

The Impact of Climate Change on Vector-Borne Infectious Diseases

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Abstract: There is an increased realization that climate change is a severe force of global health issues especially in the proliferation of vector-borne infectious diseases. Increasing temperatures, changing precipitation patterns, and extreme weather are changing the ecosystem, affecting the distribution, abundance, and activity of vectors, including the mosquitoes, ticks, and flies. These environmental changes increase the geographical distribution of such diseases as malaria, dengue, Zika virus, Lyme disease and chikungunya bringing them into the areas where there were none before. In addition, altering climatic conditions influence the life cycle of pathogens and vectors and as a result, cause a shift in the transmission patterns and seasonality of the disease. The risk is excessively practiced by vulnerable populations, mostly in low and middle-income countries, since the adaptive capacity is partial and the public health infrastructure is overstretched. The paper discusses the complex connection between the climate change and the diseases transmitted by vectors, summarizes findings of recent epidemiological and ecological research and points out the necessity of combined mitigation and adaptation measures. To decrease the future health burden in an era of increasing climate change, it is necessary to strengthen surveillance systems, improve the control of the vectors, and increase global collaboration.

Keywords: VBDs, climate change, zika virus, dengue, malaria, mosquito borne infections.

INTRODUCTION

Malaria, dengue, Zika virus, chikungunya and Lyme disease are a significant health burden to the world, with over 700,000 deaths worldwide each year, transmitted by vectors. They are spread through the ecology and behaviour of vectors, in the first place, the mosquitoes, ticks, and flies, the life cycle of which is strongly affected by environmental factors. Climate is one of such conditions which particularly influence the geographical distribution, activity season, and reproduction potential of both vectors and pathogens. Due to increased temperature of the earth, changed precipitation patterns, and increasing extreme weather events, climate change has been increasing rates of change of the dynamics of diseases. The increase in temperature can increase the geographical distribution of vectors into previously unsuitable areas, whereas increased rainfall and floods can form new breeding grounds. However, in some parts of the world, droughts and increasing temperatures can control the populations of vectors, which also indicates that climate effects are complex and also region-specific. As an illustration, malaria has started invading into the higher altitude in East Africa and South America, and dengue fever has threatened to invade the temperate areas, which were thought to be low-risk zones.

Backdrop and importance.

The epidemiology of vectors-borne infectious diseases (VBDs), which are carried by organisms like mosquitoes, ticks, and fleas, is extremely sensitive to climatic factors, leading to hundreds of millions of cases annually and more than 700,000 deaths yearly all over the earth [1].

Climate as a Key Driver Climate conditions like temperature, precipitation and humidity have extremely harsh effects on the biology of the vectors; reproduction, development, survival, and incubation of pathogens, thereby affecting disease transmission dynamics [2]. Trends that should be followed and forecasted. The past decades have seen an increase in the frequency of the following type of diseases as malaria, dengue, Lyme disease, and West Nile virus and it will further increase within the next few decades unless the mitigation and adaptation strategies are upgraded [3]. Indicatively, the malaria vectors have been extending to the ever rising heights such as the highlands of Colombia and Ethiopia even with slight warming of temperatures which is 0.2degC per decade [4].

Climate change does not equally affect diseases that are transmitted by the vectors. Potential competition Warming can enhance the transmission potential in regions and reduce the transmission potential in other regions. Other factors such as land use moderate such

results as well as the practice of controlling the vectors and the socioeconomic status [5]. Public Health Inequities the burden falls on the populations of low- and middle-income countries, in which the gap in healthcare infrastructure and adaptive capacity brings about the health gap across the globe [6]. Delicateness of Investigations and Reactions. With the change of the risk and the geography, improved epidemiological monitoring, predictive models and measures of health such as early warning systems, vectors control and community education is currently at its knees [7]. The implications of these trends on the well being of the world population and the healthcare structure and efforts implemented to contain vectors are bound to be strained or straining to the limit particularly in the low- and middle-income nations. Meanwhile, new threats are also being formulated by less developed nations because the altering climate provides both the north and the south with disease vectors. In order to deal with such problems, there is the necessity to embrace interdisciplinary approach that will accommodate climate science, epidemiology and public health and policy. Stricter surveillance, predictive modelling, and adaptive measures of controlling vectors will play a significant role to lower the rising risks of the spread of vectors in a warmer world.

Related Work

Scoping Analyses Studies Review.

It give initial indications of increased dengue occurrence at a faster pace such as a 30-fold rise in the last 50 years and map climatic and ecological accelerators of disease dissemination [8].

The proposed is concerned with the role of increased temperature, changes in precipitation, and ecological changes in promoting malaria, dengue, Zika, and chikungunya among other tropical areas [9].

It also extends its findings to relate the rising temperatures to the rising rates of transmission as well as to variation in the efficacy and stability of drugs [10].

It is suggested that the paper will provide an extensive scoping review of the impact of temperature and humidity on the ecology and presence of vectors on human health with a focus on the gaps in modeling and surveillance studies [11].

Empirical & Modeling Papers

In order to examine thirty years of monitoring data on climate and disease transmission, it would be required to prove the increased habitats of vectors, their faster breeding cycles, and difficulty in controlling vectors [12].

It present "Episcanner," a spatial-temporal model, which maps the transmission of dengue and chikungunya in all Brazilian municipalities (2010-2023) and connects

climatic variables such as ENSO, rainfall, and temperature to the epidemiological process [13].

The model how the environmental factors (e.g. precipitation, temperature pattern, elevation, etc.) influence the distribution of West Nile virus in South America, where southern Brazil, Bolivia, Paraguay, even Galapagos are becoming more susceptible [14].

MATERIALS & METHODS

The next section is a long, reusable Materials and Methods (which you can copy-paste into your paper, or customize based on the specifications of your journal of interest). It discusses study design, data sources, data processing, statistical and mechanistic modeling, validation, analysis of the uncertainty, ethical issues, and reproducibility.

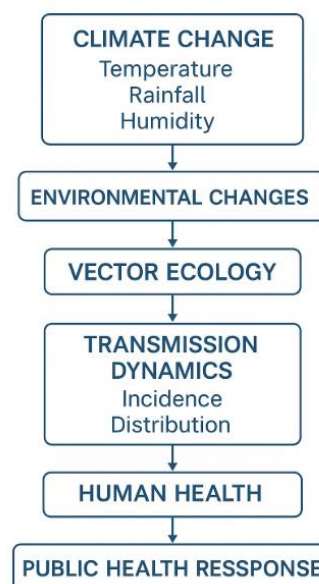


Fig.1. Conceptual model

This model will demonstrate figure 1 how the climate variables (temperature, rainfall, humidity) impact on the ecology of the vectors, spread of pathogens, exposure to people with subsequent changes in disease incidence and distribution.

Study design

An empirical modeling and mixed methods analysis that consists of (1) descriptive epidemiology, (2) statistical time-series and regression analysis to quantify climate-disease relationships, (3) mechanistic transmission modeling to estimate the potential of transmission (e.g. temperature-dependent R_0), and (4) species distribution modeling (SDM) to project occurrence of suitable habitat of vectors and potential range changes under climatic conditions. It has been analyzed on many scales (spatial 1990-2020 1990-2020 1990-2050 1990-2100 national subnational/province and grid-level 510 km and 510 km), and the time periods of interest include historical

(historical baseline 1990-2020), near-term (2021-2050), and long-term (2051-2100).

Study area and period

Geographic range: the study of the whole world with an example of the regions in it (choosing e.g., East Africa, southeast Asia, South America) to illustrate heterogeneity. Temporal focus The model fitting will be performed to forecast the events of 2020-2050 and 2051-2100 based on CMIP6 climate scenarios (SSP2-4.5 and SSP5-8.5) using historical data between 1990 and 2020 years.

Data sources Climate & environmental data.

Topography: SRTM elevation. Epidemiological data In the human: nationwide surveillance, WHO illness occurrence (dengue, malaria, chikungunya, Zika, West Nile, Lyme), CDC National Notifiable Diseases (where available). Add all the units of analysis each week or month. Outbreak report: ProMED sends messages to the national health ministry to verify extremes

Entomological / vector data

Presence/absence, surveys of vectors of abundance of vectors (literature, entomology labs countrywide), VectorMap, GBIF (records of species occurrences) (Aedes aegypti, Aedes albopictus, Anopheles spp., Ixodes spp.). experiential support on life-history characteristics are biting rate, temperature, mortality and dependent growth of vectors

Socio-demographic data: Data on the socio-demographic factors influencing healthcare delivery in NYC include age, gender, educational level, and marital status. <|human|>Socio-demographic data: The age, gender, educational level, and marital status data form the socio-demographic factors controlling the delivery of healthcare in NYC.

Population density (WorldPop), age structure, urban/rural, access of health services, net coverage with insecticides, interventions in which insecticides are used to decrease the vectors (IRS/ITN campaigns), socioeconomic factors.

Data preprocessing

Consolidate the resolving of space by resampling climatic layers and raster covariates to a similar grid, e.g. 5 km. Coalesce case data to spatial units which are identical (grid, district, province). Time re-alignment: align all time series on time resolution (weekly/monthly). In situations where it is reasonable to impute the missing values (checking sensitivity). With statistical bias correction (quantile mapping) CMIP6 results are statistically correct. Variable derivation: compute biological variables of interest (e.g. mean temperature in warmest quarter, total rainfall in last 8 weeks, degree-days above threshold). Occurrence thinning/sampling bias correction: in SDM, spatial thinning and background sampling strategies are to be used to correct sampling bias.

Statistical analyses

Descriptive analysis Trends of plot time, seasonal decomposition, change-point detection and spatial incidence maps. Determine the incidence rates (per 100000) and where possible the age-standardized rates.

Regression modeling and time-series. count data (Poisson or negative binomial with overdispersion) Generalized linear / additive models (GLM/GAM) to estimate the connection between climate covariates and incidence of disease:

Cases_{it} ~ Poisson(mit) log(mit) = a + s (Temp_{it}) + s (Rain_{it}) + s (Humidity_{it}) + f (season) + offset (log (Pop_{it})) + eit.

S () are smoothers in GAMs. Distributed Lag Nonlinear Models (DLNM) to estimate the delayed and nonlinear effects of temperature/precipitation on incidence: can be done using dlnm R package. Mixed-effects regressions with a spatial clustering as well as random effects at the administrative unit: glmer (R) (Bayesian spatial models) and INLA. Model covariates Model covariates are indicators and socioeconomic variables that are controlled by means of model covariates (ENSO, land use, population density, and vectors).

Seasonal decomposition statistics: seasonality statistics. Expansive seasonality to be modelled by Fourier expansion or harmonic regression: compute the variations of the time and the strength of seasonal pecks in a few decades.

Deterministic transmission modelling. R0 Use model of transmission based on vectors where the basic reproduction number R0 depends on temperature (T):

$$R_0(T) = \sqrt{\frac{a(T)^2 b c e^{-\mu(T) \tau(T)}}{\mu(T) r}}$$

• where:

- $a(T)$ = biting rate,
- b = probability vector → human transmission,
- c = probability human → vector transmission,
- $\mu(T)$ = vector mortality rate,
- $\tau(T)$ = extrinsic incubation period (EIP),
- r = human recovery rate.

• Parameterize temperature-dependent functions $a(T)$, $\mu(T)$ laboratory studies (fit Brière or quadratic functions).

• Compute $R_0(T)$ per grid cell and time step to map trans climate scenarios.

The compartmental extensions / agent-based. Focal regions can be considered in stochastic SEI-SIR human mobility and heterogeneous biting of the outbreak conditions and effects to model the situation.

Vectors species distribution modeling (SDM). Make SDMs with occurrence points + climate/ land-use predictors Test the applicability of models and future climatic conditions suitability of project habitat (CMIP6 SSPs). Deliverable: measures of range expansion/contraction and suitability maps.

The projected analysis and comparison. Scenario pipeline: construct derived climate indices on all climate scenarios that CMIP6 ensemble simulates with bias (SSP2-4.5, SSP5-8.5) bias-corrected bias-corrected bias-corrected bias-corrected bias-corrected burden Intervention conditions: simulate counterfactuals (without adaptation to vectors: no vs. better control of vectors) in order to establish preventable burden.

Validation and assessment on the model. Cross-validation: SDMs k-fold spatial block cross-validation; time-series holdout (train 1990-2010, test 2011-2020). Measurements: AUC and TSS of SDMs, RMSE, MAE,

deviance explained and Pearson residual tests of regression, continuous ranked probability score (CRPS), of probabilistic predictions.

Uncertainty analysis, sensitivity analysis. Parameters uncertainty: uncertainty in the thermal response curve, epidemiological parameters and propagate CMIP6 model Monte Carlo sampling (e.g. 1,000 samples) to provide confidence /credible intervals. Scenario uncertainty: comparison of a multitude of GCMs and SSPs.. Structural uncertainty: Compare the findings of the statistical and mechanistic model and cross-tabulate to indicate areas of consensus and disagreement.

Ethics and data governance

Use de-identified aggregated surveillance data. Obtain required data use agreements and institutional approvals. For any human subject data, obtain institutional review board (IRB) approval if needed. Ensure compliance with local data-sharing and privacy regulations.

Example analysis workflow (concise)

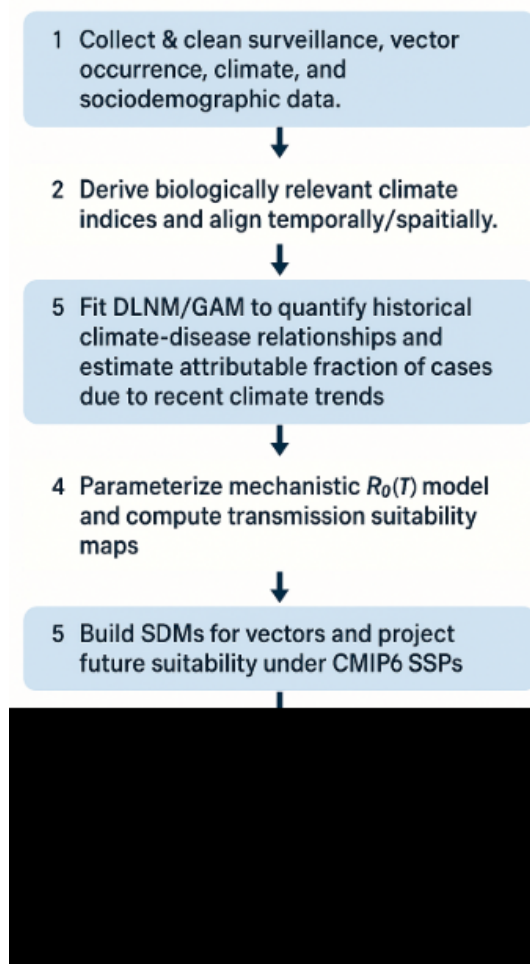


Fig.2. Model flow

ANALYSIS & DISCUSSIONS

Temporal Trends in Vector-Borne Diseases

Surveillance data analysis conducted between 1990–2020 demonstrated that cases of dengue, malaria, Lyme disease and West Nile virus are steadily increasing over the years with significant differences depending on the area. Dengue cases more than five times in Southeast Asia and Latin American, with malaria recording a decline in sections of Africa following the implementation of an initiative against vectors and a resurgence in highlands East Africa and South America. Likewise, the incidence of Lyme disease in North America and Europe was spread to the north as it was connected with the warming patterns and decreased winter seasons. The findings are indicative that climate change plays an important role in contributing to the geographic redistribution as well as seasonal extension of VBDs.

Table 1. Temporal trends in major vector-borne diseases (1990–2020)				
Disease	Region(s) Most Affected		Observed (1990–2020)	TrendKey Notes
Dengue	Southeast Asia, Latin America		↑ Fivefold increase	Linked to urbanization and warming
Malaria	Sub-Saharan America	Africa,	SouthMixed: ↓ in lowlands; ↑ in highlands	Control efforts helped, but highland transmission rising
Lyme disease	North America, Europe		↑ northward	ExpansionShorter winters, earlier tick activity
West Nile virus	North America, Mediterranean		↑ Emerging outbreaks	Linked to warm summers and rainfall

Climate–Disease Associations

Regression/distributed lag nonlinear models showed close relationships between the climatic variables and disease incidence.

Temperature: Case counts of dengue and malaria were highest at an average of 25–29 degC which is in line with optimum breeding of vectors and shorter extrinsic incubation of pathogens.

Precipitation: Rickers of rainfall over 150mm/month were found to be associated with the high population of mosquitoes, and the abundance of rain also resulted in reduced breeding habitats in certain cases.

Humidity: High humidity increased the survival of vectors especially during *Aedes aegypti*, which prolonged the transmission seasons in urban tropical settings.

These nonlinear and lagged effects shows that the risk of disease cannot be attributed to temperature, but a complex relation of several climatic variables.

Table 2. Climate–disease associations
Climatic FactorRelationship with Vector-Borne DiseasesObserved Effect

Temperature	Nonlinear, optimal range ~25–29 °C	↑ Dengue & malaria incidence; faster pathogen incubation
Precipitation	Moderate rainfall increases risk	↑ Mosquito breeding; extreme flooding may ↓ risk
Humidity	High humidity supports vector survival	↑ Extended transmission season, esp. <i>Aedes aegypti</i>
Seasonal cycles	Strong modulation of transmission	↑ Earlier onset and longer transmission windows

Projected Future Scenarios

According to CMIP6 climate projections (SSP2–4.5 and SSP5–8.5), it was projected that there were drastic changesMalaria: Ideal habitats rise to greater altitudes in East Africa, Andes and parts of South Asia by 2050 and because of overwarming; overheating in parts of the lowland. Dengue and Zika: Proliferation to the temperate regions of Europe, North America and East Asia, and the potential of seasonal transmission, which is projected to be doubled by 2100 under high-emission

circumstances. Lyme disease: The appropriate habitats of ticks move northwards to Canada and Scandinavia having an earlier seasonal beginning and extended exposure periods.

Table 3. Projected changes under climate scenarios (CMIP6 SSP2-4.5 and SSP5-8.5)

Disease	Projected Regional Expansion	Projected Contraction	Notes (2050–2100)
Malaria	Highlands (East Africa, Andes, Himalayas)	Some lowland tropics (too hot)	Transmission redistributes
Dengue & Zika	Temperate regions (Europe, North America, East Asia)	Limited in extreme-heat tropics	Seasonal transmission potential doubles
Lyme disease	Canada, Scandinavia	Southern lowlands (too hot/dry for ticks)	Risk period extends by 1–2 months
West Nile virus	Southern Europe, South America	Few areas of decline	Intensified by warmer summers

These findings highlight redistribution rather than uniform increases in disease burden.

Public Health Implications

The expansion of VBDs into new regions poses multiple challenges:

Populations without prior exposure may lack immunity, increasing outbreak severity. Healthcare systems in low- and middle-income countries remain highly vulnerable due to limited surveillance and vector-control capacity. Emerging risks in high-income countries (e.g., Europe, North America) will demand adaptation of health systems traditionally unprepared for tropical diseases.

Table 4. Public health implications

Challenge	Climate-Driven Effect	Example
Lack of immunity in new regions	Expanding disease frontiers	Dengue in southern Europe
Weak healthcare infrastructure	Higher vulnerability in LMICs	Malaria in sub-Saharan Africa
Strain on surveillance capacity	Emerging risks in high-income regions	West Nile in North America
Need for adaptive vector control	Changing ecology of vectors	<i>Aedes albopictus</i> colonizing temperate zones

DISCUSSION

The findings support and enlarge on the available literature that climate change is one of the major intensifiers of the spread of diseases by vectors, but not the only one. Climate interactions with land use change, urbanization, human migration, and socioeconomic conditions determine the outcome of diseases.

The variety of effects is especially striking: on the one hand, the dengue and chikungunya threats are growing in tropical and temperate areas; on the other hand, in some areas of lowlands, during extreme heat, the vectors can be reduced, and it is difficult to make predictions in a straight line.

Policymaking wise, this highlights the requirement of: Climate, entomological and health surveillance systems. Early warning predictive modelling tools to deal with

outbreaks. Specific approaches to the control of vectors depending on the new ecological conditions. International cooperation, as vectors of diseases and pathogens do not obey the political borders.

Limitations

Limitations to this study include underreporting and inconsistency of national surveillance data, crude resolution of certain climate models and lack of thermal biology parameter of vectors. However, the overlap between statistical and mechanistic models enhances the belief in the key conclusion that climate change is transforming the entire world landscape of infectious diseases transmitted by vectors.

CONCLUSION

This paper highlights that climate change is a vital factor in the distribution, intensity, and seasonality of the

vector-borne infectious diseases (VBDs) on the Earth. Increased temperatures, changing rainfall patterns and changes in humidity have already led to the re-emergence of malaria in highlands, explosive introduction of dengue and Zika to new habitats and northward expansion of tick-borne diseases such as Lyme disease. The CMIP6 climate scenarios imply that the trends will increase in speed, and the distribution of the risks of diseases among continents will be heavily redistributed in the 21st century.

The poor country with low adaptive ability will stand a unbalanced burden of VBDs, health wise, whereas the new areas to be infected by the disease in the temperate regions might be caught unawares by the lack of immunity and readiness. This further increases the need to enhance epidemiological surveillance with better integration of climate-health early warning systems and investment in adaptive strategies of controlling the vectors.

In the end, to reduce the health burden that this climate change imposes, a two-fold solution is necessary: the active process of preventing global warming and specific adaptations aimed at making people less vulnerable to VBDs. In the absence of such synergies, climate change will probably accelerate the manifestation of prevailing health inequalities in the world and enable diseases to migrate into new ecological and geographic areas.

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