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Temperature Anomaly and Vector-Borne Disease Incidence

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Abstract
This study looks into whether three common vector-borne diseases, such as malaria, dengue fever, and Lyme disease, are connected to temperature anomaly, with an emphasis on high-incidence areas. First, malaria study findings reveal a significant positive association between disease prevalence and temperature anomaly in a sample of the seven most common countries in the Sahara desert and portions of Oceania. Second, study results for dengue fever show a strong positive connection between disease incidence and temperature anomaly, in Asian countries like Vietnam and the Philippines. Finally, research on Lyme disease in the United States indicates that there is a significant positive association between temperature anomaly and disease incidence not just in high-incidence areas, but also in neighboring states. In conclusion, temperature anomaly may enhance the incidence of all three infectious diseases investigated in this study, according to the findings.

Key Words: Temperature Anomaly, Vector-borne Disease Incidence, Malaria, Dengue Fever, Lyme Disease

1. Introduction

Infectious diseases and humans have long coexisted. Throughout history, infectious illness epidemics have been recorded. Man has attempted to understand the natural causes and risk factors that influence the patterns of sickness and mortality in society since the dawn of time. [1] Since the 2000s, the types of infectious diseases have been increasing significantly. Not only have the varieties of infectious illnesses risen in the 2000s, but the occurrence cycle has also shortened. Globally, infectious diseases such as SARS (2002), Influenza A (2009), MERS (2012), Ebola Virus (2014), Zika Virus (2015), and COVID19 (2019) have emerged. Rising temperatures have produced an atmosphere conducive to the development of infectious illnesses. According to the World Health Organization (WHO), 150,000 people worldwide died due to infectious diseases caused by climate change in the 2000s.
Particularly, due to the recent shock of the global pandemic of COVID19, interest in countermeasures for emerging diseases likely to cause major epidemics is increasing significantly. Some countries are still experiencing mortality from the coronavirus owing to a lack of early countermeasures, and to make matters worse, mutant viruses are constantly appearing. Countermeasures against COVID19 have being investigated by G7 (Group of Seven) countries. Predicting when a pandemic will occur again, or the mediator that causes a pandemic, is a critical environmental problem.

Human health is inextricably connected to climate change. This results in heat stroke, respiratory illnesses as a result of air pollution, nutritional problems as a result of food scarcity, and the spread of infectious diseases as a result of vector habitat changes. [2] Bill Gates, who foresaw the coronavirus's spread, recently underlined the need of responding to climate change. Climate change, such as global warming, he believes, will be more dangerous than the coronavirus. The expansion of invading mosquito species may be exacerbated by global warming. [3, 4, 5, 6, 7]. Mosquitoes are the most hazardous animals to humans, according to data supplied by the Bill & Melinda Gates Foundation. As global warming occurs, infectious diseases derived by vectors such as mosquitos and ticks are spreading around the world. Such vectors are the only animals that can transmit arboviruses to vertebrates by sucking blood. [8] Malaria and dengue virus are two examples of deadly infectious illnesses spread by such vectors (725,000 fatalities in 2015, the Bill and Melinda Gates Foundation). Additionally, Lyme disease-causing ticks are on the rise. Lyme disease has long been widespread in North America, but Lyme disease is becoming more prevalent in many regions of the globe. In this aspect, this study aims to prove that when a climatic anomaly occurs, the likelihood of typical vector-borne illnesses like malaria, dengue fever, and Lyme disease increases, as does the region where the germs spread.
The rest of this paper is organized as follows. Section 2 covers theoretical background, literature review, and hypothesis development. The study samples and methods are discussed in Section 3. The results are addressed in Section 4. The discussion and conclusion are covered in the last section.

2. Theoretical Background, Literature Review, and Hypothesis Development

The earth's average temperature has increased by 1°C from pre-industrial periods (1880-1900), and by 0.8°C in the previous ten years. Figure 1 shows 'History of global surface temperature since 1880'. The surface temperature in 2020 was 1.76 degrees Fahrenheit (0.98 degrees Celsius) warmer than the twentieth-century average of 57.0 degrees Fahrenheit (13.9 degrees Celsius) and 2.14 degrees Fahrenheit (1.19 degrees Celsius) warmer than the pre-industrial period (1880-1900). Although the rise in global average surface temperature from the pre-industrial era (1880-1900) may appear little, it reflects a significant increase in stored heat. According to NOAA (National Oceanic and Atmospheric Administration)'s temperature data, 2020 was the second-warmest year on record. [9]

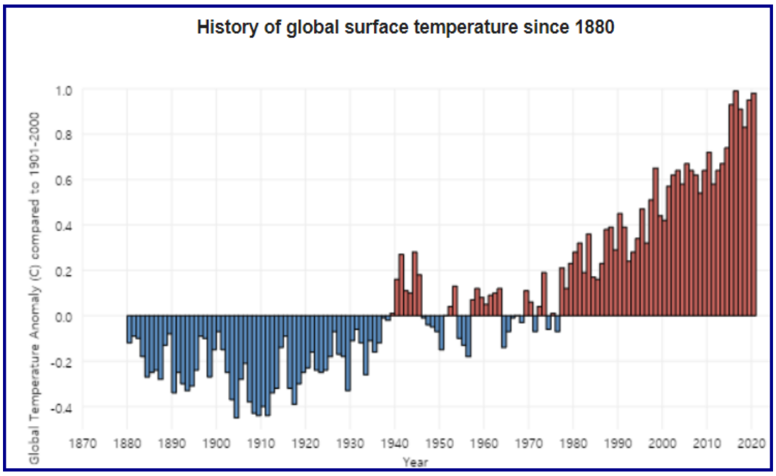

Figure 1. Climate Change: Global Temperature. [9]
Data source: https://www.climate.gov/news-features/understanding-climate/climate-change-global-temperature

Figure 2 also illustrates global warming relative to 1850–1900 and demonstrates how human-caused climate change will affect the planet in the 2100s. It is forecasted the global impact of anthropogenic carbon dioxide emissions on climate change, in Figure 2.

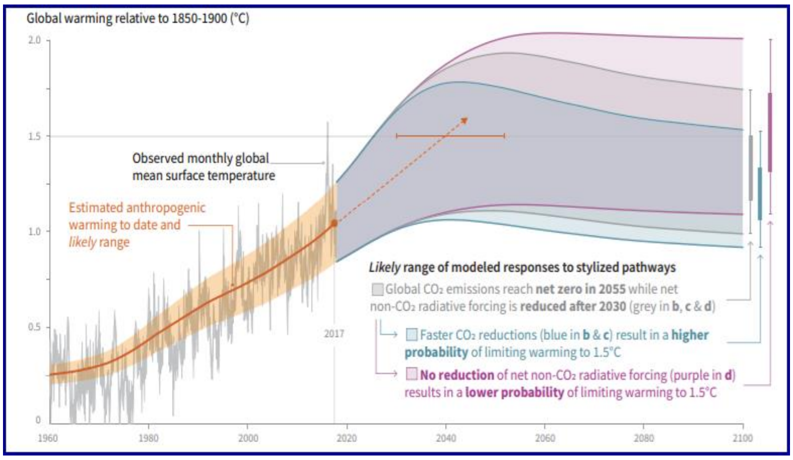

Figure 2. Global warming relative to 1850–1900, from the Intergovernmental Panel on Climate Change (IPCC) 2018 summary for policymakers. [11]
Data source: https://www.ipcc.ch/sr15/chapter/spm/

Tropical mosquitoes' habitat is growing as a result of global warming, and mosquito-borne viruses are spreading as well. Climate change is a significant factor, since global warming can exacerbate the spread of invading mosquito species and viral transmission dynamics. [5, 6, 7]. Accordingly, there has been growing interest in the impact of warming on the virus's transmission.

Arboviral disease issues, both old and new, are becoming more common and more severe. [8] In the early 1940s, scientists in California coined the name "arbovirus". [10] Among such arboviruses, West Nile virus, Japanese encephalitis, and dengue fever are all still present and can be fatal. And mosquitoes are carriers of a variety of arboviruses. [12] According to the Bill and Melinda Gates Foundation, 725,000 individuals died of encephalitis, malaria, and dengue fever after being bitten by mosquitos (as of 2015). This statistic is higher than the total number of humans killed by war and violence, which includes snakes (475,000), dogs (25,000), and crocodiles (1,000). Based on these figures, the most dangerous creatures to humans are mosquitoes.

Mosquitoes, the malaria vectors, require enough precipitation to survive, and protozoa, which cause fever in mosquitoes, require appropriate temperatures to produce fever (Centers for Disease Control and Prevention, 2018). When the weather is too cold, mosquitoes, like other insects, cannot develop into larvae. "However, as the days become warmer, the female mosquito takes blood more frequently and digests it more quickly." The fact that the more mosquitoes there are, the greater the temperature, explains why it works. [3] Global warming has caused the 'mosquito' to thrive in the Himalayas, as a result, infectious illnesses such as malaria and dengue fever afflict local populations. The likelihood of mosquito survival improves by 53% if the Arctic temperature climbs by 2 degrees Celsius. [4] Because mosquito vectors transmit infectious illnesses like malaria and dengue fever, the more conductive an environment for mosquitos is established, the greater the risk of infection with these diseases. [13] Malaria, the most common mosquito-borne disease, is being expanded as a result of climate change. An estimated 50 million more malaria cases are predicted by 2100. [14]

Figure 3 depicts a rough map of where malaria transmission occurs across the world. The region with the highest transmission rates is south of the Sahara and in parts of Oceania. Malaria distribution is largely determined by environmental conditions such as temperature, humidity, and rainfall. Malaria is spread in tropical and subtropical locations where -Anopheles mosquitos may survive and reproduce, and -Malaria parasites are able to complete their life cycle in mosquitos. [15]

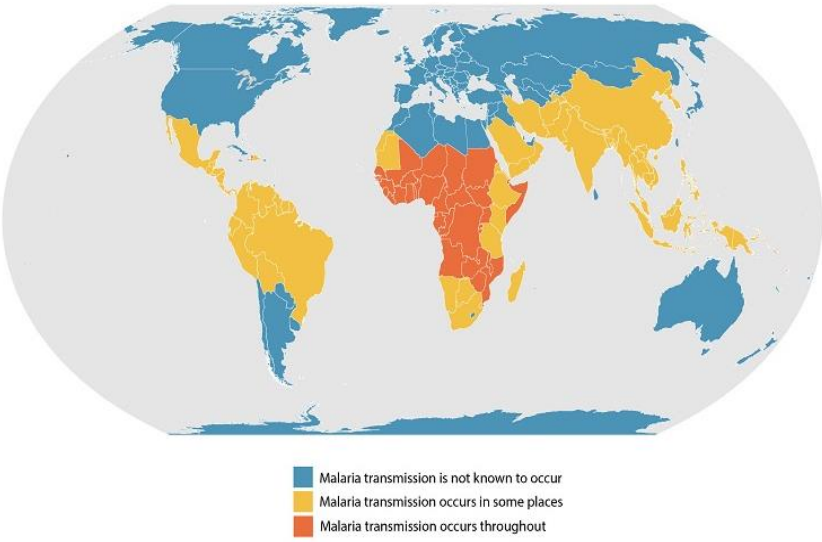

Figure 3. Where Malaria Occurs. Data source: https://www.cdc.gov/malaria/about/distribution.html

Another vector-borne illness worth noting is dengue fever. Figure 4 shows the dengue virus transmission route map in Guangzhou in 2018, which was created using paleogeography analysis. DENV-1 clusters are shown by red curves, whereas DENV-2 clusters are represented by blue curves, indicating the propagation path. The red flags represent various places, and the time accompanying the curves denotes the time period in which the viral strain is introduced.

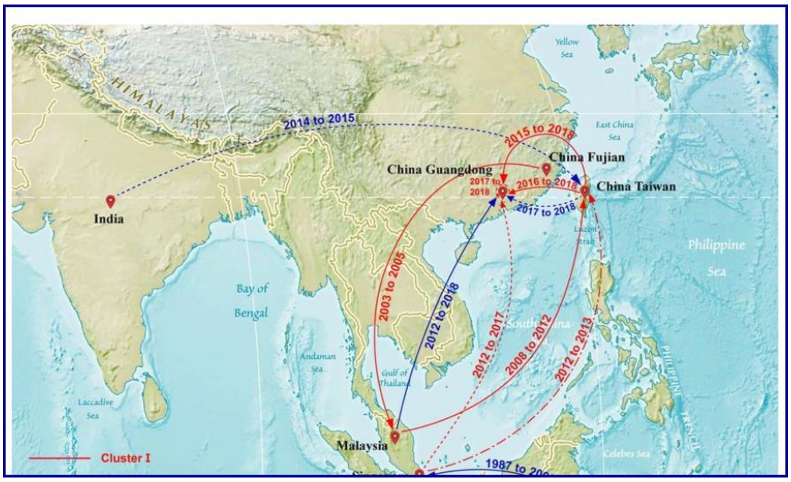

Figure 4. Molecular epidemiological characteristics of dengue virus carried by 34 patients in Guangzhou in 2018. [16] Data source: http://dx.doi.org/10.1371/journal.pone.0224676

According to the climate change scenario presented in the Intergovernmental Panel on Climate Change (IPCC) report, the habitat of Aedes albopictus will expand to around 2050 and Aedes aegypti - the main medium for the transmission of dengue fever would spread to most temperate zones by 2080. It is predicted as in Figure 5.

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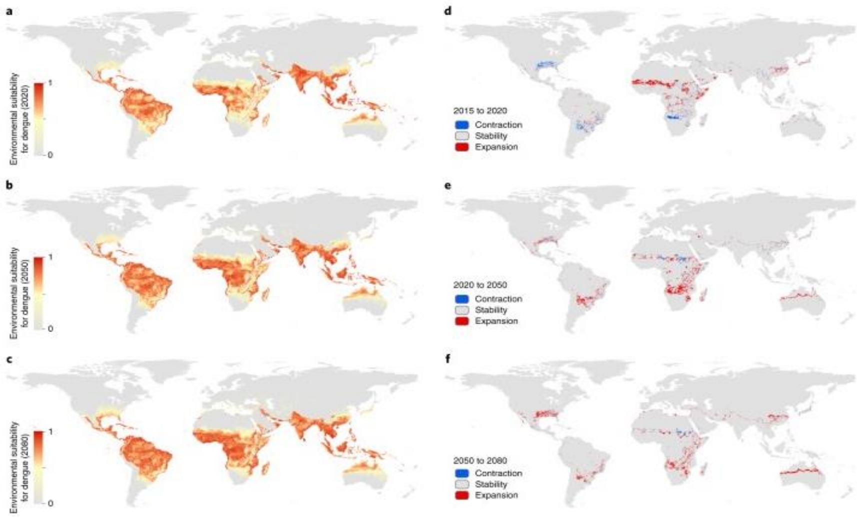

Figure 5. Predicted distribution of dengue from 2015-2080 based on socioeconomic and environmental projection scenarios. Data source: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6784886/

Aside from mosquitoes, ticks are another threatening source of infection from global warming. Lyme disease, a disease transmitted by ticks, has long been known to be endemic in the northeastern United States, but tick-borne diseases are becoming increasingly common in many parts of the world. The Centers for Disease Control and Prevention (hereafter, CDC) estimates that around 400,000 cases of Lyme disease occur each year. They've just updated that number to around 476,000, and some analysts believe it could top 500,000 in 2021. Then, why is Lyme disease becoming more prevalent? Climate change, particularly changes in temperature and humidity, may have had an impact. [17] By the mid-century (2036–2065), increasing temperatures will have increased the number of Lyme disease cases by more than 20%. [18] As seen in Figure 6, Lyme disease is prevalent in more than 80 countries across the world and 50 states in the United States, however different types of ticks and bacterium strains may be implicated. The darker the hue, the greater the number of cases. In unfilled countries or regions, no cases have been documented. [19] Despite the fact that it is found in other nations, it can be seen that infection cases are concentrated in North America.

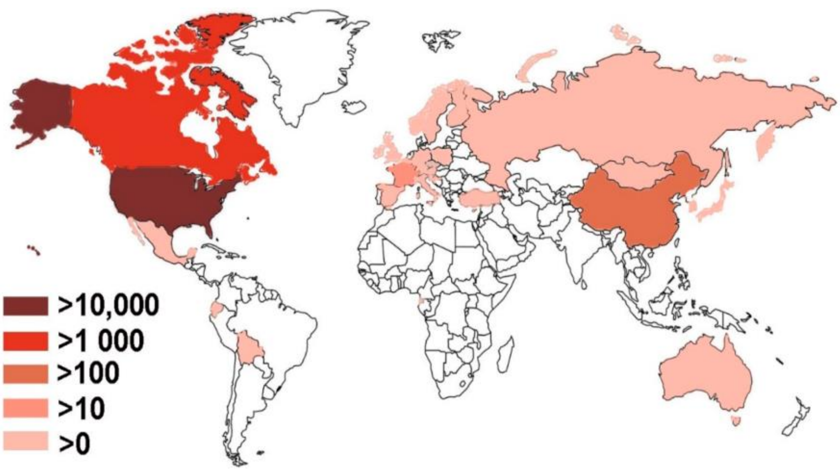

Figure 6. Lyme disease global distribution map. [19]
Data source: https://lymediseaseassociation.org/about-lyme/other-tick-borne-diseases/a-review-of-human-babesiosis/

According to the findings of the aforementioned research, this study investigates the impact of temperature anomaly on the vector-borne disease incidence. Therefore, the following hypothesis is established in this study.

Hypothesis: There is a positive relationship between temperature anomaly and vector-borne disease incidence.

3. Research Design

3.1. Sample Selection

This study makes use of weather data from NOAA (National Ocean and Atmosphere Organization, https://ncdc.noaa.gov/cdo-web/). [20] The data on vectors is obtained from the MAP (The Malaria Atlas Project, https://malariaatlas.org/), [21] the Global Health Data Exchange GBD Results Tool (http://ghdx.healthdata.org/gbd-results-tool), [22] and CDC (The Centers for Disease Control and Prevention, https://www.cdc.gov/lyme/stats/tables.html). [23]
Areas with a high incidence of infectious illnesses are considered in this study. Data for 30 countries are used for the Malaria research, with a special focus on South of the Sahara desert and in parts of Oceania, the region with the greatest transmission rates. Seven countries from regions of special interest include: Burkina Faso, Democratic Republic of the Congo, Mozambique, Nigeria, Uganda, Papua New Guinea, and Solomon Island. For dengue research, the five most common countries are used. Brazil, Viet Nam, Peru, Philippines, and France are the countries involved.
Tick-borne illnesses are growing more widespread in many regions of the world, but they are particularly prevalent in the northeastern United States. Accordingly, research on Lyme disease is limited to the United States. Table 1 displays the samples used for this study.

Table 1. Study Samples

Disease (Period)	Countries
Malaria (2000-2019)	**Burkina Faso, Democratic Republic of the Congo**, Eritrea, **Mozambique, Nigeria**, Somalia, Sudan, **Uganda**, Georgia, Turkey, Afghanistan, Bangladesh, Cambodia, India, Indonesia, Kyrgyzstan, Laos, Myanmar, Pakistan, Thailand, Turkmenistan, Uzbekistan, Vietnam, **Papua New Guinea**, **Solomon Island**, Brazil, Columbia, Guyana, Peru, Venezuela
Dengue fever (2000-2019)	Brazil, Viet Nam, Peru, Philippines, and France (+ Global)
Lyme Disease (2008-2019)	USA (50 states)

3.2. Regression Model and Variable Measurement

Hypothesis is examined using the following Ordinary Least Squares (OLS) regression model:

$$INCID_{i,t} = \alpha + \beta_1 ANOMALY_{i.t} + \sum\alpha_j COUNT\ (STATE)_j + \sum\alpha_k YEAR_l + \varepsilon_{i,t} \quad (1)$$

$INCID_{i,t,}$ a dependent variable, denotes incidence of infectious diseases. Malaria and dengue data provide the number of occurrences, so natural logarithms are taken for them. In the case of Lyme disease, it refers to confirmed cases per 100,000 people. $ANOMALY_{i.t}$ is a proxy for climate change. A temperature anomaly is a deviation from the average temperature (1910-2000 base period). NOAA

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indicates, **"**In climate change studies, temperature anomalies are more important than absolute temperature. A positive anomaly indicates the observed temperature was warmer than the baseline, while a negative anomaly indicates the observed temperature was cooler than the baseline (https://www.ncdc.noaa.gov/monitoring-references/dyk/anomalies-vs-temperature)." COUN (STATE) represents the country (state, in the case of US) dummy variable, and YEAR represents the year dummy variable.
Meanwhile, the CDC has classified Lyme disease into three groups based on its occurrence in the US: high incidence, neighboring, and low incidence. 14 states with a high incidence includes the followings: Connecticut, Delaware, Maine, Maryland, Massachusetts, Minnesota, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island, Vermont, Virginia, and Wisconsin. 11 neighboring states includes the followings: Illinois, Indiana, Iowa, Kentucky, Michigan, North Carolina, North Dakota, Ohio, South Dakota, Tennessee, and West Virginia. The remaining 25 states are classified as low incidence areas. Based on this categorization, the following analytical model is employed for further Lyme disease research.

$$\mathrm{INCID}_{i,t} = \alpha + \beta_1 \mathrm{Hano}_{i.t} + \beta_2 \mathrm{Nano}_{i.t} + \beta_3 \mathrm{Lano}_{i.t} + \sum \alpha_k \mathrm{YEAR}_l + \varepsilon_{i,t} \qquad (2)$$

Hano is ANOMALY for the states with high incidence. Nano is ANOMALY for the states classified as neighboring. Lano is ANOMALY for the states with low incidence

4. Empirical Results

4.1. Descriptive Statistics

Table 2 presents descriptive stats for each variable. The mean (median) INCID for the malaria sample is 5.5025 (5.4289), whereas the mean (median) INCID for the dengue sample is 20.6201 (19.9151), and the mean (median) INCID for the Lyme disease sample is 12.1528 (0.4500). The mean (median) ANOMALY for the malaria sample is 1.0603 (1.0300), whereas the mean (median) ANOMALY for the dengue sample is 1.0172 (0.9650), and the mean (median) ANOMALY for the Lyme disease sample is 1.5140 (1.5000).

<Table 2> Descriptive Statistics

Vector	Variables	Mean	StdDev	Median	Q1	Q3
Malaria	*INCID*	5.5025	3.1544	5.4289	3.5609	7.5205
	ANOMALY	1.0603	0.3285	1.0300	0.8300	1.2450
Dengue	*INCID*	20.6201	1.7574	19.9151	19.5834	20.9515
	ANOMALY	1.0172	0.3495	0.9650	0.7600	1.2200
Lyme	*INCID*	12.1528	22.9549	0.4500	0.1000	12.6000
	ANOMALY	1.5140	1.4868	1.5000	0.4500	2.6000

Note.
INCID : incidence of infectious diseases (for Lyme, confirmed cases per 100,000 people; for others, natural logarithms of occurrences)
ANOMALY : climate change (a deviation from the average temperature (1910-2000 base period)

4.2 Regression Results

The results of the OLS regression for the relationship between temperature anomaly and the incidence of Malaria are shown in Table 3. As can be seen in Panel A of Table 3, the results in Model 2 suggest that malaria incidence in the sample of the seven most common countries in South of the Sahara desert and in parts of Oceania has a significant positive relationship with temperature anomaly ($p < 0.05$). Model 1 displays a positive association between malaria incidence and temperature anomaly for the whole sample of 30 countries, albeit it is not statistically significant. Robust regression results in Panel B remained consistent with the OLS results. Incidence of malaria in the sample of the seven most common countries is significantly positively associated with temperature anomaly ($p < 0.1$).

<Table 3> Regression results: Temperature Anomaly - Incidence of malaria

Panel A. OLS

Variables	Expected Sign	Dependent Variable: *Incidence of malaria* Model 1 (30 countries)	Model 2 (Seven most common counties)
Constant	?	4.3787 *** (9.02)	5.0911 *** (8.22)
ANOMALY	+	**0.2690 (0.56)**	**1.5536 ** (2.07)**
Country dummies		Included	
Year dummies		Included	
F value		*16.80* ***	*13.11* ***
R^2		*0.3678*	*0.6463*
N		*509*[1]	*140*

Panel B. Robust

Variables	Expected Sign	Dependent Variable: *Incidence of malaria* Model 1 (30 countries)	Model 2 (Seven most common counties)
Constant	?	4.3787 *** (9.57)	5.0911 *** (7.24)
ANOMALY	+	**0.2690 (0.54)**	**1.5536 * (1.89)**
Country dummies		Included	
Year dummies		Included	
F value		*310.03****	*147.43****
R^2		*0.3678*	*0.6463*
N		*509*	*140*

Note.
See Table 2 for variable definitions.

[1] Missing data were generated during log transformation, in areas where the number of occurrences is zero.

t-values are shown in parentheses. * $p < 0.10$ ** $p < 0.05$ *** $p < 0.01$

Table 4 shows the findings of the dengue fever research for the global sample and each of the most common five countries sample. As can be seen in Panel A of Table 4, there was a significant positive association between dengue epidemic and temperature anomaly in Asian nations, including Vietnam and the Philippines ($p < 0.1$ and $p < 0.05$, respectively). There is a positive link between dengue epidemic and climatic anomaly in global and other national samples, however it is not significant. Robust regression results in Panel B remained consistent with the OLS results.

<Table 4> Regression results: Temperature Anomaly - Incidence of dengue fever

Panel A. OLS

Variables	Expected Sign	Dependent Variable: *Incidence of dengue fever* Model 1 (Global)	Model 2 (Brazil)	Model 3 (Viet Nam)	Model 4 (Peru)	Model 5 (Philippines)	Model 6 (France)
Constant	?	24.1464*** (331.72)	20.8476*** (418.24)	19.6746*** (603.10)	18.8801*** (397.85)	19.8808*** (408.87)	19.5229*** (646.43)
ANOMALY	+	**0.1634 (1.33)**	**0.0738 (1.03)**	**0.0655* (2.36)**	**0.0396 (0.58)**	**0.1143** (2.76)**	**0.0242 (0.86)**
Year dummies		Included					
F value		*9.57* ***	*4.62* ***	*9.55* ***	*15.19* ***	*15.90* ***	*3.34* ***
R^2		*0.9425*	*0.8879*	*0.9424*	*0.9630*	*0.9646*	*0.8512*
N		*20*	*20*	*20*	*20*	*20*	*20*

Panel B. Robust

Variables	Expected Sign	Dependent Variable: *Incidence of dengue fever* Model 1 (Global)	Model 2 (Brazil)	Model 3 (Viet Nam)	Model 4 (Peru)	Model 5 (Philippines)	Model 6 (France)
Constant	?	24.1464*** (283.48)	20.8476*** (302.27)	19.6746*** (515.35)	18.8801*** (343.44)	19.8808*** (346.32)	19.5229*** (498.01)
ANOMALY	+	**0.1634 (1.20)**	**0.0738 (0.78)**	**0.0655* (2.20)**	**0.0396 (0.54)**	**0.1143** (2.36)**	**0.0242 (0.58)**
Year dummies		Included					
R^2		*0.9425*	*0.8879*	*0.9424*	*0.9630*	*0.9646*	*0.8512*
N		*20*	*20*	*20*	*20*	*20*	*20*

Note.
See Table 2 for variable definitions.
t-values are shown in parentheses. * $p < 0.10$ ** $p < 0.05$ *** $p < 0.01$

The Lyme research is based on samples from the United States, which has the greatest prevalence of the

Lyme disease. The CDC has defined three categories of Lyme disease in regard to the incidence of Lyme disease in the US: high incidence, neighboring, and low incidence. Before performing the regression analysis, a time series graph analysis is conducted to check whether there are any distinctions between the three groups at a glance. Figure 7 shows mean annual flow of Lyme incidence by each classification. The variation of annual mean Lyme incidence appears to be considerable only in the high incidence region.

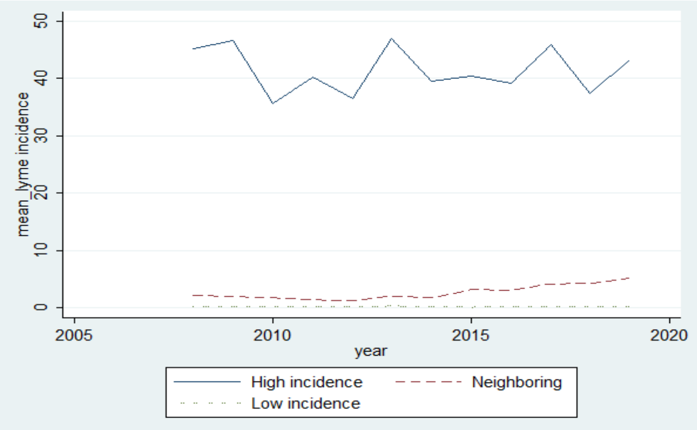

Figure 7. Time series of annual mean Lyme incidence for the three classifications

Figure 8 depicts mean annual flow of temperature anomaly by each classification. The yearly mean anomaly fluctuation range is significant in all three classes. Mean incidence and mean anomaly both exhibit substantial changes in the high incidence region, with a similar pattern of movement. As a result, in the high-incidence states, there appears to be a link between Lyme disease incidence and temperature anomaly.

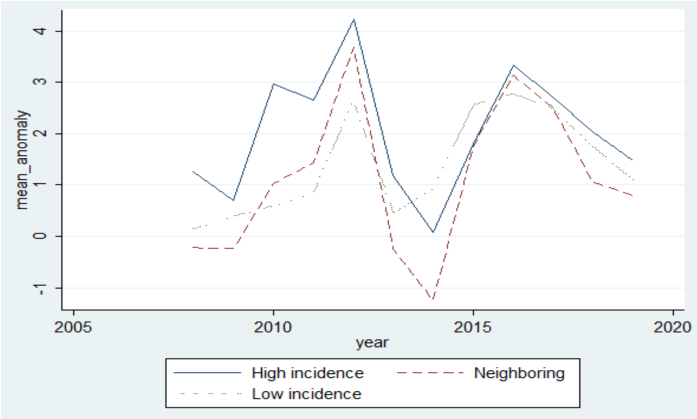

Figure 8. Time series of annual mean anomaly for each of the three classifications

Table 5 shows regression results for Lyme disease. For the whole US sample, model 1 finds no significant connection between temperature anomaly and Lyme disease. This research also examines Lyme disease using the CDC's three categories. The results in Model 2 suggest that incidence of Lyme disease in states with a high incidence has a significant positive relationship with temperature anomaly ($p < 0.01$). Additionally, the robust regression findings show a significant positive relationship between incidence of Lyme disease and temperature anomaly in both categories, encompassing 14 states with high incidence and 11 neighboring states ($p < 0.01$ and $p < 0.1$, respectively).

<Table 5> Regression results: Temperature Anomaly - Incidence of Lyme disease

Panel A. OLS

Variables	Expected Sign	Dependent Variable: *Incidence of Lyme disease*	
		Model 1 (US -50 states)	Model 2 (three CDC classifications)
Constant	?	1.1383 (0.40)	8.5035 *** (3.99)
ANOMALY	+	**-0.1149 (-0.29)**	-
Hano	+	-	**13.6695 *** (17.70)**
Nano	+	-	**1.1154 (1.12)**
Lano	?	-	**-0.9292 (-1.17)**
State dummies		Included	-
Year dummies		Included	
F value		*58.21* ***	*33.78* ***
R^2		*0.8689*	*0.4522*
N		*588*[2]	*588*

Panel B. Robust

Variables	Expected Sign	Dependent Variable: *Incidence of Lyme disease*	
		Model 1 (US -50 states)	Model 2 (three CDC classifications)
Constant	?	1.1383 (0.78)	8.5035 *** (3.47)
ANOMALY	+	**-0.1149 (-0.32)**	-
Hano	+	-	**13.6695 *** (14.37)**
Nano	+	-	**1.1154 * (1.77)**
Lano	?	-	**-0.9292 (-1.65)**
State dummies		Included	-
Year dummies		Included	
F value		*42.23* ***	*21.66* ***

[2] Except for Hawaii, which has no temperature anomaly data, only data from 49 states over a 12-year period is included.

R^2	*0.8689*	*0.4522*
N	*588*	*588*

Note.
Hano :*the interaction between ANOMALY and the high incidence dummy variable*
Nano :*the interaction between ANOMALY and the neighboring dummy variable*
Lano :*the interaction between ANOMALY and the low incidence dummy variable*
See Table 2 for other variable definitions.
t-values are shown in parentheses. * $p < 0.10$ ** $p < 0.05$ *** $p < 0.01$

5. Discussion and Conclusion

This study investigated whether three common vector-borne illnesses, such as malaria, dengue fever, and Lyme disease, were linked to temperature anomaly, with the focus mostly on high-incidence regions. The findings were not different from those that could be inferred from the incidence rate alone.
First, malaria research findings displayed a significant positive relationship between occurrence of disease and temperature anomaly in the sample of the seven most common countries in South of the Sahara desert and in parts of Oceania. Second, analysis results for dengue fever revealed a significant positive link between disease occurrence and temperature anomaly in Asian nations such as Vietnam and the Philippines. Finally, according to the findings from Lyme disease research, occurrence of Lyme disease in 14 states with a high incidence had a significant positive association with anomaly. Additional robust regression analysis confirmed that there was a significant positive correlation between temperature anomaly and disease occurrence not only in 14 high incidence states, but also in 11 neighboring states. Taken together, the findings imply that climate change may be influencing the increase in all three vector-borne diseases studied.
Previous research has indicated that rising temperatures can lead to an increase in infectious diseases, but this study backs up that hypothesis by looking at the direct link between the prevalence of three main vector-borne diseases and temperature anomalies. Other factors that could affect the emergence of infectious diseases besides temperature rises were not examined due to data collecting constraints, despite the fact that the outcome is meaningful. It is hoped that the next research would address these flaws and provide a more in-depth analysis. The findings raise awareness yet more. It serves as a reminder that, as stated in the introduction, the growing vector-borne diseases caused by global warming are the most dangerous to humans. It will be necessary to do ongoing research into countermeasures to global warming and the possible ailments that it may bring.

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