2023

The Geographic Pattern and Socioecological Factors of Helicobacter Pylori Infections in the United States

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Abstract

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by

Judith A. Merryweather

M.Ed. National Louis University, 1986

BA, Washington State University, 1980

Dissertation Submitted in Partial Fulfillment
of the Requirements for the Degree of
Doctor of Philosophy
Public Health

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May 2023

Abstract

Helicobacter pylori (*H. pylori*) is one of the most common human pathogens and may play a role in the development of several distinct diseases, which include gastric ulcer, duodenal ulcer, and gastric cancer. Studying geographic territories of the United States may reveal clusters with high rates of *H. pylori* infection and perhaps the prevalence of gastric cancer; however, geographic mapping of patterns in the United States is scarce. The purpose of this study was to investigate changes in *H pylori* infection patterns in the United States between two different time points (2000–2002 and 2016–2018). The primary hypotheses of this study concerned whether socioecological predictors were associated with any regional changes in *H. pylori* infection patterns. Data on *H pylori* cases were obtained from the National Inpatient Sample, which represents a 20% stratified sample of U.S. community hospitals and, at the time of data collection, contained data from 10 million inpatient stays in 46 states. Chi-square analyses and multiple logistic regression were used to calculate odds ratios, p-values, and confidence intervals. Although the rates of *H. pylori* infections did not change over time, there was a regional change in the distribution of infections from the South to the Northeast regions of the United States. *H. pylori* infections were most prevalent in females less than 55 years of age, and race was not a significant predictor. Medicare and Medicaid usage increased between 2016 and 2018. This study revealed the extent of *H. pylori* infection in the U.S. and identified socioecological factors that influence its occurrence. This information may help medical and public health professionals and community leaders to create programs and policies to improve infectious outcomes.

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Dedication

I dedicate this dissertation to my late mother, who departed this life 30 years ago but who left instilled in me the importance of education, hard work, and persistence. To my family, who have given unconditional support throughout this journey.

Acknowledgments

I want to thank Dr. Julia Leischner, Dr. Haba Tawfik, and Dr. David Segal for their advice, recommendations, and support.

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Chapter 1: Introduction to the Study

Helicobacter pylori (*H. pylori*) bacterial infection was first isolated in 1982 by Australian doctors Robin Warren and Berry Marshall and linked to gastritis and peptic ulceration (Kyle et al., 2016; Marshall, 2016). *H. pylori* are gram-negative helically shaped bacteria that penetrate the stomach's mucus lining and accumulate, causing a bacterial infection (Chmiela et al., 2017). Left untreated, *H. pylori* infection can lead to significant health problems such as gastritis, peptic ulcer, gastric cancer, and death (William et al., 2017). There is no consensus on the geographic distribution of the *H. pylori* bacterial infection across the United States (William et al., 2017). It has also remained unclear what role risk factors like race, age, gender, and socioeconomic status has in the prevalence of *H. pylori* infection.

H. pylori infection is an important etiologic factor for peptic ulcers, gastritis, and gastric cancer (Alfarouk et al., 2019). Gastric cancer is associated with morbidity and mortality. Gastric cancer is much more common in certain parts of the world, particularly in less developed countries (American Cancer Society, 2020). It is one of the leading causes of cancer-related deaths worldwide (American Cancer Society, 2020). Identifying high-risk factors may motivate patients to change their lifestyle. Eradication at the early stage of *H. pylori* infection could reduce gastric cancer deaths by 40% (Centers for Disease Control and Prevention [CDC], 2018). In the United States, nearly all the studies on gastric cancer have relied on the National Cancer Databases, which do not include data on *H. pylori* infection (Kumar et al., 2019). There are multiple barriers in reducing the rate of gastric cancer associated with *H. pylori* infection.

The diversity of *H. pylori* bacteria is determined by the pathogen's genetic features and the host (Jackson et al., 2020). After the bacteria enter the host stomach, several disease outcomes may occur due to the complex interplay between the bacteria, the host, and the environment (Muzaheed, 2020). *H. pylori* infection increases a person's risk of gastric cancer, mainly if the condition is not managed. Cancer is a significant concern that may affect individuals at any time. In the United States, certain population groups may be more susceptible to cancer. Cancer disparities are noted when a higher rate of new cancer diagnosis and death can be linked between population groups and race. In 2019, based on a rate per 100,000 persons, Blacks had the highest rates of cancer (445.2), followed by Hispanics (355.3), Whites (460.9), American Indian/Alaska Native (AI/AN) (315.1) , and Asian Pacific Islander (API) (307.9) (Surveillance Epidemiology and End Report, 2019). Infection rates were found to be similar for men and women. Most people who show signs of *H. pylori* infection are more than 50 years old (John Hopkins Medicine, 2022).

Past research has indicated that *H. pylori* infection is often contracted during childhood and then diagnosed later in life, resulting in critical health problems such as gastric inflammation, peptic ulcers, gastritis disease, and gastric cancer (Brown, 2020). In developed and developing countries, children living in areas without clean water supplies, in crowded homes, or with someone with *H. pylori* infection run a greater risk of contracting the bacteria infection (CDC, 2020). Children usually do not show signs or symptoms. More knowledge of the geographic pattern of, and socioecological risk factors for, *H. pylori* infection in the United States may help medical and public health researchers and practitioners to develop strategies to address the infection’s adverse health outcomes. The creation of new, effective public health interventions may support positive social change. This chapter provides the background of *H. pylori* infection, including microbiological and epidemiological factors, geographic distribution, phylogeography, oncogenesis, antibiotic resistance, and populations vulnerable to infection. Additionally, this chapter presents the problem statement, purpose of the study, theoretical and conceptual framework, research questions and hypotheses, and the scope and limitations of the study.

Background

The perspectives that have underpinned most of the research on *H. pylori* infection include epidemiology, geographic distribution, phylogeography, oncogenesis, genetics, antibiotic resistance, and vulnerable populations. Few studies have been conducted in the United States; most journal articles are focused on countries such as Africa, Asia, and Mexico, where *H. pylori* infections are prevalent. The knowledge gap in research has led to the inability of societies to eliminate a treatable disease that can be traced, in some part, to a disconnect between individual and societal incentives to prevent the spread of illness (Zullo et al., 2022). It is important to overcome the lack of knowledge in *H. pylori* disease history and the resulting socioeconomic barriers. Further knowledge in understanding microbiology and phylogeography, evidence-based practices, and geographic locations are widely overlooked.

Microbiology

H. pylori is a spiral-shaped bacterium (Agbor et al., 2018). The bacterium hides in the mucous layer of the stomach's epithelial lining, making it difficult to eradicate (Agbor et al., 2018). Approximately 65%–80% of all gastric cancers worldwide are thought to be attributed to *H. pylori* infection, a bacterium that can be treated with antibiotics (Nordestgaard et al., 2018). *H. pylori* infection is a major etiological factor in disease pathogenesis (Azhari et al., 2019).

Although bacteria can be treated with antibiotics in most cases, *H. pylori* is a bacterium that is becoming increasingly antibiotic-resistant and diverse in populations (Zhou et al., 2022). Burucoa (2018) traced patterns of antibiotic resistance of *H. pylori* in Asia, Europe, and Africa among adults and children suffering from digestive problems. Burucoa studied the impact of multiple antibiotic therapies and the point where the drug becomes resistant to the bacterium. When choosing a regimen for a specific patient, clinicians should consider geographic mapping, the researcher contended. Burucoa stated that human infection's epidemiological process is better understood through phylogeography.

Phylogeography

H. pylori infection has a high genetic diversity traced to human migration, and the bacterium is known for its genome’s ability to mirror the history of human migration (Waskito & Yamaoka, 2019). Its evolution runs parallel to that of humans; *H. pylori* infection has been coevolving with humans for the past 120,000 years (Waskito & Yamaoka, 2019). Using multilocus sequence typing, *H. pylori* infection can be classified into seven major patient population types from Africa, Asia, and Europe, namely hpAfrica1, hpAfrica2, hpNEAfrica, hpEastAsia, hpAsia2, Europe, and hpSahul (Waskito & Yamaoka, 2019). Therefore, it is highly likely that a strain found in a population today originates from a patient strain found hundreds of years before. The high genetic diversity of *H. pylori* infection has predicted host-human migration worldwide (Ono et al., 2019).

Phylogeography and Evidence-Based Practice

Phylogeographic knowledge can have an impact on evidence-based practice and patient-centered care. Traditional practices among communities are integral to cultural identity and serve as the foundation or framework for disease prevention and health promotion (Saunder, 2019). Evidence-based practice is a national movement to improve health care service quality and accountability by integrating the best research evidence with clinical expertise and patient values (Saunder, 2019). However, in implementing evidence-based practice, advocates have adequately acknowledged cultural variation despite important progress (Saunder, 2019).

The use of phylogeography can reveal the history of a bacterial epidemic. The unique reconstruction of a bacterial spread represents a valuable source of lineage and migration data that can support investigation of the underlying environmental layers of the pathogen. Burucoa (2018**)** found that the phylogeographic distribution of *H. pylori* strains isolated from subjects globally can be seen through human heredity of the descent of hpNEAfrica, hpAsia2, and hpEuropean bacterial genes. *H. pylori* infection is one of the most prevalent human pathogens in the stomach and can be found dispersed globally in human hosts (Sterbenc et al., 2019). This results in a distinct phylogeographic pattern that can be used to reconstruct ancient human migrations to present-day clusters (Newreiter et al., 2021). For example, the European population infected with *H. pylori* infection is known to be the start of the hpNEAfrica, hpAsia2, and hpEuropean, and bacterial gene migration across centuries and miles. Ailloud et al. (2019) indicated that the evolution of *H. pylori* is impacted by societal and ecological changes, and by studying the ancestry and mechanisms of genetic diversity of the bacterium, one can understand the contributing factors. Developing a map of regions of *H. pylori* infection and susceptibility patterns is critical in defining migration patterns in the United States (Hooi et al., 2017).

Geographic Territories

H. pylori colonization is prevalent throughout the world, but little is known about its territorial makeup in the United State. Studying geographic territories of the United States may reveal clusters of high rates of the infection of *H. pylori* and perhaps the prevalence of gastric cancer. The desire to cut gastric cancer rates would suggest a need for public policy to treat early signs of infection. Agbor et al. (2018) examined the evolutionary biology of the spread of a human bacterium and the factors that shape spatial distributions. Abor et al. (2018) concluded that geographic mapping of patterns in the United States is scarce. Developing a map of regions of *H. pylori* infection and susceptibility patterns is critical in defining migration patterns in the United States (Hooi et al., 2017). There is a need, therefore, to find out where the geographic clusters of *H. pylori* infection exist in the United States.

Problem Statement

H. pylori infection is an underlying cause of gastric cancer and is a severe public health problem. *H. pylori* infection is a pathogenic bacterium that lives in the stomach's epithelial lining (Agbor et al., 2018). The bacterium is a critical risk factor for associated gastric diseases such as peptic ulceration and gastric cancer (Chey, 2019). Hyo and Lee (2015) classified *H. pylori* infection as the number one carcinogen for gastric cancer. However, this is debatable because *H. pylori* infection are usually colonized in the human mucus early in life and progress to different disease states (Kienesberger, 2018; Wang et al., 2022).

H. pylori infection occurs during childhood, commonly before 5 years of age (Torres, 2017). In a recent study, Kotilia et al. (2018) assessed *H. pylori* infection in children; findings indicated eradication of *H. pylori* infection in more than 90% of children who were studied. Kotilia et al. (2018) study may support the testing of younger children before alterations caused by the bacterial infection cannot be reversed. *H. pylori* infection may cause social and health issues in a child's development, such as stomach pain, anxiety, and slow development, which can result in a lack of proper social development, the researchers concluded. Physical pain can contribute to developmental delays in children's cognitive, communication, social-emotional or behavioral skills. Experts often discuss adverse childhood experiences or traumatic events caused by physical pain. Physical pain or scars often leave emotional and psychological imprints that affect a child's mental and physical development (Kotilia et al., 2018). For these reasons, diagnosing young children early can help prevent long team health issues.

Examining the inequality of a population's heredity, environmental, and socio-economic backgrounds is crucial. *H. pylori* infects the most vulnerable and physically weak population of children and older adults (Lee & Chou, 2016**).** The prevalence of *H. pylori* infection is high in developing countries and is related to socioeconomic status and hygiene levels (Hooi et al., 2017). *H. pylori* bacteria spread via unwashed and uncooked foods, contaminated water, unsanitary conditions, and improper methods used to preserve food (Zamani et al., 2018). The prevalence of *H. pylori* infection varies widely by geographic area, age, gender, ethnicity, and socioeconomic status (Inoue, 2017). Therefore, geographic mapping of populations of the *H. pylori* infection by region and identification of individuals by age, gender, race, and other factors can enhance recommendations for treatments and eradication (O'Connor et al., 2017). The treatment of *H. pylori* infection reduces the incidence of peptic ulcers and gastric cancer (Ford, 2016). Improving geospatial data availability can give researchers measurable data allowing for a detailed conclusion. This is especially important as there is no consensus on the geographic distribution of bacterial infection across the United States (William et al., 2017). Public health authorities have slowly considered the benefits of population-based screening and treatment to reduce diseases brought about by infection (O'Connor et al., 2017). Research on the geographic distribution of, and socioecological risk factors for, *H. pylori* infections in the United States is warranted.

Purpose of the Study

In this multilevel study, I sought to identify the geographic locations of *H. pylori* infections in the United States, comparing regional changes during two time periods

(2000–2002 and 2016–2018) and also identifying the socioecological risk factors by year. This project is unique because it included the identification of clusters of populations infected by *H. pylori* bacteria in the United States. The discovery of the infectious patterns in cases or groups may help researchers to identify bacteria spread amongst different racial and socioeconomic groups (Deaton, 2013). I explored the gaps in racial and socioeconomic inequality, which Deaton (2013) identified. Perhaps this knowledge will help medical and public health researchers and practitioners to develop screening and treatment programs for specific populations (Mégraud et al., 2016). Previous researchers studying *H. pylori* distribution in the United States have examined antibiotic resistance, hygiene, and race, but state-level data for infected populations of *H. pylori* are lacking (Hooi, et al 2016). This research study aims to identify regional migration.

Research Questions and Hypotheses

In this research study, I sought to identify the patterns of *H. pylori* infection in the United States. I examined the population dynamics and the factors involved in the decline or expansion over time. The research questions (RQs) and hypotheses for the study were as follows:

RQ1: Is there a significant difference between time periods 2000–2002 and 2016–2018 and the geographic distribution of *H. pylori* infection in the United States?

$H_0$1: There is no significant difference between time periods 2000–2002 and 2016–2018 and the geographic distribution of *H. pylori* infection in the United States.

H_a1: There is a significant difference between time periods 2000–2002 and 2016–2018 and the geographic distribution of *H. pylori* infection in the United States.

RQ2: Is there an association between age, gender, race, and *H. pylori* infection in the United States?

$H_0$2: There is no association between age, gender, race, and *H. pylori* infection in the United States.

H_a2: There is an association between age, gender, race, and *H. pylori* infection in the United States.

RQ3: Is there an association between health insurance coverage (Medicare, Medicaid, Private, or No insurance) and *H. pylori* infection by region?

$H_0$3: There is no association between health insurance coverage (Medicare, Medicaid, Private, or No insurance) and *H. pylori* infection by region.

H_a3: There is an association between health insurance coverage (Medicare, Medicaid, Private, or No insurance) and *H. pylori* infection by region.

The comparison in RQ1 of two 3-year time periods was intended to capture the regional migration of *H. pylori* infection over time, which may help medical and public health researchers and practitioners in developing targeted interventions in specific geographic regions. RQs 2 and 3 focused on socioecological factors by year to identify *H. pylori* infection risk factors.

Conceptual and Theoretical Framework

In this investigation, I sought to define populations and regions of high *H. pylori* infection in the United States. To help understand various factors in this research, I used the socioecological model (SEM) as the framework. SEM has five levels and centers on the relationship between the host and the environment (Bronfenbrenner, 1977). The SEM model highlights multiple levels of influence, including age, gender, race, family history, organization, community, and public policy, and examines the interactions between risk factors at different levels (Bronfenbrenner, 1993).

The mesosystem encompasses the home, peers, family, and community (Kumar et al., 2019). This level describes how an individual affects a community and how an individual can change their surroundings (Kumar et al., 2019). The macrosystem is an ecological system theory composed of cultural patterns and values, specifically the dominant beliefs and ideas of individuals, that impacts directly or indirectly a child’s growth. I applied the SEM in examining individual-level risk factors associated with *H. pylori* infection and its spread in the U.S. population. This theory can explain and predict events or situations by identifying relationships between variables (Gott et al., 2018). Given the interaction between the pathogen (*H. pylori*), host, environment, community, and individual beliefs, the emphasis was on the ecological transition that shapes the interpersonal relationship between bacteria and human survival (see Schuwirth & van der Vleuten, 2019).

Improving health promotion efforts is essential for creating a healthy environment because fostering healthy behaviors can reduce the transmission of bacteria and lower antibiotic resistance. In this research study, I also examined specific relationships among variables to delineate between individual outcomes and ecological factors (U.S. Environmental Protection Agency, 2017). The SEM framework can be applied to determine whether humans are vulnerable to *H. pylori* due to environmental exposure (U.S. Environmental Protection Agency, 2017). By examining an individual’s biological and personal history, family relations, community levels, environment, and societal and cultural norms, public health workers may be able to identify a pattern that shows the increasing likelihood of exposure to *H. pylori* infection (U.S. Environmental Protection Agency, 2017). Any unexpected pattern of cases or clusters is a significant public health concern because of its possible epidemic spread (Dong et al., 2017). Identifying biological and personal history variables is crucial to understanding bacterial heritage and studying the progression of the disease (CDC, 2019). Understanding the geographic distribution of populations infected with *H. pylori* can provide insight for gastroenterologists on how to screen for and treat the infection.

Nature of the Study

For this multilevel quantitative study, I used a cross-sectional design incorporating hospital medical records from the National Inpatient Sample (NIS). NIS is the largest publicly available inpatient care database. The aim was to estimate the current distribution and potential spread of *H. pylori* infection. In researching the geographic patterns of *H. pylori* infection in the United States, I focused on determining the maximum number of patients infected in each region as a means of exposing the current geographic distribution of the infection. The first RQ was descriptive. To achieve spatiotemporal clustering, I used chi-square analysis. The chi-square test perfectly fits the research problem because it pinpoints the geographic location in a time-trend model. The chi-square test is a fundamental data analysis based on observing a random set of categorical variables (Scribbr, 2022). The repeated measures analysis of variance (ANOVA) test was used to calculate the differences between related population means. The second and third RQs were best examined using multiple logistic regression. Multiple logistic regression revealed whether the outcome variable was diseased or not diseased. I examined the gap between *H. pylori* infection, race, age, gender, and health insurance in potentially revealing inequality.

Definitions

The dependent variable was *H. pylori*, and the independent variables were age, race, gender, and health insurance. Following are definitions of some terms used in this research:

Healthcare Cost and Utilization Project (*HCUP*): A comprehensive source of U.S. hospital care data. The HCUP's Nationwide databases can be used to identify, track, and analyze national trends in healthcare utilization, access, charges, quality, and outcomes (AHRQ, 2022).

International Classification of Disease (*ICD-9* and *ICD-10*): The only mandated standard for defining a patient's health state, with codes used to classify different diseases (CDC, 2021).

National Inpatient Sample (*NIS*): A nationally representative database of U.S. inpatient hospital stays. NIS includes data on 97% of all discharges in the United States (Schulman, 2017). The Health Insurance Portability and Accountability Act of 1996 requires that all providers, payers, and clearinghouses electronically provide the ICD-10 code. NIS data sets can be used to test and understand the population dynamics of host-pathogen interaction through medical records, billing, and other records (Chmiel et al., 2019).

Phylogeographic: The study of the historical processes responsible for individuals' current geographic distributions (Marske, 2016).

Assumptions

A critical assumption in this research was the fundamental question regarding genetic diversity shared by the human population worldwide. Genetic diversity can sometimes interact with social processes to produce a difference in how *H. pylori* disease progresses (Waskito & Yamaoka, 2019). It is unknown how bacterial triggers transform from one person to another. Ferlay et al. (2019) stated that an ongoing transition in epidemiological patterns of *H. pylori* should be tracked. In conducting this study, I assumed that *H. pylori* infection can be tracked and traced in clusters over geographic regions. This assumption may provide knowledge on when and whom to test for *H. pylori*.

Scope and Delimitations

Several thousand species exist in the human digestive system, and unlike pathogenic *H. pylori*, most bacteria are harmless and often beneficial. It has been well established in the literature that humans and *H. pylori* infection show substantial coevolutionary traits. The evidence so far indicates that *H. pylori* infection can adapt rapidly to changing environments, which allows for higher infection rates among different population. *H. pylori* infection can also overcome antibiotic activity via various resistance mechanisms, mainly involving the reduced affinity of targets to drugs through mutational changes in the structure or movement (Hu et al., 2012). In this study, I do not explore the genetic metamorphosis of the bacteria or host; I examined the factors and environments that promote transmission. Therefore, this study will only provide a general overview of the U.S. population that has acquired *H. pylori* infection and the social-ecologic variables specific to the community.

Limitations

There are several limitations to this study. First, because I examined secondary data from each region to indicate the proportion of *H. pylori* infection per region, I was not able to identify the time of the initial infection or diagnosis. Instead, the data were analyzed to compare the differences between states from 2000–2002 and 2016–2018. I examined how often *H. pylori* infection occurs in a specific time interval and place. Second, I did not explore the genetic metamorphosis of the bacteria or the host. Solid evidence supports the ancestral origin of *H. pylori infection* in Africa and its following human migration (Mègraud et al., 2016), The progression of *H. pylori* infection into gastric cancer involves interactions between the bacteria and the host. (Padda et al., 2021). Further studies are needed to explore specific time intervals and places along with genetic metamorphosis.

Significance

A key goal of this research study was to expose possible risk factors for *H. pylori* infection. The infection is associated with the adult population, not children, even though *H. pylori* infection is a bacterium that is acquired at a young age and that contributes to diseases later in life (Matos, et al, 2020). This study's results may provide health professionals and researchers with preliminary data to identify geographic patterns for continuing research. Specifically, the study may identify potential risk factors, such as age, gender, race, and health insurance, and patterns of the high prevalence of *H. pylori* infection in various regions of the United States over time. With this knowledge, public health leaders can recommend policies for preventing and controlling *H. pylori* bacterial infection in local areas, potentially leading to positive social change (Chey, 2019; Malfertheiner, 2017).

Summary

This study may demonstrate the prevalence of *H. pylori* infection among children and adults in the United States. It may clarify whether the geographic unit of analysis (country or region) has valuable data to expose disease patterns. Past studies did not depict the natural, underlying association because of small sample sizes or low statistical power (Peek, 2016). Understanding the disease's lineage in terms of race, gender, and age might provide key insights on its transmission. The significant geographical differences can best optimize the management of *H. pylori* infection. (Kirby et al., 2017). Eliminating or reducing exposure to risk factors for *H. pylori* infection contraction can substantially affect the cancer burden in the United States (Wang et al., 2020). I review key literature on the study topic in Chapter 2

Chapter 2: Literature Review

Introduction

Much of the world's population is infected with the *H. pylori* bacterium. Over 50% of the global population has *H. pylori* infection in their upper gastrointestinal tracts, according to some researchers (Hooi et al., 2017). *H. pylori* infection is a global issue that significantly differs between and within countries (Hooi et al., 2017). Both gastric ulcer disease and gastric cancer have common etiologic factors, and *H. pylori* infection is a precursor to both. Regarding peptic ulcer and gastric cancer's global burden, international statistics showed in 2000-2017, 141.9 per 100,000-person incidence annually of peptic ulcer disease in Spain. The lowest incidence rate, 57.5, was in Sweden (Azhari, 2020). In this study, I examined the rates of *H. pylori* infection in the United States.

In 2020, approximately 4.6 million people had evidence of a peptic ulcer, and an estimated 10% will develop duodenal ulcers during their lifetime (Anand, 2021). *H pylori* infection accounts for 90% of duodenal ulcers and 70%-90% of gastric ulcers in the United States (Malik & Singh, 2019). In the United States, gastric cancer affects slightly more men than women; the American Cancer Society (2019) estimated that in 2020**,** 120,890 new cases would be diagnosed in men and 119,829 in women. In estimating the current cancer burden, cancer incidence and mortality data lags 2 to 4 years behind the current year. The disease burden may vary by race and geography.

The United States has been a melting pot for genetically diverse human beings (Thorell, 2017). *H. pylori* infection can rapidly rise, spread, and adapt to populations (Thorell, 2017). The difference in the bacterial strain between people reflects differentiations emerging during the complex transmission of *H. pylori* infection and the human host (Thorell, 2017). *H. pylori* infectious strains and a disrupted coevolution between *H. pylori* infection and its human host can potentially explain the geographic differences in the risk of *H. pylori* infection-related cancer. Any high-risk population may have its specific genetic makeup, and a new *H. pylori* infectious strains with national and regional gene pools should be considered (Bakhti et al., 2020). In the United States, strains rapidly evolved distinct *H. pylori* infectious subpopulations. As such, there needs to be a consensus on the geographic distribution of *H. pylori* bacterial infection (William et al., 2017). In this study, I sought to identify bacterial infection clusters in the United States and the socioecological risk factors associated with acquiring the bacteria in local areas.

Specifically, in this multilevel study, I aimed to identify the geographic locations of *H. pylori* infections in the United States, comparing two-time intervals, 2000–2002 and 2016–2018, and exploring the socioecological risk factors. To identify inequity in this population-based study, I used the SEM, which has individual, interpersonal, community, organizational, and policy-enabling/environment levels. This study's results may demonstrate patterns of early colonization and infection of the disease based on age, race, ethnicity, and other risks (Alimohammadi et al., 2016). Additional risk involves socioeconomic factors, such as the type of health insurance and status (i.e., private insurance, Medicare, Medicaid dual Medicare, Medicaid-eligible, and uninsured; Parikh-Patel et al., 2017). Previous studies have indicated that not all health insurance benefits patients equally; disparities exist in the quality of treatment according to demographic factors such as race/ethnicity, SES, and source of health insurance (Parikh-Patel et al., 2017).

Researchers have not used a population-based sample to assess the race, gender, age, and SES markers of *H. pylori* infection the United States, according to my review of the literature. Past research has indicated that *H. pylori* infection is contracted during childhood and leads later in life to critical health problems such as gastric inflammation, peptic ulcers, gastritis disease, and gastric cancer (Aguilera Matos et al., 2020). Current literature has shifted to identifying the need for continued research aimed at a younger age and early colonization of the bacteria (Hooi et al., 2017). In this study, I explored geographic patterns and risk factors to provide insight that policy makers can use to develop the appropriate control strategies.

Current researchers have examined the antibiotic resistance of *H. pylori* infection. They have explored the current antimicrobial drugs available to treat the infection antibiotic-resistance to those drugs, and the role of these drugs in eradicating the disease. Hooi et al., (2017) concluded that there is a significant variation among countries in infection rates. Data could be used for the development of customized strategies.

In this chapter, I will provide a synopsis of the current literature on *H. pylori* infection. This review includes epidemiology, geographic distribution, phylogeographic, oncogenesis, antibiotic resistance, vulnerable populations, race, gender, age, and how the SEM explains a paradigm shift for the transmission. This chapter includes an overview of the disease and the importance of the geographic unit of analysis (state) in exposing a cluster of disease patterns. In addition, I discuss how the study’s conceptual framework, the SEM, provided the groundwork for understanding the dynamic interrelation among various personal and environmental factors. I begin by reviewing the literature search strategy.

Literature Search Strategy

I primarily used the database Medline to identify articles on *H. pylori* infection. Peer-reviewed journal articles were also found by searching PubMed and Cochrane Library for titles and abstracts of studies on the effects of *H. pylori* infections location, age, race, gender, and health insurance. The search terms used were *H. pylori*, infectious disease, disparities, public health, antibiotic resistance, phylogeography, risk factors, gastric cancer, peptic ulcer, bacteria, prevalence, incidence, transmission, social-ecological model, health insurance, United States, and geographic. Twenty-seven articles are from 2015 to 2019; Five additional articles were added from 2019 to 2022 and seven from 2004 to 2014, and four from 1977 to 1997; these articles gave me vital information to include in the overall summary of the research.

The scope of the literature will primarily emphasize populated areas of *H. pylori* infection across the United States. Subgroups, including race, age, gender, and health insurance, are used to explain knowledge of risk factors in the geographic locations of U.S. populations. The search included peer-reviewed literature between 2015-2022. Thousands of articles have been written about *H. pylori* infection*;* most articles cover antibiotic resistance to treatment and genetic mutations.

Conceptual Framework

Epidemiology is the study of the distribution of a disease subject to the population and the course of population change. This investigation's theoretical basis is to define regions of highly concentrated areas of *H. pylori* infection in the U.S. The objectives of this research are related to epidemiologic distribution, population dynamics, and population changes. Managing the resistance to a pathogen is significant to diversity and recombination (Susi et al., 2020).

There are overlapping conceptual frameworks that dominate the study of infectious diseases. This conceptual framework manifested from the germ theory and was articulated by three medical scientists, Pasteur, Koch, and Lister (Britannica, 2021).

Epidemiologists stress the population-level infection pattern with factors that lead to an association between environmental, behavioral, and genetic influences. This conceptual framework is a risk factor approach, most often statistical. An odds ratio or relative risk statistic is predominantly used to predict an outcome. Within this framework, one can expect the time course within a given population (Susi et al., 2020). The ecologists use a complementary approach to emulating the host-pathogen interaction's natural ecological and evolutionary dynamics (Susi et al., 2020). Within this framework, one can predict the time course within a given population (Susi et al., 2020). Each layer, moving outward from the individual, is enmeshed in various ecosystems, from a private home to a more extensive school system to the most expansive society and culture.

This research will look at age, gender, and race and provide information about the population's natural ecological and evolutionary dynamics and host-pathogen interactions.

Socio-ecological models were developed to further the understanding of the dynamic interrelations among various individual and socio-ecological models. For example, poor living and sanitary conditions are often cited as significant risk factors for bacterial infection, and the risk of bacterial infection increases with lower socio-economic status and younger age. Asia’s highest risk for gastric cancer is associated with increased *H. pylori* infection. Asian foods are the major risk factor for gastric cancer, including smoked foods and salted fish pickled vegetables (Hooi et al., 2016).

Social-Ecological Model

Bronfenbrenner introduced the SEM in 1998. Health professionals may find the intersection of the different levels in the model helpful in describing and accounting for a person's health outcome. The SEM focuses on the individuals as the center and looks outward, expanding each level of social and environmental interactions to detail their complexity (Russell et al., 2022). Each class is organized from an individual to the broadest intersection of community and society. The individual level identifies natural history and one's personal history. The interpersonal level examines close relationships, while the community level explores settings such as schools, workplaces, and neighborhoods. The fourth level, organizational and final level policy/enabling environment, looks at social factors, such as health disparity, economic factors, education, and social policy, including health insurance (Bronfenbrenner, 1977).

The central theoretical hypotheses are that norms and values are prevalent within a community or setting; changing them can be challenging (Cislaghi & Heise 2018). However, changes to sectors and backgrounds can have a powerful effect on social and cultural norms, Office of Disease Prevention and Health Promotion (2020). Health depends on collective action, and whether it is through heredity, community, or society, education is a factor that can bring everything together. In looking for general patterns and picking out exceptions, we need to look at the U.S., mapping patterns of health, heredity, and wealth.

This theory has been applied through research; Parma et al., (2017) conducted a study in Texas and found that Hispanic men had higher *H. pylori* infection rates than non-Hispanic Whites. I focused on men because of their higher rate of gastric cancer. Hispanic men were 3 times as likely to be infected than non-Hispanic White Men (64% to 21%; American Cancer Society, 2016). Parma et al., (2017) examined relationships between race, age, gender, income, and family history.

This study will examine how an individual is affected by constructing an overview of infected individuals' geographic locations and the risk factors associated with age, gender, race, and health insurance. The first level of the SEM is the individual (Bronfenbrenner, 1977). No matter how we see ourselves, the concepts of race, ethnicity, and nationality set us apart. These concepts influence the past, present, and future. Race is an arbitrary classification based on various physical characteristics such as skin color, eye shape, and facial form (Pereira, 2019). Race is more complex and often not just physical features but sometimes includes ethnicity, ancestry, culture, language, and religion. Race and ethnicity do not show up on the genetic level, but the concept of race still forms our experiences (Blackmore, 2019). It has been established that race is a factor for almost half of all Americans with *H. pylori* infection (ASC, 2021). It has been noted that people who come to the U.S. from other countries bring the bacteria with them. At least 50% of Latinos and Eastern Europeans have *H. pylori* infection when entering the U.S. (Johns Hopkins Medicine, 2022). What is important is whether those race clusters found in this research can help adjust public health policy and accommodate a subpopulation of a region.

Age is a significant risk factor for *H. pylori* infection. Age-related illness and disease occur more frequently as one gets older. The disease development in old age primarily arises from an individual's physical and social environment. *H. pylori* infection is a bacterium known to be acquired during childhood and manifested as an adult in different disease states, such as gastritis, ulcer, and gastric cancer (Kalach et al., 2017). Agah et al., (2016) conducted a small study on gender disparity and infection rates in gastric cancer. The summary predicted that *H. pylori* infection was significantly higher for females. The author believes this was a novel finding since males have shown a higher risk of developing related diseases with *H. pylori* infections (Agah et., 2016).

The intrapersonal level is the second level. It relates to relationships with others, family, friends, and peers (Bronfenbrenner, 1977). At this level, the individual's parents can influence a decision that affects one's well-being, such as health care choices. Knowledge about different foods and food preparation is developed at this level.

At the interpersonal level, the communication approach encourages behavioral changes (Bronfenbrenner, 1977). Using this approach, we can target social norms and culture-specific practices and develop strategies for health interventions for the targeted population. Once the population knows the health problems, the community can begin developing health interventions.

The third level is community involvement (Bronfenbrenner, 1977). These organizations can provide resources and ideas to improve community health. Community settings include early childhood programs, education, schools, worksites, and community centers. In a combination of ways, layers of influence can influence social norms, values, and our health future (Bronfenbrenner, 1977). The National Health and Nutrition Examination Survey (NHANES) 1999-2000 examined the environmental risk factors associated with *H. pylori* seroprevalence. Howden et al., (2022) multivariable logistic regression study reported that participants aged < 20 years were seropositive, significantly associated with drinking water from a well and living in a crowded home. Adults aged >20 years that were seropositive were also related to soil-related occupations compared to those working in non-exposed disciplines. Environmental exposures such as water and occupation play a role in *H. pylori* infection transmission (Howden et al., 2022).

The fourth level is the societal, composed of the timing and duration of events used to track migration and examine environmental contributors to adverse health conditions within communities (Bronfenbrenner, 1977). Economic trends and policies continually alter the landscape. The impact of whether a patient has the appropriate insurance was studied in Japan during policy changes for *H. pylori* eradication therapy. The study results suggest that insurance coverage expansion may reduce the prevalence of *H. pylori* in other countries (Hiroi et al., 2017). The Federal and local policy decisions, including development and changing insurance requirements, can lead to the loss of manufacturing jobs and working-class neighborhoods. This study looks at the migration of bacterial infections in the United States.

Bronfenbrenner (1977) developed the SEM to understand further the dynamic interrelations among various individual and socioecological factors). Each layer, from individuals, is enmeshed in multiple ecosystems, from private homes to larger school systems to the most expansive society and culture. In a combination of ways, layers of influence can influence social norms, values, and our health future. Bronfenbrenner's model indicates that social and cultural norms govern thoughts, beliefs, and behaviors. They are shared assumptions of appropriate behaviors based on society's values and are reflected in everything. The SEM framework can show how the interplay between individual relationships, community, and societal factors affects the lives of those susceptible to *H. pylori* infection.

Literature Review Related to Key Variables

Geographic Distribution

Spatial analysis is a geographical analysis that can help illustrate drug resistance, genetics, human behavior patterns, infection rates, and clusters. Topological and geometric studies help determine the spatial distribution of many diseases and resistance. Geographic methods can be used to analyze and measure intricate behavior patterns leading to drug resistance. Complex issues in the migration of the population for health epidemics may be identified.

Pybus et al., (2015) examined the evolutionary biology of the spread of a human virus and the factors that shape spatial distributions. The author used comparative studies in the evolutionary changes of RNA and DNA viruses to highlight the generalities of patterns and processes to infer viral infections in a human population. Pybus et al., (2015) found that human bacteria's evolution relies on societal and ecological changes by studying the ancestry and genetic diversity mechanisms. Waskito and Yamaoka (2019) believe that a human virus's current phylogeographic process is more conducive to epidemiology, and the structure belongs to several distinct genetic populations. The author believes that the linkage is farther back than we think, and the infectious RNA and DNA are an offshoot of another ancient disease. The author concludes that human ecology significantly influences bacterial mutations and that we must search for evolutionary patterns to understand the intricacies of bacterial progressions. A great deal of our understanding of infectious disease begins with understanding our past.

Rosenberg and Kang (2016) compared maps of geographic variations of populations to healthcare prevention cost and utilization. The author found the geography-based analysis significant even after accounting for population differences. This study suggests that the geopolitical units of analysis (country, state, or region) needed to be refined.

Phylogeography

Phylogeography studies the historical processes that may describe the biogeography of the current or contemporary geographic distribution of individuals and the community (Weber, 2017). *H. pylori* bacterial patterns can be linked to evolutionary history and are stored in its genetic makeup (Mègraud, 2016). In the United States, we have not established patterns of phylogeographic migration or contemporary geographic distribution (Mègraud, 2016). This disease's history can be related to the phylogeographic of the migration from out of Africa (Mègraud, 2016). The difference found by exploring geographic distribution can help understand how pathogen, host, and environment propel the disease. A phylogeographic approach has been used with many diseases, such as dengue fever, HIV, and Avian influenza, which threaten human health (Mègraud, 2016). Brito et al., (2016) researched the foot-and-month disease epidemic in Argentina, using genetic data to assess the infected population's progression.

H. pylori's geographic patterns in the United States can be displayed using spatial distribution maps to define a population and its associated risk factors. Bacteria that cannot be restrained can cause significant loss of life; therefore, preventing, controlling, and eradicating infectious diseases is crucial. A phylogeographic approach will likely play a key role in understanding the vectors and *H. pylori* (Montano et al., 2015).

Gonzalez-Pons et al., (2018) examined *H. pylori* infection as implicated in many studies in the pathogenesis of many gastrointestinal conditions. The author's cross-sectional review of the population-based biorepository. The authors uncovered that *H. pylori* infections are common among Hispanics living in Puerto Rico. In the research study, the authors mention that the prevalence of *H. pylori* infection is closely linked to socioeconomic conditions, but he does not indicate which condition. The research study is unique because it noted that the *H. pylori* infection may have a racial or ethnic origin not profoundly identified in the U.S. This article is essential for identifying a subset of the population susceptible to *H. pylori* Infection. Little is known about *H. pylori* infection in the United States; what is known resonates from the nation's phylogeographic history.

Present and Past Global Awareness

The epidemiology of *H. pylori* has changed over the decades with the improvement of sanitation, food preservation and methods in eradication (Hooi, 2016). Beginning with the story of Out of Africa is an essential summary of evidence of the *H. pylori* pathogen's ancient African ancestry and the subsequent human migration. Some 60,000 to 150,00 years ago, *H. pylori* infection migrated from Africa to the Middle East and then directly to Europe and Asia (Mègraud, 2016). The variation of *H. pylori* infection is based on its human host and is driven by its host's selective choices in combination with pathogen ancestry. In the U.S., both nationally and regionally, new *H. pylori* infectious gene pools must be considered a past subpopulation (Bakhti et al., 2020). Therefore, the need to review African American, Asian American, Hispanic American, and Middle East

American past and present ancestry-specific germline alteration contributes to the ethnic population in peptic ulcers and cancer risk (Bakhti et al., 2020).

Asia

South Korea has the highest gastric cancer rate in the world (Savoldi et al., 2018). Since 1950, Asian and African countries have improved their living conditions, and the rate of gastric cancer has declined (Savoldi et al., 2018). A significant cause of gastric cancer is linked to *H. pylori* bacteria. In Japan, over the last 40 years, there have been approximately 50,000 deaths from gastric cancer annually (Tsuda et al., 2017). It has been reported that most gastric cancers in Japan are caused by *Helicobacter pylori* infection (Tsuda et al., 2017). Japanese Nation Health Insurance Approved *H. pylori* eradication therapy for patients with chronic gastritis in February 2013 for patients with an endoscopic diagnosis of chronic gastritis, which is positive for *H. Pylori* infection. Tsuda et al., (2017) examined the effect on gastric cancer death rates four years after Japan's expansion of health insurance. In conclusion, those infected with *H. pylori* infection that receive eradication therapy prescriptions for gastritis show a significant decrease in gastric cancer death (Tsuda et al., 2017). Japan's gastric cancer death toll fell yearly from 48,427 in 2013 to 45,509 in 2016 (Tsuda et al., 2017).

Wongphutorn et al., (2018) wanted to ascertain the pervasiveness of risk factors for *H. pylori* infection. The authors compared stool samples and saliva with an asymptomatic person in Northeast Thailand. The author demonstrated that genotypes of *H. pylori* infection are not identical between the oral cavity and intestinal tract. Further investigation of the genetics of the strain diversity and its ability to survive within different host conditions is warranted. *H. pylori* infection colonizes the stomach of more than half the world's population. However, only a portion will develop gastric cancer (Wongphutorn et al., 2018). The infection's long-term outcome is a multifaceted interplay between the host, the pathogen, and the environment. The authors recognize that the burden of the infectious disease carries socioeconomic implications in its diversity of hosts. Wang et al., (2019) explored the birth-cohort pattern of *H. pylori* infection in Japan, confirming the prevalence of *H. pylori* infection in various time points and age groups. He found that the majority of *H. pylori* infection increases with age and shaped trends.

Africa

The current data on *H. pylori* infection in Africa is prevalent (Smith et al., 2019). In Africa, *H. pylori* infection prevalence reaches as high as 50% as the infection is acquired during childhood (Awuku et al., 2017). Risk factors for *H. pylori* infection acquisition have been reported mainly due to overcrowding, infected siblings/patients, and unsafe water sources (Hooi et al., 2017). Africa has a record-high prevalence of *H. pylori* infection, with rates ranging from 41.3 % to 91.3% in children. The clinical manifestation of this infection has not been thoroughly studied (Smith et al., 2019).

Europe

According to new research, resistance to antibiotics commonly used to treat *H pylori* infection has more than doubled in Europe during the past 20 years. The rate was highest in southern Italy at 36.9%, Croatia at 34.6%, Greece at 30%, Poland at 28.5%, and Bulgaria at 26.9%. It was lowest in Denmark at 5%, Latvia at 6.8%, Norway at 8.9%, the Netherlands at 9.2%, and Lithuania at 13%

(Mègarad et al., 2019). The high resistance rates in some countries may reflect antibiotics overconsumption and lack of support for curbing resistance programs. Investigators will correlate the study data with data on antibiotic consumption in different European countries (Mègraud, 2019).

United States

Nolena et al., (2018) discovered that *H. pylori* infection rates are a higher risk factor for gastritis and gastric cancer among the Alaskan native population. Compared to the rest of the U.S., the Alaska Native population has an increased incidence. The study participants were 432 Alaskan Natives, with 63% female with a mean age of 49. Two hundred and seventeen individuals were positive for *H. pylori* infection (Nolena et al., 2018). The authors compared pathological changes with the diagnosis of gastritis and *H. pylori* infection. The authors used two independent pathologists to verify variation and the connections between *H. pylori* infection and gastritis found in the body. The authors emphasized the interconnection between *H. pylori* infection and gastritis. The authors suggested that community public health organizations in high-risk areas provide a population. This article was critical in understanding the association between the risk factor of *H. pylori* infection and gastric cancer. Alaska is one of the few states with a large population of *H. pylori* infection.

Choi et al., (2018) used a prospective study, a double-blind, placebo-controlled, randomized trial. A total of 396 patients were included in the modified intention-to-treat analysis. In the treatment group, 194 were treated, and 202 were in the placebo group. During a median follow-up of 5.9 years, gastric cancer developed in 14 patients (7.2%) in the treatment group and 27 patients (13.4%) in the placebo group. Patients with early gastric cancer who received *H. pylori* infection treatment had lower metachronous gastric cancer rates than patients who received a placebo.

Oncogenesis

Another contributing factor to the harmful effect of the bacteria is the oncogenesis concept, the impact of *H. pylori* infection in developing tumors. *H. pylori* infection can occur through a variety of mechanisms, including the indirect inflammatory effects of *H. pylori* infection on the gastric mucosa and the direct epigenetic impact of *H. pylori* infection on an individual cell (American Cancer Society, 2019). The epigenetic changes in a cell are influenced by several factors, including turning off the cell protein and mediating a lifelong dialog determining how *H. pylori* infection might progress to cancer (American Cancer Society, 2019). *H. pylori* infection predisposes individuals toward gastric adenocarcinoma later in life (Khatoon et al., 2016).

The pathogenesis of *H. pylori* infection is known to induce gastritis, a significant risk factor in the causes of the disease. This factor produces or predisposes toward a particular condition. *H. pylori* infection causes various reactions that damage the gastric mucosa and epithelium. The specific mechanisms involved are unknown.

Antibiotic Resistance

Antibiotic resistance is a global problem. Antibiotic resistance is a term for resistant antibiotic drugs for *H. pylori* infection. Antibiotic resistance occurs when bacteria develop the ability to survive exposure to medications designed to kill or halt their growth. A complete summary of all the peer-reviewed articles written on *H. pylori* infection was beyond this research project's scope. The finding suggests that *H. pylori* infection therapy should be based on bacterial isolates in a country or region. The information should be used to select an empirical treatment if local susceptibility patterns are known Song et al., (2016) looked at 132 patients that failed first-line therapy with bismuth quadruple compared to levofloxacin. The author concluded that the population had a high levofloxacin resistance. Park et al., 2016) multicenter retrospective cohort study for clarithromycin-resistant *H. pylori* infection was conducted in four medicinal centers in different geographic regions in the U.S. He examined clarithromycin resistance DNA sequencing of *H. pylori* 23SrRNA. The U.S. failure rate for clarithromycin exceeds the standard rate; the author cautions against the use until there is better regional and local determination.

Hu et al., (2016) study focused on using China's clarithromycin, metronidazole, amoxicillin, levofloxacin tetracycline, and furazolidone, understanding that increasing antibiotic doses does not improve its affectability and resistibility. Hu et al., (2016) explored new mechanisms for resistance therapies and novel approaches to counter resistance. In Northern India, *H. pylori* infection is widespread. Gehot et al., (2015) research stresses antimicrobial susceptibility patterns of *H. pylori* strains and drug resistance to reduce empirical drug practices. The author discussed the alarming increase in clarithromycin, metronidazole, amoxicillin, levofloxacin tetracycline, furazolidone, and the importance of resistance patterns in clinical trials.

Many research articles on a specific region focus on isolating patterns. *H. pylori's* infection is resistance to an antibiotic is poorly documented in Africa. Smith et al., (2019) recorded that the first-line empirical regimen for *H. pylori* eradication in Africa should include clarithromycin. The researcher believed that fluoroquinolone and levofloxacin-containing regimens should be discouraged without prior antimicrobial susceptibility testing. The literature review consensus is that the need for susceptibility testing and surveillance programs could improve antimicrobial regulation in some developing countries and raise public awareness. Currently, studies show an urgent need for regular antibiotic resistance surveillance studies. *H. pylori* infection can adapt rapidly to changing environments and overcome antibiotics.

Antibiotics have been one of the most transformational discoveries in medicine in the past century. Antibiotics opened new frontiers in medicine and offered not just a treatment but a cure. Many therapies could not have been possible without antibiotics, such as stem cell and organ transplants, bone marrow transplantation, and chemotherapy. These therapies weaken the patient’s immune system, which makes them vulnerable to infections.

Antibiotics were considered a miracle drug, but not anymore. The World Health Organization has admitted that we live in a post-antibiotic era (CDC, 2020). Antibiotic resistance is no longer a prediction for the future (CDC, 2020). Antibiotic resistance is happening right now in every region of the world and has the potential to affect anyone (CDC, 2020). What caused this phenomenal bacterium, a living organism that spreads, to cause infections? Bacteria have no borders; bacteria will find a way to survive. One bacterium in many bacteria will resist an antibiotic and create a new life form. To date, the overuse of all antibiotics has lost its effectiveness against target bacteria. Losing the ability to treat severe bacterial infections significantly threatens public health. Today physicians have limited antibiotics to fight new, stronger germs.

Vulnerable Populations

H. pylori infection is a chronic, infectious, and inflammatory gastric condition that leads to gastritis, ulcer, and gastric cancer, infecting the most vulnerable and physically weak population of children and older adults (Lee et al., 2016). *H. pylori* is commonly found in children; it is acquired between the ages of one and five (Alimohammadi, et al., 2016). Alimohammadi et al., (2016) studied the childhood recurrence of abdominal pain (RAP) and found a positive relationship between *H. pylori* infection and RAP. The author found that the relationship between *H. pylori* infection and socio-economic status was statistically significant. The spread of *H. pylori* is facilitated by a socially deprived environment and the effects of socioeconomic class (Kavali et al., 2018).

The National Health and Nutrition Examination Survey (NHANES) 1999-2000 examined the environmental risk factors associated with *H. pylori* infection seroprevalence. Krueger's et al., (2015) multivariable logistic regression study; reported that participants aged < 20 years were seropositive with significantly associated with drinking water from a well as the source and living in a crowded home. Adults aged >20 years who were seropositive were associated with soil-related occupations and healthy water compared to those working in non-exposed adults. Environmental exposures such as water and discipline play a role in *H. pylori* infection transmission (Krueger et al., 2015). Kumar et al., (2017) used the SEM to explore veterans with a diagnosis of *H. pylori* infection. They found a significantly higher risk of gastric cancer in racial and ethnic minorities. The theory raised questions about the disadvantaged population and focused on prevention, early intervention, and public awareness. Nagy and Moll-Bland, (2016) state that the risk of infection increases in lower socioeconomic and ethnic groups within many geographical populations. Reviewing an individual's ethnic background, heritage, and inherited living conditions is essential. Our social and cultural norms govern our thoughts, beliefs, and behaviors. They are shared assumptions of appropriate behaviors based on society's values and are reflected in everything. The SEM framework can show how the interplay between individual relationships, community, and societal factors affects the lives of those susceptible to *H. pylori* infection.

In the U.S., another factor to consider is the geographic variability in the types of healthcare insurance coverage. Variable healthcare costs and utilization at local, regional, and state levels affect co-morbidities and mortality outcomes. Population co-morbidity and healthcare availability account for between 18-64% of the variability in mortality outcomes, 3-39% of the variability outcomes, and 22-70% in the variability in prevention (Rosenberg, 2016).

Summary and Conclusions

The literature indicates that *H. pylori* infection can adapt rapidly to changing environments. Moreover, it has been known to be biologically and genetically unstable. Today, research is mainly focused on antibiotic resistance to drug treatments. The present study will focus on understanding which geographic location presents a more conducive environment for *H. pylori* infections. In summary, the knowledge of *H. pylori* infection pathogenesis and disease development has been improved by studies focusing on investigating bacterial factors with understanding sanitation, childhood hygiene, and food. Some individuals are infected and develop symptoms of *H. pylori* infection; others are not. The present study may fill a gap in the geographic location in the U.S. and provide sub-groups more susceptible to the bacteria with possible risk factors.

Continually clarifying and refining *H pylori* pathogenesis's roles will benefit vaccine and alternative therapy development. *H. pylori*-infected areas have yet to be well known in the U.S. This study will examine the presence of *H. pylori* infection geographically. Changes in patterns of life and causes of death are the paradigm of science and philosophies that forage the theories, research methods, and standards that constitute a legitimate contribution to the field of epidemiology, keeping that inherent heterogeneity is present in all ecological systems. To address the gap in the literature, in chapter three, a method will be proposed to identify individuals who host this bacterium, along with risk factors that are a critical component of future research in disease ecology (Kumar et al., 2019). *H. pylori's* infection cumulative incidence related to the primary cause of peptic ulcers and other associated chronic gastritis and adenocarcinoma of the stomach in the U.S. may be defined. Furthermore, this study may encourage testing younger children before alterations caused by the bacterial infection cannot be reversed at the adult level (El-Serag et al., 2018).

Chapter 3: Research Method

Introduction

In this multilevel study, I sought to identify the geographic locations of *H. pylori* infections in the United States. I compared time intervals 2000–2002 and 2016–2018 and identified the socioecological risk factors. This project is unique because it may determine the population clusters of *H. pylori* infection across the United States. Humans and *H. pylori* infection show substantial coevolutionary traits (Hu et al, 2016). Previous research indicates that *H. pylori* infection can rapidly adapt to changing environments and resist antibiotic treatments (Hu et al., 2016).

An unusual occurrence of a disease and any exceptional cases or clusters of the disease distribution may help identify bacterial spread amongst the populations and point to how to eliminate it (Deaton, 2013). If the geographic distribution of *H. pylori* infection reveals risk factors for specific populations, then screening and treatment programs can be adequately developed for a geographic population (Mégraud et al., 2016). Identifying the age of transmission of *H. pylori* infection may also indicate a need for parent education strategies to assist in early recognition of the disease among children.

In Chapter 3, I will discuss the research method used in this study. I begin by presenting the study design and research approach. The setting and sample are then described, along with a sample size justification. Next, the data collection and analysis procedures are detailed. Then, I present the instruments used to measure the variables, including purpose, methods, scoring, and statistical parameters. The data collection and analysis procedures are then described. Before concluding the chapter, I discuss ethical issues.

Research Design and Rationale

I surmised that a cross-sectional study would best answer the question about the prevalence of *H. pylori* infection. It may establish the norm for a specific demographic in a particular region during an exact time. Due to the time constraints, I faced as a doctoral student, I found a cross-sectional study to be ideal because it was relatively inexpensive and quick to conduct. One issue considered is that in October 2015, HCUP modified the version of the ICD-9-CM code. The 10th revision (ICD-10-CM) replaced the ICD-9-CM system for inpatient hospital procedures after the third quarter; therefore, some state data were not captured (Healthcare Cost and Utilization Project, 2022). This cross-sectional study may infer a relationship or correlation and pave the way for future investigations. This cross-sectional observational study included an extensive sample of the U.S. population to examine the prevalence of *H. pylori* and test whether a variable’s effects on the predictor were significantly different. I used the chi-square test to answer RQ1 and logistic regression analysis using SPSS to answer RQs 2 and 3.

Chi-square is a test that is a test of independence used to determine the frequency distribution between groups. The chi-square test was appropriate for this research study because the data being analyzed were from a random sample and the variable in question was categorical (Dietz & Kalof, 2009). I used this statistical test to tell which of the categorical variables occurred more frequently. This application is an observation of mutually exclusive classes.

To analyze RQs 2 and 3, I performed multiple logistic regression, which is a statistical method used to understand the relationship between multiple predictor variables and a response variable. The method is used to calculate the probability of multiple various sets of variables to estimate the probability of it having a value on the dependent variable (Scribbr, 2022). MLR was used to examine the relationship between one or more predictor variables.

I used SPSS to perform multiple logistic regression on the age, race, gender, and health insurance independent variables. Multiple logistic regression can handle multiple independent variables, whether continuous or categorical (Laerd, 2018). The question can be asked about the odds probability of the dependent variable occurring as the independent variable value changes. The procedure allows for the reporting of the p-value and the significance of the relationship between the dependent and independent variables.

Methodology

Population

The study population for this research study came from the NIS, which is part of the HCUP, an entity that is sponsored by the Agency for Healthcare Research and Quality (HCUP, 2022). NIS databases consist of hospital inpatient stays collected from billing data submitted from the hospital to statewide organizations across the United States. NIS uses ICD codes and includes all patient health insurance types, including Medicare, Medicaid, private insurance, and uninsured (HCUP, 2022). NIS has a large sample size that enables analyses for all populations. I used the ICD-9-CM and ICD-10-codes for *H.*

pylori infection (041.86). ICD codes were revised in 2015. Therefore, ICD-9-CM and ICD-10-CM cover the period of data needed for 2000 to 2020 (HCUP, 2022).

Sampling and Sampling Procedures

For this study, I used the NIS databases. The NIS is a set of longitudinal hospital inpatient databases. The database owner is the Agency for Healthcare Research and Quality, under which is the HCUP. The data are coded in the HCUP databases; the descriptions are cumulative across all the years of NIS data from 1988 to the current data year. As of 1988, NIS contained information on a stratified sample of over 1,000 U.S. hospitals with approximately 8 million hospital stays per year (HCUP, 2022). The introduction of ICD-10-CMcode for reporting clinical diagnoses and inpatient procedures was introduced in 2015 (HCUP, 2022). The sample size will vary according to the NIS-reported data. NIS has an online website where a researcher can apply for access to the data. The researcher must complete the HCUP Data Use Agreement training course required by all users. Once the training is completed, a researcher can purchase access to the data. Guo (2021) also used the NIS database to examine temporal trends in peptic ulcers.

I used G*Power to calculate the minimum sample size needed. The statistical z test was used, the means: Difference between two dependent means (matched pairs) (2000-2002) and (2016 -2018). I chose a medium effect size. The 2-tailed test with alpha = .05 and power = 80% equated to a total sample size of 105. When G*Power was used to calculate the minimum sample size for the independent variables race, age, gender, and health insurance, the statistical z-test was used. The means: The difference between the two dependent means (two groups) effect size was 0.5 at 80% power. The sample size needed was 619.

The NIS represents a 20% stratified sample of the U.S. community hospitals, currently containing data from 10 million inpatient stays in 46 states. Data used for this research study included clinical and nonclinical elements: diagnoses at admission, patient demographics, payment source, and hospital provider characteristics. Data collection is ongoing. The database was initiated in 1988, with the number of states contributing data growing over time. This database has many advantages, and the NIS is used widely to address an array of RQs. Data analysis is a sampling of admissions, but it is somewhat unequal in this database: individual states or types of patients (usually defined by demographic variables might be over-and under-represented. Examples of the use of this database can be found in the publications by Alemu, (2022), Castellanos (2022), and Wang (2022). Patel (2022) used the NIS database to publish an article on Hospital Factors and Socioeconomic Status. Alemu (2022) used NIS to determine maternal comorbidities using hospital discharge status. Castellanos, (2022) used in-hospital mortality records associated with childhood racial/ethnic disparities. Wang (2022) used NIS in-hospitalized data on the influence of clinical outcomes of chronic thrombocytopenia on clinical outcomes of hip and knee arthroplasty.

Procedures for Recruitment, Participation, and Data Collection

The collection of data from hospital databases is secondary data. Secondary data analysis allows the researcher to test new ideas, theories, and frameworks. Re-analyzation and re-interpretation will enable us to create further RQs and generate new knowledge from existing research (Ruggiano and Tamm, 2019). This study’s larger sample data set represents the target population and allows for greater validity (Ruggiano and Tamm, 2019).

Variables

Numerous hypothesized factors relate to the decline in the prevalence of *H. pylori*. For example, higher socioeconomic status, better hygiene practices, and lower household crowding (Sonnenberg, et al., 2020). These factors, genetics, and antibiotics contribute significantly to prevalence (Sexton, S., 2018). As more of the world’s infrastructure develops access to clean water and sanitation, fewer people than before are exposed to bacteria. Ultimately, prevalence rates in a population will become lower but remain different between regions based on environmental and biological contributions (Hooi et al., 2017). I aim to evaluate where demographically, *H. pylori* infection may be associated with potential risk factors of race, age, gender, and health insurance. *H. pylori* infection is the dependent variable, and the independent predictors are race, age, gender, and health care insurance.

Dependent Variable

The purpose of the research is to discover the cluster locations of *H. pylori* infection in the U.S. *H. pylori* infection data will be collected from the NIS database and captured in SPSS for the range 2000-2002 and 2016-2018. Regional data aims to estimate the distribution of *H. pylori* infection and to document trends using the chi-square method of distribution and graphs. Data will be entered into the SPSS Version 28 and graphed. The p-value of <0.05 is significant, and an 80% (median) confidence interval for the association between the groups. The goal is to collect statistical data to evaluate and identify infection groups of *H. pylori* infection clinically and compare the migration over time. From this point we can develop a management plan. (Castelli, 2017).

Independent Variables

The second part of this research collects individuals' data to see whether the dependent variable (*H. pylori infection*) is linked to several independent variables (age, race, gender, and health insurance). A multivariable logistic regression model using SPSS will examine *H. pylori* infection as the dependent variable and age, race, gender, and health insurance as the independent variables. These patient-level factors are within the hospital-level factors admission day demographic.

This research aims to discover the independent variable (IV) that significantly impacts the dependent variable (*H. pylori* infection). The independent variables (IV) for this proposed study are categorical. The purpose is to categorize the data into groups based on age, race, gender, and health insurance. Hospital characteristics for variables are standard on admissions, for example, race; (Hispanics, Asian Pacific Islander, Whites, Blacks, and American Indian/Alaska Native); age; (≤55) and (>55); gender; (male and female) and health insurance; (Medicare, Medicaid, Private, Self-paid or no Insurance). I will compare two-time groups (2000-2002) and (2016 -2018) the age, race, gender, and health insurance as independent variables that will help isolate the impact of the dependent contribution on the disease's progression.

In this research study, health insurance is an independent variable. It can have either a positive or a negative measure on the progress of *H. pylori* infection. I will examine whether health insurance is a variable that can influence the outcome. We can determine whether the type of health insurance positively or negatively affects the population and *H. pylori* infection. This research study will look at data elements for health insurance such as Medicare, Medicaid, private insurance, self-pay, and no insurance. This multivariable logistic regression analysis model identified hospitalizations for *H. pylori* infection diagnosis. The p-value gives us the likelihood of acquiring *H. pylori infection* related to race, gender, age, and health care coverage will be determined.

Quantitative Sample

Descriptive statistics and central tendency measures will help identify the shape of the distribution geographically and the bulk of the cases. The means of central tendency are commonly used to describe a data set and the variability or dispersion. We can capture the mean, median, and mode and measure the standard deviation or variance, the maximum values, the kurtosis, and the skewness. The probability of *H. pylori* infection occurrences will be calculated using the cumulative probability. I will use a chi-square analysis and a multiple logistic regression model. In 2015 the ICD-9 codes were updated to the ICD-10 code in October 2015. In 2015 statistics were calculated using only months 1-3 quarter data for ICD-9 and the fourth quarter for the ICD-10 code. As for ICD -10 data, the statistics available are limited. Data element descriptions explain how the data element is coded in the HCUP database. Not all data elements are uniformly coded across states. Not all data elements are available each year. In addition, only discharge rates are displayed, not the number of discharges; logistic regression will be used to calculate the maximum likelihood of observing the presence of *H. pylori* infection with a relationship to race, age, gender, and health insurance. The categorical variable solves a classification problem as an independent variable predictor.

Data Analysis Plan

Data analysis will be conducted using the computer software program SPSS, version 28. Data will be used for the two groups (2000-2002) and (2016-2018) and the demographic variables of age, race, gender, and health insurance. In preparation data cleaning for data analysis, was done with SPSS descriptive, frequency identifying and replacing, incorrect or incomplete data, using series mean value. Chi-square was used to identify changes in *H. pylori* infection rates in the Northeast, Midwest, Southern, and Western regions of the U.S. A multiple logistic regression model was used to predict the outcome of a dependent variable and estimate the relationship between a dependent and independent variable (age, race, gender, and health insurance. Multiple logistic regression can be used to analyze one or more independent variables that may be categorical or continuous when the dependent variable is dichotomous (StatsTest, 2023). The question can be asked about the p-value of the DV occurring as the values of the IVs change from year to year.

A visual presentation of *H. pylori* infectious areas on maps is needed, given that spatial data is currently limited. Improving geospatial data availability can provide researchers with a measurable relationship that can allow a detailed conclusion. The United States needs more recent comparative clinical trials, more knowledge of *H. pylori* infection antibiotic resistance patterns, local cure rates, relevant demographic details (age, race, and ethnicity), and more recent data on temporal trends (Shah et al., 2021). Spatial analysis is a geographical analysis that seeks to explain drug resistance, genetics, and human behavior using map technology to show the global distribution of *H. pylori* infections (Hooi et al., 2017). Topological and geometric data can study the spatial distribution of many products, diseases, and resilience.

I used geographic location to address RQ1, which was, Is there a significant difference between time periods 2000–2002 and 2016–2018 and the geographic distribution of *H. pylori* infection in the United States? The chi-square test of independence was used to determine those individuals diagnosed with *H. pylori* during admission hospitalization, defining the study population from the total population for each year 2000, 2001, 2002, 2016, 2017, and 2018. I will take the observed frequency minus the expected frequency to find the significant difference using the chi-square test.

Restatement of the Research Questions and Hypotheses

RQ1: Is there a significant difference between time periods 2000–2002 and 2016–2018 in the geographic distribution of *H. pylori* infection in the United States?

$H_0 1$: There is no significant difference between 2000–2002 and 2016–2018 in the geographic distribution of *H. pylori* infection in the United States.

$H_a 1$: There is a significant difference between 2000–2002 and 2016–2018 in the geographic distribution of *H. pylori* infection in the United States.

RQ2: Is there an association between age, gender, race, and *H. pylori* infection in the United States?

$H_0 2$: There is no association between age, gender, race, and *H. pylori* infection in the United States.

H_a2: There is an association between age, gender, race, and *H. pylori* infection in the United States.

RQ3: Is there an association between health insurance coverage (Medicare, Medicaid, private, or no insurance) and *H. pylori* infection by year?

H_03: There is no association between health insurance coverage (Medicare, Medicaid, private, or no insurance) and *H. pylori* infection by year.

H_a3: There is an association between health insurance coverage (Medicare, Medicaid, private, or no insurance) and *H. pylori* infection by year.

A non-experimental design will be used because the categorical groups are already determined, non-manipulable, and not subject to random assignment. I will use the chi-square, repeated measure ANOVA, and multiple logistic regression Model. The dependent variable is *H. pylori* infection, which can be found under Infectious and Parasitic Diseases 001.139 ICD-9 code (041.86) and ICD -10 (B986). Multiple logistic regression will be used to calculate the maximum likelihood of observing the presence of *H. pylori* infection with a relationship to race, age, gender, and health insurance. The tables will include odd rational 95% C.I. and p-value. The p-value will indicate the probability of the independent variable.

Threats to Validity

Threats to validity can affect - the data collected in a study sample. These threats to validity include internal validity threats, external validity threats, statistical conclusion validity threats, and construct validity threats. Because most of the participants live in one regional area, a threat is posed to the validity of generalizing results from this study to other countries. Information from HCUP database input is valid, but not all states make their data available, which can cause gaps in data when comparing conditions. The integrity of the data is known to be complete to create a database. Data cleaning and repairing data for analysis can be done by removing or modifying incorrect or incomplete data, for missing by simplifying by creating a missing category.

Ethical Procedures

This research project uses data from a secondary resource, HCUP, and agreed upon. Research involving children is subject to many ethical hazards. In this proposed study, these hazards will be mitigated using archival data to have no direct contact with any study participant. No new data will be collected. The clinic has assigned each case a numerical code. These codes will be collected. These codes are entered into the database; no names or other identifying information will be contained in the researcher's computer data file. Data will be reported, but no identifying information and no information on single cases will be registered. This way, it will not be possible to identify any participants in the final written document. The Walden University Institutional Review Board approved this secondary data analysis (approval no. 09-28-21-0599140).

Summary

This is a multilevel study to identify the geographic locations of *H. pylori* infections in the U.S., comparing time intervals from 2000-2002 to 2016-2018 and the socio-ecological risk factors of age, gender, race, and health insurance. The methodology used in this research study includes the chi-square and multivariable logistic regression model to evaluate the impact of the independent variables on *H. pylori* infection. I examined the odds probability of the dependent variable occurring as the values of the independent variable change. This quantitative study will use a non-experimental design to compare *H. pylori* infection using inpatient hospital admission. Before determining the prevalence of *H. pylori* infection in various geographic areas, some studies were not designed to investigate risk factors for *H. pylori* infection positivity but to observe the multitude of mutations and the antibiotic response to drugs. It could have been clearer whether prevalence rates for the various groups compared were directly or indirectly standardized to adjust for historical differences. Future research may determine the link to gastric cancer by identifying the population, location, and social and economic factors.

Chapter 4: Results

Introduction

In this cross-sectional observational study, I sought to identify the geographic migration of *H. pylori* infections in the United States by comparing time intervals 2000–2002 and 2016–2018 and identifying socioecological risk factors. The primary hypothesis of this study is that understanding the regional changes in *H. pylori* infection clusters over time will significantly improve the health awareness of the disease, considering its prevalence in gastric cancer. The total estimated gastric cancer in 2020 is 1.1 million new cases (Morgan et al. 2022). For this research study, I used secondary data from an extensive population-based nationwide inpatient hospital database, the NIS. The data were obtained from the Agency for Healthcare Research and Quality. The HCUP includes the most extensive longitudinal hospital care data collection in the United States (HCUP, 2022). For this study, patients diagnosed with *H. pylori* infection were compared between 2000 and 2002 and 2016 and 2018. The total population varied each year (see Tables 1 and 2).

To perform the statistical analysis, I used SPSS Version 28. The data analysis techniques used to address the hypothesis were descriptive statistics, chi-square analysis, and multiple logistic regression. Multiple logistic regression was used to evaluate the association between the independent variables (age, gender, race, insurance, and region) to determine whether there is an association with *H. pylori* infections. *H. pylori* was coded as a dichotomous variable, *+HP* and *-HP*, for multiple logistic regression.

Data Collection

States in NIS vary by data years. In 2000, NIS was limited to 28 states. In 2018 it increased to 48 states. In 2012, NIS hospitals changed from area to zip codes management by census divisions (HCUP, 2022). For this research. . In this chapter, I discuss the data analysis for each RQ using inferential statistics. RQ1 compared 2000–2002 to 2016–2018 population distribution and geographic region changes over time. Each NIS sample was taken from admission data submitted to HCUP by its partners. I used chi-square for the admitted population hospitalized and the total population of *H. pylori* infection between 2000–2002 and 2016–2018. The data set for the year in NIS has over 7 million cases entered annually. The cases from the data sets for *H. pylori* infection that met the inclusion criteria for this study were weighted to make national estimates. The variables were selected from the data set and as demonstrated in *n* = millions. The total population varies year to year, 2000 (*n* = 7,450), 2001 (*n* = 4,585), 2002 *(n* = 4,140), and 2016 (7,135), 2017 (7,159) and 2018 (7,105).

The number of states that contributed varied each year. Approximately 20% of all U.S. community hospitals were represented in the databases. The predictor variables for the study were regional location (Northeast, Midwest, South, and West), and the covariates that could affect the outcomes were age, gender, race, and health insurance. I explored these using descriptive statistics and multiple logistic regression. The population of interest for this study was individuals with *H. pylori* infection diagnosed at hospitalization. The sample size for each year was calculated using the total number of infected individuals per total population.

Procedures for Addressing the Volume of Data

The definition of big data is data that contains a greater variety, arriving in increasing volumes and having the velocity to be acquired quickly and the need to process at a faster rate (Yunita et al., 2022). NIS is big data. One downfall of NIS's big data is the misrepresentation across states in any given year; NIS suggests not using a state-to-state comparison basis on state-specific estimates from the NIS (HCUP, 2020). Moreover, there is a misrepresentation of the number of states each year per region and the entry and exit of states and hospitals in the sampling frame. NIS draws several hospitals from the sampling frame to net 20% nationally. (HCUP, 2020) Therefore, the representation of states in a region changes from year to year.

NIS staff are collecting an enormous volume of data every day, resulting in a limited number of statistical tests that could be computed on a standard laptop combining all the data from year to year. Originally for RQ1, I was going to use the Poisson statistics, but running the Poisson model on the data within a mapping system was not practical for this research study. There was a need for latitudinal and longitude data points. Therefore, it was impossible to calculate distance because states enter and exit at will. Instead, frequency tables, summaries, and crosstabulation were used to determine statistics over time from the region. Multiple logistic regression could only be calculated from year to year. Due to the size of the population, comparing time ranges was not practical because the population numbers would triple in size, which is beyond the capabilities of a standard computer.

Once downloaded into SPSS, there were two reasons for changing the time span from 1999-2003 and 2014-2018 to 2000-2002 and 2016-2018. The first issue was that in October 2015, HCUP modified the version of the ICD-9-CM code. A new tenth revision (ICD-10-CM) replaced the ICD-9-CM system for inpatient hospital procedures after the third quarter; therefore, some state data was not captured. The ICD was revised to incorporate changes in the medical field to ICD 10. The tenth revision (ICD 10) differs from ICD 9. ICD-10 is printed in a three-volume set compared with ICD-9's two-volume group. Second, group ICD-10 has alphanumeric categories rather than numeric categories. Some chapters have been rearranged, some titles have changed, and conditions have been regrouped. ICD-10 has twice as many categories as ICD-9.

The second reason is that the number of disease categories increases yearly in the database. The term dx in the system represented a disease category. There are 14,000 ICD 9 codes and 283 categories, and 70,000 ICD 10 codes and 530 categories represent primary and secondary diseases. As time progressed from 1989 to 2021, the database changed increasingly. For Group A 2000-2002, the diagnosis code for *H. pylori* was ICD 9 code 04186, and for Group B, the ICD 10 code was B9681.

Chi-square and repeated measure ANOVA analysis was used to determine the relationship between *H. pylori* infection (dependent variable) and region (independent variable). The assumptions met included categorical variables and two or more categorical independent variables. The confidence interval was 95%, and the p-value was < 0.05 for the statistical analysis. This chapter discusses the data analysis for each RQ using inferential statistics.

Baseline Descriptive and Demographic Characteristics of Sample

Secondary data from large data sets can be complex, incomplete, misinterpreted, and missing. Missing data was not used for this study. Table 1 includes a summary of the number and percentage of patients with *H. pylori* infection by age, gender, race, region, and health insurance for 2000-2002. In 2000, 16,182 patients were diagnosed with *H. pylori* infection. Most were female, 8,452 (52%), while 7,730 (48%) were male. Most of the patients were White, 7473 (65%), followed by Black 2014 (13%), Hispanic 1422 (12%); Asian, 89 (7%); and Native American, 89 (7 %). The predominate health insurance type was Medicare 8,607 (56%), followed by Private Insurance 4,121 (27%), Medicaid 1,523 (9%), Self-pay 1,026 (7%), and No charge 88 (1%). Most patients fell into the age category ≤55 11,016, 68%), while 5,163 (32 %) were > 55. The region with the most diagnoses was the Midwest 5,738 (36%), followed by the West 3,869 (24%), South 4446 (28%), and Northeast 1,836 (12%).

In 2001, 959 patients were diagnosed with *H. pylori* infection. Most were females, 489 (51%), while 470 (49%) were male. Most of the patients were White 543 (58%), followed by Hispanic 216 (23%), Asian 108 (12%), Black 60 (6%), and Native American 7 (1%). The predominate health insurance type was Medicare 476 (54%), followed by Private insurance 214 (24%), Medicaid 159 (18%), Private 214 (24%), Self-pay 1021 (7%), and No charge 0 (0%). Most patients fell into the age category >55, 675 (70 %), while 284 (30%) >55. The region with the most diagnoses was the South 425 (45%), followed by the West 245 (26%), Midwest 227 (24%), West 245 (26%), and Northeast 42 (5%).

In 2002, 6577 patients were diagnosed with *H. pylori* infection. Most were female, 3,387 (51%), while 3,190 (49%) were male. Most of the patients were White 2,256 (53%), followed by Black 800 (19%), Hispanic 759 (18%), Asian 405 (9%), and Native American 3 (1%). The predominant health insurance type was Medicare 3314 (52%), followed by Private Insurance 1783 (28), Medicaid 730 (11%), Self-pay 401 (6%), and No charge 29 (3%). Most patients fell into the age category > 55 4222 (64%), while 2355 (36 %) were ≤ 55. The region with the most diagnoses was the South, 2683 (42%), followed by the West, 1705 (27%), Midwest, 1560 (24%), and Northeast, 404 (7%).

Table 1

Stratified Number of Patients with H. pylori Infections for 2000–2002

	Year					
	2000		2001		2002	
Variable	*n*	%	*n*	%	*n*	%
Gender						
Male	7,730	48	470	49	3,190	49
Female	8,452	52	489	51	3,387	51
Race						
White	7,473	65	543	58	2,256	53
Black	2,014	13	60	6	800	19
Hispanic	1,422	12	216	23	759	18
Asian	422	3	108	12	405	9
Native American	89	7	7	1	3	1
Missing	4,762		25		2,354	
Health insurance						
Medicare	8,607	56	476	54	3,314	52
Medicaid	1,523	10	159	18	730	11
Private	4,121	26	214	24	1,783	28
Self-pay	1,021	7	35	4	401	6
No charge	88	9	0	0	29	3
Missing	822		75		320	
Age (years)						
≤ 55	11,016	68	284	30	2,355	36
≥ 55	5,163	32	675	70	4,222	64
Missing	3					
Region						
Northeast	1,836	12	42	5	404	7
Midwest	5,738	36	227	24	1,560	24
West	3,869	24	245	26	1,705	27
South	4,446	28	425	45	2,683	42
Missing	293		20		225	

Note. *N* = 16,182 in 2000, *N* = 959 in 2001, *N* = 6,577 in 2002.

Table 2 shows that 6,067 patients were diagnosed with *H. pylori* infection in 2016. Most were male, 3186 (52%), while 2881 (48%) were female. Most of the patients were White 2,416 (43%), followed by Black 1559 (28%), Hispanic 1198 (22%), Asian 356 (6%), and Native American 54 (1%). The predominant health insurance type was

Medicare 2442 (47%), followed by Medicaid 1513 (30%), Private Insurance 703 (13), Self-pay 485 (9%), and No charge 55 (1%). Most patients fell into the age category ≥ 55, 3,398 (56%), while 2,659 (44%) were ≤ 55. The region with the most diagnoses was the Northeast, 233 (44%), followed by the Midwest, 1424 (24%; West, 1260 (21%), and South, 89 (15%).

In 2017, 6059 patients were diagnosed with *H. pylori* infection. Most were male, 3,235 (53%), while 2,824 (48%) were female. Most of the patients were White, 2,379 (43%), followed by Black 1,619 (29%), Hispanic 1,156 (21%), Asian 355 (6%), and Native American 82 (1%). The predominant health insurance type was Medicare 2,549 (43%), followed by Medicaid 1,520 (21%), Private Insurance 1,294 (22), Self-pay 482 (8%), and No charge 36 (6%). Most patients fell into the age category ≥ 55 3,478 (57%), while 2,576 (43%) were ≤ 55. The region with the most diagnoses was the Northeast, 2396 (40%, followed by the Midwest, 1,390 (24%); West, 1,236 (21%); and the South, 896 (15%).

In 2018, 5,828 patients were diagnosed with *H. pylori infection*. Most were male, 3,119 (53%), while 2709 (47%) were female. Most of the patients were White 2,214 (41%), followed by Black 1,593 (30%), Hispanic 1,165 (21%), Asian 365 (7%), and Native American 69 (1%). The predominant health insurance type was Medicare 2,455 (43%), followed by Medicaid 1,498 (26%), Private Insurance 1,224 (22), Self-pay 456 (8%), and No charge 31 (1%). Most patients fell into the age category ≥ 55 3,449 (59%), while 2,379 (41%) were ≤ 55. The region with the most diagnoses was the Northeast, 2,250 (40%), followed by the Midwest, 1,403 (25%); West, 1,168 (20%; and the South, 882 (15%).

Table 2

Stratified Number of Patients with H. pylori Infections for 2016-2018

	2016		2017		2018	
	n	%	n	%	n	%
Gender						
Males	3186	52	3235	53	3119	53
Females	2881	48	2824	47	2709	47
Race						
White	2416	43	2379	43	2214	41
Black	1559	28	1619	29	1593	30
Hispanic	1198	22	1156	21	1165	21
Asian	356	6	355	6	365	7
Native American	54	1	82	1	69	1
Missing	484		468		422	
Health Insurance						
Medicare	2442	47	2549	43	2455	43
Medicaid	1513	30	1520	21	1498	26
Private	703	13	1292	22	1224	22
Self-pay	485	9	482	8	456	8
No charge	55	1	36	6	31	1
Missing	869		180		164	
Age						
age ≤55	2659	44	2576	43	2379	41
age >55	3398	56	3478	57	3449	59
Missing	10		5			
Region						
Northeast	2338	40	2396	40	2250	40
Midwest	1424	24	1390	24	1403	25
West	1260	21	1236	21	1168	20
South	895	15	896	15	882	15
Missing	150		141		125	

Results

Research Question 1

The focus of RQ1 is on comparing 2000–2002 to 2016–2018 *H. pylori* infection population distribution and geographic region changes over time.

RQ1: Is there a significant difference between the time periods 2000–2002 and 2016–2018 in the geographic distribution of *H. pylori* infection in the United States?

$H_0$1: There is no significant difference between 2000–2002 and 2016–2018 in the geographic distribution of *H. pylori* infection in the United States.

H_a1: There is a significant difference between 2000–2002 and 2016–2018 in the geographic distribution of *H. pylori* infection in the United States.

Table 3 displays the number of states and hospitals contributing to the HCUP's NIS database each year. A state that appears in a previous year might not be able to provide data to HCUP in the following years; therefore, it may not be listed in the next year. Table 4 shows the region in which each state is located. Figure 1 is the regional map provided by HCUP.

Table 3

State Providing Data to HCUP by Year

Calendar year	States in the frame	# Of States	# Of Hospitals
2000	AZ CA CO CT FL GA HI IA IL KS KY MA MD ME MO NC NJ NY OR PA SC TN TX UT VA WA WI WV	28	994
2001	AZ CA CO CT FL GA HI IA IL KS KY MA MD ME MI MN MO NC NE NJ NY OR PA RI SC TN TX UT VA VT WA WI WV	33	986
2001	CA CO CT FL GA HI IA IL KS KY MA MD ME MI MN MO NC NE NJ NV NY OH OR PA RI SC SD TN TX UT VA VT WA WI WV	35	995
2016	AK AR AZ CA CO CT DC FL GA HI IA IL IN KS KY LA MA MD MI MN MO MS MT NC ND NE NJ NM NV NY OH OK OR PA RI SC SD TN TX UT VA VT WA WI WV WY	47	4,573
2017	AK AR AZ CA CO CT DC DE FL GA HI IA IL IN KS KY LA MA MD ME MI MN MO MS MT NC ND NE NJ NM NV NY OH OK OR PA RI SC SD TN TX UT VA VT WA WI WV WY	48	4,584
2018	AK AR AZ CA CO CT DC DE FL GA HI IA IL IN KS KY LA MA MD ME MI MN MO MS MT NC ND NE NJ NM NV NY OH OK OR PA RI SC SD TN TX UT VA VT WA WI WV WY	48	4,550

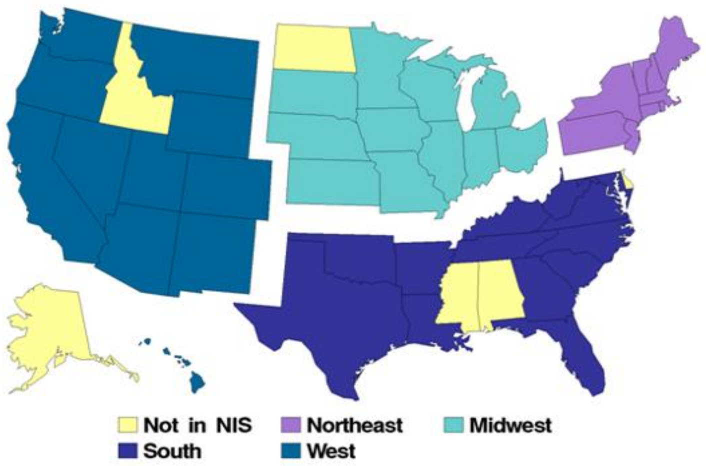
Table 4

List of States that Comprise Each Region

Region	States
Northeast	Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island, Vermont
Midwest	Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, Wisconsin
South	Alabama, Arkansas, Delaware, District of Columbia, Florida, Georgia, Kentucky, Louisiana, Maryland, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Texas, Virginia, West Virginia
West	Alaska, Arizona, California, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, Wyoming

Figure 1

National Inpatient Sample (NIS) Regions



Note. From Agency for Healthcare Research and Quality, Center for Delivery, Organization, and Markets, Healthcare Cost and Utilization Project, National Inpatient

Sample (NIS) 2000-2018. In the public domain. Authorization for the map is found in the appendix.

Preliminary Analysis

A preliminary analysis was completed using a chi-square test of independence to determine those participants diagnosed with *H. pylori* infection during admission hospitalization, defining the study population from the total population for each year 2000, 2001, 2002, 2016, 2017, and 2018. I chose chi-square because the assumptions that were met included a categorical dependent variable of whether the population has the disease. The independent category consists of two or more categorical variables. The variables were mutually exclusive categories. This distribution-free test examines the association between categorical variables in SPSS; I created two nominal variable levels (+ H. pylori and – H. pylori) infection. I used the NIS data sets to answer RQs 1, 2, and 3.

Following the outcome of this analysis, I used Repeated Measure ANOVA. The Repeated Measure ANOVA was used to determine whether there is a statistically significant difference between the means comparing 2000-2002 to 2016-2018 by region. For the years 2000, 2001, and 2002, I used ICD 9 Code, 04186 = positive for +HP; for years 2016, 2017, and 2018, I used ICD 10 Code, B9681= positive for +HP. The objective of this study is to compare the years 2000-2001 to the years 2016-2018 geographically to identify if there was a change across the passage of time and regional migration. The results from the repeated measure ANOVA greenhouse geisser indicate, if the *p*-value is more than .05, then there is not a statistically significant difference between the two observations identified in the outcomes. The Greenhouse-Geisser (F).036) p=.854 and

Time*Region (F) 1.849 p=.217 result, we find that the null hypothesis can be accepted for the independent variables.

Table 5

Repeated Measure ANOVA

Source		Sum of Squares	df	Mean Square	F	Sig.
factor1	Greenhouse Geisser	1.382E-9	1	1.382E-9	.036	.854
factor1 * Region	Greenhouse Geisser	2.107E-7	3	7.023E-8	1.849	.217

The result showed that for each of the means where p >.05, we indicate that the null hypothesis “There is no significant difference between 2000-2002 and 2016-2018 and geographic distribution of *H. pylori* infection in the United States by Region” can be accepted and that we can reject the alternate hypothesis.

Chi-square was used to calculate marginal means. Figure 2 reveals a decrease and increase in interaction between the effects of time and region. In 2000-2002, the Southern region of the United States had more *H. pylori* infection admissions compared to the other regions and decreased from 2016 to 2018. The main effects analysis showed that within the region, there was a statistically significant effect (p = <.001). Figure 2 shows that *H. pylori* infection rates did not change in the Midwestern region. There was a decrease in *H. pylori* infection between 2000-2002 and 2016-2018 in the Western region. The Northeastern region had the lowest number of patients with *H. pylori* infection in 2000-2002 and the highest in 2016-2018. However, the periods were not statistically significant from each other. Below in Table 6 you will the frequency data for 2000-2002 and 2016-2018.

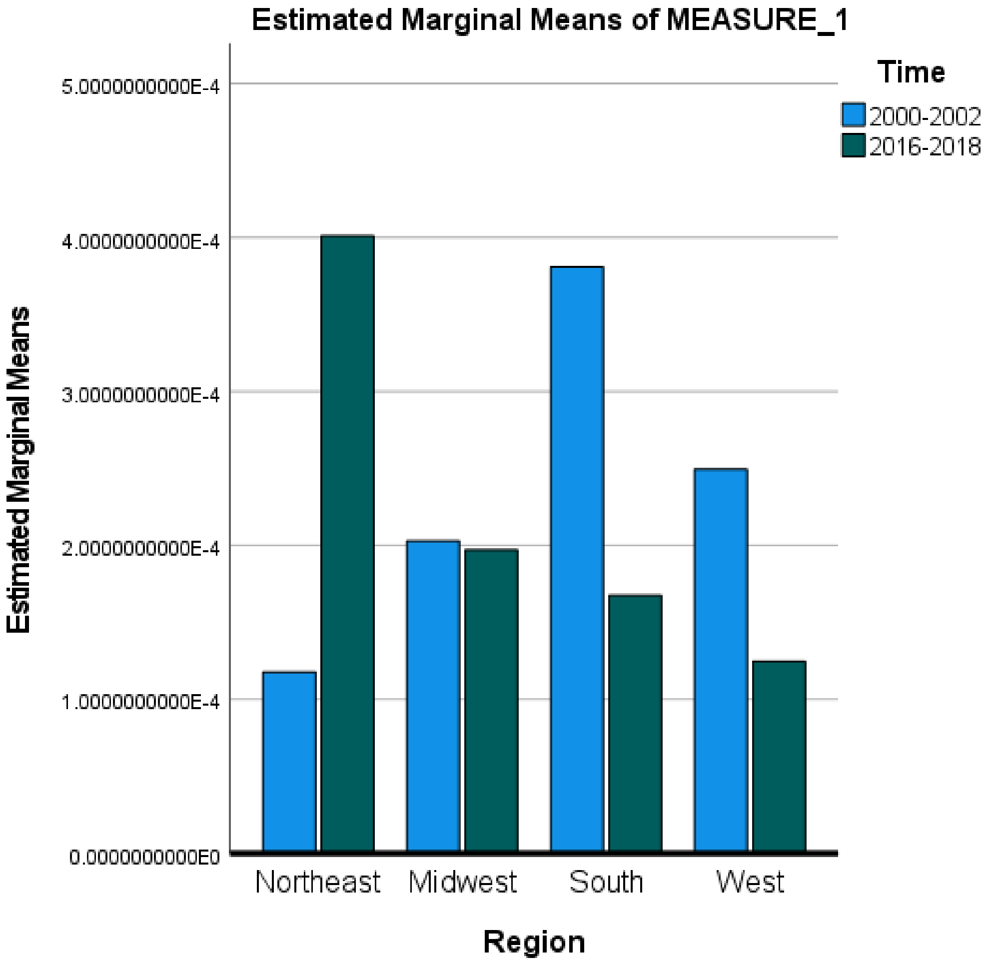
Table 6

Frequency Table 2000-2012 and 2016-2018

	2000	2001	2002	2016	2017	2018
Northeast	1836	42	404	2338	2394	2250
Midwest	5738	227	1560	1424	1390	1403
West	3869	245	1705	1260	1236	1168
South	4446	425	2683	895	896	882

Figure 2

Estimated Margin



Research Question 2

RQ2: Is there an association between age, gender, race, and *H. pylori* infection in the United States?

$H_0$2: There is no association between gender, race, and *H. pylori* infection in the United States.

H_a2: There is an association between age, gender, race, and *H. pylori* infection in the United States.

Table 7

Research Questions 2 and 3 Variable and Coding

Variable Name	Operational Definition
Race	White**
	Black
	Hispanic
	Asian/Islander
	Native American
Age	≤55**
	>55
Gender	Male **
	Female

** reference group

Multiple Logistic Regression for 2000 and 2002 Data

RQ2 aimed to examine whether an underlying variation in age, gender, and race between-group (years) has an effect. Table 5 presents the variable coding for RQs 2 and 3. For this RQ, the methodology used was multiple logistic regression. The comparison was between group A (2000, 2001, 2002) to group B (2016, 2017, and 2018); this sixteen-year span allows us to see changes in the regional infections for age, race, and gender. I create a dummy variable for each category. The dummy variable coding represents a category of a categorical independent variable except for the reference (**) category. Each year indicates the relationship between *H. pylori* infection and age, gender, and race.

The following tables provide the statistical significance, Odds Ratio (Exp (B), 95% CI, and p-value for each variable category. For RQ2, I used binary logistic regression to test the correlation between the dependent variables and significant predictors being diagnosed with *H. pylori* infection and the perceived susceptibility of the demographic variables. Multiple logistic regression was computed for 2000-2002 and 2016-2018.

Data From 2000. Using the 2000 results in Table 8, the model predicts that respondents less than 55 years old are more than five times more likely to be diagnosed with HP infection, OR= 5.302, 95% C.I. 1316, 21.366, p-value = .019.

Hispanic respondents are a significant predictor of being diagnosed with HP infection OR = 4.483, 95% C.I., 1.113, 18.058, p-value .035. All other race categories, Black, Asian, and Native American, were not significant predictors of being diagnosed with HP infection, at a p-value >.05. The reference group for Race is White respondents. Lastly, females' odds of being diagnosed with HP infection were less significant than males' in 2000. Females, OR= 1.021, C.I.274, 3.801, p-value .976. Male gender was a significant predictor. The reference category in the table below is white, >55, and male. This implies that dummy variables were created representing the other categories.

Table 8

Multiple Logistic Regression for Age, Race, and Gender in 2000

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Age (≤ 55)	.019*	5.302	1.316	21.366
Age (> 55) **				
Black	.869	1.203	.134	10.765
Hispanic	.035*	4.483	1.113	18.058
Asian	.990	.000	.000	
Native American	.987	.000	.000	
White**				
Gender (Female)	.976	1.021	.274	3.801
Gender (Male)**				
Constant	< .001*	.000		

**p* < .05
**reference group

Data From 2001. Using the 2001 results in Table 9, respondents less than 55 years old are a significant predictor of being diagnosed with HP infection, OR=.229, 95% C.l.198, .265, p-value <.001.

Black, Hispanic, and Asian Respondents are significant predictors of being diagnosed with *H. pylori* infection. When a respondent is Hispanic, the model predicts the respondent is more likely to be diagnosed with HP infection, OR = 1.631, 95% CI: 1.383, 1.924 p-value <.001. When a respondent is Asian, the model predicts the respondent is more likely to be diagnosed with HP infection OR = 3.05, 95% C.I. 3.050, 2.480, p-value <.001. For Blacks, the model predicts they are more likely to be diagnosed with HP infection, OR= 1.348, 95% C.I. 1.187, 2437, p-value <.001. When a respondent is Native

American, the model predicts the respondent is less likely to be diagnosed with HP infection, OR = .000, 95% CI: .743, p-value <.215.

Lastly, being female is a significant predictor of being diagnosed with HP infection, OR=1.348, 95%C.I. 1.187, 1.53, p-value < .001. The reference category in the table below is white, >55, and male. This implies that dummy variables were created representing the other categories.

Table 9

Multiple Logistic Regression for Age, Race, and Gender in 2001

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Age (≤ 55)	< .001*	.229	.198	.265
Age (> 55) **				
Black	< .001*	1.348	1.187	2.437
Hispanic	< .001*	1.631	1.383	1.924
Asian	< .001*	3.050	2.480	
Native American	.215	.000*	.743	
White**				
Gender (Female)	< .001*	1.348	1.187	1.531
Gender (Male)**				
Constant	.000	.003		

**p* < .05
**reference group

Data From 2002. Using the 2002 results in Table 10, respondents less than 55 years old are significant predictors of being diagnosed with HP infection, Age, (≤ 55) OR=.393 95% C.I. 373, .414, p-value <.001. When a respondent is less than 55 years old, the model predicts the respondent is more likely to be diagnosed with *H. pylori* infection.

All race categories, Black, Asian, Hispanic, and Native American, were significant predictors of being diagnosed with HP infection, p <.05. Lastly, being female is an essential predictor of being diagnosed with HP infection, OR = 1.428, 95% CI. 1.331, 1.533, p-value <.001. When a respondent is female, the model predicts that they are more likely to be diagnosed with HP infection than males. The reference category in the table below is white, >55, and male. This implies that dummy variables were created representing the other categories.

Table 10

Multiple Logistic Regression for Age, Race, and Gender in 2002

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Age (≤ 55)	< .001*	.393	.373	.414
Age (> 55) **				
Black	< .001*	2.299	2.127	2.484
Hispanic	< .001*	1.503	1.388	1.628
Asian	< .001*	2.483	2.239	2.753
Native American	.006*	2.105	1.244	3.562
White**				
Gender (Female)	< .001*	1.428	1.331	1.533
Gender (Male)**				
Constant	.000	.002		

**p* < .05
**reference group

Multiple Logistic Regression for 2016 and 2018 Data

Data From 2016. Using the 2016 results in Table 11, when a respondent is less than 55 years old, the model predicts the respondent is likely to be diagnosed with HP infection: OR = 1.667, 95% CI: 1.583, 1.757, p-value <.001.

Race was a significant predictor of being diagnosed with *HP* infection, p<.05. The reference group for race is White respondents. When a respondent is Black, the model predicts the respondent is more likely to be diagnosed with HP infection: OR = 2.978, 95% CI: 2.795, 3.173, p-value <.001. When a respondent is Hispanic, the model predicts the respondent is more likely to be diagnosed with HP infection, OR = 2.898, 95% CI: 2.700, 3.110, p-value <.001. When a respondent is Asian, the model predicts the respondent is s more likely to be diagnosed with HP infection, OR = 3.455, 95% CI: 3.088, 3.,864 and p-value <.001. Last, when a respondent is Native American, the model predicts the respondent is more likely to be diagnosed with HP infection OR = 2.454, 95% CI: 1.869, 3.221, p-value <.006.

Lastly, being female is a significant predictor of being diagnosed with HP infection, OR = 1.427, 95% C.I. 1.356, 1.502, p-value <.001. When a respondent is female, the model predicts that they are more likely to be diagnosed with HP infection than males. The reference category in the table below is white, >55 and male. This implies that dummy variables were created representing the other categories.

Table 11

Multiple Logistic Regression for Age, Race, and Gender in 2016

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Age (≤ 55)	< .001*	1.667	1.582	1.757
Age (> 55) **				
Black	< .001*	2.978	2.795	3.173
Hispanic	< .001*	2.898	2.700	3.110
Asian	< .001*	3.455	3.088	3.864
Native American	.006*	2.454	1.869	3.221
White**				
Gender (Female)	< .001*	1.428	1.356	1.502
Gender (Male)**				
Constant	.000	.000		

**p* < .05
**reference group

Data From 2017. Using the 2017 results in Table 12, respondents less than ≤55 years old are not a significant predictor of being diagnosed with HP infection, OR =1.094, 95% CI .283 4,239, p-value .896. Race was not a significant predictor of being diagnosed with *HP* with a p-value >.05. When a respondent is Black, the model predicts the respondent is less likely to be diagnosed with HP infection OR = 2.823, 95% CI: .569, 13.995, p-value .204. When a respondent is Hispanic, the model predicts the respondent is less likely to be diagnosed with HP infection OR = 2.870, 95% CI: .641, 12.837, p-value .168. When a respondent is Asian, the model predicts the respondent is less likely to be diagnosed with HP infection, R = .000, 95% CI: .000, p-value 0.988. This indicates that there is no statistically significant association. Last, when a respondent is Native American, the model predicts the respondent is less likely to be diagnosed with HP infection, OR=.000, 95% CI: .000, p-value .993. Female gender was not a significant predictor of being diagnosed with HP infection OR =1.172, 95% C.I. 331, 4.157, p-value .805. Male gender was a significant predictor. The reference category in the table below is white, >55, and male. This implies that dummy variables were created representing the other categories.

Table 12

Multiple Logistic Regression for Age, Race, and Gender in 2017

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Age (≤ 55)	.896	1.094	.283	4.239
Age (> 55) **				
Black	.204	2.823	.569	13.995
Hispanic	.168	2.870	.641	12.837
Asian	.988	.000*	.000	
Native American	.993	.000*	.000	
White**				
Gender (Female)	.805	1.172	.331	4.157
Gender (Male)**				
Constant	.000	.000		

**p* < .05
**reference group

Data From 2018. Using the 2018 results in Table 13, - the respondents less than 55 years old are not significant predictors of being diagnosed with HP infection, OR=1375895.229 95% C.I. .000, p-value .995. When a person is more significant >55, they are more likely to be diagnosed with HP infection than if they are less than <55 years old. Race was a significant predictor of being diagnosed with HP infection, p<.05. When a respondent is Black, the model predicts the respondent is more likely to be diagnosed with

HP infection, OR = 3.077, 95% CI: 2.887, 3.279, p-value <.001. When a respondent is Hispanic, the model predicts the respondent is more likely to be diagnosed with HP, OR = 2.679, 95% CI: 2.497, 2874, p-value <.001. When a respondent is Asian, the model predicts the respondent Is more likely to be diagnosed with HP infection, OR = 3.4765, 95% CI:3.112, 3882, p-value <.001. Last, when a respondent is Native American, the model predicts they will likely be diagnosed with HP infection, OR = 3.017, 95% CI:2.374, 3.833, and p-value <.001

Female gender was a significant predictor of being diagnosed with HP infection, OR= 1.517, 95% C.I. 1.441, 1.597, p-value <.001. When a respondent is female, the model predicts that they are more likely to be diagnosed with HP infection than males. The reference category in the table below is white, >55, and male. This implies that dummy variables were created representing the other categories.

Table 13

Multiple Logistic Regression for Age, Race, and Gender in 2018

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Age (≤ 55)	.995	1375895229	.000*	
Age (> 55) **				
Black	< .001*	3.077	2.887	3.279
Hispanic	< .001*	2.697	2.497	2.874
Asian	< .001*	3.476	3.112	3.882
Native American	< .001*	3.017	2.374	3.833
White**				
Gender (Female)	< .001*	1.517	1.441	1.597
Gender (Male)**				
Constant	.000	.000		

**p* <.05 **reference group

The RQ2 summary table describes the population characteristics by year for the target sample, *H. pylori* infection. The decision was made to reject or accept the null hypotheses based on the finding in the group by years; group A is from 2000 to 2001, and group B is from 2016 to 2018. The population size for this research from the NIS 2000-2002 and 2016-2018 files contained primary and secondary diagnoses of *H. pylori* infection from hospital admission. This included age, gender, and race at admission using the diagnoses with the ICD 9 code 04186 and ICD 10 code B9681.

As Table 14 shows, the results revealed a significant change in the age of the independent variable from ≤ 55 in 2000, 2001, 2002, and 2016 to an increasingly older generation of ≥55 in 2017 and 2018. This could be explained by the progression of the disease from the start of the infection to the manifestation of the illness during a person's lifetime. There is a significant association between age and *H. pylori* infection between decades.

For gender, females were most likely to be infected with *H. pylori* infection than males, except in 2000 and 2017. In 2000 and 2017, males were more likely to be diagnosed with *H. pylori* infection The association between groups was equal in males verse females, with males being 1 out of 3 years between decades. Females were a substantial factor for gender.

Race was an essential factor, except in 2001 and 2017 when the p-value was >.05. Race was a significate factor between the other years. The descriptive and demographic characteristics are shown in Table 11 through Table 16 for each year. Age, gender, and race were significate between 2000-2002 and 2016 -2018. Therefore, we accept the alternative hypotheses.

Table 14

Summary Table for Age, Gender, and Race

Year	2000	2001	2002	2016	2017	2018
Age	≤ 55	≤ 55	≤ 55	≤ 55	>55	> 55
Gender	Female	Female	Female	Female	Female	Female
	.976	<.001*	<.001*	<.001*	.806	<.001*
Black	.869	<.001*	<.001*	<.001*	.204	<.001*
Asian	.990	<.001*	<.001*	<.001*	.998	<.001*
Hispanic	.035*	<.001*	<.001*	<.001*	.168	<.001*
NA	.987	.215	.006*	.006*	.993	<.001*

$*p < .05$

Research Question 3

RQ3: Is there an association between health insurance coverage (Medicare, Medicaid, private, or no insurance) and *H. pylori* infection by region?

$H_0$3: There is no association between health insurance coverage (Medicare, Medicaid, private, or no insurance) and *H. pylori* infection by region.

H_a3: There is an association between health insurance coverage (Medicare, Medicaid, private, or no insurance) and *H. pylori* infection by region.

The final RQ tested the effects of health insurance on the predictors' susceptibility to *H. pylori* infection. Multiple logistic regression was used to analyze the relationship between health insurance and regions on the probability of the impact on *H. pylori* infection. The following tables provide the statistical significance and the p-value for each variable category. Predictor variable one is health insurance, two is regions, and the response variable is *H. pylori* infection.

Insurance Coverage by Regions for the year 2000

Using the 2000 results in Table 15, the results for the health insurance indicate a highly significant overall effect; Medicaid, OR=.732, 95% C.I. .690, .777, p-value <.001; Self-pay, OR=1.871, 95% CI 1.730, 1.986, p-value <.001; No charge OR=2.085 95% CI 1.681, 2.586, p-value <.001 and Medicare OR= 2.096, 95% C.I. 2.022, 2.172, p-value <.000. Those patients on Medicare with a p-value <.000 have a greater probability of infection than other types of health insurance.

The results for regions showed an association between the region and the target group (*H. pylori*) infection p-value <.05. The p-value for regions association was Northeast, p-value <.001; Midwest, OR=.846, 95% CI .802, .569, p-value <.001 and South, OR=.656, 95% CI .620, .641, p-value <.001. For all regions, the results were significant, and the odds ratios are all less than one, indicating a negative association, which means individuals in these regions are less likely to be diagnosed with *H. pylori* infection. The reference category in the table below is West and Private insurance. This implies that dummy variables were created representing the other categories.

Table 15

Multiple Logistic Regression for Insurance Coverage by Region 2000

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
West**				
Northeast	<.001*	1.321	1.256	1.389
Midwest	<.001*	.846	.802	.569
South	<.001*	.656	.620	.641
Private**				
Medicare	.000*	2.096	2.022	2.172
Medicaid	<.001*	.732	.690	.777
Self-pay	<.001*	1.854	1.730	1.986
No charge	<.001*	2.085	1.681	2.586
Constant	.000	.002		

**p* < .05
**reference group

Insurance Coverage by Regions for the 2001

Using 2001 results for regions is insignificant. The regions were Northeast, OR=924, 95% CI .671, 1.272, p-value .627; Midwest, OR=.1.139, 95% CI. .969, 1.340, p-value .115 and South, OR=.1.064, 95% CI 909, 1.246, p-value .441 show p-value >.05 indicating no significant.

Using the 2001 results in Table 16, the results for the healthcare insurance indicate a highly significant overall effect, the p-value at a significance level, < 0.05: Medicare, OR=.2.096, 95% C.I. 2.022, 2.172, p-value <.001; Medicaid, OR= .732 95% CI .690, .777, p-value <.001; Self-pay, OR =1.854, 95% CI.1.730, 1.986, p-value.0.10. Other OR=.975, 95% C.I. .705, 1.349, p-value .881 was less likely to be diagnosed with *H. pylori* infection. Results indicate there was no association with *H. pylori* infection between regions. There was less association between Regions and Health Care Insurance in 2001.

The reference category in the table below is West and Private insurance. This implies that dummy variables were created representing the other categories.

Table 16

Multiple Logistic Regression for Insurance Coverage by Region 2001

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
West**				
Northeast	.627	.924	.671	1.272
Midwest	.115	.139	.969	1.340
South	.441	1.064	.909	1.246
Private**				
Medicare	<.001*	2.096	2.022	2.172
Medicaid	<.001*	.732	.690	.777
Self-pay	.010*	1.854	1.730	1.986
No charge	.881	.975	.705	1.349
Constant	.000	.002		

*p<.05 **reference group

Insurance Coverage by Regions for the Year 2002

Using 2002 results for regions showed an association between the region and the target group (*H. pylori*) infection. Regions association were Northeast, OR= 1.511, 95% C.I. 1.360, 1.360, 1.679, p-value <.001; Midwest, OR=1.381, 95% C.I. 1.298, 1.470, p-value <.001 and South, OR= 1.064, 95% C.I. 1.100, 1.241, p-value <.001. Regions results indicated an association with *H. pylori* infection. An odds ratio greater than 1 indicates that the event will likely occur as the predictor (H. *pylori*) infection increases.

Using the 2002 results in Table 17, the results for the health insurance indicate a highly significant overall effect; the p-value is less than the significance level, p-value <0.05: Medicare, OR=.2.096, 95% C.I. .376, .442 p-value <.001; Medicaid, OR, .732 95% CI, .484, .543, p-value <.001; Self-pay, OR=1.854, 95% CI .964, 1.187, p-value .202; No charge OR=.000 95% C.I. .490, 1.020, p-value .064 and Other, OR=.975, 95% C.I. .642 .843, p-value <.001. Those patients who are self-paid and at no charge are less likely to have *H. pylori* infection over other types of insurance and not affected by regions' overall positive *H. pylori* infection. The reference category in the table below is West and Private insurance. This implies that dummy variables were created representing the other categories.

Table 17

Multiple Logistic Regression for Insurance Coverage by Region 2002

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
West**				
Northeast	< .001*	1.511	1.360	1.679
Midwest	< .001*	1.381	1.298	1.470
South	< .001*	1.064	1.100	1.241
Private**				
Medicare	< .001*	2.096	.376	.442
Medicaid	< .001*	.732	.484	.543
Self-pay	.202	1.854	.964	1.187
No charge	.064	.000	.490	1.020
Other	< .001*	.975	.642	.843
Constant	.000	.002		

**p* < .05
**reference group

Insurance Coverage by Regions for the year 2016

Using the 2016 results for regions showed an association between regions and health insurance. The association were Midwest, OR= .759, 95% CI .711 .811, p-value<.001; South, OR=.726 95% CI .678, .778, p-value <.001; West: OR=.635, 95% CI.587, .687, p-value-<.001. Regions results indicate an association with *H. pylori* infection. The overall p-value of < .001 indicates the probability of falling into a target group.

In 2016 results in Table 18 show healthcare insurance indicates a highly significant overall effect; the p-value is less than the significance level, p-value < 0.05: Self-pay OR=1.871, 95% CI .972, 2.176, p<.001; No charge OR=.000 95% CI 2.062, 3.539, p<.001 and Private, OR=<.00, 95% CI. .790,.739, p<.001. The probability of the event falling into the targeted group (*H. pylori*) infection is greater than the non-target group. Medicaid, OR=1.017, 95% C.I. .953. 1.086, p<.606 was not significate. The reference category in the table below is Northeast and Medicare insurance. This implies that dummy variables were created representing the other categories.

Table 18

Multiple Logistic Regression for Insurance Coverage by Region 2016

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Northeast**				
West	< .001*	.635	.587	.687
Midwest	< .001*	.759	.711	.811
South	< .001*	.726	.678	.778
Medicare**				
Private	< .001*	.790	.739	.845
Medicaid	.606	1.017	.953	1.086
Self-pay	< .001*	1.854	.972	2.176
No charge	< .001*	.000	2.062	3.539
Other	< .001*	.975	.857	1.161
Constant	.000	.001		

*$p < .05$
**reference group

Insurance Coverage by Regions for the year 2017

Using the 2017 results in Table 19, the results for the health insurance indicate a highly significant overall effect; the p-value is less than the significance level, p-value < 0.05: Medicaid, OR=1.047, 95% C.I. .981, 1.117, p-value.167; Self-pay, OR=1.766, 95% CI 1.597, 1.952 p-value <.001; No charge OR=1.552, 95% C.I. 1.088, 2.212, p-value<.015. The probability of the event falling into the targeted group (*H. pylori*) infection is greater than that of the non-target group (Regions). Medicaid, OR=1.047, 95% C.I. .981, 1.117, p-value. 167 and others indicate a significant relationship. The results for regions showed an association between region and health insurance. Midwest, OR= .759, 95% C.I. .711, .811, p<.001; South, OR=.726, 95% CI .6678,.778, p<.001; West, OR=.635, 95% C.I. .587, .687, p-value <.001. Regions results indicate a significate relationship between *H. pylori* infection and a mixed relationship with healthcare insurance. The reference category in the table below is Northeast and Medicare. This implies that dummy variables were created representing the other regions.

Table 19

Multiple Logistic Regression for Insurance Coverage by Region 2017

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Northeast**				
West	< .001*	.635	.587	.687
Midwest	< .001*	.759	.711	.811
South	< .001*	.726	.678	.778
Medicare**				
Private	< .001*	.735	.686	.787
Medicaid	.167	1.047	.981	1.117
Self-pay	< .001*	1.766	1.597	1.952
No charge	.015*	1.552	1.088	2.212
Other	.437	.938	.798	1.102
Constant	.000	.001		

*$p < .05$ **reference group

Insurance Coverage by Regions for the year 2018

Using the 2018 results in Table 20, the results for the health insurance indicate a highly significant overall effect. Medicaid, OR= 1.033, 95%C.I. .968, 1.102, p-value.328; Self-pay, OR=1.742, 95% CI 1.576, 1.926, p<.001; No charge OR=1.533, 95% CI 1.076, 2.186, p<.018. 1.102, p-value. 328 and Other, OR=.932. 95% C.I. .793, 1.095, p-value .389 did not show a difference. The results indicate that Medicaid, self-pay, and no charge are 1% more likely to fall into the non-target group. The results for regions showed an association between region and health insurance. Midwest, OR= .759, 95% CI .711, .811 p<.001; South, OR=.726, 95% CI .678, .728, p<.001; West, OR= .635, 95% CI .587, .687, p<.001. Regions results indicate that affluence is associated with increased odds with *H. pylori* infection. Depending on the Social and economic class and the environment, one could expect more infections found in a particular region regardless of insurance coverage, which would cause the probability of the event occurring to increase. Regions results indicate a significate relationship between *H. pylori* infection and a mixed relationship with healthcare insurance. The reference category in the table below is Northeast and Medicare. This implies that dummy variables were created representing the other regions and insurances.

Table 20

Multiple Logistic Regression for Insurance Coverage by Region 2018

			95% CI for OR	
	Sig.	Odds ratio	Lower	Upper
Northeast**				
West	< .001*	.635	.587	.687
Midwest	< .001*	.759	.711	.811
South	< .001*	.726	.678	.778
Medicare**				
Private	< .001*	.730	.681	.782
Medicaid	.328	1.033	.968	1.102
Self-pay	< .001*	1.742	1.576	1.926
No charge	< .018*	1.533	1.076	2.186
Other	.389	.932	.793	1.095
Constant	.000	.001		

*$p < .05$
**reference group

The RQ3 summary table describes the population characteristics of Health Insurance by Region by year for the target sample, *H. pylori* infection. The decision was made to reject or accept the null hypotheses based on the finding in the group by years; group A is from 2000 to 2001, and group B is from 2016 to 2018. The population size for this research from the NIS 2000-2002 and 2016-2018 files contained primary and secondary diagnoses of *H. pylori* infection from hospital admission. This included region and health insurance at admission using the diagnoses with the ICD 9 code 04186 and ICD 10 code B9681.

Using summary table 21, the results revealed that regions were significate factors except in 2001, where *H. pylori* infection was not a significant variable and insurance was. From 2000 to 2002 and 2016 to 2018, there was a positive association between *H. pylori* infection in all regions. The summary table indicates that regions and healthcare insurance are affected by *H. pylori* infection. Insurance coverage did not show a definitive connection between *H. pylori* infection within a region.

Table 21

Summary Table for Region and Insurance

Year	2000	2001	2002	2016	2017	2018
Northeast	< .001*	.627	< .001*	**	**	**
Midwest	< .001*	.115	< .001*	< .001*	< .001*	< .001*
South	< .001*	.441	< .001*	< .001*	< .001*	< .001*
West**	**	**	**	< .001*	< .001*	< .001*
Medicare	.000*	<.001*	<.001*	**	**	**
Medicaid	<.001	<.001*	<.001*	.606	.167	.328
Private**	**	**	**	<.001	<.001	<.001*
Self-pay	<.001	.010	.202	<.001	<.001	<.001
No charge	< .001*	< .001*	.064	< .001*	.015*	.018*
Other	**	.881	<.001	<.001*	.437	.389

*$p < .05$
**reference group

Summary

In summary, each year of the data sources documentation discussed has its strengths and weaknesses. To answer the final RQ, I used binary logistic regression to test the correlation between the dependent variables and significant predictors of being diagnosed with *H. pylori* infection and the perceived susceptibility of the demographic variables. The research could not be advanced further because a standard computer cannot merge large data sets. The results indicated region and health insurance status correlated to increases in perceived susceptibility, and health status was related to increased number. In Chapter 5, I will further discuss the results of the RQs, including my interpretations of the findings.

Chapter 5: Discussion, Conclusions, and Recommendations

Introduction

In this quantitative cross-sectional study, I sought to determine whether *H. pylori* infection over time (2000–2002 to 2016–2018) is affected by geographical location and the relationships between the predictors and the outcome variable. This study was justified because no studies had addressed the changes in *H. pylori* infection over the years in the United States, according to my review of the literature. The goal was to identify statistically significant information that could be incorporated into understanding other epidemiologic migrations and long-term health complications of *H. pylori* infection to reduce the risk of gastric cancer. The study's findings are essential because *H. pylori* infection, when detected early, can be treated and eradicated in some individuals (Bakhti, 2020). Findings within the literature indicated that compared to populations with high socioeconomic status, the lower the socioeconomic status of a group, the higher the incidence of *H. pylori* infection (Bakhti et al., 2020). However, studies have also pointed out that this relationship may depend on various factors, such as genetics, oncogenesis, antibiotics, and socio-economic factors. Communities must be aware of clusters of *H. pylori* infection within a region to combat the infection. I examined the geographic migration of *H. pylori* infection and associated socioeconomic factors through extensive data analysis.

The concept of big data may strengthen the direction of new research. Future researchers might examine the results of this study for predictive analysis, policy development recommendations, and program intervention to improve outcomes, such as gastric cancer. The benefits of eradicating *H. pylori* infection may apply to all levels of risk of gastric cancer.

Interpretation of the Findings

There is no consensus on the geographic distribution of *H. pylori* infection across the United States, as William et al. (2017) noted. Most *H. pylori* infection research has been conducted in developing countries overseas, such as Asia, India, South America, and Africa. Findings show that sanitation, overcrowding, and food sources cause contribute to the infection (Hooi, 2017). My findings provide a regional snapshot of *H. pylori* infection in the United States and how the SEM helps to explain a shift in the transmission of the migration of *H. pylori* infection over time. Research in the United States has been sporadic; researchers have conducted studies in Texas (Parma, 2017) and Alaska (Nolena et al., 2018). However, there needs to be more of an understanding of where *H. pylori* infection rates are high and the states and regions in which infection rates are increasing.

In this research study, I conducted repeated measure ANOVA to examine the *H. pylori* infection across the United States. The *H. pylori* infection was the highest in the southern (2000-2002) then shifted to the northeastern (2016-2018) part of United States over time. These results indicate that researchers must look closely at other variables (e.g., education, income, and housing markets) to determine other possible influencing factors. For example, increases in housing prices and higher interest rates may cause overcrowding in single-family homes (Mayo Clinic, 2023). During the COVID-19 pandemic, many children and grandchildren moved into their parent’s houses (Varshney, 2021). Varshney (2017) indicated that overcrowding in households was a significant risk factor for COVID-

19, as was also found by Zamani (2018) for *H. pylori*. I conducted multiple logistic regression to ascertain the extent of the relationship between *H. pylori* infection (dependent variable) and age, gender, race, and type of health insurance (independent variables). Significant predictors (P-value < 0.05) were identified using multivariable logistic regression analyses.

The most recent data relating to *H. pylori* infection, at the time of the study, came from countries outside the United States. Wu et al.'s (2022) research indicates that males are the predominant carrier, the older adult population is the most likely to have *H. pylori* infection, and Hispanics and Asian are the dominant racial and ethnic groups infected. (Wu et al., 2022). Their results also indicate that socioeconomic status is a critical determinant negatively correlated with *H. pylori* infection. Moreover, *H. pylori* infection varies based on geographical locations. Other factors, such as environmental, sociodemographic characteristics, and SES, have yet to be firmly established in the United States. I now present the finding of the regression analysis.

The results of this study revealed that in 2000, 2001, 2002, and 2016, *H. pylori* ages were significant for those younger than 55. Only in 2017 and 2018 was it important for those who were older than 55 years of age. Most researchers studying *H. pylori* infection have focused on patients with gastric cancer, gastritis, and peptic ulcers Huang, 2021). Researchers are looking for minor genetic differences. This research study is unique because it captured hospitalized patients of all ages diagnosed with *H. pylori* infection. Most studies on *H. pylori* infection have focused on late-stage disease in older patients (Huang et al., 2021: Wang, et al. 2022.

In this research, in 2001, 2002, 2016, and 2018 being a female was a significant factor p= <.001 compared to males but not in 2000 and 2017. It is possible that females could be carriers of *H. pylori* infection due to their more nurturing nature and intrafamilial transmission. Females being the predominant gender in this research make you wonder if females possess a trait that allows them to be carriers of the disease. However, these results conflict with a previous study, which indicated that males were the predominant gender (Ibrahim, 2017).

Race was a factor; Native Americans ranged from 1% to 40%, Hispanics ranged from 25% to 96%, Asians ranged from 1% to 58%, and Blacks ranged from 16% to 40%, greater than Whites, the reference category. Oddly enough, when race changed from significant to insignificant, it was by year for all four race categories simultaneously. Previous studies are usually based on countries or states with larger populations of a certain race. For example, Hispanics, population used in Texas or Native American population in Alaska Predominant race studies in regions with a concentrated population of a race; are predictable outcome to the given race of that country (Parma, 2017) (Nolen,2018) . Most of these studies. dies were usually executed in developing countries, such as Africa, Nigeria, South America, and Asia (Diaconu et al., 2017; Brown, 2022; Nguyen, 2021; Hooi, 2017). It is essential to evaluate race in countries of mixed populations, such as the U.S., for an overall understanding of the race predominance of *H. pylori* infection.

Those with Medicare and Medicaid health insurance were the predominant type of insurance associated with *H. pylori* infection hospitalization. Health insurance is a significant factor in the fourth level of the SEM, which includes the organizational and policy/enabling environment. It also looks at social factors, such as health disparity, economic factors, education, and social policy (Bronfenbrenner, 1977). Medicare-covered patients aged 65 and older and lower-income patients typically use Medicaid coverage; both are related to socio-economic status. The single type of health insurance did not predict *H. pylori* infection each year. Medicare and Medicaid are noted as used by lower socioeconomic groups; therefore, it is not surprising that Medicare and Medicaid are the predominant type of insurance used by *H. pylori* infected patients for many years (Landers et al., 2020).

Limitations of the Study

The geographic differences in the pathology of *H. pylori* infection may be explained by the presence of different types of *H. pylori* infection virulence factors (Chang, 2018). Virulence factors may be coded within the bacterial genome, thus being inherent aspects of the organism's structure, or may be coded within transmissible genetic elements and thus acquired from the environment (Chang et al., 2018). We did not investigate this. The phylogeographic origin of *H. pylori* infectious strains and the disrupted co-evolution between *H. pylori* infection and its human host may explain the geographic differences. Also, the different rates of gastric cancer can be partly attributed to the different genotypes of *H. pylori* circulation in other geographic areas (Piscione, 2021). Therefore, high and low-incidence regions of *H. pylori* infection can show us how the differences in transmission ecology primarily affect the composition of the *H. pylori* infection population. In the U.S. evolution of a distinct *H. pylori* infection subpopulation has occurred (Bakhti, 2020).

Another limitation is the NIS sampling frame which includes all community and non-rehabilitation hospitals that could match the corresponding American Hospital Association (AHA) Annual Survey data. While 20% of the hospitals from each region are selected for the NIS, the comprehensiveness of the sampling varies by region. The regions in the NIS sampling frame contain 97.6% of the population in the Northwest, 89.6% in the Midwest, 83.7% in the West, and 81.2% in the South. (NIS, 2018). The sampling of the NIS frame is a disproportionate representation of the more populous states. The use of secondary data has increased over the years. Secondary data analysis of large data sets can have limitations, invalid date entry, not appropriately coded, or data just eliminated. For this study, missing data was not used.

Recommendations

Keeping track of population movement over time (trends) can help researchers understand whether progress is being made. Additional research is needed to address new challenges, such as improving screening or finding better treatment. *H. pylori* infection can affect the risk of developing gastric cancer. In 2019, there will be 1, 762,450 new cases of gastric cancer, and an estimated 606,880.00 people will die of this disease (American Cancer Society, 2020).

Improvement in education and *H. pylori* infection awareness is needed for social change to occur. The community needs to understand the long-term implications of a disease that could result in gastric cancer. I recommend more studies comparing peptic ulcer and gastric cancer attributed to *H. pylori* infection by region to see if there is a pattern, locally and regionally.

Implications

Disease management could be initiated through a healthcare community adviser. Healthcare providers could educate the public and physicians on the community's needs. The SEM was used to integrate the effects of internal and external factors for patients with *H. pylori* infection. Improvements in education with awareness of *H. pylori* infection are the first steps for social change.

Accessibility to health care is affected by insurance coverage. People enrolled in both Medicare and Medicaid are usually considered at-risk populations. Some common factors are overcrowding, contaminated drinking water, handwashing, lower family income, and educational level. Since the increase in medical expansion of Medicaid in 2021, states have been provided the opportunity for Medicaid to be offered to uninsured and low-income individuals to acquire Health care (Branham et al., 2021). Since the expansion of Medicaid, there has been an improvement in insurance coverage and overall health care, and the narrowing of racial disparities has improved (CEA, 2021; Guth et al., 2020).

Collaborating and communicating with healthcare professionals is essential to enhance healthcare delivery to patients with *H. pylori* infection. Physician continuing education on chronic disease could benefit *H. pylori's* infection improvements and health outcomes regionally. Factors that require consideration are education about the disease and treatments incorporated into the patients' region.

A positive aspect that resulted from the COVID-19 pandemic is the awareness of washing hands to eliminate the transmission of that virus and we may find that this results in a decline in new cases of *H. pylori* infection. This awareness should be used in campaigns as a parallel to strengthen community understanding of other diseases. I would recommend future research in analyzing early hospitalization data, as well as hygiene, and other environmentally related factors.

Conclusion

In recent years new methods have been proposed to predict the risk of *H. pylori* infection: the phylogeographic origin of *H. pylori* infectious strains and the disrupted co-evolution between *H. pylori* infection and its human host, which can potentially explain the geographic differences in the risk of *H. pylori* infection (Bakhti et al., 2020). Areas with high and low *H. pylori* infection rates have shown differences in transmission ecology, mainly affecting the composition of *H. pylori* infection populations. The mechanisms of *H. pylori* infection transmission have yet to be entirely understood. In the U.S., there is a rapid evolution of different *H. pylori* infection subpopulation genetically impact *H. pylori* infection migrations. In this study, we looked at variables to see the impact of overtime. Examining changes over time can help researchers understand whether progress is being made to control *H. pylori* infection.

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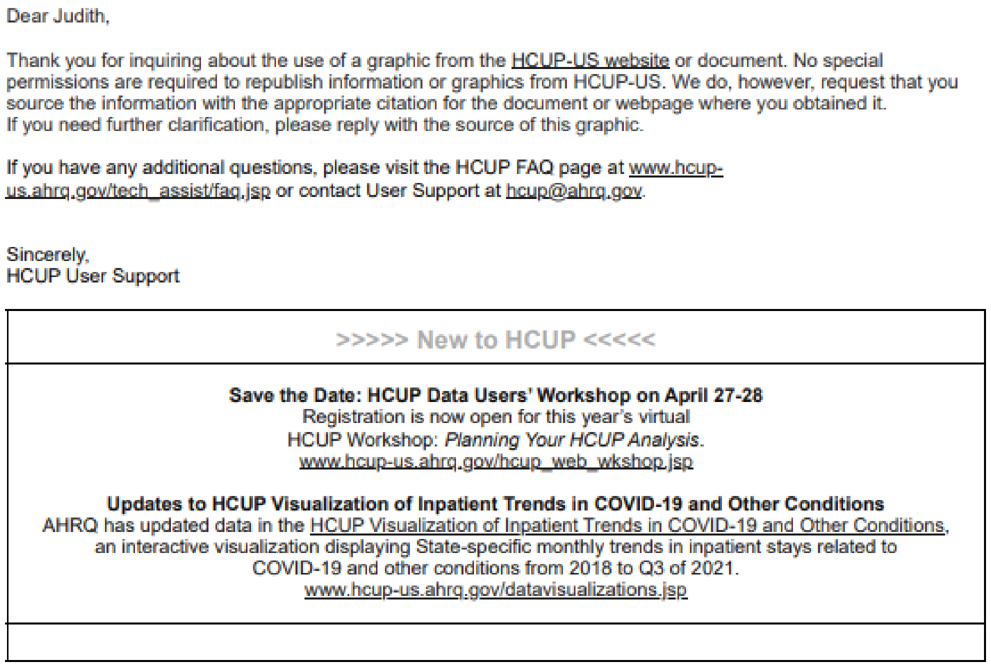
Appendix: Authorization to Use Healthcare Cost and Utilization Project Regional Map



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