using the BMI as a tool, healthcare professionals may perform a physical exam to measure height and weight, obtain a health history, measure waist size and check for additional health issues (high blood pressure, high cholesterol, underactive thyroid, diabetes, etc). Once BMI calculations are performed, values obtained are compared to established parameters to determine if a person has normal weight, is overweight, obese or extreme obese. NIH established that for a person to be considered normal weight BMI recording must be 18.5 to 24.9, for overweight 25.0 to 29.9, obese 30.0 to 39.9 and for extreme obese 40.0 or higher (NIH, 2021). Although BMI measurements are a great way to estimate a person's fat index, it is not a reliable tool for such purposes. For example, a person might have a higher weight measurement because of being an athlete carrying more muscle tissue. In such a scenario, BMI recording might be higher, but this could not mean the person had excessive body fat.

Hypertension

A person's heart muscle is responsible for pumping blood through arteries, blood vessels and organs of the human body. Blood pressure is the pressure exerted by the blood passing through arteries (Cabrera et al., 2023). Hypertension or high blood pressure is when pressure in the blood vessels is considered too high or above normal (140/90 mmHg or higher) (WHO, 2023). Although some people might not know if they are experiencing high blood pressure since symptoms might not be felt, some factors can increase the risk of a person experiencing high blood pressure. Factors can include older age, genetics, obesity, physical inactivity, high salt diets and increased alcohol intake (WHO, 2023). When high blood pressure is left untreated, it can increase the risk of experiencing a heart attack, stroke and other health issues. Studies have shown that hypertension can be considered one of the most important modifiable risk factors for all-cause morbidity and mortality worldwide, associated with increased risk of developing cardiovascular diseases, including coronary heart disease, heart failure, stroke, myocardial infarction, and atrial fibrillation (Oparil, et al., 2018).

Epidemiology of Hypertension in Puerto Rico and the United States

Hypertension remains the most significant and modifiable risk factor for cardiovascular disease worldwide. It is estimated that 1.28 billion adults between the ages of 39-79 have been diagnosed with hypertension, most living in low- and middle-income countries worldwide (WHO, 2023). In the United States for 2021, hypertension was one of the primary or contributing causes of mortality with 691,095 deaths (CDC, 2023e). The estimated economic burden of hypertension in the United States is about $131 billion annually. The National prevalence of hypertension in the USA population was 49.64%, corresponding to 115 million persons (Chobufo, et al., 2020). In the USA, rates of hypertension vary from sex and race. For example, 50% of men and 44% of women reported having high blood pressure (CDC, 2023e). When it comes to race, in the United

States, high blood pressure is more common in non-Hispanic blacks (56%) than in non-Hispanic white adults (48%), non-Hispanic Asian adults (46%) or Hispanic adults (39%) (CDC, 2023e).

In Puerto Rico, men 18 and older, had higher prevalence (40.8%) than men 65 and older (66.4%) (Cabrera, Felici, Diaz, & Martinez, 2023). In 2019, Puerto Rico reported a prevalence of hypertension of 36.1%, compared to the prevalence of hypertension in the USA was 32.3%. From 2011 to 2019, the prevalence of hypertension on the island fluctuated from 36.1 % to 41.0%. However, although some variations are present, prevalence has remained somehow constant. Hispanic Americans are one of the fastest-growing ethnic minorities in the USA, expected to double within the next four decades, considered a population compromise of many ethnic subgroups with diverse lineages and cultural mores (Thomas & Allison, 2019). Although different, such groups are often classified as a single ethnic group. However, when it comes to their prevalence of hypertension, Puerto Rican reported the third highest prevalence, with 27.4% men and 29.1% women, when compared to Dominican men 32.6% and women 26.1%. (Thomas & Allison, 2019). A similar variation in hypertension prevalence has been observed in the US mainland Hispanic population. In a cross-sectional-based study of individuals aged 25-64 years living in seven Latin American cities, the prevalence of hypertension was close to the US average (25-30%) (Thomas & Allison, 2019).

Current Diagnostic Protocol for Hypertension

For a person to be considered hypertensive, they first must have their blood pressure measured in a medical clinic, on which the patient must have two or more high blood pressure readings at separate medical appointments (NIH, 2022). To have the most appropriate readings, the patient must not exercise, drink coffee or smoke cigarettes 30 minutes before the test. Also, it is recommended to sit and relax 5 minutes before the test and ensure that feet are flat on the floor. Blood pressure reading is taken by using a pressure cuff (sphygmomanometer) around the upper arm. The readings obtained from the technique are recorded as two numbers. The first number is the systolic blood pressure (top number), which indicates how much pressure the blood exerts among the arteries when the heart is contracting during heartbeats. The second number is the diastolic blood pressure (bottom number), which indicates how much pressure the blood exerts among the arteries when the heart is resting between heartbeats (AHA, 2023). American Heart Association established blood pressure categories based on systolic and diastolic blood pressure readings.

Blood Pressure Category

- normal blood pressure: less than 120 mmgh systolic and less than 80 mmgh diastolic
- elevated blood pressure: 120-129 mmhg systolic and less 80 mmgh diastolic
- high blood pressure Stage 1: 130-139 mmhg systolic and 80-89 mmgh diastolic
- high blood pressure Stage 2: 140 or higher mmhg systolic and 90 or higher mmgh diastolic
- hypertensive crisis: 180 or higher mmhg systolic and 120 or higher mmgh diastolic

Gap in the Literature

Although studies have evaluated the impact of non-communicable diseases on the severity of COVID-19, there is limited data on how non-communicable diseases (diabetes mellitus, hypertension) and risk factors like obesity that contribute to mortality rates in Puerto Rico could be affecting the probability of being diagnosed with a COVID-19 test result on the island. Non-communicable diseases can present different challenges and burden a population, affecting their health, economy and healthcare system. As a disease, (DM) is a major public health issue in the United States, affecting a total of 28.7 million people of all ages diagnosed with diabetes, which is equivalent to 8.7% of the entire United States population in the year of 2019 (NIH, 2023a). In 2018, Hispanics were 1.3 times more likely than non-Hispanic whites to die from diabetes; as adults, they were 70 percent more likely to be diagnosed by a physician (HHS, 2021). The Hispanic population is more affected by DM when compared to the general population. It is considered the largest minority group in the United States, compromising 17.4% (55.4 million) of the entire population and is expected to increase to 28.9% (119 million) by 2060 (Mondragon et al., 2016). Additionally, there are substantial differences between subgroups that could affect the prevalence of DM-associated risk factors, since there are differences in their culture (Johnson, et al., 2017). For example, the Puerto Rican population compromised the second largest subgroup with 9.6% and reported the second highest prevalence of DM of Hispanic groups in the USA with 12.4% second to Hispanics of Mexican origin with 14.4% (CDC, 2022e; HHS, 2023). Considering another non-communicable disease like hypertension in Puerto Rico, the groups 18 and older that reported higher prevalence were men (43.3%). However, for both sexes groups 65 years and older reported a prevalence of 69.0% (Cabrera et al., 2023). Compared to the United States in 2019, Puerto Rico reported a prevalence of hypertension for 36.1%, higher than the prevalence of hypertension in the USA was 32.3%. As for obesity as a risk factor, the Puerto Rican population reported higher obesity prevalence when compared to the USA. In 2016 the obesity prevalence on the island was 66.45% and increased to 66.39% (Cabrera et al.,2023). Hispanic can be disproportionally affected by the condition of daily life, structural and social factors that could affect their rates of obesity.

Evaluating the impact of hypertension, obesity, and diabetes on COVID-19 outcomes in the Puerto Rican population, it was important to recognize that this demographic, like other Hispanic groups, was disproportionately affected by transmissible diseases such as COVID-19. Hispanic individuals accounted for 16,138,064 (24.2%) of confirmed and probable COVID-19 cases in the United States, second only to White, non-Hispanic individuals, who comprised 35,838,547 (53.8%) of reported cases. Puerto Ricans, as a subgroup of the Hispanic population, faced numerous health challenges and risk factors that may have contributed to higher rates of chronic diseases and increased vulnerability to COVID-19.

As non-communicable diseases, DM and hypertension, and obesity together as a risk factor constantly impact the health of the targeted population, having higher rates when compared to the general US population. According to the United States Census Bureau, Hispanic or Latino refers to people who classify themselves as Mexican, Puerto Rican, or Cuban. In addition to those categories, a person could classify as Hispanic if they originate from either Spain, Spanish-speaking countries of South America or another Spanish culture (USCB, n.d.). According to the data from the 2020 Census, there are 62.1 million Hispanics as part of the USA population. That said, Hispanic subgroups are often combined in health research. Being Hispanic American, one of the fastest-growing ethnic minorities in the USA, expected to double within the next four decades, they are considered a population compromise of a number of ethnic subgroups with diverse lineages and cultural mores (Thomas & Allison, 2019). Being Puerto Rican, the second largest among the Hispanic population with 9.6% and expected to keep growing, it is crucial to evaluate and obtain a better understanding of how non-communicable diseases and risk factors that affect chronic disease mortality rates on the island, could be affecting their probability to become infected with COVID-19.

Previous Research Using Proposed Methodology

Similar studies have evaluated how different factors could affect the diagnosis and prognosis of COVID-19. Piedra (2022) using logistic regression examined the relationship between exposure variables (household size, reliance on outside help for everyday tasks, experience of change in work due to the pandemic), material hardship and COVID-19 diagnosis within the household environment on a sample of the U.S. Latino population. Logistic regression revealed that exposure variables such as material hardship and reliance on outside help were significantly correlated with COVID-19 infection. Such a result can help explain the disproportionate burden when it comes to COVID-19 rates experienced by the Latino population during the pandemic. A second study aimed to describe the characteristics of COVID-19 patients with T2DM and risk factors for severity. Used logistic regression to explore risk factors that could be associated with disease severity. Results from the logistic regression analysis established decreased CD4 lymphocyte count (*OR* = 0.988, 95% *CI* 0.079 - 0.997) and increased serum amyloid A (SAA) at admission were confirmed as independent risk factors of severity on COVID-19 patients with suffering from T2DM (Zhang, et al., 2020). By that established that CD4 T cells play a crucial role when it comes to various immunological responses during infection. Overall, the study established that hyperglycemia and dyslipidemia coupled with impaired immunological response in each population, might be associated with susceptibility to virus infections (Zhang, et al., 2020). A study performed in Iran, aimed to investigate the risk factors of COVID-19 in order to obtain a better understanding and control. Such study established using logistic regression that COVID-19 had correlations with history of cardiac disease ($p = 0$, $OR = 5.7$), blood hypertension ($p = 0$, $OR = 7.1$ and diabetes ($p = 0$, $OR = 7.4$) (Keshavarzian, Biranvand, & Khalifpour, 2021). Based on demographic and clinical characteristics, results showed that from the 407 confirmed COVID-19 diagnosed patients 565 were men, 9 % had history of cardiac disease, 16% history of high blood pressure and 18% reported history of diabetes. A study evaluating the association of obesity and diabetes with the risk of mortality in critically ill patients that are diagnosed with COVID-19, established that patients with diabetes alone has a increased risk of mortality with an *OR* of 2.68 (*CI* 95% 1.1 - 7.4, $p = .026$) (Cruz, et al., 2021). However, when patients had both diabetes and obesity as risk factors, their risk of mortality was 3.17 (*CI* 95% 1.9 - 10.2, $p = .038$)., concluding that patient with both diabetes and obesity could be considered as risk factors increasing severity of COVID-19 infection, since they both were associated with an increased mortality.

Definitions

Dependent Variables

COVID-19 diagnosis (Categorical in Nature)

Defined as individuals of Puerto Rican heritage who were tested for COVID-19 by detection of SARS-CoV-2 ribonucleic acid (RNA) in a clinical specimen using a molecular amplification test performed by a Clinical Laboratory Improvements Amendments (CLIA) certified provider (CDC, 2021b). Levels of measurement for this variable will be set as positive vs negative.

Chronic Disease/Noncommunicable Disease

Defined a condition that lasts at least 1 or more years, that needs ongoing medical attention or limits daily activities (CDC, 2022e).

Incidence

Rate of new cases or events over a specific period for the specific population at risk (Tenny & Boktor, 2023)

Independent Variables

Obese (Categorical in Nature)

For a person to be considered obese, he or she must fall in the BMI category of obese or extreme obese or have a yes answer for sever obesity on the person under investigations form (PUI). Using those two categories, a new variable was created where participants who reported BMI recordings that fell in both categories (obese, severe obese) were counted as obese. BMI measures are considered an estimate of the body fat that compares to a person's weight and height (NIH, 2021). BMI results were then compared to the NIH BMI measures that established their obesity status. For example, 18.5 to 24.9, for overweight 25.0 to 29.9, obese 30.0 to 39.9 and for extreme obese 40.0 or higher (NIH, 2021). Measurements of body weight and height were obtained from the patient medical record.

Hypertension (Categorical in Nature)

Persons under investigation form (PUI) were evaluated for a yes or no answer on the hypertension variable. Medical records were evaluated for hypertension diagnosis for patients who did not have the variable answered on the PUI. (CDC, 2020a).

Diabetes Mellitus (Categorical in Nature)

Persons under investigations form (PUI) were evaluated for a yes or no answer on the DM variable. Medical records were evaluated for DM diagnosis for patients who did not have the variable answered on the PUI. (CDC, 2020b)

Pandemic

When diseases spread over several countries or continents, often affecting a large amount of the population (CDC, 2023 f).

Polymerase Chain Reaction (PCR)

Laboratory technique for rapidly producing (amplifying millions to billions of copies of a particular segment of deoxyribonucleic acid (DNA) (NIH, 2023c).

Prevalence

Proportion of the population suffering from a condition at a specific time period (Tenny & Boktor, 2023)

Assumptions

When conducting this study, the following assumptions were made. When asked about their medical history by their medical provider, participants in the study answered truthfully. It was also assumed that when variables such as DM and hypertension were present in the medical records, such information was provided when patients were officially diagnosed with a specific disease and not just based on self-diagnosis for DM or hypertension. Additionally, it was assumed that the height and weight measured used for calculating BMI were properly measured by a healthcare provider and not solely reliant on patients' responses, assuming there was no response bias in the process. The sample was considered representative of the entire population. However, in terms of generalizability, it was assumed that rates of hypertension, diabetes mellitus, obesity, and COVID-19 varied across geographic regions of the island. This assumption was made because the health centers or clinics from which the data was collected were primarily focused on the northern and eastern parts of the island.

Scope and Delimitations

There was limited research specifically examining how chronic diseases and modifiable risk factors predisposed the Puerto Rican population to COVID-19 infection. This gap was not only due to a lack of research but also because the Puerto Rican population while being the third-largest subgroup within the Hispanic population in the

United States, was often aggregated into broader Hispanic categories. Although Puerto Ricans are part of the Hispanic ethnicity, research frequently treated Hispanic populations as a single group, overlooking the unique challenges faced by individual subgroups. As a result, findings from such studies could not be generalized to the entire Hispanic community, as each subgroup may be affected differently based on cultural values, resource availability, and other contextual factors.

This study focused on participants from the Puerto Rico Community Engagement Alliance (PR-CEAL) dataset. Only individuals who were tested for COVID-19 using PCR were included in the analysis, as PCR testing was considered the gold standard for COVID-19 diagnosis; antigen testing was not available at the time of the study. The study specifically examined chronic conditions such as obesity, hypertension, and diabetes as predictors, alongside age group, sex, and personal exposure. Data were primarily collected from community health clinics located in the northern and eastern regions of Puerto Rico, which may not have fully represented the entire population of the island. Without this specific focus, the study could have been expanded to include other regions, given that trends in the selected predictor variables often varied across different areas of the island. Thus, having a better understanding of how such predictors could affect COVID-19 diagnosis.

Limitations

The cause and effect for the predictors and outcome variable could not be established with a correlational study. Although correlational studies uncovered relationships that may not have been previously known in the literature, they did not equate to causation when used as a method. Additionally, correlational research helped to determine connections between variables; however, it did not provide information on which variable could have been affecting another variable. Some concerns with the present data related to data processing and data quality, as well as the potential for limited generalizability, which were known challenges when using electronic medical records data for secondary data research (Edmondson & Reimer, 2020). Additional limitations to the study related to the sources used to create the secondary data set. Data was extracted from revisions of medical records in the health centers around the island. Such usage posed greater challenges at the time of making the necessary statistical analysis, since the quality of the data depended on consistency and availability. Furthermore, human errors when entering and collecting data were also taken into consideration. The study had two main limitations. First, the health clinics from which the data were obtained could not hospitalize patients. As a result, the dataset lacked information related to hospitalization and post-diagnosis complications of COVID-19. This limited the study's ability to assess disease severity and long-term outcomes. Second, although the study population included patients from across the island, the participating clinics were primarily located in the northern and eastern regions. This may have affected the external validity of the findings, as rates of chronic diseases and associated risk factors can vary geographically across Puerto Rico. Therefore, the exposure and prevalence of chronic conditions in the study sample may not fully reflect those of the entire island population.

Significance

Obtaining a better understanding of how chronic diseases and contributing risk factors to mortality rates in Puerto Rico could impact their predisposition for being diagnosed with COVID-19 can help guide clinicians and public health professionals create targeted public health interventions. Prevention strategies that target specific groups not only can help reduce rates of COVID-19 infection but can also help reduce the risk of DM, obesity and hypertension health complications associated with COVID-19 infection. Also, understanding the role of such risk factors in COVID-19 infections could encourage more careful surveillance and earlier interventions among the population, thus leading to higher quality and more robust interventions.

Summary and Conclusion

The focus of this study was to evaluate the association between chronic diseases and risk factors that included DM, hypertension, and obesity with COVID-19 diagnosis in Puerto Rico, with the primary goal of understanding how such predictors could affect the probability of infection among the targeted population. At the time of this study, the territory of Puerto Rico reported a total of 1,104,605 diagnosed patients of COVID-19, with an average of 286 daily diagnoses and accumulated deaths of 5,837. In 2021, it was estimated that in Puerto Rico, a total of 456,640 individuals, or 16.8% of the adult population, lived with diabetes; this meant that 1 in every 6 adults had diabetes (PRDH, 2021). When it came to obesity, Puerto Ricans had a higher obesity prevalence rate compared to the general population in the USA. In 2021, the obesity prevalence on the island was 66.4%, which increased to 66.9% (1,778,464 individuals in 2019) (Cabrera, Felici, Diaz, & Martinez, 2023) In 2019, Puerto Rico reported a prevalence of hypertension of 36.1%, compared to the prevalence of hypertension in the USA, which was 32.3%. Because the Puerto Rican population on the island was heavily affected by chronic diseases, it was of great importance to public health to obtain a better understanding of how such diseases could have affected the predisposition of a population to become infected with a novel virus, like COVID-19, during the early stages of a pandemic.

In Section 2, the correlational study design to evaluate the association between DM, obesity, hypertension, and COVID-19 infection among the population in Puerto Rico will be discussed. Included is a discussion of how logistic regression was used to evaluate the relationship between predictor variables (DM, obesity, hypertension) and COVID-19 diagnosis among the population.

Section 2: Research Design and Data Collection

This quantitative correlational study examined the association between risk factors affecting Puerto Rico's mortality rates, including obesity status, hypertension, and diabetes mellitus (DM) and COVID-19, adjusted for age, sex, and person exposure. The main topics of Section 2 include the research design and rationale for the study, focusing on the variable under investigation and its connection to the research questions. This section also describes the study population and sampling procedures used by the original creators of the secondary data set for the study. The data analysis plan consists of descriptive statistics using univariate, bivariate, and multivariate analysis plans. Charts and contingency tables were used for data visualization. The last section focuses on the internal and external threats to the study's validity. The IRB approval number for this study is 11-06-24-0580552

Research Design and Rationale

The research design included a secondary data analysis using epidemiologic and clinical features of COVID-19 data from the Puerto Rico Community Engagement Alliance (PR-CEAL) database. The study's design was correlational to examine the association between risk factors (obesity, hypertension, and DM) and the probability of being diagnosed with COVID-19 infection while controlling age, sex, and person exposure. Independent variables were obesity, hypertension, and DM. The dependent variable was COVID-19 diagnosis in Puerto Rico. Control variables were age, sex, and person exposure. All dependent, independent, and control variables were categorical.

Correlational analysis of secondary data allows researchers to increase research expertise and avoid data collection challenges that could be present when using primary data (Wickham, 2019). Correlational analysis allows the researcher to evaluate a larger number of variables. Studies could be used to generate hypotheses and examine multiple outcomes at the same time without any loss to follow-ups. Some disadvantages of correlational studies include that correlational studies can determine associations between exposure and outcomes but cannot predict causation (Lau & Kuziemsky, 2017; Wickham, 2019).

Methodology

Population

Patients attending primary health clinics in Puerto Rico were tested for COVID-19 diagnosis. The sample for the study was N = 1,463 adult patients age 18 years and older who underwent a PCR test for COVID-19 when visiting the selected primary health clinics.

Sampling Procedures Used by Original Creators of the Data Set

The original study's data collectors used a convenience sampling method. The study personnel established agreements with primary health care clinics in different municipalities of Puerto Rico. They visited clinics that were available for data collection, specifically those with the time and space for the study staff. Due to time constraints, the data collectors were able to visit a total of four primary health care clinics. Data were collected through the evaluation of electronic medical records by trained staff. Training consisted of discussing relevant data required for analysis, identifying the location of variables within the electronic medical record, and utilizing a standardized electronic form for data abstraction, along with a protocol that outlined how the data had to be abstracted. The collected data included case classification, sociodemographic characteristics, health care worker information, exposure history, clinical course, symptoms, and start date of symptoms, diagnosis of COVID-19, clinical comorbidities, complications, and COVID-19 vaccine status. Patients included in the study were classified as suspected (serology testing) and confirmed (PCR) COVID-19 patients who visited the primary health care clinics in Puerto Rico from April 1, 2020, to March 31, 2021. The clinics shared a list of patients who met the inclusion criteria, and patients who were on the list but did not have laboratory evidence in their records were excluded.

Dataset used for this study was part of the study titled “Epidemiologic and clinical features of patients with suspected or confirmed COVID-19 evaluated in primary healthcare centers in Puerto Rico, part of the Puerto Rico Community Engagement Alliance” (PR-CEAL). Professionals led this study with years of experience in the public health and medical field. The dataset was generated using the REDCap tracking database to minimize any breach in the subjects’ confidentiality. Healthcare clinics that participated in the study came from different municipalities across Puerto Rico, generating information about populations with diverse backgrounds and characteristics. Because of the detailed information collected in this dataset, this study sought to provide a better understanding of the Puerto Rican population receiving healthcare services in these clinics who suffered from various chronic conditions, including DM, hypertension, obesity, and diagnoses of COVID-19. These findings aimed to help bridge the gap regarding COVID-19 in this Hispanic population.

Sampling Procedures for the Current Study

The original data set provided by the Puerto Rico Community Engagement Alliance (PR-CEAL) included a total of N=1,463 participants. For this study, we utilized the entire sample since all cases met the inclusion criteria. Specifically, all participants underwent COVID-19 testing using PCR diagnostics, which was central to the study's focus. Initially, the plan was to include only those participants who tested positive for COVID-19 (n = 1,028). However, during the planning phase of the inferential analysis, it became necessary to also include participants who tested negative via PCR (n = 435). This decision allowed for a more comprehensive analysis and enhanced the statistical power of the study. Using the full sample helped minimize sampling error and provided more reliable estimates for the population being studied. Additionally, including all available data improved the generalizability of the findings, particularly given that the health clinics contributing data were not evenly distributed across Puerto Rico.

Operationalization of Constructs

Dependent Variable

COVID-19 diagnosis (Categorical in nature) was defined as individuals of Hispanic ethnicity in Puerto Rico who were tested for COVID-19 by detection of SARS-CoV-2 ribonucleic acid (RNA) in a clinical specimen using a molecular amplification test performed by a Clinical Laboratory Improvements Amendments (CLIA) certified provider (CDC, 2021b). The level of measurement for the variable was nominal (categorical). The variable consisted of two levels coded 0 = Negative and 1 = Positive.

Independent Variables

Obesity as a predictor variable was defined as a person with a BMI category of obese or extremely obese or who had a yes answer for severe obesity on the person under investigation's form (PUI). BMI measures were considered an estimate of body fat that compared to a person's weight and height (NIH, 2021). BMI results were then compared to the NIH BMI measures that established their obesity status. For example, normal weight was classified as 18.5 to 24.9, overweight as 25.0 to 29.9, obese as 30.0 to 39.9, and extreme obesity as 40.0 or higher (NIH, 2021). Body weight and height measurements were obtained from the patient's medical record. Using those two categories, a new variable was created in which participants who reported BMI recordings that fell within both categories (obese, severe obese) were counted as obese. The level of measurement for the variable was nominal (categorical). The variable consisted of three levels coded as 0 = No, 1 = Yes, and 99 = Unknown.

Hypertension as a variable was defined as a person who answered yes on the standardized person under investigation form (PUI) hypertension variable. Medical records were evaluated for hypertension diagnosis for patients who did not have the variable answered on the PUI (CDC, 2020a). The level of measurement for the variable was nominal (categorical). The variable consisted of three levels coded 0 = No, 1 = Yes, and 99 = Unknown.

For DM as a predictor, patients had to answer yes in the standardized person under investigation form (PUI) for that specific variable. Additionally, medical records were evaluated for DM diagnosis for patients who did not have the variable answered on the PUI (CDC, 2020a). The level of measurement for the variable was nominal (categorical). The variable consisted of three levels coded as 0 = No, 1 = Yes, and 99 = Unknown.

Control Variables

Age group and sex control variables were obtained from answers of the standardized patient under investigation forms (PUI) that were used to collect the data. When answers were not obtained via PUI, then variables were extracted from the patient medical records. Age variables were collected as numerical continuous variables. When patients were infants, months were converted to years. For sex, answers were obtained in a categorical nature specifically coded as 1 = males, 2 = females, 3 = other, and 99 = unknown. As for person exposure, was defined as individuals that had contact with a known COVID-19 confirmed two days to onset of symptoms, without protective equipment within 6 feet radio.

Data Analysis Plan

The data set provided by the Puerto Rico Community Engagement Alliance (PR-CEAL) was initially reviewed in Excel before being imported into SPSS version 29 for analysis. I started by visually scanning the data and utilizing sorting and filtering tools in Excel to identify any duplicate entries, incorrect values, or structural errors. After that, I employed SPSS to generate frequency tables and descriptive statistics, which helped me detect any out-of-range values and inconsistencies among the variables. Evaluation revealed no missing values in the dataset, and there were no extreme values that could be classified as outliers. Since all variables were complete and relevant to the study objectives, none were deleted. Finally, I ensured that the dataset was organized and properly formatted for logistic regression and chi-square testing. After completing these steps, the data was ready for statistical analysis.

Research Questions and Hypotheses

RQ1: What is the association between obesity and COVID-19 diagnosis while controlling for age, sex and person exposure?

H_o1: There is no significant association between obesity and COVID-19 diagnosis while controlling for age, sex and person exposure.

H_a1: There is a significant association between obesity and COVID- diagnosis while controlling for age, sex and person exposure.

RQ2: What is the association between DM and COVID-19 diagnosis while controlling for age, sex and person exposure?

H_o2: There is no significant association between DM and COVID-19 diagnosis while controlling for age, sex and person exposure.

H_a2: There is a significant association between DM and COVID-19 diagnosis while controlling for age, sex and person exposure.

RQ3: What is the association between hypertension and COVID-19 diagnosis while controlling for age, sex and person exposure?

H_o3: There is no significant association between hypertension and COVID-19 diagnosis while controlling for age, sex and person exposure.

H_a3: There is a significant association between hypertension and COVID-19 diagnosis while controlling for age, sex and person exposure?

RQ4: What is the association of (obesity, DM and hypertension) and COVID-19 diagnosis while controlling for age, sex and person exposure?

H_o4: There is a negative predictive value of (obesity, DM and hypertension) and COVID-19 diagnosis while controlling for age, sex and person exposure.

H_a4: There is a positive predictive value of (obesity, DM and hypertension) and COVID-19 diagnosis while controlling for age, sex and person exposure.

Descriptive Statistical Analysis

Univariate descriptive statistics (using table, percentages, and frequencies for each variable). Considering the categorical nature of variables used for this study, frequency distribution analysis that included tables to summarize data values using numbers and percentages was proposed. (See Table 1). Univariate descriptive analysis helped describe the population regarding their COVID-19 results and history of hypertension, diabetes, or obesity. Numerical variables in the study was age as a control variable, which was reported using measures of central tendency like mean and standard deviation (SD).

Table 1

Frequency Distribution of Study Population by Sex (N = x)

Sex	Frequency	Percentage	Total
Male	Number	%	Number
Female	Number	%	Number
Missing	Number	%	Number
Total	Number	%	Number

Table 2

Age Group Frequency Distribution of the Study Population (N = x) Descriptive Statistics of Age Control Variable

Age group	Frequency	Percentage	Total
< 18	Number	%	Number
18–40	Number	%	Number
41–59	Number	%	Number
≥ 60	Number	%	Number
Total	Number	%	Number

Table 3

Frequency Distribution of Obesity Independent Variable

Obesity	Frequency	Percentage	Total
Yes	Number	%	Number
No	Number	%	Number
Missing	Number	%	Number
Total	Number	%	Number

Table 4

Frequency Distribution of Hypertension Independent Variable

Hypertension	Frequency	Percentage	Total
Yes	Number	%	Number
No	Number	%	Number
Missing	Number	%	Number
Total	Number	%	Number

Table 5

Frequency Distribution of Diabetes Mellitus Independent Variable

Diabetes mellitus	Frequency	Percentage	Total
Yes	Number	%	Number
No	Number	%	Number
Missing	Number	%	Number
Total	Number	%	Number

Table 6

Frequency Distribution of COVID-19 Diagnosis Dependent Variable

COVID-19 diagnosis	Frequency	Percentage	Total
Positive	Number	%	Number
Negative	Number	%	Number
Missing	Number	%	Number
Total	Number	%	Number

Bivariate Analysis

Bivariate analysis was used to evaluate the association between categorical variables that included risk factors (obesity, hypertension, and DM) contributing to mortality rates in Puerto Rico related to COVID-19. For data visualization, a description of this association included contingency tables. Each independent predictor variable was evaluated with the dependent variable to explore if there was a relationship between them. Contingency table displayed percentages on the predictor variable since it was the best choice when wanting to establish a relationship between independent and dependent variables (Bertani et al., 2018). Associations were established using the Chi-square test (χ^2) (Bertani et al., 2018). Assumptions for using the Chi-square test included that the variables used in the analysis were categorical in nature and mutually exclusive of each other. Univariate logistic regressions were used to evaluate the impact of each predictor variable on the odds ratio at the event of interest, thus avoiding the expected confounding when variables were analyzed altogether (Sperandai, 2014). Measures of association between exposure and outcomes, odds ratios (*OR*) at a 95% confidence interval (*CI*), were used.

Table 7

Contingency Table with Chi-Square and Fisher for Obesity and COVID-19 Diagnosis Test Analysis

		COVID-19 Diagnosis		
		Positive	Negative	Total
Obesity	Yes	Number	Number	Number
	No	Number	Number	Number
	Total	Number	Number	Number

	Value	Df	Asymptotic Significance (2-sided)	Exact Sig (2-sided)	Exact Sig (1-sided)
Pearson Chi-Square	Number	Number	Number	Number	Number
Continuity Correction	Number	Number	Number	Number	Number
Likelihood Ratio	Number	Number	Number	Number	Number
Fishers Exact Test	Number	Number	Number	Number	Number
N of Valid Diagnosis	Number	Number	Number	Number	Number

Table 8

Contingency Table with Chi-Square and Fisher for Hypertension and COVID-19 Diagnosis Test Analysis

		COVID-19 Diagnosis		
		Positive	Negative	Total
Hypertension	Yes	Number	Number	Number
	No	Number	Number	Number
	Total	Number	Number	Number

	Value	Df	Asymptotic Significance (2-sided)	Exact Sig (2-sided)	Exact Sig (1-sided)
Pearson Chi1-Square	Number	Number	Number	Number	Number
Continuity Correction	Number	Number	Number	Number	Number
Likelihood Ratio	Number	Number	Number	Number	Number
Fishers Exact Test	Number	Number	Number	Number	Number
N of Valid Diagnosis	Number	Number	Number	Number	Number

Table 9

Contingency Table with Chi-Square for DM and COVID-19 Diagnosis Test Analysis

		COVID-19 Diagnosis		
		Positive	Negative	Total
Diabetes Mellitus (DM)	Yes	Number	Number	Number
	No	Number	Number	Number
	Total	Number	Number	Number

	Value	Df	Asymptotic Significance (2-sided)	Exact Sig (2-sided)	Exact Sig (1-sided)
Pearson Chi-Square	Number	Number	Number	Number	Number
Continuity Correction	Number	Number	Number	Number	Number
Likelihood Ratio	Number	Number	Number	Number	Number
Fishers Exact Test	Number	Number	Number	Number	Number
N of Valid Diagnosis	Number	Number	Number	Number	Number

Binary logistic regression analysis was used to establish the magnitude of association between predictor variables (DM, hypertension, obesity) and obtain a COVID-19 diagnosis. Model was utilized to calculate and predict the probability of a binary event occurring, in the sense that the patient would or would not have positive

COVID-19 diagnostic test results after being exposed to the selected predictor variables. Because the dependent variable was dichotomous, a binomial logistic regression analysis was suited for this study (See Table 10). Assumptions included the following: one or more independent variables were either continuous or categorical. For example, the independent variables used in the study included obesity, hypertension, and DM, which were all categorical in nature. There should not have been multicollinearity between more than two independent variables; independent variables should have been highly correlated with the dependent variable and not with each other. To detect multicollinearity, variance inflation factors (VIF) were implemented. VIF estimated how much the variance of the regression coefficient was inflated due to multicollinearity.

Confounding variables were identified by assessing whether predictor variables were related to both the outcome variable and other predictors within the dataset. To evaluate confounding, a multivariate logistic regression analyses was performed, which enabled me to control multiple confounders at the same time. This approach yielded adjusted odds ratios (AORs) that illustrated the relationship between each predictor and COVID-19 diagnosis after accounting for the confounding variables.

Table 10

Classification Table for Dependent Variable

Observed		Predicted		
		COVID-19 Diagnosis		
		No	Yes	%
COVID-19	No	Number	Number	%
Diagnosis	Yes	Number	Number	%
Overall Percentage		%	%	%

Table 11

Contribution of Each Independent Variable to the Model and its Statistical Significance

	B	S.E.	Wald	Df	Sig.	Exp(B)	95% C.I. for Exp (B)	
							Lower	Upper
Obesity	Number	Number	Number	Number	Number	Number		
DM	Number	Number	Number	Number	Number	Number		
Hypertension	Number	Number	Number	Number	Number	Number		

A Priori Power Analysis

A priori power analysis involved estimating the sample size needed in order to reach the desired level of power in the study. For this study, power analysis and sample size were calculated by using the G*Power Statistical Analysis tool. G*Power was a tool that helped compute the statistical power analysis for different tests proposed in the study, which included χ^2 (Faul et al., 2007). In a priori power analysis, sample size N was computed as a function of the required power level (1-ß), the prespecified level of alpha, and the population effect size to be detected with probability 1-ß (Faul et al., 2007). Overall, a priori sample analysis provided an effective method for controlling the statistical power before the study was actually conducted.

Data Analysis Matrix

Table 12

Analysis for the COVID-19 Probability Study

Study Objective or Research Questions	Concept	Data Source	Level of Measurement	Analysis Procedures
RQ I: What is the association between obesity and COVID-19 diagnosis while controlling for age, sex and person exposure	Evaluate if being obese affect the probability of being diagnosed with COVID-19	Secondary data analysis from the Epidemiologic and clinical feature of COVID-19 of the Puerto Rico Community Engagement Alliance (PR-CEAL). Data from patients of COVID-19 attending primary healthcare clinics in Puerto Rico was conducted from April 1, 2020 to March 31, 2021.	(Categorical)	A: Inferential Statistical Analysis Chi-square test (χ^2) = compare the distribution of a categorical variable on sample with the distribution of another sample or groups Fishers exact test= establish the association between outcome and predictor variables Binary logistic regression= presence or absence of a characteristic or outcome based on values of a set of predictor variables Odds Ratio=measures the association between exposure and outcome
RQ II: What association between DM and COVID-19 diagnosis while controlling for age, sex and person exposure	Evaluate if having a diagnosis of DM affect the probability of being diagnosed with COVID-19	Secondary data analysis from the Epidemiologic and clinical feature of COVID-19 of the Puerto Rico Community Engagement Alliance (PR-CEAL). Data of patients of	(Categorical)	A: Inferential Statistical Analysis Chi-square test (χ^2) = compare the distribution of a categorical variable on sample with the distribution of another sample or groups

		COVID-19 attending primary healthcare clinics in Puerto Rico was conducted from April 1, 2020 to March 31, 2021.		Fishers exact test= establish the association between outcome and predictor variables Binary logistic regression= presence or absence of a characteristic or outcome based on values of a set of predictor variables Odds Ratio=measures the association between exposure and outcome
RQ III. Association between hypertension and COVID-19 diagnosis while controlling for age, sex and person exposure	Evaluate if having hypertension affects the probability of being diagnosed with COVID-19	Secondary data analysis from the Epidemiologic and clinical feature of COVID-19 of the Puerto Rico Community Engagement Alliance (PR-CEAL). Data of patients of COVID-19 attending primary healthcare clinics in Puerto Rico was conducted from April 1, 2020 to March 31, 2021.	(Categorical)	A: Inferential Statistical Analysis Chi-square test (χ^2) = compare the distribution of a categorical variable on sample with the distribution of another sample or groups Fishers exact test= establish the association between outcome and predictor variables Binary logistic regression= presence or absence of a characteristic or outcome based on values of a set of predictor variables Odds Ratio=measures the association between exposure and outcome
RQ IV. Association of (obesity, DM and hypertension) COVID-19	Evaluate if risk factors for mortality rates in Puerto Rico affect the	Secondary data analysis from the Epidemiologic and clinical feature of	(Categorical)	A: Inferential Statistical Analysis Chi-square test (χ^2) = compare the

diagnosis while controlling for age, sex and person exposure	probability of being diagnosed with COVID-19	COVID-19 of the Puerto Rico Community Engagement Alliance (PR-CEAL). Data of patients of COVID-19 attending primary healthcare clinics in Puerto Rico was conducted from April 1, 2020 to March 31, 2021.		distribution of a categorical variable on sample with the distribution of another sample or groups Binary logistic regression= presence or absence of a characteristic or outcome based on values of a set of predictor variables Odds Ratio=measures the association between exposure and outcome

Threats to Validity

Internal validity referred to the design characteristics that provided confidence in the findings or the relationships examined in the study. Internal validity defined how well the relationship between outcome and predictor variables could be established (Mazurek & Morrison, 2019). A lack of internal validity meant that the findings might not have reflected what was intended. To enhance internal validity or reduce threats, study employed binary logistic regression to control for variables like sex, age group, and known COVID-19 exposure, isolating the effects of chronic conditions. Participants were included based on confirmed PCR test results, ensuring objective measurement and minimizing misclassification bias. Data integrity was upheld through rigorous cleaning, eliminating errors and inconsistencies, while a consistent sampling approach from community health clinics participating in the PR-CEAL initiative standardized data collection methods. Finally, using the entire sample of $N = 1{,}463$ participants increased statistical power and reduced sampling error. Collectively, these methodological steps strengthened internal validity by minimizing biases and ensuring reliable findings.

Ethical Procedures

Data Management and Confidentiality

All data used for this study was de-identified, and no personal identifiers were used to analyze and report findings. The data management process was confidential. As mentioned, patient identifiers, which included name, address, or any other identifiable information, were not present at the moment of receiving or obtaining permission to use the data set. When access to the data for analysis was obtained, the data set was cleaned from identifiers by data analyst personnel from the original developers of the data set. For this reason, the data that was worked on did not have any identifiers present at the moment of analysis. The PR-CREAL Program Coordinators removed identifiers from the data set.

Data Protection

Risk to patient data was minimal since secondary data analysis was performed using a data set that had already been cleaned of patient identifiers. The data was stored in an external hard drive protected by a password. The only people who had access to the data were me (Mr. Julian R. Rivera Rodriguez as the principal investigator) and my committee members, Dr. Richard Jimenez and Dr. Ndetan Harrison. Data was stored in encrypted files for a minimum of 5 years as required by the IRB. The IRB approval number for this study is 11-06-24-0580552.

Summary

The study was a correlational design to explore the association between risk factors (obesity, hypertension, and DM and the probability of being diagnosed with COVID-19 infection while controlling for age, sex, and person exposure. Population for this study consisted of patients attending primary health clinics in Puerto Rico who underwent testing for COVID-19 diagnosis. The sample for the proposed study was 1,463 (N = 1,463) adult patients ages 18 years and older who underwent a PCR test for COVID-19 when visiting the selected primary health clinics. Dataset used for this study was part of the research titled "Epidemiologic and clinical features of patients with suspected or confirmed COVID-19 evaluated in primary healthcare centers in Puerto Rico, part of the Puerto Rico Community Engagement Alliance" (PR-CEAL). The statistical analysis conducted for this study included univariate descriptive statistics displayed using percentages, and frequency tables for each variable. Bivariate analysis was used to establish the association between outcome and predictor variables using the Chi-square test (χ^2). Multivariate analysis included binary logistic regression to establish the magnitude of the association between predictor variables (DM, hypertension, obesity) and obtaining a diagnosis for COVID-19. Next section focused on presenting the results and findings of the study.

Section 3: Presentation of the Results and Findings

The purpose of this quantitative study was to examine the association between various risk factors and noncommunicable diseases, including DM, obesity, hypertension, and COVID-19 diagnosis, while controlling for age and sex in Puerto Rico. The primary research question centered on the relationship between obesity and COVID-19 diagnosis, accounting for age, sex, and personal exposure. Additional research questions examined similar associations regarding COVID-19 diagnosis, with hypertension and DM serving as predictor variables. The study investigated how these predictors (DM, hypertension, and obesity) were related to COVID-19 diagnoses in Puerto Rico. The analysis included descriptive statistics for predictor and outcome variables. The inferential analysis included chi-square tests and binary logistic regression. The secondary data set utilized for this study provided details on the epidemiological and clinical features of COVID-19, sourced from the PR-CEAL database. This section offers a description of the data set, a presentation of the results, and a summary of the findings.

Assessing the Data Set Used for Secondary Analysis

The study population was composed of patients who attended primary health clinics in Puerto Rico from April 1, 2020, to March 31, 2021, and who underwent testing for COVID-19 diagnosis. The sample included $N = 1{,}463$ adult patients age 18 years and older who received a PCR test for COVID-19 during their visits to the selected clinics. The original data set used for the study incorporated both suspected (serology) and confirmed (PCR) COVID-19 cases; however, this study excluded the population of suspected cases. In assessing the adjusted variables, ethnicity was not included as a control variable in the analysis due to the fact that 98.8% ($N = 1{,}446$) of participants identified as Hispanic/Latino. Furthermore, the original data set did not include age group as a variable, leading to the creation of a new categorical variable that divided participants into four distinct age groups (< 18, 18–40, 41–59, and ≥ 60). This categorization was justified for its potential to simplify the adjustment process in age-related analyses, with age groupings informed by previous studies (H. Zhang et al., 2022).

It is noteworthy that the data set did not contain any missing data or values. Given that convenience sampling was employed by the creators of the original data set, the external validity of the findings may be limited because the results might not accurately represent the entire population. Nonetheless, descriptive analysis of the study population revealed that the prevalence of diabetes was 11.6%, in contrast to a reported prevalence of 13.3% in Puerto Rico during the year 2020. Additionally, according to hypertension rates, the general population on the island recorded an incidence rate of 36.1% in 2020, whereas the study population exhibited a significantly lower rate of 22.1%. In terms of sex distribution, the broader Puerto Rican population comprised 52.8% females and 47.2% males, while the study sample showed a distribution of 58.9% females and 41.1% males (United States Census, 2024).

Results

Descriptive Analysis

A total of 1,463 participants visited primary health clinics in Puerto Rico and underwent PCR testing for COVID-19. The baseline characteristics for participants who tested positive for PCR (*n* = 1,028, 70.3) most of them were female (*n* = 594, 68.9) compared to males (*n* = 434, 72.2). Participants who tested negative for PCR (*n* = 435, 29.7) also reported a similar pattern in terms of male and female distribution being females (*n* = 268, 31.1) and males (*n* = 167, 28.8). The distribution for ethnicity in this sample population was: Hispanic/Latinos were the majority of the population (*n* = 1,446, 98.8), followed by non-Hispanic/Latino (*n* = 13, 0.9). Considering known risk age groups for COVID-19, age was categorized into four different age groups: (H. Zhang, et al., 2022). Age group <18 years (*n* = 240, 16.4), 18–40 years (*n* = 568, 38.8), 41–59 years (n = 429, 29.3), and 60 years or older (*n* = 226, 15.5). The frequency distribution of this age group with COVID-19 diagnosis, varied across age groups. However, the highest percentage of positive PCR testing was in the youngest age group <18 (*n* = 217, 90.4) vs negative PCR results (*n* = 23, 9.6). In contrast, the oldest age groups ≥60 reported fewer positive PCR results (*n* = 121, 53.5) vs patients with negative PCR results (*n* = 105, 46.5). Considering the risk exposure of participants, such as having contact with a confirmed COVID-19 case, the highest percentage of the population reported not having contact with a COVID-19 confirmed case (*n*=896, 61.2) compared to participants who reported having contact (*n* = 567, 38.8). Although the smallest percentage of the population reported having contact with a confirmed COVID-19 case, participants who reported contact reported the largest number of positive PCR results obtained in that group (*n* = 507, 89.4) vs (*n* = 60, 10.6) that reported a negative PCR result.

Results for outcome variables indicated that most participants were non-obese (*n* = 1,072, 73.3) compared to obese participants (*n* = 391, 26.7). Looking at groups of obese participants and their COVID-19 diagnosis, most tested positive (*n* = 301, 77) vs participants that tested negative (*n* = 90, 23.0). The second evaluation suggested that a more significant proportion of the sample population was considered non-diabetic (*n* = 1,294, 88.4) vs the side of the population that reported having diabetes (*n* = 169, 11.6). Considering the diabetic population, most participants tested PCR positive (*n* = 116, 68.6) when compared with the diabetic groups that tested PCR negative (*n* = 53, 31.4). Results for participants that reported having a diagnosis of hypertension, it was clear that most of the population was not diagnosed as hypertensive (*n* = 1,139, 77.9) when compared to the side of the population that was diagnosed as hypertensive (n = 324, 22.1). A similar pattern was observed when looking at the population's hypertension status and a COVID-19 diagnosis. The majority hypertensive population reported a positive PCR test (*n* = 234, 72.2) when compared to the hypertensive population that tested negative for COVID-19 (*n* = 90, 27.8). Table 13 depicts the descriptive statistics for these results.

Table 13

Selected Characteristics of the Study Population by COVID-19 Diagnosis Status (N = 1,463)

Baseline characteristic	COVID-19 diagnosis positive PCR result *n = 1,028 (70.3)*	COVID-19 diagnosis negative PCR result *n = 435 (29.7)*	Total *N = 1,463 (100.0)*
Sex			
Male	434 (72.2)	167 (27.8.)	601 (41.1)
Female	594 (68.9)	268 (31.1)	862 (58.9)
Ethnicity			
Hispanic/Latino	1014 (70.1)	432 (29.9)	1446 (98.8)
Non-Hispanic/Latino	11 (15.4)	2 (84.6)	13 (0.9)
Unknown	3 (75.0)	1 (25.0)	4 (0.3)
Age group			
< 18	217 (90.4)	23 (9.6)	240 (16.4)
18–40	409 (72.0)	159 (28.0)	568 (38.8)
41–59	281 (65.5)	148 (34.5)	429 (29.3)
≥ 60	121 (53.5)	105 (46.5)	226 (29.3)
Person exposure			
Contact with positive COVID-19 case	507 (89.4)	60 (10.6)	567 (38.8)
Noncontact with positive COVID-19 case	521 (58.1)	375 (41.9)	896 (61.2)
Obesity status			
Obese	301 (77.0)	90 (23.0)	391 (26.7)
Non-obese	727 (67.8)	345 (32.2)	1072 (73.3)
Diabetes status			
Diabetic	116 (68.6)	53 (31.4)	169 (11.6)
Non-diabetic	912 (70.5))	382 (29.5)	1294 (88.4)
Hypertension status			
Hypertensive	234 (72.2)	90 (27.8)	324 (22.1)
Non-hypertensive	794 (69.7)	345 (30.3)	1,139 (77.9)

Inferential Analysis

A priori power analysis using Gpower as statistical software was conducted. Assuming alpha = 0.05 and one predictor variable of obesity, a minimum sample size of 36 participants was required to achieve a power of 0.80. Results from the Chi-square analysis to examine the association between obesity and COVID-19 diagnosis without control variables were considered significant with small effect size, X^2 (1, N = 1,463) = 11.5, $p < .001$, *phi* = 0.89, suggesting a statistically significant association between obesity and COVID-19 diagnosis. Similarly, individuals with obesity reported 1.59 times higher odds of being diagnosed with COVID-19 (*OR* = 1.59, 95% *CI* [1.214 - 2.075]). Table 14 depicted the descriptive statistics for these results.

Table 14

Cross-Tabulation for Obesity and COVID-19 Diagnosis

Case Processing Summary for Obesity and COVID-19 Diagnosis

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
Obesity * COVID-19 Diagnosis	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests for Obesity and COVID-19 Diagnosis

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	11.518[a]	1	<.001		
Continuity Correction[b]	11.084	1	<.001		
Likelihood Ratio	11.901	1	<.001		
Fisher's Exact Test				<.001	<.001
Linear-by-Linear Association	11.511	1	<.001		
N of Valid Cases	1463				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 116.26.
b. Computed only for a 2x2 table

Symmetric Measures for Obesity and COVID-19 Diagnosis

		Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
Nominal by Nominal	Phi	.089			<.001
	Cramer's V	.089			<.001
Interval by Interval	Pearson's R	.089	.025	3.405	<.001[c]
Ordinal by Ordinal	Spearman Correlation	.089	.025	3.405	<.001[c]
N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate (Odds Ratio) for Obesity and COVID-19 Diagnosis

	Value	95% Confidence Interval	
		Lower	Upper
Odds Ratio for obesity (No / Yes)	1.587	1.214	2.075
For cohort COVID-19 diagnosis = Negative	1.398	1.144	1.709
For cohort COVID-19 diagnosis = Positive	.881	.823	.943
N of Valid Cases	1463		

A chi-square test of association using the Yates Continuity method was conducted to examine the association between obesity and COVID-19 diagnosis, controlling for person exposure, defined as having contact with a COVID-19 prior to the onset of symptoms. The results were statistically significant when there was no exposure to a COVID-19 case, χ^2 (1, N = 1,463) = 12.6, p < .001, *phi* = 0.121. When patients reported exposure to known COVID-19 case the results were not significant, χ^2 (1, N = 1,463) = 0.00, p = .95, *phi* = 0.009. This concludes that there is a strong association between obesity and COVID-19 when participants were not exposed to COVID-19 cases prior to the onset of their symptoms. However, when analyzing the entire sample s (N = 1,463), regardless of whether they had exposure to known COVID-19 cases, results were statistically significant, χ^2 (1, N = 1,463) = 11.1, p < .001, *phi* = 0.089. Considering the reported effect of the control variables of no exposure ($n = 896$), $p < .001$, and individuals with exposure ($n = 567$), $p = .95$, the overall significant result is mainly driven by individuals who have not reported contact with known COVID-19 cases. Odds ratio estimates support this interpretation. In the full sample, obese individuals were 1.59 times more likely to test positive for COVID-19 compared to non-obese individuals (*OR* = 1.59, 95% *CI* [1.21, 2.08]). Among individuals without exposure, the odds of testing positive were significantly higher for obese participants (*OR* = 1.79, 95% *CI* [1.30, 2.45]). In contrast, among exposed individuals, obesity was not significantly associated with testing positive (*OR* = 1.07, 95% *CI* [0.59, 1.96]). Table 15 depicts the descriptive statistics for these results.

Table 15

Cross-Tabulation Analysis for Obesity and COVID-19 Diagnosis When Controlled by Person Exposure

Case Processing Summary for Obesity and COVID-19 Diagnosis when controlled by person exposure

	Valid		Cases Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
Obesity * COVID-19 Diagnosis * Person Exposure	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests for Obesity and COVID-19 Diagnosis Controlled by Person Exposure

Person Exposure		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
No	Pearson Chi-Square	13.181[c]	1	<.001		
	Continuity Correction[b]	12.626	1	<.001		
	Likelihood Ratio	13.460	1	<.001		
	Fisher's Exact Test				<.001	<.001
	Linear-by-Linear Association	13.166	1	<.001		
	n of Valid Cases	896				
Yes	Pearson Chi-Square	.048[d]	1	.827		
	Continuity Correction[b]	.004	1	.947		
	Likelihood Ratio	.048	1	.826		
	Fisher's Exact Test				.880	.480
	Linear-by-Linear Association	.048	1	.827		
	n of Valid Cases	567				
Total	Pearson Chi-Square	11.518[a]	1	<.001		
	Continuity Correction[b]	11.084	1	<.001		
	Likelihood Ratio	11.901	1	<.001		
	Fisher's Exact Test				<.001	<.001
	Linear-by-Linear Association	11.511	1	<.001		
	N of Valid Cases	1463				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 116.26.
b. Computed only for a 2x2 table
c. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 97.52.
d. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.72.

Symmetric Measures for Obesity and COVID-19 Diagnosis Controlled by Person Exposure

Person Exposure			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
No	Nominal by Nominal	Phi	.121			<.001
		Cramer's V	.121			<.001
	Interval by Interval	Pearson's R	.121	.032	3.653	<.001[c]
	Ordinal by Ordinal	Spearman Correlation	.121	.032	3.653	<.001[c]
	n of Valid Cases		896			
Yes	Nominal by Nominal	Phi	.009			.827
		Cramer's V	.009			.827
	Interval by Interval	Pearson's R	.009	.041	.219	.827[c]
	Ordinal by Ordinal	Spearman Correlation	.009	.041	.219	.827[c]
	n of Valid Cases		567			
Total	Nominal by Nominal	Phi	.089			<.001
		Cramer's V	.089			<.001
	Interval by Interval	Pearson's R	.089	.025	3.405	<.001[c]
	Ordinal by Ordinal	Spearman Correlation	.089	.025	3.405	<.001[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate for Obesity and COVID-19 Diagnosis Controlled by Person Exposure

Person Exporure		Value	95% Confidence Interval Lower	Upper
No	Odds Ratio for obesity (No / Yes)	1.787	1.303	2.449
	For cohort PCR = Negative	1.429	1.163	1.756
	For cohort PCR= Positive	.800	.716	.895
	n of Valid Cases	896		
Yes	Odds Ratio for obesity (No / Yes)	1.070	.585	1.957
	For cohort PCR = Negative	1.062	.618	1.827
	For cohort PCR = Positive	.993	.933	1.057
	n of Valid Cases	567		
Total	Odds Ratio for obesity (No / Yes)	1.587	1.214	2.075
	For cohort PCR = Negative	1.398	1.144	1.709
	For cohort PCR = Positive	.881	.823	.943
	N of Valid Cases	1463		

A chi-square test of association using Yates Continuity was conducted to examine the association between obesity and COVID-19 diagnosis, controlling for sex. Results were statistically significant when sex of the participants were female, χ^2 (1, n = 862) = 8.46, $p < .004$, *phi* = 0.102, indicating a small effect size. In contrast, results for male participants were not considered significant, χ^2 (1, n = 601) = 2.91, $p = .09$, *phi* = 0.074. However, the combined effect of all individuals (N = 1,436), regardless of sex status, results were considered significant, χ^2 (1, N = 1,436) = 11.1, $p < .001$, *phi* = 0.089. Results strongly suggest that obesity is associated with the dependent variable of COVID-19 diagnosis across the entire sample. Considering the reported effect of sex within the population and the association of obese individuals and COVID-19 diagnosis, results indicate that sex can modify the relationship between variables. Adjusted Odds ratio analysis reflected that obese females were significantly more likely to test positive for COVID-19 than non-obese females, *OR* = 1.67, 95% *CI* [1.19, 2.33], indicating a 67% increase in odds. Among males, the odds of testing positive were also higher for obese individuals (*OR* = 1.51), but this result was not statistically significant, 95% *CI* [0.97, 2.35]. Obesity was associated with significantly higher odds of testing positive for COVID-19 in the total sample, *OR* = 1.59, 95% *CI* [1.21, 2.08], suggesting that obesity may be a general risk factor for COVID-19 infection, particularly among females. Overall results indicated that sex as a control variable has a meaningful effect on obesity and COVID-19. However, females drove the statistical significance compared to males, which did not reflect the same pattern. Table 16 depicts the descriptive statistics for these results.

Table 16

Cross-Tabulation Analysis for Obesity and COVID-19 Diagnosis when Controlled for Sex

Case Processing Summary for Obesity and COVID-19 Diagnosis when Controlled by Sex

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
Obesity_COVID-19 Diagnosis sex	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests Obesity and COVID-19 Controlled by Sex

	sex	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Female	Pearson Chi-Square	8.939[c]	1	.003		
	Continuity Correction[b]	8.460	1	.004		
	Likelihood Ratio	9.225	1	.002		
	Fisher's Exact Test				.003	.002
	Linear-by-Linear Association	8.929	1	.003		
	n of Valid Cases	862				
Male	Pearson Chi-Square	3.287[d]	1	.070		
	Continuity Correction[b]	2.910	1	.088		
	Likelihood Ratio	3.404	1	.065		
	Fisher's Exact Test				.086	.042
	Linear-by-Linear Association	3.282	1	.070		
	n of Valid Cases	601				
Total	Pearson Chi-Square	11.518[a]	1	<.001		
	Continuity Correction[b]	11.084	1	<.001		
	Likelihood Ratio	11.901	1	<.001		
	Fisher's Exact Test				<.001	<.001
	Linear-by-Linear Association	11.511	1	<.001		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 116.26.
b. Computed only for a 2x2 table
c. 0 cells (.0%) have expected count less than 5. The minimum expected count is 77.42.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 39.46.

Symmetric Measures Tests Obesity and COVID-19 Controlled by Sex

sex			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
Female	Nominal by Nominal	Phi	.102			.003
		Cramer's V	.102			.003
	Interval by Interval	Pearson's R	.102	.032	3.002	.003[c]
	Ordinal by Ordinal	Spearman Correlation	.102	.032	3.002	.003[c]
	n of Valid Cases		862			
Male	Nominal by Nominal	Phi	.074			.070
		Cramer's V	.074			.070
	Interval by Interval	Pearson's R	.074	.039	1.815	.070[c]
	Ordinal by Ordinal	Spearman Correlation	.074	.039	1.815	.070[c]
	n of Valid Cases		601			
Total	Nominal by Nominal	Phi	.089			<.001
		Cramer's V	.089			<.001
	Interval by Interval	Pearson's R	.089	.025	3.405	<.001[c]
	Ordinal by Ordinal	Spearman Correlation	.089	.025	3.405	<.001[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate Tests for Obesity and COVID-19 Controlled by Sex

sex		Value	95% Confidence Interval Lower	Upper
Female	Odds Ratio for obesity (No / Yes)	1.666	1.190	2.332
	For cohort COVID-19 diagnosis = Negative	1.439	1.122	1.845
	For cohort COVID-19 diagnosis = Positive	.864	.790	.945
	n of Valid Cases	862		
Male	Odds Ratio for obesity (No / Yes)	1.508	.965	2.354
	For cohort COVID-19 diagnosis = Negative	1.357	.964	1.910
	For cohort COVID-19 diagnosis = Positive	.900	.810	1.000
	n of Valid Cases	601		
Total	Odds Ratio for obesity (No / Yes)	1.587	1.214	2.075
	For cohort COVID-19 diagnosis = Negative	1.398	1.144	1.709
	For cohort COVID-19 diagnosis = Positive	.881	.823	.943
	N of Valid Cases	1463		

Controlling for age groups, the chi-square test of association using Yates Continuity indicated that age group < 18 χ^2 (1, *n* = 240) = 0.068, *p* = .79, *phi* = 0.043 reported no significant association and a weak effect size. Following the same pattern, age group 41 – 59 χ^2 (1, *n* = 429) = 3.34, *p* = .67, *phi* = 0.093 reported no significant association and a weak effect size for obesity and COVID-19 diagnosis. However, obesity was significantly associated with COVID-19 in the 18 – 40 and ≥ 60. Significant association and a weak to moderate effect size for age group 18-40 χ^2 (1, *n* = 568) = 9.74, *p* = .002, *phi* = 0.14 was reported. The strongest association and effect size was reported for age group ≥ 60 χ^2 (1, *n* = 226) =10.58, *p* < .001, *phi* = 0.23. Overall, Chi-square and continuity correction for all age groups established a significant association between obesity and COVID-19 diagnosis χ^2 (1, *N* = 1,463) =11.08, *p* < .001, *phi* = 0.09.

However, based on the mentioned phi value, the overall strength is weak, with obesity having the strongest effect in older adults ≥ 60. Crude odds ratio analysis suggested that across all age groups, obesity is associated with a positive COVID-19 diagnosis (*OR* = 1.59, 95% *CI* [1.21 - 2.08]), and this association is statistically significant diagnosis χ^2 (1, *N* = 1,463) = 11.08, *p* < .001, *phi* = 0.09. However, variation exists within individual age groups. Table 17 depicts the descriptive statistics for these results.

Table 17

Cross-Tabulation Analysis for Obesity and COVID-19 Diagnosis When Controlled by Age Group

Case Processing Summary for Obesity and COVID-19 Diagnosis when controlled by age group

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
obesity * COVID-19 diagnosis * age group	1463	100.0%	0	0.0%	1463	100.0%

Chi-square tests obesity and COVID-19 diagnosis when controlled by age group

Age_Group		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
<18	Pearson Chi-Square	.444[c]	1	.505		
	Continuity Correction[b]	.068	1	.794		
	Likelihood Ratio	.516	1	.472		
	Fisher's Exact Test				1.000	.435
	Linear-by-Linear Association	.443	1	.506		
	n of Valid Cases	240				
18-40	Pearson Chi-Square	10.425[d]	1	.001		
	Continuity Correction[b]	9.758	1	.002		
	Likelihood Ratio	11.054	1	<.001		
	Fisher's Exact Test				.001	<.001
	Linear-by-Linear Association	10.406	1	.001		
	n of Valid Cases	568				
41-59	Pearson Chi-Square	3.735[e]	1	.053		
	Continuity Correction[b]	3.343	1	.067		
	Likelihood Ratio	3.780	1	.052		
	Fisher's Exact Test				.061	.033
	Linear-by-Linear Association	3.727	1	.054		
	n of Valid Cases	429				
≥60	Pearson Chi-Square	11.643[f]	1	<.001		
	Continuity Correction[b]	10.580	1	.001		
	Likelihood Ratio	12.129	1	<.001		
	Fisher's Exact Test				<.001	<.001
	Linear-by-Linear Association	11.592	1	<.001		
	n of Valid Cases	226				
Total	Pearson Chi-Square	11.518[a]	1	<.001		
	Continuity Correction[b]	11.084	1	<.001		
	Likelihood Ratio	11.901	1	<.001		
	Fisher's Exact Test				<.001	<.001
	Linear-by-Linear Association	11.511	1	<.001		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 116.26.
b. Computed only for a 2x2 table
c. 1 cells (25.0%) have expected count less than 5. The minimum expected count is 1.82.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 43.39.
e. 0 cells (.0%) have expected count less than 5. The minimum expected count is 57.27.
f. 0 cells (.0%) have expected count less than 5. The minimum expected count is 23.69.

Symmetric Measures Tests Obesity and COVID-19 Diagnosis when Controlled by Age Group

Age_Group			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
<18	Nominal by Nominal	Phi	.043			.505
		Cramer's V	.043			.505
	Interval by Interval	Pearson's R	.043	.050	.664	.507[c]
	Ordinal by Ordinal	Spearman Correlation	.043	.050	.664	.507[c]
	n of Valid Cases		240			
18-40	Nominal by Nominal	Phi	.135			.001
		Cramer's V	.135			.001
	Interval by Interval	Pearson's R	.135	.038	3.253	.001[c]
	Ordinal by Ordinal	Spearman Correlation	.135	.038	3.253	.001[c]
	n of Valid Cases		568			
41-59	Nominal by Nominal	Phi	.093			.053
		Cramer's V	.093			.053
	Interval by Interval	Pearson's R	.093	.047	1.937	.053[c]
	Ordinal by Ordinal	Spearman Correlation	.093	.047	1.937	.053[c]
	n of Valid Cases		429			
≥60	Nominal by Nominal	Phi	.227			<.001
		Cramer's V	.227			<.001
	Interval by Interval	Pearson's R	.227	.061	3.488	<.001[c]
	Ordinal by Ordinal	Spearman Correlation	.227	.061	3.488	<.001[c]
	n of Valid Cases		226			
Total	Nominal by Nominal	Phi	.089			<.001
		Cramer's V	.089			<.001
	Interval by Interval	Pearson's R	.089	.025	3.405	<.001[c]
	Ordinal by Ordinal	Spearman Correlation	.089	.025	3.405	<.001[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate Tests obesity and COVID-19 Diagnosis when Controlled by Age Group

Age_Group		Value	95% Confidence Interval Lower	Upper
<18	Odds Ratio for obesity (No / Yes)	1.990	.253	15.633
	For cohort COVID-19 diagnosis = Negative	1.891	.270	13.274
	For cohort COVID-19 diagnosis = Positive	.950	.847	1.066
	n of Valid Cases	240		
18-40	Odds Ratio for obesity (No / Yes)	2.107	1.332	3.333
	For cohort COVID-19 diagnosis = Negative	1.756	1.220	2.527
	For cohort COVID-19 diagnosis = Positive	.833	.755	.920
	n of Valid Cases	568		
41-59	Odds Ratio for obesity (No / Yes)	1.508	.993	2.290
	For cohort COVID-19 diagnosis = Negative	1.315	.990	1.747
	For cohort COVID-19 diagnosis = Positive	.872	.761	.998
	n of Valid Cases	429		
≥60	Odds Ratio for obesity (No / Yes)	3.240	1.615	6.500
	For cohort COVID-19 diagnosis = Negative	2.062	1.264	3.366
	For cohort COVID-19 diagnosis = Positive	.637	.509	.796
	n of Valid Cases	226		
Total	Odds Ratio for obesity (No / Yes)	1.587	1.214	2.075
	For cohort COVID-19 diagnosis = Negative	1.398	1.144	1.709
	For cohort COVID-19 diagnosis = Positive	.881	.823	.943
	N of Valid Cases	1463		

Results from the Chi-square analysis to examine the association between hypertension and COVID-19 diagnosis were not significant, χ^2 (1, N = 1,463) = 0.65, p = .421, *phi* = 0.23, suggesting that there is no association between hypertension and COVID-19 diagnosis.

Table 18

Cross-Tabulation Analysis for Hypertension and COVID-19 Diagnosis

Case Processing Summary for Hypertension and COVID-19 Diagnosis

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
Hypertension * COVID-19 Diagnosis	1463	100.0%	0	0.0%	1463	100.0%

Cross tabulation for Hypertension and COVID-19 Diagnosis

			COVID-19 Diagnosis		Total
			Negative	Positive	
Hypertension	No	Count	345	794	1139
		% within hypertension	30.3%	69.7%	100.0%
		% within COVID-19 Diagnosis	79.3%	77.2%	77.9%
		% of Total	23.6%	54.3%	77.9%
	Yes	Count	90	234	324
		% within hypertension	27.8%	72.2%	100.0%
		% within COVID-19 Diagnosis	20.7%	22.8%	22.1%
		% of Total	6.2%	16.0%	22.1%
	Total	Count	435	1028	1463
		% within hypertension	29.7%	70.3%	100.0%
		% within COVID-19 Diagnosis	100.0%	100.0%	100.0%
		% of Total	29.7%	70.3%	100.0%

Chi-Square Tests for Hypertension and COVID-19 Diagnosis

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.762[a]	1	.383		
Continuity Correction[b]	.646	1	.421		
Likelihood Ratio	.769	1	.381		
Fisher's Exact Test				.409	.211
Linear-by-Linear Association	.761	1	.383		
N of Valid Cases	1463				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 96.34.

b. Computed only for a 2x2 table

Symmetric Measures for Hypertension and COVID-19 Diagnosis

		Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
Nominal by Nominal	Phi	.023			.383
	Cramer's V	.023			.383
Interval by Interval	Pearson's R	.023	.026	.872	.383[c]
Ordinal by Ordinal	Spearman Correlation	.023	.026	.872	.383[c]
N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate for Hypertension and COVID-19 Diagnosis

	Value	95% Confidence Interval	
		Lower	Upper
Odds Ratio for hypertension (No / Yes)	1.130	.859	1.486
For cohort COVID-19 diagnosis = Negative	1.090	.896	1.327
For cohort COVID-19 diagnosis = Positive	.965	.893	1.043
N of Valid Cases	1463		

When evaluating the association of hypertension and COVID-19 diagnosis when controlling by person exposure, the overall chi-square using Yates continuity correction was not significant for both hypertensive that were exposed and not exposed, with a phi value close to zero suggesting no strong relationship between variables χ^2 (1, N = 1,463) = 0.64, p = .42, *phi* = 0.23. Results from the risk estimate suggest that none of the odds ratios are statistically significant, since all the confidence intervals include 1 (*OR* = 1.13, 95% *CI* [0.86 - 1.49]), suggesting that there is no strong evidence that hypertension affects COVID-19 diagnosis. Although some odd ratios reflect a slight increase or decrease risk, these results could be due to random variation. Table 19 depicts the descriptive statistics for these results.

Table 19

Cross-Tabulation Analysis for Hypertension and COVID-19 Diagnosis When Controlled by Person Exposure

Case Processing Summary for Hypertension and COVID-19 Diagnosis when Controlled by Person Exposure

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
hypertension*COVID-19 diagnosis * person exposure	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests hypertension and COVID-19 Diagnosis when Controlled by Person Exposure

person_exposure		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
No	Pearson Chi-Square	1.998[c]	1	.158		
	Continuity Correction[b]	1.773	1	.183		
	Likelihood Ratio	2.015	1	.156		
	Fisher’s Exact Test				.164	.091
	Linear-by-Linear Association	1.996	1	.158		
	n of Valid Cases	896				
Yes	Pearson Chi-Square	1.190[d]	1	.275		
	Continuity Correction[b]	.861	1	.353		
	Likelihood Ratio	1.137	1	.286		
	Fisher’s Exact Test				.328	.176
	Linear-by-Linear Association	1.188	1	.276		
	n of Valid Cases	567				
Total	Pearson Chi-Square	.762[a]	1	.383		
	Continuity Correction[b]	.646	1	.421		
	Likelihood Ratio	.769	1	.381		
	Fisher’s Exact Test				.409	.211
	Linear-by-Linear Association	.761	1	.383		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 96.34.
b. Computed only for a 2x2 table
c. 0 cells (.0%) have expected count less than 5. The minimum expected count is 81.61.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 13.65.

Symmetric Measures hypertension and COVID-19 Diagnosis when Controlled by Person Exposure

person exposure			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
No	Nominal by Nominal	Phi	.047			.158
		Cramer's V	.047			.158
	Interval by Interval	Pearson's R	.047	.033	1.413	.158[c]
	Ordinal by Ordinal	Spearman Correlation	.047	.033	1.413	.158[c]
		n of Valid Cases	896			
Yes	Nominal by Nominal	Phi	-.046			.275
		Cramer's V	.046			.275
	Interval by Interval	Pearson's R	-.046	.045	-1.090	.276[c]
	Ordinal by Ordinal	Spearman Correlation	-.046	.045	-1.090	.276[c]
		n of Valid Cases	567			
Total	Nominal by Nominal	Phi	.023			.383
		Cramer's V	.023			.383
	Interval by Interval	Pearson's R	.023	.026	.872	.383[c]
	Ordinal by Ordinal	Spearman Correlation	.023	.026	.872	.383[c]
		N of Valid Cases	1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate Hypertension and COVID-19 Diagnosis when Controlled by Person Exposure

person exposure		Value	95% Confidence Interval Lower	Upper
No	Odds Ratio for hypertension (No / Yes)	1.265	.913	1.753
	For cohort COVID-19 diagnosis = Negative	1.151	.942	1.406
	For cohort COVID-19 diagnosis = Positive	.910	.802	1.032
	n of Valid Cases	896		
Yes	Odds Ratio for hypertension (No / Yes)	.717	.394	1.306
	For cohort COVID-19 diagnosis = Negative	.745	.440	1.261
	For cohort COVID-19 diagnosis = Positive	1.039	.965	1.118
	n of Valid Cases	567		
Total	Odds Ratio for hypertension (No / Yes)	1.130	.859	1.486
	For cohort COVID-19 diagnosis = Negative	1.090	.896	1.327
	For cohort COVID-19 diagnosis = Positive	.965	.893	1.043
	N of Valid Cases	1463		

When controlling for sex, the overall chi-square using Yates continuity correction was not statistically significant for both hypertension and COVID-19 diagnosis, with a phi value close to zero suggesting no strong relationship between variables χ^2 (1, *N* = 1,463) = 0.64, *p* = .42, *phi* = 0.23. Result from the risk estimate, suggest that none of the odd's ratio are statistically significant, since all the confidence intervals include 1 (*OR* = 1.13, 95% *CI* [0.86 - 1.49]), suggesting that there is no strong evidence that hypertension affects COVID-19 diagnosis. Table 20 depicts the descriptive statistics for these results.

Table 20

Cross-Tabulation Analysis for Hypertension and COVID-19 Diagnosis When Controlled by Sex

Case Processing Summary for Hypertension and COVID-19 Diagnosis when Controlled by Sex

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
hypertension*COVID-19 diagnosis * sex	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests for Hypertension and COVID-19 Diagnosis when Controlled by Sex

sex		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Female	Pearson Chi-Square	.913[c]	1	.339		
	Continuity Correction[b]	.755	1	.385		
	Likelihood Ratio	.924	1	.336		
	Fisher's Exact Test				.384	.193
	Linear-by-Linear Association	.912	1	.340		
	n of Valid Cases	862				
Male	Pearson Chi-Square	.071[d]	1	.790		
	Continuity Correction[b]	.023	1	.878		
	Likelihood Ratio	.071	1	.790		
	Fisher's Exact Test				.822	.443
	Linear-by-Linear Association	.071	1	.790		
	n of Valid Cases	601				
Total	Pearson Chi-Square	.762[a]	1	.383		
	Continuity Correction[b]	.646	1	.421		
	Likelihood Ratio	.769	1	.381		
	Fisher's Exact Test				.409	.211
	Linear-by-Linear Association	.761	1	.383		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 96.34.
b. Computed only for a 2x2 table
c. 0 cells (.0%) have expected count less than 5. The minimum expected count is 62.49.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 34.18.

Symmetric Measures Hypertension and COVID-19 Diagnosis when Controlled by Sex

sex			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
Female	Nominal by Nominal	Phi	.033			.339
		Cramer's V	.033			.339
	Interval by Interval	Pearson's R	.033	.033	.955	.340[c]
	Ordinal by Ordinal	Spearman Correlation	.033	.033	.955	.340[c]
	n of Valid Cases		862			
Male	Nominal by Nominal	Phi	.011			.790
		Cramer's V	.011			.790
	Interval by Interval	Pearson's R	.011	.040	.265	.791[c]
	Ordinal by Ordinal	Spearman Correlation	.011	.040	.265	.791[c]
	n of Valid Cases		601			
Total	Nominal by Nominal	Phi	.023			.383
		Cramer's V	.023			.383
	Interval by Interval	Pearson's R	.023	.026	.872	.383[c]
	Ordinal by Ordinal	Spearman Correlation	.023	.026	.872	.383[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

c. Based on normal approximation.

Risk Estimate for Hypertension and COVID-19 Diagnosis when Controlled by Sex

sex		Value	95% Confidence Interval Lower	Upper
Female	Odds Ratio for hypertension (No / Yes)	1.185	.837	1.677
	For cohort COVID-19 diagnosis = Negative	1.126	.880	1.440
	For cohort COVID-19 diagnosis = Positive	.950	.859	1.052
	n of Valid Cases	862		
Male	Odds Ratio for hypertension (No / Yes)	1.062	.680	1.659
	For cohort COVID-19 diagnosis = Negative	1.045	.755	1.447
	For cohort COVID-19 diagnosis = Positive	.984	.872	1.110
	n of Valid Cases	601		
Total	Odds Ratio for hypertension (No / Yes)	1.130	.859	1.486
	For cohort COVID-19 diagnosis = Negative	1.090	.896	1.327
	For cohort COVID-19 diagnosis = Positive	.965	.893	1.043
	N of Valid Cases	1463		

Controlled by age, the only age group that reported a significant association was ≥ 60, meaning that hypertension has a significant association with COVID-19 diagnosis within that specific age group with a phi value greater than zero suggesting a moderate positive relationship χ^2 (1, n = 226) = 22.74, p < .001, *phi* = 0.33. However, when looking at the association and its strength across all age groups, it can be said that results were non-significant with no relationship χ^2 (1, N = 1,463) = 0.65, p = .42, *phi* = 0.02. Evaluating risk estimated, odds ratio analysis suggests that hypertensive patients have 3.94 greater chances of being diagnosed with COVID-19 (*OR* = 3.94, 95% *CI* [2.25 - 9.89]). Across all age groups the odds ratio did not suggest a statistically significant relationship for hypertensive patients being diagnosed with COVID-19 (*OR* = 1.13, 95% *CI* [0.86 - 1.49]). Table 21 depicts the descriptive statistics for these results.

Table 21

Cross-Tabulation Analysis for Hypertension and COVID-19 Diagnosis When Controlled by Age Group

Case Processing Summary Hypertension and COVID-19 Diagnosis when Controlled by Age Group

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
hypertension*COVID-19 diagnosis * age group	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests Hypertension and COVID-19 Diagnosis when Controlled by Age Group

Age Group		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
<18	Pearson Chi-Square	.214[c]	1	.644		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.405	1	.525		
	Fisher's Exact Test				1.000	.817
	Linear-by-Linear Association	.213	1	.645		
	n of Valid Cases	240				
18-40	Pearson Chi-Square	1.954[d]	1	.162		
	Continuity Correction[b]	1.524	1	.217		
	Likelihood Ratio	2.087	1	.149		
	Fisher's Exact Test				.192	.106
	Linear-by-Linear Association	1.951	1	.162		
	n of Valid Cases	568				
41-59	Pearson Chi-Square	2.515[e]	1	.113		
	Continuity Correction[b]	2.195	1	.138		
	Likelihood Ratio	2.538	1	.111		
	Fisher's Exact Test				.119	.069
	Linear-by-Linear Association	2.509	1	.113		
	n of Valid Cases	429				
≥60	Pearson Chi-Square	24.029[f]	1	<.001		
	Continuity Correction[b]	22.735	1	<.001		
	Likelihood Ratio	24.565	1	<.001		
	Fisher's Exact Test				<.001	<.001
	Linear-by-Linear Association	23.923	1	<.001		
	n of Valid Cases	226				
Total	Pearson Chi-Square	.762[a]	1	.383		
	Continuity Correction[b]	.646	1	.421		
	Likelihood Ratio	.769	1	.381		
	Fisher's Exact Test				.409	.211
	Linear-by-Linear Association	.761	1	.383		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 96.34.
b. Computed only for a 2x2 table
c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .19.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 14.28.
e. 0 cells (.0%) have expected count less than 5. The minimum expected count is 57.61.
f. 0 cells (.0%) have expected count less than 5. The minimum expected count is 48.32.

Symmetric Measures Hypertension and COVID-19 Diagnosis when Controlled by Age Group

Age Group			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
<18	Nominal by Nominal	Phi	.030			.644
		Cramer's V	.030			.644
	Interval by Interval	Pearson's R	.030	.011	.461	.645[c]
	Ordinal by Ordinal	Spearman Correlation	.030	.011	.461	.645[c]
	n of Valid Cases		240			
18-40	Nominal by Nominal	Phi	.059			.162
		Cramer's V	.059			.162
	Interval by Interval	Pearson's R	.059	.038	1.398	.163[c]
	Ordinal by Ordinal	Spearman Correlation	.059	.038	1.398	.163[c]
	n of Valid Cases		568			
41-59	Nominal by Nominal	Phi	.077			.113
		Cramer's V	.077			.113
	Interval by Interval	Pearson's R	.077	.048	1.587	.113[c]
	Ordinal by Ordinal	Spearman Correlation	.077	.048	1.587	.113[c]
	n of Valid Cases		429			
≥60	Nominal by Nominal	Phi	.326			<.001
		Cramer's V	.326			<.001
	Interval by Interval	Pearson's R	.326	.062	5.162	<.001[c]
	Ordinal by Ordinal	Spearman Correlation	.326	.062	5.162	<.001[c]
	n of Valid Cases		226			
Total	Nominal by Nominal	Phi	.023			.383
		Cramer's V	.023			.383
	Interval by Interval	Pearson's R	.023	.026	.872	.383[c]
	Ordinal by Ordinal	Spearman Correlation	.023	.026	.872	.383[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate Hypertension and COVID-19 Diagnosis when Controlled by Age Group

Age Group		Value	95% Confidence Interval Lower	Upper
<18	For cohort COVID-19 diagnosis = Positive	.903	.867	.942
	n of Valid Cases	240		
18-40	Odds Ratio for hypertension (No / Yes)	1.660	.810	3.400
	For cohort COVID-19 diagnosis = Negative	1.470	.830	2.604
	For cohort COVID-19 diagnosis = Positive	.885	.765	1.025
	n of Valid Cases	568		
41-59	Odds Ratio for hypertension (No / Yes)	1.398	.923	2.118
	For cohort COVID-19 diagnosis = Negative	1.249	.944	1.653
	For cohort COVID-19 diagnosis = Positive	.893	.780	1.024
	n of Valid Cases	429		
≥60	Odds Ratio for hypertension (No / Yes)	3.936	2.250	6.887
	For cohort COVID-19 diagnosis = Negative	2.131	1.528	2.973
	For cohort COVID-19 diagnosis = Positive	.541	.419	.699
	n of Valid Cases	226		
Total	Odds Ratio for hypertension (No / Yes)	1.130	.859	1.486
	For cohort COVID-19 diagnosis = Negative	1.090	.896	1.327
	For cohort COVID-19 diagnosis = Positive	.965	.893	1.043
	N of Valid Cases	1463		

Results from the Chi-square analysis to examine the association between DM and COVID-19 diagnosis were not significant, χ^2 (1, *N* = 1,463) = 0.16, *p* = .687, *phi* = 0.13, suggesting that there is no association between diabetes and COVID-19 diagnosis. Individuals with diabetes reported 0.917 higher odds of being diagnosed with COVID-19 (*OR* = 0.917, 95% *CI* [0.648 - 1.296]). However, since *CI* includes one, results are not considered significant. Table 22 depicts the descriptive statistics for these results.

Table 22

Cross-Tabulation Analysis for Diabetes Mellitus and COVID-19 Diagnosis

Case Processing Summary for Diabetes Mellitus and COVID-19 Diagnosis

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
Diabetes * COVID-19 Diagnosis	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests for Diabetes Mellitus and COVID-19 Diagnosis

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.242[a]	1	.623		
Continuity Correction[b]	.162	1	.687		
Likelihood Ratio	.240	1	.624		
Fisher's Exact Test				.655	.341
Linear-by-Linear Association	.242	1	.623		
N of Valid Cases	1463				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 50.25.
b. Computed only for a 2x2 table

Symmetric Measures for Diabetes Mellitus and COVID-19 Diagnosis

		Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
Nominal by Nominal	Phi	-.013			.623
	Cramer's V	.013			.623
Interval by Interval	Pearson's R	-.013	.026	-.492	.623[c]
Ordinal by Ordinal	Spearman Correlation	-.013	.026	-.492	.623[c]
N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate for Diabetes Mellitus and COVID-19 Diagnosis

	Value	95% Confidence Interval Lower	Upper
Odds Ratio for diabetes (No / Yes)	.917	.648	1.296
For cohort COVID-19 diagnosis = Negative	.941	.742	1.195
For COVID-19 diagnosis = Positive	1.027	.922	1.144
N of Valid Cases	1463		

Considering the association between DM and positive COVID-19 diagnosis. When controlling by persons exposure, Chi-square analysis using Yates continuity correction suggested that there is no significant association between the variables on the exposed, non-exposed and across all groups with no relationship established χ^2 (1, N = 1,463) = 0.16, p = .69, *phi* = 0.013. Odds ratio analysis suggested that across all groups exposed and non-exposed diabetic patients did not had significant risk of having a positive COVID-19 diagnosis (*OR* = 0.91, 95% *CI* [0.65 - 1.29]). Overall chi-square analysis and phi effect size and odds ratio analysis suggested that diabetes was not a major predictor or risk factor for COVID-19 diagnosis regardless of their exposure. Table 23 depicts the descriptive statistics for these results.

Table 23

Cross-Tabulation Analysis for Diabetes Mellitus and COVID-19 Diagnosis When Controlled by Person Exposure

Case Processing Summary Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Person Exposure

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
diabetes * COVID-19 diagnosis * person exposure	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Person Exposure

Person exposure		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
No	Pearson Chi-Square	.002[c]	1	.964		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.002	1	.964		
	Fisher's Exact Test				1.000	.522
	Linear-by-Linear Association	.002	1	.964		
	n of Valid Cases	896				
Yes	Pearson Chi-Square	.396[d]	1	.529		
	Continuity Correction[b]	.169	1	.681		
	Likelihood Ratio	.376	1	.540		
	Fisher's Exact Test				.513	.327
	Linear-by-Linear Association	.396	1	.529		
	n of Valid Cases	567				
Total	Pearson Chi-Square	.242[a]	1	.623		
	Continuity Correction[b]	.162	1	.687		
	Likelihood Ratio	.240	1	.624		
	Fisher's Exact Test				.655	.341
	Linear-by-Linear Association	.242	1	.623		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 50.25.
b. Computed only for a 2x2 table
c. 0 cells (.0%) have expected count less than 5. The minimum expected count is 44.78.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 6.56.

Symmetric Measures Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Person Exposure

Person exposure			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
No	Nominal by Nominal	Phi	-.002			.964
		Cramer's V	.002			.964
	Interval by Interval	Pearson's R	-.002	.033	-.045	.964[c]
	Ordinal by Ordinal	Spearman Correlation	-.002	.033	-.045	.964[c]
	n of Valid Cases		896			
Yes	Nominal by Nominal	Phi	-.026			.529
		Cramer's V	.026			.529
	Interval by Interval	Pearson's R	-.026	.045	-.629	.530[c]
	Ordinal by Ordinal	Spearman Correlation	-.026	.045	-.629	.530[c]
	n of Valid Cases		567			
Total	Nominal by Nominal	Phi	-.013			.623
		Cramer's V	.013			.623
	Interval by Interval	Pearson's R	-.013	.026	-.492	.623[c]
	Ordinal by Ordinal	Spearman Correlation	-.013	.026	-.492	.623[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Person Exposure

Person exposure		Value	95% Confidence Interval Lower	Upper
No	Odds Ratio for diabetes (No / Yes)	.991	.658	1.491
	For cohort COVID-19 diagnosis= Negative	.995	.785	1.261
	For cohort COVID-19 diagnosis = Positive	1.004	.845	1.192
	n of Valid Cases	896		
Yes	Odds Ratio for diabetes (No / Yes)	.775	.350	1.718
	For cohort COVID-19 diagnosis= Negative	.798	.398	1.601
	For cohort COVID-19 diagnosis = Positive	1.030	.932	1.139
	n of Valid Cases	567		
Total	Odds Ratio for diabetes (No / Yes)	.917	.648	1.296
	For cohort COVID-19 diagnosis= Negative	.941	.742	1.195
	For cohort COVID-19 diagnosis = Positive	1.027	.922	1.144
	N of Valid Cases	1463		

The performed Chi-square test of association using Yates continuity to evaluate the association between diabetes and COVID-19 diagnosis, controlling for sex, provided a non-significant association across all groups (male / female) with negligible relationship on Phi analysis χ^2 (1, N = 1,463) = 0.16, p = .69, *phi* = - 0.13. Odds ratio analysis suggested no association for diabetes and COVID-19 diagnosis across all groups (*OR* = 0.91, 95% *CI* [0.65 - 1.29]). Overall chi-square analysis and phi effect size and odds ratio analysis suggest that diabetes does not appear to be a major predictor or risk factor for COVID-19 diagnosis regardless of their sex. Table 24 depicts the descriptive statistics for these results.

Table 24

Cross-Tabulation Analysis for Diabetes Mellitus and COVID-19 Diagnosis When Controlled by Sex

Case Processing Summary Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Sex

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
diabetes * COVID-19 diagnosis * sex	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Sex

sex		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Female	Pearson Chi-Square	.235[c]	1	.628		
	Continuity Correction[b]	.140	1	.708		
	Likelihood Ratio	.238	1	.626		
	Fisher’s Exact Test				.661	.357
	Linear-by-Linear Association	.235	1	.628		
	n of Valid Cases	862				
Male	Pearson Chi-Square	1.987[d]	1	.159		
	Continuity Correction[b]	1.579	1	.209		
	Likelihood Ratio	1.900	1	.168		
	Fisher’s Exact Test				.170	.106
	Linear-by-Linear Association	1.983	1	.159		
	n of Valid Cases	601				
Total	Pearson Chi-Square	.242[a]	1	.623		
	Continuity Correction[b]	.162	1	.687		
	Likelihood Ratio	.240	1	.624		
	Fisher’s Exact Test				.655	.341
	Linear-by-Linear Association	.242	1	.623		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 50.25.
b. Computed only for a 2x2 table
c. 0 cells (.0%) have expected count less than 5. The minimum expected count is 34.20.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 16.39.

Symmetric Measures Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Sex

sex			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
Female	Nominal by Nominal	Phi	.017			.628
		Cramer's V	.017			.628
	Interval by Interval	Pearson's R	.017	.034	.485	.628[c]
	Ordinal by Ordinal	Spearman Correlation	.017	.034	.485	.628[c]
	n of Valid Cases		862			
Male	Nominal by Nominal	Phi	-.057			.159
		Cramer's V	.057			.159
	Interval by Interval	Pearson's R	-.057	.043	-1.410	.159[c]
	Ordinal by Ordinal	Spearman Correlation	-.057	.043	-1.410	.159[c]
	n of Valid Cases		601			
Total	Nominal by Nominal	Phi	-.013			.623
		Cramer's V	.013			.623
	Interval by Interval	Pearson's R	-.013	.026	-.492	.623[c]
	Ordinal by Ordinal	Spearman Correlation	-.013	.026	-.492	.623[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

Risk Estimate Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Sex

sex		Value	95% Confidence Interval Lower	Upper
Female	Odds Ratio for diabetes (No / Yes)	1.115	.718	1.730
	For cohort COVID-19 diagnosis= Negative	1.079	.791	1.471
	For cohort COVID-19 diagnosis = Positive	.968	.850	1.101
	n of Valid Cases	862		
Male	Odds Ratio for diabetes (No / Yes)	.667	.379	1.175
	For cohort COVID-19 diagnosis= Negative	.757	.523	1.096
	For cohort COVID-19 diagnosis = Positive	1.134	.932	1.381
	n of Valid Cases	601		
Total	Odds Ratio for diabetes (No / Yes)	.917	.648	1.296
	For cohort COVID-19 diagnosis= Negative	.941	.742	1.195
	For cohort COVID-19 diagnosis = Positive	1.027	.922	1.144
	N of Valid Cases	1463		

When controlling age groups, results indicated that diabetes has a weak association for a COVID-19 within the ≥ 60 age groups χ^2 (1, *n* = 226) = 5.77, *p* = .02, *phi* = 0.17. However, when it comes to the overall impact of diabetes in COVID-19 diagnosis across all groups, results were not significant χ^2 (1, *N* = 1,463) = 0.16, *p* = .69, *phi* = - 0.01. Odds ration analysis reported similar results in the sense that diabetic patients within age groups ≥ 60 have a 2.2 greater opportunity of being diagnosed with COVID-19 (*OR* = 2.24, 95% *CI* [1.20 - 4.18]). However, across all age groups there was no significant association established for diabetes and being diagnosed with COVID-19 (*OR* = 0.92, 95% *CI* [0.65 - 1.30]). Overall chi-square analysis and phi effect size and odds ratio analysis suggested that diabetes does not appear to be a major predictor or risk factor for COVID-19 diagnosis regardless of their age. Table 25 depicts the descriptive statistics for these results.

Table 25

Cross-Tabulation Analysis for Diabetes Mellitus and COVID-19 Diagnosis When Controlled by Age Group

Case Processing Summary Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Age Group

	Cases					
	Valid		Missing		Total	
	N	Percent	*N*	Percent	*N*	Percent
diabetes * COVID-19 diagnosis * age group	1463	100.0%	0	0.0%	1463	100.0%

Chi-Square Tests Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Age Group

Age group		Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
<18	Pearson Chi-Square	.214[c]	1	.644		
	Continuity Correction[b]	.000	1	1.000		
	Likelihood Ratio	.405	1	.525		
	Fisher's Exact Test				1.000	.817
	Linear-by-Linear Association	.213	1	.645		
	n of Valid Cases	240				
18-40	Pearson Chi-Square	1.866[d]	1	.172		
	Continuity Correction[b]	1.296	1	.255		
	Likelihood Ratio	2.077	1	.150		
	Fisher's Exact Test				.253	.125
	Linear-by-Linear Association	1.863	1	.172		
	n of Valid Cases	568				
41-59	Pearson Chi-Square	.123[e]	1	.725		
	Continuity Correction[b]	.050	1	.824		
	Likelihood Ratio	.123	1	.726		
	Fisher's Exact Test				.797	.409
	Linear-by-Linear Association	.123	1	.726		
	n of Valid Cases	429				
≥60	Pearson Chi-Square	6.524[f]	1	.011		
	Continuity Correction[b]	5.772	1	.016		
	Likelihood Ratio	6.657	1	.010		
	Fisher's Exact Test				.015	.008
	Linear-by-Linear Association	6.495	1	.011		
	n of Valid Cases	226				
Total	Pearson Chi-Square	.242[a]	1	.623		
	Continuity Correction[b]	.162	1	.687		
	Likelihood Ratio	.240	1	.624		
	Fisher's Exact Test				.655	.341
	Linear-by-Linear Association	.242	1	.623		
	N of Valid Cases	1463				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 50.25.
b. Computed only for a 2x2 table
c. 2 cells (50.0%) have expected count less than 5. The minimum expected count is .19.
d. 0 cells (.0%) have expected count less than 5. The minimum expected count is 7.00.
e. 0 cells (.0%) have expected count less than 5. The minimum expected count is 28.63.
f. 0 cells (.0%) have expected count less than 5. The minimum expected count is 27.41.

Symmetric Measures Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Age Group

Age group			Value	Asymptotic Standard Error[a]	Approximate T[b]	Approximate Significance
<18	Nominal by Nominal	Phi	.030			.644
		Cramer's V	.030			.644
	Interval by Interval	Pearson's R	.030	.011	.461	.645[c]
	Ordinal by Ordinal	Spearman Correlation	.030	.011	.461	.645[c]
	n of Valid Cases		240			
18-40	Nominal by Nominal	Phi	.057			.172
		Cramer's V	.057			.172
	Interval by Interval	Pearson's R	.057	.035	1.366	.173[c]
	Ordinal by Ordinal	Spearman Correlation	.057	.035	1.366	.173[c]
	n of Valid Cases		568			
41-59	Nominal by Nominal	Phi	-.017			.725
		Cramer's V	.017			.725
	Interval by Interval	Pearson's R	-.017	.049	-.350	.726[c]
	Ordinal by Ordinal	Spearman Correlation	-.017	.049	-.350	.726[c]
	n of Valid Cases		429			
≥60	Nominal by Nominal	Phi	.170			.011
		Cramer's V	.170			.011
	Interval by Interval	Pearson's R	.170	.064	2.580	.011[c]
	Ordinal by Ordinal	Spearman Correlation	.170	.064	2.580	.011[c]
	n of Valid Cases		226			
Total	Nominal by Nominal	Phi	-.013			.623
		Cramer's V	.013			.623
	Interval by Interval	Pearson's R	-.013	.026	-.492	.623[c]
	Ordinal by Ordinal	Spearman Correlation	-.013	.026	-.492	.623[c]
	N of Valid Cases		1463			

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

c. Based on normal approximation.

Risk Estimate Diabetes Mellitus and COVID-19 Diagnosis when Controlled by Age Group

Age group		Value	95% Confidence Interval Lower	Upper
<18	For cohort COVID-19 diagnosis = Positive	.903	.867	.942
	n of Valid Cases	240		
18-40	Odds Ratio for diabetes (No / Yes)	2.097	.708	6.209
	For cohort COVID-19 diagnosis= Negative	1.784	.720	4.423
	For cohort COVID-19 diagnosis = Positive	.851	.711	1.018
	n of Valid Cases	568		
41-59	Odds Ratio for diabetes (No / Yes)	.914	.555	1.507
	For cohort COVID-19 diagnosis= Negative	.944	.684	1.301
	For cohort COVID-19 diagnosis = Positive	1.032	.863	1.234
	n of Valid Cases	429		
≥60	Odds Ratio for diabetes (No / Yes)	2.235	1.197	4.175
	For cohort COVID-19 diagnosis= Negative	1.599	1.074	2.382
	For cohort COVID-19 diagnosis = Positive	.715	.565	.905
	n of Valid Cases	226		
Total	Odds Ratio for diabetes (No / Yes)	.917	.648	1.296
	For cohort COVID-19 diagnosis= Negative	.941	.742	1.195
	For cohort COVID-19 diagnosis = Positive	1.027	.922	1.144
	N of Valid Cases	1463		

A Priori Power Analysis for binary logistic regression using obesity as the main categorical predictor variable was conducted to determine the minimum required sample size. Results indicated that a minimum of 419 cases were required to achieve a minimum power of 0.80.

Binary logistic regression analysis was conducted to examine the relationship between obesity, hypertension, DM and COVID-19 diagnosis. Using variance inflation factor (VIF) for testing multicollinearity, results suggested that there was no multicollinearity present between the variables, reporting the largest VIF of 1.3. The logistic regression analysis results were significant χ^2 (3, N = 1,463) = 13.133, p = .004, indicating the model could distinguish between respondents that were diagnosed positive or negative for COVID-19 diagnosis. The model explained between 0.9% (Cox & Snell R2) and 1.3% (Nagelkerke R2) of the variance in COVID-19 diagnosis and correctly classified 70.3% of the cases. Sensitivity was 100.0% and specificity was 0.0%. Obesity can be considered the only significant predictors with $p < .001$. Additional independent variables like hypertension and diabetes reports not significant results with OR = 0.586 and 0.286 respectively. Among the predictors, only obesity showed a significant effect on the odds of COVID-19 diagnosis (B = 0.467, SE = 0.140, $p < .001$), with an OR = 1.60 (95% CI), indicating individuals with obesity were 1.6 times more likely to be diagnosed with COVID-19 compared to those without obesity. Hypertension (p = .586) and diabetes (p = .27) were not significantly associated with COVID-19 diagnosis in this model. Table 26 depicts results from the binary logistic regression analysis.

Table 26

Binary Logistic Regression Analysis for Obesity, Hypertension, Diabetes Mellitus, and COVID-19 Diagnosis

Case Processing Summary for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis

Unweighted Cases[a]		*N*	Percent
Selected Cases	Included in Analysis	1463	100.0
	Missing Cases	0	.0
	Total	1463	100.0
Unselected Cases		0	.0
Total		1463	100.0

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

Omnibus Tests of Model Coefficients for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis

		Chi-square	df	Sig.
Step 1	Step	13.133	3	.004
	Block	13.133	3	.004
	Model	13.133	3	.004

Model Summary for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	1767.597[a]	.009	.013

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

Classification Table for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis

Observed			Predicted COVID-19 Diagnosis Negative	Predicted COVID-19 Diagnosis Positive	Percentage Correct
Step 1	COVID-19 Diagnosis	Negative	0	435	.0
		Positive	0	1028	100.0
	Overall Percentage				70.3

a. The cut value is .500

Variables in the Equation for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	Obesity	.467	.140	11.088	1	<.001	1.595
	Hypertension	.085	.156	.297	1	.586	1.089
	DM	-.215	.194	1.228	1	.268	.806
	Constant	.751	.070	114.765	1	<.001	2.119

a. Variable(s) entered step 1: obesity, hypertension, diabetes.

RQ1: What is the association between diabetes mellitus (DM) and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

Binary logistic regression analysis was conducted to examine the relationship between DM and COVID-19 diagnosis while controlling age, sex and person exposure. Using variance inflation factor (VIF) for testing multicollinearity, results suggested that there was no multicollinearity present between the variables, reporting the largest VIF of 1.09. The logistic regression analysis model for DM alone were significant χ^2 (4, *N* = 1,463) = 233.10, $p < .001$, indicating the model could distinguish between respondents that were diagnosed positive or negative for COVID-19 diagnosis. The model explained between 0.15% (Cox & Snell R2) and 0.21% (Nagelkerke R2) of the variance in COVID-19 diagnosis and correctly classified 72.5% of the cases. Sensitivity was 93.9% and specificity was 22.1%. As a variable, DM did not reported a significant association (*B* = 0.33, *SE* = 0.20, *Wald* = 2.84, *p* = .092), *OR* = 1.39, 95% *CI* [0.95, 2.05]. Among control variables, only Age group showed a significant association (*B* = - 0.51, *SE* = 0.72, *Wald* = 49.87 p < .001), with an *OR* = 0.62, 95% *CI* [0.52 - 0.69], indicating older age group had 40% lower odds of being diagnosed with COVID-19 compared to younger. Person exposure was also a strong and statistically significant predictor, with individuals reporting contact with a known COVID-19 case being more than five times as likely to be diagnosed compared to those with no known exposure, (*B* = 1.70, SE = 0.155, *Wald* = 120.67, p < .001), *OR* = 5.48, 95% *CI* [4.05, 7.42]. Overall, the logistic regression models showed that DM was not a statistically significant predictor for COVID-19 diagnosis after adjusting for age, sex and person exposure. Does failing to reject the null hypothesis, that established that there was no significant association between DM and COVID-19 diagnosis when adjusting for age, sex and person exposure. Table 27 depicts the descriptive statistics for these results.

Table 27

Binary Logistic Regression Analysis for Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex, and Age Group

Case Processing Summary for DM and COVID-19 Diagnosis

Unweighted Cases[a]		N	Percent
	Included in Analysis	1463	100.0
Selected Cases	Missing Cases	0	.0
	Total	1463	100.0
Unselected Cases		0	.0
Total		1463	100.0

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

Omnibus Tests of Model Coefficients for Diabetes Mellitus and COVID-19 Diagnosis

		Chi-square	df	Sig.
Step 1	Step	233.102	4	<.001
	Block	233.102	4	<.001
	Model	233.102	4	<.001

Model Summary for Diabetes Mellitus and COVID-19 Diagnosis

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	1547.628[a]	.147	.209

a. Estimation terminated at iteration number 5 because parameter estimates changed by less than .001.

Classification Table for Diabetes Mellitus and COVID-19 Diagnosis

Observed			Predicted: Covid-19 Diagnosis Negative	Predicted: Covid-19 Diagnosis Positive	Percentage Correct
Step 1	Covid-19 Diagnosis	Negative	96	339	22.1
		Positive	63	965	93.9
	Overall Percentage				72.5

a. The cut value is .500

Variables in the Equation for Diabetes Mellitus and COVID-19 Diagnosis

		B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I.for EXP(B) Lower	Upper
Step 1[a]	Diabetes	.331	.196	2.836	1	.092	1.392	.947	2.045
	Age group	-.508	.072	49.874	1	<.001	.602	.522	.693
	Sex	.115	.127	.815	1	.367	1.121	.874	1.438
	Person exposure	1.701	.155	120.969	1	<.001	5.478	4.046	7.417
	Constant	.614	.297	4.286	1	.038	1.848		

a. Variable(s) entered on step 1: diabetes, age group, person exposure, sex.

Coefficients[a] for Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

Model		Unstandardized Coefficients B	Std. Error	Standardized Coefficients Beta	t	Sig.	Collinearity Statistics Tolerance	VIF
1	(Constant)	1.626	.054		30.025	<.001		
	Diabetes	.065	.036	.045	1.792	.073	.917	1.090
	Age group	-.090	.013	-.186	-7.192	<.001	.883	1.133
	Sex	.018	.023	.019	.789	.430	.994	1.006
	Person exposure	.281	.023	.299	12.115	<.001	.964	1.037

a. Dependent Variable: covid-19 diagnosis

RQ2: What is the association between obesity and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

Binary logistic regression analysis was conducted to examine the relationship between Obesity and COVID-19 diagnosis while controlling age, sex and person exposure. Using variance inflation factor (VIF) for testing multicollinearity, results suggested that there was no multicollinearity present between the variables, reporting the largest VIF of 1.02. The logistic regression analysis results for obesity were significant χ^2 (4, N = 1,463) = 246.79, p < .001, indicating the model could distinguish between respondents that were diagnosed positive or negative for COVID-19 diagnosis. The model explained between 0.15% (Cox & Snell R^2) and 0.22% (Nagelkerke R2) of the variance in COVID-19 diagnosis and correctly classified 73.8% of the cases. Sensitivity was 90.4% and specificity was 34.5%. Obesity reported a significant association (B = 5.85, SE = 0.15, $Wald$ = 15.90 p < .001), with an OR = 1.79, 95% CI [1.35, 2.39]., indicating that obese patients had a 79% increase chance of being diagnosed with COVID-19. Among control variables, only Age group showed a significant association (B = - 0.50, SE = 0.70, $Wald$ = 51.71, p < .001), with an OR = 0.61, 95% CI [0.53, 0.70], indicating older age group had 40% lower odds of being diagnosed with COVID-19 compared to younger. Person exposure was also a strong and statistically significant predictor, with individuals reporting contact with a known COVID-19 case being more than five times as likely to be diagnosed compared to those with no known exposure, (B = 1.69, SE = 0.16, $Wald$ = 119.37, p < .001), OR = 5.45, 95% CI [4.028, 7.38]. Overall, the logistic regression models showed that Obesity was statistically significant predictor for COVID-19 diagnosis after adjusting for age, sex and person exposure. Rejecting the null hypothesis, that established that there was no significant association between Obesity and COVID-19 diagnosis when adjusting for age, sex and person exposure. Table 28 depicts the descriptive statistics for these results.

Table 28

Binary Logistic Regression Analysis for Obesity and COVID-19 Diagnosis when Controlling by Person Exposure, Sex, and Age Group

Case Processing Summary for Obesity and COVID-19 Diagnosis

Unweighted Cases[a]		*N*	Percent
Selected Cases	Included in Analysis	1463	100.0
	Missing Cases	0	.0
	Total	1463	100.0
Unselected Cases		0	.0
Total		1463	100.0

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

Omnibus Tests of Model Coefficients for Obesity and COVID-19 Diagnosis

		Chi-square	df	Sig.
Step 1	Step	246.791	4	<.001
	Block	246.791	4	<.001
	Model	246.791	4	<.001

Model Summary for Obesity and COVID-19 Diagnosis

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	1533.940[a]	.155	.221

a. Estimation terminated at iteration number 5 because parameter estimates changed by less than .001.

Classification Table for Obesity and COVID-19 Diagnosis

Observed			Predicted Covid-19 Diagnosis Negative	Positive	Percentage Correct
Step 1	Covid-19 Diagnosis	Negative	150	285	34.5
		Positive	99	929	90.4
	Overall Percentage				73.8

a. The cut value is .500

Variables in the Equation for Obesity and COVID-19 Diagnosis

		B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I.for EXP(B) Lower	Upper
Step 1[a]	Obesity	.585	.147	15.903	1	<.001	1.795	1.346	2.392
	Age Group	-.500	.070	51.710	1	<.001	.607	.529	.695
	Sex	.126	.128	.980	1	.322	1.135	.884	1.457
	Person Exposure	1.695	.155	119.366	1	<.001	5.446	4.018	7.381
	Constant	.221	.287	.594	1	.441	1.248		

a. Variable(s) entered on step 1: obesity, age group, sex, person exposure.

Coefficients[a] for Obesity and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

Model		Unstandardized Coefficients B	Std. Error	Standardized Coefficients Beta	t	Sig.	Collinearity Statistics Tolerance	VIF
1	(Constant)	1.554	.051		30.534	<.001		
	Obesity	.111	.025	.108	4.427	<.001	.979	1.021
	Age Group	-.091	.012	-.187	-7.525	<.001	.944	1.059
	Sex	.022	.022	.023	.967	.334	.992	1.008
	Person exposure	.278	.023	.296	12.050	<.001	.964	1.038

a. Dependent Variable: Covid-19 Diagnosis

RQ3: What is the association between hypertension and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

Binary logistic regression analysis was conducted to examine the relationship between hypertension and COVID-19 diagnosis while controlling age, sex and person exposure. Using variance inflation factor (VIF) for testing multicollinearity, results suggested that there was no multicollinearity present between the variables, reporting the largest VIF of 1.81. The logistic regression analysis results for hypertension alone were significant χ^2 (4, N = 1,463) = 244.10, $p < .001$, indicating the model could distinguish between respondents that were diagnosed positive or negative for COVID-19 diagnosis. The model explained between 0.15% (Cox & Snell R^2) and 0.22% (Nagelkerke R2) of the variance in COVID-19 diagnosis and correctly classified 73.4% of the cases. Sensitivity was 89.9% and specificity was 34.5%. Hypertension reported a significant association (B = 0.59, SE = 0.16, $Wald$ =13.45, $p < .001$), with an OR = 1.81, 95% CI [1.32, 2.49], indicating that hypertensive patients had an 81% increased risk of being diagnosed with COVID-19. Among control variables, only Age group showed a significant association (B = - 0.58, SE = 0.76, $Wald$ = 59.18, $p < .001$), with an OR = 0.56, 95% CI [0.49, 0.65], indicating older age group had 44% lower odds of being diagnosed with COVID-19 compared to younger. Person exposure was also a strong and statistically significant predictor, with individuals reporting contact with a known COVID-19 case being more than five times as likely to be diagnosed compared to those with no known exposure, (B = 1.67, SE = 0.155, $Wald$ = 115.75, $p < .001$), OR = 5.30, 95% CI [3.91, 7.19]. Overall, the logistic regression models showed that hypertension was statistically significant predictor for COVID-19 diagnosis after adjusting for age, sex and person exposure. Rejecting the null hypothesis, that established that there was no significant association between hypertension and COVID-19 diagnosis when adjusting for age, sex and person exposure. Table 29 depicts the descriptive statistics for these results.

Table 29

Binary Logistic Regression Analysis for Hypertension and COVID-19 Diagnosis when Controlling by Person Exposure, Sex, and Age Group

Case Processing Summary for Hypertension and COVID-19 Diagnosis

Unweighted Cases[a]		*N*	Percent
Selected Cases	Included in Analysis	1463	100.0
	Missing Cases	0	.0
	Total	1463	100.0
Unselected Cases		0	.0
Total		1463	100.0

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

Omnibus Tests of Model Coefficients for Hypertension and COVID-19 Diagnosis

		Chi-square	df	Sig.
Step 1	Step	244.105	4	<.001
	Block	244.105	4	<.001
	Model	244.105	4	<.001

Model Summary for Hypertension and COVID-19 Diagnosis

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	1536.625[a]	.154	.218

a. Estimation terminated at iteration number 5 because parameter estimates changed by less than .001.

Classification Table for Hypertension and COVID-19 Diagnosis

Observed			Predicted		
			Covid-19 Diagnosis		Percentage Correct
			Negative	Positive	
Step 1	Covid-19 Diagnosis	Negative	150	285	34.5
		Positive	104	924	89.9
	Overall Percentage				73.4

a. The cut value is .500

Variables in the Equation for Hypertension and COVID-19 Diagnosis

		B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I.for EXP(B) Lower	Upper
Step 1[a]	Hypertension	.594	.162	13.452	1	<.001	1.812	1.319	2.489
	Age group	-.581	.076	59.182	1	<.001	.559	.482	.649
	Sex	.114	.127	.806	1	.369	1.121	.873	1.440
	Person exposure	1.669	.155	115.754	1	<.001	5.304	3.914	7.189
	Constant	.377	.273	1.912	1	.167	1.458		

a. Variable(s) entered on step 1: hypertension, age group, person exposure, sex.

Coefficients[a] for Hypertension and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.	Collinearity Statistics	
		B	Std. Error	Beta			Tolerance	VIF
1	(Constant)	1.579	.049		32.391	<.001		
	Hypertension	.119	.029	.108	4.085	<.001	.828	1.207
	Age group	-.106	.013	-.218	-8.064	<.001	.796	1.256
	Sex	.017	.022	.018	.762	.446	.994	1.006
	Person exposure	.273	.023	.291	11.800	<.001	.956	1.045

a. Dependent Variable: covid-19 diagnosis

RQ4: What is the association of (diabetes mellitus, obesity and hypertension) and COVID-19 diagnosis among Puerto Rican population while controlling for age, sex, and person exposure?

Binary logistic regression analysis was conducted to examine the relationship between obesity, hypertension, DM and COVID-19 diagnosis when controlling for person exposure, age and sex. Preliminary analyses were conducted to assess the assumptions of outliers, multicollinearity and linearity. Results indicated that 13 cases were considered outliers reporting a ZResid ≤ 2.5. Using variance inflation factor (VIF) for testing multicollinearity, results suggested that there was no multicollinearity present between the variables, reporting the largest VIF of 1.3. The logistic regression analysis results were significant χ^2 (6, N = 1,463) = 255.88, $p < .001$, indicating the model could distinguish between respondents that were diagnosed positive or negative for COVID-19 diagnosis. The model explained between 16% (Cox & Snell R2) and 23% (Nagelkerke R2) of the variance in COVID-19 diagnosis and correctly classified 74.3% of the cases. Accuracy for predicting a COVID-19 diagnosis the sensitivity for positive was 90.0% and specificity for negative was 37.2%. Although obesity, person exposure, hypertension and age groups were significant predictors with p value of < .001, <0.001, .007 and < .001 respectively. Person exposure reported being the most significant predictor as a control variable reporting and odds OR = 5.26, indicating that a one unit increase in exposure to COVID-19 respondents are 5.25 times more likely of being diagnosed with COVID-19.

Overall, the multivariable logistic regression model was statistically significant, indicating that the predictors collectively improved classification of COVID-19 diagnosis. At the individual level, obesity and hypertension were significantly associated with COVID-19 diagnosis, whereas diabetes was not, after adjusting for sex, age group, and person exposure. Therefore, the null hypothesis of no association was rejected for obesity and hypertension but not rejected for DM. Table 30 depicts the descriptive statistics for these results.

Table 30

Binary Logistic Regression for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex, and Age Group

Case Processing Summary for Obesity, Hypertension, DM n and COVID-19 Diagnosis

Unweighted Cases[a]		*N*	Percent
Selected Cases	Included in Analysis	1463	100.0
	Missing Cases	0	.0
	Total	1463	100.0
Unselected Cases		0	.0
Total		1463	100.0

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

Omnibus Tests of Model Coefficients for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

		Chi-square	df	Sig.
Step 1	Step	255.818	6	<.001
	Block	255.818	6	<.001
	Model	255.818	6	<.001

Model Summary for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	1524.913[a]	.160	.228

a. Estimation terminated at iteration number 5 because parameter estimates changed by less than .001.

Classification Table[a] for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

	Observed		Predicted COVID-19 Diagnosis Negative	Predicted COVID-19 Diagnosis Positive	Percentage Correct
Step 1	COVID-19 Diagnosis	Negative	162	273	37.2
		Positive	103	925	90.0
	Overall Percentage				74.3

a. The cut value is .500

Variables in the Equation for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis Controlled for Person Exposure, Sex and Age group

		B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I.for EXP(B) Lower	95% C.I.for EXP(B) Upper
Step 1[a]	Obesity	.497	.149	11.099	1	<.001	1.644	1.227	2.204
	Hypertension	.472	.175	7.271	1	.007	1.603	1.138	2.259
	DM	.073	.211	.119	1	.730	1.075	.712	1.625
	Person exposure	1.660	.156	113.988	1	<.001	5.261	3.879	7.136
	Sex	.131	.128	1.038	1	.308	1.140	.886	1.465
	Age group	-.588	.077	59.012	1	<.001	.555	.478	.645
	Constant	-.190	.347	.300	1	.584	.827		

a. Variable(s) entered on step 1: obesity, hypertension, diabetes, person exposure, sex, age group.

Coefficients[a] for Obesity, Hypertension, Diabetes Mellitus and COVID-19 Diagnosis when Controlling by Person Exposure, Sex and Age Group

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.	Collinearity Statistics	
		B	Std. Error	Beta			Tolerance	VIF
1	(Constant)	1.470	.062		23.885	<.001		
	obesity	.096	.026	.093	3.744	<.001	.946	1.058
	hypertension	.096	.031	.087	3.093	.002	.730	1.370
	DM	.014	.038	.010	.381	.703	.827	1.210
	person exposure	.271	.023	.289	11.734	<.001	.956	1.046
	sex	.022	.022	.023	.960	.337	.991	1.009
	age group	-.109	.013	-.224	-8.230	<.001	.778	1.285

a. Dependent Variable: COVID-19 diagnosis

Summary

Chi-square analysis suggested a strong association between obesity and COVID-19 diagnosis. However, when adding the effect of person exposure, obesity is a significant risk factor for COVID-19 only in people without exposure, since results were not significant when patients had previous exposure to COVID-19, suggesting that COVID-19 diagnosis is mainly driven by exposure. Results indicated that sex as a control variable has a meaningful effect on obesity and COVID-19. However, females drove the statistical significance compared to males, which did not reflect the same pattern. As for age, the results of the Odds ratio analysis suggested that across all age groups, obesity is associated with a positive COVID-19 diagnosis. However, variation exists within individual age groups. When it comes to hypertension as a predictor variable, results indicated that there was no significant association between both variables. However, when controlling age groups. Sample greater than 60 years reported a significant association, but when looking across all groups results were not significant. As for DM as a predictor variable results also established that there was no significant association between DM and COVID-19 diagnosis regardless of their exposure, sex or age group. Overall Chi-square analysis results study indicated that obesity can be considered a strong predictor variable for COVID-19 diagnosis, indicating that obese individuals are at greater risk of being diagnosed with COVID-19 when not previously exposed to a positive COVID-19 case. Section 4 will interpret the study findings, discuss study limitations, recommendations and the implication of the study results for professional practice and social change.

Across all logistic regression models, obesity and hypertension emerged as significant independent predictors of COVID-19 diagnosis in the Puerto Rican population, even after adjusting for demographic and exposure variables. DM did not show a significant association. Person exposure was the strongest predictor, and age group showed a protective effect, while sex was not significant.

Section 4: Application to Professional Practice and Implications for Social Change

The purpose of this quantitative study was to evaluate the association between risk factors and non-communicable diseases that included DM, obesity, hypertension, and COVID-19 diagnosis, adjusted for age, sex, and person exposure in Puerto Rico. As a population, Hispanics were the largest racial minority group in the United States, comprising 17.4% of the entire population and expected to increase to 28.9% by 2060 (Velasco-Mondragon et al., 2016). The Puerto Rican population comprised the second largest subgroup at 9.6% (HHS, 2023). Chronic disease continued to be one of the leading causes of death in Puerto Rico, and around 58% of the island’s population suffered from at least one chronic disease. The Puerto Rican population, as the second largest group within the Hispanic community, also presented higher rates of diagnosed diabetes (13.8%) when compared to more studied Hispanics of Mexican ancestry (13.3%), while at the same time experiencing considerable health disparities that included obesity (Johnson et al., 2017). Current study findings suggested obesity and hypertension emerged as significant independent predictors of COVID-19 diagnosis in the Puerto Rican population, even after adjusting for demographic and exposure variables. DM did not show a significant association. Person exposure was the strongest predictor, and age group showed a protective effect, while sex was not significant.

Interpretation of the Findings

Results suggested that obesity was significantly associated with COVID-19 diagnosis, primarily among individuals who had not reported contact with a known COVID-19 case. The absence of a significant association among exposed individuals indicated that, when direct transmission was likely, the effect of obesity on infection risk was reduced or masked by the stronger influence of exposure. Distinction highlighted the potential role of obesity as a risk factor in community-acquired transmission, where individual susceptibility played a larger role than direct exposure. In chi-square analysis obesity and COVID-19 diagnosis while controlling for sex, findings indicated that obesity was a significant risk factor for COVID-19 diagnosis, particularly among women. Among women, the association between obesity and testing positive for COVID-19 was statistically significant, both in terms of the chi-square test and odds ratio. As for age as a control variable, findings suggested that the association between obesity and COVID-19 diagnosis remained statistically significant for adults age 18–40 and those age ≥ 60. The association was strongest among the oldest age group, suggesting that obesity may have played a compounding role in vulnerability to COVID-19 among older individuals. The relationship was not significant among children or middle-aged adults, though the 41–59 age group showed a trend toward significance.

Regarding how hypertension impacted the probability of being diagnosed with COVID-19, chi-square tests and risk estimates indicated no meaningful relationship when controlled by person exposure, with odds ratios and confidence intervals including 1, suggesting that hypertension did not significantly affect the likelihood of testing positive for COVID-19. Regarding how sex affected this relationship, the chi-square values, both for women and men, as well as the overall test, did not reach statistical significance, indicating that hypertension might not have been a major factor in determining COVID-19 diagnosis in this data set. However, in the ≥ 60 age group, hypertension was significantly associated with an increased likelihood of testing positive for COVID-19, which is consistent with previous findings indicating greater vulnerability in older adults.

Study findings evaluating the impact of DM on COVID-19 diagnosis suggested that when controlling person exposure, DM was not significantly associated with COVID-19 diagnosis, regardless of whether participants had known exposure to a COVID-19 case. Similar results were observed when evaluating how sex affected this association, with findings suggesting that diabetes did not serve as a major predictor or risk factor for COVID-19 diagnosis, even when controlling for sex. As for age as a control variable, results indicated that diabetes was not significantly associated with COVID-19 diagnosis among individuals in the < 18, 18 – 40, or 41 – 59 age groups, with negligible effect sizes. Although a statistically significant association was observed among individuals aged ≥ 60, these findings suggested that while DM may have increased risk among older adults, it did not appear to be a strong independent predictor of COVID-19 diagnosis across the broader population within the study.

Overall, findings suggested that obesity was significantly associated with an increased likelihood of a COVID-19 diagnosis. Although the strength of the association was small, the elevated odds among obese individuals aligned with existing evidence linking obesity to greater susceptibility and severity of infectious diseases, highlighting the importance of considering obesity as a potential risk factor in both public health surveillance and targeted prevention strategies (Elizabeth Pérez-Cruz, 2021). The logistic regression analyses showed that, at the individual-variable level, obesity and hypertension were significant predictors of COVID-19 diagnosis, whereas diabetes was not. These findings were consistent in the multivariable analysis, with obesity and hypertension remaining significant after adjusting for age, sex, and person exposure, while DM continued to show no significant association. The overall multivariable model was statistically significant, indicating that the combined set of predictors improved the classification of COVID-19 diagnosis. Accordingly, the null hypothesis of no association was rejected for obesity and hypertension in both the individual-variable and multivariable analyses, confirming their independent association with COVID-19 diagnosis. In contrast, the null hypothesis was not rejected for DM in either analysis, indicating no significant independent effect. Together, these results highlight obesity and hypertension as independent risk factors for COVID-19 in the Puerto Rican population, whereas DM does not appear to have a significant independent effect.

Limitations of the Study

One of the first limitations of the study related to its generalizability to the entire population of Puerto Rico. Although the study included participants from all of the regions or geographic locations of the island, most of the population consisted of patients who visited the designated health clinics located in the northeastern part of the island. Another limitation of the study fell on the type of sampling used by the original researchers collecting the data. Since convenience sampling was used, which meant that participants were selected based on availability rather than randomness, this could have resulted in the overrepresentation or underrepresentation of certain groups within the targeted population. For example, chronic disease rates like DM, hypertension, and obesity varied within regions in Puerto Rico. In 2021, residents from the south (20.2%)

and west side (18.3%) of the island reported the highest rates of DM. Another limitation of the study was that, as a result of time challenges, the original study creators selected health clinics that agreed to participate in the study and established the collaborative agreement. The time frame of the study affected this health clinic recruiting process, which reduced the capacity to include health clinics from the west and south of the island. Since all of the health clinics from which the original sampling was performed did not have the capacity to hospitalize incoming patients, this did not provide the study with the ability to evaluate health complications that could have arisen after the infection of COVID-19 on the targeted population. Although the study sample provided adequate power for the study, in every study that used convenience sampling, there was a risk that external validity or the study's ability to generalize to other settings, populations, or times might have been affected, along with the presence of type II error. One risk of type II error lay in the inability to reflect the full population, thus affecting real associations between predictor and outcome variables.

Recommendations

To address the limitations identified in this study, future research should aim to improve geographic representation by including a more balanced distribution of participants from all regions of Puerto Rico, particularly from the southern and western areas where chronic disease rates—such as diabetes and hypertension—are notably higher. This would ensure a more accurate reflection of the island's health landscape and strengthen the generalizability of findings. Employing probability-based sampling methods, such as random or stratified sampling, is also recommended to minimize selection bias and allow for more reliable conclusions across different population subgroups. Additionally, extending the data collection period would give more time for health clinics across the island to engage in the study, especially those that may face administrative or logistical constraints in forming collaborative agreements. Including a broader range of health facilities, especially those with inpatient care capacity, would enhance the ability to monitor and assess post-COVID-19 health outcomes and complications that may not be observable in outpatient settings. To reduce the risk of Type II errors—where real associations may go undetected—future studies should prioritize larger, more diverse samples and ensure adequate representation of key demographic and clinical groups.

Implication for Professional Practice and Social Change

Study findings can guide clinicians and public health professionals in creating targeted interventions to address current health issues on the island that may increase the risk of emerging diseases. Given the high rates of obesity and hypertension in Puerto Rico, it is essential for health professionals to gain a better understanding of how this existing health problems can contribute to the burden of COVID-19. Research, not only help reduce COVID-19 infection rates but also lower the risk of complications related to diabetes, obesity, and hypertension associated with COVID-19. Overall, study findings can aid in the development of targeted public health interventions and provide insight into how to effectively allocate resources for groups at risk of health complications. In our selected population groups, which are significantly impacted by chronic diseases like obesity, diabetes, and hypertension, this understanding is crucial.

Conclusion

The Puerto Rican population has reported higher rates of obesity, hypertension, and DM compared to the overall United States population. It is crucial to understand how existing diseases on the island could interact with and affect the predisposition to emerging diseases, such as novel viruses like COVID-19, during the early stages of a pandemic. Hispanics are the largest and fastest-growing minority group in the United States, with Puerto Ricans being the second largest subgroup. Research targeting this population is important because Hispanic subgroups are often combined in studies and treated as a single population. However, there are cultural differences and challenges within each Hispanic subgroup that influence how health issues affect each population. This highlights the need for research that provides a better understanding of how chronic diseases impacting groups like the Puerto Rican population can influence their susceptibility to emerging diseases, such as those experienced during the COVID-19 pandemic. Overall, the study found that obesity and hypertension were significant predictors of COVID-19 diagnosis, whereas DM was not. Accordingly, the null hypothesis of no association was rejected for obesity and hypertension in both the individual-variable and multivariable analyses, confirming their independent association with COVID-19 diagnosis

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