

# Ⓜ Potential effect of population and climate changes on global distribution of dengue fever: an empirical model

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## Summary

**Background** Existing theoretical models of the potential effects of climate change on vector-borne diseases do not account for social factors such as population increase, or interactions between climate variables. Our aim was to investigate the potential effects of global climate change on human health, and in particular, on the transmission of vector-borne diseases.

**Methods** We modelled the reported global distribution of dengue fever on the basis of vapour pressure, which is a measure of humidity. We assessed changes in the geographical limits of dengue fever transmission, and in the number of people at risk of dengue by incorporating future climate change and human population projections into our model.

**Findings** We showed that the current geographical limits of dengue fever transmission can be modelled with 89% accuracy on the basis of long-term average vapour pressure. In 1990, almost 30% of the world population, 1.5 billion people, lived in regions where the estimated risk of dengue transmission was greater than 50%. With population and climate change projections for 2085, we estimate that about 5–6 billion people (50–60% of the projected global population) would be at risk of dengue transmission, compared with 3.5 billion people, or 35% of the population, if climate change did not happen.

**Interpretation** We conclude that climate change is likely to increase the area of land with a climate suitable for dengue fever transmission, and that if no other contributing factors were to change, a large proportion of the human population would then be put at risk.

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## Introduction

There is increasing scientific interest in the potential effects on health of global climate change. One area that has received particular attention is the association between climate variation and vector-borne diseases.<sup>1,2</sup> Dengue fever is the most important viral vector-borne disease in the world.<sup>3</sup> The disease affects hundreds of millions of people every year, and is transmitted predominantly by one species of mosquito, *Aedes aegypti*, which has adapted to living near areas of human habitation. It feeds during the day and prefers human beings to other animals. No effective vaccine or drug treatment for dengue fever is yet available, so management of the disease has relied on vector control measures, such as reduction of breeding sites and use of insecticides. Such measures have succeeded in eradicating mosquitoes in some regions, but have proved difficult to maintain in the long term.

Mosquito-borne disease transmission is climate sensitive for several reasons; mosquitoes require standing water to breed, and a warm ambient temperature is critical to adult feeding behaviour and mortality, the rate of larval development, and speed of virus replication.<sup>4,5</sup> If the climate is too cold, viral development is slow and mosquitoes are unlikely to survive long enough to become infectious. Although a suitable climate is necessary for disease transmission, other factors are needed for an epidemic to take place, including a source of infection, vector populations, and a susceptible human population.

Mathematical models project substantial increases in transmission of vector-borne diseases in various climate change situations.<sup>1,6,7</sup> However, these models have been criticised on the grounds that they do not adequately account for rainfall,<sup>8</sup> interactions between climate variables,<sup>9</sup> or relevant socioeconomic factors.<sup>10</sup> An empirical model of malaria transmission risks, which accounted for interactions between climate variables,<sup>9</sup> predicted little change in the size of the at-risk population by the year 2050.

The decline of malaria in Europe and the southern USA in the 20th century was attributable to social and economic development and improved public health services, and not to change in climate.<sup>10</sup> However, this finding does not mean that ambient temperature and rainfall are irrelevant from a health perspective. Climate is one of the fundamental forces behind epidemics, and its effects become evident if adaptive measures falter or cannot be extended to all populations at risk.

Our aim was to describe the current geographical limits of dengue fever transmission on the basis of climate. In an empirical model, we incorporated future projections of climate, to estimate changes in the geographical limits of dengue fever transmission and the size of populations at risk.

## Method

### Data

Dengue fever was defined as present if any outbreak of the disease had been reported between 1975 and 1996.<sup>10</sup> Every country was a geographic unit, except where more detailed information was available, in which case subnational administrative regions were used.

Population projections were based on the spatial pattern in 1990,<sup>11</sup> and region-specific projections for 2055 and 2085.<sup>12</sup> Monthly averages of vapour pressure, rainfall, and temperature recorded between 1961 and 1990,<sup>13</sup> and global circulation model projections of future climate were obtained from the Intergovernmental Panel on Climate Change (IPCC) data distribution centre.<sup>14</sup>

Data were entered into a geographic information system, converted into ASCII grid format. Global circulation model data were interpolated to a resolution of 0.5° latitude and longitude, or 720 grid cells east-west and 360 cells north-south, with a total of 259 200 cells. Of these, the 61 538 cells that represented land were included in the analyses.

### Model

We used logistic regression, fitted by the method of maximum likelihood, to model the presence (1) or absence (0) of dengue, on the basis of 1961–90 climate reports. We used monthly average rainfall, vapour pressure, and maximum, minimum, and mean temperature as exposure variables, singly, and in combination, with or without statistical interaction terms. For model selection, the gridded data were aggregated by administrative region (n=2000). This approach allowed us to keep to a minimum the effect of spatial autocorrelation in the data, while avoiding over-fitting of the model with 20-fold cross-validation. Leaving out each twentieth part in turn, we compared recorded values for the omitted part, with predictions from a model that is fitted to the remaining 19/20ths of the data.

Data were exported from the geographic information system as a text file containing columns for presence or absence of dengue fever, and estimates of climate variables, and rows for each grid cell. Our selected

model was then fitted with these data, and resulted in a modelled baseline risk of dengue fever transmission between zero and one for each grid cell, on the basis of climate data for 1961–90. The accuracy of the model was assessed by comparing our results with the known distribution of dengue fever.

### Future climate predictions

The model results were applied to future climate change situations to generate projections of dengue fever risk in the 2050s and 2080s. As recommended by the IPCC,<sup>15</sup> we estimated future climate by combining recorded baseline data with projections. In 1992, the IPCC defined six alternative scenarios of greenhouse gas emissions, named IS92a to IS92f. These scenarios use a range of assumptions about how future greenhouse gas emissions might evolve in the absence of mitigation policies. All of our analyses used the IS92a scenario, which results in a 1% per year increase in greenhouse gas concentrations leading to about a three-fold rise of CO<sub>2</sub> concentration by the year 2100 compared with 1990 values. This step resulted in a modelled risk of dengue transmission between zero and one for each grid cell.

### Population at risk

A crude estimate of the population living within countries or administrative regions where at least one outbreak of dengue fever had been reported was generated in the geographic information system by overlaying the map of dengue fever occurrence with the gridded 1990 population data. Next, we used output from the regression model to estimate the population at risk of dengue fever.

Previously generated baseline data for risk of dengue fever transmission were reimported into the geographic information system as a text file with a standard ASCII header and one row per grid cell. Following accepted practice, we defined the population at risk according to a probability cutoff of 0.5—ie, estimated populations living in an area where the modelled probability of transmission was greater than 50% were defined as at risk. Transmission probabilities were generated for three situations; the estimated population in 1990 with

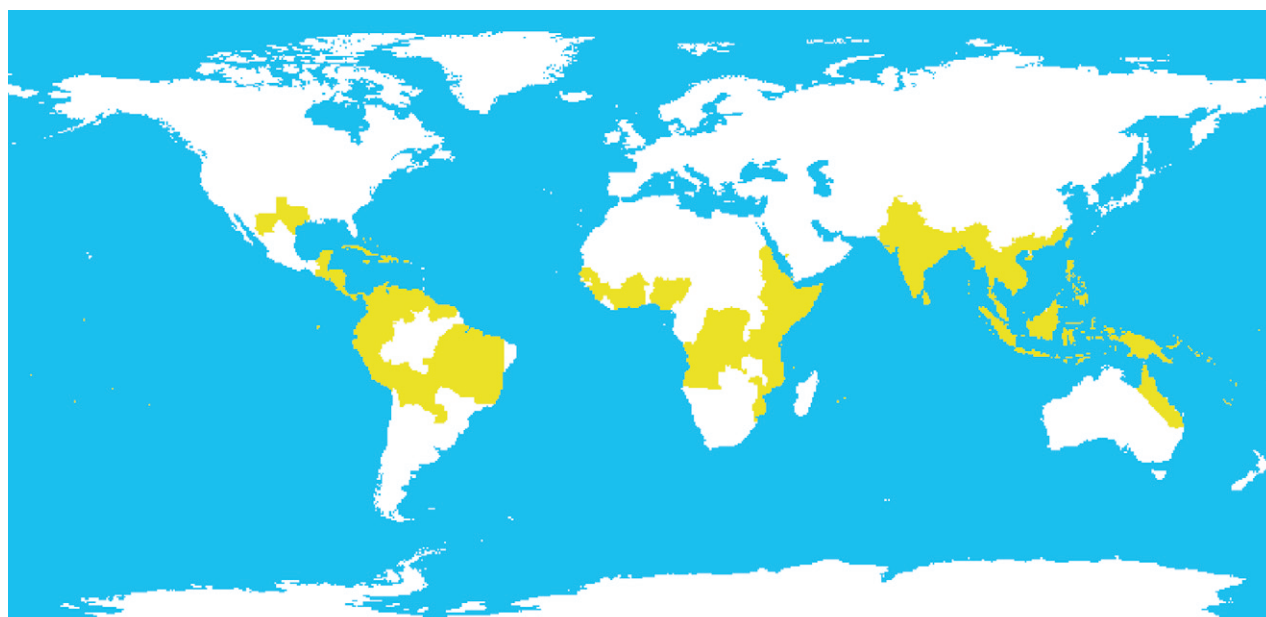


Figure 1: The distribution of dengue fever between 1975 and 1996

In yellow areas there was at least one outbreak between 1975 and 1996.<sup>3</sup>

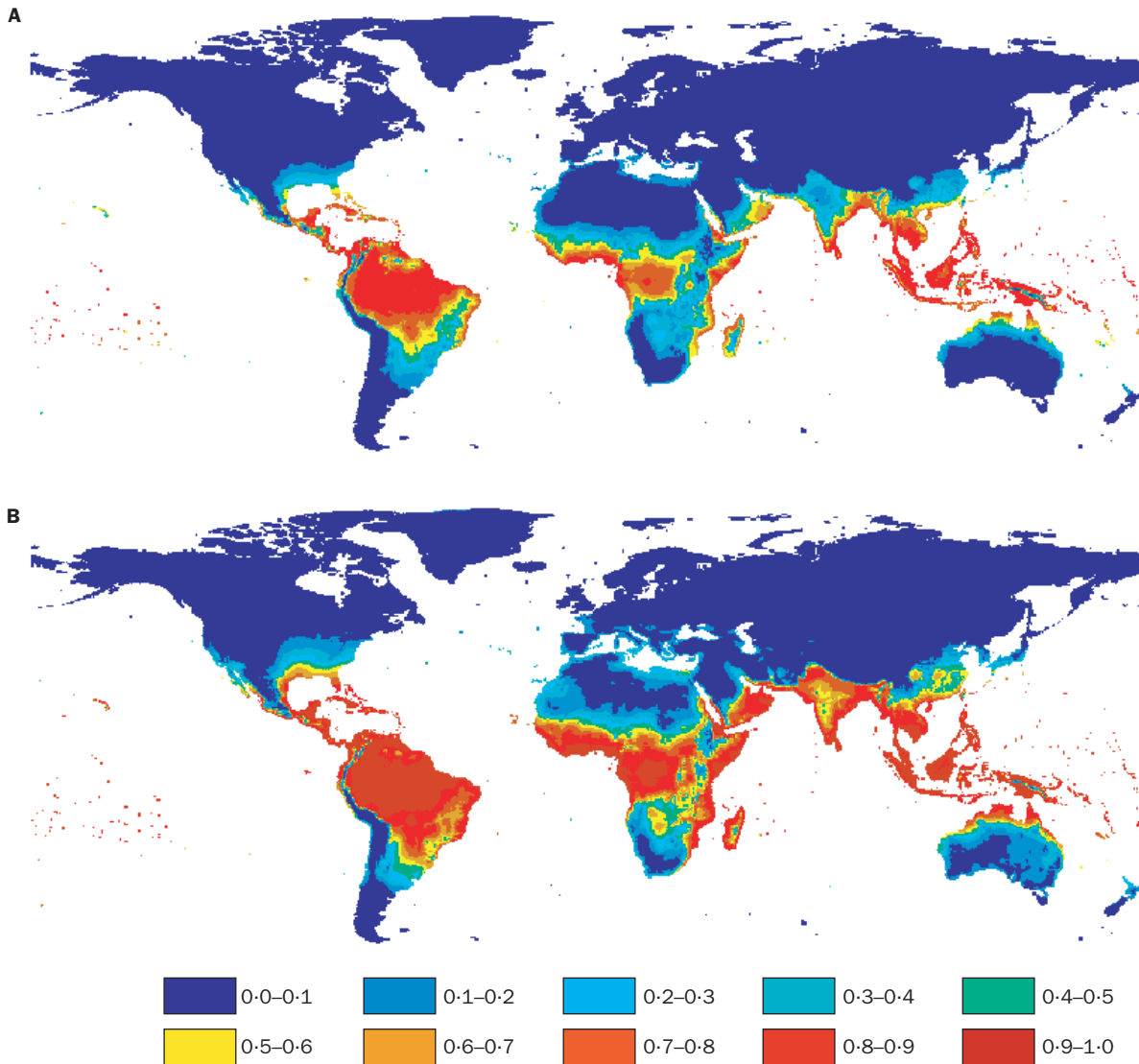


Figure 2: **Estimated baseline population at risk in 1990 (A) and estimated population at risk in 2085 (B)**

Results of a logistic regression model with vapour pressure (humidity) as the predictor of dengue fever risk, using climate data from 1961 to 1990 (A). Forecast geographical distribution of dengue transmission based on climate projections for 2080–2100 from a global circulation model (CGCMA2) (B). Colours represent probability of dengue fever transmission.

1961–90 (baseline) climate data, the projected population in 2055 and 2085 with baseline climate data, and projected population in 2055 and 2085 with climate change projections for those years.

#### Sensitivity analysis

Risk data for dengue fever transmission with expected climate change, and for predicted climate change and population growth were regenerated with alternative global circulation models (ECHAM4,<sup>16</sup> HADCM2,<sup>17</sup> CCSR/NIES,<sup>18</sup> CGCMA2,<sup>19</sup> and CGCMA1<sup>20</sup>); and three alternative models (all of which were for the CGCMA2 model, but with slightly different initial conditions). Because global circulation model data were not readily available, slightly different comparison periods were used for generating model change fields. For the HADCM2, CGCMA1 and ECHAM4 models, average changes in vapour pressure from several models runs (2070–99 *vs* 1961–90) were available from the intergovernmental panel for climate change. For CGCMA2 and CCSR/NIES models, these results were

not readily available and change fields for specific humidity were calculated as ratios for 2080–2100 versus 1975–95 for single global circulation model runs.

Examination of a map of the residuals from our model which generated baseline risk of dengue fever transmission on the basis of baseline climate data, suggested that spatial autocorrelation was not completely removed by the model. We investigated the effect of including further humidity variables in the model, which we hoped would account for some, or all, of this residual autocorrelation. Using the geographic information system, we estimated the maximum humidity for each grid cell within radii of 5, 10, and 20 cells. These data were included in multivariate logistic regression models, with or without statistical interaction terms.

#### Role of the funding source

The funding source did not have a role in the study design, data collection, data analysis, data interpretation, or writing of the report.

## Results

We showed that annual average vapour pressure was the most important individual predictor of dengue fever distribution. Therefore, we chose a cautious final model that contained humidity as the only explanatory variable, which is in keeping with recommendations of the US Committee on Climate, Ecosystems, Infectious Diseases, and Human Health.<sup>2</sup> Vapour pressure proved a significant predictor of dengue fever risk (OR 1.3; SE 0.003;  $p < 0.0001$ ). When areas at risk of dengue fever were defined by a cutoff probability of 0.5, the model fitted with gridded data classified 89% of the grid cells accurately.

On the basis of the reported distribution of dengue fever and the estimated population in 1990, we calculated that 2 billion people, (about 40% of the 1990 world population) lived in regions where at least one outbreak of dengue was reported between 1975 and 1996 (figure 1).<sup>3</sup> We refined this estimate using gridded data to obtain highest accuracy of the estimates of population at risk. However, this method was not perfect, and nearly 5% of the population living near, or on boundaries of land and sea could not be assigned to a risk category by the geographic information system. On the basis of this regression model, we conservatively estimated the baseline population that was at risk in 1990 to be 1.5 billion people (about 30%) (figure 2). If humidity remains at baseline values, and projected increases in population are realised, we forecast that 3.2 billion people (34% of the total population) will be at risk of dengue fever in 2055 and 3.5 billion people (or 35% of the total) in 2085. With these same increases in population, but with changes in humidity projected by the HADCM2 global circulation model, we forecast an increase in the population at risk of dengue fever to 4.1 billion people (44%) by 2055 and 5.2 billion (52%) by 2085. Using four alternative global circulation models, we estimated the population at risk to be in the region of 5–6 billion by 2085 (figure 2).

Model accuracy was improved, and spatial patterning of the residuals reduced, by inclusion of a variable indicating the maximum of humidity within a specific radius in the neighbourhood of each grid cell. The most accurate model included local humidity, and the maximum humidity within a radius of ten grid squares, which is equivalent to 5° latitude, and a variable representing statistical interaction between these two variables. This multivariate model achieved an overall accuracy of 92%, with a sensitivity of 85% and specificity of 93%. We repeated risk calculations for population and climate projections for 2085 using one global circulation model (CGCM2). The population at risk was shown to be 7 billion people (70% of the total).

## Discussion

Our findings confirm that the geographical limits of dengue fever transmission are strongly determined by climate. On the assumption that other factors affecting dengue fever transmission remain the same, we forecast that climate change will contribute to a substantial increase in the number of people and proportion of global population at risk of dengue fever. The finding that the baseline distribution of dengue is well predicted on the basis of reported vapour pressure is biologically credible. Humidity, defined as vapour pressure or specific humidity, is high only where rainfall and temperatures are high, and these are conditions that are conducive to breeding and survival of vector populations, and rapid replication of the virus.<sup>4</sup>

With a suitable climate, other factors, including a source of infection, a vector, and susceptible human populations would also need to be present for an epidemic to happen. Where and when dengue occurs in the future will therefore depend on diverse economic, social, and environmental factors. Although we do not deny the importance of these factors in determining the actual transmission of vector-borne disease, we do not attempt to account for them in our model.

The data for the distribution of dengue fever epidemics are of uncertain quality. However, data for presence or absence of dengue fever, though crude, are likely to be more reliable for our purpose than reports of number of cases. Because we used dengue fever epidemiology data that covered many years, the effect of human interventions is likely to be small. Successful vector eradication campaigns would have biased results towards prediction of the absence of dengue fever. However, because of unfavourable climate conditions, vector control measures are difficult to sustain over time, except in regions where vector survival is precarious.

Spatial autocorrelation is likely to have increased the apparent significance of the results. However, the main results are likely to be conservative, since when we attempted to model residual spatial autocorrelation by including additional variables in the model, the population at risk increased. Furthermore, in this study we are mainly interested in applying the model to predict the effects of an incremental change in humidity at the margins of the present distribution of dengue fever; this prediction should be almost unaffected by spatial autocorrelation. A model that predicts the current distribution with high cross-validation accuracy should continue to perform well when there are incremental changes to humidity as a result of climate change.

Future social trends might move in a favourable direction, which would reduce the likelihood that disease potential is translated into disease occurrence. However, there are other possible situations that might have negative consequences.<sup>1</sup> We have not attempted to account for all possible economic and social futures, nor do we claim to be able to predict the distribution of dengue fever at the end of the 21st century. Instead we have examined the relations between climate variability and dengue fever, independent of other variables. This is vital information for policy makers who want to understand the potential effects of climate change, and to set priorities for mitigation and adaptation. The resurgence of dengue fever and global climate change are driven by similar issues, which include excessive resource consumption in rich countries, an increase in social inequality, and population increases in poor countries. Addressing these issues will help to reduce dengue fever prevalence and global climate change in the future.

### Contributors

S Hales initiated the study and collected and analysed the data. J Maindonald and A Woodward contributed to the study design. All authors contributed to the interpretation of results and writing the paper.

### Conflict of interest statement

None declared.

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