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A State-of-the-Science Review of Long-Term Predictions of Climate Change Impacts on Dengue Transmission Risk

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Background: Climate change is predicted to profoundly impact dengue transmission risk, yet a thorough review of evidence is necessary to refine understanding of climate scenarios, projection periods, spatial resolutions, and modeling approaches.

Objectives: We conducted a state-of-the-science review to comprehensively understand long-term dengue risk predictions under climate change, identify research gaps, and provide evidence-based guidelines for future studies.

Methods: We searched three medical databases (PubMed, Embase, and Web of Science) up to 5 December 2024 to extract relevant modeling studies. An a *priori* search strategy, predefined eligibility criteria, and systematic data extraction procedures were implemented to identify and evaluate studies.

Results: Of 5,035 studies retrieved, 57 met inclusion criteria. Prediction for dengue risk ranged from 1950 to 2115, and 52.63% ($n=30$) of all studies used Representative Concentration Pathways (RCPs). Specifically, RCP 8.5 (34.94%; $n=29$), Shared Socioeconomic Pathways (SSPs) 2 (32.35%; $n=11$), and the Special Report on Emissions Scenarios (SRES) A1 (58.33%; $n=7$) were utilized the most among all the RCPs, SSPs, and SRES climate change scenarios. Most studies (57.89%; $n=33$) used only climatic variables for the prediction, and 21.05% ($n=12$) of studies employed fine spatial resolution (≈ 1 km) for the climate data. We identified that correlative approach was used mostly across the studies for modeling the future risk (61.40%; $n=35$). Among mechanistic models, 35% ($n=7$) lacked outcome validation, and 75% ($n=15$) did not report model evaluation metrics.

Discussion: We identified the urgent need to strengthen dengue databases, use finer spatial resolutions to integrate big data, and incorporate potential socioenvironmental factors such as human movement, vegetation, microclimate, and vector control efficacy in modeling. Utilizing appropriate spatiotemporal models and validation techniques will be crucial for developing functional climate-driven early warning systems for dengue fever. https://doi.org/10.1289/EHP14463

Introduction

By the 2050s, at least 3 billion people in the world will be at risk of dengue,[1,2] accounting for 31–47% of the global population projected for that period.[3] Annually, ∼390 million human beings are infected by this vectorborne virus, which is spread by *Aedes aegypti* and *Aedes albopictus* mosquitoes.[4] On 30 April 2024, the World Health Organization (WHO) collected data on over 7.6 million incidents of dengue, which included 3.4 million cases, over 16,000 severe cases, and more than 3,000 deaths.[5] *A. aegypti* transmits several other viruses, such as chikungunya, yellow fever, and Zika virus.[6] There are four distinct serotypes of the dengue virus (DENV1–4), transmitted between infected and susceptible humans by blood-feeding *Aedes* mosquito vectors.[5] Environmental factors influence the feeding behavior of vectors and the incubation period of the virus.[7] Higher temperature may reduce the virus incubation period and increase the probability that an infected mosquito will survive long enough to incubate and then transmit virus, escalating the infection risk.[8] Studies further provided evidence that heavy precipitation may reduce the transmission potential by carrying away mosquito's eggs, larvae, and pupae from standing water[9]; and a relative humidity level of at least 60% assisted in *A. aegypti* survival.[10] Along with various climatic factors, several nonclimatic variables—including urbanization,[11] gross domestic product (GDP),[12] microclimate,[13] and land use and land cover—are highly related to virus transmission potential.[14] In recent years, there have been substantial advances in interventions such as vaccines and the introduction of *Wolbachia* strains in *Aedes* mosquito populations. For example, Dengvaxia, a tetravalent, live-attenuated dengue vaccine, is licensed by 20 countries[15]; Qdenga has the capability to induce a wider immune response involving both humoral and cell-mediated mechanisms, and it has already been authorized by the European Medicines Agency[16]; and 14 countries are implementing the *Wolbachia* project, which benefits ∼11 million people.[17] Despite these advancements, the recent surge in infections highlights critical weaknesses in our preparedness for this vectorborne disease, while the ongoing effects of climate change pose an additional threat that may further exacerbate the situation in the future.

The World Meteorological Organization (WMO) projected that the mean surface temperature will be 1.5°C over preindustrial levels for at least 1 year between 2023 and 2027, with a 66% likelihood.[18] Similarly, the Shared Socioeconomic Pathways (SSPs), developed by an international consortium of researchers and utilized by the Intergovernmental Panel on Climate Change (IPCC) in their Sixth Assessment Report (AR6), project a global temperature rise (best estimate) of 1.6–2.4°C from 2041 to 2060 and 1.4–4.4°C from 2081 to 2100, depending on various projection scenarios.[19] Climate change has significant consequences for vectorborne diseases due to its impact on pathogens, vectors, and hosts.[20] Globally the tropical and subtropical regions are historically affected by different vectorborne diseases, such as dengue fever, malaria,

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chikungunya, yellow fever, lymphatic filariasis, leishmaniasis, Zika virus, and Japanese encephalitis.[7] A previous IPCC report published in 2022 mentioned that the occurrence of diseases transmitted by vectors has risen in recent decades and further projected with a high confidence that the occurrence of dengue fever, malaria, and Lyme disease will continue to rise over the next 80 years if no action is taken to improve control strategies.[21] Most importantly, dengue has emerged as the most widespread mosquitoborne viral infection of humans in the past two decades.[22] Mosquito thermal adaptation—through physiological, behavioral, and genetic-based compliant response,[23] combined with changes in blood feeding behavior, mosquito survival rate, and vectorial capacity due to climate change,[24] may amplify virus transmission. This effect is likely to be further intensified by global population growth which is projected to reach 9.4 to 10.0 billion by 2050 and 8.9 to 12.4 billion by 2100.[25] Anticipated changes in land use and land cover patterns, development of new economic zones, and international migration or travel may create new transportation pathways for this vector, such as shipping routes, travel for leisure, or festival- or job-related rapid human movement, which may assist in carrying mosquitos or their eggs and viremic humans from one place to another.[26]

Taking this into account, we conducted a state-of-the-science review of the existing literature, which quantified the pattern of dengue transmission risk in the long-term future based on climate change and predictive modeling. First, we searched the database to identify studies that explored any type of dengue transmission risk using climate change scenarios. Then, we extracted the necessary information to check the modeling approach used, the spatial resolution of the climate database, the modeling performance techniques applied, the model outcome validations, and the data used (e.g., climatic, nonclimatic, and the type of dengue data included). We utilized our findings to explore research gaps and provide scientific evidence that needs to be addressed in future climate change-oriented decision making.

Methods

Study Selection

Inclusion criteria focused on utilizing climate change scenarios to develop a long-term prediction for the risk associated with dengue. Therefore, we included studies on human exposure to dengue virus transmitted by *A. aegypti* or *A. albopictus*, excluding any nonhuman primates or other animals as study subjects. Besides, studies that included predictions for infectious diseases other than dengue were excluded to maintain the focus of this review. Articles reporting long-term projection of dengue based on climate change scenarios were included. Although there is no fixed definition of long-term projection, for the purposes of this study, we defined long-term projection as predicting the pattern of risk for more than 10 years beyond the date at which the prediction was performed. Therefore, we excluded any studies related to short-term predictions of 10 years or less.

Inclusion criteria required that articles be peer-reviewed and written in English, while systematic reviews and meta-analyses were excluded. We organized the publications and removed duplicates using Endnote X9. We then examined the title and abstract to discover articles that included the necessary data. J.I. and W.H. screened all retrieved citations, titles, and abstracts for inclusion before conducting a thorough analysis of the reported findings. Selections were made independently based on the inclusion and exclusion criteria and tracked using a spreadsheet, and disagreements were resolved through discussion.

Literature Search

We conducted literature searches in three electronic bibliographic databases: PubMed, Embase (which includes MEDLINE), and Web of Science. Where applicable, controlled vocabularies such as Medical Subject Headings (MeSH terms) were used in PubMed, and equivalent terms in other databases were utilized.

A research librarian affiliated with the authors' institution provided guidance on search terms and database selection. The literature search was conducted in two phases: first on 15 October 2023 and subsequently on 5 December 2024 to capture the most recent studies. The search strategy focused on three core themes—forecasting, climate, and dengue—and incorporated an extensive range of synonyms for each concept to ensure a comprehensive review of relevant literature (Table S1).

Boolean terms "OR" and "AND" were used for specification and elaboration of the searches. The reference lists within the included studies were also searched for any publications missing from the initial database search. This state-of-the-science review was registered in the International Prospective Register of Systematic Reviews (PROSPERO; registration number CRD42023425448).

Data Extraction

Findings relevant to our study objectives were extracted and entered into a spreadsheet from which a standardized table was created. The table included key information about the study location, year, spatial resolution of dengue and climate data, climate change scenarios, baseline period for the climate data, pattern of climate change–related risk, modeling approaches, outcome validation methods, performance checking metrics, and finally the strengths and limitations of the studies. We analyzed the techniques employed by the included studies to validate model outcomes and assess model performance. R programming language (version 2023.06.0; R Development Core Team) was used to create figures and conduct descriptive analysis to explain the findings, and ArcGIS Pro (version 3.1.2; Esri Inc.) was used for mapping the study locations.

Climatic and Nonclimatic Variables

The dengue mosquito's lifecycle, fecundity, vectorial capacity, and transmission intensity are influenced by various climatic and nonclimatic factors. Therefore, temperature, precipitation, extreme weather, relative humidity, microclimate, urbanization, human movement, and many other climatic and nonclimatic factors are important to assess the risk of dengue transmission.[27,28] In our review, we explored all of the climatic and nonclimatic variables used for future prediction of dengue transmission risk to critically evaluate their role. We categorized climatic variables as those directly related to atmospheric and environmental conditions (e.g., temperature, rainfall, humidity), following established literature, while the nonclimatic variables were defined as social, demographic, or behavioral factors influencing transmission dynamics.[29] For the future climate projection, IPCC-based assessment reports are predominantly used among different disciplines. Since 1988, IPCC has delivered six assessment reports in which different climate projections are characterized. These include Scenario A (SA90), IPCC 1992 emission scenarios (IS92), the Special Report on Emissions Scenarios (SRES), Representative Concentration Pathways (RCPs), and SSPs.[30] In climate modeling, SA90 and IS92 represent early greenhouse gas emission scenarios designed to project future climate conditions. Developed in the 1990s, the SA90 scenario was among the first to estimate future emissions based on varying assumptions about economic and population growth.[31] Similarly, the IS92 scenarios, introduced by the IPCC in its 1992 supplementary report, include six distinct

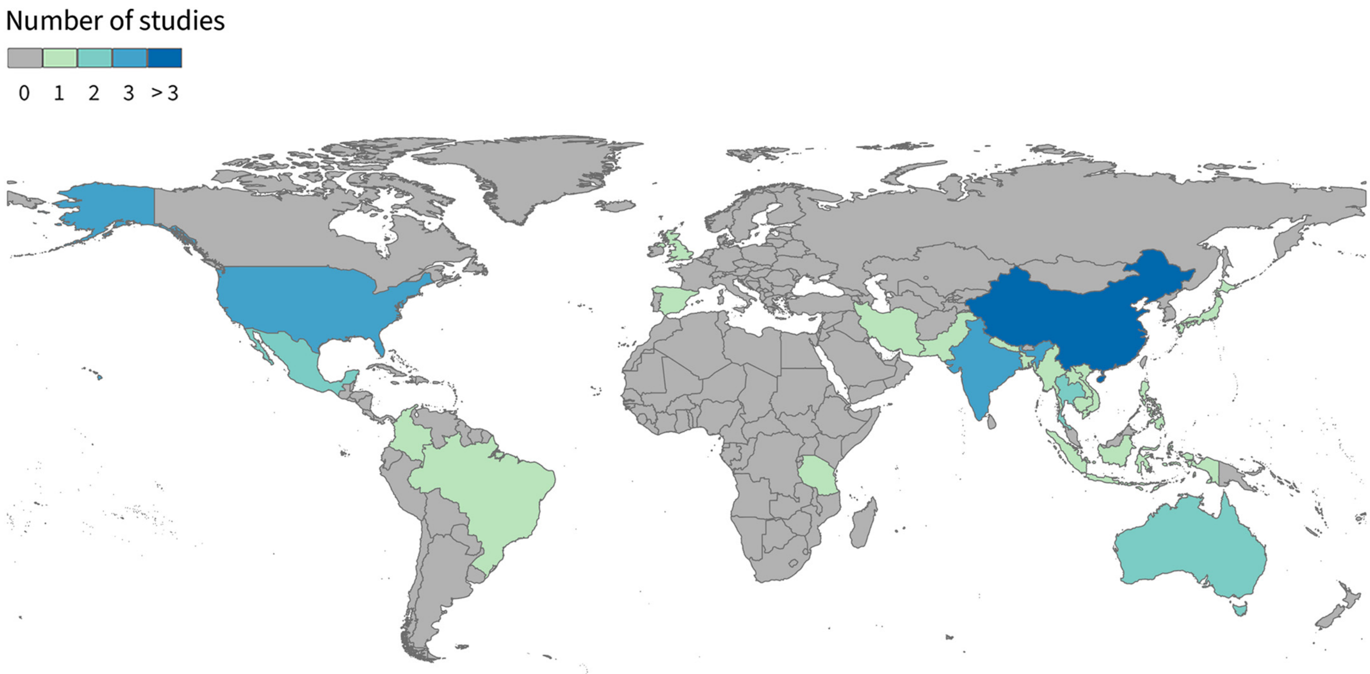

Figure 1. Geographical distribution of country-based studies included in the review ($n = 57$). Refer to the corresponding references provided in Excel Table S1 for the source data. This figure was produced using ArcGIS Pro (version 3.1.2, Esri Inc.) based on the background map data sourced from Esri's "World Countries Generalized" dataset (available at https://hub.arcgis.com/datasets/esri::world-countries-generalized/explore).

pathways (IS92 a–f).[32] Overall, all of the six assessment reports present a comprehensive overview of scientific, technical, and socioeconomic insights regarding climate change, its impacts, future risks, and strategies for mitigating its progression, thereby, significantly contributing to the advancement of climate change research and modeling. These scenarios play a crucial role in informing and guiding national and international legislation.[33]

Methods for Calculating Spatial Resolution in Climate Data

We found that different studies employed varying spatial resolutions of climate data. To enable comparisons and standardize the diverse datasets assessed in this study, all spatial resolutions were converted to their equivalents in kilometers (km). These conversions were based on geodetic conventions, assuming a constant value of 1 degree of latitude equal to $\sim$111.1 km. This value was derived from the Earth's approximate circumference of 40,000 km divided by 360 degrees ($40{,}000/360 = 111.1$ km). Longitudinal distances were similarly adjusted for latitude to account for the Earth's curvature.

The spatial resolution of 30 arc seconds was calculated as 30 arc seconds = 0.00833 degrees which, when multiplied by 111.1 km/degree, equals $\sim$1 km. Similarly, a resolution of 5 arc minutes was calculated as 0.0833 degrees or $\sim$9.3 km, while a resolution of 2.5 arc minutes was found to be equivalent to $\sim$5 km.[34] For coarser resolutions, 0.04 degrees or $\sim$4 km[35] and 10 arc minutes or roughly 18.5 km at the equator were determined.[36,37] These calculations were essential to standardizing the spatial resolution of the geospatial data across the studies analyzed. The methodology ensured consistent resolution adjustments and provided a basis for reliable comparisons of spatially varying climate data.

Results

We identified 5,035 studies in total from the database, with 3,034 studies accepted for screening after the deduplication of 2,001 studies. After screening the title and abstract, we accepted 122 articles for full-text screening. We found that 56 studies followed the inclusion and exclusion criteria. Only one study was added from checking the references, and finally, 57 studies were chosen for the review (Figure S1; Excel Table S1).[1–3,24,34,38–89]

Location, Climate Scenarios, and Projection Period Used

Initially, we combined all studies that focused on single countries, multiple regions, or smaller localized areas. Among these, 38.60% ($n = 22$) of the studies were conducted at the single-country level, while 10.53% ($n = 6$) examined multiple regions or locations. Additionally, 21.05% ($n = 12$) focused on city- or region-based analyses, 17.54% ($n = 10$) adopted a global perspective, and 12.28% ($n = 7$) were continent-based studies (Figures 1 and 2). Although the study locations were heterogeneous, studies of entire continents were primarily concentrated in Europe.[40,43,55] Studies focusing on single country or multiple locations were predominantly conducted in China (20%; $n = 7$),[52,65,69,74,77–79] followed by India (8.57%; $n = 3$),[34,61,88] and the US (9.09%; $n = 3$).[47,53,62] Other countries, including Australia,[38,65] Mexico,[41,85] and Thailand were represented in 5.71% ($n = 2$) of the studies.[65,70] The remaining country-based studies encompassed a diverse range of nations, including Bangladesh,[67] Brazil,[85] Colombia,[60] Indonesia,[65] Iran,[80] Japan,[71] Nepal,[49] Pakistan,[73] Tanzania,[45] the UK,[57] the Philippines,[65] Vietnam,[65] Singapore,[81] Laos,[70] Myanmar,[70] and Cambodia.[70] For multilocation-based studies, Bonnin et al.[70] focused on Southeast Asia, while Davis et al.[65] examined six countries: Australia, China, Indonesia, The Philippines, Thailand, and Vietnam. Kraemer et al.[53] explored both the US and the European continent, whereas Wang et al.[81] analyzed both country-level and cities, specifically Singapore, Colombo (Sri Lanka), Selangor (Malaysia), and Chiang Mai (Thailand). Additionally, Pardo-Araujo et al.[87] focused their study on Europe and Spain, and the research of Wang et al.[89] was concentrated on South and Southeast Asia.

After a thorough examination of continent-based studies, we observed that the analysis conducted by Bouzid et al.[43] primarily focuses on the European Union (EU) member states rather than the entirety of Europe. The study relies on data sources such as

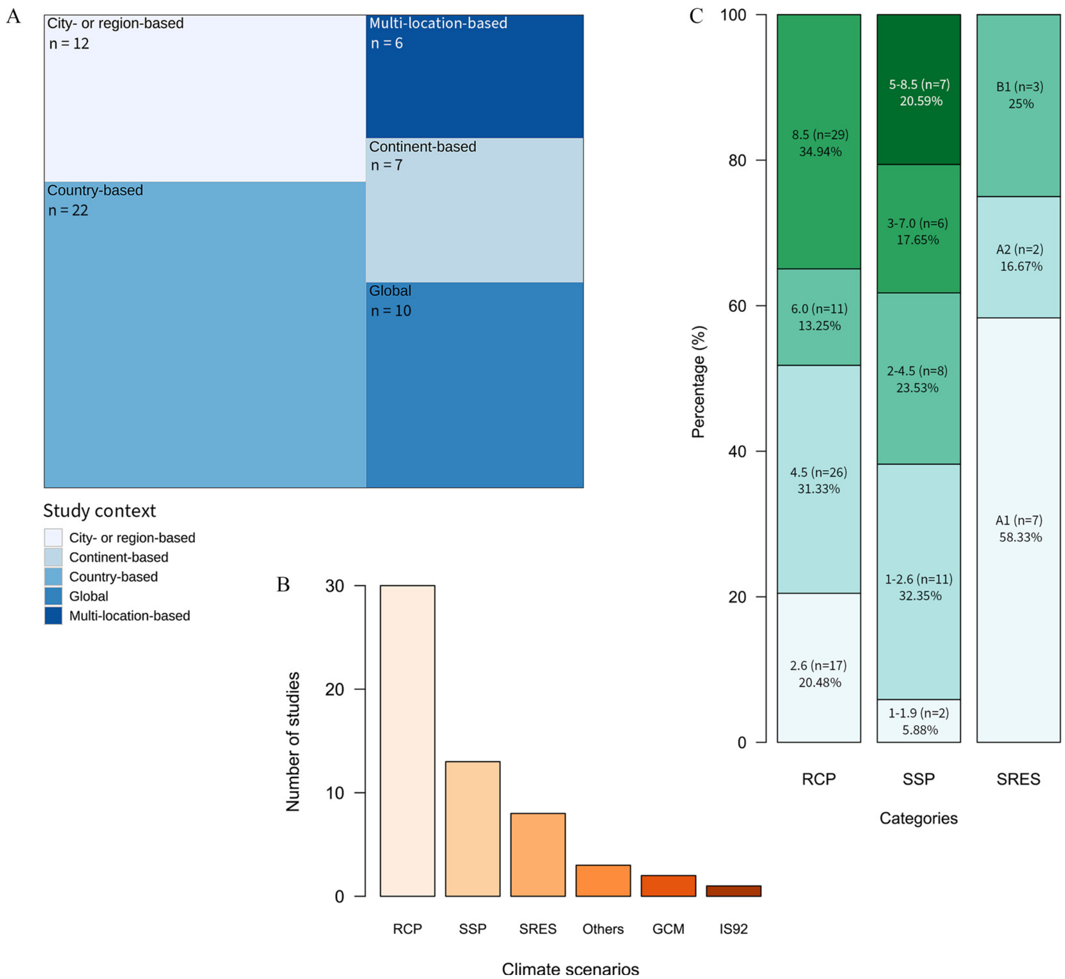

Figure 2. Overview of locations and climate change scenarios in included studies: (A) Treemap of study locations ($n = 57$), (B) frequency of climate change scenarios, and (C) distribution of specific climate change scenarios across studies. Other scenarios represented in bar plot B include observed historical climate data,[78] manually selected probable temperature patterns,[42] and four climate scenarios predicted by Australia's Commonwealth Scientific and Industrial Research Organization (CSIRO).[38] Note: GCM, general circulation model; IS92, interim scenarios of 1992; RCP, representative concentration pathways; SSP, shared socioeconomic pathways; SRES, special report on emissions scenarios.

EUROSTAT and the GEOSTAT 2006 population grid dataset, both of which predominantly encompass the 27 EU countries. Although the term "Europe" is frequently employed throughout the article, the study's reliance on EU-centric datasets indicates a lack of comprehensive coverage for non-EU countries, including Norway, Switzerland, Ukraine, Russia, Iceland, and Belarus. Consequently, the study's projections and conclusions are primarily applicable to the EU region, with limited relevance to non-EU European countries. In contrast, the study by Colón-González et al.,[50] which provides predictive scenarios for the entirety of Latin America, categorizes certain nations under the term "others". This grouping likely refers to aggregated data for Latin American countries that are not individually listed, either due to data limitations or because projected changes in dengue cases are relatively minor compared to explicitly mentioned nations. While the study offers detailed projections for countries such as Brazil, Colombia, Venezuela, Mexico, Ecuador, Guatemala, Haiti, the Dominican Republic, Peru, and Argentina, the "others" category encompasses the remaining Latin American nations included in the analysis, including Bolivia, Paraguay, Chile, Uruguay, Nicaragua, and El Salvador.

Conversely, studies by Fischer et al.[40] and Liu-Helmersson et al.[55] encompass the entire European continent. Fischer et al.[40] utilized *A. albopictus* presence records from its native range in Asia and its global distribution, including established populations in Europe. Meanwhile, Liu-Helmersson et al.[55] employed a process-based model to examine the lifecycle of *A. aegypti* and projected the species' potential distribution under future climate scenarios across Europe. Notably, their analysis was not confined to the EU, ensuring the inclusion of regions both within and outside the EU. This comprehensive approach enhances the study's applicability across the full European continent. Similarly, the studies conducted by Sintayehu et al.,[63] Gorris et al.,[84] and Jing et al.[86] provide predictions for entire continents, specifically Africa, North and South America, and Asia, respectively. These studies adopt robust methodologies to ensure continent-wide coverage, addressing both regional and subregional variabilities and offering broader projections that are not limited to specific political or economic boundaries.

For climate change scenarios, the majority of the studies used RCPs (52.63%; $n = 30$), 22.81% ($n = 13$) used SSPs, and 14.04% ($n = 8$) used SRES (Figure 2). Bambrick et al.[38] used four climate change scenarios where three of the scenarios assumed that "no action" will lead to a temperature increase of 4.5°C at the end of the century and that, by taking strong action, the temperature increase will be 2°C. Banu et al.[42] assumed temperature increases of 1, 2, or 3°C by the end of this century. As RCPs, SSPs, and SRES constituted 88% of all of the climate change scenarios used, we further explored the specific scenarios used. Among the SRES, we found 58.33% ($n = 7$) used the A1 scenario, 25% ($n = 3$) used the B1, and 16.67% ($n = 2$) used the A2 scenario. For the SSPs, the majority used SSP 2 (32.35%; $n = 11$), SSP 3 (23.53%; $n = 8$), SSP 5 (20.59%; $n = 7$), and SSP 4 (17.65%; $n = 6$). Within the RCPs, the majority of studies used RCP 8.5 (34.94%; $n = 29$), RCP 4.5 (31.33%; $n = 26$), RCP 2.6 (20.48%; $n = 17$), and RCP 6.0 (13.25%; $n = 11$). The SRES B2 scenario was not used in any of the selected studies (Figure 2).

Spatial Resolution, Variable Types, and Projection Period Used for the Prediction

Of the studies, 26.32% ($n = 15$) did not report the spatial resolution of the climatic data, 21.05% ($n = 12$) used 30 arc seconds (≈1 km), and 15.79% ($n = 9$) used 0.5° (≈55 km). A substantial proportion of studies (57.89%; $n = 33$) used climatic data, while 42.11% ($n = 24$) incorporated both climatic and nonclimatic data. Among the climatic variables analyzed, temperature was universally included (100%; $n = 57$), followed by precipitation (71.21%; $n = 47$) and humidity (18.18%; $n = 12$). Less frequently utilized variables included evapotranspiration, vapor pressure, solar radiation, downward longwave radiation, wind speed, photoperiod, and saturation deficit, each reported in 1.52% of studies ($n = 1$). The majority of nonclimatic variables employed in the studies included population (38.46%; $n = 15$), GDP (12.82%; $n = 5$), population density (12.82%; $n = 5$), land use and land cover (10.26%; $n = 4$), and human mobility (5.13%; $n = 2$). Less commonly utilized variables encompassed urban and nonurban areas, urban growth, sanitation indices, traffic networks, elevation, enhanced vegetation index, tasseled cap brightness, and tasseled cap wetness, each represented in 2.56% of studies ($n = 1$). The temporal resolution of the temperature data varied monthly (35.09%; $n = 20$), daily (21.05%; $n = 12$), and annually (15.79%; $n = 9$), while 28.07% ($n = 16$) of studies did not mention this (Table 1). The earliest time observed for the dengue prediction period started from 1950[64] and extended to 2115 (Figure 3).[50]

Modeling Techniques and Statistical Analysis

Correlative models (i.e., no processes or mechanisms identified) were used in 61.40% ($n = 35$) of the studies, and 35.08% ($n = 20$) used mechanistic models (i.e., identifying underlying processes and mechanisms that represent the biological, environmental, and social processes driving dengue transmission) (Table 2). Only two studies by Colón-González et al.[24] and Harish et al.[85] used a mixed method. For the correlative models, 48.57% ($n = 17$) used human case data, 40.47% ($n = 14$) used vector occurrence data, and 11.43% ($n = 4$) used both human cases and vector occurrence data. We differentiated the modeling techniques used in the included studies as follows: mechanistic models were used to predict the future risk based on the influence of the climatic factors on the mosquito's biological mechanism. For example, studies employed a mathematical model based on the life cycle of *A. aegypti* to determine the size of mosquito population over time,[47] measuring the vectorial capacity,[24] creating a suitable condition index (SCI) by considering the vectorial capacity and basic reproduction number,[65] and defining the potential transmission index by examining the extrinsic incubation period of dengue virus within both dengue vectors.[52] In contrast, correlative models or statistical correlation models were used to identify and quantify the relationships between risk factors and dengue transmission.[83] These models do not imply causation but instead measure the degree to which two or more variables are related.

Correlative models primarily included the ecological niche models, which were observed in 40% ($n = 14$) of the studies. This includes the maximum entropy modeling (Maxent) that employs the principle of maximum entropy by considering the dengue occurrence data to predict the species distribution. In addition, 25.71% ($n = 9$) used generalized linear models, 8.57% ($n = 3$) used a classification and regression tree, and 5.71% ($n = 2$) used a distributed lag model. We found that 20% ($n = 7$) of the studies used six different predictive models, including the reproductive rate model (R_o), empirical model, support vector machines classifier, generalized boosted regression tree, and calculating the risk of arboviral diseases by considering the general potential index of the vector. Internal validation was conducted in 80% ($n = 28$) of the correlative models, and 20% ($n = 7$) of the studies did not report it. Among the model performance techniques, 22.86% ($n = 16$) used area under the curve (AUC), 15.71% ($n = 11$) used cross-validation, 14.29% ($n = 10$) used sensitivity test, 10% ($n = 7$) used Akaike information criterion, and 8.57% ($n = 6$) used split sample strategy. For the mechanistic models, 95% ($n = 19$) of the studies used process-based models, while only one study used the mechanistic generalized linear model. Model performance was not checked in 75% ($n = 15$) of the

Table 1. Data types and characteristics from state-of-the-science review of dengue prediction studies ($n = 57$).

Data type used for dengue prediction	n (%)
Climatic data	33 (57.89%)
Climatic and nonclimatic data	24 (42.11%)
Total	57
Climatic data	
Temperature	57 (100%)
Temporal resolution	—
Daily	12 (21.05%)
Monthly	20 (35.09%)
Annual	9 (15.79%)
Not reported	16 (28.07%)
Spatial resolution (≈ km)	—
Not reported	15 (26.32%)
1 (30 arc seconds)	12 (21.05%)
55 (0.5°)	9 (15.79%)
5 (2.5 arc minute)	7 (12.28%)
18.5 (10 arc minute)	5 (8.77%)
4 (0.04°)	2 (3.51%)
10 (5 arc minute)	2 (3.51%)
12	1 (1.75%)
15	1 (1.75%)
27.8	1 (1.75%)
30	1 (1.75%)
144–433	1 (1.75%)
Precipitation	47 (71.21%)
Humidity	12 (18.18%)
Evapotranspiration	1 (1.52%)
Vapor pressure	1 (1.52%)
Solar radiation	1 (1.52%)
Downward longwave radiation	1 (1.52%)
Wind speed	1 (1.52%)
Photoperiod	1 (1.52%)
Saturation deficit	1 (1.52%)
Nonclimatic data	
Population	15 (38.46%)
GDP	5 (12.82%)
Population density	5 (12.82%)
Land use land cover	4 (10.26%)
Human movement	2 (5.13%)
Urban and nonurban area	1 (2.56%)
Urban growth	1 (2.56%)
Sanitation index	1 (2.56%)
Traffic network	1 (2.56%)
Elevation	1 (2.56%)
Enhanced vegetation index	1 (2.56%)
Tasselled cap brightness	1 (2.56%)
Tasselled cap wetness	1 (2.56%)

Note: —, no data; GDP, Gross domestic product.

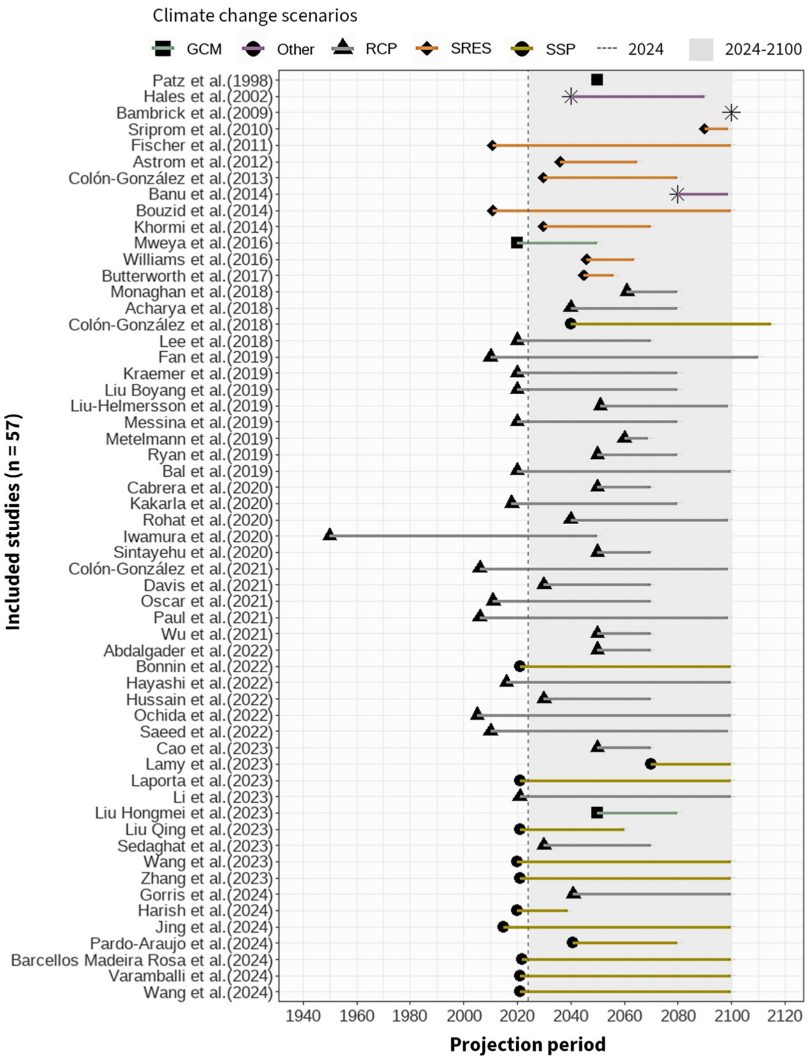

Figure 3. Distribution of climate change scenarios and projection periods across studies ($n = 57$). Studies included: Patz and others (1998),[3] Hales and others (2002),[2] Bambrick and others (2009),[38] Sriprom and others (2010),[39] Fischer and others (2011),[40] Astrom and others (2012),[1] Colón-González and others (2013),[41] Banu and others (2014),[42] Bouzid and others (2014),[43] Khormi and others (2014),[44] Mweya and others (2016),[45] Williams and others (2016),[46] Butterworth and others (2017),[47] Monaghan and others (2018),[48] Acharya and others (2018),[49] Colón-González and others (2018),[50] Lee and others (2018),[51] Fan and others (2019),[52] Kraemer and others (2019),[53] Liu Boyang and others (2019),[54] Liu-Helmersson and others (2019),[55] Messina and others (2019),[56] Metelmann and others (2019),[57] Ryan and others (2019),[58] Bal and others (2019),[59] Cabrera and others (2020),[60] Kakarla and others (2020),[61] Rohat and others (2020),[62] lwamura and others (2020),[64] Sintayehu and others (2020),[63] Colón-González and others (2021),[24] Davis and others (2021),[65] Oscar and others (2021),[66] Paul and others (2021),[67] Wu and others (2021),[68] Abdalgader and others (2022),[69] Bonnin and others (2022),[70] Hayashi and others (2022),[71] Hussain and others (2022),[34] Ochida and others (2022),[72] Saeed and others (2022),[73] Cao and others (2023),[74] Lamy and others (2023),[75] Laporta and others (2023),[76] Li and others (2023),[77] Liu Hongmei and others (2023),[78] Liu Qing and others (2023),[79] Sedaghat and others (2023),[80] Wang and others (2023),[81] Zhang and others (2023),[82] Gorris and others (2024),[84] Harish and others (2024),[85] Jing and others (2024),[86] Pardo-Araujo and others (2024),[87] Barcellos Madeira Rosa and others (2024),[83] Varamballi and others (2024),[88] and Wang and others (2024).[89] Note: GCM, general circulation model; RCP, representative concentration pathways; SRES, special report on emissions scenarios; SSP, shared socioeconomic pathways.

studies, while 20% ($n = 4$) of studies used a sensitivity test, and 5% ($n = 1$) performed both AUC and cross-validation. We found that 35% ($n = 7$) of studies did not conduct any model outcome validation, while 50% ($n = 10$) of studies conducted external validation, 10% ($n = 2$) conducted internal validation, and one study conducted both external and internal validation. Model validation was performed by the real-world dengue cases (50%; $n = 6$), observed climate database (25%; $n = 3$), kappa coefficient (16.67%; $n = 2$), and Pearson correlation (8.33%; $n = 1$).

A Critical Overview of Methodological and Data Constraints in the Included Studies

On examining the sample representativeness of the chosen studies, we note that Patz et al.[3] excluded regions with current epidemic potential (EP) below 0.1. The EP parameter, which serves as a concise measure based on mosquito population and viral introduction, provides a useful comparative index for assessing the impact of temperature variations on dengue transmission. However, such exclusionary criteria might limit the generalizability of findings, as regions currently exhibiting low EP might experience significant increases in risk due to future environmental changes, such as temperature changes or other environmental shifts.[90] Barcellos Madeira Rosa et al.[83] acknowledged these limitations, highlighting that the potential for overlooking several factors—such as natural impediments, geographical occupation, and microclimate—could influence future transmission dynamics.

Data spanning 3 years of dengue incidence from a province of Thailand was used by Sriprom et al.[39] While the study provides valuable localized insights, this limited temporal scope might not

Table 2. Summary of modeling approaches and performance evaluation in dengue prediction studies ($n = 57$).

Modeling approach	n (%)
Correlative models	35 (61.40%)
Ecological niche models[34,40,45,49,54,60,68,74,80,82–84,88,89]	14 (40%)
Generalized linear model[1,2,39,41,43,50,59,86,89]	9 (25.71%)
Classification and regression tree[53,54,56]	3 (8.57%)
Distributed lag model[42,77]	2 (5.71%)
Others[38,48,61,63,66,72,76]	7 (20%)
Modeling performance evaluation	
Internal evaluation	28 (80%)
Not reported	7 (20%)
Model performance techniques	
AUC	16 (22.86%)
Cross-validation	11 (15.71%)
Sensitivity	10 (14.29%)
AIC	7 (10%)
Split sample strategy	6 (8.57%)
Specificity	6 (8.57%)
TSS	4 (5.71%)
MAE	2 (2.86%)
TER	2 (2.86%)
Boyce index	2 (2.86%)
Kappa coefficient	1 (1.43%)
LDIC	1 (1.43%)
Jaccard and Sorensen	1 (1.43%)
RMSE	1 (1.43%)
Mechanistic models	20 (35.08%)
Process-based model[3,44,46,47,51,52,55,57,58,62,64,67,69–71,73,75,81,87]	19 (95%)
Others[65]	1 (5%)
Model outcome validation	
External validation	10 (50%)
No validation	7 (35%)
Internal validation	2 (10%)
External and Internal validation	1 (5%)
Total	20
Model validation techniques	
Observed dengue case	7 (53.85%)
Observed climatic data	3 (23.08%)
Kappa	2 (15.38%)
Pearson correlation	1 (7.69%)
Model evaluation metrics	
Not reported	15 (75%)
Sensitivity	4 (20%)
AUC, cross-validation	1 (5%)
Mixed models[24,85]	2 (3.51%)

Note: AIC, Akaike information criterion; AUC, area under the curve; LDIC, lowest deviance information criterion; LTO-CV, leave-time-out cross-validation; MAE, mean absolute error; RMSE, root mean square error; ROC, receiver operating characteristics; TSS, true skill statistic; VC, vectorial capacity.

capture longer-term trends and variations, such as multiyear climate cycles or socioeconomic changes, potentially affecting the robustness of predictions. Similarly, Bouzid et al.[43] relied on the Mexican database to estimate the association between dengue and climatic factors and then applied these estimates to create dengue projections for Europe. Although this approach offers a pragmatic solution to data scarcity, its reliability could be enhanced by cross-validation with independent datasets from any other regions or time. Furthermore, differences in health care systems, vector control measures, and public health policies between Mexico and Europe may limit the applicability of these projections. A comparable issue was identified in a previous study where dengue data from Taiwan were utilized, based on the assumption that Jeju Island, South Korea, may experience analogous climatic conditions in the coming decades. However, this assumption may necessitate further validation in future research.[51] Dengue data constraints were also mentioned by Sedaghat et al.[80] and Cabrera and Selvaraj.[60]

Khormi and Kumar[44] provided a comprehensive global dataset but noted data deficiencies in sub-Saharan Africa due to limited diagnostic capacity. Most data were sourced from Latin America, Southeast Asia, and the Pacific islands, which may skew global risk assessments. Monaghan et al.,[48] building on Eisen et al.,[91] classified *A. aegypti* presence into four categories based on city-specific temperature and precipitation thresholds. This categorization may oversimplify the complex ecological variability of *A. aegypti* populations across diverse regions. Mweya et al.[45] utilized data on dengue-infected *A. aegypti* mosquitoes collected solely in Dar es Salaam, Tanzania, to predict risk areas for the entire country. Such extrapolation may require further refinement, as mosquito distribution is influenced by localized factors, such as breeding site availability, human behavior, and environmental conditions, which can vary significantly across regions. Paul et al.[67] obtained climate data from the Bangladesh Meteorological Department, with coverage limited to 35 stations. This clustering around 64 districts might not adequately represent temperature variability nationwide. Saeed et al.[73] limited their temperature range from 28°C to 32°C to determine the appropriate number of days for dengue transmission. This approach may not fully represent the intricate dynamics of dengue transmission, which are influenced by a combination of factors, such as temperature, humidity, human behavior, and mosquito biology.[73] The study by Lamy et al.[75] primarily relied on entomological surveys, which might overestimate or underestimate mosquito populations in certain regions due to variation in sampling methods, such as the use of adult traps[92,93] vs. oviposition traps.[94] However, they further collected weekly dengue case numbers to explore whether there is any correlation with the entomological data that would validate their model outcome. Variations of outcome related to collecting entomological data should be carefully investigated to maintain the accuracy of vector population estimates.

Several other studies—Patz et al.,[3] Paul et al.,[67] Hayashi et al.,[71] and Ryan et al.[58]—relied highly on temperature parameters for modeling dengue transmission. Bambrick et al.[38] excluded the 2008–2009 epidemic period, which may underestimate future dengue burden if recent outbreaks reflect shifting transmission trends. We identified several studies, including Fischer et al.,[40] Cabrera and Selvaraj,[60] and Gorris et al.,[84] that provided valuable insights but highlighted challenges related to limited dengue occurrence records, which may bias toward the presence only data, temporal mismatch, and limited environmental predictors. Such a smaller samples issue might be resolved by setting up probability threshold and conducting accuracy assessment.[95] Presence-only data refer to datasets that record locations where a phenomenon (e.g., dengue cases or mosquito vectors) has been observed or reported but may lack corresponding information about locations where the phenomenon is absent.[96] Limited availability of dengue incidence databases was highlighted in studies such as Liu et al.,[54] while the temporal scope of data in Mweya et al.,[45] Lamy et al.,[75] and limited transmission months used by Williams et al.[46] may not adequately address the seasonal and annual variability. The statistical method or equation used by Bambrick et al.[38] was not explicitly set out in the methodology. The validation of global reference maps by Monaghan et al.,[48] with an uncertainty of $\pm 10\%$, reflects a degree of methodological uncertainty. While the authors outlined their validation process, further detailing of error sources, including model parameterization and data quality, could strengthen confidence in their findings.

The Role of Climatic Drivers in Expanding Regional Dengue Transmission Risk in the Future

Climatic variables play a crucial role in predicting future dengue transmission risks; for example, rising temperatures are projected to enhance epidemic potential by shortening the virus's incubation period,[3] increasing vectorial capacity,[51,52,86] boosting vector density,[70]

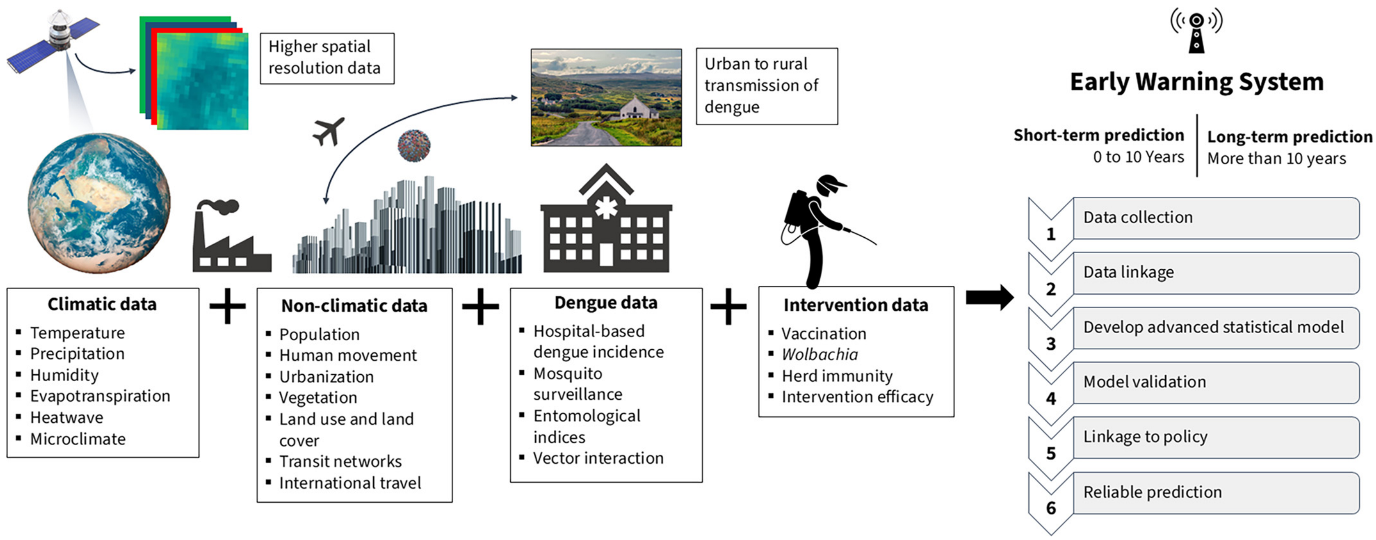

Figure 4. Comprehensive approach to developing a dengue early warning system with multisource data integration. The figure was created by the author using Microsoft PowerPoint (version 2411 Build 16.0.18227.20082).

and extending breeding or transmission season,[24,47,61,62,64,67,71,78] thereby facilitating greater transmission risk. Furthermore, increased humidity and vapor pressure are anticipated to expand the geographical limits of dengue transmission, with the global population at risk projected to rise significantly—from 30% in 1990 to an estimated potentially 50–60% by 2085.[2] Without robust mitigation measures, the population at risk could increase by up to eightfold by the end of the century due to combined effects of rising temperature and humidity.[38] In Sakon Nakhon province, Thailand, higher temperatures are expected to extend the dengue transmission period from 5 to 9 months, shifting high-risk areas from densely populated districts to less populated ones and significantly increasing the number of districts at medium to high transmission risk.[39]

Climatically suitable regions for dengue transmission are anticipated to expand, with notable increases observed in western and central Europe,[40] southern Europe,[55,56,76] the Mediterranean and Adriatic coasts and northern Italy,[43] Mexico,[41,50] North Africa, the Arabian Peninsula, and parts of inland Australia.[44] Coastal areas, such as Dar es Salaam and Zanzibar in Tanzania will also observe higher transmission risk.[45] Similarly, dengue transmission suitability is expected to rise in Nepal,[49] Jeju Island in South Korea,[51] temperate zones,[53,58,60,65] higher altitudes,[24,34,58,63,73,75,85] and northern and eastern regions of Taiwan.[54] In India, regions such as Kolkata[59] and southern, central, and eastern parts of the country are projected to observe increased risk.[61] Other high-risk areas include Rio de Janeiro[66] and Espírito Santo state in Brazil[83]; the Pearl River Delta[68]; the southern, southeastern, eastern,[69] northwestern, and northeastern regions of China,[79] including the mainland[77]; parts of North and South America[84]; the southeastern USA[47]; and northern Europe, including England, Ireland, and Scandinavia.[87] These expansions are driven by enhanced climatic conditions favorable for mosquito breeding and virus transmission.[41,42,48]

Evaluation of the Future Risk of Dengue: Global Perspective

Between 2040 and 2070, the predicted total population at risk of contracting dengue is estimated to be 4.46 (4.44–4.50) billion by Khormi and Kumar.[44] About 3.6 billion people at risk of dengue is estimated by Colón-González et al.,[24] 3.2/4.1 billion will be at risk depending on baseline/Hadley Centre Coupled Model version 2 projected humidity (Hales et al.[2]), and 2.98–4.60 billion people will be at risk (during 2061–2080 specifically) as projected by Monaghan et al.[48] Overall risk may increase based on the length of transmission season in higher altitudes (>1,500 m) in the African region[24] but may be reduced in continental Europe over coming decades due climate variability and absence of a more competent *A. aegypti* vector.[56,64] Nonetheless, Khormi and Kumar,[44] Ryan et al.,[58] and Laporta et al.[76] predicted higher risk in Europe due to increased *A. aegypti* climate suitability, population exposure, and distribution of dengue vectors. Besides, the life cycle completion per decade will accelerate by 4.4% (3.5–5.4%) per decade from the 2000s while invading ∼2–6 km per year by 2050.[64]

The global-based predictive analyses were primarily conducted on the basis of dengue occurrence records,[1,44,56,76] creating mechanistic models,[3,48,58,64] collecting incidence data from government websites,[24] or by reviewing existing scientific literature.[2] The occurrence data provide presence-only information, indicating where a vector species has been found but often lacks true absence data on where the species is not present. To account for this, techniques like generating pseudo-absences or background sampling are used in modeling.[64,76] However, sampling selection bias may occur due to the underlying assumption that the background data (occurrence record) implies true absence. Moreover, the strength of entomological surveys may bias to hot spots and site distance.[97] In such a situation, the model output may not represent the true distribution of the species. This sample selection bias can be mitigated by analyzing the dataset by presence/absence labeling within a large sample, which represents the range of environmental conditions.[98] We found this labeling in some included studies[1,2,56,76] but not all. Several important climatic variables such as temperature, precipitation, humidity, and vapor pressure were used for assessing the risk while the nonclimatic variables included population, GDP, and urban or nonurban areas data.

Discussion

Despite the escalated risk of dengue transmission,[1–3,39,41,42] increased vector suitability,[44,45,47,49,51] and geographical expansion[38,40,52] projected in the long-term future, the use of credible epidemiological and entomological dengue data at a higher spatial resolution is necessary. This data should consider various sociodemographic, economic, and environmental risk factors during modeling and require the evaluation of both model performance and outcome validation. The WHO Southeast Asian region consists of 10 dengue-endemic countries, which account for 52% of the global risk of dengue.[5] South Asia and East Asia and the Pacific regions have ∼4.3 billion in population in total.[99] Therefore, the most important factor in the future will be to understand how large-scale population movement, internal and external migration, and international travel will influence dengue transmission under different climate change scenarios. In this case, SSPs will provide a better understanding, as they take into consideration several crucial issues such as fossil fuel development, regional rivalry, and inequality, which we discussed elaborately below.

Selecting appropriate climate models is a critical challenge as advancements in climate science continue. For example, Liu et al.[78] compared climate data from local meteorological stations and general circulation models (GCMs) in China, identifying discrepancies in their mean temperature projections. Linear regression analysis of historical data projected a mean temperature of 2.17°C (1.88–2.46°C) for 2050, while GCM projections were ∼1°C lower.[78] Addressing such discrepancies requires further exploration and alignment.

The IPCC has played a pivotal role in assessing climate science. Established by the WMO and United Nations Environment Program in 1988, the IPCC has provided a robust scientific foundation for policymaking.[100] Starting with its First Assessment Report in 1990 (SA90), the IPCC has advanced our understanding of climate change.[31] In 1992, six scenarios (IS92 a–f) were introduced in a supplementary report, integrating new data.[101] Subsequent reports, such as the Second Assessment Report in 1995,[102] highlighted anthropogenic climate impacts, while the Third (2001)[103] and Fourth (2007)[104] Assessment Reports incorporated SRES scenarios and observed trends, including increased atmospheric water vapor and improved climate models. The SRES scenarios were developed through an intensive international process to create new projections. The Fifth Assessment Report (2014) introduced RCPs, which focused on emissions trajectories and their implications.[105] The most recent AR6 (2023) integrates a broader range of factors, including greenhouse gas emissions, land use, and air pollution, while introducing SSPs (Excel Table S2).[106] SSPs provide socioeconomic narratives that complement the physical focus of RCPs, capturing variables like demographics, economic growth, urbanization, and technology that influence emissions and climate outcomes.[106]

Therefore, AR6 represents the most comprehensive and advanced assessment of climate change science to date, providing a foundation for improving the accuracy of future climate projections by incorporating the latest findings and methodologies. Our review observed that most studies relied on RCPs, particularly the high-emission pathway RCP 8.5, to assess dengue risk under extreme climate scenarios. However, pathways like RCP 4.5, which assumes moderate climate actions, aim to stabilize radiative forcing at 4.5 W/m^2 by the year 2100, representing a scenario that seeks to balance economic and environmental objectives.[107] These findings highlight the importance of aligning climate modeling with both physical and socioeconomic contexts to improve accuracy in disease risk assessments.

Spatial resolution for the climate database plays a major role because several environmental factors, such as land use and land cover, fresh water sources, ocean conditions, habitat type, and built environment, are important confounding factors, and finer spatial resolution can improve the accuracy of these data. Dengue transmission is highly sensitive to microclimatic conditions like temperature and humidity, which vary significantly and diverge dramatically from general air temperature data, even within a small geographic area such as a city.[108] Therefore, higher spatial resolution is crucial to measure future dengue risk more accurately. Moreover, for the smaller countries or regions, without a finer spatial scale, it will be hard to determine the actual population movement and conduct thorough risk assessments. Alongside finer spatial resolution being a limitation, several studies mentioned concerns regarding dengue data. For example, small sample sizes,[49,80] coarse spatial scale,[1] poor surveillance systems,[42,77] and the absence of *A. albopictus* data[78] were the major dengue data-related problems. Furthermore, only a limited number of studies could incorporate both entomological and epidemiological data, which is essential for the evidence-based decision making suggested by the WHO.[109]

Based on the human case or disease occurrence records, performing the probabilistic modeling by Maxent may provide some advantages, as it incorporates interactions between environmental factors and vector species. It can utilize both categorical and continuous data and can create continuous maps of species distribution. Additionally, it observes the species distribution under space and environmental conditions and determines the maximum entropy,[110] even with fewer than 25 occurrence data points (depending on the spatial resolution of the study location).[111] However, the result should be used with caution by acknowledging the limitations of the actual representation of many biological realities, sampling bias, and regularization (add a penalty to the complexity of the model) to reduce the possibility of overfitting.[112] Approaches to predicting dengue transmission risk vary significantly by understanding changes in the mosquito life cycle, spatiotemporal analysis using case notification, using dengue occurrence point to predict the future probabilistic distribution, creating an SCI to measure the spatial and temporal risk, calculating potential transmission index, measuring the R_o, and many more. While determining the R_o, the calculation of contagiousness should be updated by any variabilities caused by vaccination programs driven by any difference in individual susceptibility to the dengue virus.[113]

To improve future projections of dengue under climate change, development of big data such as dengue case surveillance and entomological data, socioenvironmental data, climatic data at higher spatial resolution, immunity level survey, and human movement data should be prioritized to ensure quality and reliability. While modeling approaches may vary based on the available data, the optimal approach should perform both internal and external validation, reduce different types of biases, and continue to check whether the prediction is reliable. To our knowledge, the SCI approach is a unique mechanistic modeling framework that can detect any climate-suitable region for *A. aegypti* and *A. albopictus*.[114] Davis et al.[65] used this approach to understand the influence of regional temperature on the vectorial capacity. As climate change progresses, the SCI can help forecast areas that may become suitable for dengue transmission due to climatic and nonclimatic factors favoring vector proliferation as well as provide insights within the regions lacking entomological surveillance data.[115] Reliable dengue prediction in the future will also depend on the accurate representation of high-resolution spatiotemporal data and incorporating random effects and interactions in models. Spatiotemporal models have the advantage of addressing these uncertainties.[116] Knowledge regarding the Breteau index, house index, pupal index, and prevalence of anti-dengue antibodies after an outbreak also could be essential to understand the trend.[117] It is worth further including the herd immunity of the population,[118] vaccine efficacy,[119] and *Wolbachia* intervention in the modeling and analyzing the contributing factors behind the autochthonous cases in novel locations. Herd immunity to dengue is strain specific, and subsequent infections with different serotypes can lead to more severe disease, such as dengue hemorrhagic fever or dengue shock syndrome.[120] We strongly recommend utilizing ensemble modeling for forecasting, which integrates both spatiotemporal models and machine learning methods. Relying on a single model is challenging due to inherent problems related to the dengue database used, random effects, and their complex interactions. Ensemble modeling can enhance the robustness and accuracy of predictions by combining the strengths of multiple approaches, thereby addressing these underlying difficulties more effectively.[121]

Based on the studies reviewed, we suggest several actions to improve predictions of dengue under climate change scenarios and thus increase preparedness. First, update surveillance databases to integrate clinical records, social media data,[122] and entomological data for *A. aegypti* and *A. albopictus* mosquitoes. In short-term prediction, surveillance may involve abrupt rises in dengue notification resulting from rapid human mobility situations,[123] such as festivals, concerts, or displacement induced by political instability, travel, internal or international migration, and heatwaves.[124] Second, employing an integrated network and modern monitoring technology, along with establishing a system that enables real-time data exchange between regions and countries, is advisable.[125] Allocating additional resources to develop advanced remote sensing, geographic information systems, and artificial intelligence to improve the identification of dengue epidemics is further practical.[126] Comprehensive and extensive dengue data may significantly enhance the accuracy of long-term predictions. In addition, it is crucial to build a genomic surveillance system to monitor global or regional variation in the dengue virus serotypes. Third, track future research and development on vaccine effectiveness, human mobility, and microclimate by surveying dengue vectors, employing *Wolbachia*-infected mosquitos to assess the impact, and measuring climatic suitability in the respective areas. Methods for controlling insects include the use of insecticides, reducing their sources, employing the sterile insect approach, and implementing *Wolbachia* intervention. Fourth, create a linkage between databases from different sectors and develop advanced statistical models. Employing higher geographical resolution for dengue case data, including meteorological and nonclimatic datasets, considering many aspects of risk assessment, confirming study findings, and enhancing model performance through various methodologies might yield reliable results. Future research should prioritize the evaluation of model performance in various places and the acquisition of more accurate location-specific data for model parameterization. Fifth, develop dashboards to visualize and communicate local and global risks with all of the policymakers and stakeholders, and establish an efficient integrated network for an early warning system. Our overall recommendation for a data-driven early warning system to enhance the future preparedness of public health infrastructure is visualized in Figure 4. Furthermore, the recent development of the TV005,[127] Dengvaxia,[15] and Qdenga vaccines[16] and *Wolbachia* implementation in several regions may require redefining susceptibility to dengue infection in different populations in the future.[128]

Based the reviewed literature, dengue transmission is projected to infect a larger population in the future, expanding to new geographic locations, including high-altitude regions,[53] low-lands,[49] metropolitan cities,[69] coastal zones,[34] rural landscapes,[24] and even desert environments.[34] Future patterns of dengue transmission will be heavily influenced by climatic factors and human activities. Notably, previous studies indicate that mobility restrictions imposed during the COVID-19 pandemic had an unpredictable effect on the transmission of dengue.[129–131] This highlights the necessity of assessing the influence of such interventions on the regular transmission dynamics, as well as exploring the underlying causal mechanisms and vector behavior during periods of human movement restriction. Several key limitations identified in the studies include challenges in tracking the effects of climate variability and human interventions on dengue virus transmission. Factors such as water networks, aquatic habitats, internal travel, vegetation, land use and land cover changes, urbanization, increased globalization, transportation system, income disparities, and the interaction between *A. aegypti* and *A. albopictus* was often inadequately addressed. Understanding these interconnected elements will be critical to refining future strategies for dengue prevention and control.

There are several limitations of this review that warrant consideration. First, as the study was restricted to peer-reviewed publications in English, the exclusion of studies published in other languages, unpublished works, non–peer-reviewed studies, or gray literature cannot be ruled out. Second, the heterogeneity in geographical scope, spatial and temporal variations in prediction scales, and methodological differences across the studies presented challenges in performing statistical analyses to synthesize outcomes from the extracted results. Future research should aim to conduct more targeted statistical analyses to provide nuanced insights into the risks of climate change-related dengue transmission. Third, while short-term prediction of dengue transmission is possible, the exclusion of such studies limits our ability to assess near-future risk comprehensively. This review also did not identify or recommend a definitive methodology for predicting dengue transmission, as the phenomenon remains highly complex; however, we emphasize the importance of employing multiple approaches to enhance prediction accuracy. Finally, our study did not explain the future risk of dengue transmission for every specific location mentioned within the studies included.

Despite these limitations, this review combined fundamental information from 57 studies intended to assist policymakers in managing dengue transmission in the context of global warming. Despite notable variability in projection periods, study locations, sample sizes, dengue data types, spatial resolutions, and analytical techniques, a clear conclusion emerged: the overall risk of dengue exposure is expected to increase considerably in the future. This trend underscores the immediate importance for adequate and preventive measures to minimize the effects of climate change on dengue transmission. This review identifies a significant challenge related to the availability and quality of dengue-related data, especially in developing countries with inadequate surveillance infrastructure. Accurate predictive models require reliable data on dengue incidence and transmission. The absence of standardized reporting systems, along with deficiencies in spatial and temporal coverage, hinders effective disease monitoring. Human mobility and international travel significantly contribute to the spread of pathogens across geographic regions. The absence of human movement data, especially real-time mobility patterns, in conjunction with climate variables, undermines climate-based predictive models and limits our capacity to accurately forecast outbreaks. Minimizing the discrepancy between modeling-based predictions and real-time dengue incidence should be a primary objective moving forward. Integrating high-resolution climate, human mobility, and socioenvironmental data into robust spatiotemporal models will facilitate this achievement. These approaches would facilitate the development of sophisticated, real-time early warning systems that can deliver prompt alerts to high-risk regions and communities.

This review identified deficiencies in geographic representation within the current body of research. Numerous dengue-endemic nations identified by the WHO were not found in the studies reviewed. Further investigation of those regions is necessary to ensure a comprehensive assessment and accounting of global dengue transmission risks. Future research must focus on addressing these geographic gaps by implementing standardized methodologies across various contexts, which will facilitate comparisons and improve the generalizability of results. Finally, the overall limitations of previous studies explored in this review should be addressed in the future by using robust spatiotemporal models to develop an advanced early warning system. Based on the current evidence, the shape of the future burden of dengue may be managed through bolstering established policies and strategic efforts to limit anthropogenic climate change.

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