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Jasmine Carter Date

Favorable Conditions:
How Climate Change Impacts Infectious Disease Dynamics in Circumpolar Regions

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An abstract of
A thesis submitted to the Faculty of the
Rollins School of Public Health of Emory University
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2021

Abstract

Favorable Conditions:
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in Circumpolar Regions

By Jasmine Carter

OBJECTIVE: To locate previously published research on the actual and potential role of climate change in increasing exposure to emerging/re-emerging diseases among human populations within arctic regions, especially neglected tropical diseases and vector-borne diseases.

BACKGROUND: Climate change poses a threat to human health in circumpolar regions. Shifts in temperature and precipitation patterns could create conditions that contribute to pathogen, vector, and reservoir persistence in new areas, increasing the potential for human exposure to emerging and re-emerging infectious diseases, especially zoonotic, parasitic, and vector-borne diseases. The detrimental effects of climate change on these diseases could impact indigenous populations disproportionately, given the relationship of these communities with the land.

METHODS: A systematic literature review was performed of peer-reviewed literature published from 2000-2021 in PubMed and Web of Science. Search terms such as “zoonotic diseases OR zoonoses,” “vector borne diseases,” “tick borne OR tick OR mosquito borne OR mosquito,” “parasitic diseases OR parasite,” “neglected tropical diseases,” and “infectious diseases OR communicable diseases,” were used and combined with “AND” connectors to terms related to circumpolar location and climate/environmental factors. The articles were uploaded into Covidence, and findings from the final selected articles were entered into a matrix and organized by disease category.

RESULTS: Of 161 articles identified and uploaded for selection, 48 studies were determined to fit all of the selection criteria for inclusion. Of those, 43 studies focused on infectious diseases, and five were studies of the impact of climate/environmental factors and infectious diseases on indigenous populations. The most common disease groups researched were vector-borne diseases and zoonotic diseases. Tick-borne encephalitis (TBE) and Lyme Disease were considered the emerging diseases of most concern, while anthrax was described as a main re-emerging disease for circumpolar populations. There were fewer studies about Neglected Tropical Diseases, which were discussed as potentially re-emerging in the arctic regions. Some studies also examined antimicrobial-resistant pathogens and fungal diseases as possible emerging diseases. Only limited research was found addressing the risk for enhanced climate change driven transmission of diseases among indigenous communities.

CONCLUSION: The findings of this systematic literature review indicated that vector-borne diseases, primarily TBE and Lyme Disease, were prominent emerging diseases for circumpolar regions. More research is needed to determine the potential for emergence/re-emergence of other specific diseases in these regions to prepare communities to control such disease threats. In addition, the presence of indigenous voices in global conversations regarding the effects of a changing arctic environment on health and well-being needs to be increased.

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Hook 'Em Horns and Eat 'Em Up Cats!

Table of Contents

CHAPTER 1: INTRODUCTION

In circumpolar regions, the effects of anthropogenic climate change are “unprecedented,” and the situation will become even more critical in the future in the absence of global mitigation efforts (IPCC, 2019). Between 1971-2017, the Arctic annual surface air temperatures increased 2.4 times faster than the average for the entire northern hemisphere (AMAP, 2019). The annual Arctic surface air temperatures from 2014-2018 were higher than any observed year since 1900, with the second warmest year being from October 2017-September 2018 (IPCC, 2019). Climate change poses a clear and present threat to human health in circumpolar regions. We can expect drastic shifts in temperature and precipitation to cause extreme changes to ecosystems, impacting biodiversity, abundance, and geographic distribution of animal and insect populations (AMAP, 2019). Conditions could become more favorable to support pathogen, vector, and reservoir persistence in new areas, increasing the potential for human exposure to emerging and re-emerging infectious diseases, especially zoonotic, parasitic, and vector-borne diseases (Parkinson et al., 2014; Pauchard et al., 2015).

An estimated 4 million people currently live in the circumpolar regions, and about 10% of residents are indigenous (Arctic Council, 2021). The detrimental effects of climate change on these diseases would likely impact indigenous populations disproportionately, as these communities tend to have a different relationship with the land than non-indigenous Arctic residents (Davydov & Mikhailova, 2011). By living in remote areas, indigenous populations have increased potential susceptibility to emerging and re-emerging infections that have expanded to northern territories, such as vector-borne diseases and neglected tropical diseases. There may be absent or limited immunity to these pathogens due to lack of previous exposure

(Omazic et al., 2019b). In addition, these communities often suffer from limited resources, lacking surveillance, and accessibility barriers to healthcare services, which could impact their capacity to effectively control and stamp out infectious disease outbreaks (Nelson, 2013).

1.1 Problem Statement

Despite the circumpolar north containing several high-income countries, there exists a lack of adequate public health research and resources in the more remote areas. Previous global health research efforts often failed to recognize and include a separate analysis of health disparities in arctic territories, “dilut[ing] and hid[ing] important regional challenges within countries” (Chatwood et al., 2012). In response to the negligence, national and international working groups were established to assess how climate change could impact circumpolar health. However, the assessment of the full impact, especially on indigenous populations, is still limited. Many areas lack the baseline data that could identify climate-sensitive diseases of importance in circumpolar regions to inform surveillance efforts and help epidemiological models forecast patterns of these diseases among humans, animals, and vectors. There is also an unequal distribution of research among the arctic countries themselves, with more than 75% of publicly available reports from North America (IPCC, 2019). In addition, more up-to-date regional climate and environmental data are needed to detect possible relationships between local external factors and these diseases (Parkinson et al., 2014). Current evidence on external drivers of disease is conflicting, as non-climate/environmental factors could influence infectious disease transmission dynamics, such as changes in land use and human behavior (Omazic et al., 2019b).

1.2 Purpose Statement

This systematic literature review will investigate peer-reviewed literature published from the past two decades to examine how climate change potentially influences exposure to emerging/re-emerging zoonotic, vector-borne, and parasitic diseases among human populations within circumpolar regions and attempt to answer the following research questions:

- *What infectious diseases are emerging/re-emerging in the circumpolar regions?*
- *How has the burden of these diseases changed over time (focusing over the past 20 years)?*
- *What climate/environmental factors may be impacting the dynamics of these diseases?*
- *How are indigenous communities affected by these climate-sensitive diseases?*

1.3 Significance Statement

As temperatures continue to increase, we can expect to see conditions become more suitable for infectious diseases to be introduced to higher latitudes through importation and establishment and re-released back into the environment, such as through thawing permafrost (Gourdazi, 2016; Omazic et al., 2019b). Limited research efforts of these projected disease patterns in arctic regions combined with inadequate surveillance and healthcare infrastructure create difficulties in adequately assessing the presence and actual burden of diseases among human populations, especially indigenous communities (Parkinson et al., 2014). The traditional and cultural connection that indigenous residents have with the environment makes them even more at risk for exposure to these climate-sensitive diseases. Measures for studying the Arctic's unique ecology and disease transmission patterns need to heighten to increase community awareness and preparedness for infectious disease threats encroaching upon these northern areas (Hotez, 2010). This systematic literature review will contribute to this need by providing an overview of the current body of evidence that describes the suspected influence of climate change on the exposure of infectious diseases in the eight circumpolar countries.

1.4 Definition of Terms

This study will use the terms “arctic” and “circumpolar” interchangeably to represent the geographic region of focus for this review. These terms represent the areas covered by both the previously defined “Arctic” and “Subarctic” territories in the world’s northernmost countries, also known as “The Arctic 8”: Canada, The United States (Alaska), Finland, Denmark (Greenland, Faroe Islands), Iceland, Russia, Sweden, and Norway (Arctic Council, 2021; UArctic, 2021).

CHAPTER 2: BACKGROUND

2.1 Climate Change and Infectious Diseases

Anthropogenic climate change is expected to continue to cause global disruptions to the environment and human society, with heavier effects in the Arctic. Temperatures could increase faster and over two times higher in the northern regions than those in temperate or tropical climates (IPCC, 2018). The effect of climate change on infectious diseases in the arctic areas has sparked both curiosity and fear in the general public and academic community. Dramatic variations in temperature and precipitation have led to increased speculation about how climate change could potentially affect “what lies beneath” the ice and risk the release of these pathogens into the environment, exposing surrounding residents to such agents as *Bacillus anthracis* (Gourdazi, 2016). Climate change could affect the abundance and distribution of pathogens, vectors, and their non-human hosts and reservoirs. These factors, such as increased temperature, can directly impact pathogens' persistence and life cycle by challenging them to develop under shifting conditions (Wu et al., 2016). Changes in temperature and precipitation could also influence the environment and habitats of animal or insect hosts and reservoirs. More favorable conditions could promote importation and establishment of these invaders at the higher latitudes and altitudes of northern territories (Pauchard et al., 2015; Slenning, 2010). Such variations could “narrow available habitats,” as animal hosts may crowd in smaller areas searching for food and increase the risk of disease transmission between other animals and humans (Slenning, 2010).

According to Parkinson et al., the climate-sensitive etiologic agents of particular concern to the arctic regions include “*Brucella spp., Toxoplasma gondii, Trichinella spp., Clostridium* *botulinum, Francisella tularensis, Borrelia burgdorferi, Bacillus anthracis*, *Echinococcus spp.*, *Leptospira spp*., *Giardia spp., Cryptosporidia* spp., *Coxiella burnetti*, rabies virus, West Nile virus, Hantaviruses, and tick-borne encephalitis viruses" (Parkinson et al., 2014).

2.1.1 Special Interest: Vector-Borne Diseases

Over the past three decades, most emerging diseases were of zoonotic or vector-borne origin (Waits et al., 2018). Vector-borne diseases (VBDs) are commonly transmitted by arthropod vectors, such as ticks and mosquitoes. Their body systems can be directly and indirectly affected by the conditions of the surrounding environment (Caminade et al., 2019). The increased movement of people and goods between countries contributes to importing VBDs in countries not previously reported, such as those in Europe and circumpolar regions. Depending on the capabilities of the vector, changing climatic and environmental conditions could support the survival and potential establishment of the vectors once there (Semenza & Suk, 2018).

In tropical regions, high temperature and precipitation settings help arboviruses like dengue, ZIKA, and chikungunya dominate the VBD realm. However, tick-borne bacterial and viral diseases tend to be more common at higher latitudes, such as those in temperate regions (Caminade et al., 2019). Colder temperatures in northern territories were previously defined as latitudinal and altitudinal constraints of certain tick species, limiting their transmission in circumpolar regions. However, climate change could create more favorable conditions for both ticks and their animal hosts that enable expansion into arctic territories. Warmer winters and earlier springs can affect vegetation growth patterns and extend the period of seasonal tick activity, influencing both animal host and human behaviors, increasing the risk of transmission of diseases like Lyme Disease and Tick-borne encephalitis (Semenza & Suk, 2018).

2.1.2 Special Interest: Neglected Tropical Diseases

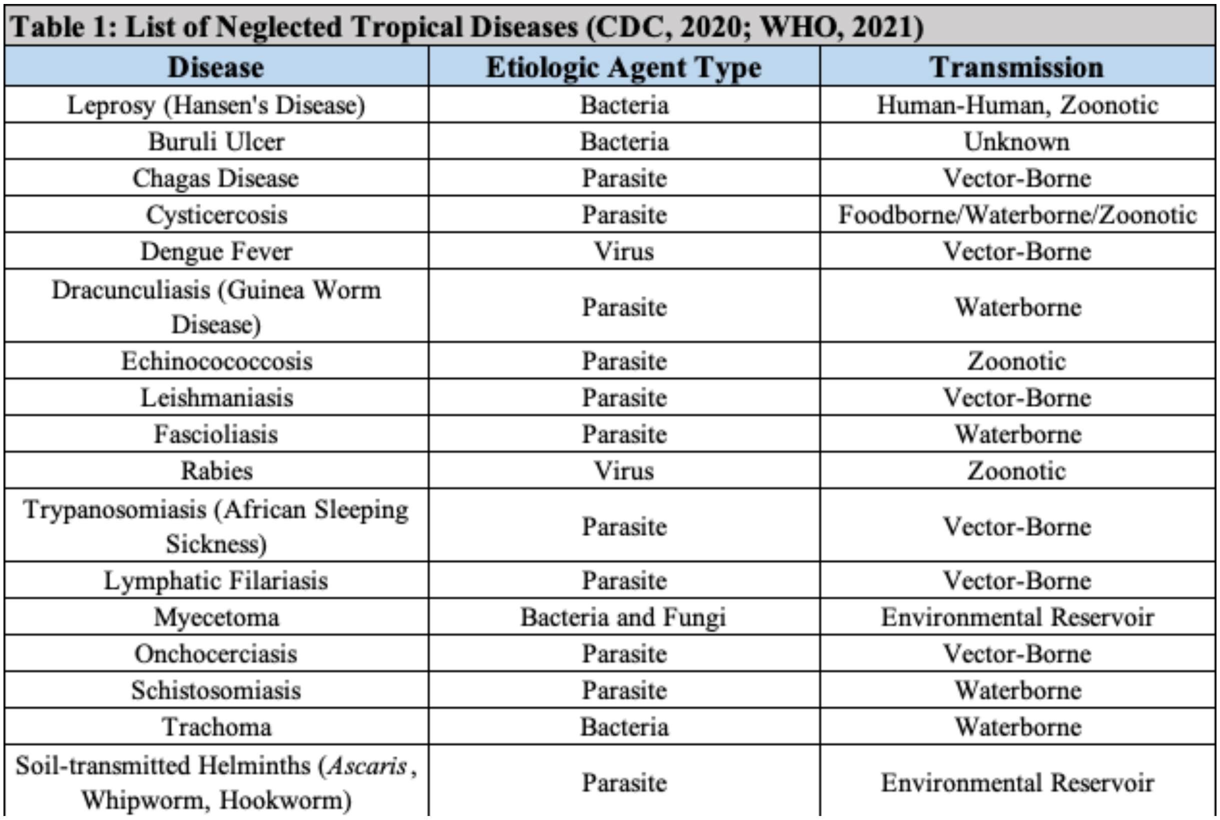
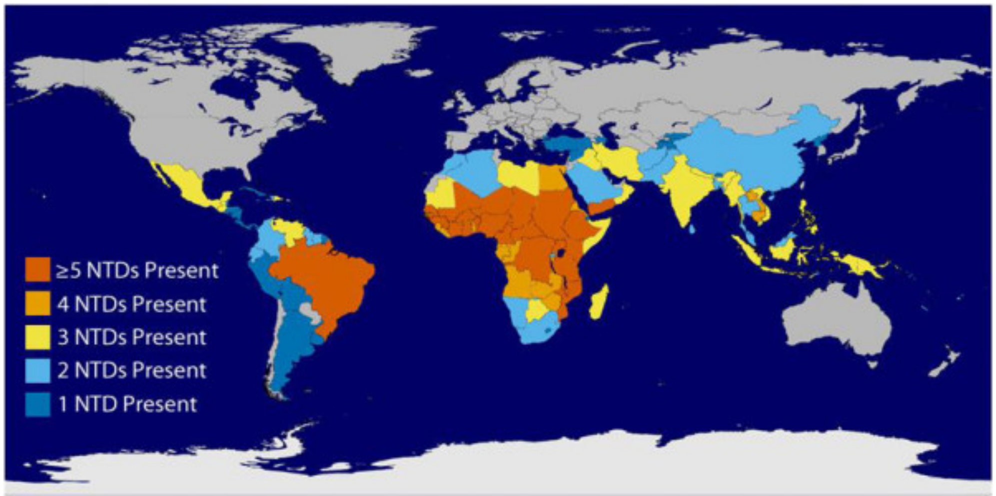


Table 1: List of Neglected Tropical Diseases (CDC, 2020; WHO, 2021)

Disease	**Etiologic Agent Type**	**Transmission**
Leprosy (Hansen's Disease)	Bacteria	Human-Human, Zoonotic
Buruli Ulcer	Bacteria	Unknown
Chagas Disease	Parasite	Vector-Borne
Cysticercosis	Parasite	Foodborne/Waterborne/Zoonotic
Dengue Fever	Virus	Vector-Borne
Dracunculiasis (Guinea Worm Disease)	Parasite	Waterborne
Echinocococcosis	Parasite	Zoonotic
Leishmaniasis	Parasite	Vector-Borne
Fascioliasis	Parasite	Waterborne
Rabies	Virus	Zoonotic
Trypanosomiasis (African Sleeping Sickness)	Parasite	Vector-Borne
Lymphatic Filariasis	Parasite	Vector-Borne
Myecetoma	Bacteria and Fungi	Environmental Reservoir
Onchocerciasis	Parasite	Vector-Borne
Schistosomiasis	Parasite	Waterborne
Trachoma	Bacteria	Waterborne
Soil-transmitted Helminths (*Ascaris* , Whipworm, Hookworm)	Parasite	Environmental Reservoir

Neglected tropical diseases (NTDs) are bacterial, viral, and parasitic diseases of zoonotic, vector-borne, waterborne, foodborne, and environmental transmission that particularly affect communities experiencing poverty (Table 1). These conditions can lead to debilitating physical disabilities and impairments that impact the livelihoods of affected individuals and ultimately "trap" communities in the cycle of poverty (WHO, 2021). As shown in Figure 1, NTDs are most common in Sub-Saharan Africa, Asia, and the Americas, and attributable mortality from NTDs has reportedly increased to approximately 152,000. The burden is estimated to be much higher due to underreporting (Bhutta et al., 2014).

Figure 1: Map Showing Global Distribution of Most Common NTDs (Bhutta et al., 2014)



Despite their given name, NTDs are not exclusive to tropical and subtropical regions. They can be found in any location among populations experiencing extreme poverty, such as in the Arctic (WHO, 2021). As described by Hotez,

> *"The single most important determinant of neglected infections among human populations is the observation that these conditions occur among the poorest people living in the Arctic."*

Indigenous people make up an estimated 5% of the global population and 15% of the extremely poor (World Bank, 2021). Most residents in circumpolar regions classified as possessing low socioeconomic status are indigenous persons, as employment is usually related to lower-wage positions in hunting and fishing, government, or the service industry (Hotez, 2010). Indigenous individuals in the circumpolar regions also suffer from higher rates of infectious diseases than non-indigenous persons, especially zoonotic NTDs (Hotez, 2010; Pauchard et al., 2015). Limited community resources combined with economic and geographical barriers to receiving adequate healthcare services contribute to the disproportionate risk of severe health outcomes from these infections (Nelson, 2013).

Previous research of parasitic NTDs has explained that though tropical conditions provide more diversity among plants and animals that contributed to pathogen niches, there may no longer be a fundamental difference between niche diversity among tropical sites compared to arctic sites (Kerfahi et al. 2016). The limited ranges that restricted pathogens to these tropical areas may no longer apply, as there is increasing evidence of more species able to tolerate other climatic conditions (Kerfahi et al., 2016). The most common NTDs described for arctic regions are rabies, trichinellosis, and echinococcosis. For circumpolar communities, the risk of transmission of these NTDs connects with wildlife exposure due to the environmental involvement associated with rural and indigenous lifestyles (Hotez, 2010; Nelson 2013). Residents could come in contact with infected animals directly or accidentally ingest food materials contaminated with the parasites due to proximity to infected animal feces or failure of traditional food preparation methods to effectively eliminate the parasites (Himsworth et al., 2010; Nelson, 2013).

2.2 Indigenous Populations and Climate Change

The number of indigenous individuals worldwide ranges from 370-500 million people (World Bank, 2021). Indigenous communities are often used to gauge the more local and regional effects of climate change, as they are “uniquely sensitive” to the impacts of climate change due to the rich cultural history with the land and natural resources (Belfer et al., 2017). Of the approximate 4 million people that live in the arctic, 10% are indigenous (IPCC, 2019). Variations in climate can impact access to safe drinking water and food obtained through hunting and gathering practices and the health status of wild and domestic animals interacting with residents. In addition, increased temperatures that promote the thawing of permafrost have severe implications for the fortification of rural infrastructure, as many homes and buildings constructed relied on permafrost as the foundation (IPCC, 2019). Some communities have indicated feeling that climate change and other environmental stressors were forcing them to essentially adapt away from the older, more traditional ways of performing tasks. The recent shifts in climate conditions reduced the relevance of traditional methods because they were now operating under a “different weather regime” than when the modes were first applied (Furberg et al., 2018). Despite these threats to their livelihoods, many indigenous residents have not expressed signs of planned “outmigration” to areas that may be less impacted by climate change (Davydov et al., 2011; IPCC, 2019).

2.3 Current Circumpolar Disease Research and Surveillance Efforts

There has been a noted lack of representation of the circumpolar perspective in global health, which has pushed public health leaders in these regions to facilitate their own surveillance and research working groups (Chatwood, 2012). Groups reportedly investigating the intersection of climate and environmental factors with public health issues include the International Union for Circumpolar Health, the Arctic Council, and the Circumpolar Health Research Network (Parkinson et al., 2014). The Arctic Investigations Program (AIP) through the Centers for

Disease Control and Prevention supports infectious disease research activities in Alaska. It is part of the International Circumpolar Surveillance (ICS) system in conjunction with the Arctic Council and the International Union for Circumpolar Health (AIP, 2011).

The ICS was created to establish a network of public health laboratories, institutions, and hospitals to help monitor infectious diseases in all arctic countries except for Russia. Invasive bacterial diseases such as *Streptococcus pneumoniae* and *Neisseria meningitidis* have been the primary focus of the group, but other diseases could be included for surveillance activities depending on the threat level (Bruce et al., 2016). A subgroup was born from this project known as the "ICS Climate Change and Infectious Diseases" working group, formed to facilitate data-sharing between circumpolar researchers about climate-sensitive infectious diseases in the region. The main objective of this working group is to examine how climate and environmental factors could impact the emergence or re-emergence of infectious diseases, particularly in the context of "One Health" (AIP, 2011; Parkinson et al., 2014). However, regional challenges still exist in reporting infectious diseases plaguing the Arctic, as more rural settings could experience resource disparities that hinder preparedness and response efforts. The barriers to receiving care, absence of adequate diagnostic infrastructure, limited staff capacity, and general logistical complications managing remote sample collection processes impede any potential research and surveillance progress (Parkinson et al., 2014).

CHAPTER 3: METHODS

The primary objective of this systematic literature review was to locate previously published research on the role of climate change in increasing exposure to emerging/re-emerging diseases among human populations within arctic regions, especially neglected tropical diseases and vector-borne diseases. Using a set of parameters outlined below, a systematic literature review was performed of the existing literature in PubMed and Web of Science to address the following research questions:

- *What infectious diseases are emerging/re-emerging in the arctic/circumpolar regions?*
- *How has the burden of these diseases changed over time (focusing over the past 20 years)?*
- *What climate/environmental factors may be impacting the dynamics of these diseases?*
- *How are indigenous communities affected by these climate-sensitive diseases?*

3.1 Initial Study Selection Criteria

Articles were screened for inclusion based on the relevance to the circumpolar regions, year published (Jan 2000 – Jan 2021), disease areas of interest and the discussion of the presence of the vector or reservoir that facilitates transmission, mention of climate or latitude/altitude, access to the paper itself (Open Access or available through Emory University Library databases), and languages offered (excluded if English version was unavailable). Excerpts from books and other literature reviews were excluded, but we examined the reference lists of the other reviews, and any relevant studies were selected for screening.

3.2 Search Terms

The search was conducted using general MeSH in both smaller segments of each topic in separate searches and larger segments containing all topics of interest in one search. Search terms were verified by looking at terms listed in existing literature reviews.

The following terms used for the climate-sensitive disease areas of interest: “zoonotic diseases OR zoonoses,” “vector borne diseases,” “tick borne OR tick OR mosquito borne OR mosquito,” “parasitic diseases OR parasite,” “neglected tropical diseases,” “infectious diseases OR communicable diseases,” “emerging diseases OR emerging pathogens OR emergence OR re-emerging OR re-emergence OR novel diseases OR novel pathogens,” “antibiotic resistance OR drug resistance OR antimicrobial resistance OR multidrug resistance,” and “fungal pathogen OR fungal diseases OR pathogenic fungi OR fungal infection.” These terms were combined with “AND” connectors to the following terms related to circumpolar location and climate/environmental factors: “arctic OR circumpolar OR polar,” “sea ice OR permafrost OR polar ice,” and “climate OR latitude OR altitude.”

To obtain results about studies about indigenous/rural populations, the previously outlined terms were combined with “AND” connectors to “indigenous OR rural OR native.”

Additional targeted searches were performed for specific parasitic diseases previously described as being relevant to the circumpolar region. The search terms used were “echinococcus OR echinococcosis,” “trichinella OR trichinellosis OR trichinosis,” “helminth AND human.” These terms were combined with “AND” connectors to the previously mentioned terms concerning the circumpolar location and climate/environmental factors.

3.3 Data Synthesis

Articles were uploaded and screened for consideration by abstract and full-text content using the Covidence web application. Studies were excluded for the following reasons: the actual location of the study was not within the arctic/circumpolar region, the microbial agent could not be transmitted to and cause disease in humans (via the environment, animal, vector, or another person), the vector was not known to interact with humans, and the authors did not address the concern of the potential impact of climate factors (temperature, precipitation, etc.) or the significance of latitude/altitude on the disease. Diseases of bacterial or viral origin classified as strictly waterborne or foodborne transmission were not included in this review.

To confirm that the study location was conducted within an arctic region, the site was cross-checked with arctic state territory information listed on the Arctic Council website (Arctic Council, 2021) and Google/Google Maps.

To determine if the pathogen or vector was significant to human health, the given species name was cross-checked using the search functions in PubMed, the CDC, or the WHO websites for evidence of reported transmission and disease in humans.

Findings from the final selected articles were entered into a matrix and organized by disease category (zoonotic, vector-borne, parasitic, and other – fungal and antimicrobial-resistant) in Microsoft Excel (Table 2).

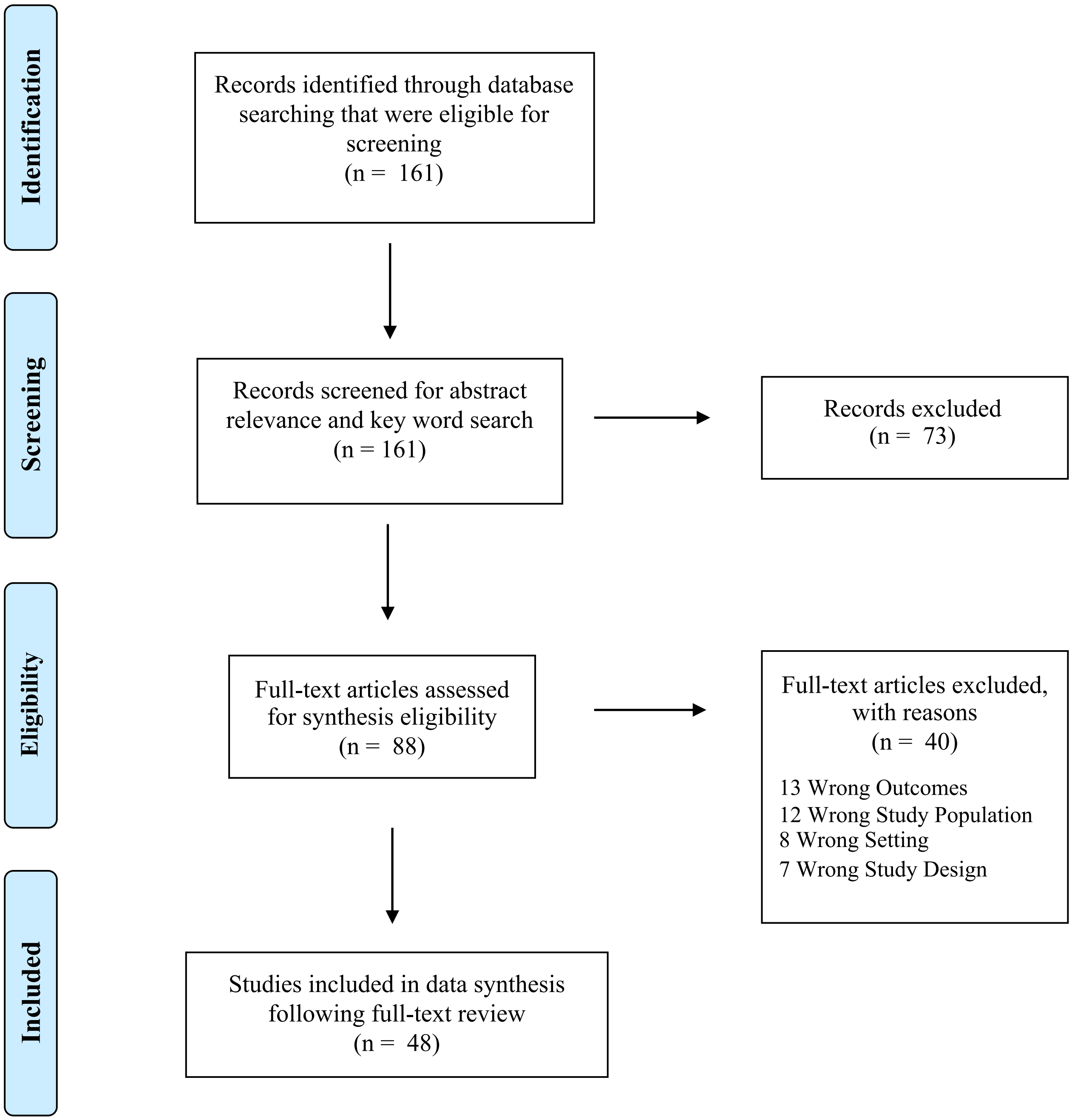
3.4 Ethical Approval

Approval from the Emory University Institutional Review Board was not needed because the research did not involve human subjects, as it summarizes the existing published literature.

CHAPTER 4: RESULTS

The searches of PubMed and Web of Science databases resulted in 161 articles uploaded for selection. Of these, 48 studies were determined to fit all of the selection criteria and were included in this systematic literature review (Figure 2). There were 43 studies that focused on infectious diseases or the presence of their corresponding vectors and reservoirs, and the remaining five studies assessed the impact of climate/environmental factors and infectious diseases on different indigenous communities.

Figure 2: PRISMA Flow Diagram of Study Selection (Page, 2021)



4.1 Regions of Study

All of the 8 countries in the arctic regions were represented in the selected studies, with most research conducted for the arctic territories of Canada. (10). There were several studies performed in more than one country (9) and different parts of Norway (7) and Russia (6). Another seven studies researched pertained to Alaska, United States, and four studies were about Sweden. There were two studies completed in Iceland and another two in Finland, with one study conducted in Greenland/Denmark.

4.2 Impact of Climate and Latitude on Diseases of Interest

The studies addressed the impact of changes in climate, latitude, and altitude on diseases of interest in different ways. Some studies used climate data to reach conclusions about the influence of different climate factors and pathogen/vector dynamics, but most presented hypotheses or speculations on the interaction based on other published work or the author's general thoughts and observations. The majority of studies (19) discussed or analyzed how increased temperatures as an effect of climate change could influence the incidence, prevalence, persistence, and range of the studied disease(s) in animal hosts, humans, and the environment. Of these, 14 studies mentioned increased temperatures in general as possibly affecting the diseases, and five specifically focused on the melting and thawing of sea ice and permafrost due to higher temperatures. Several studies (18) only mentioned climate change in general as a concern, with the implication connected to increased temperatures. There were eight studies that discussed more than one factor possibly influencing diseases, with four studies commenting on the combined effects of latitude/altitude and climate factors in general, three studies referencing variations in temperature and precipitation, and one study mentioning the potential impact of temperature and humidity. Only three studies specified the influence of latitude alone on diseases, and it was in the context of the distribution and range expansion of the corresponding vector. There were no studies that addressed altitude as a separate factor impacting disease or vector presence.

Table 2: Relevant Study Findings by Disease Category

Disease Category	Study	Human Disease(s) Studied	Location
Zoonotic (13)	Revich & Podolnaya, 2011	Anthrax	Russia
	Stella et al., 2020	Anthrax	Russia
	Timofeev et al., 2019	Anthrax	Russia
	Walsh et al., 2018	Anthrax	Canada, Russia, Iceland, Sweden, Finland, Norway, United States - Alaska
	Huettmann et al., 2017	Rabies	United States - Alaska
	Kim et al., 2014	Rabies	United States - Alaska
	Aenishaenslin et al., 2021	Rabies	Canada
	Groeschel et al., 2019	Bacterial Disease caused by: *Erysipelothrix rhusiopathiae*	Canada
	Forde et al., 2016	Bacterial Disease caused by: *Erysipelothrix rhusiopathiae*	Canada, United States - Alaska
	Pettersson et al., 2008	Nephropathia Epidemica (Puumala virus)	Sweden
	Haredasht et al., 2012	Nephropathia Epidemica (Puumala virus)	Finland
	Lee et al., 2020	Avian influenza	Norway
	Buhler et al., 2020	Cat Scratch Disease	Canada
Vector-Borne (17)	Tokarevich et al., 2011	Tick-borne Encephalitis	Russia
	Tokarevich et al., 2017	Tick-borne Encephalitis	Russia
	Tronin et al., 2019	Tick-borne Encephalitis	Russia
	Soleng et al., 2018	Tick-borne Encephalitis	Norway
	Deardorff et al., 2013	Tick-borne Encephalitis	Russia, United States - Alaska
	Jääskeläinen et al., 2011	Tick-borne Encephalitis	Finland
	Lindgren et al., 2000	Tick-borne Encephalitis, Lyme Disease	Sweden
	Alfredsson et al., 2017	Tick-borne Encephalitis, Lyme Disease	Iceland
	Hvidsten et al., 2015	Lyme Disease	Norway
	Ogden et al., 2006	Lyme Disease	Canada
	Ogden et al., 2015	Lyme Disease	Canada
	Hvidsten et al., 2020	Lyme Disease, Spotted Fever	Norway
	Jore et al., 2011	Lyme Disease, Babesiosis	Norway
	Hahn et al., 2020	Lyme Disease, Babesiosis	United States - Alaska
	Larsson et al., 2018	Neoehrlichiosis (*Candidatus N. mikurensis*)	Norway
	Ryden et al., 2009	Tularemia	Sweden
	Mullerova et al., 2018	Viral Diseases of the genera: *Alphavirus (family Togaviridae), Orthobunyavirus, Phlebovirus (Bunyaviridae), Flavivirus (Flaviviridae), Orbivirus (Reoviridae)*	Greenland, Norway
Parasitic (5)	Jensen et al., 2010	Toxoplasmosis	Norway
	Seymour et al., 2014	Trichinellosis	United States - Alaska
	Masuoka et al., 2009	Trichinellosis	Canada, United States - Alaska
	Andreassen et al., 2017	Toxocariasis, Coenurosis, Strongyloidiasis	Greenland
	Salb et al., 2008	Toxoplasmosis, Giardiasis, Echinococcosis, Toxocariasis, Taeniasis, Cystoisosporiasis, Sarcocystosis, Cutaneous larva migrans	Canada
Other Diseases (4)	Mogrovejo et al., 2020	Antimicrobial Resistance	Greenland, Norway
	Haan et al., 2021	Antimicrobial Resistance	United States - Alaska
	Diaz et al., 2017	Antimicrobial Resistance	Sweden
	Perini et al., 2019	Mycosis of the following: *Naganishia albida, Rhodotorula mucilaginosa, Aureobasidium melanogenum*	Greenland, Norway
Multiple Diseases Across Different Categories (4)	Atwood et al., 2017	Toxoplasmosis, Tularemia, Q Fever	United States - Alaska
	Andersen-Ranberg et al., 2018	Bacterial Diseases of the species: *Erysipelothrix, Bacteroides, Bacillus, Actinomyces, Fusobacterium, Pseudomonas, Rhodococcus, Yersinia*	Greenland, Norway
	Omazic et al., 2019	Anthrax, Borreliosis, Cryptosporidiosis, Leptospirosis, Nephropathia Epidemica (Puumala virus), Q-fever, Tick-borne encephalitis, Tularaemia	Sweden, Finland, Norway, Iceland, Greenland
	Hornok et al., 2020	Trypanosomiasis, Babesiosis, Anaplasmosis, Ehrlichiosis, Lyme Disease, Spotted Fever Rickettsiosis	Iceland

4.3 Diseases of Interest, By Transmission Category

4.3.1 Zoonotic Diseases

Of the 43 studies selected relating to infectious diseases, 13 pertained strictly to zoonotic diseases. These studies observed direct transmission from animals to humans or mentioned the prevalence of disease among a zoonotic host or reservoir. Table 2 contains a summary of the diseases referenced in the 43 studies by transmission category, based on the presence of the pathogenic agent or vector/reservoir in the locations researched.

ANTHRAX

The most common pathogen discussed among these studies was *Bacillus anthracis* (4). Of these four, three focused on the concern of the pathogen re-emerging in Russia's arctic territories. In their 2011 correlational study, Revich and Podolnaya used local weather station data from 1961-2010 to estimate the impact of temperature changes on permafrost thawing near the burial grounds of cattle that succumbed to anthrax. Because of this, the team hypothesized that communities close to these cattle burial grounds were at risk of exposure to anthrax. During their analysis, Revich and Podolnaya discovered a statistically significant annual temperature increase among the region that corresponded with districts that reported the highest numbers of anthrax outbreaks. They also found that the territory with the highest variation in temperature also contained a higher number of cattle burial grounds. The presence of viable spores in the thawed permafrost was not studied but mentioned as necessary research to assess the actual risk of exposure (Revich and Podolnaya, 2011). By creating their own compartmental epidemiological model, Stella et al. also investigated the potential influence of temperature on permafrost dynamics and how that could affect anthrax transmission. In the model, the team found that high permafrost thawing rates supported endemic anthrax transmission because of the role the deeper active layers and top surface layers play in long-term spore storage. Warmer temperatures due to climate change could thaw these permafrost layers and ultimately result in the re-circulation of and exposure to anthrax spores from animal carcasses (Stella et al., 2020).

Timofeev et al. explored the possible origins of the 2015-2016 anthrax outbreak believed to be promoted by thawing permafrost. Environmental samples (soil, water, animal carcasses, insects) were collected and analyzed using DNA extraction, PCR, and Whole Genome Sequencing (WGS) to test for the presence of *B. anthracis* and the phylogeny of any positive samples. Most soil, water, and animal carcass samples tested positive, while all insects were negative for the presence of *B. anthracis*. Based on samples pulled from different depths of the permafrost, Timofeev et al. were able to distinguish three separate anthrax transmission "events" in Russia. One strain, MLVA25, appeared to circulate during the 2016 epidemic and hinted at a connection between human and animal infection. Timofeev et al. noted that the temperature during this epidemic was higher than usual and theorized that such temperature increases could have thawed permafrost and pushed preserved spores to the surface (Timofeev et al., 2019). The final study was a modeling study by Walsh et al. that looked at how different factors in selected northern regions promoted favorable conditions for anthrax transmission. In their model, an association was found between anthrax suitability and climate, livestock (cattle, goat, etc.) densities, and wild ungulate species richness. This suitability increased substantially with warmer temperatures and higher livestock densities but decreased with higher wild ungulate biodiversity and areas with extreme or low water stress. The model predicted that by 2050, continued warming could keep the risk of anthrax exposure the same in circumpolar regions and expand into newer territories. This study provided evidence of increasing global temperatures promoting high anthrax suitability at northern latitudes (Walsh et al., 2018).

RABIES

Another etiologic agent discussed in the literature was rabies virus, the focus of three studies. There were two studies conducted in Alaska and one in Canada. Huettmann et al. used both GIS and 153 confirmed enzootic rabies cases reported in terrestrial animals within Alaska to inform ecological niche models used to understand rabies transmission dynamics and possibly predict areas most at risk for outbreaks. With this model, the authors forecasted future transmission under specific climate scenarios, which showed a reduction in arctic rabies ecological niche in Alaska by 2050. Huettmann et al. also mentioned that changing environmental conditions and increased human infrastructure could facilitate virus adaptation and variations in host distribution, which would challenge these projections. In addition, the model did not consider the possibility of importation from other regions (Huettmann et al., 2017).

Similarly, Kim et al. used passive surveillance of rabies in foxes from 1980-2010 combined with different climate factors and sea ice extent to model trends of rabies transmission for parts of Alaska. They found that rabies in arctic fox populations would be greater impacted by climate change than red fox populations. Increases in temperature and precipitation were negatively associated with red fox cases, while only an increase in temperature showed a negative association in arctic foxes. Kim et al. found a correlation between sea ice extent and fox rabies cases, reportedly reducing as the sea ice extent also decreased, possibly due to limited long-range mobility by the fox hosts. As changes in climate promote red fox range expansion and establishment into new arctic regions, arctic rabies may have “the opportunity to perpetuate” in red foxes (Kim et al., 2014). Aenishaenslin et al. used retrospective descriptive analyses of fox rabies cases (historical cases, human population density, fox abundance) from 1953-2017 to predict the areas that should be prioritized for early detection systems of arctic rabies virus variant (ARVV). While there were no climate/environmental factors included in the analysis, Aenishaenslin et al. mentioned how climate change in the Northern (arctic) Canada could encourage the re-emergence of ARVV in densely populated areas in the Southern region. Their findings indicated that Northern Canada was the source of more ARVV cases than southern areas and should remain the primary focus of public health interventions (Aenishaenslin et al., 2021).

ERYSIPELOTHRIX RHUSIOPATHIAE

There were two studies that focused on the pathogen *Erysipelothrix rhusiopathiae*. Groeschel et al. presented a case study of an infected elderly resident of Canada. The patient suffered from a prosthetic joint infection and had a known history of wild animal exposure. Through diagnostic medical testing (including radiography), physicians determined the cause of the infection to be *E. rhusiopathiae* and performed WGS to compare the patient’s sample to other isolates in an attempt to identify a zoonotic source. Unfortunately, Groeschel et al. were unable to connect this case to the possible zoonotic sources as the closest animal relatives of the strain did not match the patient's exposure history. Climate change was mentioned as a potential factor for increased zoonotic transmission of *E. rhusiopathiae* (Groeschel et al., 2019). In Forde et al., the authors used a “bacterial genomic approach” to determine the potential emergence of *E. rhusiopathiae* in wild ungulates of arctic regions in North America (Canada and Alaska). Tissue and fecal samples were collected from 89 carcasses of muskoxen, caribou, and moose. Samples were cultured, isolated, and analyzed using qPCR and WGS. Based on the findings, the authors determined that a single strain was not responsible despite cases sharing similar geographical locations. Host factors were speculated to be influenced by climate change, referencing that hosts could become more susceptible to opportunistic agents under a changing climate (Forde et al., 2016).

HANTAVIRUS

Two studies were conducted on nephropathia epidemica (NE), a condition caused by Puumala virus, a type of hantavirus. Pettersson et al. described the 2007 outbreak of Puumala virus in Västerbotten County, Sweden that resulted in 313 cases of NE. The team investigated the possible relationship between the outbreak and milder weather, rodent populations, and reduced snow cover. A formal correlational analysis was not performed, but general observations found above-average temperatures in December 2006 and an uncharacteristic delay of snow cover, hypothesized to impact bank vole behaviors and push them towards habitats in human spaces (Pettersson et al., 2008). Haredasht et al. developed mathematical models to help predict NE cases as early as three months ahead for multiple countries, but the arctic country of focus was Finland. The model used Lab-confirmed NE cases from 1995-2008, climate factors, bank vole trapping data from 1995-2008, and enhanced vegetation index. For Finland, Haredasht et al. found that air temperature and bank vole population dynamics could be used to predict cases of NE 3 months ahead (Haredasht et al., 2012).

AVIAN INFLUENZA

Only one relevant study found that discussed avian influenza virus (AIV). In Lee et al., the authors screened for AIV antibodies from 66 bird host serum samples of 2 kittiwake and glaucous gull breeding colonies in Svalbard, Norway from 2014 to 2017. There 14 birds that tested positive for AIV antibodies during the 3-year study period, which the authors noted as presenting the first evidence of AIV exposure among birds in this arctic region. No additional research was conducted to confirm potential active infections or identify influenza subtypes or strains in the birds that tested positive. Climate change was briefly mentioned as possibly impacting the dynamics of AIV, especially for circumpolar regions (Lee et al., 2020).

CAT SCRATCH DISEASE

The final zoonotic study focused on *Bartonella henselae*. For the purposes of this review, *B. henselae* was categorized as a zoonotic agent because of the limited evidence of direct transmission from flea and tick vectors to humans (CDC, 2019). Through an animal field study from 2014-2018, Buhler et al. analyzed flea samples from fox dens, goose nests, and goose corpses in Nunavut, Canada that for *Bartonella* spp. using DNA extraction and qPCR. Blood samples were also obtained and analyzed from live foxes for evidence of *Bartonella* spp. infection. *B. henselae* was present in fleas collected from fox dens and goose nests, but minimal prevalence among live fox samples. Increased temperatures in arctic regions were discussed as necessary to the distribution and prevalence of cases, especially through the movement of migratory birds (Buhler et al., 2020).

4.3.2 Vector-Borne Diseases

The highest number of studies selected focused on vector-borne diseases, accounting for 17 of the 43 articles. These studies shared evidence of direct transmission to humans from vectors, the presence of the pathogen within the vector, or the implications of potential exposure to the pathogen based on the presence or establishment of the vector in the area observed. Of the 17 studies, 15 centered around exposure to tick-borne diseases, one study focused on mosquito-borne diseases, and another pertained to a disease of both mosquito and tick transmission. Several studies researched the presence of multiple pathogens in the designated vector.

TICK-BORNE ENCEPHALITIS

There were six studies that focused primarily on Tick-borne Encephalitis (TBE) or Tick-borne Encephalitis Virus (TBEV) and the vector *Ixodes persulcatus*. In their 2011 study, Tokarevich et al. used local meteorological data, monthly tick abundance counts, and TBE incidence data from 1980-2009 in Arkhangelsk Oblast (AO), Russia to investigate the influence of climate factors on range expansion of *I. persulcatus* and TBE cases. Changes in both temperature and precipitation conditions were found to make AO a favorable environment for the life cycle of *I. persulcatus*, promoting its invasion. Additionally, biting incidence rate increased over time in different AO zones, starting from 0 bites in the 1980s, before the invasion of *I. persulcatus* was suspected (Tokarevich et al., 2011). Tokarevich et al. focused on the effects of air temperature alone on TBE incidence and *Ixodes* spp. distribution in their 2017 study based in the Komi Republic (RK), Russia. Using resident reports and other methods to estimate TBE incidence, the team discovered that the human-biting incidence rate increased substantially from 1998-2011, with more biting events reported in the north. The reports also indicated the extension of seasonal tick activity. Combining TBE case data with average air temperature and seasonal air temperature data from 1960-2013, Tokarevich et al. found that TBE incidence was associated with variations in air temperature, indicating a potential connection with tick activity and climate (Tokarevich et al., 2017).

Similarly, Tronin et al. studied the influence of air temperature on tick-bite incidence in RK, using reported medical visits for *I. persulcatus* tick bites and a tick-bite incidence rate equation (number of tick-bite victims per 100,000 of the population). The use of medical visits for tick bites was an alternative to using tick collection via flagging to measure *I. persulcatus* tick abundance. Temperature data was collected from the National Centers for Environmental Information for 1948-2016. From their analysis, Tronin et al. found that annual air temperatures were associated with the number of tick-bite victims (Tronin et al., 2019). In Soleng et al., the authors wanted to investigate the distribution of *Ixodes ricinus* and the prevalence of TBEV in questing ticks in higher latitudes, specifically Norway. Ticks were collected using the flagging and dragging techniques in different locations below and above the Arctic Circle (66°N).

In Soleng et al., the ticks were randomly selected for TBEV testing via RT-PCR and confirmed using pyrosequencing. Soleng et al. found that ticks positive for TBEV were present as far north as 65.3°N, previously thought of as not being an endemic area for TBEV. Though, only a limited number of ticks, in general, were found north of the Arctic Circle, indicating a possible lack of established tick populations for that area (Soleng et al., 2018). Deardorff et al. also investigated latitude for the distribution and prevalence of the emerging TBE serogroup virus known as Powassan virus (POWV) in Siberia and Alaska. The authors collected serum samples from northern red-backed voles and southern red-backed voles and used strip immunoblot assays to test for the presence of antibodies to Deer Tick Virus, a virus serologically similar to POWV and other TBE serogroup viruses. Ticks were also collected from captured mammals at different latitudes and tested for the presence of POWV RNA using RT-PCR. Deardorff et al. found serologic reactivity in 6.2% of northern red-backed voles and 6.7% of southern red-backed voles in higher latitudes but found no presence of viral RNA in ticks. Despite using DTV as a surrogate to measure seropositivity, the authors did not believe that this indicated that the rodents had DTV compared to POWV due to the lack of its recorded presence in these species. However, they also noted that the actual agent responsible could be another TBE serogroup virus besides POWV, but more research would be needed to confirm. While unable to make a direct connection, the presence of antibodies in rodents within Siberia and Alaska provided more data on the spread of TBE serogroup viruses in higher latitudes undergoing rapid environmental changes (Deardorff et al., 2013). Jääskeläinen et al. studied TBEV prevalence among humans, *I. persulcatus*, and bank voles in Simo, Lapland, Finland. They interviewed 2 of 4 reported human cases from 2008-2009 and used the data collected from those interviews to determine two possible locations to perform sampling. Ticks were collected and tested for the presence of TBEV RNA using RT-PCR. Blood, brain, and lung samples were obtained from bank voles, with the blood tested for antibodies to TBEV and the organ samples tested for TBEV RNA using RT-PCR. Jääskeläinen et al. found that about 6% of ticks and at least one organ in almost 88% of bank voles were RNA positive for TBEV, in addition to 4 bank voles presented with antibodies to TBEV. From these findings, the team concluded that the shifting distribution of TBEV into new areas of higher altitudes and latitudes such as Simo could be influenced by changes in climate (Jääskeläinen et al., 2011).

LYME DISEASE

Three studies focused on vectors of Lyme Disease caused by *Borrelia* spp. Two were written by Ogden et al., who discussed the distribution of the vector *Ixodes scapularis* under a changing northern climate. In the 2006 article, Ogden et al. used a tick population model and climate scenarios (A2, B2) to map how climate change could impact the expansion of tick ranges in Canada. From the model, they predicted that climate change would push tick populations towards more northern regions in Canada as early as the 2020s and other circumpolar territories between the 2050s-2080s, as conditions became ideal for *I. scapularis* establishment. As a result of such changes in population size and geographic distribution, the range of transmission for *Borrelia burgdorferi* would also expand into new areas (Ogden et al., 2006). In their 2015 study, Ogden et al. used stable isotope analysis of tail feathers collected from migratory passerine birds in Canada to approximate how far north the birds were transporting *I. scapularis*. Feathers and ticks from the heads of birds were collected from migration monitoring stations. Through the isotope analysis, Ogden et al. discovered that 70% of the birds carrying ticks could import them to more northern regions, including Canadian arctic territories. The authors' concern was that as northern regions continued to endure the effects of climate change, conditions could become more suitable for *I. scapularis* to promote expansion and establishment with the assistance of migratory birds (Ogden et al., 2015).

Hvidsten et al. conducted the other study, intending to determine *I. ricinus* activity, abundance, and carriage of different *Borrelia* spp. From April to November 2011, the authors collected ticks at two separate sites in Norway using the flagging technique and used PCR to detect the presence of *Borrelia* spp. Climatic conditions were also assessed, with meteorological conditions at collection sites and historical data collected from 1961-2012 from the Norwegian Meteorological Institute. Hvidsten et al. found a total of 582 *I. ricinus* ticks at all stages during the study period, with 135 ticks testing positive for *Borrelia* spp. The most prominent species was *Borrelia afzelii,* which was present in 97% of the positive ticks. In addition, 2011 was characterized as a warmer year with an extended growing season, presenting more favorable conditions for tick activity. The team speculated that the combination of abundance, prevalence, and conditions contributed to the increased incidence of Lyme Disease in the region (Hvidsten et al., 2015).

CANDIDATUS NEOEHRLICHIA MIKURENSIS

There was only one study found related to *Candidatus Neoehrlichia mikurensis*, another species of bacteria transmitted by *I. ricinus*. Larsson et al. wanted to investigate the range of *I. ricinus* carrying *Ca. N. mikurensis* in northern latitudes. Vegetation flagging and veterinary (dogs, cats) sampling and surveillance methods were used to collect ticks in northern Norway. These ticks were then analyzed using DNA extraction, real-time PCR, and nucleotide sequencing to test for the presence of *Ca. N. mikurensis*. Larsson et al. found that of the 1104 ticks collected, 124 tested positive for *Ca. N. mikurensis*, with 34 ticks from dogs/cats and 90 ticks from vegetation. There were also 42 ticks from the vegetation collection that had coinfections with both *Ca. N. mikurensis* and *B. burgdorferi*. This study provided evidence of *Ca. N. mikurensis* in *I. ricinus* at northern latitudes, increasing human risk of exposure if bitten by a tick (Larsson et al., 2018).

TULAREMIA

One study involved research into tularemia, a disease caused by the etiologic agent *Francisella tularensis* that is transmitted by infected animals or vectors, particularly mosquitoes, ticks, and deer flies. Of vector transmission, the bites of ticks are typically the most common (Abdellahoum et al., 2020; CDC, 2018). However, mosquito-associated tularemia is noted as the main mode of transmission in Northern Scandinavian countries, such as Sweden (Abdellahoum et al., 2020). In their 2009 research, Ryden et al. wanted to create a model that could use climate and epidemiological data to help forecast future mosquito-borne tularemia activity in different areas of Sweden. The model used case information from the Swedish Institute of Infectious Disease Control for all regions of Sweden from 1997-2008 plus regional (RCA3) and international (A2, B2) climate scenarios. Their model predicted that increased temperatures due to climate change could extend the duration of tularemia outbreaks between 2010-2100, but minimal influence was seen for precipitation (Ryden et al., 2009).

MULTIPLE TICK-BORNE PATHOGENS

Five studies focused on more than one disease, such as TBE, Lyme Disease, Babesiosis, and Spotted Fever. Four of these studies specifically focused on *I. ricinus* ticks and 1 study that included data for multiple tick species. Lindgren et al. questioned the influence of climate change on previously reported range expansion of *I. ricinus* into Sweden and increased abundance of the tick population. To collect tick information, the team used retrospective data from a study that documented the geographical distribution of *I. ricinus* and another study that analyzed survey results targeting responses from hunters, dog and cat owners, and house and cottage owners. Lindgren et al. collected temperature data from 20 meteorological stations for 1979-1981 and 1991-1993. Tick abundance appeared to be associated with milder winters and longer spring/autumn seasons, suggesting that tick distribution may spread to higher latitudes and altitudes as the climate in these northern regions continues to warm (Lindgren et al., 2000). The research in Alfredsson et al. was part of a larger surveillance program to report potential established habitats of *I. ricinus* in Iceland. Active surveillance (flagging) and passive surveillance (public submissions of encounters) were performed to collect tick data from different areas in Iceland. While Alfredsson et al. did find *I. ricinus* questing in Iceland, there was no evidence of an apparent established population. The current climate was speculated to be a limiting factor for some regions within Iceland, despite other areas already being favorable for *I. ricinus.* Seasonal dynamics of key animal hosts could also be impacting the ability for tick establishment (Alfredsson et al., 2017).

Hvidsten et al. conducted a field research study from 2010-2018 to explore the distribution of ticks and the potential pathogens they carried in northern Norway in the context of increasing temperatures and extension of growing season length (GSL). Tick sampling was conducted using the dragging technique, veterinary surveillance, and removal from pets and captured small mammals. The ticks were tested for *Borrelia* spp. and *Rickettsia* spp. genetic material through PCR and the prevalence of both pathogens among the 518 ticks collected was low (1-15%). Climate data were obtained and differences in median GSL were calculated using the Mann-Whitney test. Temperature was discovered to increase for all study locations, which supported longer vegetation GSL and provided evidence of an established population of *I. ricinus* (Hvidsten et al., 2020). In Jore et al., the study's objective was also to determine the distribution of *I. ricinus* in Norway for any evidence of latitudinal or altitudinal shifts based on previous measurements from 1935-1983 compared to more recent data. To estimate this, the authors used tick-sighting reports (from veterinarians, hunters, and the general public) and surveillance data of both human and animal tick-borne infections (Lyme Disease and bovine babesiosis). Jore et al. determined from their analysis that the updated data provided evidence of shifts in latitudinal and altitudinal range, as ticks were recorded beyond the previous northern limit. Despite this expansion, there were no reported cases of bovine babesiosis or Lyme Disease in humans found for the study period. Though, this may have been due to other factors involved, such as changes in human behavior and socioeconomic factors (Jore et al., 2011).

In the fifth study regarding multiple tick-borne pathogens, Hahn et al. wanted to provide baseline information to establish a passive tick surveillance program in Alaska to prepare for potential tick range expansions due to increasing temperatures. A combination of sources was used to determine historical and current tick occurrence, such as using retrospective tick data from 1909-2019, a literature review, active surveillance using the dragging technique, and creating a civic reporting system called the Alaska "Submit-A-Tick Program." In addition to establishing a baseline measurement, Hahn et al. discovered that three non-native *Ixodes* species significant to human health (*I. pacificus, I. scapularis,* and *I. ricinus*) were reported in Alaska, indicating importation or expansion of these into the region due to climate or other factors. Through the development of the passive surveillance program, "Submit-A-Tick," the authors created a way to support future monitoring of tick distribution and activity, especially in a changing climate (Hahn et al., 2020).

MULTIPLE MOSQUITO-BORNE PATHOGENS

One study by Mullerova et al. examined the prevalence of multiple arboviruses in mosquito vectors in Greenland and Norway. In a field research study, the authors collected mosquitoes during the summers of 2012-2016, totaling over 11,000 specimens. RNA was isolated from the mosquitoes and used for analysis via RT-PCR to test for arboviruses of the genera *Alphavirus (family Togaviridae), Orthobunyavirus, Phlebovirus (Bunyaviridae), Flavivirus (Flaviviridae),* and *Orbivirus (Reoviridae)*. All mosquitoes were classified as *Aedes nigripes*, but no arboviruses of the targeted genera were detected in any mosquitoes. Existing climate conditions for the region and other factors were noted as possibly restricting the current circulation of these arboviruses. However, future effects of climate change could pose new opportunities for transmission (Mullerova et al., 2018).

4.3.3 Parasitic Diseases

Interestingly, only five of the 43 studies focused on parasitic diseases. These studies addressed the potential of human exposure and infection based on the presence of the parasite in other animals or the environment.

TRICHINELLOSIS

Two studies pertained to etiologic agents of the *Trichinella* spp., both performed in North America. Seymour et al. conducted a laboratory-based research study that examined the presence of *Trichinella* spp. in Alaskan marine-associated mammals, such as pacific walruses, ice seals (ringed, bearded, spotted), arctic foxes, sea lions, and polar bears. A “double-separatory funnel digestion assay diagnostic method” was used to simulate digestion and detect larvae in archived animal tissue samples, which were then categorized and subjected to DNA extraction and PCR analysis for species identification. Of the 380 marine animals, 1 ringed seal, 1 polar bear, and 3-7 arctic foxes tested positive for *Trichinella* spp. and the larval DNA analyzed from these infected mammals was revealed to be *T. nativa*. Seymour et al. concluded that confirmation of *T. nativa* indicated it to be the likely dominant *Trichinella* species in arctic ecosystems. More research is needed to determine how the impacts of climate change will affect the pathogen’s distribution and ability to persist in altering environments (Seymour et al., 2014). Masuoka et al. used

Maxent-based modeling to predict ranges for sylvatic *Trichinella* spp. in different parts of North America based on environmental conditions. To support the model, climate data were obtained from WorldClim 1.4, information about land cover was gathered from the U.S. Geological Survey's Global Land Cover Characteristics Database, and *Trichinella* case information was collected from published literature and accession records with the International Trichinella Reference Center. For the arctic regions, the models predicted that ranges for *T. spiralis* extended to Alaska and also estimated that higher latitudes and elevations characterized *T. nativa* ranges. The authors hoped that using predictive modeling could be very useful in monitoring future impacts of climate change and other anthropogenic factors on *Trichinella* distribution (Masuoka et al., 2009).

TOXOPLASMOSIS

One study focused on *Toxoplasma gondii,* the pathogen responsible for toxoplasmosis. Jensen et al. conducted an animal research study in Norway to investigate the transmission pathway(s) and prevalence of *T. gondii* in polar bears and their marine mammal prey, especially in the context of warming sea temperatures. Blood samples were collected from 1992-2008 from captured animals (polar bears, whales, seals) and analyzed for the presence of antibodies to *T. gondii* using a direct agglutination test. From this research, Jensen et al. found that 45.6% of polar bears, 18.7% of ringed seals, and 66.7% of adult bearded seals tested positive for *T. gondii*, a prevalence that doubled compared to previous measurements. It was speculated that this might have been due to the increased persistence of oocysts in ocean water, likely due to warming water temperatures (Jensen et al., 2010).

MULTIPLE PARASITIC DISEASES

The remaining two studies that centered around parasitic diseases involved research in more than one etiologic agent. Andreassen et al. conducted an ecological study to explore the prevalence of *Toxascaris leonine, Taenia crassiceps, Taenia serialis,* and *Strongyloides stercoralis* among arctic foxes in Greenland. Fecal samples were collected near fox dens located in two areas from May to August of 2006-2008 and examined using microscopy, DNA extraction, and PCR. About 45.5% of samples contained eggs or larvae from *T. serialis, T. crassiceps*, and *Toxascaris leonine*, in addition to some that had *Strongyloides*-like larvae. The team concluded that the results from their study could help provide a baseline that could be used for future investigation of the influence of climate change on parasitism dynamics for the region (Andreassen et al., 2017).

Salb et al. collected fecal and blood samples to measure gastrointestinal parasite prevalence among domesticated dogs in northern Canada and evaluate the role of dogs as sources of zoonotic parasitic diseases. Veterinarians collected the samples, which were analyzed for the presence of parasites (fecal) using quantitative sugar flotation and microscopy or antibodies (blood) using direct agglutination and immunofluorescence assays. At least 11 different parasite genera were detected and 47% of dogs tested positive for more than one parasite. It was also discovered that various characteristics of the dogs influenced the parasites present. Dogs housed outdoors were more likely to be infected with *Toxocara* spp., *Toxascaris* spp., and *Cystoisospora* spp., and dogs that consumed wild game meat were more likely to be infected with *Sarcocystis* spp., *Taenia* spp., and *Echinococcus* spp. *Giardia* spp. and *T. gondii* were also recovered from samples. Based on these results, domesticated dogs in northern communities could act as reservoirs of parasites present in foods consumed by humans and dogs or as direct sources of transmission for zoonotic parasitic diseases, which could be exacerbated by warming climate trends (Salb et al., 2008).

4.3.4 Other Notable Diseases

The search for emerging and re-emerging pathogens in the arctic region also yielded four studies related to antimicrobial-resistant organisms and pathogenic fungi. These were included because of their public health significance, possible sensitivity to climate or other environmental factors, and potential risk of human exposure via environmental interactions.

ANTIMICROBIAL RESISTANCE

Three studies focused on the presence of resistant genes among clinically significant bacterial pathogens in arctic environments. In their 2020 study, Mogrovejo et al. tested 118 isolates from environmental samples in Greenland and Norway for evidence of virulent and antimicrobial-resistant phenotypes. Samples from lake ice, glacial and subglacial ice, glacial meltwater, tap water, pond water, seawater, sediment were collected and analyzed for identification and phenotypic resistance using culturing, hemolytic assays, and antimicrobial susceptibility tests. Mogrovejo et al. observed that most isolates were resistant to at least one antimicrobial, including ciprofloxacin, chloramphenicol, and cefotaxime. Isolates of the *Pseudomonas* spp. were found to have the highest multidrug resistance abilities. In addition, there was also evidence of some isolates showing carbapenem resistance among *Bacillus*, *Cryobacterium*, *Leifsonia*, and *Streptomyces*. Mogrovejo et al. concluded that while more research would be needed, their study provided insight into evidence of potential adaptations and origins of resistance in bacteria in the arctic environment, especially in the context of climate change (Mogrovejo et al., 2020).

Haan et al. conducted a study in Alaska to determine how permafrost thaw due to external factors impacted the abundance and mobility of antimicrobial resistance genes among bacterial isolates. In September 2017, bacteria were cultured and isolated from collected soil core samples from the Fairbanks Experiment Station, a research station that measures different levels of permafrost disturbance. The isolates were analyzed for antimicrobial resistance genes using whole-genome sequencing and antimicrobial susceptibility tests. Over 90% of the isolates showed phenotypic resistance to at least one of the clinically important antimicrobials tested, with ampicillin and chloramphenicol having the highest prevalence of resistance. It was also found that as disturbance increased, so did the abundance of antimicrobial genes. Haan et al. found genes encoding for antimicrobial efflux, antimicrobial inactivation, antimicrobial target modification, and antimicrobial target protection that seemed to be clustered by bacterial phylum instead of the collection site. The team emphasized that studies like theirs would contribute to our understanding of how climate and other anthropogenic causes of permafrost thaw impact resistance characteristics among bacteria in arctic environments (Haan et al., 2021).

In the third study about antimicrobial resistance, Diaz et al. investigated the presence of antimicrobial resistance genes among the permafrost microbial community in Sweden. In 2012, core samples were collected from different sites along a thawing permafrost gradient and then analyzed using DNA extraction and genome sequencing. Diaz et al. found the presence of antimicrobial protein-coding genes in 0.72–1.29% of core samples. They did not observe a difference between antimicrobial resistance abundance across collection sites but did find differences in the class and gene types of antimicrobial resistance. Similar to Haan et al., the authors of this study explained that the data obtained would provide insight into antimicrobial resistance for this region and how climate-induced permafrost thaw could influence antimicrobial resistance (Diaz et al., 2017).

MYCOSES

The remaining study researched fungi in arctic environments for phenotypes associated with pathogenicity and resistance in humans: growth at 37^{o}C, hemolytic activity, and antifungal resistance to common fungicidal therapeutics. Perini et al. cultured and isolated different fungal species among environmental samples (snow, glacial meltwater, subglacial ice, supraglacial ice and water, and air) collected from 2016-2018 in parts of Greenland and Svalbard, Norway. The isolates underwent DNA extraction and Sanger sequencing for identification, as well as antifungal susceptibility tests and assays for thermotolerance and hemolytic activity. Perini et al. found thermotolerance and high hemolytic activity was present for *Naganishia albida, Rhodotorula mucilaginosa,* and *Aureobasidium melanogenum*, fungal pathogens previously documented to infect and cause disease humans. There was also antifungal resistance seen in *N. albida*, *A. melanogenum*, and 2 species of *Glaciozyma*, a fungal pathogen not previously documented to cause disease in humans. Perini et al. expressed that their study indicated the importance of identifying potentially pathogenic and virulent fungi in arctic regions, especially as climate change could promote conditions that cause an increased release of spores into the environment (Perini et al., 2019).

4.3.5 Multiple Diseases Across Different Transmission Categories

There were four studies that explored multiple diseases across the different categories of transmission. These studies analyzed the prevalence of many different types of pathogens within a specific animal host or reservoir and the human population of a particular region.

ZOONOTIC, PARASITIC, AND VECTOR-BORNE DISEASES

Two articles researched zoonotic, parasitic, and vector-borne diseases within the same study. Atwood et al. examined how different factors, including changing environmental conditions, could impact the seroprevalence of various pathogens among polar bears in the Alaskan region of the Beaufort Sea, such as *Coxiella burnetii*, *Brucella* spp., *T. gondii*, and *F. tularensis*. Blood samples were collected from 139 polar bears from 2007-2014 and analyzed for prevalence using pathogen-specific antigen/serologic testing. The authors found evidence of a possible increase in the seroprevalence of *Brucella* spp. (27%) and *T. gondii* (81%) in polar bears, as well as the potential exposure to *C. burnetti* and *F. tularensis*. Atwood et al. also noted that climate-induced changes in pathogen range expansion and polar bear behavior might have impacted the chances for exposure (Atwood et al., 2017). The 2019 study by Omazic et al. focused on assessing the differences in reporting of climate-sensitive zoonotic and vector-borne diseases across Sweden, Norway, Finland, Iceland, and Greenland. Authors reviewed nationally reported data from 1965-2016 on nine diseases: anthrax, borreliosis, brucellosis, cryptosporidiosis, leptospirosis, NE, Q-Fever, TBE, and tularemia. Omazic et al. found differences in the availability, quality, and requirements of reporting disease data across the countries, especially for diseases such as TBE, Q-Fever, cryptosporidiosis, leptospirosis, and brucellosis. These discrepancies were viewed as barriers to effectively comparing incidence and prevalence across Nordic countries, an important aspect of monitoring possible impacts of climate change on infectious disease dynamics (Omazic et al., 2019a).

BACTERIAL DISEASES OF DIFFERENT TRANSMISSION TYPES

Another study researched various bacterial diseases of different transmission categories, specifically zoonotic, vector-borne, and environmental. In their 2018 study, Andersen-Ranberg et al. investigated the fecal bacterial community among muskoxen in Greenland and Norway by trying to quantify the effects of physiological, temporal, and geographical changes on the fecal bacterial community's composition. Fecal samples were collected in September 2013 and September 2015, then analyzed using DNA extraction, PCR, and bioinformatics analysis. There were 13 genera of zoonotic [and vector-borne] pathogens collected, with the ones relevant to this review being *Erysipelothrix, Bacteroides, Bacillus, Actinomyces, Fusobacterium, Pseudomonas, Rhodococcus,* and *Yersinia*. Andersen-Randberg et al. speculated that changes in annual climate might impact muskoxen health, as previous literature provided that increased temperatures and humidity are associated with changes in the gut microbiomes of other ruminants (Andersen-Randberg et al., 2018).

VECTOR-BORNE PARASITIC AND BACTERIAL DISEASES

One study focused on different vector-borne diseases of parasitic and bacterial transmission. Hornok et al. tested liver samples using DNA extraction, qPCR, and sequencing to examine the prevalence of different diseases among arctic foxes in Iceland from 2011-2012. Of the 60 samples analyzed, only 1 tested positive for a vector-borne pathogen transmitted by *I. ricinus* ticks, *Anaplasma phagocytophilum*. Hornok et al. noted that this could be the first molecular evidence of the agent in arctic foxes and the first autochthonous occurrence in Iceland, though the finding could not be confirmed by sequencing. All 60 samples were negative for other pathogens or contained genetic material too low to be detected by qPCR. The lack of pathogens implied to the authors that the effects of warming temperatures in Iceland might not have impacted the distribution of tick-borne pathogens during this period (Hornok et al., 2020).

4.4 Impact of Climate on Indigenous Populations

Five studies researched the direct and indirect health impacts of climate change and the disease categories of interest on indigenous communities.

4.4.1 Canada

Blangy et al. discussed projects and objectives of the International Observatory of Human–Environment Interactions (OHMi) Nunavik program, such as reducing Inuit and non-Inuit community exposure to zoonoses and strengthening awareness of these diseases influenced by the effects of climate change. The authors described OHMi Nunavik as a multidisciplinary "ecosystemic" approach that kept the community involved at every stage of the research project. For the project concerning zoonoses, Blangy et al. used an "Ecohealth" perspective to investigate both the negative and positive effects of domesticated dogs on human health and wellness, such as rabies. A survey about community perceptions regarding dog-human interactions was distributed, followed by a focus group discussion after collecting initial data. Many residents agreed that dogs were important, but they also agreed that the dog population was too high and that either themselves or someone in their family had been bitten or scratched by a dog. The results from the focus group were adapted into posters to help spread awareness of the concern of dog-human interactions in the community (Blangy et al., 2018).

In Masina et al., the authors also used an Ecohealth approach to investigate the potential presence of *Giardia* spp. and *Cryptosporidium* spp. in untreated surface water used for drinking by Inuit communities in Canada. Water samples were obtained from June to September 2016 from Sylvia Grinnell and Apex Rivers, as they were considered culturally significant to the Inuit community members. The samples were tested for bacteria and parasites, and any oocysts recovered were analyzed using immunofluorescence, microscopy, DNA extraction, and PCR. Masina et al. also tested for association with measured environmental factors, such as air temperature, precipitation, water temperature, turbidity, and water level. The team found that 22% of samples tested positive for *Giardia* and 2% tested positive for *Cryptosporidium* using microscopy but were unable to detect either pathogen using PCR which also restricted the determination of species or genotype. Lower air and water temperatures were associated with higher parasite presence. Masina et al. extrapolated that climate-induced changes to seasonal ice dynamics could lead to longer periods of low water temperature that support growth and contamination of *Giardia* and *Cryptosporidium* (Masina et al., 2019). In a 2014 study by Aenishaenslin et al., the authors used data from 1999-2012 to research the health impacts of arctic rabies dynamics on Inuit communities in Canada. The team used a One Health approach to best characterize arctic rabies epidemiology by using dog vaccination records in the Ministère de l’Agriculture, des Pêcheries et de l’Alimentation du Québec (MAPAQ) database, documented tests and confirmed cases among animals from the Canadian Food Inspection Agency (CFIA) database, and reports of potential human exposures from the Nunavik Regional Board of Health and Social Services. Aenishaenslin et al. found that the proportion of confirmed rabies cases was higher among wild animals compared to domestic, dog vaccination rates varied between the regions studied and that children were considered the most at-risk for rabies exposure. There was also a brief discussion about how climate change could impact wild animal rabies cases by influencing variations in prey availability in natural habitats, causing animals to forage closer to human housing (Aenishaenslin et al., 2014).

Campagna et al. explored the seroprevalence of different zoonotic, parasitic, and vector-borne infections in two Cree communities to help provide a baseline reference in a region expected to be heavily impacted by climate change. Residents were randomly selected and asked to complete three different surveys relating to demographics and lifestyle, wildlife and zoonosis exposures: hunting, fishing, and trapping habits, and traditional food consumption. Blood samples were also obtained and analyzed using ELISA to detect the presence of antibodies to 10 specific pathogens: *C. burnetti, F. tularensis, Leptospira* spp., hantavirus, Jamestown Canyon virus, California serogroup viruses, snowshoe hare virus, *T. gondii, Echinococcus granulosus, T. canis,* and *Trichinella* spp. Of the 251 participants, almost 50% expressed seropositivity at least one for the targeted pathogens, with the highest rates being for *F. tularensis, Leptospira* spp., and California serogroup viruses. According to the authors, the critical risk factors determined from their analysis were age, gender, owning a dog, and hunting (Campagna et al., 2011).

4.4.2 Alaska

As a project for the Center for Climate and Health of the Alaska Native Tribal Health Consortium, Brubaker et al. conducted a community-scale assessment on how the effects of climate change impacted the health of members of two indigenous communities in Northwest Alaska. The vulnerabilities found from the evaluation placed community members at risk for potential exposure to infectious diseases from water and food insecurity. Brubaker et al. shared how increased temperatures limited the freeze time for outdoor food storage, promoted the development of mosquito larvae in water filters, and reduced the amount of shore ice available to prevent impact from storm surges which resulted in the closure of a facility that offered sanitation and hygiene services to community members. The assessment was promoted to help understand the link between health and climate change and be an essential step towards creating sufficient adaptation plans for these communities (Brubaker et al., 2011).

CHAPTER 5: DISCUSSION

This systematic literature review explored the different emerging and re-emerging infectious diseases in the circumpolar regions and how climate change has already or could in the future impact incidence, prevalence, pathogen persistence, vector abundance and distribution, and pathogen-host dynamics. Literature database searches were conducted to find studies about zoonotic, vector-borne, and parasitic diseases affecting arctic populations, as well as the potential future threat of antimicrobial-resistant and fungal pathogens. These searches yielded 43 studies that described the patterns of the disease itself or the environmental vectors, hosts, and reservoirs involved in transmission and five studies that discussed how these diseases impacted indigenous populations in the arctic regions. Different types of research were included in this review, such as ecological/field research studies, animal research studies, correlational/epidemiological studies, case reports, and multi-method studies. The most relevant themes and findings regarding diseases of public health importance in the circumpolar regions are discussed below.

5.1 Key Diseases of Public Health Importance in Circumpolar Regions

While a broad range of infectious diseases was covered in this systematic literature review, some transmission categories were represented in the body of research more than others, especially in the context of climate change, latitude, and altitude. These findings could imply that emerging and re-emerging zoonotic diseases and emerging vector-borne diseases may present the greatest public health risks towards circumpolar populations under a rapidly changing environment.

5.1.1 Re-Emerging Disease: Anthrax

Zoonotic diseases were the second most common transmission category of studied reviewed, with most studies researching *B. anthracis* in circumpolar territories. Anthrax has been reportedly found on every continent and island inhabited by humans, with most of the estimated 20,000 to 100,000 cases a year occurring in rural areas. Current research into the global burden of anthrax identified parts of East Asia, Australia, North America, Eastern Europe, and Africa as the places for high-endemicity and high human vulnerability. Interestingly, high-latitude regions have been described as poorly represented among this group, likely due to reduced reporting and limited research on what climate factors impact *B. anthracis* transmission in the circumpolar areas (Carlson et al., 2019). In this systematic literature review, anthrax was indicated as a re-emerging disease of concern for arctic regions, as spores from past anthrax outbreaks were suspected of causing recent and future epidemics.

Rising temperatures were found to advance the thawing of permafrost and potentially push viable anthrax spores preserved in animal carcasses to the surface, creating new exposure opportunities for animals and humans. Communities living near cattle burial grounds were considered the most at risk for anthrax exposure due to the role that deep active and top surface permafrost layers play in long-term spore storage (Revich and Podolnaya, 2011; Stella et al., 2020). Temperatures during an outbreak in 2016 were higher than average, leading researchers to speculate that the warm conditions facilitated exposure via permafrost thaw (Timofeev et al., 2019). Arctic regions reportedly have the factors necessary to support suitable conditions for anthrax transmission, such as increased temperatures and livestock densities. Similar to vector-borne diseases, this continued rise in global temperatures was predicted to not only keep anthrax endemic in certain arctic regions but also allow further expansion into other areas (Walsh et al., 2018). Future research could continue to measure the prevalence of viable spores in the permafrost and compare different anthrax strains identified in epidemics with those present in the local environment.

5.1.2 Emerging Diseases: Tick-Borne Encephalitis and Lyme Disease

The transmission category with the most studies was vector-borne diseases, with 15 studies about tick-borne diseases alone, specifically Tick-borne Encephalitis (TBE) and Lyme disease. Both diseases have been previously described as being “the most important tick-borne diseases” in Europe. Of all of the other vector-borne diseases, Lyme disease is the most commonly reported, closely followed by TBE. Over the past three decades, cases of TBE have increased by over 400% in endemic areas (Semenza & Suk, 2018). Similar to Europe, the most frequently reported vector-borne disease in the United States is Lyme disease, with about 476,000 people diagnosed and treated for the disease every year (CDC, 2021). In North America, TBE is exceptionally rare and is considered an imported disease from more endemic areas like Europe (CDC, 2020). In both countries, the ranges of these tick-borne diseases have expanded, as newer areas are reporting cases and the presence of tick populations (Caminade et al., 2019; CDC, 2021; Semenza & Suk, 2018). TBE and Lyme disease were described as emerging in arctic regions, as climate and environmental factors enhanced introduction and establishment in these new areas previously described as unfavorable for tick activity. The tick species discussed in the context of emergence were those previously described to be significant to human health, *I. scapularis, I. ricinus, I. persulcatus,* and *I. pacificus*.

Many studies relating to tick-borne diseases addressed increasing temperatures as impacting vector dynamics and disease trends in the arctic regions. Rising temperatures were discussed as promoting more favorable conditions in the environment to support vector abundance, lengthen seasonal activity, and expand vector distribution, potentially resulting in more TBE and Lyme disease cases. Higher temperatures were found to be associated with a greater incidence of human biting rates and tick-borne diseases, as well as an extended growing season for vegetation (Hvidsten et al., 2015; Tokarevich et al., 2017; Tronin et al., 2019). These warming conditions could create even more ideal settings that facilitated extended seasonal tick activity, importation, and establishment of tick populations in new areas (Hvidsten et al., 2020). Tick abundance and distribution were associated with milder winters and longer spring and autumn seasons, spreading to higher latitudes and altitudes as temperatures increased over time (Lindgren et al., 2000).

Non-climate related northward expansion into higher latitudes and altitudes was only briefly referenced. Epidemiological data and other modes of surveillance showed ticks being reported beyond the previously defined northern limit, indicating substantial shifts in latitudinal and altitudinal ranges (Jore et al., 2011). The presence of new species in different latitudes marked importation or possibly even expansion and establishment in the new region (Hahn et al., 2020). There was also a discussion of the role that animals played in the spread of tick-borne diseases and the distribution of vectors. Climate-induced tick range expansion towards the arctic regions was found to be likely aided by migratory birds traveling to these regions. As conditions become more favorable, this bird-facilitated importation of ticks could lead to the establishment of new tick populations in new areas (Ogden et al., 2015).

Increased prevalence of tick-borne pathogens found in animals at higher altitudes could also reflect changes in climate and the presence and potential establishment of ticks in new regions (Deardorff et al., 2013; Jääskeläinen et al., 2011). However, there was also evidence that challenged the potential for tick range expansion and increased transmission of tick-borne diseases in certain arctic regions. For some northern locations, ticks have been found only in limited quantities, indicating a possible lack of substantial establishment. Latitudinal and climatic conditions could also act as limiting factors for tick establishment, especially when considering how both could affect seasonal dynamics of animal hosts necessary for establishment (Soleng et al., 2018; Alfredsson et al., 2017). Future research could revisit past analyses based on previous climate scenario projections and assess if the vector range did expand to the predicted areas. There could also be investigations into what other factors, like animal host dynamics and human behaviors, could be influencing the limited presence of tick populations in locations.

5.1.3 Potential Re-Emerging Diseases: Neglected Tropical Diseases

As previously mentioned, the “tropical” misnomer of these types of diseases can lead researchers to confine them to strictly tropical regions, when they can occur anywhere that impoverished conditions exist (Hotez, 2010). Several neglected tropical diseases (NTDs) were identified in the studies as important to the arctic regions, with most of the studies reporting findings for rabies and trichinellosis transmission. Some of the studies in this review provided analysis explaining a negative association between a changing climate and rabies transmission. Increasing temperatures were predicted to decrease rabies transmission among terrestrial animals, especially in certain species of foxes (Huettmann et al., 2017; Kim et al., 2014). However, as climate variations promote more favorable settings in newer areas, the opportunity for rabies to expand to other territories and amplify in a new species may present itself (Aenishaenslin et al., 2021; Kim et al., 2014). Domestic and wild dogs were described as posing a potential risk to humans of both rabies virus and parasitic diseases. (Aenishaenslin et al., 2014; Campagna et al., 2011). Though, marine-associated animals were also considered direct and indirect sources of transmission, through consumption of hunted meat or interacting with the waste products of animals that may have become infected (Jensen et al., 2010; Seymour et al., 2014). Increased temperatures in the air and ocean may have also increased the survival capabilities of parasitic oocysts, leading to higher disease prevalence among marine animals (Jensen et al., 2010).

Surprisingly, echinococcosis was mentioned in the context of climate change in only one study that discussed multiple parasitic diseases. This was particularly interesting because *Echinococcus multicularis* is the more common species found at higher latitudes and can withstand freezing temperatures (Booth, 2018). What may have impacted the diminished recovery of studies of echinococcosis and other NTDs for this review was the requirement for the reference of climate change affecting transmission dynamics. Previous queries into the limited evidence of climate change on NTDs and other infectious diseases in the arctic have looked into why many of these studies may not refer to long-term variations in weather as being classified as climate change (Omazic et al., 2019b). In addition, there is not enough research being performed on infectious diseases in circumpolar regions in the context of climate change in general, which results in a smaller pool of evidence to draw from (Parkinson et al., 2014). As with tropical regions, more interest and funding should be allocated to support future research and disease surveillance activities of NTDs in the Arctic. A key difference between tropical and circumpolar areas impacted by NTDs is the capability to push those efforts forward because arctic countries are among the wealthiest nations in the world (Chatwood et al., 2012). However, wherever extreme poverty exists, such as among circumpolar indigenous populations where conditions may resemble those in lower-income countries, NTDs will be found more often. National governmental bodies should attempt to correct the limited resources available to support adequate disease reporting and diagnostic efforts to prioritize research into NTDs.

5.1.4 Potential Emerging Diseases: Antimicrobial Resistance and Fungal Pathogens

Antimicrobial-resistant pathogens and fungal pathogens were investigated for this review because of their significance to public health, being linked to potential human exposure through interacting with the environment, and their possible sensitivity to climate or other environmental factors. These diseases are significant in their own right but could also be important opportunistic or coinfections due to increased host susceptibility from exposure to other diseases addressed in this review.

A report from the U.K. estimated that if climate mitigation efforts did not occur by 2050, global mortality from antimicrobial-resistant pathogens could reach as high as 10 million deaths per year. This is considered a response to climate-induced resistance shared between microbes in the natural environment and the increase in climate-sensitive infectious diseases that may require antimicrobials (Gudipati et al., 2020). Of the studies about antimicrobial resistance, researchers expressed interest in the prevalence and origins of clinically important resistance genes and mechanisms hidden in pathogens persisting in permafrost, ice, and sediment. All three studies found evidence of antimicrobial resistance to at least one antimicrobial, with 2 studies recovering resistance in permafrost samples. Alarmingly, there was evidence of carbapenem resistance in some of the bacteria, an emerging class of resistance presenting significant challenges in the treatment of certain bacterial pathogens, especially those under the order of Enterobacterales (CDC, 2019). The question remained of the true origin of such resistance among the researched environmental pathogens researched, mainly due to some resistance noted as a natural adaptive process of microorganisms. The authors speculated the potential for factors like increased temperatures applying stress to the environment, such as through permafrost thaw, and thus inducing adaptations for virulence and resistance characteristics (Diaz et al., 2017; Haan et al. 2021; Mogrovejo et al., 2020). To better understand the role of exposure to environmental reservoirs in antimicrobial resistance among arctic residents, future research could attempt to measure the association of the prevalence of genetic/phenotypic resistance to that of suspected/confirmed clinical cases, ideally under different climatic conditions.

Climate change’s influence on mycoses has been referenced in the context of increased temperatures impacting the intensity and duration of extreme weather events, which create conditions that support fungal growth (Jaksic et al., 2020). In more recent years, however, with the emergence of the infamous drug-resistant fungal pathogen *Candida auris*, theories are surfacing about the direct influence of temperature fungi. As the fungi adapt to these higher temperatures, the view is that this could enable them to possibly be able to infect humans, as they would gain thermotolerance (Casadevall et al., 2019). Only 1 study discussed fungal pathogens in the circumpolar regions and how climate change may impact human risk of fungal diseases. In Greenland and Norway, previously documented pathogenic fungi to humans, *Naganishia albida, Rhodotorula mucilaginosa,* and *Aureobasidium melanogenum,* were found in different environmental samples, including that of snow, ice, air, and water sources. Antifungal resistance was discovered for *N. albida*, *A. melanogenum*, and species of *Glaciozyma*, a species not reported to have any prior pathogenic potential in humans. Climate change could promote more suitable conditions that facilitate the increased release of pathogenic fungal spores into the surrounding environment (Perini et al., 2020). Future research could examine the presence of clinically relevant fungi in the environments close to arctic communities to assess the risk of human exposure and assist in fungal disease surveillance. Studies could also be conducted to measure the carriage distance of these fungal spores to new areas, in addition to the likelihood of establishment based on climate conditions.

5.2 Indigenous Populations and Climate-Sensitive Infectious Diseases

This review also attempted to investigate the impact of climate-sensitive diseases on indigenous populations in the circumpolar regions. These communities have a significant cultural relationship with the environment that could place them at a disproportionate risk for the effects of climate change and exposure to certain infectious diseases. Climate-related health risks among other indigenous populations, such as Australia's Aboriginal communities, differ from those in circumpolar regions. Extreme weather events that lead to flooding, high heat days, and rising sea-level concerns mainly affect these residents, with the infectious diseases of concern being mainly mosquito-borne and waterborne (Ford, 2012). As supported by this review, Arctic indigenous populations seem to be most affected by changes in temperature increasing risks of zoonotic diseases, waterborne diseases, and foodborne diseases via proximity to wildlife, food preparation, and disturbances to water infrastructure and food storage capabilities. Only five studies recovered from the database search directly addressed the risk of infectious disease exposure among indigenous communities in the context of climate change. Despite there being indigenous populations in all of the arctic regions except Iceland (Arctic Council, 2021), there were only two countries represented in the results of this review, Canada and the United States (Alaska).

Several studies employed Ecohealth or One Health approaches to help assess the risk of infectious disease exposure and promote public awareness of these risks (Aenishaenslin et al., 2014; Blangy et al., 2018; Brubaker et al., 2011; Masina et al., 2019). One Health is a collaborative, holistic approach that affirms to improve human health and well-being, we must concurrently enhance the health of animals and the environment. Ecohealth is similar in that it focuses on improving the health of humans, animals, and the environment, while also including socioeconomic stability and environmental sustainability. This approach also emphasizes the importance of biodiversity and the protection of the lives of microbial organisms (Lerner & Berg, 2017). Zoonotic diseases were of great concern, particularly concerning rabies and other zoonoses transmitted to humans by domestic dogs and wild animals. Climate change was hypothesized to alter interactions between dogs and humans and affect prey availability for wild animals by pushing them closer to human residences in search of food and increasing chances of human exposure (Aenishaenslin et al., 2014; Blangy et al., 2018; Campagna et al., 2014). Food and water security for these communities were addressed as likely being impacted by the effects of climate change. Higher temperatures reduced the amount of outdoor food storage time, and lower temperatures resulted in a higher prevalence of *Giardia* and *Cryptosporidium* parasites in traditional, untreated water sources (Masina et al., 2019). Future research needs to focus efforts on investigating disease burden in indigenous communities that are less represented in the global conversations, such as those in Russia. These studies should also review and reference the historical marginalization of these communities that exacerbate the effects of climate change and infectious diseases.

5.3 Limitations

There were limitations to this systematic literature review that likely influenced the quality and quantity of studies included. First, this study only included articles with versions available in English due to the lack of reviewer linguistic skills and access to proper document translation tools. Articles or reports in other languages could have been helpful to include, especially when considering research addressing indigenous populations. Second, only two databases were used, and only articles with Open Access or otherwise accessible through Emory University's library partnerships were considered for inclusion, which impacted the number of search results. Undoubtedly, other relevant articles with a paywall may have been beneficial to include (especially regarding international research and indigenous populations) but were excluded because of this financial barrier for the reviewer. Third, the use of specific keywords over others may have also impacted search results. More general terms were used in an attempt to yield a broader range of results instead of using more disease-specific or country-specific keywords. Fourth, studies that addressed the bacterial and viral diseases of waterborne and foodborne transmission were not included in this review. By not focusing on the full burden of these types of diseases concerning the others discussed, it may have impacted which diseases should be considered a higher priority for public health action and research in the arctic regions. Finally, only articles that addressed climate change, latitude, and altitude as factors influencing the researched infectious diseases were included. This is considered a limitation because studies could still be relevant without directly mentioning these factors, as they may research climate-sensitive diseases without actually identifying them as such or discussing climate/environmental factors involved. In addition, by only requiring the brief mention of climate and environmental factors, many studies discussed their theories of how these factors would impact diseases based on previous research performed in other studies or their own general observations. Future reviews may focus on studies that analyze measured relationships between climate or environmental factors and infectious diseases.

CHAPTER 6: IMPLICATIONS/RECOMMENDATIONS

This systematic review investigated the existing body of literature to assess what infectious diseases were reported in the circumpolar regions and how changes in climate and environmental factors impacted their dynamics with host and vector populations. TBE and Lyme Disease were the most prominent emerging diseases studied in the context of climate change in the Arctic, as rising temperatures promoted more favorable conditions for tick populations to grow and expand their ranges. Anthrax was the main zoonotic disease studied, warned as potentially re-emerging due to thawing permafrost exposing rural communities to pristinely preserved spores. Certain parasitic diseases, such as those also classified as neglected tropical diseases, were limited in the results, despite previous research indicating establishment in circumpolar regions. Antimicrobial-resistant and fungal pathogens were briefly discussed as potential emerging threats due to climate change promoting particular advantageous adaptations.

On the global scale, the health trends and disparities experienced in circumpolar health should be added to the global health objective. Because circumpolar regions are projected to be the most impacted by the effects of climate change (AMAP, 2017), more research must be targeted towards these areas to address the potential emergence and re-emergence of specific diseases in these regions, increase public awareness of these diseases, and adequately prepare communities to control such threats to circumpolar health. As mentioned by Chatwood in their 2012 article, “global health concerns do not stop at high latitudes.”

Indigenous leaders have started to be included in the greater conversation about the environmental and health effects of a changing climate in the Arctic, but overall involvement is limited (Ford, 2012; IPCC, 2019). The inclusion of indigenous voices in these conversations needs to increase in all circumpolar countries, not just those most actively involved like Canada or the United States. This would also help ensure that future response efforts would no longer fail to consider how the historical marginalization of indigenous communities causes health disparities. Indigenous communities should be offered more opportunities and spaces to share what actions are needed from national and international health systems, associations, and working groups to support their livelihoods and improve health outcomes.

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