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Leslie Waller Date

Exploratory Analysis of Climate Drivers of *Vibrio vulnificus* Wound Infections in the Southeastern US

By

Leslie Waller
Master of Public Health

Environmental Health

_____

Jeremy Hess, MD MPH
Committee Chair

_____

Jesse Bell, PhD
Committee Member

_____

Paige Tolbert, PhD
Committee Member

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By

Leslie Waller

B.A., B.A., University of Tennessee, 2011

Thesis Committee Chair: Jeremy Hess, MD MPH

An abstract of
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Abstract

Exploratory Analysis of Climate Drivers of *Vibrio vulnificus* Wound Infections in the Southeastern US

By Leslie Waller

Introduction: Vibrio vulnificus is a gram-negative marine bacteria that causes gastroenteritis and skin and soft tissue infections through exposure of open wounds to sea water. The infection is known as a seasonal infection, with cases peaking in the late summer. Due to the pathogens affinity for brackish and salty warm water, there is much concern surrounding the impacts of climate change on its behavior and likelihood of cases to increase. This research aims to test associations between environmental parameters and reported cases of *v. vulnificus* skin and soft tissue infections.

Methods: Poisson time series regressions were used to test precipitation and maximum daily temperature as predictors of cases at different lag times. Cases were mapped and analyzed using Local Moran's I and kernel density functions to assess clusters of cases.

Results: Precipitation was only rarely significant, whereas temperature was significant in most models. Three full models were significant: Mississippi and Florida at the 5 day lag time, and Alabama at the 30 day lag time.

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Table of Contents

Introduction

Substantial amount of scientific evidence shows that global climate change is occurring, with widespread impacts on hydrological, geological, and atmospheric systems [1-3]. With these broad impacts, there is concern that climate change may be altering the ecology of disease-causing pathogens on a large scale[4]. Diseases like dengue, chikungunya, and malaria have been affected by climatic changes in regional ecology in ways that allow vectors and pathogens to capitalize on changing environmental factors like higher rainfall amounts and longer hot periods to further spread disease in human populations [5-6]. Researchers in the areas of new and emerging infectious diseases are particularly keen to investigate changes in climate and the subsequent environmental fluctuations on disease ecology as the consequences of these changes can be widespread and expensive [7]. This type of research will be even more pertinent as changes in climate progress.

An important aspect of this research is investigating the extent to which the environment may impact disease proliferation. One pathogen that appears to be mediated by environmental factors is *Vibrio vulnificus,* a member of the genus of the pathogen that causes cholera[8]. *The* genus *Vibrio* is also known for foodborne outbreaks related to oysters and other raw shellfish due mainly to *Vibrio vulnificus* and *Vibrio parahaemolyticus* [9]. Both of these species prefer warm marine and brackish waters, and have demonstrated survivability in sediment, aquatic plants, fish, shellfish, and as free-floating organisms during warmer months and in salinity ranges of [10-12]. However, *V. vulnificus* has the distinguishing characteristic of readily causing skin and soft-tissue infections in humans as a result of open wound exposure in the setting of habitats where the bacteria occur naturally [13, 14].

These skin infections have been documented in the media as the 'flesh-eating bacteria' since the hallmark symptom is necrotizing fasciitis of the infected area [15, 16], which sometimes leads to limb amputation [13]. Other common symptoms include septicemia, fever, nausea, vomiting, and organ failure [13]. Individuals are much more likely to develop an infection if they have one of several preexisting conditions, including hepatic or renal diseases, or alcoholism[17]. Upon exposure, cases typically develop symptoms within 48 hours, but often sooner and sometimes within just a few hours. From there, infected cases must seek prompt medical attention because these infections progress rapidly and have led to death within 2 days of being exposed for some people [13, 17]. *Vibrio vulnificus* has a high mortality rate for its skin infections, estimates of which have been reported around 20%[18]. Three biotypes of the pathogen exist: A, B, and AB, where B is the most virulent in humans [10]. The mechanism by which the bacteria infect humans is the release of an RTX toxin upon contacting endothelial cells [19]. Additionally, *v. vulnificus* has dual morphology, which is a hypothesized mechanism by which it survives in sediment or aquatic plants in suboptimal environmental conditions like lower water temperatures [20].

Many *in situ* studies have shown the association of higher temperatures and a wide range of salinities with greater *v. vulnificus* survival, which has also been repeated in laboratory settings [21-24]. Cases of reported vibriosis, the resulting illness from infection with a member of vibrio genus, also peak in warm summer months, further suggesting that the presence of *v. vulnificus* increases when environmental conditions are prime [9] (Figure 1). As it becomes more critical to understand the impacts of a changing climate on human health, the body of knowledge and data on

v. vulnificus is growing so that further research can be done to test its significance to human health as well as using it as a case study for impacts resulting from climate change. The National Climate Assessment also calls for increased surveillance of *v. vulnificus* as its affinity to cause skin and soft tissue infections could act as an indictor of climate change, particularly warming oceans[25]. The Centers for Disease Control and Prevention (CDC) began mandated reporting of all cases of vibriosis beginning in 2007; the data set currently extends to 2012. Additionally, environmental and climate change data exist for the entire timeframe of the data set which allows for associations between reported cases and various environmental parameters to be drawn.

Methods

The goal of this exploratory analysis was to evaluate postulated associations between several environmental factors known to be important to *v. vulnificus* ecology and skin and soft tissue infections acquired in the organism's natural environment in the coastal areas of the Southeastern United States using Poisson time series regressions. We hypothesized that cases would be significantly associated with temperature at the location of exposure at the shorter lag times of 0, 3, and 5 days while precipitation would be significantly associated with cases at longer lag times of 15, 30, and 45 days. We also hypothesized that precipitation would be an adequate proxy for water salinity since this data was unavailable. The research also investigated demographic trends in the data set using univariate and multivariate analyses, and cluster density analysis of cases throughout the study

area. It was hypothesized that cases would be clustered in areas where large estuaries and freshwater inflows were present.

Data Sources and Preparation

Two data sets were used in this analysis. One is the Cholera and Other Vibrio Illness Surveillance (COVIS) data set, which contains demographic, health, and medical information on the reported cases. The second is the Daily Global Historical Climatological Network (GHCN-D), which contains meteorological and climatological variables. The COVIS data set includes variables on cases, locations of exposure, type of exposure, water type associated with each exposure in each case, preexisting conditions, employment, age, sex, and how they were exposed. Exposure type includes fish, boats, sediment, water, and other aquatic life. The information contained within is self-reported data that was collected by a state or local public health official, and it was common for some information to be omitted for variables throughout the data set, according to no theme. Environmental parameters were downloaded from the National Oceanic and Atmospheric Association's (NOAA) National Climatic Data Center's (NCDC) Daily Global Historical Climatological Network (GHCN-D)[26], an online database of regularly acquired daily readings. State and county level daily environmental parameters were sourced, and only stations within each of these boundaries reporting readings at least 80% of the time during the study period were used in the analysis. More specifically, state level data had to be downloaded from NCDC, then averaged from all weather data stations from the state. This was performed using Microsoft Excel 2013 (Redmond, Washington). Both

of these data sets were then merged in Excel at their respective dates within the study timeframe and given an ObjectID and daily case count.

Data Analysis

Univariate and multivariate analyses were done for exploratory analysis of the data. Cases were mapped to visualize locations and visually assess regional distributions, as well as to analyze case densities and spatial autocorrelation. Lastly, a Poisson time series analysis was conducted to analyze the association between environmental parameters and cases.

Using SAS 9.4 (Cary, NC), case data were described based on sex, age, how the case was infected, whether it was a recreational or occupational exposure, and pre-existing conditions with frequency tables and univariate analyses. Cases were mapped using ArcGIS 10.2 (Redlands, CA) using reported locations of the exposure that caused the infection, and stratified by year of infection. Cases were visually inspected for their distribution throughout the study area, and case density was analyzed using a kernel density function to assess areas of higher case concentrations. Significant spatial autocorrelations were assessed with a local Moran's I statistic using ClusterSeer (BiomedWare, Ann Arbor, MI).

Multiple environmental parameters were assessed for use in regression models to test associations between reported cases and corresponding environmental parameters at different lag times, including Palmer Drought Severity Index, minimum temperature, maximum temperature, average daily temperature, precipitation, and sea surface temperature. Tests for multicolinearity were performed on these environmental parameters using Pearson's chi-square statistic

to determine if any parameters could be thrown out to prevent over-fitting the models using SPSS 22(Armonk, NY). From this analysis, maximum daily temperature (°C) and daily precipitation (mm) were chosen as two parameters for regression analysis, and daily case counts were regressed against these two parameters. Associations between environmental parameters and reported infections were modeled at the state and county level, and assessed for their significance, model fit, and power using SAS. Models were developed for a variety of lag times that include testing associations with environmental parameters at 3, 5, 15, 30, and 45 days prior to the date of exposure. The 5 different lag structures modeled were chosen based on lab-based revival studies that showed *V. vulnificus* could return from a viable but not culturable state (VBNC) to a culturable state at 3 days after optimal environmental conditions were returned[27]. Therefore, we started with 3 days and went up from there to 45 days, which was selected as an arbitrary cutoff. The interspersed lag times were also arbitrary. Some counties did not have enough data coverage to analyze each lag structure, so in those instances analyses were only run where data allowed, which accounts for the lack of models at the county level. In addition, some counties only had one case, so a regression would not be possible. Zero-inflated Poisson distributions were also performed using the same inputs and the same lag structures to account for low case counts and to test a different model.

Results

General Trends

There were 276 vibriosis cases in total and 182 in the Southeastern US region that were infected with *v. vulnificus* and acquired the infection through wound exposure to environmental media from 2007 to 2012. The analysis went forward with these 182 cases.

Since vibriosis became nationally notifiable to the CDC in 2007, annual reported case counts exhibited an upward trend, with the highest peak in cases reported in 2010, with possible plateauing or slight fluctuations between 2010 and 2012 (Figure 2). Reported monthly case counts stratified by year exhibit increasingly normal distributions as time progresses, with 2010-2012 displaying the most normal distributions (Figure 3). There were some interesting and unsuspected findings regarding case frequency distributions and demographic information. Some months, like June 2012, where relatively high case counts would be expected showed low or no cases reported. Next, 2008 and 2012 had anomalous frequencies of reported cases with 2008 reporting relatively low frequencies across the entire region, and 2012 exhibited the longest season for reported cases. When stratified by year and state, reported case counts had high variability. For example, Alabama and Mississippi had years when they did not report any cases. Other states had wide ranges of frequencies, like Florida with a minimum of 3 cases in 2007 and 2008 to 22 cases reported in 2010. There is no apparent trend in yearly peaks across all states in the region, as each state hits a maximum of annual reported cases in mostly different years (Table 1). Of the cases in the region, 88% of cases in the study area

were males with a mean age of 58.3, in contrast to women who had a mean age of 50.6 (Table 2). The distribution of ages was normal about the mean. 93.9% of cases (171/182) were exposed during recreational activities, predominantly in saltwater followed by brackish water. Lastly, analysis shows that 50.5% of exposures to *vibrio vulnificus* occurred as a result of bodily contact with water, followed by multiple exposure types (33.6%) (Table 3). The locations of the cases are spread from South Texas all the way to Key West and up the Atlantic Coast of Florida, with some areas exhibiting an apparently higher frequency of cases based on significant spatial autocorrelation results (p-value <0.001), indicating significant local clusters of cases (Figure 4). Kernel density analysis also revealed high densities of cases surrounding areas where there are large estuaries and bays relative to areas where these large bodies of brackish water do not exist (Figure 5).

Regression Analysis

Tests for model fit were run in SAS, and statistics for each model had a very high p-value for model fit, indicating that the Poisson distribution was a good fit for the data. Likewise, model diagnostics showed the data were not over- or under-dispersed for any of the states or counties at the various lag times. Zero-inflated poisson model diagnostics were also run, and this distribution was deemed not a good fit for the data.

Analysis of multicolinearity among the environmental parameters showed that nearly all of them were highly correlated, with the exception of maximum temperature and precipitation. The regression models were therefore carried out using just daily maximum temperature and precipitation to test associations with

reported cases of vibriosis through wound exposure to the *vulnificus* species without oversaturating the models (Appendix 1). A total of 151 models were run at the county level and 25 at the state level. No full model was significant at the county level, although temperature was frequently a significant predictor in the models whereas precipitation was only a significant predictor at this finer scale in 11 out of the 151 models. However, temperature was significant at a variety of lag times according to no apparent trend. Two examples categorize the county level results well. Two Texas counties, Harris and Aransas, are located on Trinity Bay and Aransas Bay, respectively. Analysis performed on Harris County showed temperature to be significant at every lag time with no significant precipitation, whereas temperature was only significant in Aransas County at 15 and 45 days and significant precipitation at the 30 day lag time. Second, maximum daily temperature is significant at the 30 and 45 day lag in Orleans County, but is not significant at any lag times in neighboring LaFourche County, just south of New Orleans. This type of pattern, or rather lack thereof, is typical throughout all models in the analysis. At the state level analysis, there were complete models that were significant, namely the Alabama analysis at the 45 day lag time, the Florida analysis at the 5 day lag time, and Mississippi at the 5 day lag time. Only temperature was in the Texas model due to missing precipitation data. Temperature was significant in all state level models except for two, Alabama at the 30 day lag, and Mississippi at the 45 day lag. Also at this level, much like at the county level, models did not demonstrate a clear trend in the significance of the predictors at various lag times.

Discussion

General Trends

This is the first time to our knowledge that the association between incidence of vibriosis resulting from wound exposure to *Vibrio vulnificus* and daily precipitation and maximum temperature has been analyzed.. While some data points were missing in each of the data sets, which made analysis of some features difficult or impossible, there were novel and reaffirming results nonetheless.

Upon deeming vibriosis nationally notifiable from 2007, it could have taken states some time to adjust policies and procedures for compliance with new CDC reporting standards. Missing or contradicting variables for some cases reduced the reliability of the information reported, particularly in the case of the type of water present where the case was exposed, time and date of exposure, and the location of exposure itself. There were also questions of whether increasing frequency of reported cases was due to reporting habits as well. This increase could be due to several reasons, including states adapting to new standards. This is the most likely scenario, and would explain the increasingly normal distributions in monthly data by year.

Alternately, cases are truly increasing, but data from more recent years would need to be added to the data set to give such a statement any power. Even though there are increasing frequencies of reported cases over time, the stratified data by year hold the same seasonal pattern as previously described in the literature, with most

cases reported in warmer months. Additionally, when cases are stratified by year, there are months where no cases were reported. For example, in 2012 there were no cases reported in June throughout the entire region, which is anomalous considering every other year saw between 2 and 10 cases reported in June. Other curious findings are relatively low frequency of reported cases in 2008, and a relatively long season in 2012. Potential factors contributing to these findings include environmental and sociological factors. First, there are a number of parameters not used in this study, like chlorophyll a concentrations in water that could influence the fluctuation in reported cases. 2008 was also the first year of the Great Recession, so it's possible that fewer people took vacations, therefore exposing fewer people to the bacteria.

The analysis reaffirmed findings in previous studies, as well as produced some novel findings. It was interesting to see that a large percentage of cases were males over 55 years old. One study has suggested that estrogen can be protective against *v. vulnificus* infection, providing a possible explanation why men are more likely to be infected[28]. This also brings up questions of interaction between being a male with no significant estrogen, older age and weaker immune systems, and changing environmental factors associated with climate change. It could be possible, and provides an important area of research, that shifting demographics in the face of warmer and longer summers as a result of climate change are impacting frequencies of reported cases of *v. vulnificus.*

Contrary to our assumption that many cases would be occupationally acquired, the vast majority of cases (93.5%) were recreationally acquired. This is

interesting because our data point to older individuals being more susceptible to infection, on average, with a hypothesis regarding this distribution being that many people infected are retired and/or vacationing at the time of infection. The prevalence of saltwater reported at the location of exposure was also surprising, since previous studies have noted that there is an optimal salinity of 10-25 ppt for the bacterium. This salinity level is well below the salinity of typical oceanwater in the Gulf of Mexico[29], insinuating that either the reporting of the water type is sometimes miscategorized, or *V. vulnificus* can live in much higher salinities than previously described. One question that arises from this finding is based on hydrological changes in marine systems when precipitation mixes with oceans. During periods of rain, the salinity levels of the top 2-3 inches of ocean water can drop so low that it can be considered potable[30]. Due to this feature, it may be possible for *vulnificus* to survive in local clusters in open oceans that have high salinities and frequently experience rain.

The climate data sets contained a wealth of information on environmental parameters, although some variables that could have been useful were missing, or some locations had very low reporting frequency. For example, salinity varies greatly even within short distances and by the time of day, so a daily average would not truly capture the salinity at the time and location of an exposure in the COVIS data set. Other desired variables were relative and absolute humidity, chlorophyll a, and sea surface temperature at the state and county level. These variables either did not exist, were not regularly reported enough to run a powerful regression in our specific locations, or would not apply to a state level analysis. In doing the analysis,

precipitation was assumed to be somewhat of a proxy for salinity, since accumulation of rainwater in ocean water can alter salinity.

Analysis

Upon designing the study, it was assumed that precipitation would be a good proxy measure for ocean salinity, since this particular measurement was hard to find at the daily level and salinity frequently changes throughout the day. It was hypothesized that it may take several days for rain upstream to flow to brackish bays and the Gulf of Mexico, making statewide precipitation important to the habitat of *vulnificus*, thereby leading to more reported cases. This was not the case, as most of the models produced showed no significance for precipitation at the state or county level.

The fact that significance of the models at the various lag structures adheres to no apparent pattern was another surprising result of the analysis. In the models for both state level and county level associations, maximum temperature's significant associations with a higher frequency of reported cases was not surprising, as it corresponds to previous studies' assertions that cases spike in the summer months[40], it was expected that it would be significant at more lag times and locations. Precipitation was also expected to be significant more often than it was. There was again no clear pattern in the state level analyses, although three states did have significant full models. Some factors contributing to difficulty in identifying a pattern include the nature of the varied landscapes throughout the region, soil texture and type, and groundwater saturation levels in each state. For example, Florida's significant model at the 5 day lag time could be significant due to the

narrowness of the state, its low elevation, and the soil type. All of these things can impact water flow and groundwater mixing zones in coastal areas, and therefore precipitation may more quickly impact salinity levels of estuaries, bays, and oceans. Statewide precipitation in other locations could still be relevant to levels of *vulnificus* populations in marine habitats despite the results of being significant only in 3 locations. One previous study has shown that drought conditions in North Carolina correlated to lower frequency of positive environmental samples of *v. vulnificus* in the Chesapeake Bay[31]. This relationship deserves more analysis and scrutiny to determine links between precipitation and frequency of reported cases in terms of its effects on salinity of bays and estuaries and therefore its potential to impact cases. While we can attest to the substantiated influences of higher temperatures on increasing frequency of cases, from previous literature and these analyses, we still cannot attest to a clear pattern in the different lag times.

Limitations

This study has several limitations. The first relates to the data available for the study. The study period and region provide a small number of cases for the time studied, which reduces the power of the findings. There is also a chance that less severe infections are not diagnosed and subsequently treated as a skin infection, and therefore not reported. The information contained in the data sets are all self-reported, so there is the possibility for recall bias. The environmental and climatological data sets also present with missing data and a lack of variables pertinent to the study of marine bacteria. Chlorophyll, salinity, dissolved oxygen, and turbidity are not regularly measured as part of any national monitoring

program at distances from shore that are relevant to our study. Monitoring on coastlines are limited to short, spatially defined independent studies performed mostly by universities. Lastly, to our knowledge no one has been able to analyze the association between environmental samples positive for *v. vulnificus*, reported cases, and relevant environmental parameters. Regular monitoring of the bacterium in the environment is rare, when it is conducted it is done in a narrow timeframe and a fine spatial scale, often to inform studies.

The regression analysis was performed using a Poisson distribution to accommodate case counts and the rarity of reported cases. While some of the models were significant and tests performed in SAS supported good model fit for the data, it would be prudent to re-analyze any trends when more data become available since there remain no clear patterns of significance.

Future Directions

Some studies have shown associations and interactions between the presence of free floating particles and chlorophyll a with temperature and salinity in predicting the presence of *v. vulnificus* in the environment[32-34]. Using these types of studies to look at associations between the parameters in these larger models and frequency of reported cases is an area that could benefit our understanding of climate's impact on this bacterium. This type of analysis has not been done, and is a next logical step in the field. Additional surveillance for the pathogen in the environment could facilitate future analyses of this sort. More regular monitoring would allow for correlation analysis between environmental parameters like temperature, drought indices, and precipitation and levels of the pathogen in its habitat. Likewise, health

officials could also correlate the levels of the pathogen with numbers of reported cases to see if increased pathogen populations leads to increased reported cases, or if the rise in numbers of reported cases is merely due to human population fluctuations or random chance.

Conclusions and Recommendations

The analyses within this research have shown spatial and temporal distributions of *vibrio vulnificus* cases in the Southeastern US. This research is important as *v. vulnificus* infections are seemingly increasing in frequency. At the same time, evidence that the earth is warming and habitats are changing as a result is indisputable. It is important to discover relationships between this pathogen and its environment in order help public health agencies in prevention and adaptation measures.

Clusters of cases in space and time were assessed, and several local clusters around bays and estuaries were shown to be significant. The results here also reaffirm evidence that *v. vulnificus* infections are seasonal, with peaks at the end of summers when water temperatures are their warmest. Precipitation was not as significant as we had hoped to find, however there are many hydrological and geological factors that could play into this complex relationship, and must be studied further.

A primary recommendation is further research into the ecology of the pathogen itself. Many factors like pathogen virulence in a variety of conditions, the variety of habitats of *vulnificus*, and the impacts of the hydrology of bays and estuaries still needs to be fully described. More immediately, and usable by public health officials is a recommendation to inform beachgoers, fishermen, and stakeholders of the potential for wound infection by this pathogen. Particular parties that should use extra caution are older men, and anyone with a pre-existing condition that would weaken the immune system.

References

1. Altizer S, Ostfeld RS, Johnson PTJ, Kutz S, Harvell CD. Climate Change and Infectious Diseases: From Evidence to a Predictive Framework. *Science*. August 2, 2013 2013;341(6145):514-519.

2. Tirado MC, Clarke R, Jaykus LA, McQuatters-Gollop A, Frank JM. Climate change and food safety: A review. *Food Research International*. 8// 2010;43(7):1745-1765.

3. Greer A, Ng V, Fisman D. Climate change and infectious diseases in North America: the road ahead. *Canadian Medical Association Journal*. March 11, 2008 2008;178(6):715-722.

4. Epstein PR. Emerging diseases and ecosystem instability: new threats to public health. *American Journal of Public Health.* 1995/02/01 1995;85(2):168-172.

5. Ermert V, Fink AH, Morse AP, Paeth H. The impact of regional climate change on malaria risk due to greenhouse forcing and land-use changes in tropical Africa. *Environ Health Perspect*. Jan 2012;120(1):77-84.

6. Burge CA, Mark Eakin C, Friedman CS, et al. Climate change influences on marine infectious diseases: implications for management and society. *Ann Rev Mar Sci*. 2014;6(1):249-277.

7. Young I, Gropp K, Fazil A, Smith BA. Knowledge synthesis to support risk assessment of climate change impacts on food and water safety: A case study of the effects of water temperature and salinity on Vibrio parahaemolyticus in raw oysters and harvest waters. *Food Research International*.

8. Baker-Austin C, Trinanes JA, Taylor NGH, Hartnell R, Siitonen A, Martinez-Urtaza J. Emerging Vibrio risk at high latitudes in response to ocean warming. *Nature Clim. Change*. 01//print 2013;3(1):73-77.

9. Martinez-Urtaza J, Bowers JC, Trinanes J, DePaola A. Climate anomalies and the increasing risk of Vibrio parahaemolyticus and Vibrio vulnificus illnesses. *Food Research International*. 8// 2010;43(7):1780-1790.

10. Chase E, Harwood VJ. Comparison of the effects of environmental parameters on growth rates of Vibrio vulnificus biotypes I, II, and III by culture and quantitative PCR analysis. *Applied and environmental microbiology*. Jun 2011;77(12):4200-4207.

11. Chase E, Young S, Harwood VJ. Sediment and vegetation as reservoirs of Vibrio vulnificus in the Tampa Bay Estuary and Gulf of Mexico. *Applied and environmental microbiology*. Jan 30 2015.

12. Givens CE, Bowers JC, DePaola A, Hollibaugh JT, Jones JL. Occurrence and distribution of Vibrio vulnificus and Vibrio parahaemolyticus--potential roles for fish, oyster, sediment and water. *Letters in applied microbiology*. Jun 2014;58(6):503-510.

13. Kuo YL, Shieh SJ, Chiu HY, Lee JW. Necrotizing fasciitis caused by Vibrio vulnificus: epidemiology, clinical findings, treatment and prevention. *Eur J Clin Microbiol Infect Dis*. 2007/11/01 2007;26(11):785-792.

14. Hollis DG, Weaver RE, Baker CN, Thornsberry C. Halophilic Vibrio species isolated from blood cultures. *Journal of Clinical Microbiology*. April 1, 1976 1976;3(4):425-431.

15. Herriman R. Vibrio vulnificus case reported in Polk County, brings state total to 25. U.S. News 2014; http://outbreaknewstoday.com/vibrio-vulnificus-case-reported-in-polk-county-brings-state-total-to-25-72895/. Accessed December 23, 2014, 2014.

16. KFOR-TV. Texas woman recounts her 'unreal' fight against flesh-eating bacteria. News 2014; http://kfor.com/2014/08/04/texas-woman-recounts-her-unreal-fight-against-flesh-eating-bacteria/. Accessed December 23, 2014, 2014.

17. Newton A, Kendall M, Vugia DJ, Henao OL, Mahon BE. Increasing Rates of Vibriosis in the United States, 1996–2010: Review of Surveillance Data From 2 Systems. *Clinical Infectious Diseases*. June 1, 2012 2012;54(suppl 5):S391-S395.

18. Oliver JD. Wound infections caused by Vibrio vulnificus and other marine bacteria. *Epidemiology and infection*. Jun 2005;133(3):383-391.

19. Kim YR, Lee SE, Kook H, et al. Vibrio vulnificus RTX toxin kills host cells only after contact of the bacteria with host cells. *Cellular microbiology*. Apr 2008;10(4):848-862.

20. Franco SL, Swenson GJ, Long RA. Year round patchiness of Vibrio vulnificus within a temperate Texas bay. *Journal of applied microbiology*. Mar 2012;112(3):593-604.

21. Griffitt KJ, Grimes DJ. Abundance and distribution of Vibrio cholerae, V. parahaemolyticus, and V. vulnificus following a major freshwater intrusion into the Mississippi Sound. *Microbial ecology*. Apr 2013;65(3):578-583.

22. Johnson CN, Flowers AR, Noriea NF, 3rd, et al. Relationships between environmental factors and pathogenic Vibrios in the Northern Gulf of Mexico. *Applied and environmental microbiology*. Nov 2010;76(21):7076-7084.

23. Turner JW, Malayil L, Guadagnoli D, Cole D, Lipp EK. Detection of Vibrio parahaemolyticus, Vibrio vulnificus and Vibrio cholerae with respect to seasonal fluctuations in temperature and plankton abundance. *Environmental microbiology*. Apr 2014;16(4):1019-1028.

24. Motes ML, DePaola A, Cook DW, et al. Influence of water temperature and salinity on Vibrio vulnificus in Northern Gulf and Atlantic Coast oysters (Crassostrea virginica*). Applied and environmental microbiology*. Apr 1998;64(4):1459-1465.

25. Program, U. 2014 National Climate Assessment Full Report. Retrieved from http://www.energyandclimatechange.org/view/article/537bc46d0cf226e0bdbfef38. 2014.

26. Menne, Matthew J., et al. "An overview of the global historical climatology network-daily database." *Journal of Atmospheric and Oceanic Technology* 29.7 (2012): 897-910

27. Nowakowska J, Oliver JD. Resistance to environmental stresses by Vibrio vulnificus in the viable but nonculturable state. *FEMS Microbiol Ecol*. Apr 2013;84(1):213-222.

28. Merkel SM, Alexander S, Zufall E, Oliver JD, Huet-Hudson YM. Essential Role for Estrogen in Protection against Vibrio vulnificus-Induced Endotoxic Shock. DiRita VJ, ed. *Infection and Immunity*. 2001;69(10):6119-6122. doi:10.1128/IAI.69.10.6119-6122.2001.

29. World Ocean Atlas Regional Climatology-NODC's Ocean Climate Laboratory Products. Silver Spring,MD: National Oceanographic Data Center; 2014.http://www.nodc.noaa.gov/cgi-bin/OC5/GOMclimatology/gomregclfig.pl. Accessed 12 March 2014.

30. Skinner, BJ, Murck BW. *The Blue Planet: An Introuction to Earth System Science*. 3rd ed. Wiley. 2011.

31. Jacobs JM, Rhodes M, Brown CW, et al. Modeling and forecasting the distribution of Vibrio vulnificus in Chesapeake Bay. *Journal of applied microbiology*. Nov 2014;117(5):1312-1327.

32. Hsieh JL, Fries JS, Noble RT. VIBRIO AND PHYTOPLANKTON DYNAMICS DURING THE SUMMER OF 2004 IN A EUTROPHYING ESTUARY. *Ecological Applications*. 2007/07/01 2007;17(sp5):S102-S109.

33. Fukushima H, Seki R. Ecology of Vibrio vulnificus and Vibrio parahaemolyticus in brackish environments of the Sada River in Shimane Prefecture, Japan. *FEMS Microbiol Ecol*. May 1 2004;48(2):221-229.

34. Nigro OD, Hou A, Vithanage G, Fujioka RS, Steward GF. Temporal and spatial variability in culturable pathogenic Vibrio spp. in Lake Pontchartrain, Louisiana, following hurricanes Katrina and Rita. *Applied and environmental microbiology*. Aug 2011;77(15):5384-5393.

Tables and Figures

Figure 1: Causal pathway diagram for *vibrio vulnificus*

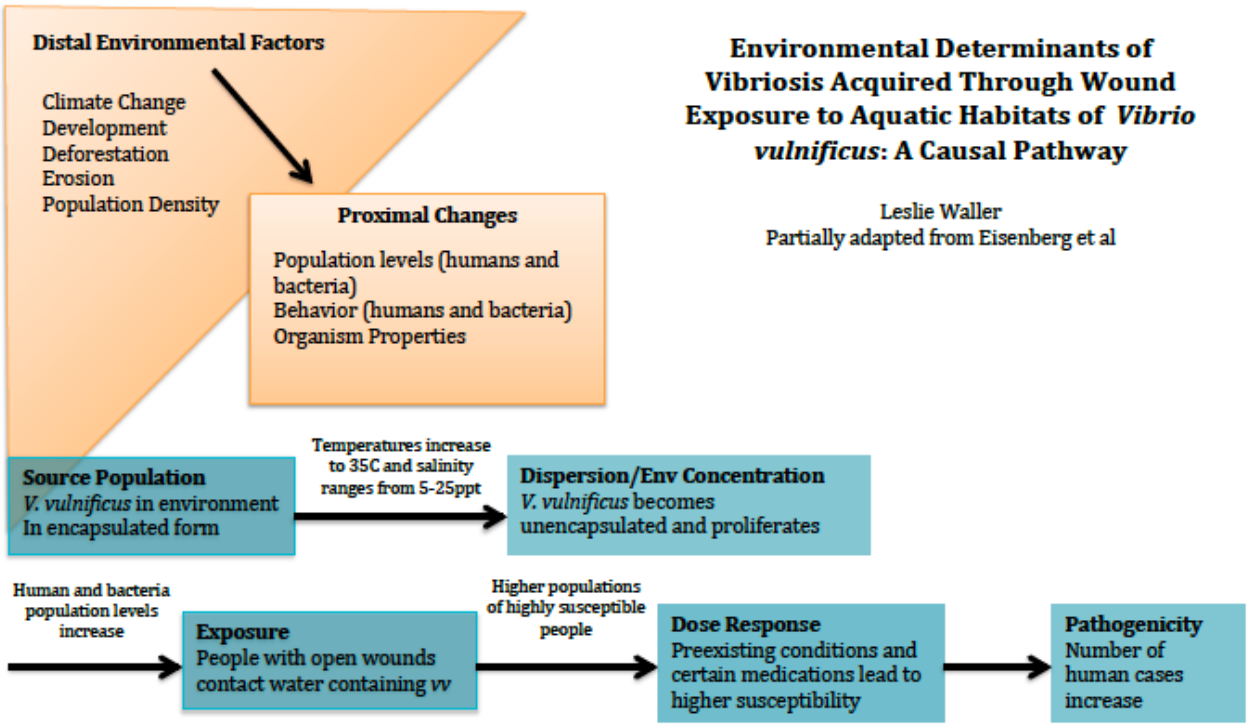


Figure 2: Frequency of reported cases stratified by year

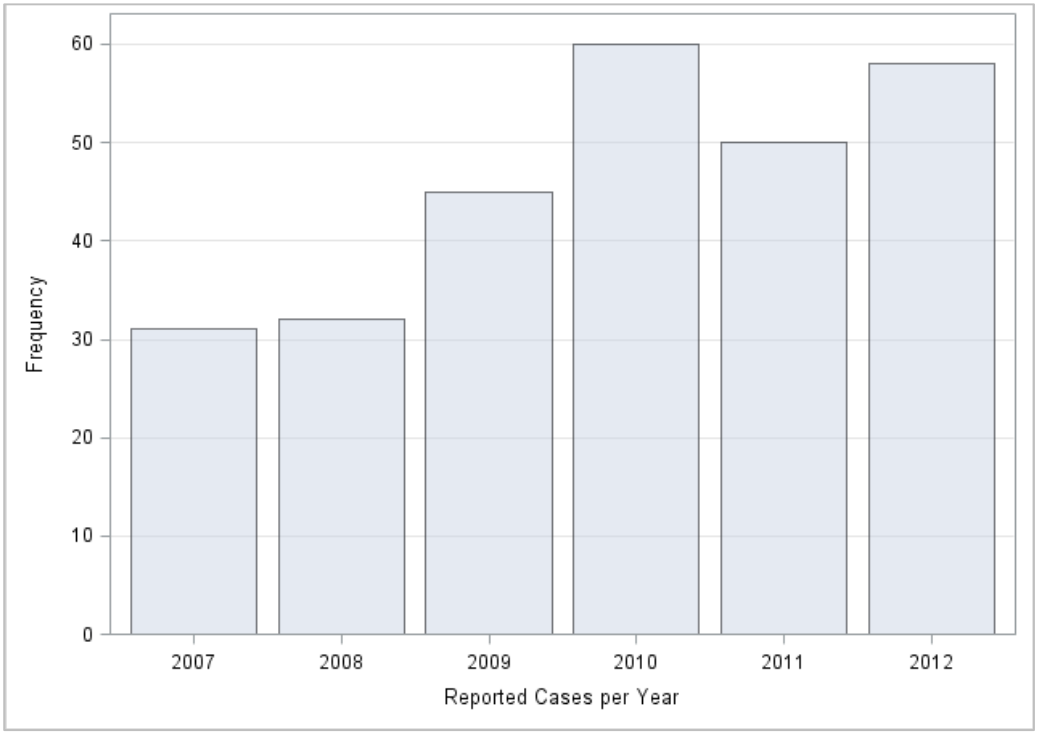


Figure 3: Monthly case counts stratified by year in the Southeastern US

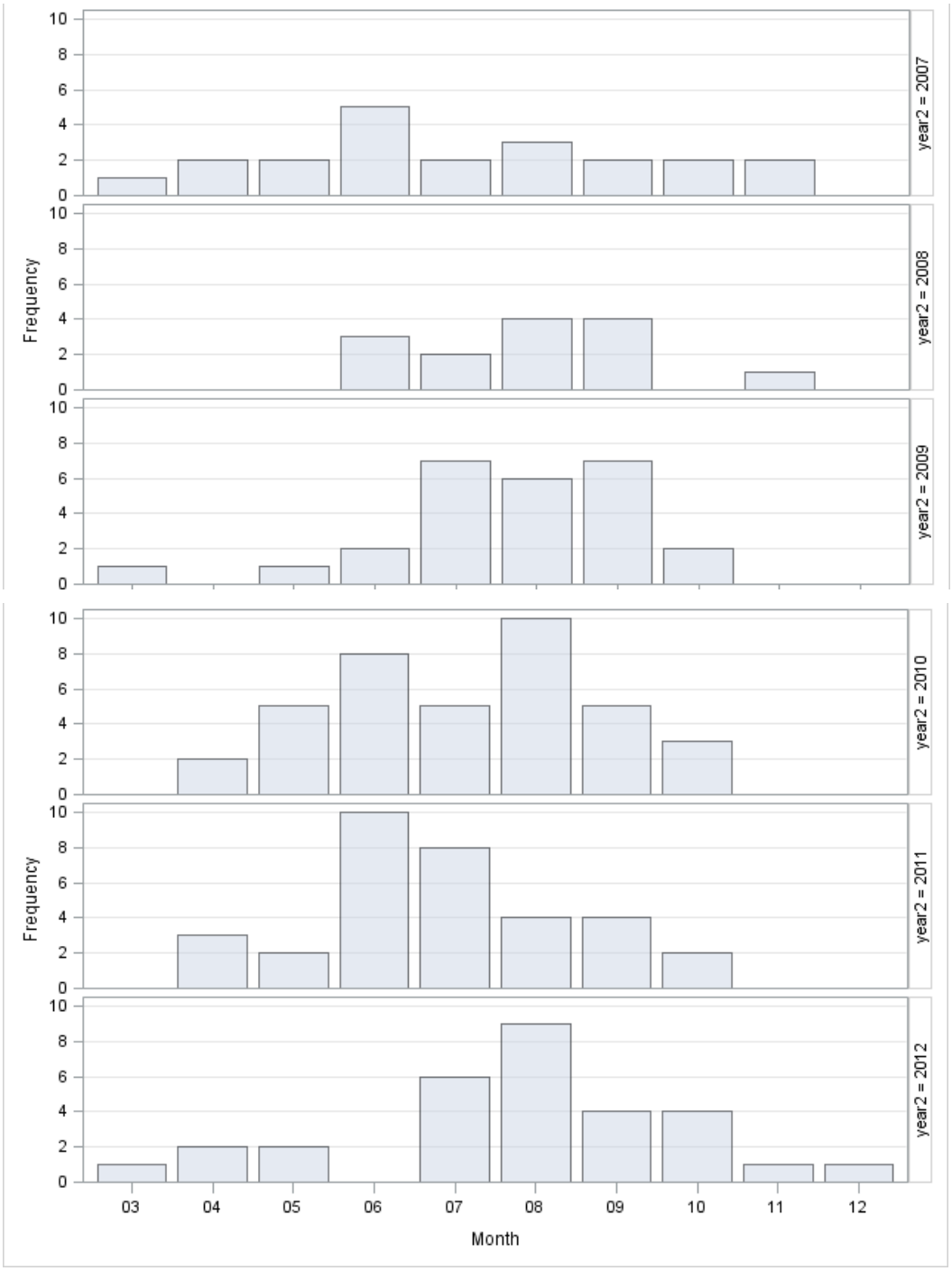


Table 1: Case counts by state and year, with counts stratified by sex and type of exposure (recreational versus occupational). There are some discrepancies in the totals, as there were many unknowns denoted, and those have not been listed in the table.

	Alabama (13)	Florida (73)	Louisiana (45)	Mississippi (12)	Texas (39)	Total (182)
2007	none	**3** male=1 female=2 rec=2	**9** male=9 rec=4 occ=3	**1** male=1 rec=1	**10** male=9 female=1 rec=7	23
2008	**2** male=2 rec=1	**3** male=3 rec=3	**5** male=5 rec=4	none	**4** male=4 rec=4	14
2009	**3** male=2 female=1 rec=2	**17** male=16 female=1 rec=14 occ=1	**7** male=5 female=2 rec=4	none	**5** male=5 rec=2 occ=1	32
2010	**3** male=3 rec=3	**22** male= 20 female=2 rec=18 occ=1	**6** male=6 rec=3	**2** male=1 female=1 rec=1	**10** male=10 rec=8 occ=1	43
2011	**2** male=2 rec=1 occ=1	**16** male=12 female=4 rec=11 occ=2	**8** male=8 rec=2 occ=2	**3** male=2 female=1 rec=1	**6** male=4 female=2 rec=5	35
2012	**3** male=3 rec=3	**12** male=12 rec=10 occ=1	**10** male=8 female=2 rec=5	**6** male=6 rec=3	**4** male=3 female=1 rec=3	35

Table 2: Age statistics of cases, stratified by gender

Male Mean Age	**Female Mean Age**
58.34	50.61
Median	**Median**
61	51
Standard deviation	**Standard deviation**
18.23	18.24

Table 3: Counts and percent of exposure types

Exposure Type	Frequency	Percent
Contact with fish	30	18.5
Bodily contact with water	58	35.8
Swimming	15	9.3
Multiple exposures	58	35.8
Unknown	1	.62

Figure 4: Spatial distribution of cases, graphed by year of exposure and subsequent infection

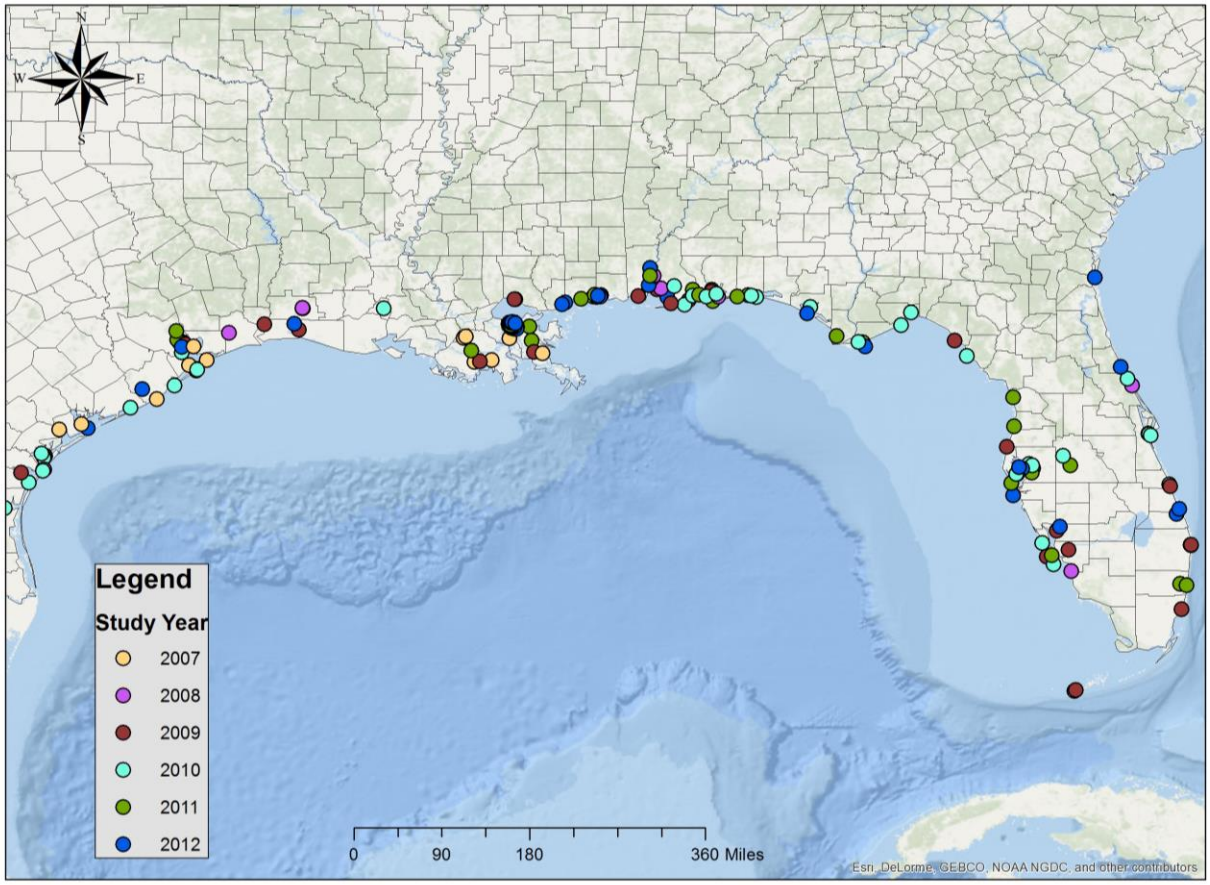
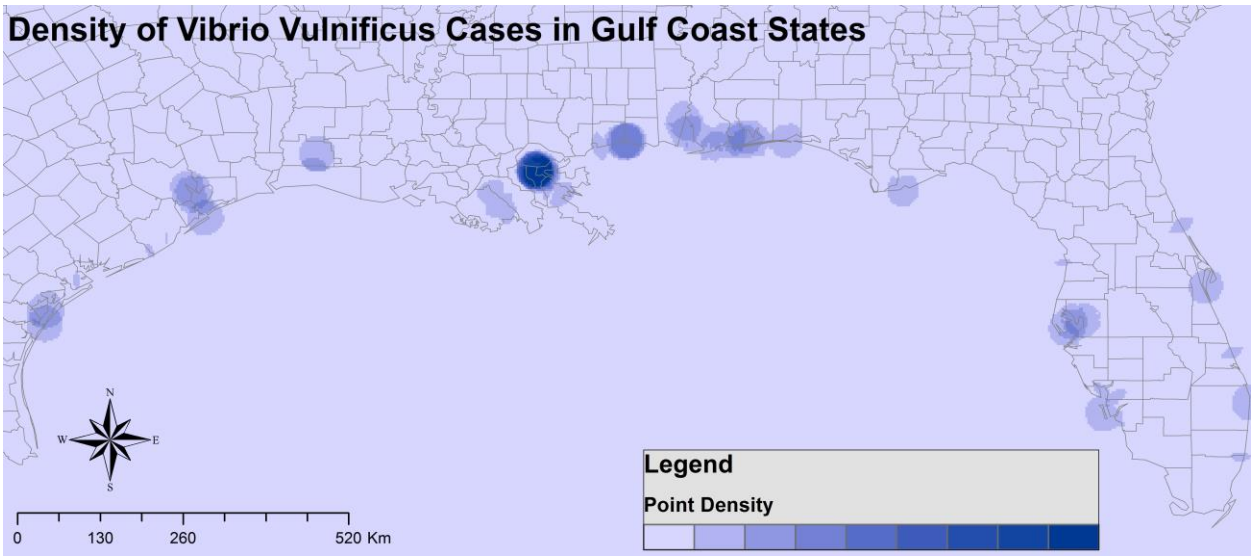


Figure 5: Kernel density analysis results showing spatial clusters of cases, predominantly in areas located around larger bays and estuaries



Appendix 1: Correlation Test Between Environmental Parameters

Correlations

			PCP	TMIN	TMAX	PDSI	SP01	SP02
Spearman's rho	PCP	Correlation Coefficient	1.000	.260**	.172**	.399**	.824**	.569**
		Sig. (2-tailed)	.	.000	.000	.000	.000	.000
		N	2380	2380	2380	2380	2380	2380
	TMIN	Correlation Coefficient	.260**	1.000	.970**	-.126**	.031	-.005
		Sig. (2-tailed)	.000	.	.000	.000	.135	.796
		N	2380	2380	2380	2380	2380	2380
	TMAX	Correlation Coefficient	.172**	.970**	1.000	-.213**	-.063**	-.094**
		Sig. (2-tailed)	.000	.000	.	.000	.002	.000
		N	2380	2380	2380	2380	2380	2380
	PDSI	Correlation Coefficient	.399**	-.126**	-.213**	1.000	.483**	.619**
		Sig. (2-tailed)	.000	.000	.000	.	.000	.000
		N	2380	2380	2380	2380	2380	2380
	SP01	Correlation Coefficient	.824**	.031	-.063**	.483**	1.000	.684**
		Sig. (2-tailed)	.000	.135	.002	.000	.	.000
		N	2380	2380	2380	2380	2380	2380
	SP02	Correlation Coefficient	.569**	-.005	-.094**	.619**	.684**	1.000
		Sig. (2-tailed)	.000	.796	.000	.000	.000	.
		N	2380	2380	2380	2380	2380	2380

**. Correlation is significant at the 0.01 level (2-tailed).

Appendix 2: County and State-level Model Outputs

Aransas County, TX

Variable Name	Regression Coefficient	P-Value	P-Value
TMAX0	0.0162	.	.
PCP0	-0.3764	.	.
TMAX3	0.0093	0.2327	0.2327
PCP3	0.0013	0.2666	0.2666
TMAX5	0.0097	0.2193	0.2193
PCP5	0.0013	0.3257	0.3257
TMAX15	0.0239	0.0366	0.0366
PCP15	-0.0253	0.6371	0.6371
TMAX30	0.0181	0.0699	0.0699
PCP30	0.0021	0.0023	0.0023
TMAX45	0.0361	0.0104	0.0104
PCP45	-0.0003	0.9468	0.9468

Bexar County, TX

Variable Name	Regression Coefficient	P-Value	P-Value
TMAX0	0.0020	0.7896	0.7896
PCP0	0.0001	0.9565	0.9565
TMAX3	0.0040	0.6161	0.6161
PCP3	0.0001	0.9604	0.9604
TMAX5	0.0003	0.9713	0.9713
PCP5	0.0001	0.9533	0.9533
TMAX15	0.0033	0.6708	0.6708
PCP15	-0.0005	0.0001	0.0001
TMAX30	0.0046	0.5669	0.5669
PCP30	0.0001	0.9620	0.9620
TMAX45	0.0086	0.3362	0.3362
PCP45	0.0001	0.9695	0.9695

Brazoria County, TX

Variable Name	Regression Coefficient	P-Value	P-Value
TMAX0	0.0297	0.2324	0.2324
PCP0	0.0052	0.1657	0.1657
TMAX3	0.0398	0.1509	0.1509
PCP3	-0.0592	0.7352	0.7352
TMAX5	0.0302	.	.
PCP5	-1.3532	.	.
TMAX15	0.0204	0.3104	0.3104
PCP15	0.0049	0.1554	0.1554
TMAX30	0.0413	0.2261	0.2261
PCP30	0.0093	0.0013	0.0013
TMAX45	0.0236	.	.
PCP45	-1.3881	.	.

Calhoun County, TX

Variable Name	Regression Coefficient	P-Value	P-Value
TMAX0	0.0080	0.4742	0.4742
PCP0	0.0004	0.7006	0.7006
TMAX3	-0.0011	0.8956	0.8956
PCP3	0.0004	0.6953	0.6953
TMAX5	0.0073	0.5040	0.5040
PCP5	0.0004	0.7135	0.7135
TMAX15	0.0096	0.4064	0.4064
PCP15	-0.0001	0.3446	0.3446
TMAX30	0.0091	0.4265	0.4265
PCP30	0.0004	0.7147	0.7147
TMAX45	0.0280	0.1106	0.1106
PCP45	0.0005	0.7309	0.7309

Galveston County, TX

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0047	0.5354	0.5354
PCP0	-0.0002	0.8550	0.8550
TMAX3	0.0035	0.6338	0.6338
PCP3	-0.0002	0.8596	0.8596
TMAX5	0.0021	0.7660	0.7660
PCP5	-0.0002	0.8699	0.8699
TMAX15	0.0080	0.3376	0.3376
PCP15	-0.0002	0.8488	0.8488
TMAX30	0.0056	0.4687	0.4687
PCP30	-0.0002	0.8530	0.8530
TMAX45	0.0159	0.1312	0.1312
PCP45	-0.0002	0.8315	0.8315

Harris County, TX

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0564	0.0021	0.0021
PCP0	-0.0030	0.7154	0.7154
TMAX3	0.0632	0.0011	0.0011
PCP3	-0.0006	0.9222	0.9222
TMAX5	0.0745	0.0004	0.0004
PCP5	0.0012	0.7760	0.7760
TMAX15	0.0413	0.0085	0.0085
PCP15	0.0020	0.1170	0.1170
TMAX30	0.0279	0.0252	0.0252
PCP30	0.0014	0.3574	0.3574
TMAX45	0.0398	0.0083	0.0083
PCP45	-0.0074	0.5491	0.5491

Jefferson County, TX

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	-0.0005	0.9200	0.9200
PCP0	0.0010	0.4101	0.4101
TMAX3	0.0018	0.7168	0.7168
PCP3	-0.0234	0.3962	0.3962
TMAX5	0.0016	0.7453	0.7453
PCP5	-0.0022	0.6259	0.6259
TMAX15	0.0058	0.2948	0.2948
PCP15	-0.0042	0.5144	0.5144
TMAX30	0.0121	0.0698	0.0698
PCP30	-0.0026	0.5939	0.5939
TMAX45	0.0203	0.0177	0.0177
PCP45	0.0013	0.2927	0.2927

Nueces County, TX

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0145	0.4050	0.4050
PCP0	0.0026	0.4854	0.4854
TMAX3	0.0057	0.6677	0.6677
PCP3	-0.0070	0.8173	0.8173
TMAX5	0.0157	.	.
PCP5	-0.6245	.	.
TMAX15	0.0285	.	.
PCP15	-0.8149	.	.
TMAX30	0.0299	.	.
PCP30	-0.8042	.	.
TMAX45	0.0093	0.5262	0.5262
PCP45	-0.0024	0.8817	0.8817

LaFourche Parrish, LA

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0142	0.2184	0.2184
PCP0	-0.0000	0.9685	0.9685
TMAX3	0.0010	0.8994	0.8994
PCP3	0.0000	0.9770	0.9770
TMAX5	-0.0037	0.5905	0.5905
PCP5	-0.0001	0.9040	0.9040
TMAX15	-0.0035	0.6223	0.6223
PCP15	0.0011	0.5287	0.5287
TMAX30	0.0110	0.2894	0.2894
PCP30	0.0001	0.9632	0.9632
TMAX45	0.0010	0.8995	0.8995
PCP45	-0.0001	0.9341	0.9341

Orleans Parrish, LA

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0051	0.2238	0.2238
PCP0	0.0008	0.5202	0.5202
TMAX3	0.0066	0.1332	0.1332
PCP3	0.0006	0.6776	0.6776
TMAX5	0.0035	0.3768	0.3768
PCP5	-0.0000	0.9946	0.9946
TMAX15	0.0069	0.1119	0.1119
PCP15	-0.0028	0.4861	0.4861
TMAX30	0.0140	0.0104	0.0104
PCP30	-0.0029	0.4792	0.4792
TMAX45	0.0181	0.0036	0.0036
PCP45	-0.0002	0.9148	0.9148

St. Tammany Parrish, LA

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0121	0.2382	0.2382
PCP0	0.0000	0.9975	0.9975
TMAX3	0.0238	0.1041	0.1041
PCP3	-0.0001	0.9303	0.9303
TMAX5	0.0177	0.1494	0.1494
PCP5	-0.0001	0.9490	0.9490
TMAX15	0.0135	0.2063	0.2063
PCP15	-0.0000	0.9769	0.9769
TMAX30	0.0164	0.1689	0.1689
PCP30	0.0019	0.3144	0.3144
TMAX45	0.0156	0.1705	0.1705
PCP45	0.0003	0.9191	0.9191

Hancock County, MS

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0216	.	.
PCP0	-0.3417	.	.
TMAX3	0.0107	.	.
PCP3	-0.3482	.	.
TMAX5	0.0123	.	.
PCP5	-0.3470	.	.
TMAX15	0.0100	0.4581	0.4581
PCP15	0.0007	0.8134	0.8134
TMAX30	0.0037	.	.
PCP30	-0.3455	.	.
TMAX45	0.0014	.	.
PCP45	-0.3446	.	.

Harrison County, MS

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0564	0.0021	0.0021
PCP0	-0.0030	0.7154	0.7154
TMAX3	0.0632	0.0011	0.0011
PCP3	-0.0006	0.9222	0.9222
TMAX5	0.0745	0.0004	0.0004
PCP5	0.0012	0.7760	0.7760
TMAX15	0.0413	0.0085	0.0085
PCP15	0.0020	0.1170	0.1170
TMAX30	0.0279	0.0252	0.0252
PCP30	0.0014	0.3574	0.3574
TMAX45	0.0398	0.0083	0.0083
PCP45	-0.0074	0.5491	0.5491

Jackson County, MS

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0172	0.1482	0.1482
PCP0	-0.0001	0.8848	0.8848
TMAX3	0.0068	0.4610	0.4610
PCP3	0.0023	0.0159	0.0159
TMAX5	0.0299	0.0695	0.0695
PCP5	0.0024	0.0496	0.0496
TMAX15	0.0355	0.0481	0.0481
PCP15	0.0001	0.9524	0.9524
TMAX30	0.0195	0.1301	0.1301
PCP30	0.0022	0.0599	0.0599
TMAX45	0.0124	0.2263	0.2263
PCP45	0.0005	0.8635	0.8635

Baldwin County, AL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0141	0.0823	0.0823
PCP0	-0.0013	0.7786	0.7786
TMAX3	0.0287	0.0146	0.0146
PCP3	-0.0038	0.5953	0.5953
TMAX5	0.0205	0.0361	0.0361
PCP5	0.0001	0.9795	0.9795
TMAX15	0.0209	0.0362	0.0362
PCP15	0.0027	0.1468	0.1468
TMAX30	0.0184	0.0474	0.0474
PCP30	0.0022	0.3007	0.3007
TMAX45	0.0278	0.0164	0.0164
PCP45	0.0025	0.2069	0.2069

Mobile County, AL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0051	0.4529	0.4529
PCP0	-0.0022	0.7023	0.7023
TMAX3	0.0014	0.8331	0.8331
PCP3	0.0018	0.2956	0.2956
TMAX5	0.0000	0.9948	0.9948
PCP5	-0.0034	0.6386	0.6386
TMAX15	0.0046	0.4828	0.4828
PCP15	-0.0304	0.4665	0.4665
TMAX30	0.0091	0.2269	0.2269
PCP30	-0.0056	0.5669	0.5669
TMAX45	0.0067	0.4031	0.4031
PCP45	0.0035	0.0001	0.0001

Bay County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0151	0.2519	0.2519
PCP0	-0.0001	0.8830	0.8830
TMAX3	0.0128	0.3021	0.3021
PCP3	0.0013	0.6796	0.6796
TMAX5	0.0270	0.1304	0.1304
PCP5	0.0033	0.0564	0.0564
TMAX15	0.0109	0.3485	0.3485
PCP15	-0.0001	0.9108	0.9108
TMAX30	0.0388	0.0651	0.0651
PCP30	-0.0001	0.9050	0.9050
TMAX45	0.0186	0.1946	0.1946
PCP45	-0.0001	0.9426	0.9426

Escambia County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0204	0.0213	0.0213
PCP0	0.0010	0.3023	0.3023
TMAX3	0.0196	0.0235	0.0235
PCP3	0.0005	0.7759	0.7759
TMAX5	0.0173	0.0329	0.0329
PCP5	-0.0095	0.5012	0.5012
TMAX15	0.0259	0.0087	0.0087
PCP15	-0.0058	0.5701	0.5701

Franklin County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0074	0.4901	0.4901
PCP0	-0.0002	0.8777	0.8777
TMAX3	0.0163	0.2326	0.2326
PCP3	-0.0001	0.9129	0.9129
TMAX5	0.0154	0.2476	0.2476
PCP5	-0.0001	0.9100	0.9100
TMAX15	0.0257	0.1345	0.1345
PCP15	-0.0001	0.9338	0.9338
TMAX30	0.0292	0.1128	0.1128
PCP30	-0.0001	0.9448	0.9448
TMAX45	0.0256	0.1328	0.1328
PCP45	-0.0000	0.9910	0.9910

Hillsborough County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0053	.	.
PCP0	-0.4993	.	.
TMAX3	0.0053	.	.
PCP3	-0.4989	.	.
TMAX5	0.0012	.	.
PCP5	-0.4877	.	.
TMAX15	0.0022	0.8175	0.8175
PCP15	0.0026	0.0268	0.0268
TMAX30	0.0293	0.0881	0.0881
PCP30	-0.0050	0.6425	0.6425
TMAX45	0.0298	0.0838	0.0838
PCP45	-0.0086	0.5852	0.5852

Indian River County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0332	.	.
PCP0	-0.4519	.	.
TMAX3	0.0348	0.1131	0.1131
PCP3	-0.0520	0.5829	0.5829
TMAX5	0.0403	0.0858	0.0858
PCP5	-0.0169	0.6252	0.6252
TMAX15	0.0629	0.0182	0.0182
PCP15	0.0001	0.9865	0.9865
TMAX30	0.0228	0.2382	0.2382
PCP30	0.0002	0.9743	0.9743
TMAX45	0.0208	.	.
PCP45	-0.4402	.	.

Martin County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	-0.0065	0.6735	0.6735
PCP0	0.0035	0.0190	0.0190
TMAX3	0.0138	0.5099	0.5099
PCP3	0.0040	0.0037	0.0037
TMAX5	0.0061	0.7380	0.7380
PCP5	0.0002	0.9575	0.9575
TMAX15	-0.0052	0.7180	0.7180
PCP15	-0.0000	0.9982	0.9982
TMAX30	0.0050	0.7908	0.7908
PCP30	0.0037	0.0086	0.0086
TMAX45	-0.0062	0.6601	0.6601
PCP45	-0.0000	0.9732	0.9732

Monroe County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0520	0.2018	0.2018
PCP0	0.0022	0.5716	0.5716
TMAX3	0.0756	0.0537	0.0537
PCP3	-0.0000	0.9624	0.9624
TMAX5	0.0552	0.0867	0.0867
PCP5	0.0000	0.9722	0.9722
TMAX15	0.0191	0.2914	0.2914
PCP15	0.0000	0.9779	0.9779
TMAX30	0.0363	0.1447	0.1447
PCP30	0.0020	0.4467	0.4467
TMAX45	0.0609	0.0748	0.0748
PCP45	-0.0000	0.9719	0.9719

Okaloosa County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0236	0.0977	0.0977
PCP0	-0.0000	0.9997	0.9997
TMAX3	0.0099	0.3005	0.3005
PCP3	-0.0032	0.7224	0.7224
TMAX5	0.0164	.	.
PCP5	-0.5243	.	.
TMAX15	0.0291	0.0732	0.0732
PCP15	0.0007	0.8791	0.8791
TMAX30	0.0317	0.0518	0.0518
PCP30	-0.0556	0.4620	0.4620
TMAX45	0.0646	0.0073	0.0073
PCP45	0.0021	0.5953	0.5953

Palm Beach County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	-0.0113	0.5837	0.5837
PCP0	-0.0247	0.7569	0.7569
TMAX3	-0.0045	.	.
PCP3	-0.5877	.	.
TMAX5	-0.0231	.	.
PCP5	-0.7421	.	.
TMAX15	-0.0536	0.0214	0.0214
PCP15	0.0066	0.1192	0.1192
TMAX30	-0.0003	0.9902	0.9902
PCP30	-0.0803	0.7175	0.7175
TMAX45	0.0236	.	.
PCP45	-0.6511	.	.

Pinellas County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0268	0.1560	0.1560
PCP0	0.0001	0.9835	0.9835
TMAX3	0.0268	.	.
PCP3	-0.3739	.	.
TMAX5	0.0162	0.2750	0.2750
PCP5	0.0014	0.4414	0.4414
TMAX15	0.0322	0.1308	0.1308
PCP15	0.0019	0.2286	0.2286
TMAX30	0.0134	0.3253	0.3253
PCP30	0.0008	0.7847	0.7847
TMAX45	0.0211	0.1831	0.1831
PCP45	-0.0215	0.4893	0.4893

Polk County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.1225	0.0172	0.0172
PCP0	-0.0000	0.9843	0.9843
TMAX3	0.0756	0.0537	0.0537
PCP3	-0.0000	0.9624	0.9624
TMAX5	0.0552	0.0867	0.0867
PCP5	0.0000	0.9722	0.9722
TMAX15	0.0191	0.2914	0.2914
PCP15	0.0000	0.9779	0.9779
TMAX30	0.0363	0.1447	0.1447
PCP30	0.0020	0.4467	0.4467
TMAX45	0.0609	0.0748	0.0748
PCP45	-0.0000	0.9719	0.9719

Santa Rosa County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0351	0.0662	0.0662
PCP0	0.0010	0.8381	0.8381
TMAX3	0.0248	0.1186	0.1186
PCP3	0.0003	0.8731	0.8731
TMAX5	0.0311	0.0855	0.0855
PCP5	0.0002	0.8591	0.8591

Volusia County, FL

Variable Name	*Regression Coefficient*	*P-Value*	*P-Value*
TMAX0	0.0214	0.3149	0.3149
PCP0	0.0019	0.7200	0.7200
TMAX3	0.0201	0.3253	0.3253
PCP3	-0.0055	0.7374	0.7374
TMAX5	0.0180	0.3630	0.3630
PCP5	0.0009	0.9035	0.9035
TMAX15	0.0765	0.0337	0.0337
PCP15	0.0071	0.0446	0.0446
TMAX30	0.1137	.	.
PCP30	-0.4971	.	.
TMAX45	0.0416	0.1673	0.1673
PCP45	-0.0016	0.8822	0.8822