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Relationship Between Homelessness, Substance Use, Employment, Living on a Reservation and Tuberculosis Among Northern Plains Native Americans

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Walden University
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Abstract

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MPH, Independence University, 2011

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Dissertation Submitted in Partial Fulfillment

of the Requirements for the Degree of

Doctor of Philosophy

Epidemiology

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Abstract

Native Americans in the Northern Plains have a long history of tuberculosis (TB) infections. There is limited research on the causes of latent TB infections (LTBI) and TB in this population. The purpose of this quantitative study was to assess the relationship between latent TB and factors of homelessness, substance use, employment, living on a reservation, and active or latent TB among this population using the eco-social theory as the theoretical framework. Data from 146 TB cases of Native Americans living in the Northern Plains and diagnosed with TB from 1999 to 2019 were analyzed using chi-square tests that showed a relationship between LTBI and active TB disease. Binary logistic regression analyses showed no statistically significant association between the variables. Age was found to be significantly related to TB, with the odds of active TB decreasing and the odds of latent TB increasing as the study population grew older. The study outcomes could inform the development of policies, processes, and educational resources geared toward decreasing the public health burden of TB among Native American populations. This would refocus TB prevention and treatment programs on the social conditions and inform how public health programming addresses every TB case using a three-pronged approach: public health, medical, and socioeconomic. The potential positive social change that could result is due to the use of the three-pronged approach which could reduce health disparities and increase awareness of TB risks and potential strategies for risk avoidance in marginalized groups.

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Dedication

This study is dedicated to all the Native Americans sent to the Sioux Sanitarium in Rapid City, South Dakota, from 1939 until the 1960s. Many of the patients succumbed to the TB disease, and some were buried on the grounds of the Sioux Sanitarium. It was not until 1943 with the advent of Streptomycin that these patients received health care other than rest and sunshine.

Acknowledgments

To Mary Louise McCloskey, my mother, who was a 4-year-old child sent from the St. Francis Mission Boarding School in St. Francis, South Dakota to the Sioux Sanitarium in 1946. As told by her, the white van parked in the front of the school, the sister called her and several other children outside, and then she put them in the van. For a year, my mother rarely saw her parents, Olive and Albert, who struggled with being able to travel the 3-day trip from Rosebud Reservation to Rapid City, South Dakota. After a year, Mary Louise was sent back to the boarding school, only to return to the sanatorium in 1948 for another year. It was hearing of her strength and ability to adapt to hardships that profoundly changed my professional focus and passion.

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Chapter 1: Introduction to the Study

Native Americans in the Northern Great Plains of the United States have a long history of tuberculosis (TB) infections. Despite effective treatments and Native Americans moving to urban communities from reservations, they continue to be disproportionately affected by TB. Native Americans continue to have high rates of TB (3.7/100,000) compared to the general population (2.5/100,000; Stewart, 2018), even though Indian Health Services (IHS) and the state health departments provide access to the same medication and treatment as other Americans. The current study was conducted to ascertain the causes of ongoing TB among this population, focusing on underlying latent TB infection (LTBI), socioeconomic status, and living in urban centers or reservations. The findings of this study could contribute to social change by informing preventive programs designed to reduce TB infections among the Native American population in underserved areas, thereby improving public health directly and indirectly within the community.

Chapter 1 addresses the history of TB rates among the Native American population in the Northern Plains and their socioeconomic conditions. I also address the new surveillance techniques involving the use of genotyping to define TB clusters. The capability to genotype *Mycobacterium tuberculosis* (*M. tuberculosis*) affords public health professionals the ability to differentiate between LTBI and newly contracted infections. The ability to identify these differences during an outbreak of active TB disease will allow public health programs to identify clusters in a population. Information from the Centers for Disease Control and Prevention (CDC, 2005) TB cluster

investigations outlined how identifying clusters during studies of active TB disease offers a benefit in determining treatment, surveillance, community outreach, and public health programming. A combination of genotyping and epidemiological data collection can identify TB transmission between individuals from different communities, and identify TB reactivation among populations with LTBI through analysis of mutation of the TB genome (Hatherell et al., 2017; Mattelli et al., 2017). TB genetic information could be used as part of a TB elimination program, including early diagnosis and treatment, to improve patient outcomes.

In Chapter 2, I explore the history of TB among Native Americans and cover TB surveillance innovations through analysis of TB genetic testing and a focus on socioeconomic conditions of populations at the highest risk of contracting TB. Chapter 3 details the use of the eco-social theory to analyze the TB cases and how they are affected by the socioeconomic variables: homelessness, multigenerational households, low socioeconomic status, living in an urban area or on a reservation, and substance abuse. The secondary data used were TB genotype and data from contact studies conducted by the Northern Plains state departments of health.

Background

M. tuberculosis has afflicted humans for thousands of years and continues to threaten vulnerable populations around the world. The current countermeasures, which include contact studies and surveillance programs, have been inadequate for vulnerable people, as seen by the continuing infections in the homeless, racial minority groups, and substance abusers (CDC, 2017b). The current TB contact and surveillance guidelines by

the CDC focus on active TB cases and new transmissions. Most U.S. public health TB elimination programs do not address LTBI due to cost and time (CDC, 2017b).

New techniques in genotyping to trace TB cases and distinguish between clusters and new cases (CDC, 2017b) have been applied in high-risk populations such as the homeless and immigrants (Stewart, 2018). The literature showed that genotyping can improve the surveillance of TB in high-risk populations (CDC, 2017b). The literature also showed that Native Americans are at high risk for TB (Stewart, 2018) and adverse socioeconomic conditions (Holm et al., 2010). However, there was a lack of studies related to TB genotyping and the socioeconomic conditions in the TB cases among Native Americans.

The need to identify LTBI in vulnerable populations is vital to effectively and efficiently implementing TB surveillance programs to reach the World Health Organization's (WHO, 2018) goal for TB elimination. The WHO and CDC (2017b) have added genotyping analysis for differentiation between reactivation and new TB cases in populations at the highest burden for TB infections as one way to work toward elimination. One of those populations is the American Indians living in the Northern Plains. There are several populations of American Indians of North Dakota, South Dakota, Nebraska, and Iowa in this region: Cheyenne River Sioux Tribe; Crow Creek Sioux Tribe; Ponca Tribe; Flandreau Santee Sioux Tribe; Yankton Sioux Tribe; Oglala Sioux Tribe; Lower Brule Sioux Tribe; Omaha Tribe of Nebraska, Winnebago Tribe of Nebraska; Turtle Mountain Band of Chippewa; Mandan, Hidatsa, and Arikara Nation;

Rosebud Sioux Tribe; Sac and Fox Tribe of the Mississippi; Santee Sioux Nation; Sisseton-Wahpeton Oyate; Spirit Lake Dakota Nation; and Standing Rock Sioux Tribe.

The Tribal members intermarry, live and work on each other's reservations, and reside in urban areas together. The states in the Northern Plains are considered a low burden for TB. However, the American Indian/Alaska Native (AI/AN) population is among the ethnic groups that have a higher rate of TB infections than other U.S. populations. This population also has high rates of homelessness, low socioeconomic status, and substance abuse (CDC, 2017a; Cormier et al., 2019; O'Leary et al., 2019).

The gap in knowledge in the discipline of public health that the current study addressed was TB and its effects on the AI/AN population living in the Northern Plains of the United States. The recent use of genotyping in other parts of the United States to identify clusters has helped public health professionals move toward improved treatment, surveillance, and eradication of TB in these communities. Therefore, the current study was needed to address the gap in the literature on TB disease in the AI/AN population living in Northern Plains, including TB genotyping and the influence of socioeconomic status, homelessness, multigenerational households, and substance abuse on disease occurrence.

Problem Statement

There was a paucity of recent research on TB in Native Americans in the Northern Plains. Based on a search of online health research literature databases, I found no recent reports or published research on this issue and limited references from 4 to 5 years ago. However, reports from the last 10 years showed the Native American

populations of the Northern Plains had TB on their reservations and urban communities for decades (Cheek et al., 2014). According to the most recent studies on Native Americans and TB, their TB prevalence rates remain higher than the general population. At least 40%–50% of the TB cases reported in studies conducted in 2016 and 2017 by the Departments of Health were in the Northern Plains (CDC, 2017a). The highest TB incidence for U.S.-born people was among Native Hawaiians/Pacific Islanders (6.5 per 100,000) followed by AI/AN (3.1 per 100,000) and Whites (0.4 per 100,000) as reported by the CDC in 2017. The most recent evidence-based information available on Native Americans with TB indicated that although there have been declines in mortality rates across the United States, the decline has been much slower in the Native American community (Reilley et al., 2014). The Center for disease control and prevention (2018) identified that the U.S. population TB rates declined from 1.1% in 2015 to 1.0% in 2018. During the same period, AI/AN TB rates were 7.0% in 2015 and decreased to 4.0% in 2018 (Talwar et al., 2018).

The CDC (2017a) stated that the general population rate of active TB contacts in the United States was 7.8%, but AI/AN rates were 30.8% of all cases. The CDC also noted that nationwide genotyping of TB clusters from 2015 to 2017 showed that the AI/AN population had an overall rate of 46.5% for single cases of TB that do not share genetic characteristic compared to 53.5% for those with clustered genetic markers (these are variations and mutations on the TB gene) shared between the cases. In two states in the Northern Plains where the largest population of the Northern Plains populations live, North Dakota rates for individual cases were 28.6%, and South Dakota had 42.9%, the

highest percentage (CDC, 2017a). Being among the AI/AN ethnic group is one of the four main risk factors identified by the CDC for contracting TB, other than being foreign-born from a country where TB is endemic (Yuen et al., 2016).

After an extensive literature review of TB within the Native American population in the Northern Plains of the United States, I found a literature gap because the most current peer-reviewed research on this topic was from 2014 and 2015. Reilley et al. (2014) stated that more research on this topic was needed. Reilley et al. compared diagnostic codes for HIV and TB deaths between Native Americans and non-Hispanic Whites. The data for the years 1990–1998 showed that TB mortality in the Native American population was 3.3/100,000 and was statistically significantly higher than non-Hispanic Whites at 0.3/100,000. Although the TB mortality rates for both decreased over the next 10 years from 1999 to 2009, Native Americans' mortality continued to be higher than non-Hispanic Whites (1.5/100,000 compared to 0.1/100,000).

Yuen et al. (2016) analyzed the epidemiology of TB cases that considered recent infections related to transmissions in the United States from January 2011 to September 2014. Yuen et al. looked at specific groups and found that being in certain groups (Native Americans, Native Hawaiian/Pacific Islander, Blacks, and homeless) was more of a factor in TB transmission risk than being foreign-born. Cheek et al. (2014) analyzed the relationship between health disparities and TB in the AI/AN population in the United States. Since the 1950s, AI/ANs living on the reservations had the same health outcome from TB, measles, and smallpox as those living off the reservations and a high morbidity

and mortality rate. The most significant numbers of admissions for TB occurred in Alaska, the Southwest, and the Northern Plains.

I found very few research articles on this subject by reviewing articles regarding genotyping TB and latent TB in Native Americans. I noted gaps in research using TB genotyping, including variates and mutations found in Native Americans living in the Northern Plains, to identify latent TB within the community. Specifically, the following were unknown or unclear:

1. The TB incidence rates among the Native American population living in the Northern Plains in the United States are related to LTBI or are affected by low socioeconomic status and physical location.
2. There is a difference between the TB incidence rates of those living on the reservations and those living in urban areas.
3. There is a correlation between reinfection (LTBI), socioeconomic status, homelessness, multigenerational households, and substance abuse among the Native Americans in the Northern Plains living on the reservation compared to those living in urban areas based on genotyping data.

Interrante et al. (2015) discussed genotyping to identify the difference between reactivation and reinfection of TB disease. Interrante et al. recognized the method of genotyping and defined *reactivation* as recurrent TB 12 months or more after treatment completion. Interrante et al. identified social and environmental conditions that affected the U.S. population-based cohort with data entered into the National TB Surveillance System as exposed to TB. According to Interrante et al., genotyping may help define the

cause of ongoing TB disease in some high-risk populations, including recent immigrants. Interrante et al. also found that if a person remained in a low socioeconomic environment with the first infection, they had a 60% greater chance of a second infection.

Godwin et al. (2017) analyzed, with CDC assistance, TB outbreaks requested by state, tribal, or territorial health departments. Godwin et al. studied how genotyping was applied in identifying the transmission and detection of TB epidemiologic linkage. The CDC assisted with 21 outbreaks during 2009–2015, and Godwin et al. assessed the demographic and social conditions that may have contributed to the outbreak in that area. Godwin et al. found that 79% of cases were U.S.-born, 45% were homeless, and 83% had a history of heavy alcohol or substance abuse. Godwin et al. stated that these data showed that TB prevention and control programs need to address the needs of vulnerable populations. The lack of research on TB infections in Native Americans living in the Northern Plains and genotyping to identify clusters in this population indicated a gap in the literature. Overall, there was a lack of evidence on how low socioeconomic status, homelessness, and substance abuse affect the response to infectious diseases such as TB among Native Americans living in the Northern Plains.

Purpose of the Study

The purpose of this quantitative study was to examine the association between active TB status, low socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans living in urban areas or on reservations in the Northern Plains. I aimed to determine whether a relationship exists between (a) TB cases that are reinfections (LTBI) found by genotype variations and

mutations that convert to active TB disease and (b) low socioeconomic status, homelessness, multigenerational households, or substance abuse. I sought to determine whether there was a correlation between the reinfection (LTBI) using genotyping and socioeconomic status, homelessness, and substance abuse among Native Americans in the Northern Plains living on the reservation compared to urban areas.

The data from Talkpoverty.org (2017) identified living conditions for American Indians in urban and reservation settings. Talkpoverty.org found that poverty rates for South Dakota were 13.3% overall, of which 49.3% identified as American Indians, while in North Dakota the overall poverty rate was 10.3%, of which 33.8% identified as American Indians, and in Nebraska the overall rate was 10.8%, of which 22.4% identified as American Indians. Warne and Wescott (2019) discussed the socioeconomic conditions that led this population to have poor health outcomes relating to substance abuse and poverty. Bloss et al. (2011) also identified in an analysis of Native Americans with TB from 2003–2008 that this population was more likely to be homeless (21.9%), suffer from drug use (3.8%) and alcohol use (42.6%), and be unemployed (70.8%). The use of genotyping of TB to identify clusters in vulnerable populations has been invaluable in public health programs. In a Canadian study, Tuite, et al., (2013) found that although the clusters identified by genotyping were small, TB clusters in aboriginal populations showed an odds ratio of 1.41 (95% CI 0.61–3.24), and being homeless had an even higher odds ratio at 3.98 (95% CI 2.44–6.49).

Research Questions and Hypotheses

The research questions (RQs) for this study were as follows:

RQ1: What is the association between socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains) and active TB status?

H_o1: There is no association between socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains) and active TB status.

H_a1: There is an association between socioeconomic status, homelessness, multigenerational households, substance abuse, place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains), and active TB status.

RQ2: Is there a relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse and reinfections cases (LTBI) among Native Americans living in urban centers compared to reservations in the Northern Plains?

H_o2: There is no relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse and active TB cases identified as reinfections among Native Americans living in urban centers compared to reservations in the Northern Plains.

H_a2: There is a relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse and active TB cases identified as

reinfections among Native Americans living in urban centers compared to reservations in the Northern Plains.

Theoretical Framework

In this study, the eco-social theory, first presented by Krieger (2012), was used to discuss integrating the social inequalities and biological effects of TB as it spread among the American Indian population. Krieger (2014) stated that the central function of this theory is to look at how environmental and social exposures affect the level of health and the distribution of disease among any population. The Native American reservations have many conditions that put this population at risk for harmful social conditions, unemployment, violence, alcohol and drug abuse, poverty, poor health, and high morbidity and mortality rates. The IHS (2018) noted that Native Americans' life expectancy is 73 years compared to the general population at 78.5 years. The unemployment prevalence for AI/ANs increased from 8.8% to 15.8% between 2006 and 2010 (CDC, 2013). The eco-social theory outlines the "socially patterned exposure-induced pathogenic pathways, mediated by physiology, behavior and gene expression, that affect the development, growth, regulation, and death of an individual's biological systems, organs and cells, culminating in disease, disability, and death" (Krieger, 2014, p. 653). The theory was used to examine the possible connection between the socioeconomic and living conditions of TB patients and how these conditions affect the disease process or outcomes.

Nature of the Study

I used the quantitative method to analyze TB incidence rates among the Native American population living in the Northern Plains and determine whether the rates of LTBI are related to socioeconomic status and where individuals physically reside. I also analyzed whether there was a difference between the TB incidence rates of those living on the reservations compared to those living in an urban area and their socioeconomic conditions. I analyzed retrospective data and conducted statistical analyses using chi-square tests to answer Research Question 1. The chi-square test is designed to test the association between two nominal or ordinal variables (Frankfort-Nachmias & Leon-Guerrero, 2015).

I also used binary logistic regression to analyze data to answer Research Question 2. These research methods enabled me to investigate the variable relationships by integrating disease processes and environmental conditions (see Statistics Solutions, 2019b). This study's categorical and nominal dependent variables were active TB and LTBI (reinfections). The categorical and nominal independent variables were socioeconomic status, homelessness, multigenerational households, and history of alcohol use/abuse. I studied these variables to identify the effects on the rates of TB among this population. A confounding variable (age) was also considered in the analysis.

Creswell (2014) stated that a quantitative survey design provides numerical data representing the population's trends, attitudes, and opinions. I drew inferences about the chosen sample to define an issue in the general population that I studied. Rudestam and Newton (2015) described how quantitative methodology moves through the epistemic

(meaning the nature of knowledge) to theoretical (models and theories) and empirical levels (obtaining learning through observation).

Definitions

Great Plains area: The states identified by IHS (2018) in the Great Plains area are North Dakota, South Dakota, Iowa, and Nebraska. This relates to TB patients or contacts with addresses on the State Department of Health TB contact study Section 2 and the IHS Registration section 5.0 Demographics. The address includes street address, city, state, zip, community, and home location.

Homelessness: without a home (Dictionary (2020a). This relates to TB patients or contacts without an address on the State Department of Health TB contact study form Section 2 and the IHS Registration section 5.0 Demographics. The address includes street address, city, state, zip, community, and home location.

Reservation: A tract of public land set apart for a special purpose, as for use of an Indian Tribe (Dictionary, 2020b). This relates to TB patients or contacts with address on the State Department of Health TB contact study Section 2 and the IHS Registration section 5.0 Demographics. The address includes street address, city, state, zip, community, and home location.

Multigenerational households: The American Community Survey Briefs 2009-2011 (Lofquist, 2012) identified these households as family households consisting of three or more generations. This relates to TB patients or contacts with the same address on the State Department of Health TB contact study Section 2 and the IHS Registration

section 5.0 Demographics. The address includes street address, city, state, zip, community, and home location.

Socioeconomic status: The position of standing of a person or group in society as determined by a combination of social and economic factors that affect access to education and other resources crucial to an individual's upward mobility (Dictionary, 2020c). These data are found in the IHS Registration regarding insurance, those on Medicaid and those who use IHS health care services for free, data entered into registration section 5.4, alternate resources.

Substance abuse: Long-term pathological use of alcohol or drugs, characterized by daily intoxication, inability to reduce consumption, and impairment in social or occupational function; broadly, alcohol or drug addiction (Dictionary, 2020d). This relates to TB patients' history and physical used to diagnosis and treat TB found in the IHS Electronic Health Record and in the State Department of Health TB contact study pre-investigation section. This section includes other diagnoses (e.g., substance abuse, mental illness, or dementia) that impinge directly on the interview.

Urban area: In population census, a city area considered as inner city plus built-up environments, irrespective of local body administrative boundaries (Dictionary, 2020e). This relates to TB patients or contacts with address on the State Department of Health and Human services TB contact study Section 2 and the IHS Registration section 5.0 Demographics. The address includes street address, city, state, zip, community, and home location.

Assumptions

The primary assumptions from the eco-social theory of disease distribution proposed by Krieger (2012) and Evan et al. (2019) related to the connection between socioeconomic status, living conditions, substance abuse, and how the disease progresses within a population. Based on this theory, I assumed a person's interaction with other people and their environment may increase certain types of infectious and chronic diseases in that population and increase inequities to suffering from the disease. An assumption regarding the IHS registration and history /physical data was that patients provided accurate information when registering for health care services or providing historical health information in the IHS clinics and hospitals. Another assumption was that patients provides accurate details when asked about substance abuse, whom they were in contact with, or where they lived when questioned by the health department during the TB case contact study.

Scope and Delimitations

This study focused on the AI/AN population living in the Northern Plains of the United States. The states included in the Great Plains area are North Dakota, South Dakota, Nebraska, and Iowa. These states also have moderate to large Native American populations who live on Native American tribal lands or in urban areas. All tribal members and those with tribal lineage within the Great Plains area have access to IHS, hospitals, clinics, or tribal health clinics for health care.

This group was chosen because of the ongoing high rates of TB in the United States and the Great Plains area per capita, even though these groups compose a tiny

percentage of the total population. NA/AIs also have higher poverty rates, drug/alcohol abuse, violence, mortality /morbidity rates, and homelessness than non-Native Americans living in the same non-reservation communities. The rates for TB and the socioeconomic status of the Native American population in the Great Plains area have not improved at the same rates as non-Native American communities in the same location (Center for disease control and prevention, 2018; Substance abuse and mental health services administration (SAMHSA). (2018).

Limitations

This study's limitations and challenges included the incompleteness of genotype data entry and TB data from state health departments and IHS contact studies conducted for each incident and studying TB in low-burden states. Concerning the first limitation, genotyping data and information from the contact studies were voluntary, and data completion depended on the people entering it. The second limitation related to when each state started uploading TB data into the TB Genotyping Information Management System (TB GIMS). When different states started uploading at different time points over the years, some genotype data were available for confirmed TB incidents in some states for specific periods. The third limitation was that the research focused on American Indians in the Northern Plains, where most live on reservations compared to small towns and cities in low population states. Therefore, the study findings may not be generalizable to American Indians living in large cities with high-density populations.

Significance

This study was significant in examining the relationship between active TB status, low socioeconomic status, homelessness, multigenerational households, substance abuse, and residence of Native Americans living in urban areas or on reservations in the Northern Plains. TB risk increases as social conditions such as poverty, inadequate housing, and substance abuse rise in a population (Ortblad et al. 2015). These social conditions among the American Indians in both urban areas and reservations contribute to persistent health disparities relating to TB infections, as shown by morbidity rates of 3.9%, which are higher than the general population's 1.0% (CDC, 2017a). Public health organizations could use this study's findings to plan TB prevention programs for American Indians living in poverty, having substance abuse or poor housing conditions, and living on or off reservations.

The research findings could also inform health care programs for the treatment and management of LTBI, such as during the provision of directly observed therapy in this population. The results of this study could add to the limited literature regarding TB reinfections connected to social conditions for those living on the reservations compared to reinfections rates of those living in urban areas consistently for more than 5 years.

The findings of this study could refocus TB prevention and treatment programs on the social conditions that patients experience, which increase the risks of TB spreading in this population and reinfection. At the community and societal level, the findings from this study could inform decisions on the future prevention of TB cases in the Native American people in the Northern Plains. This study could also influence how public

health programming addresses every TB case using a three-pronged approach: public health, medical, and socioeconomic. Use of the three-pronged process could reduce health disparities by allowing the public health professional to determine when the TB case is closed, instead of the current process in which the case is closed when the individual is no longer infectious. At the individual level, the findings could increase awareness of TB reinfection and its risks and inform potential strategies for risk avoidance in marginalized groups, thereby contributing to positive social change.

Summary and Transition

In Chapter 1, I addressed how AI/ANs continue to have a high rate of TB infections in the Great Plains area compared to other populations in North Dakota, South Dakota, Nebraska, and Iowa. The TB rates in this group have decreased but at a slower pace compared to other ethnic and racial groups. This quantitative study addressed the possible correlation between TB cases and factors such as low socioeconomic status, homelessness, multigenerational households, and substance abuse among the AI/ANs in the Northern Plains living on the reservation compared to urban areas. Chapter 2 provides a review of the literature on TB and previous studies relating to eliminating the disease among high-risk populations. I examine the evidence from Western countries on public health programs focused on surveillance, testing, and treating the most vulnerable people, such as the homeless and migrants, and comorbidities such as HIV or diabetes.

Chapter 2: Literature Review

This quantitative study involves analyzing TB incidence rates among the Native American populations in the Northern Plains in the United States. This study had a dependent variable of a positive test for active TB and independent variables of low socioeconomic status (below the poverty line), homelessness, multigenerational households, and substance/alcohol use among Native Americans in the Northern Plains living on the reservation compared to urban areas. TB cases were reported to the CDC by the state health departments from 1999 to 2019 in the Northern Plains states including South Dakota, North Dakota, Iowa, and Nebraska.

Most of the research on TB in the Native American population was conducted on chronic disease with TB as a coinfection. However, there was little research on using genotyping TB cases to assess the relationship between latent TB and social conditions in the communities where Native Americans live in the Northern Plains as a cause of the persistently high TB morbidity rates in this population. Chapter 2 presents the literature review of TB history, epidemiology, pathophysiology, genotyping of TB as part of surveillance and identification of clusters, and social and environmental conditions of the Native Americans living in the United States.

Literature Search Strategy

Database and Resources

Preparation for this literature review was conducted by searching online resources using the Preferred Reporting Items for Systemic Reviews and Meta-Analysis. Databases searched included the Walden Library online search engines PubMed, CINAHAL,

EBSCO, Thoreau, Medline, Sage Knowledge, Science Direct, Sage Journals, World Health Organization (WHO), and CDC. Also included in the review are articles from Native American publications *Indian Country Today*, *Native Times*, and advocate flyers and handouts because data on Native Americans were limited when reviewing life in urban settings and living on the reservations.

Concepts and Terms Used

The search included the following conditions, concepts, indices, and truncated terms as individual conditions or a combination of all three during this search. The search terms included *Native American*, *American Indian*, *poverty*, *low socioeconomic status*, *TB*, *latent Tuberculosis*, *TB genotyping*, *TB cluster*, *TB contact studies* and *Native American*, *demographics*, *socioeconomic status*, *alcohol use*, *substance abuse*, *violence*, *homelessness*, *homeless*, *poor housing*, *lack of housing* and *eco-social theory, human rights theory,* and *Native American*, *active Tuberculosis*, *LTBI*, *abuse*, *physical abuse*, *genotype*, and *whole genotype*.

Article or Study Inclusion and Exclusion Criteria

The criteria for the articles included in this study were the following: published date from January 2015 to October 2019, peer-reviewed or seminal literature, interventions, or public health policy related to one of the following or a combination of TB, latent TB, TB genotyping, American Indians, Native Americans, homelessness, poverty, or related to substance or alcohol abuse. All articles were in English or were translated into English. Most items were limited to the United States, but some articles related to TB, genotyping, poverty, and eco-social theory were from outside the

continental United States. I used articles and studies using the eco-social theory to report on original development, concepts, and rationale dating from 2001 to 2012. Some materials on social and environmental issues among the American Indians were older than 2008–2015 due to a lack of recent articles or literature.

Little Recent Research or Literature

Because there was limited peer-reviewed research on Native Americans and TB, I identified some related information based on secondary data from programs that worked with Native Americans regarding alcohol use and poverty. These programs' reporting was supported by federal programs or grants from Health Resources and Services Administration (HRSA), SAMHSA, IHS, and Health and Human Services.

Theoretical Foundation

Krieger (2014) identified eco-social theory to explain the effects of a population's exposure to societal and ecological conditions and how these exposures affect disease distribution within that population. The eco-social theory takes this concept and addresses the idea of inequities both in race and the social and environmental effects on the overall health of an entire group that shares a race or ethnicity (Krieger, 2014). Bey et al. (2019) used the eco-social theory as the foundation of an Identity Pathway framework to study the effects of discrimination on cardiovascular disease occurrence. Bey et al. analyzed whether the daily racial discrimination had any effect on the rates of cardiovascular disease among African American men and women compared to their White counterparts. Bey et al. questioned whether the social environment, such as poverty, negative lifestyle choices, and disease progression, is affected by the daily barrage of racial discrimination.

The framework predicted that each group had a different outcome on the cardiovascular disease effects, and these outcomes were similar to the rates of racial and gender discrimination identified by the subject.

In another study, Evans (2020) relied on Krieger's concept of eco-social theory that a population's social and political conditions can affect their physical responses to disease conditions. Evans looked at how Krieger's concept of social inequalities' effects on health should have intersectional terminology added. Social and health inequities were expressed as an interlocking system to deal with inequities related to discrimination. Evans outlined the idea that Krieger focused on only the disease causality but not on how social and political inequities affected the population's reaction to disease. The next steps from this concept were to add operationalization and institutional discrimination to the list of inequities. Evans recommended that the eco-social theory should be expanded to address the larger issue of health, including social and ecological disparities between groups.

These studies showed how important the person's environment and social standing are to their overall health and how they are affected by disease. The Native American population is affected by social, ecological, and political policies that have historically failed with outcomes of increased poverty, drug/alcohol use, and homelessness (Talkpoverty, 2017). Adding to this fact, Native Americans also suffer from diseases such as TB at a higher rate (4.0%) compared to the general population 1.0% (CDC, 2017a).

Review of Literature

TB: World's Silent Epidemic

Charged with the goal of eliminating or eradicating TB around the world and in the United States, the TB elimination program has been in place since 1989; however, this goal has not been met (LoBue & Mermin, 2017; MacNeil et al., 2019). There has been a decrease in TB cases in Western countries such as the United States, but the vulnerable populations have been left behind in the TB elimination program strategy. The CDC 2009-2015 as cited in Godwin et al., 2017 found that of those affected, 79% were U.S.-born, 45% were homeless, and 83% had a history of heavy alcohol or substance abuse. The World Health Organization (2014, as cited in Matteelli et al., 2017; Rangaka et al., 2015; Stock, 2017) also found that TB elimination programs have decreased rates but failed to eradicate TB and determined it was essential to focus on LTBI, especially with the increase in migration from third world countries to first world countries.

A key reason why LTBI has not been addressed is because of the lack of funding for TB elimination programs and resources (Schito et al., 2017). Many public health programs, health care systems, and providers could use current research evidence to support the reallocation of resources for surveillance, faster testing, better treatment, and vaccines (Centis et al., 2017; Hannah et al., 2017; Padayatchi et al., 2017). Increased funding may also improve testing access such as point-of-care testing to improve detection times (Gkika et al., 2018). Prevention programs could also focus on identifying the TB transmission paths from infection to active disease to be able to break the cycle earlier in the disease process (Séraphin et al., 2016). Improved genetic testing to

determine TB clusters and transmission factors will allow TB elimination programs to dedicate resources to the areas in the country or state that are still reporting TB cases (Blanco-Guillot et al., 2018; Center for disease control and prevention, 2018).

The spread of TB can only be mitigated by interfering with the transmission process; this includes the process from LTBI to developing the active disease (Glynn et al. 2015; Guirado et al. 2015; Hunter, 2016). Early diagnosis of TB is required to interfere with the transmission process; this means that public health practitioners must be able to detect valid *M. tuberculosis* cases separating them from *M. Bovis* and multidrug-resistant TB cases to make sure that treatment is timely and effective (Marks et al. 2019; McBryde et al. 2017; Scott et al. 2016). Follow-up on all testing and diagnosis is essential to meet the goal of TB eradication or elimination, and public health practitioners must move past passive surveillance and increase the use of new tools to improve outcomes (Fox et al., 2018). However, it is important to remember that each person has natural conditions that account for increased susceptibility to contracting TB and developing the disease, which increases morbidity and mortality in high-risk communities (Lindenau et al., 2016; Restrepo, 2016; Zak, 2016).

Epidemiology of TB in Native Americans

In the Northern Plains, American Indians are a small group in low-incident states, but per capita they have always had a higher rate than the general population (Cheek et al., 2014; Reilley et al., 2014). Also, Podewils et al. (2014) noted that TB in the AI/AN population is not a historical affliction but a current health issue that has silently targeted their communities. The rates of TB in this population have decreased over time but are

still much higher per capita than in other ethnic and racial groups in the United States (Stewart et al., 2017; Yuen et al., 2016). This small population is sometimes lost in the data collection because they are mixed with other small racial minority populations or identified in the group called non-Hispanic, and national data analysis does not show AI/AN as an individual group (Adekoya et al., 2015; Salinas et al. 2016). Combining races leads to a lack of accurate data on TB morbidity and mortality in the AI/AN population throughout the United States and Northern Plains (Talwar et al., 2018).

Social and Environmental Issues Impacting the Health of Native Americans Living in the United States

Low socioeconomic status, homelessness, and substance abuse have been and are plaguing the American Indian/Alaska Natives for generations (Patterson et al., 2015). Miserable social conditions have led to a stagnating rate in the incidence of infectious diseases like TB, and many believe that socioeconomic conditions are a significant factor in the adverse outcomes that this population suffers from (Ponicki et al., 2018). There does not seem to be a difference between AI/ANs who live in urban areas versus reservations when it comes to substance abuse, violence, or infectious diseases. However, many experience a loss of connectedness to their tribe, following traditional practices, and a loss of spirituality. Although urban AI/ANs are found to have issues with the loss of traditions, (Brown, et al., 2016), those AI/ANs living on the reservations also suffer from this loss. AI/ANs not only have higher rates of TB, but also, they are infected at a young age; this increases mortality and morbidity rates in the adult population (Stanley & Swaim, 2018). It is this deterioration of health that adult AI/ANs suffer from that leads to

an increased risk of poverty, homelessness, and contracting infectious diseases (Cunningham, et al., 2016; Chartier, et al., 2013; Volkmann, 2016).

American Indians and Alaska Natives still deal with issues such as racism that increase disconnect from the community at large and lead to a rise in substance and alcohol abuse (Vaeth, et al., 2017; Huyser et al., 2018). The American Indian tribes in the Northern Plains have higher rates of substance abuse than tribes from other areas in the United States, but funding for prevention and treatment are the same for all tribes (Vaeth, et al., 2017; Burduli et al., (2018). Awareness of substance abuse of opioids is critical but interventions must be designed to meet the needs of communities where they live. A study found that opioid use might not have high rates on the Northern Plains reservations because of a lack of access to and availability of cheaper drugs like Meth and alcohol (Tipps, et al., 2018).

The AI/AN communities suffer from poverty, substance abuse, and homelessness, which increase infectious diseases like TB, and these are the same high-risk conditions identified by the CDC and WHO for TB transmission. The American Indians in the Northern Plains may be the smallest ethnic groups but have a high rate of health disparity increased due to behavioral factors that lead to adverse outcomes (Holm, et al, 2010). The social and socioeconomic conditions that Native Americans live in put them at significant risk for having LTBI and thus increased testing should be part of their health care, (Holman et al., 2011; Bibbins-Domingo, 2016; Gounder et al., 2017).

The Northern Plains has two of the ten largest reservations in the United States and suffers from large numbers of social, poverty, hunger, and homeliness (Thorton,

2015; Bread for the world, 2018). This group also suffers from a lower health status, lower life expectancy, inadequate education, high poverty rates, economic adversity, and poor social, and environmental conditions. This population tends to die younger, and suffer more from chronic disease, infectious disease, self-injury, unintentional injury, and assaults/homicide per capita than any other demographic (Indian Health Services, 2018; Burnette and Figley, 2017).

Kong, et al. (2018) looked at how American Indians in the Northern Plains (South Dakota) reacted to childhood abuse and how it affected their chances of being abused by an intimate partner. They found that childhood abuse leads to an increase in violence, close and physical. They also found that they were also at a higher risk of depression and despair (Kong et al., 2018). Strategies for working with this population must focus on the population's perception of their health and must be engaged positively and productively (Leston, et al., 2018; Duwe, et al., 2014).

If American Indians inhabit a sick, violent, poverty-stricken environment, it is challenging to be healthy bodily or mentally (Narhi & Matthies, 2018; Evans, et al., 2018; Lawrence & Forbat, 2019). It is important these populations reconnect with their traditions and culture when trying to improve their lives and environment (Krieger, 2012; Matamonasa-Bennett, 2017). The eco-social framework emphasized the need for all the policies, resources, and strategies to incorporate the person's perception of their environment and social interactions (McGinnis & Ostrom, 2014).

The eco-social framework by Krieger, & Guskin, (2001) when applied to women's health related to TB, showed that women progress from infection to disease at a

faster rate. It also reflects that current public health policy focuses on treatment to stop infections from occurring and not focusing on when that population continues to have active cases. However, the eco-social framework does not address why some are affected by social, racial, economic, or biological conditions that put them at risk for adverse outcomes. Krieger and Guskin (2001) stated that public policy and research must consider these issues when developing or implementing strategies for populations that have social and economic inequities.

Genotyping TB to Improve Surveillance and Public Health Policy and Practice

The use of whole-genome sequencing (WGS) during TB outbreaks, especially in areas of low disease burden, is vital to the goal of eliminating TB. Whole-genome testing would provide a faster and more accurate diagnosis of the virulence of the disease, define the transmission process, and connect to probable sources (Gilchrist et al., 2015). Using whole-genome-sequencing to determine transmission and its effects in high-risk groups, including the use of TB lineages along with epidemiological investigations, can improve overall disease management (Nikolayevaskyy, et al., 2016; Hatherall, et al., 2016; Guthrie et al., 2018).

The CDC explains why genotyping is used to describe a disease cluster, and how to link unsuspected cases through epidemiological connections in the genotype isolates, and variations (Center for disease control and prevention, 2018; Teeter et al. 2017). Whole genomic sequencing has been used in small outbreaks efficiently, and effectively to identify TB and treatment to meet the needs of the World Health Organization TB response around the world (Votintseva, et al., 2017). Another use for whole genomic

testing is in the diagnosis of multidrug-resistant TB (MDR), identification of the biotinylated RNA explicitly designed to bait M. tuberculum DNA. This identifies the entire TB genome from the sputum sample by using whole genomic sequencing.

WGS thus eliminates the need for culture, however, one major issue is that currently the technology for WGS is in countries with relatively small numbers of multidrug-resistant TB (Brown et al., 2015; Pankhurst, et. al., 2015; Lee & Behr, 2016). The use of WGS could more accurately determine if a case were to be MDR and enable more timely and appropriate treatment. The use of whole genomic sequencing would allow for the identification of MDR, transmission between hosts, and the general pattern of transmission during an outbreak (Yang et al., 2017; Witney, et al., 2016; Puerto, et al., 2015). Analysis of the genome of TB to identify any differences in the genes expressed in TB disease, and pathways, or polygenic/Omni genic research could potentially aid in the development of new treatments, or vaccines. It could also address the diversity in the host's genetic susceptibility, the genetics of the TB in that region, and environmental conditions that allow infections to occur in that specific family, community, or country Stein, et al. (2017).

The use of whole-genome sequencing (WGS) could pave the way for future TB research. Data collected from WGS collected around the world could be entered into a database that would provide access to TB DNA genomes to those countries that are not financially able to use this process on all TB and LTBI patients. Further down the line, all the parts of this process will improve, faster, with expanded capabilities for sequencing, lower costs, faster diagnosis of multidrug resistance TB and an increase in data for

research studies to improve our chances of eliminating TB in the future (Colijn, & Cohen, 2016). Genotyping can be used to determine new transmission versus reactivation of latent TB. Using genotyping means that the TB control programs must adjust disparities and reallocate resources to decrease it (Noppert, et al., 2017).

The Individual-based model for TB

Researchers and providers cannot forget that, along with all the TB genetic data, social and environmental conditions need to be considered. Such as, the living conditions that TB patients encounter which puts them at risk of contracting or advancing from TB infection to a disease state. For TB elimination programs to move toward eliminating latent TB disease, it is important to first determine the rates within the populations. One way is to use mathematical models, including the use of age-structured socio-demographic individual-based models (IbM) with the addition of a time-evolving structure in a defined population with a low burden for TB. The IbM by including age structure to focus on contact studies or investigations on an index case may enable researchers to determine the factors linked to the reactivation of LTBI cases in that population accurately. By adding the socio-demographic aspects, they could analyze the transmission rates in specific settings where the contacts are located. This model has worked well with longitudinal research, whether or not there was a new transmission (Ackley et al., 2015). It has been applied to assess the effectiveness of TB elimination programs and is malleable enough to evaluate TB in different environments (Guzzetta et al., 2011; Burzynski, 2017).

The Individual-based model for TB can be used to analyze the effects of TB on a sample and to analyze how their social, environmental, and physical conditions affect the TB process from infection to disease. The IbM model can be used to analyze data from low incident populations, and assess all the stages of TB infection, and illness. The data on latent TB infection can also be calculated, and it allows a researcher to use variables that are more specific to any population or community (Prats et al., 2016). Zhang, Li & Zhang (2015) studied the epidemiological consequences of both the prevention and health care of TB patients. They found that three main measures were needed to eradicate TB in this population, decrease transmission, increase hospitalizations for infectious patients, and increase treatment of latent TB in the community. The article discussed the models for TB that could simulate the transmission, and disease process for TB to allow predictions on rates for that population. These models were based on multiple mathematical systems that can be differential equations or simulation models, including the Markov Chain Monte Carlo methods (Ozcaglar, et al., 2012). Simple estimations of LTBI in a community have used the data from genotyping the active TB cases to estimate the number of LTBI cases in that community then. Thus, finding LTBI cases can be resolved by the move to whole-genome sequencing as this form of analysis is cost-effective because it uses the data on active cases reported, and decreases the need to test or evaluate the population for LTBI (Haddad, et al., 2018).

The evidence found in the literature review shows a link between TB, and socioeconomic conditions. Yuen et al. (2016) analyzed the epidemiology of TB cases for recent infections related to transmissions in the US from January 2011- September 2014,

and found that being Native American, Native Hawaiian/Pacific Islander, Black, and homeless were more of a factor for TB transmission than being foreign-born. Another article by Cheek et al. (2014) reported that TB rates of hospitalizations among the A.I./ANs declined from 1998 – 2006 but remained higher than the general population. The most significant number of admissions for TB occurred in Alaska, Southwest, and the Northern Plains. These same areas also had a high rate of disparities, and the Northern Plains average mortality was 4-5 times higher than that of the general population.

The connection between social conditions such as alcohol use and TB was noted by Godwin et al. (2017) who analyzed the CDC data from 21 outbreaks from 2009 to 2015 and looked at the demographic and social conditions that may have contributed to the outbreaks. They found that of those affected, 79% were US-born, 45% were homeless, and 83% had a history of heavy alcohol or substance abuse. As did the study by Ponicki et al., (2018) who analyzed the high rates of alcohol and drug-related health conditions or injuries in the Northern Plains Indian populations. They looked at inpatient records for hospitals in South Dakota, and Nebraska, and focused on the zip codes in areas with the highest Native American population. The zip codes included the reservations, and areas with a large population of Native Americans. The results showed that Native American populations living on the reservations had higher rates of self-inflicted injury and drug/alcohol abuse.

Finally, Volkmann, et al. (2016) studied the connection between TB infection and alcohol abuse. The alcoholics were at high risk of poverty, housing issues, and lack of

health care along with an ability to complete treatment provided by directly observed therapy. They were uncertain if the increase in TB transmission was due to the physical damage the alcohol had done, or the social conditions that the person was living in, poor diet, poor housing, poor general health and lowered immune system. Overall, the literature shows that there is a link between low socioeconomic status, substance abuse, lack of housing, and TB infections.

Summary

In Chapter 2, I identified the historical aspect of TB in the AI/AN population in the US. The review also focused on the social and economic conditions that support TB morbidity, and mortality in the communities that suffer from lower socioeconomic status, such as AI/ANs. The literature and research review included a discussion of how the eco-social theory could be used to evaluate the connection between TB disease, and social conditions in the AI/AN population in the United States. The review addressed the use of genotyping TB as part of a TB elimination program and the links to the public health policy needed to decrease TB rates.

Chapter 3 will outline the study methods, define the independent variables (socioeconomic status, homelessness, physical location, cohabitation, substance, and alcohol use in the AI/NA population). I will also describe statistical methods used in the study such as chi-square analyses and binary logistic regression.

Chapter 3: Research Method

The research design was a quantitative study using secondary data to analyze the relationship between TB infection/reinfection and socioeconomic factors in Native Americans in the Northern Plains. The dependent variable was TB infections. The independent variables were socioeconomic status, multigenerational households, homelessness, residence, and substance abuse. The target population was Native Americans in the Northern Plains of all ages diagnosed with TB infections from 1999 to 2019.

The sample size was 150 cases from the secondary data based on G*power analysis, which included an effect size of 0.3 and a power of 80%. The methodology involved manually collecting secondary TB data from each state's department of health contact study, including TB genotyping and treatment. The statistical analysis was conducted using chi-square tests and binary logistic regression. Threats to internal validity are outlined in this chapter, which included time and order and historical threats. Ethical considerations are also described, which included using numerical identifiers for each TB case and excluding contact with vulnerable populations.

Research Design and Rationale

According to Creswell (2014), a quantitative survey design provides numerical data representing the population's trends, attitudes, and opinions. Rudestam and Newton (2015) described the quantitative approach in a more defined manner from the epistemic levels, meaning the nature of knowledge, theoretical meaning models and theories, and

empirical meaning obtaining learning through observation. I aimed to draw inferences about the chosen sample to define the study topic in the general population studied.

I used a quantitative method to analyze retrospective data and statistical analysis including a chi-square test to answer Research Question 1 regarding potential associations. The chi-square test is nonparametric and designed to test the statistical significance or relationship between categorical variables (Frankfort-Nachmias & Leon-Guerrero, 2015). I analyzed two nominal variables: active TB and LTBI cases.

I conducted binary logistic regression analysis to answer Research Question 2 and determine the relationship between the nominal dependent variable (TB acute and latent) and one or more nominal, ordinal, interval, or ratio independent variables: residency, socioeconomic status, homelessness, multigenerational households, and substance abuse. This design is used to identify the relationship between the dependent and independent variables by looking for an association between the variances in the dependent variable (McDonald, 2014). This research approach allows the investigation into the variable relationship to be more holistic and robust by integrating disease processes and environmental conditions (Yin, 1994).

Methodology

Study Population

The study population consisted of people identifying as Native American/American Indian living in the Great Plains area of South Dakota, North Dakota, Nebraska, and Iowa. The sample was active cases of TB or on a contact list for a TB case. Patients of all ages were sample cases during this study; the sample included all

cases due to a small number of overall TB cases in these low-burden states. Inclusion criteria were American Indians from a tribe in the Northern Plains, including males and females of all ages who had contracted and developed the TB disease. Eligible individuals were identified using the demographic and diagnostic data retrieved from the South Dakota Department of Health's data during the TB contact investigation. Patients not on both data systems were excluded.

The sample size was based on 150 cases derived from the secondary data using the following parameters: CI = 95%, alpha Type I error = 0.05, beta Type II error = 0.2, power = .8. The G*power analysis for this study included an effect size of 0.3 and a power of 80% and required a total sample of 150 to test the association at 5% levels using a two-tailed test. The G*power Version 3.1.9.7 was used to carry out the sample size calculation.

The cases were determined by the completeness of the records collected by the state health departments, and IHS Resource and Patient Management System (RPMS) databases. To answer Research Question 1, I compared the level of TB outbreaks in Native American counties and determined how many were related to reinfection or whether these were cases of LTBI breaking down. I used the secondary data from the patient records for the IHS RPMS registration database and the state TB contact study data for the past 2 years to determine location category (reservation or urban). These data were added to the spreadsheet with the genotyping data for each case. To answer Research Question 2, I used data from the IHS RPMS database, State Health Department contact studies to determine whether there was ongoing LTBI in the population that was

leading to the outbreaks or whether there was a relationship between the non-Native American community and demographic shifts.

Sources and Methods of Data Collection: Archival Data

The data source for Research Question 1 was secondary data from IHS on active TB and LTBI. I searched the data for each state in the Northern Plains; each one had a specific code that identified its data. I used a spreadsheet to analyze the data after the system provided a list type report for each state. The data source for the secondary data to answer Research Question 2 included socioeconomic data obtained from contact studies that followed the CDC contact study process guidelines for TB surveillance. The forms contained the patient's name, address, age, gender, community, family, and household members, and everyone who worked with or socialized with the patient.

The department of health collects all labs, X-rays, and treatments the patient received and their history, if available. The CDC (2005) has a specific set of algorithms that direct the investigator on each step of the process. Once retrieved, these studies can be obtained from each state department of health and IHS public health departments. The medical data on TB diagnosis and patient demographics collected from IHS RPMS patient records and registration system include age, gender, and insurance (IHS only, Medicaid/Medicare/private insurance). This system also contains substance abuse diagnosis for active TB cases and residence on reservation (zip code identified as being on the reservation lands for larger reservations and address with the town, or the city within the reservation boundaries). I then compared these records to those not falling into either of these categories identified by the patient from a contact study from the South

Dakota Department of Health: no data provided by IHS RPMS registration and State Department of Health for North Dakota, Nebraska, and Iowa.

Operationalization of Each Variable

The genotype data from the TB cases in the Northern Plains were not available from the CDC GIMS program database, the IHS RPMS system, and state health departments. The South Dakota Department of Health entered these cases and contact study data and TB sputum samples, providing both demographic on each case. Predictors of interest included demographic information regarding gender, insurance (IHS only, Medicaid/Medicare/private insurance), address, and substance abuse diagnosis for active TB cases from contact study from IHS RPMS registration and electronic health record and state department of health for North Dakota, South Dakota, Nebraska, and Iowa investigation data. These secondary data provided information on tribal affiliation, substance abuse, residence, and TB data. I manually entered data into a spreadsheet using the following codes: positive for TB 0 = reinfection, 1 = new infection; substance abuse 0 = yes, 1 = no; socioeconomic status related to the poverty line 0 = below, 1 = above, 2 = unknown; homelessness 0 = yes, 1 = no; multigenerational households 0 = yes, 1 = no; and residence 0 = reservation, 1= urban. The data were then be analyzed using binary logistic regression to assess relationships. Address was coded as "live on reservation" (zip code identified as being on the reservation lands for larger reservations and address within a town or city within the reservation boundaries). The data were compared to those not falling into either of these categories identified by a patient from a contact study

from IHS RPMS registration and the state department of health for North Dakota, South Dakota, Nebraska, and Iowa.

Data Analysis Plan

The data collected from state health departments' contact study form were manually entered into a spreadsheet. The data were cleaned up by identifying outliers in the data, starting with pronounced errors (inverted numbers, misspelled words). Next, I looked at strange patterns to determine whether most of the data had a lower possibility of containing skewed or erroneous data compared to a minority that were obvious errors. I analyzed all contact studies conducted by the state departments of health for each patient for erroneous errors to fix the error or omit it from the sample. Once the data spreadsheet was clean, the data were analyzed using SPSS Version 23 to conduct the chi-square and binary logistic regression tests.

Research Question 1

What is the association between socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains) and active TB status? This research question was addressed using a chi-square test of association. The chi-square test is nonparametric and designed to test the significant association between categorical variables (Frankfort-Nachmias & Leon-Guerrero, 2015). I analyzed two nominal variables: TB cases and LTBI cases.

The chi-square test does not require assumptions regarding the distribution of data points from the population analyzed (Frankfort-Nachamias and Leon-Guerrero, 2015).

The TB was two categories of nominal variables, one active and those that have a history of LTBI. Each variable was dichotomous with or without a history of LTBI.

Research Question 2

Is there a relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse and reinfections cases (LTBI) among the Native Americans living in urban centers versus reservations in the Northern Plains? This research question was addressed using binary logistic regression analyses. Binary logistic regression is used when predicting a nominal binary outcome of the dichotomous variable. Logistic regression explains the relationship between the nominal dependent variable: TB (active and LTBI) and one or more (nominal, ordinal, interval, or ratio-level) variables. I used nominal independent variables: residency, socioeconomic status, homelessness/ multigenerational households, and substance abuse. If needed, the R2 using the Hosmer-Lemeshow goodness of fit test could be used (Statistics Solutions, 2019).

Assumptions

Assumption 1 was dependent variables are dichotomous variables. Assumption 2 was one or more of the independent variables are categorical (ordinal, nominal). Assumption 3 was the dependent variable should have exclusive and exhaustive categories. Assumption 4 was logits of any dependent variable will check with the SPSS program (see Statistic Solutions, 2019).

The descriptive analysis of this study showed how new TB cases compared to reinfections based on confirmatory testing and categories were measured against the

independent variables identified as low socioeconomic status (below the poverty line), homeless or multigenerational households, substance abuse, and residency (urban or reservation) findings were assessed for effects on TB infection rates. I used binary logistic regression analysis to identify potential associations between TB genotype with or without variables and social conditions among the Native American population in the Northern Plains.

The binary dependent variable was positive for TB: 0 = reinfection, 1 = new infection. TB cases from 2000 to 2019, new infections and reinfection. The independent variables were the following:

- homelessness 0 = yes, 1 = no
- socioeconomic status employment; 0 = below, 1 = above, 2 = unknown
- history of substance abuse 0 = yes, 1 = no
- reservation address zip code within the boundaries of a federally recognized Indian Reservation 0 = reservation, 1 = urban.

The confounder was age.

Individual-Based Model for TB

For the identification of the rates of latent TB infection in this population, a mathematical model was used. The IbM model can analyze data from low-incident populations by looking at all the stages of TB infection and disease, and the data calculated on latent TB infection. An individual-based model for TB can be used to analyze the effects of TB on the sample and analyze how their social, environmental, and physical conditions affect the TB process from infection to disease. This model can add

issues with political, or public health policy, and take into consideration the social, environmental, and physical aspects of the population. This IbM model for TB allows a researcher to use variables that are more specific to any demographic or community (Prats et al. 2016).

This model was based on TB patients in two categories: one who is infected, and has no disease, and one with disease, and symptoms. The WHO and CDC identify that only 10% of those infected will develop the disease, so the longer they have been infected, the chance of developing the disease decreases. The IbM analyses of the TB sequelae focus on patient's age at the time of infection, time from infection to disease, disease to diagnosis, time from diagnosis to start treatment (identify if treatment is abandoned or finished), time from treatment to recover, and death (Prats et al., 2016).

Parameters

The parameters for TB data: patients with TB diagnosis, which includes: TB detection active cases diseased state identified through contact study, or present of a cavitary lesions. Any diagnosis delay = time from contact to positive test in days, was treatment started, completed, or abandoned. Review of risk factors: lower socioeconomic status, homeless, history of substance abuse, or multigenerational households. Place of residence lives on reservation with an address within reservation boundaries or do they live in an urban area with populations > 2,000 not located within the boundaries of the reservation.

Threats to Validity

Internal Validity

The internal threats to the validity of this study are historical and time order. Both time order, and historical treats can lead to selection bias while collecting each TB case data. Time order threat can occur when the researcher cannot determine the time sequence of the events being studied (Urban & van Eeden-Moorefield, 2018). In this study, the timing of demographic information regarding residence, cohabitants, substance use, or income was collected, and TB exposure, or disease. The historical threat is identified when an event occurs before, or during the study that could influence the results (Urban & van Eeden-Moorefield, 2018). This study could have included missed, inaccurate or incomplete data that may result from changes in data collection and changes to the contact study process from 1999 – 2019. The data on a spreadsheet was analyzed, excluding data that is incomplete or inaccurate if data is not available in another report form that was collected.

External Validity

Using genotyping in vulnerable or minority populations to identify latent tuberculosis infections, enhances the accuracy of identification of LTBI in a population which allows public health programs to mitigate the risk posed to the community by TB, and increases early treatment before they become contagious, thus decreasing overall TB cases. However, the findings may only be generalized to Native Americans in the study population.

Potential Issues With Validity

This study considered confounding bias due to co-morbid conditions, or conditions that lower the immune system of the TB patient. These could be confounding variables because they are also risk factors for contracting TB. In order to mitigate this bias, I included only cases where the subject with co-morbidities are within limits identified as controlled per medical guidelines.

Selection bias is possible due to completeness and accuracy of data entered into the IHS RPMS database on TB cases. To decrease this discrepancy, a comparison of the demographic and historical medical data from both the contact study conducted by the state health departments to the IHS RPMS data to be sure that they used complete and accurate data.

Information bias could occur due to misdiagnosed TB cases, or patients lost to follow up when confirming TB diagnosis. Only active cases with diagnostic confirmation (chest x-ray, genotype) testing were included in this study. Thus, the only cases included in this study were TB cases in Native Americans with confirmed TB.

Construct Validity of the Genotyping of the M. Tuberculosis for Each Active Case Conducted by the CDC

The CDC allows a standardized system of genotyping M. tuberculosis isolates with new methods of spoligotyping and MIRU analysis; these testing methods are based on the PRC, and provide a validated approach with much more rapid results (CDC, 2012). However, due to lack of data, I was not able to utilize genotyping to identify the

variation, and mutations based on secondary data from the CDC, based on the genotyping process involving the use of IS6110-based RFLP genotyping.

Ethical Procedures

For this study, all the data was secondary, and no partnerships with external organizations were needed. Government agencies with secondary data have processes for accessing the data. The IHS has a data application process to obtain data on demographic, and medical information on patients in the RPMS data bank. I applied for IRB approval from the following data sources after I gained approval from Walden University 08-30-21-0652590; all IRB requests require prior approval from Walden. To access the IHS RPMS, I sent the proposal to the Great Plains Area Institutional Review Boards for review, and approval. I submitted applications to South Dakota, North Dakota, Nebraska, and Iowa State Health Departments to access data on the TB contact investigations. To access the Nebraska State Health department, I completed the written request, and proposal to DHHS. To access the South Dakota Health Department, I completed the application for IRB approval. To access the North Dakota Health Department, I completed the IRB request, and send it to NDDoH, to determine if my request needs IRB approval. To access the Iowa health department, I completed the online form requesting IRB approval.

All reporting identified Native Americans living in the Northern Plains in urban areas, or on reservations. A numerical identifier was used to de-identify all data from each case, and a master list of numbers was assigned to each patient for the study. For each of the organizations that own their databases, an IRB application was submitted

asking the organization if they wanted to be the IRB of record; their response was added to the IRB application for Walden University. This study was not a part of any "piloting" or regarded as a part of a pilot.

The data used in this study was secondary data from records already collected. The research and data collection are not a part of my regular job duties; I do work for IHS but not in the operation where the TB data is collected, analyzed, or stored. IHS database RPMS retains the data on patient demographics, TB tests, and treatment. This study was reported without any names or identifiers from the cases used.

Summary

The data collection was secondary data from the State departments of health in the Northern Plains contact studies, and the registration and electronic health records in Indian Health Services. I analyzed TB among the Native Americans living in the Northern Plains, and assessed the link between TB incidence rates, and socioeconomic status, housing, and substance abuse history in the proposed study manually entering data into the spreadsheet and analyzing the outcomes. All data was protected by removing all identifiable patient data during the collection, analysis, and final report. Chapter 4, describes the results of the study based on analyses involving the chi-square test, and binary logistic regression test, integrating the individual-based model for TB to examine the latent TB infection rates.

Chapter 4: Results

This chapter presents the descriptive statistics, chi-square results, and binary logistic regression analysis results. Plans for data analysis were outlined in Chapter 3. To determine whether a relationship existed between the TB cases that were reinfections (LTBI), and socioeconomic status, employment, homelessness, living on a reservation, or substance abuse, I addressed the following questions using the analytical methods outlined in Chapter 3.

Research Questions

RQ1: What is the association between socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains) and active TB status?

H_o1: There is no association between socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains) and active TB status.

H_a1: There is an association between socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans (living in urban areas or on reservations in the Northern Plains), and active TB status.

RQ 2: Is there a relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse and reinfections cases (LTBI) among the Native Americans living in urban centers versus reservations in the Northern Plains?

H_o2: There is no relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse among the Native Americans living in urban centers versus reservations in the Northern Plains and active TB cases identified as reinfections.

H_a2: There is a relationship between socioeconomic status, multigenerational households, homelessness, and substance abuse among the Native Americans living in urban centers versus reservations in the Northern Plains and active TB cases identified as reinfections.

Data Analyses

Once Walden Institutional Review Board (IRB) was obtained, I obtained secondary data sets on 145 cases of Native Americans with TB from 1999 to 2019. This study's target population was adult Native Americans with TB living in the Northern Plains. The data were complete except for the genotype data due to changes in testing and access to genetic testing conducted by the CDC. The data were collected by the South Dakota State Health Department, and included the contact study data, hospital data, CDC reportable data, and information that local health departments provided.

Descriptive Statistics

The sample size was 145 cases from 1999–2019, consisting of 69 males and 76 females (47.6% and 52.6%, respectively; see Table 1). Age was considered to be a

potential confounder and was included in the analyses. The ages ranged from 1 year to 88 years, with 110 cases out of 145 having ages ranging between 40 and 75 years (75.9%). The other ages were 1–18 years (11.0%) and >75 years (13.1%; see Table 2). The sample included 52 cases other than pulmonary TB infections, and 93 had active pulmonary TB (35.9% and 64.1%, respectively). Most of the sample population lived within reservation lands (76%); the data also showed that 127 cases (87.6%) were not seeking employment, and 14 TB patients (9.7%) stated they were homeless. The number of TB patients who had an issue with substance use was 59 (40.7%).

Table 1

*Descriptive Statistics (*N = *145)*

Variable	Frequency	Percentage
Gender		
Male	69	47.6%
Female	76	52.4%
Age		
1–18 years	16	11.0%
20–29 years	13	9.0%
30–39 years	9	6.2%
40–49 years	22	15.2
50–59 years	28	19.3%
60–75 years	38	26.2%
76+	19	13.1%
Reservation		
Off	111	76.6%
On	34	23.4%
Employment		
Employed/retired	18	12.4%
Not seeking employment	126	87.6%
Homelessness		
Yes	13	9.7%
No	131	90.3%
Substance use		
Substance use	59	40.7%
No substance use	86	59.3%
Tuberculosis		
Acute TB	52	35.9%
Latent TB	93	64.1%

Table 2

Age Frequency Data for Cases With Latent TB Infection and Active TB

Category	Frequency	Percentage	Valid percentage	Cumulative percentage
1–18 years	16	11.0%	11.0%	11.0%
19–29 years	13	9.0%	9.0%	20.0%
30–39 years	9	6.2%	6.2%	26.2%
40–49 years	22	15.2%	15.2%	41.4%
50–59 years	28	19.3%	19.3%	60.7%
60–75 years	38	26.2%	26.2%	86.9%
76+ years	19	13.1%	13.1%	100.0%

Study Results

To test the model fit for my study, I conducted a chi-square test and the Hosmer-Lemeshow test. These results showed the degree to which the model could take each case and put them into the groups identified on the dependent variable being used. The chi-square was conducted to identify an association between dependent variables (LTBI and active TB disease) and the independent variables: homelessness, substance use, occupation, and living on reservation. The null hypothesis in Research Question 1 was that there is no association between those with active TB and the independent variables of homelessness, occupation, substance use, and living on a reservation. No expected cells had fewer than five samples during this test.

The chi-square results showed that there were statistically significant associations at 5% significance level between active TB (11.593, $df = 1$, $p = <.001$; see Table 3), homelessness (213.572, $df = 2$, $p = <.001$; see Table 3), substance use (73.090, $df = 2$, $p = <.001$; see Table 3), occupation (312.448, $df = 5$, $p = <.001$; see Table 3), and living on reservation (40.890, $df = 1$, $p = <.001$; see Table 3). This meant that active TB,

homelessness, substance use, occupation, and living on the reservation were reliant on each other. Therefore, I accepted the null hypothesis.

Table 3

Chi-Square Analysis for Model Fit Using Dependent Active TB

Category	Acute TB infection	Homelessness	Substance use	Occupation	Reservation
Chi-square	11.593	213.572	73.090	312.448	40.890
df	1	2	2	5	1
Asymp. sig.	<.001	<.001	<.001	<.001	<.001

The null hypothesis in Research Question 2 was there is no relationship between those with latent TB and the independent variables homelessness, occupation, substance use, and living on a reservation. No expected cells had fewer than five samples during this test. The chi-square results showed that there was a statistically significant relationship at 5% significance level between latent TB (5.800, $df = 1$, $p = <.016$; see Table 4), homelessness (213.572, $df = 2$, $p = <.001$; see Table 4), substance use (73.090, $df = 2$, $p = <.001$; see Table 4), occupation (312.448, $df = 5$, $p = <.001$; see Table 4), and living on reservation (40.890, $df = 1$, $p = <.001$; see Table 4). This meant that active TB, homelessness, substance use, occupation, and living on the reservation were reliant on each other. Therefore, I accepted the null hypothesis.

Table 4

Chi-Square Analysis for Model Fit Using Dependent Latent TB

Category	Latent TB infection	Homelessness	Substance use	Occupation	Reservation
Chi-square	5.800	213.572	73.090	312.448	40.890
df	1	2	2	5	1
Asymp. sig.	<.016	<.001	<.001	<.001	<.001

Although the results showed that there was a statistically significant association with active TB (p = <.001) and a relationship with latent TB (p = .016), the results showed that there may be a slightly stronger association with active TB and the independent variables of homelessness, substance use, occupation and living on a reservation. A Hosmer and Lemeshow test was conducted for model fit for active TB infections compared to a null model without independent variables (chi-square = 10.752, df = 8; p = .216), Omnibus tests of Model Coefficients (Model [chi-square = 14.018, df = 5, p = .015]), which was statistically significant. When the Hosmer and Lemeshow test was conducted for LTBI with full predictor with that of a null model without any other predictors showed (chi-square = 14.651, df = 8; p = .066); the likehood ratio chi-square Omnibus tests of Model Coefficients (chi-square = 18.766, df = 5, p = .002). The Hosmer and Lemeshow test results were conducted for the active TB and LTBI models (p = .216; p = .066, respectively). Both were not statistically significant, which showed a good fit.

The Chi-square was significant for both active TB and Latent TB to the alternate model out performs the null model. The results may show that there is an increase multicollinearity and the possibility of a type II error, meaning that there could be a false

rejection of the null hypothesis. The overall model fit for both models for the dependent variable compared to the null model was good.

For analysis of the research questions, a binary logistics regression was conducted. There were three assumptions: independence of errors, linearity in logit for continuous independent variables, and absence of multicollinearity (see Stoltzfus, 2011). The first assumption used was independence of errors; this was met because the dependent variables for this study were active TB and LTBI. The dependent variables were categorical with two levels (yes/no), and there were no duplicate responses. The second assumption was related to independent variables that must be separate and independent of each other. This assumption was met because TB data from each of the health departments was not influenced or affected by the other public health departments that were also reporting TB data to the South Dakota Department of Health. Binary logistic regression assumes very little or no multicollinearity between any continuous independent variable (Yasin, 2017). The continuous variables that would be colinear were not met because all the independent variables used in this study were nonlinear, so the chances of multicollinearity were decreased and would not skew the results.

Research Question 1 Results

Age, a confounder was found to have a statistically significant (p=.049, see Table 5) impact on the risks of active TB. These results showed that only those aged 1-18 years (OR=9.840, 95%CI [1.673, 57.892], p=.011, see Table 5) and aged 19-29 years (OR=16.256, 95%CI [1.669, 158.369], p=.016, see Table 5) were statistically significantly more likely to have active TB by 9.840 and .16.256 times (respectively).

Table 5

Binary Logistic Regression for the Relationship Between Dependent Variable Active Tuberculosis and Independent Predictors

						EXP(B)		
Variable	B	*SE*	Wald	*df*	Sig.	Exp(B)	Lower	Upper
Homelessness	.554	.757	.535	1	.464	.575	.130	2.535
Reservation	-.022	.450	.002	1	.961	.978	.405	2.364
Substance use	-.217	.408	.284	1	.594	.805	.362	1.789
Not seeking employment	-.062	.637	.009	1	.923	.940	.270	3.277
Age (years)			12.624	6	.049			
Age 1 (1–18)	2.286	.904	6.395	1	.011	9.840	1.673	57.892
Age 2 (19–29)	2.788	1.161	5.764	1	.016	16.256	1.669	158.369
Age 3 (30–39)	1.565	.964	2.637	1	.104	4.782	.723	31.613
Age 4 (40–49)	.304	.637	.227	1	.634	1.355	.389	4.718
Age 5 (50–59)	1.066	.623	2.928	1	.087	2.903	.856	9.839
Age 6 (60–75)	.632	.587	1.159	1	.282	1.881	.596	5.942
Gender	.025	.385	.004	1	.949	1.025	.482	2.178
Constant	.326	.849	.144	1	.704	1.380		

These results showed that there was some effect by the independent variables on active TB, but they were not statistically significant, ages 1-18 years (p=.006, see Table 6), and aged 19-29 years (p=.001, see Table 6) were statistically significantly making the finding multicollinearity increasing chance of Type II error, I accepted the null hypothesis. The study's findings showed there was no significant association between active TB infections, and the predictor variables: employment, substance abuse,

homelessness, and living on reservation land among the Native American population in the Northern Plains in the United States.

Research Question 2 Results

The binary logistic regression was used to analyze the relationship, between the dependent variable latent TB diagnosis, and independent variables: not seeking employment (p= .908, see Table 6); substance use (p=.337, see Table 6); reservation (p=.952, see Table 6); homelessness (p= .386, see Table 6) that showed the relationships were not statistically significant.

Table 6

Binary Logistic Regression for the Relationship Between Dependent Variable Latent Tuberculosis Infection (LTBI) and Independent Predictors

						EXP(B)		
Variable	B	*SE*	Wald	*df*	Sig.	Exp(B)	Lower	Upper
Homelessness	-.660	.761	.751	1	.386	1.934	.435	8.594
Reservation	-.027	.452	.004	1	.952	.973	.401	2.361
Substance use	.392	.409	.922	1	.337	1.481	.664	3.299
Not seeking employment	-.074	.646	.013	1	.908	.928	.261	3.295
Age (years)	-	.911	15.123	6	.019			
Age 1 (1–18)	2.491	1.167	7.481	1	.006	.083	.014	.494
Age 2 (19–29)	-	.974	6.502	1	.001	.051	.005	.502
Age 3 (30–39)	2.977	.654	3.297	1	.069	.171	.025	1.151
Age 4 (40–49)	-	.624	.056	1	.812	.856	.238	3.085
Age 5 (50–59)	1.769	.598	2.472	1	.116	.375	.110	1.274
Age 6 (60–75)	-.155	.385	1.490	1	.222	.482	.149	1.556
Gender	-.981							
	-.730		.017	1	.896	1.052	.495	2.236
	.050							
Constant	-.326	.857	.145	1	.704	.722		

Age a confounder, was found to have a statistically significant (p=.019, see Table 6) impact on the risks of latent TB. Within these results that only those aged 1-18 years (OR=.083, 95%CI [.014, .494], p=.006, see Table 6), and aged 19-29 years (OR=.051, 95%CI [.005, .502], p=.001, see Table 6) were statistically significantly less likely to have latent TB.

So, I concluded that the independent variables had no significant effect on the odds of developing latent TB in this population. Therefore, the I accepted the null

hypothesis as the study identified no significant relationship between Latent TB Infections, and the socioeconomic, homelessness, substance use, and reservation living conditions in the Native American population in the Northern Plains of the United States.

Summary

The binary logistic regression results on RQ1 regarding active TB infection, and independent variables: homelessness, not seeking employment, substance abuse, and rural/urban were not statistically significant. So, I failed to reject the null hypothesis. These findings mean there is no statistically significant association between a diagnosis of active TB, and where they live, whether rural or urban, their occupation, homelessness, or substance use.

Regarding the binary logistic regression analysis conducted on latent TB infections, and independent variables: homelessness, not seeking employment, substance abuse, and reservation, found that there was no statistical significance. This finding meant accepting the null hypothesis that there is no relationship between the dependent variable, and the predictors identified, but age was statistically significant, age was significant for both active TB and Latent TB increase the odd of a Type II error when accepting the null hypothesis.

Chapter 5: Discussion, Conclusions, and Recommendations

This chapter includes a discussion of the findings, limitations, and implications. The purpose of this quantitative study was to examine the association between active and latent TB status, socioeconomic status, homelessness, multigenerational households, substance abuse, and place of residence of Native Americans living in urban areas or on reservations in the Northern Plains. Although studies had been conducted regarding TB in the Native American population, there was a paucity of studies examining the effects of social and environmental conditions on the transmission and development of TB. Current findings showed a failure to reject the null hypotheses in RQ1 and RQ2. There was no relationship between a diagnosis of active or latent TB infection and the predictor variables.

Interpretation of Findings

The results of the first RQ did not show a statistically significant result, and the I accepted the null hypothesis; this also occurred with the second RQ. I found that age which was not a variable in RQ but was statistically significant for both RQ questions. This made the results multicollinearity increasing chance of Type II error. The reviewed literature in Chapter 2 suggested predictor variables such as homelessness, substance use, poverty, and multigenerational housing may increase the chances of contracting active TB or progressing from LTBI to active disease. Literature from previous studies showed that homelessness, poverty, and crowded households were the most significant variables in the transmission and progression from LTBI to active disease. Godwin et al. (2017) identified that alcohol or illicit drug use, homelessness, and those with mental illness had

a higher rate of TB transmission. Lee et al. (2021) found that "people of color, notably Blacks and Native Americans, are shown to be overrepresented in the homeless populations of each community, in part because of the barriers they face to housing, and economic mobility." (p. 3). Although there were data showing that Native Americans have high rates of TB, low income, lack of housing, and violence, there are few studies on how these social issues affect the TB cases in that population. There were issues with obtaining homelessness data depending on how the question was posed, or interpreted. Hannah et al. (2017) identified that recent homelessness might not be reported, and a history of homelessness may not show how long individuals were homeless; this could have skewed the responses from the subjects.

In the current study, another variable addressed was poverty (i.e., income and employment). The level of those not seeking employment was 86.9%; however, as noted in the results ($p = .927$, $p = .908$), this did not affect the diagnosis of TB. The data did not indicate any other sources of income and only provided employment information. The literature showed that poverty is one of the leading conditions that leads to social and environmental conditions that increase the risk of contracting TB. Living in poverty is considered high risk for developing TB (Bread for the World, 2018). Bloss et al. (2011) identified that AI/ANs were more likely than other groups of people to suffer from homelessness, use alcohol, and live-in communities, or counties that have a more significant proportion of those living in poverty, and without health care insurance.

In a review of recent literature, I found that substance use was a significant issue, and risk for contracting TB (TB alert, n.d), which was not confirmed in the current study

because the association, or relationship between substance abuse, and active TB, and LTBI was not statistically significant (p = .594, p = .337, respectively). The results also showed that nearly one third of the respondents reported substance use, leaving two thirds who reported no substance use. The literature indicated that Native Americans have a high rate of substance use, and substance use is also a considerable risk for TB transmission, and progress to active disease. Volkman et al. (2016) showed that progression from LTBI to active disease is accelerated by homelessness, and alcohol use.

The data used for the variable reservation were zip codes. I used them to determine whether the community where individuals lived was on, or off the reservation. The findings showed that 76% of those with TB lived on lands identified as Native American reservations. Lack of housing increases living with multiple families in the same household, and cohabitation with many people puts them at risk of contracting, transmitting, and progressing to TB disease, as outlined by de Castro et al. (2018) who found that the indigenous populations in the Amazon with high rates of TB were affected by poor housing, poor health care, food inequities, and poverty.

Limitations of the Study

This study was conducted using data from a reliable source, and rigorous statistical analysis to test the hypothesis for this study. Very few cases were investigated directly by the state health department, but they were reported to their staff by public health programs, hospitals, and county health departments, all using their system of collecting and reporting TB data. Because I was able to obtain data from only one source, this meant that all the predictor variables reported could have been affected by various

reporting issues. There was enough information to conduct the study, but not to definitively confirm the strength of the effect of the independent variables on each case of active, or latent TB.

In the respondents' perceptions regarding the data, 89.6% stated they were not seeking employment simultaneously, and 90% denied being homeless. The high percentage of unemployment but low percentage of homelessness could mean that many respondents were living in multigenerational households, and did not consider themselves homeless. These findings may be why homelessness in the study was not associated with active TB and LTBI (p = .464, p = .386, respectively). Secondary data collected from the South Dakota Department of Health contained age, gender, active pulmonary disease, latent disease other than pulmonary, cavitary lesions, zip codes, homelessness, occupation, and substance use in each case. Secondary data on genotyping and identified clusters were based on spligotypes and mycobacterial interspersed repetitive unit (MIRU) mutations in only 50% of the 145 cases, so I did not use these data in the analysis.

I obtained data on pulmonary TB active and TB found in other parts of the body that were identified as latent because I could not use genotyping. The data obtained represented the sample needed for the TB cases in the Northern Plains among the Native Americans, and the study sample population was 100% of all cases identified in South Dakota. This state had the most TB cases and the largest Native American population in the Northern Plains.

The limitations related to reliability were due to data in this study that were self-reported. The values provided by self-reporting can be prone to errors, misinterpretation

of questions, shame, guilt, and data entry mistakes because several people collected the data over the past 20 years. These issues increased the limitation regarding the independent variable data used in this study that were self-reported, such as occupation, homelessness, address zip code, and substance use.

I could not determine whether those who stated they were not homeless were living in a multigenerational home with the data provided. I found the same issue with substance use, the data collection process did not identify whether this was current or prior substance use, which may have influenced the results for this variable. The data also showed that most of the cases identified were not looking for employment. However, because no data were collected on other types of resources, I could not determine whether they had regular income.

Another limitation was having only one source for the data collected. Even though most of the TB cases in the Northern Plains were in South Dakota, and reported to the health department, the data collection did not allow for cross-checking of the self-reported data. The results were not statistically significant, and not generalizable. Several attempts to obtain data from the IHS after IHS IRB approval for data collection were unsuccessful. North Dakota had four cases, but could not conclude that they were Native American, while Iowa and Nebraska refused to provide any data, limiting my ability to cross-check the data. Another variable that needs more investigation is substance use, because of the time between TB exposure and disease development, it would be helpful to ask about historical use, and other environmental conditions accompanying drug, or alcohol use. Multiple health department staff collected the data for this variable, but the

question was inconsistent between the forms used. Different survey tools were used to collect the same demographic data, so the person may not have identified prior drug use. Data only identified substance use or no substance use but did not specify current or historical use.

Recommendations

Although the current study's findings did not indicate a statistically significant association between active TB infections and LTBI, studies are needed to reveal complex causal effects that impact the TB diagnosis in this population. To answer this question, there needs to be wide-ranging data collection to increase the reliability and validity of the study. Identifying multigenerational households was not possible with the data obtained. There needs to be further research conducted to assess the impact of multigenerational households on the outcome variables.

Implications

I found after a review of the findings there is a need for more investigation into why this population is still affected by TB, substance use, homelessness /multigenerational living, and poverty more than the general population. The manifestation of the social, and environmental risks that increase the odds of a Native American contracting TB, and progressing to a disease state needs further study to determine the causes.

This study's results bring attention to the Native Americans' social/environmental plight leading to improved public health programs and policies. The idea that a population had such high rates of poverty, unemployment, homelessness, substance use,

mental illness, and poor health is the antithesis of the current public health goals in the United States of equality and equity. An important public health goal is to improve the health conditions in this population, and to decrease the cases and deaths from tuberculosis. This study highlights that there must be a cohesive system/process when collecting infectious disease data and measuring the effects of TB policies and programming among this population.

These findings have positive implications for social change. The results of this study could form changes that improve the data collection, staff training, and reporting of TB cases among the Native American populations leading to improved TB intelligence systems that could inform programming to decrease TB cases found in these populations. This would mean changes to processes, and improved collaboration, and record-keeping between local, state, and federal agencies that work in this community. Successful implementation of these strategies would allow public health, and social programs to work together to address all aspects of TB patients' environment and needs.

Conclusions

Overall findings supported an inability to reject the study's null hypotheses. Although results were not statistically significant between active, and latent TB infection, and the independent variables poverty, homelessness, substance use, and residence, only one variable, age was statistically significant. Nevertheless, age was not one of the identified independent variables in the hypotheses, but was included in the analyses to account for potential confounding effects. Thus, further investigations including other potential confounders are needed to ascertain their influence on the outcome of interest.

The risk of tuberculosis, and other infectious diseases, substance use, homelessness, mental illness, and poverty has been high in the Native American population based on the data collected by the CDC each year. This group continues to have higher rates than most of the other ethnic groups (Center for disease control and prevention, 2018; Cormier et al., 2019; O'Leary et al., 2019). Nevertheless, the ability to collect, analyze, and maintain data so that a multidisciplinary system can coordinate services is nonexistent. The lack of a cohesive process means that population health needs assessments remain inadequate, and when public policy, regulations, and funding decisions are made they are not data-driven further increasing the levels of unmet population health needs as they relate to TB. Social change will happen if we apply positive ideals into every step of this process, we must have an unwavering mindset of kindness, unlimited time and unmitigated dignity when dealing with Tuberculosis and the socioeconomic conditions that burdens the Native American population.

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