

Vibrio vulnificus infections from water exposure in the Chesapeake Bay: are they predictable?

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Highlights

- The intent is to enhance the utility of the Chesapeake Bay *Vibrio vulnificus* model
- Show the ability of an operational habitat suitability model for *Vibrio vulnificus*
- Increase understanding of the distribution of *Vibrio vulnificus* waterborne cases in the state of Virginia
- Examine the relationship of a habitat suitability model for a waterborne pathogen to public health outcomes

Abstract

Vibrio vulnificus is a naturally occurring pathogenic marine bacterium that is found in coastal waters. Infections from *V. vulnificus* infections can occur from wound exposure to contaminated water as well as consuming raw or undercooked seafood. Despite low case numbers of 50-60 per year in the United States, *V. vulnificus* is commonly found in brackish water like in Chesapeake Bay. Predictive models have been developed to predict occurrence of *V. vulnificus* based on temperature and salinity, two known drivers of *V. vulnificus* abundance. Though these models can predict the abundance of bacteria, they do not predict the likelihood of infection due to the lack of understanding surrounding virulence. Also, the individual health status of the person exposed is an important predictor of illness but is not typically available for research purposes. This work utilizes *V. vulnificus* case numbers from the Virginia Department of Health coupled with model predictions from an operational habitat suitability model that would predict the

number of infections. The results indicate a relationship between per capita wound infection cases and the probability of the pathogen being present in tidal waters of the Chesapeake Bay (VA).

Introduction

Vibrio vulnificus (*Vv*) is a gram negative, halophilic bacterium that is endemic to coastal waters world-wide. It is most notable for illness it causes through both wound exposure and consumption of raw or undercooked seafood. Wound infections account for roughly 50% of the illnesses and while severe in nature, are exceedingly rare with approximately 50-60 cases reported per year in the United States (CDC). The bacterium, however, is not rare and may account for up to 10% of the total heterotrophic bacterial community in estuarine systems like the Chesapeake Bay (Heidelberg, Heidelberg et al. 2002).

Of particular interest are soft tissue infections associated with *Vv*, in that they appear to be on the rise. In general, necrotizing soft tissue infections are divided into two types dependent on whether the infection is polymicrobial and marked by gas formation in the tissue (Type I) or monomicrobial as is the case with *Vv* (Type II), where gas formation is possible but unlikely (Urschel 1999 Stevens and Bryant 2017). In most cases, the infections are preceded by trauma or minor breaches of the skin followed by fever, soft tissue edema, skin necrosis, and bullae. Treatment often includes aggressive wound care, such as surgical debridement, and antibiotic therapy. Of the bacterial species involved in Type II necrotizing soft tissue infections besides *Vv*, streptococcus is the most common, followed by methicillin resistant *Staphylococcus aureus* (MRSA). In cases related to water exposure, *Aeromonas hydrophila* is a common cause in fresh

to brackish waters, while *Vv* is responsible for many marine wound infections. *Vv* infections are largely treatable, but hesitation in seeking medical attention can dramatically alter the outcome.

Vv represents a significant challenge in public health communication. First, dose response for exposure related illness is largely unknown. In their risk assessment for the consumption of raw oysters, the World Health Organization (WHO) estimated the infectious dose to be between 10^3 and 10^7 CFU per gram of meat (WHO 2005). In iron dextran treated mice, subcutaneous inoculation with 10^3 CFU reliably leads to skin infection, while intraperitoneal inoculation dose response can occur with as little as 10 CFU (Thiaville, Bourdage et al. 2011). Shaw, Sapkota et al. (2015) demonstrated that dermal concentrations of *Vv* are linearly related to environmental concentrations, and estimated an average exposure dose of 360 CFU for a 2 cm² wound in studies with human swimmers. In this study, the average environmental concentration swimmers were exposed to was 10^3 . This concentration is typical of estuarine systems in the summer, yet illness is exceedingly rare. Thus, there is no concentration criteria to initiate management action. Additionally, annual media coverage in recent years tends to dramatize the issue, which creates fear and potentially public avoidance of water activities.

Second, *Vv* virulence is poorly understood. In Thiaville et al.'s (2011) study with iron dextran treated mice, both clinical and environmentally derived strains were equally capable of causing illness, although infections from clinical strains were generally more severe. Therefore, the question that has driven much of the *Vv* research in recent times has been why a pathogen that is ubiquitous in the estuarine environment at high concentrations causes so few illnesses. Although some strides have been made in identifying specific strains that are more likely to be associated with illness (Baker-Austin, 2010), there is currently no criteria on which to base closures of waterways or public warnings.

Studies have shown that *Vv* abundance is positively correlated with mesohaline salinity and warmer temperatures above 15°C (Baker-Austin et al. 2012). This has facilitated the development and validation of predictive models, which can fairly accurately predict occurrence, and to a lesser degree abundance, using environmental observation data (Jacobs et al. 2014). The caveat, however, is that knowing the distribution and abundance of the species may not provide adequate information concerning public health outcomes.

Since 2018, NOAA has offered an operational *Vv* forecast for the Chesapeake Bay, predicting the daily and 48 hour probability of occurrence throughout the bay at a 0.5 to 5km variable resolution ([Vibrio vulnificus in Chesapeake Bay](#)). Since 2014, the Virginia Department of Health (VDH) has maintained records of reported *Vv* infections and their exposure locations. Here, we demonstrate the relationship between an operational habitat suitability model for *Vv* and the number of infections. The intent is to enhance the utility of the model over time for public health practitioners by validating the model predictions with observed *Vv* infection exposure locations.

Material and Methods

Data Sources

Illness Data

Vibrio infections are both nationally notifiable and [reportable in Virginia, thus](#) relevant information about each case is gathered by county health officials, maintained at the state level, and submitted to the CDC [Cholera and Other *Vibrio* Illness Surveillance](#) (COVIS) program. In this effort, we used surveillance data compiled and provided by the VDH for non-foodborne, culture confirmed *Vv* cases, whose exposure was from Virginia waters during the years 2014 –

2021. Data fields provided included the date and location of exposure, with no personally identifiable or medical information. Each case was assigned a latitude and longitude based on best available information as described below.

Modeled Data

The first exercise examined the predictive capability of the existing NOAA Operational *Vv* habitat suitability model for illness outcomes spatially. The model generates daily average probability of occurrence of *Vv* throughout the Chesapeake Bay based on an empirical relationship derived for sea surface temperature and salinity (Jacobs, Rhodes et al. 2014). Each illness location and date were paired with archived modeled data by using the following criteria:

1) Exact location provided - When a case location was available with resolution equal to or exceeding the model grid resolution (.5 km), the nearest or exact grid point was used (N=14). In some cases, exact locations were adjacent to the model grid, and again nearest grid point was used.

2) Mid-level resolution - In cases where resolution exceeded the modeled grid (N=23), grids were averaged over the general location. An example would be “Potomac River near 301 bridge”. In such cases, +/- 4 grid points were averaged to characterize the general area.

3) Low-level resolution - In cases where only the river system was recorded (N=5), modeled data was averaged over a transect representing the mid river portion of the entire system for the day of exposure.

4) Excluded - Cases were excluded in instances where either 1) location recorded was broader than river scale (e.g.; Chesapeake Bay) or insufficient information was available to prescribe a location; 2) multiple locations were listed; 3) case occurred outside of Virginia waters; or 4) related to handling of seafood from unknown source.

This study utilized MATLAB to find the model indices for the given latitude and longitude of each exposure site, to rerun the model with a salinity correction using independent buoy observations when required and to retrieve the model probabilities. A salinity correction was included in the model runs starting in 2015 forward. For days with infections in 2014, the model was rerun and the salinity correction applied from historical data provided by the Chesapeake Bay Interpretive Buoy System (CBIBS). The preceding three days of CBIBS buoy salinities and model salinities were compared by averaging the data over each day. If more than a 1 psu RMS difference in salinity was found, then a salinity correction was performed. A linear regression was found between the model and observed salinities with a polynomial of $n=2$. The y intercept of the regression was forced to zero, so salinities at fresh water stations were not artificially increased or decreased from zero. The coefficients of the fit were then used to recalculate the output salinity grid for the day of interest. This corrected model salinity grid was then used along with the model's top 1-meter averaged surface temperature to find a new probability of occurrence field.

Population Data

Census data of the 3 closest counties was used as a proxy for relative rate of water exposure in the Virginia population. Yearly county population estimates were obtained from the University of Virginia's Cooper Center (<https://demographics.coopercenter.org/virginia-population-estimates>).

Statistical analysis

For comparison of the operational habitat model to *Vv* cases in Virginia, modeled probability of occurrence was binned by salinity (4 ppt bins) and averaged for comparison to corresponding cases over the time interval. Lower and higher salinity bins were combined in

order to maintain a minimum of 4 cases per bin. Cases were further adjusted to reflect “cases per capita” by dividing the number of cases by the average population of the 3 neighboring counties where each case occurred. Pearson’s correlation analysis was used to examine the strength of the relationship (SAS v 9.2, Cary NC).

Results

A total of 86 non-foodborne *Vv* cases were reported in Virginia from 2014 – 2021. Of these, slightly under half (N= 42, 49%) had sufficient data to identify the location and date of exposure. The remaining cases (N=44) either lacked a date or location, were generalized to a regional scale (i.e.; Chesapeake Bay), or occurred in a neighboring state, but sought medical attention in Virginia. While these remaining cases could not be used in our analysis of our predictive model, they are included where possible in summary figures.

Over the time period examined, Virginia averaged 11 non-foodborne *Vv* cases per year, with a high of 17 in 2016 and low of 7 in 2021 (Figure 1A). *Vv* cases in Virginia followed a typical seasonal epi-curve with the majority of cases in the summer months, and tailing off in the spring and fall. June consistently had either the highest number of cases or tied for the distinction, and subsequently the most cases overall during the 5-year period (Figure 1B). By river/region (where identifiable), the most cases (n=17) were reported with exposure to the Rappahannock River, followed by Hampton Rhodes/VA Beach (n=11) region, the Potomac River (n=8), the York River (n=7), and 2 each in the James and tributaries on the Eastern Shore (Figure 1C).

Using the 42 cases available from 2014 -2021 where location of exposure within the river system and date were known (11 cases less than shown in Figure 1C), we matched cases in space and time to the probability of *Vv* occurrence provided by NOAA’s Operational *Vv* forecast. Data

were further binned by salinity to allow for direct comparison of number of cases versus average predicted probability (Figure 2A). A strong correlation between the number of cases and model probabilities was not found (Pearsons, $r = 0.06$, $P = 0.93$). Using nearest 3-county population estimates as a proxy for recreational water activity, a period prevalence of illness was calculated. Considering population density, a strong correlation was noted between modeled probability and period prevalence (Pearsons, $r = 0.91$, $P = 0.03$; Figure 2B).

Conclusions

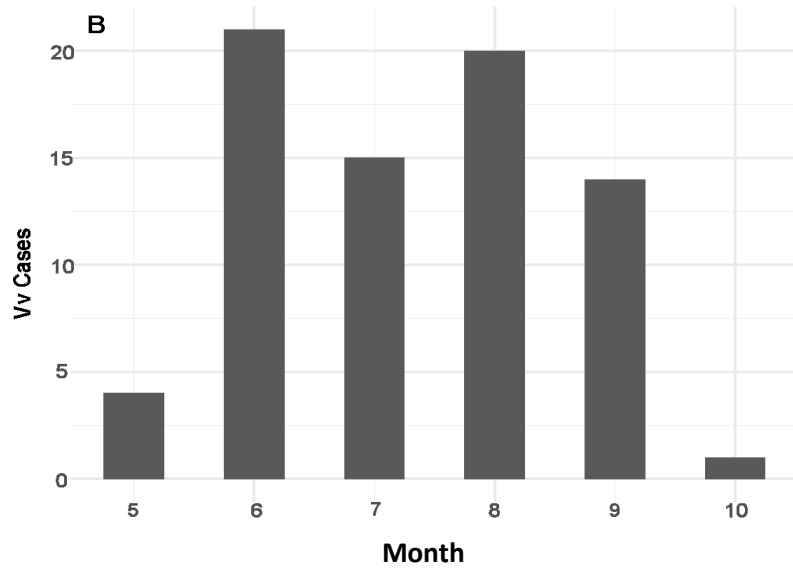
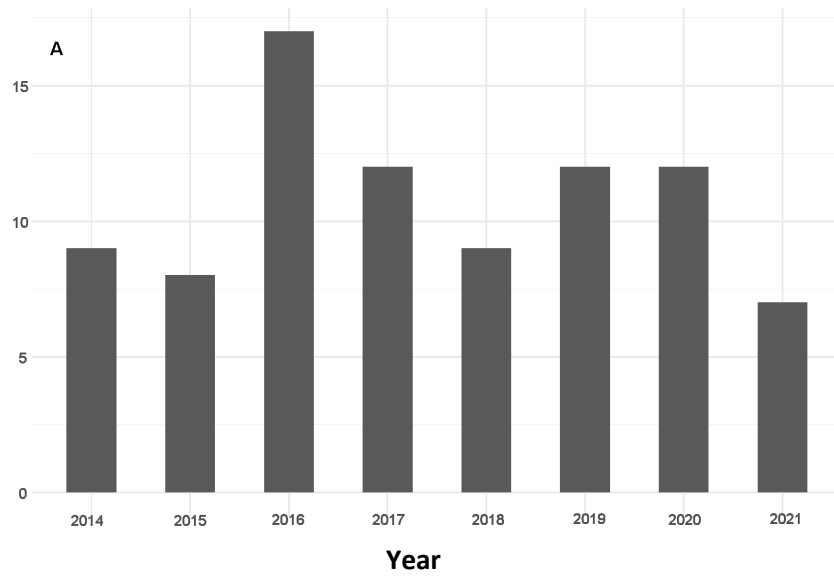
To our knowledge, this effort represents the first attempt to relate a habitat suitability model for a waterborne pathogen to public health outcomes. We demonstrate a strong relationship between population adjusted *Vv* exposure/wound infection cases and the probability of the pathogen being present over the range of salinities encountered in tidal waters of Virginia's Chesapeake Bay. Collectively, this effort demonstrates the promise of a habitat suitability model of a waterborne pathogen in helping explain public health outcomes, and increases our understanding of the distribution of cases in the state of Virginia.

The relationship between *Vv* and temperature is well established, generally emerging at temperatures greater than 15°C and correlating positively as temperature increases (Kaspar and Tamplin, 1993, Baker-Austin et al. 2012). *Vv* also exhibits a strong salinity preference for mesohaline waters, being far less abundant in high or low salinity waters. The NOAA Operational *Vv* forecast uses these relationships to predict the probability of occurrence (Jacobs et al. 2014). Based on the occurrence of *Vv* in water, more cases were noted in the high salinity region of Virginia Beach/Hampton Roads than might otherwise be expected. Adjusting to per capita incidence clearly improved the model fit (Figure 2B) by accounting for regional differences in population, and by proxy, exposure opportunity.

There are several limitations of this exercise that should be noted. First, reported *Vv* recreational exposure cases are rare, and thus the total number of cases available for inclusion in this analysis is low. This is an inherent issue in the study of rare disease, necessitating clustering of data to understand broader geographic trends with water body or salinity range as demonstrated here. Second, only case occurrence and location data are available for this study, thus underlying conditions or comorbidities are not part of this analysis. It is well documented that those with pre-existing immunocompromising conditions, such as cirrhosis, are more susceptible to *Vv* infection. Finally, the use of demographic data to serve as a relative proxy for water exposure is not ideal and it would be helpful to involve social science methods to better estimate the number of people who recreated in the Virginia waters of the Chesapeake Bay. Perhaps a combination of the many methods available, each with its own strength and weakness as demonstrated in a literature review by Burns et al (2019) for smaller areas like National Marine Sanctuaries and National Parks, could enhance the estimates of recreational water use across a wider region.

Acknowledgements

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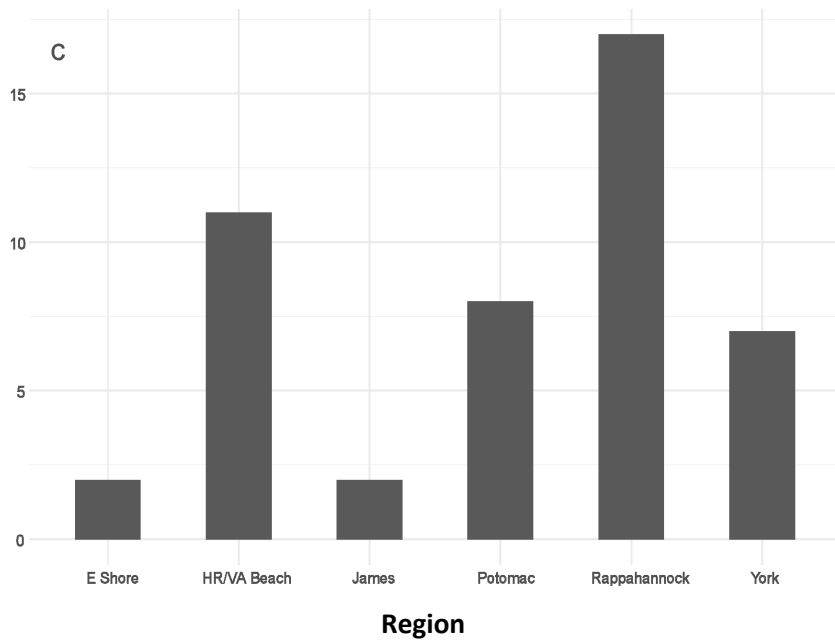
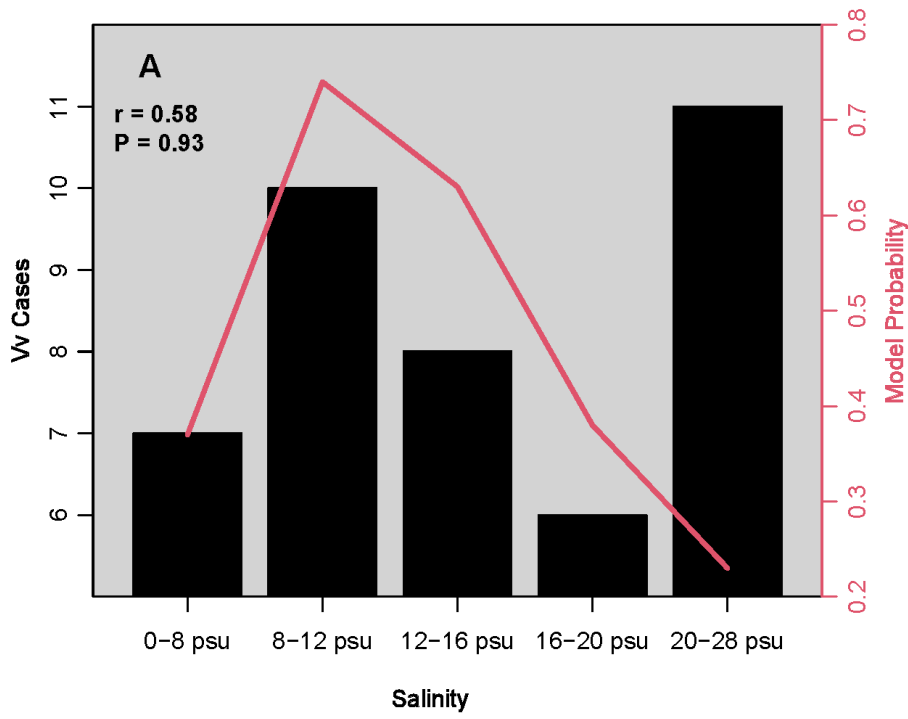


Figure 1. A- Total number of Vv exposure/wound infection cases from 2014 – 2021 reported as occurring in Virginia waters (out of state cases excluded; N=4). B - Number of cases by month of exposure (out of state and unknown dates excluded; N=15). C - Total number of Virginia cases by river/region (Out of state and unknown locations excluded; N=17).



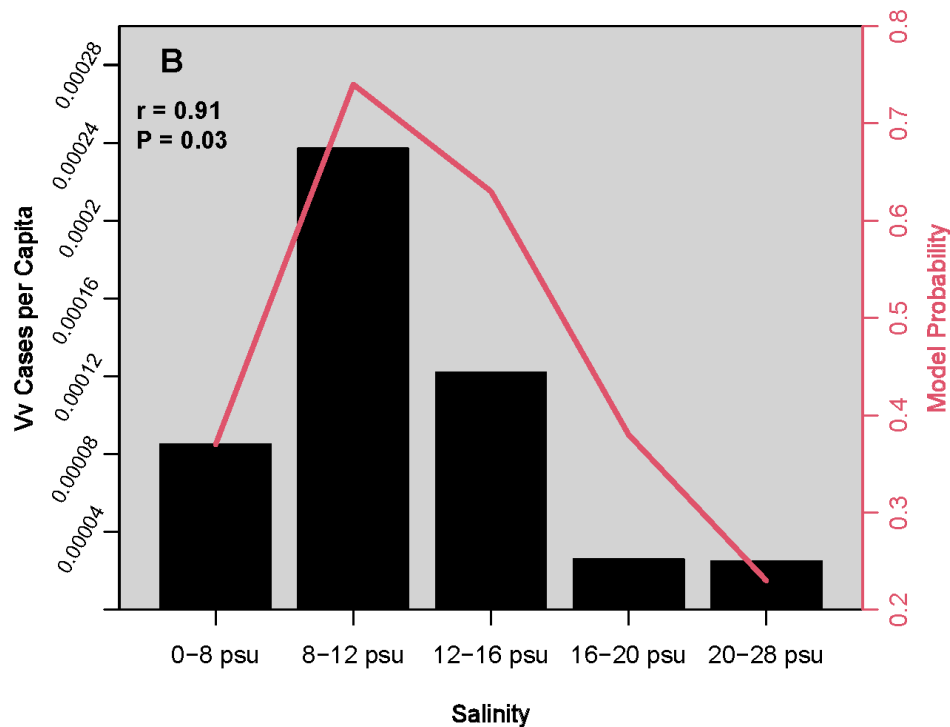


Figure 2. A- *Vv* cases as related to NOAA *Vv* modeled probability of occurrence. Data were sub-setted into salinity bins to demonstrate the relationship with average number of cases. Binning was conducted at 4 ppt intervals and collapsed where necessary to obtain a minimum of 4 observations per bin. B- Modeled probability as related to *Vv* cases per capita.

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