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<http://dx.doi.org/10.1289/EHP218>

**Received: 24 March 2016**

**Revised: 19 August 2016**

**Accepted: 19 August 2016**

**Published: 7 October 2016**

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National Institute of  
Environmental Health Sciences

## **An Analysis of the Potential Impact of Climate Change on Dengue Transmission in the Southeastern United States**

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Running title: Climate change and dengue fever in the southeastern US

This work was supported in part through the CLIMAS project at the University of Arizona, funded by the National Oceanic and Atmospheric Administration's Climate Program Office through grant #NA12OAR4310124, a National Science Foundation Doctoral Dissertation Research Improvement Grant #1302209, and a National Aeronautics and Space Administration Postdoctoral Fellowship. The authors declare that they have no competing financial interests

## Abstract

**Background:** Dengue fever, caused by a mosquito-transmitted virus, is an increasing health concern in the Americas. Meteorological variables such as temperature and precipitation can impact disease distribution and abundance through biophysical impacts on the vector and virus. Such tightly coupled links may facilitate further spread of dengue fever under a changing climate. In the southeastern United States, the dengue vector is widely established and exists on the current fringe of dengue transmission.

**Objectives:** This paper assesses projected climate change-driven shifts in dengue transmission risk in this region.

**Methods:** We used a dynamic mosquito population and virus transmission model driven by meteorological data to simulate *Aedes aegypti* populations and dengue cases in 23 locations in the southeastern US under current climate conditions and future climate projections. We compared estimates for each location to simulations based on observed data from San Juan, Puerto Rico, where dengue is endemic.

**Results:** Our simulations based on current climate data suggest that dengue transmission at levels similar to San Juan is possible at several US locations during the summer months, especially in southern Florida and Texas. Simulations that include climate change projections suggest that conditions may become suitable for virus transmission in a larger number of locations, and for a longer period of time during each year. However, in contrast with San Juan, US locations would not sustain year-round dengue transmission according to our model.

**Conclusions:** Our findings suggest that dengue virus transmission is limited by low winter temperatures in the mainland US, which are likely to prevent its permanent establishment.

Although future climate conditions may increase the length of the mosquito season in many locations, projected increases in dengue transmission are limited to the southernmost locations.

## Introduction

The impacts of climate and climate change on infectious disease dynamics, distribution, and spread have been the subject of significant discussion (Brisbois and Ali 2010; Chaves and Koenraadt 2010; Lafferty 2009; Ostfeld 2009; Pascual and Bouma 2009; Randolph 2009), as temperature can impact the seasonality and intensity of infectious disease transmission (Harvell et al. 2002). Dengue fever, a virus spread predominantly by *Aedes aegypti* mosquitoes, is emblematic of a disease whose rapid expansion may be partly fueled by changing climatic conditions. Bhatt et al. (2013) estimate that the four dengue serotypes (DEN-1, 2, 3, 4) cause 390 million annual infections, 96 million of which are symptomatic, representing a significant global disease burden. Therefore, understanding links between local and global climate and weather patterns, and disease outbreaks, is an important topic of inquiry.

Dengue virus transmission predominantly occurs in tropical regions. However, there has been an increase in the outbreak intensity and spatial distribution of dengue in the Americas over the past decade (Bouri et al. 2012; Brathwaite Dick et al. 2012). Travel within and across countries, the growth of sub-standard urban conditions, and the cessation of public health and vector control programs are collectively understood as contributing to this increase (Gubler & Clark 1995; Wilder-Smith and Gubler 2008). The possibility of concurrent circulation of up to four DEN serotypes in a given location (Halstead 1992) and changing environmental conditions further complicate dengue ecology. Laboratory and field-based studies indicate that climate has an important role in mosquito and dengue viral development and transmission (discussed below). However, linking these variables to actual outbreaks remains challenging.

Meteorological variables such as temperature and precipitation impact the biophysical functioning of the mosquito and breeding habitat (e.g., Christophers 1960). Precipitation can

increase vector density by providing breeding habitat (Moore et al. 1978), while temperature impacts mosquito hatching rate, development time (Mohammed and Chadee 2009) and survival (Tun-Lin et al. 2000). Temperature further influences virus transmission dynamics by shortening the extrinsic incubation period (EIP). Watts et al. 1987 reported that the EIP for the DEN-2 serotype declines from 12 days at temperatures  $\leq 30^{\circ}\text{C}$  to 7 days at  $32\text{--}35^{\circ}\text{C}$ . Similarly, Rohani et al. (2009) noted mosquitoes became infectious with DEN-2 and DEN-4 at day 5 at  $30^{\circ}\text{C}$ , four days sooner than mosquitoes held at  $26^{\circ}\text{C}$  and  $28^{\circ}\text{C}$ . A shorter EIP heightens the transmission potential to humans and outbreak intensity (Jetten and Focks 1997; Patz et al. 1998). These biophysical processes underpin the links between climate variability and observed dengue fever cases across multiple spatio-temporal scales (Cazelles et al. 2001; Gagnon et al. 2001; Hopp and Foley 2003; Johansson et al. 2009), and have led to concerns that virus transmission may increase in regions where has been uncommon (Patz et al. 1998). Recent empirical work in Mexico found a decreasing number of *Ae. aegypti* with increased elevation along an altitudinal transect (Lozano-Fuentes et al. 2012). This study also found populations of *Ae. aegypti* at higher elevations in Mexico than previously recorded within the country. Collectively the results point to the possibility of temperature induced *Ae. aegypti* expansion into areas beyond current geographical boundaries in the future.

Several model-based studies have focused on relationships between climate and dengue, highlighting the utility of these approaches (Bannister-Tyrrell et al. 2013; Focks et al. 1993; Hales et al. 2002; Hopp and Foley 2001; Martens et al. 1997; Patz et al. 1998). Such models are useful tools given a lack of long-term mosquito population records (Morin and Comrie 2010). Dynamic models, in particular, can address data constraints by simulating mosquito populations based on local climate and environmental inputs (Focks et al. 1993; Morin and Comrie 2010).

This is an important advance in understanding the links between climate change and disease because current and future climate scenarios can be used to simulate local mosquito populations for comparison. At the same time, the complexity of mosquito-borne disease ecology means that not all locations will see an increase in disease, and some may actually see a decrease under future climate conditions (Lafferty 2009).

Understanding how the geography of outbreaks may change under future climate is a particular concern in the southern United States because it exists along the periphery of transmission in the Americas. Dengue is epidemic and endemic through parts of Central and South America. While the US has a history of dengue epidemics through the 1940's, decreased transmission is often attributed to changes in social and built environments (Reiter 2001). However, it remains possible that a more favorable climate may render current strategies less useful. For example, recent dengue outbreaks in Florida, Texas, and Hawaii (Bouri et al. 2012), could be indicative of how changing climate may enhance transmission risk.

This paper addresses these concerns by using downscaled projected climate conditions from global climate model (GCM) ensembles to drive a Dynamic Mosquito Simulation Model (DyMSiM) coupled with a virus transmission component. Model parameter values were derived from successful simulations in San Juan, Puerto Rico (Morin et al. 2015), a nearby location with significant dengue burden and the requisite data necessary for model validation. Present and future meteorological data were produced by a statistical weather generator and used to drive DyMSiM and simulate total mosquito populations and human dengue cases for 23 sites in the southeastern US. These sites were selected because they (1) are population centers, (2) completeness of climatic datasets ( $> 98\%$ ), and (3) are regionally at greater risk of tropical disease emergence (Gubler and Clark 1995; Hotez et al. 2014). To isolate the climatic

component, the present and future meteorological inputs were the only variables changed among the sites. We simulated mosquito populations and dengue transmission under current and future climate change projections in the southeastern US to address two primary study questions:

1. *What sites in the southeastern US can currently support dengue fever transmission, and how might this shift under future climate projections?*
2. *How does climate impact the seasonality of the mosquito vector, and the potential transmission of dengue virus in the southeastern US?*

## **Methods & Analysis**

### *Collection and Generation of Climate Data and GCM scenarios*

We downloaded 20 years (1981-2000) of observed daily weather station measurements (temperature and precipitation data) from the Global Historical Climatology Network Database [National Centers for Environmental Information] for each of the 23 sites. Future climate change data were accessed from GCM data housed in the statistical weather generator LARS-WG5 (LARS) (Rothamsted Research). Daily-level data from GCMs are not directly comparable to observed daily data, therefore we used LARS to produce a comparable series. LARS uses historical data to create a new synthetic time series, statistically similar to the observed data at each site, enabling translation between monthly and daily time scales. We evaluated the observed and synthetic time series to assess the software's ability to reproduce realistic daily data. The daily probability distributions (Kolmogorov-Smirnov test) and monthly means (t-test) for precipitation, minimum, and maximum temperatures for each site showed only one statistically significant value ( $p < .01$ ; Jackson, MS, Sept minimum temp). The minimal significance

differences between the observed and synthetic datasets for these values suggests that the synthetic time series reasonably capture the overall patterns of the observed datasets.

We produced time series for the future climate scenario by calculating GCM ensemble projected average monthly changes in temperature (absolute) and precipitation (proportion) between the GCM simulated baseline (1961-1990) and future (2045-2065) periods. We applied the changes in LARS for each site, using the closest location for which the GCMs (1.3-3.9° resolution) were run, to the synthetic time series to create 21 years of downscaled, daily time series of site-specific future mid-century climate conditions (2046-56). We applied the same procedure to generate comparable baseline data to use in place of the observed data. We used an ensemble of 15 GCMs (table 1) to account for models that over-or-under-predict specific variables. The projections used the IPCC SRA1B Special Report on Emissions scenario, which assumes, "A future world of very rapid economic growth, global population that peaks in mid-century and declines thereafter, and rapid introduction of new and more efficient technologies, with the development balanced across energy sources" (IPCC 2007a). This scenario was selected because it was available for all models and is a mid-range emissions and warming scenario (IPCC 2007b).

### *Dynamic Mosquito Simulation Process*

DyMSiM is a meteorologically driven, process-based model containing entomological and epidemiological components. The model was first parameterized to simulate *Culex quinequefasciatus* populations (Morin and Comrie 2010), and has now been adjusted to simulate *Ae. aegypti* and dengue virus development. Using daily temperature and precipitation data,

mosquito populations are simulated by calculating daily rates of development and mortality for mosquito cohorts as they proceed through their life cycle (egg, larvae, pupae, and adult). Development rates are calculated using temperature while mortality rates are dependent on temperature and, in the case of larvae and pupae, water availability. Water habitat is calculated for rain-filled containers (precipitation minus evaporation and spilling) and permanent water sources (levels remain constant). During the adult stage cohorts of mosquitoes proceed through their gonotrophic cycle, including blood meal questing, ovarian development, and egg laying. Rates of feeding and ovarian development are temperature dependent. Once ovarian development is complete and water is available, the eggs are deposited. During feeding, mosquitoes can become infected with the dengue virus at a probability based on human infection rates (see below) and will then proceed through a temperature regulated EIP. We input new cohorts of eggs into the model if the mosquito population drops to zero. This prevents extinction of the mosquito within the model during inhospitable climate conditions.

The human population is simulated using a compartmental Susceptible-Exposed-Infectious-Recovered model. Susceptible humans move to the exposed stage based on the number of infected mosquitoes that have completed the EIP. Exposed individuals remain in the exposed and infectious stages for a period of 5-7 days before recovering from the infection. Mosquito infection rates are calculated using the number of humans in the infectious stages. In order to prevent extinction of the virus, a minimum human infection rate is used when there are few or no infections in the human population. The governing equations for each stage (mosquito and human) as well as the parameters and their equations can be found in Morin et al. (2015).

San Juan was used for model evaluation because of the availability of multiyear dengue case records, which are unavailable in the mainland US due to a lack of long-term transmission.

The climate of San Juan is an important driver of local transmission, and DyMSiM is able to effectively capture inter- and intra-annual variability (Morin et al. 2015). We used the same predictors (7 variables, 96 total parameter values, Table 2) applied in the previous analysis of transmission in San Juan for the present analysis, and while we acknowledge the potential for variation among individual locations, it was not possible to validate these parameters for each location in the present analysis. In addition, standardizing model outputs for each US site against San Juan data, while holding all model parameters other than climate constant, allowed us to estimate the specific effects of climate and climate change on dengue transmission.

The daily meteorological data sets generated by LARS, described above, were used to drive DyMSiM to simulate current and projected future mosquito populations and human dengue cases. DyMSiM also requires the parameterization of additional environmental variables and the site latitude to determine the duration of sunlight hours (which influences the evaporation of standing water). To account for spatio-temporal variability in parameter values and climate conditions, 96 simulations were performed at each site using different combinations of model parameter values. The parameter values were selected to represent ranges of values reported in the literature (Morin et al. 2015). Six of the seven parameters included in our suite of simulations were represented by only two or three possible values because their values are well established (Table 2). In contrast, we included 12 possible values for habitat area (determined by the number and surface area of containers available for egg laying) because of greater uncertainty and potential for variation in this parameter (Morin et al. 2013; Morin et al. 2015). Parameter values for the simulation were chosen from the best-fit 1% of simulations for San Juan, PR for the period 2010-2013, due to their superior ability to replicate patterns of dengue (Morin et al. 2015, table 2). We simulated a total of 21 years of daily total mosquito populations and dengue case

data for each site driven by baseline climate, and repeated this process with the future climate scenarios. After discarding the first year of DyMSiM results to allow for model spin-up time, each of the 23 mainland US sites had four associated 20-year daily time series: (1) total mosquitoes, present climate, (2) total dengue cases, present climate, (3) total mosquitoes, future climate, (4) total dengue cases, future climate.

### *Analysis and Map Visualization Process*

We compared the outputs of the model runs to output from San Juan for each site. The analysis results are indicative of one of two possibilities for each location: (1) transmission in the mainland US site occurs at the same level as San Juan, indicating that the climate is suitable for transmission, but socio-economic factors, lack of importation, or other unaccounted for factors are limiting transmission, or (2) dengue transmission in the mainland US site is significantly reduced or absent compared to San Juan, suggesting that the site climate is not suitable for epidemic dengue. By repeating these steps for the future climate scenarios, we also assessed future transmission potential for each location.

Maps were created from the model output to visualize spatio-temporal variance. For visualization purposes, the daily model outputs (mosquito population and dengue cases) were aggregated to seasonal values by dividing the year into four 13-week periods (approximately JAN/FEB/MAR; APR/MAY/JUN; JUL/AUG/SEP; OCT/NOV/DEC). For each mainland US location and parameterization, data values were averaged across the 20-year runs and then compared with the corresponding data for San Juan, PR. The comparison metric (% of value in San Juan) was then averaged across parameterizations and mapped (Figures 1 & 2).

In addition to estimating mosquito populations and dengue cases during each season for the 23 locations, we conducted a separate analysis to estimate weekly variation in dengue cases for the Key West, FL and Brownsville, TX sites. Specifically, we averaged estimated numbers of weekly dengue cases across the 20-year period to create a single annual time series (at weekly resolution) for each simulation and location. The time series were then standardized against the cumulative annual San Juan dengue cases using the equation below:

$$StDen_{ijx} = \frac{MDen_{ijx}}{\sum_{i=1}^{52} SMDen_{ij}}$$

*StDen* = standardized dengue causes, *MDen* = modeled dengue averaged over the 20 years, *SMDen* = modeled dengue in San Juan averaged over the twenty years, *i* = epi week, *j* = simulation #, *x* = site. An epidemiological week (epi week) is a standardized way of defining the aggregation of days into weeks so that data is comparable across years. We then averaged across all the simulations to create one annual time series each for Key West and Brownsville, respectively, under the base and future climate scenarios. This method is similar to the method used to estimate seasonal averages for all 23 locations. Here, however, the standardization process only serves to highlight the seasonality of transmission (i.e., the percent of the total annual dengue cases that occurred each week).

## Results

Our estimates suggest that under baseline climate conditions, dengue transmission may be possible in several sites in the southeast US (Figure 1). The estimated transmission potential was highest during summer (JUL/AUG/SEP), while some locations in Florida and Texas may

have transmission during the spring and fall as well. In addition, our estimates suggest that South Florida is as climatically capable of supporting dengue transmission as Puerto Rico during the summer months, denoted by estimated values that are 100% of values estimated for San Juan. Absent caseloads during the winter at all 23 sites suggest that for all locations the current winter temperatures are too low to allow virus transmission. However, our estimates suggest that mosquito populations during the winter in southern Florida may be only slightly less than mosquito populations in San Juan (Figure 2). Although our model estimates suggest that *Ae. aegypti* populations may be present at the northernmost sites during the summer and fall, there is little likelihood of local transmission (dengue cases) at during any season in these locations.

Our simulations suggest similar seasonal and regional patterns under projected future scenarios. Estimated numbers of cases (transmission potential) are highest during summer, with a larger number of northern sites showing some potential for transmission during the summer (Figure 1). In the far south, estimated cases are similar to San Juan during the summer, and some transmission could continue in the fall and spring. Model projections also indicate an increase in the length of the adult mosquito season, but with less of an increase in the number of sites affected compared with the estimated expansion of transmission potential (Figure 2).

#### *Site-specific results – Key West, FL and Brownsville, TX*

We conducted additional analysis on Key West, FL and Brownsville, TX because both have had recent dengue cases (see Bouri et al. 2012), but have contrasting climate characteristics. Figure 3 shows dengue cases at these sites as a percentage of total cases in Puerto Rico, along with plotted climate data. Presently, Key West climate conditions are more favorable for transmission than San Juan during the summer (weeks 30-44), with the window widening to

weeks 27-51 under the future scenario. Our modeled output data showed, on average, low but continual transmission throughout winter in San Juan. However, this year round transmission is not maintained in Key West or Brownsville (see also Figure 1). The climate data in Figure 3 show that San Juan has a smaller annual temperature range, with warmer winter temperatures able to support year-round transmission. Conversely, cooler winter conditions are likely to prevent or limit transmission in Key West, even under future climate conditions. Estimates show a similar pattern for Brownsville, but with a shorter time window for transmission that does not currently exceed San Juan. However, transmission is projected to increase in future climate scenarios, exceeding current case numbers in San Juan during summer (weeks 27-35). However, temperatures remain substantially cooler than in San Juan during fall and winter, thus limiting the potential for year round transmission..

## **Discussion**

Our results suggest that the current climate is capable of supporting dengue transmission throughout much of the southeast US during limited periods of the summer months. Evidence of climatic suitability for dengue is not surprising given historic epidemics in this region. According to our model, southern Florida has the highest likelihood of transmission, consistent with the fact that Florida has reported locally-acquired cases every year since 2009 (Khan 2016; USGS 2016). Our estimates for Brownsville under baseline climate conditions also indicate a relatively long infectious mosquito season, consistent with current data for dengue transmission in this location (Bouri et al. 2012).

Although our baseline climate projections suggest that the potential for dengue transmission in southern Florida during the summer is similar to San Juan, outbreaks are much less common in southern Florida than San Juan. This difference is likely to be partly due to differences in social factors that influence transmission, such as housing infrastructure and public health services, which may also mitigate future risk. However, our estimates suggest that environmental factors may also play a role: specifically, the climate in south Florida appears to be too cold to maintain regular dengue transmission throughout the winter months, whereas transmission is sustained year-round in Puerto Rico, albeit at lower levels during the winter.

Our model projections for future climate scenarios suggest that the potential for dengue transmission will continue to be seasonal throughout the southeastern US, without becoming a year-round phenomenon except perhaps in southern Florida, which may have a some winter dengue activity. This could increase the possibility of virus maintenance throughout the winter, at least during warmer than average years. Our estimates also suggest that the length of the potential transmission season will increase for most sites. Although our projections suggest a small possibility of summer dengue transmission at northern sites that currently do not support it (e.g., Virginia, North Carolina, Tennessee, Kentucky, and Missouri), time windows for transmission would be short, and at most, only a few, localized cases would be expected to occur.

In all locations considered, and for both current and future scenarios, the projected time window for dengue transmission is shorter than the seasonal time window for *Ae. aegypti* populations. Studies show that the EIP shortens as temperatures rise above 26 ° C (Watts et al. 1987; Rohani et al. 2009). The ideal temperature range for *Ae. aegypti* is as low as 20°C (Tun-Lin et al. 2000), but the mosquito can remain active until temperatures drop approximately to

between 10°-15° C (Christophers 1960). Our results suggest that conditions favorable for the virus (when simulated dengue cases occur) only arise during the warmest times of the year, likely due to the lengthening of the EIP at lower temperatures. Furthermore, our model suggests that even in locations where mosquitos may survive year round, such as southern Florida, temperatures are too low to permit dengue transmission during an infected mosquito's lifespan during much of the year. Therefore, outbreaks occur only when dengue is reintroduced during favorable conditions, i.e. when the length of the EIP is shorter than the lifespan of the mosquito. In most US locations dengue outbreaks are rare because this potential time window is very short, whereas cases are more common in southern Texas and Florida where the time window for conditions that favor transmission is longer.

Although our findings suggest that current climate conditions during the summer in southern Florida are capable of supporting dengue transmission at levels similar to San Juan, dengue outbreaks are much less common in southern Florida, and while our model projections suggest that lower winter temperatures and a lack of year-round transmission contribute to this difference, social factors, public health infrastructure, and other influences may also play a role, and have been proposed to explain the decline in dengue fever transmission in the southern US over time. Nonetheless, the likely influence of these factors on the risk of dengue does not negate the potential for an increase in transmission under more favorable climate conditions in the future, and our findings suggest that public health departments should be prepared to adapt to new levels of risk that may result from longer mosquito seasons with wider transmission windows.

Geographic proximity also plays a role in disease transmission and spread. Places with significant tourism, such as southern Florida, or places with increased migration between

endemic and non-endemic locations, such as the US-Mexico border region, have recently experience localized dengue outbreaks (Adalja et al. 2012). Therefore, if dengue were to become endemic in Florida, or at least overwinter during some years, the risks to neighboring states could be considerably higher

### *Limitations and Future Work*

A number of important factors known to impact dengue, such as humidity, herd immunity, vector competition, insect resistance, viral mutation, and socio-economic factors, are not included in the model. Nor do we account for land cover variation, geographic relationships to endemic areas, or potential human adaptation strategies. Dengue disease dynamics are complex, and future research should aim to develop more comprehensive models that can better assess the role of such variables.

In light of the above factors, our results should be interpreted as climate-based projections of relative differences in estimated risks, not as concrete predictions of future climate change impacts on dengue fever. The generated climate data provide only possible values for daily temperature and precipitation. Synthetic baseline and GCM datasets are inherently subject to inaccuracies, for example some standard deviation metrics between the observed and synthetic datasets did not perform as well as the evaluation metrics described in the methods section. We attempted to partially address this concern by using the synthetic baseline data in place of the observed data to standardize such inaccuracies across the baseline and future time series for comparative purposes. The use of longer datasets and improved downscaling techniques may improve this in future studies.

Case studies have shown that the spatial distribution of *Ae. aegypti* is heterogeneous within cities and regions (Hayden et al. 2010; Murray et al. 2012). We have attempted to account for this by using the average from 96 different parameterizations that were selected to optimize model performance based on an analysis of data from Puerto Rico. Nevertheless, it remains that some locations in our study may have different spatial patterns of breeding sites than those captured in the San Juan validation, and readers should keep in mind that these results were modeled using San Juan parameters. Further field studies are needed to quantify the distribution of *Ae. aegypti* across US urban landscapes.

While it would be ideal to have accurate mosquito population and breeding site data for each location, the paucity and accuracy of such records and the length of time needed to generate methodologically sound data sets is an ongoing problem in climate and health research. DyMSiM seeks to fill such a void by generating environmentally-driven mosquito populations in the absence of mosquito data. Future work should be focused on evaluating model performance in multiple locations and obtaining better location-specific information for model parameterization. This includes re-validating the model periodically as longer dengue datasets become available.

Finally, more detailed risk assessments are needed to better understand site-specific vulnerabilities. This may include parameterizing the model against local mosquito data, if available, or running the model at finer spatial scales within a city. Given that micro-climatic variations within a community can impact mosquito abundance (Hayden et al. 2010), this may be useful for determining local risk. Inter and intra-annual future climate variations may also impact the seasonality of dengue transmission in ways that current GCMs are unable to account for when downscaled to the local level. As GCM capabilities improve, along with our understanding

of shifting weather patterns, additional analysis may be useful to understanding dengue transmission potential.

These limitations are inherent in modeling approaches. Nevertheless, this technique is useful for demonstrating the contributing role of climate in shaping dengue fever transmission risk within the southeastern US. The impact of climate on *Ae. aegypti* abundance patterns is also important for Chikungunya and Zika viruses. The current DyMSiM model does not incorporate specific characteristics of these viruses, but the potential for an increase in *Ae. aegypti* seasonality may have implications for the transmission of these viruses as well. Future studies incorporating specific temperature thresholds for Zika and Chikungunya viruses would be helpful.

## **Conclusion**

Hosking and Campbell-Lendrum (2012) note a lack of studies quantifying the links between climate and human health. This is particularly true for analyses of future dengue in the southeastern US. We used a dynamic modeling approach to estimate future impacts of climate change on *Ae. aegypti* and dengue cases in the US. Our results highlight the potential influence of climate on both the vector and virus. Some locations may see an increase in both disease risk and vector abundance, while others may see an increase in *Ae. aegypti* populations, but remain on the fringe of dengue transmission. Our estimates suggest that the dengue transmission window is narrower than the *Ae. aegypti* season length at all of the locations evaluated, consistent with stringent climatic limitations on the virus. While social and public health infrastructure play an important role in preventing transmission, this research shows that current

climatic conditions may also be limiting the virus. Our findings indicate that it is too cold during the winter months for viral transmission to be sustained under present mainland US climate conditions. If so, virus re-introduction is required for dengue outbreaks to occur. However, future climate changes may expand transmission potential in the southeast, making dengue a public health challenge in the future.

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## Tables

**Table 1.** The 15 GCMs used to create a single ensemble scenario for each site, obtained through the LARS-WG5 interface (Rothamsted Research n.d.).

<b>GCM Name</b>	<b>Description</b>
BCM2	Bergen Climate Model (BCM) Version 2
CGMR	Canadian Centre for Climate Modeling and Analysis, CGCM2.1(T47)
CNCM3	Centre National de Recherches Meteorologiques
CSMK3	CSIRO Mark 3.0
FGOALS	LASG, Institute of Atmo. Physics, Chinese Academy of Sciences
GFCM21	Geophysical Fluid Dynamics Lab, NOAA
GIAOM	NASA Goddard Institute AOM
HADCM3	Hadley Centre for Climate Prediction and Research
HADGEM	Hadley Centre Global Environmental Model
INCM3	Institute of Numerical Mathematics (Russian Academy of Science)
IPCM4	Institut Pierre Simon Laplace (ISPL)
MIHR	National Institute for Environmental Studies, Japan, MRI-CGCM2.3.2
MPEH5	Max-Planck Institute
NCCCSM	NCAR Community Climate System Model
NCPCM	NCAR/NSF/DOE/NASA/NOAA Parallel Climate Model

**Table 2.** Parameter names, values, and total number of values used to create the 96 different model parameterizations (from Morin et al. 2015).

Parameter Name	Values	# of Values
1 Habitat Area	1.0x10 <sup>7</sup> , 1.4x10 <sup>7</sup> , 1.8x10 <sup>7</sup> , 2x10 <sup>7</sup> , 2.4x10 <sup>7</sup> , 2.6x10 <sup>7</sup> , 2.8x10 <sup>7</sup> , 5.0x10 <sup>7</sup> , 6.0x10 <sup>7</sup> , 7.0x10 <sup>7</sup> , 9.0x10 <sup>7</sup> , 1.0x10 <sup>8</sup> cm <sup>2</sup>	12
2 Container Height	8,12 cm	2
Minimum Human Infection Rate	4x10 <sup>-5</sup> , 6x10 <sup>-5</sup> , 8x10 <sup>-5</sup>	3
Maximum Larval Density	0.5, 1 per cm <sup>3</sup>	2
Adult Survival Rate	0.86, 0.88	2
Length of Human Infectious Period	5, 7 days	2
3 Maximum Mammal Transmission Probability	0.5, 1	2

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1

Habitat area refers to the surface area of water containers (both manual and precipitation filled).

2

Container height refers to the maximum height of water in a container before additional precipitation will spill.

3

Maximum mammal transmission probability refers to the highest probability of transmission of the virus from mosquito to human during a blood meal dependent on temperature.

## Figure Legends

**Figure 1.** Baseline and future dengue cases by season (Winter: JFM, Spring: AMJ, Summer: JAS, Fall: OND). The larger circle denotes present dengue and the inner circle denotes projected future dengue. The scale bar refers to percent of dengue cases compared to San Juan, PR model output for the same period. The sites are: Atlanta, GA; Birmingham, AL; Brownsville, TX; Charleston, SC; Charlotte, NC; Dallas, TX; Jackson, MS; Jacksonville, FL; Key West, FL; Little Rock, AR; Louisville, KY; Miami, FL; Nashville, TN; New Orleans, LA; Oklahoma City, OK; Orlando, FL; Port Arthur, TX; Raleigh, NC; Richmond, VA; San Antonio, TX; St. Louis, MO; Tallahassee, FL; Tampa, FL.

**Figure 2.** Baseline and future mosquitoes by season (Winter: JFM, Spring: AMJ, Summer: JAS, Fall: OND). The larger circle denotes present mosquitoes and the inner circle denotes projected future mosquitoes. The scale bar refers to percent of mosquitoes compared to San Juan, PR model output for the same period.

**Figure 3.** The top panel shows the weekly (averaged across the simulations and years) dengue cases (% of Puerto Rico annual total dengue) for San Juan and the base and future scenarios for Key West, FL and Brownsville, TX. The bottom panel shows the corresponding temperature and precipitation values.

Figure 1.

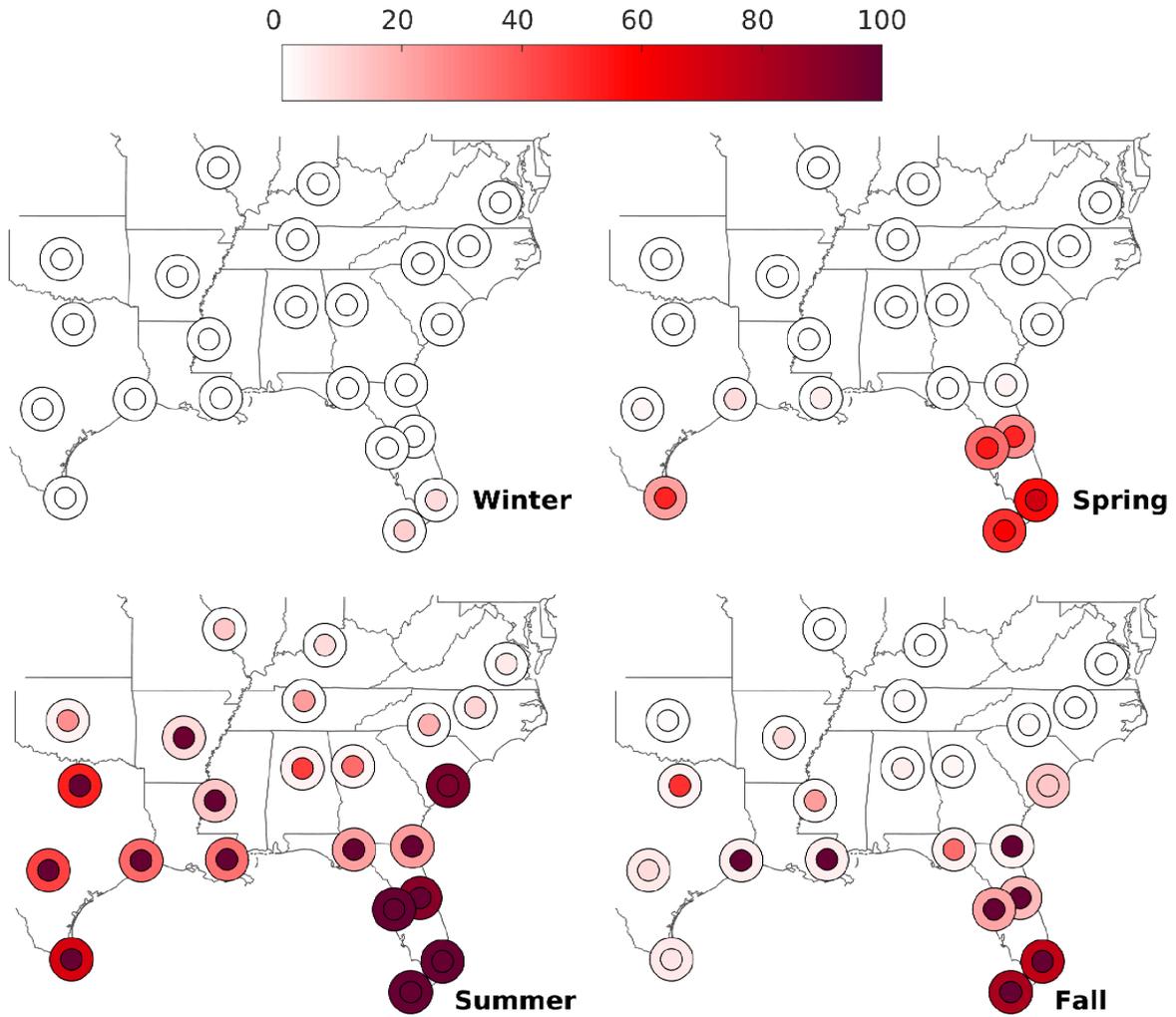


Figure 2.

