Crowded and warmer: unequal dengue risk at high spatial resolution across a megacity of India

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Abstract

The role of climate factors on transmission of mosquito-borne infections within urban landscapes must be considered in the context of the pronounced spatial heterogeneity of such environments. Socio-demographic and environmental variation challenge control efforts for emergent arboviruses, a major class of pathogens responsible for dengue, Zika and chikungunya, transmitted via the urban mosquito *Aedes aegypti*. We address at high resolution, the spatial heterogeneity of dengue transmission risk in the megacity of Delhi, India, as a function of both temperature and the carrying-capacity of the human environment for the mosquito. Based on previous results predicting maximum mosquitoes per human for different socio-economic typologies, and on remote sensing temperature data, we produce a map of the reproductive number of the disease at a resolution of 250m by 250m. We focus on dengue risk hotspots during inter-epidemic periods, places where chains of transmission can persist for longer. We assess the resulting high-resolution risk map of dengue with reported cases for three consecutive winters. We find that both temperature and vector carrying-capacity per human co-vary in space because of their respective dependence on population density. The synergistic action of these two factors results in larger variation of dengue’s reproductive number than when considered separately, with poor and dense locations experiencing the warmest conditions and becoming the most likely reservoirs off-season. The location of observed winter cases is accurately predicted for different risk threshold criteria. Results underscore the inequity of risk across a complex urban landscape, whereby individuals in dense poor neighborhoods face the compounded effect of higher temperatures and mosquito carrying capacity. Targeting chains of transmission in inter-epidemic periods at these locations should be a priority of control efforts. A better mapping is needed of the interplay between climate factors that are dominant determinants of the seasonality of vector-borne infections and the socio-economic conditions behind unequal exposure.
Introduction

Climate change, globalization, and rapid population growth are accelerating the spread of established pathogens and facilitating the emergence of novel ones, modifying geographical limits and environmental suitability for transmission (1,2). Spatial resolutions finer than those of countries and cities are becoming critical to understand the epidemiology of vector-borne infections, including those transmitted by the widespread urban mosquito *Ae. aegypti* and caused by arboviruses such as dengue and Zika (3–5). Although traditional “well-mixed” mathematical models provide a foundation for epidemiological theory (6,7), the increasing availability of fine-scale data has underscored the importance of explicitly considering the spatial dimension (e.g. 8,9). Consideration of highly-resolved spatial scales is essential to the prediction of transmission risk and efficiency of control efforts in urban landscapes where human density and mosquito abundance can vary widely.

The persistence of dengue virus transmission in urban settings is challenging to control efforts given the pronounced heterogeneity in environmental, demographic and socio-economic conditions. Because humans effectively generate breeding sites for *Ae. aegypti* in the form of a variety of small water containers (10), vector abundance within cities depends on population density and infrastructure (11). The generation of water containers can vary spatially also as a function of socio-economic conditions, especially in developing countries where unplanned urbanization and limited resources leave a part of the population without regular or continuous access to pipe water and garbage collection.

Temperature, another important determinant of vector-borne transmission, can also vary within cities because of the urban heat island effect (UHI). Temperature influences the demographic parameters of mosquitoes, as well as transmission parameters, ultimately determining vectorial capacity (12–14). Importantly, land surface modifications make urban areas warmer than their surrounding peri-urban or rural landscapes (3). Although the local cause of the UHI can vary, several high-resolution remote sensing studies have shown that...
the intensity of UHI can correlate positively with human population density (15–17). Usually, these temperature differences are larger at night than during the day and are more noticeable during summer and winter (18,19). A better understanding of how UHI contributes to dengue transmission hotspots would be invaluable to optimize deployment of mosquito control resources across the scale of a metropolis. Thus, high-resolution datasets allowing translation of temperature heterogeneity into transmission risk especially outside the epidemic season could help us locate environmental niches where mosquitoes survive and breed, enabling viral persistence. Hypothetically, targeting such localized reservoirs could interrupt or minimize chains of transmission across seasons.

Here we examine dengue transmission risk at a high resolution (250m by 250m) in the megacity of Delhi, India. By considering the basic reproduction number, we explore the interplay of temperature in winter with the vector’s carrying capacity in relation to human population density. We show that these two environmental factors act synergistically, producing a larger variation in local disease risk than when considered separately. Case reports for three winters are used to evaluate our risk map. Results underscore the inequity of risk across a complex urban landscape: individuals in dense poor neighborhoods face the compounded effect of warmer temperatures. We then discuss this result in the greater context of global climate change.

Results

We focus on the basic reproduction number, $R_0$, one of the most fundamental quantities in epidemiology measuring the average number of secondary infections produced by one single infection in a totally susceptible population. Although the precise form of $R_0$ depends on the model, its general expression for mosquito-borne diseases (with a single host and vector) can be typically written in such a way to separate the respective effect of two key factors, namely temperature and the maximum number of mosquitoes per human the environment can support, hereafter referred to as the vector’s carrying capacity. Specifically,
$R_0$ can be decomposed into the product of two terms: a function of temperature (that impacts biological parameters of the mosquito and the pathogen within the mosquito), and the ratio of the vector’s carrying capacity ($V$) to the human population ($N$) (Methods). We can thus write $R_0 = f(T) \sqrt{\frac{V}{N}}$, an expression decomposing the effects of climate and socio-economic conditions.

These two variables in the general expression for $R_0$ are spatially heterogeneous within the city of Delhi in the winter season (Fig. 1A). Spatial temperature ($T$) varies about five degrees Celsius (mean $T=18.6 \, ^\circ C$) and the ratio of the vector’s carrying capacity to the human population ($V/N$) shows values ranging from zero to 1.5 (mean $V/N=0.4$). Importantly, both quantities, $T$ and $V/N$, can vary as a function of human density and therefore share a common source of spatial variation. To first address this dependence for $V/N$, we note that mosquito recruitment in urban landscapes is intrinsically related to human activity. The map for $V/N$ specifically relies on the previously inferred dependence of the vector carrying capacity on human density in (20) (Fig. 1B, see Methods). The shape of the function was shown to vary for different socio-economic categories (low, medium and high) as defined in (20,21). In particular, 87% of the spatial units correspond to socio-economic conditions for which $V/N$ increases with population density, with locations that exhibit the most deprived conditions experiencing the fastest increment. Second, for winter temperature, we find here that values, at the same high resolution of interest, are also affected by human density. Although the least dense areas show the highest variability, those most populated tend to be systematically warmer (Fig. 1C). Together, these two patterns suggest the potential synergy of the two environmental variables on dengue risk across the city. In particular, population density would drive the spatial co-localization of elevated winter temperature and vector’s carrying capacity.

**Fig. 1.** Temperature ($T$) and vector carrying capacity per human ($V/N$) in Delhi. A Maps
for a spatial resolution of 250m by 250m for temperature (November night-time) and \( V/N \) in the city of Delhi. B Vector carrying capacity (maximum number of mosquitoes per human) as a function of population density for deprived (triangles), medium (circles) and rich (dots) typologies. C Boxplot of November night-time temperature as a function of population density (boxes illustrate, as is standard, the median with the 25th and 75th percentiles, and the dotted lines indicate the extremes of the distribution).

To address this hypothesis, we examine first the separate effect of each of the two variables and then their joint influence on the spatial variability of \( R_0 \). Frequency distributions in the form of histograms show that both \( T \) and \( V/N \) generate broad ranges in \( R_0 \)'s spatial variability. Compared to the spatial average of \( R_0 \) (about 0.4), consideration of temperature introduces a variation of up to 40% (Fig. 2A) and consideration of \( V/N \) of up to 75% (Fig. 2B). The associated maps exhibit variation that would be absent not only under constant temperatures as expected, but also under the common assumption of a linear increase of vectors with humans in standard coupled vector-human mathematical models (Fig. 2A, B and C). Importantly, when both factors are considered together, the range of \( R_0 \) is larger than when they are considered separately, with many more units at the two extremes of high and low risk conditions (Fig. 2C). In particular, units that do not exhibit a high dengue risk under either factor alone, can do so when their joint effect is considered together (Fig. 2D).

Thus, comparison of the maps indicates that \( T \) and \( V/N \) act synergistically in a considerable part of the city.

**Fig. 2. The effect on the basic reproductive number \( R_0 \) of temperature (\( T \)) and vector carrying capacity per human (\( V/N \)).** Maps and histograms of local \( R_0 \) at 250 m by 250 m spatial resolution for: (A) local temperature with spatially averaged \( V/N \), (B) local \( V/N \) with spatially averaged temperature and, (C) local temperature and \( V/N \). Blue, aqua green and red colors represent respectively a low (\( R_0 < 0.3 \)), medium (\( 0.3 < R_0 < 0.55 \)) and high (\( R_0 > 0.55 \)) risk of local dengue transmission. (D) Percentage of units at high risk for different risk threshold values, computed for: local \( T \) with spatially averaged \( V/N \) (green dots), local \( V/N \) with spatially averaged \( T \) (red dots), and both local \( T \) and \( V/N \) (black dots).

To examine whether the generated risk map has predictive value, we rely on surveillance data over three winter seasons for reported dengue cases at high spatial resolution (Methods). First, we establish a threshold \( R_0^* \) to classify spatial units at risk of dengue...
transmission when $R_0$ is above this value ($R_0 > R_0^*$, $u=1,2,\ldots, U$, where $U$ is the total number of units). Since small values of $R_0^*$ imply a higher number of units at risk, we expect the percent of “hits”, defined as units whose observed cases surpass the threshold, to decrease with increasing $R_0^*$. However, a high number of hits is not necessarily informative.

We can illustrate this by the trivial extreme of $R_0^*=0$, for which we would obtain a 100% trivial success rate because the whole city would be at risk. Thus, to evaluate the $R_0$ criterion, we compute as a baseline the probability of the number of realized hits under the assumption of a random spatial distribution of infected units (for a given threshold). We specifically compute the $p$-value of a binomial process:

$$p-value = \sum_{i=K}^{U_f} \binom{U_f}{i} p^i (1-p)^{U_f-i}$$

where the number of trials is the number of infected units $U_f$, the number of units with cases classified at risk is the number of hits $K$, and the probability that a risk unit is randomly infected is $p=UR/U$, for the number of risk units $UR$. We find that the $p$-value is consistently below 0.05 as $R_0^*$ increases, leading us to reject a random distribution of cases relative to our risk map. (A $p$-value larger than 0.05 is only obtained when $R_0^*$ equals the 97.5th quantile, that is when 2.5% of the units are classified at high risk).

Because population density underlies both components of $R_0$, we can further ask whether considering a threshold defined directly on the basis of local human density would also be informative. We repeat the calculation of a binomial probability now with a minimum population density threshold as an indicator of dengue transmission during the winter season. We find that this condition works as well as one defined on the basis of $R_0$ as an indicator of winter hotspots (see Fig. 3).

**Fig. 3.** Performance of risk maps for the prediction of dengue cases in winter (at a resolution of 250 m by 250 m). The $p$-value is computed from a binomial process for different risk thresholds. The threshold values are defined by the percent of units at risk (quantiles), for the criterion based on either $R_0$ (black dashes) or population density ($N$) (red...
circles).

Discussion

The spatial distributions of the two dengue drivers taken together, for temperature and vector carrying capacity to human ratio, are here shown to produce important variability in local suitability for virus transmission at high resolution within the city. Although the influence of these drivers could be expected, their joint action reflects a common underlying influence of population density, which proves critical for the localization of winter hotspots. Identification of such hotspots will be invaluable for interrupting the chain of transmission during the low season when it should be most vulnerable to intervention.

The synergistic action of the two drivers especially affects the least developed areas of the city, with 70% of the winter cases reported from within socio-economic units classified as deprived, and only 22% and 8%, from medium and rich typologies respectively. Deprived units are typically densely populated with only a few green areas, which can favor the UHI effect. In addition, the number of vectors per human is higher in poor areas of the city, where one can expect a higher production of breeding containers (10). This socio-economic disparity in dengue suitability is also clear in our risk map, which yields a higher percentage of risk units in the deprived typology as the threshold $R_0^*$ increases (Fig. S1).

The location of reported cases over three winter periods validates the high-resolution risk map obtained here when compared to the random distribution of infections across units. Although the values of $R_0$ obtained for our map remain below one, this does not necessarily imply the absence of transmission (22,23). The commonly used threshold of $R_0=1$ assesses the risk of an outbreak from a purely deterministic perspective. Although such an outbreak is not expected in Delhi during the off-season and transmission in small areas is inherently stochastic, higher values of $R_0$ even below one, should indicate higher transmission suitability, and therefore a higher chance of persistence of transmission chains off-season.
Because human density influences local vector carrying capacity and temperature, this quantity can also be used effectively as an indicator of dengue transmission risk in winter. As a purely statistical indicator, the associated threshold can be less informative, however, than a more mechanistic and direct understanding of how population density ultimately impacts risk (24–26).

A limitation of our results is the reliance on a single detailed remote sensing image. The pattern of increasing temperature with density should, however, hold more generally as it has been reported by other studies (15,16).

Direct measures of mosquito abundance across the urban landscape would be valuable but extremely challenging in practice, especially at fine scales (27). Mathematical models of coupled vector-human transmission commonly assume a constant vector-to-human ratio (28). This implicit assumption implies a constant risk landscape across the city in terms of $V/N$ and, therefore, precludes the variation in risk described here. We have relied, for our risk map, on an indirect estimate of maximum mosquito numbers per human (20). Interestingly, the predictive power of the $R_0$ threshold provides support for this indirect estimation of $V/N$.

The challenges posed by climate change require a robust and holistic approach to understanding infectious disease dynamics (23). Understanding climate change effects on infectious disease transmission remains a crucial gap within urban landscapes at sufficiently high spatial resolutions, including potential synergies with various demographic and socio-economic drivers. We have shown that the fine-scale interaction of temperature and socio-economic conditions (related to vector production) amplifies local dengue transmission suitability. Both these factors are sensitive to climate change directly and indirectly. Warmer winter temperatures where cold temperatures limit transmission can favor persistence of
mosquito populations outside the epidemic season. Climate change can also favor breeding site production, as climate instability in the form of extreme events can contribute to poverty and overcrowding as the result of enhanced and unplanned human migration (29). Although our findings are for dengue in the megacity of Delhi, we expect the described synergistic effect of temperature and mosquito carrying capacity to apply more broadly to other urban landscapes and other climate-sensitive infections, especially in developing countries with seasonal transmission.

Methods and Materials

Expression of the basic reproductive number as a function of temperature and vector carrying capacity per human.

The basic reproductive number gives the average number of secondary infections that would result from introducing a single infective individual into an entirely susceptible population. Calculation of \( R_0 \) for dengue infection involves a two-step process: host to vector, then vector back to host (or vice versa). To illustrate this process, we rely on the following standard equations for the infectious classes in coupled vector-human models:

\[
\frac{dI}{dt} = a P_{MH} Z S / N - (\mu_H + \gamma) I \quad \text{(1a)}
\]

\[
\frac{dZ}{dt} = a P_{HM} W I / N - \mu_M Z \quad \text{(1b)}
\]

where \( W, Z \) and \( M \) (for mosquitoes), and \( S, I \) and \( N \) (for humans), denote susceptible, infectious and total populations, respectively. Parameter \( a \) denotes the biting rate, \( P_{MH} \) (for a human) and \( P_{HM} \) (for a mosquito) are the respective probabilities that an infectious bite results in an infection, \( \gamma \) is the recovery rate of infected humans,
and $\mu_h$ and $\mu_M$ the respective mortality rates for humans and mosquitoes.

Let $R_{0_{MH}}$ be the number of hosts directly infected by the introduction of a single infective vector into an entirely susceptible host population. Similarly, let $R_{0_{HM}}$ denote the number of vectors that become directly infected upon the introduction of a single infectious host into an entirely susceptible vector population. When the host population is entirely susceptible ($I=0$ and then $S=N$), the transmission rate from the vector population to the host population is given by $a \cdot P_{MH} \cdot Z$. Thus, the transmission rate per infective vector equals $a \cdot P_{MH}$ (eq. 1a). Since infective vectors live for an average of $1/\mu_M$ time units, a single infective vector will give rise to $R_{0_{MH}} = a \cdot P_{MH} / \mu_M$ infective hosts. Employing a similar argument for an entirely susceptible vector population ($Z=0$ and thus $W=M$), we obtain (eq. 1b)

$$R_{0_{IM}} = \left[ a \cdot P_{IM} / (\mu_M + \gamma) \right] \cdot (M/N).$$

Therefore, over the entire transmission cycle we obtain the following expression,

$$R_0 = \sqrt{R_{0_{HM}} \cdot R_{0_{MH}}} = \sqrt{\frac{a^2 P_{IM} P_{MH}}{\mu_M (\gamma + \mu_H)}} \cdot \frac{M}{N} = h(T) \cdot \frac{M}{N}$$

(eq. 2).

We can decompose this expression into two main factors: one that depends on demographic and biological parameters which are constant or depend on temperature ($h(T)$, where $T$ is temperature), and another that is the ratio between mosquito and human numbers.

Because the developmental life cycle of Ae. aegypti is complex, coupled mosquito-human models commonly assume that the total abundance of mosquitoes follows logistic growth, with for example an equation of the form
\[ \frac{dM}{dt} = \lambda M \left(1 - \frac{M}{K}\right) \quad (3) \]

where \( \lambda \) represents the number of offspring per adult female per unit time, and, \( K \), the carrying capacity supported by the environment. By making a quasi-stationary assumption whereby the population dynamics of the vector equilibrates quickly to temporal variation, we can consider that \( M \sim K \) (by equating eq. (3) to zero). Variations of this expression for mosquito abundance are of course obtained depending on model details. For example, (30,31) proposes that

\[ \frac{dM}{dt} = EFD \cdot p_{EA} \cdot M_{DR} \cdot \mu_{M}^{-1} \cdot M \left(1 - \frac{M}{K}\right) - \mu_{M} \cdot M \]

(4) (an expression obtained by adding equations (1), (2) and (3) for susceptible, exposed and infectious mosquitoes populations in the original article), and therefore

\[ M \left(1 - \frac{\mu_{M}^2}{(EFD \cdot p_{EA} \cdot M_{DR})}\right) \cdot K \]

where \( EFD \) is the number of eggs laid per female per day, \( p_{EA} \) is the probability of mosquito egg-to-adult survival, and \( M_{DR} \) is the mosquito egg-to-adult development rate. Another example is found in (20) where

\[ M \left(\frac{\lambda}{\mu_{M}}\right) \cdot K \]

In short, models in which the differential equation for mosquito abundance follows a form in the family of logistic functions (eq. (3)), produce generically the form

\[ M \cdot g(T) \cdot K \]

where the particular expression of the function \( g(T) \) depends on the model.

Here, we specifically used the following differential equation for adult mosquitoes

\[ \frac{dM}{dt} = EFD \cdot p_{EA} \cdot M \left(1 - \frac{M}{K}\right) - \mu_{M} \cdot M \quad (4) \]

Then, by introducing the value of \( M \) obtained from equating the left-hand side of this equation to zero into the expression in eq. (2), we specifically obtain
\[ R_0 = \sqrt{\frac{a^2 P_{HM} P_{MH}}{\mu_M(y^+ \mu_H)}} \] \[ M = \sqrt{\frac{a^2 P_{HM} P_{MH}}{\mu_M(y^+ \mu_H)}} \left(1 - \frac{\mu_M}{EFD pEA} \right) \frac{K}{N} \] \[ h(T) g(T) \frac{K}{N} = f(T) \left(1 - \frac{\mu_M}{EFD pEA} \right) \frac{K}{N} \] (5)

The values of the parameters of \( f(T) \) and their dependence with temperature are given in Table 1. We emphasize that although we illustrate the risk maps for this model and therefore this specific form of \( f(T) \), the results should generalize to other models.

The carrying capacity as a function of the human population per spatial unit is computed with the curves inferred in (20). We summarize here the basic approach. For \textit{Ae. aegypti}, it is reasonable to consider that \( K \) depends on \( N \), or \( K=K(N) \), since humans generate the breeding sites for the mosquito. We can expect that this production of breeding sites and therefore the shape of the \( K(N) \) function, depend in turn on socio-economic conditions of the local human population. Because it remains extremely challenging to sample and quantify mosquito numbers, we rely on the results obtained in (20) where mosquito numbers were inferred from human population density. Importantly, \( K(N) \) was shown to vary with socio-economic conditions on the basis of the typologies classified in (21), with \( K \propto N^2 \) and \( K \propto N^{1.24} \) for typologies denoted respectively as deprived and intermediate, and a non-monotonic, increasing and then decreasing, behavior for those denoted as rich (see Fig. 1B).

<table>
<thead>
<tr>
<th>symbol</th>
<th>description</th>
<th>formula</th>
<th>parameters value</th>
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<tbody>
<tr>
<td>( a )</td>
<td>biting rate (days(^{-1}))</td>
<td>( c \cdot T \cdot</td>
<td>T - T_{min}</td>
</tr>
<tr>
<td>\textit{EFD}</td>
<td>rate of eggs laid per female (days(^{-1}))</td>
<td>( c \cdot T \cdot</td>
<td>T - T_{min}</td>
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TABLE 1. Model parameter specifications. Values without references indicate that they have been determined for this article (see Fig S1).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Value</th>
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<tbody>
<tr>
<td>$p_{EA}$</td>
<td>probability of mosquito egg-to-adult survival</td>
<td>$c \cdot (T - T_{\text{min}}) \cdot (T_{\text{max}} - T)$</td>
</tr>
<tr>
<td>$\mu_{M}$</td>
<td>mosquito mortality (days$^{-1}$)</td>
<td>const.</td>
</tr>
<tr>
<td>$P_{HM}$</td>
<td>probability virus transmission from human to mosquito</td>
<td>const.</td>
</tr>
<tr>
<td>$P_{MH}$</td>
<td>probability virus transmission from mosquito to human</td>
<td>$c \cdot T \cdot (T - T_{\text{min}}) \cdot \sqrt{T_{\text{max}} - T}$</td>
</tr>
<tr>
<td></td>
<td></td>
<td>&amp; $T_{\text{max}}=13$</td>
</tr>
<tr>
<td>$\gamma$</td>
<td>human recovery rate (days$^{-1}$)</td>
<td>const.</td>
</tr>
<tr>
<td>$\mu_{H}$</td>
<td>human mortality (days$^{-1}$)</td>
<td>const.</td>
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**Temperature data from remote sensing**

Satellite brightness temperature was retrieved from LANDSAT 8 TIRS (band 10). The thermal image was taken on November 15, 2013 at around 5:00 AM. Land surface temperature was computed by the methods of [Walawender 2014] (by incorporating the correction equations for land surface emissivity and atmospheric bias). Surface temperatures were obtained at a 38 m scale and then aggregated to the 250 m by 250 m spatial resolution (see details on (36)).

**Dengue cases for the winter season**

The dengue cases were geo-localized for the winter seasons from 2013 to 2015. These are the seasons for which dengue cases were reported in winter for the first time. Dengue cases were confirmed for the presence of IgM antibodies against DENV by MAC ELISA using a kit prepared by the National Institute of Virology, Pune, India as an integral part of the National Vector Borne Disease Control Programme.
These confirmed cases were geo-coded with QGIS (36).

**Ethics Statement**

Written consent to participate in the study was obtained from all participants and ethical approval was granted by the ethics committees of the Indian Council for Medical Research, India (N° TDR/587/2012-ECD-11, 10 December 2012) and Institut Pasteur, France (N° 2011–20, 29 April 2011). If human subjects were not adult, a parent or guardian of the child provided written informed consent on their behalf.

Patient data were anonymized.

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**References**


Fig. S1. Model parameters (eq. 5) as a function of temperature. The black circles represent experimental data (from (32) Supp Material), the red dots the mean value (with respect to temperature) and the dashed red lines the curves used as a model to describe the parameters variation. A biting rate (data values from (37,38)). B Number of eggs laid per
female per day (data from (39,40)), C probability of mosquito egg-to-adult survival (data from (41–45)). D Probability of virus transmission from a bite of an infected mosquito to a susceptible human. E Probability of a susceptible mosquito to get the virus following a bite on an infectious human (D and E data are from (46–49)). The parameters of the curves shown in panels A, B and C are taken from (32) and those of panels D and E were determined in this article.

**Fig S2.** Percent of units at risk that belongs to the different socio-economics typologies as a function of $R_0^*$ (threshold to classify spatial units at risk of dengue transmission when $R_0$ is above this value). Pink triangles denote low socio-economic typologies, whereas black circles and gray dots represent medium and rich socio-economic conditions, respectively.
Figure 1: 

A: Spatial distribution of temperature (°C) and V/N ratio. 

B: Scatter plots showing the relationship between carrying capacity (V) and population size (N) in different units. 

C: Box plot illustrating the distribution of temperature (°C) across different population sizes (N).
Figure
Figure supporting information
Figure supporting information