ECOGRAPHY

Research article

Climate change is aggravating dengue and yellow fever transmission risk

Alisa Aliaga-Samanez[1], David Romero[1], Kris Murray[2,3], Marina Cobos-Mayo[1], Marina Segura[4], Raimundo Real[1,5] and Jesús Olivero[1,5]

[1]Grupo de Biogeografía, Diversidad y Conservación, Departamento de Biología Animal, Universidad de Málaga, Malaga, Spain
[2]Medical Research Council Unit the Gambia at London School of Hygiene and Tropical Medicine, Fajara, Gambia
[3]Centre on Climate Change and Planetary Health, London School of Hygiene & Tropical Medicine, London, UK
[4]Centro de Vacunación Internacional, Ministerio de Sanidad, Consumo y Bienestar Social, Estación Marítima, Malaga, Spain
[5]Instituto IBYDA, Centro de Experimentación Grice-Hutchinson, Malaga, Spain

Correspondence: Alisa Aliaga-Samanez (alisaliaga@uma.es)

Ecography
2024: e06942
doi: 10.1111/ecog.06942
Subject Editor: Timothée Poisot
Editor-in-Chief: Jean-François Guégan Accepted: 21 May 2024

Dengue and yellow fever have complex cycles, involving urban and sylvatic mosquitoes, and non-human primate hosts. To date, efforts to assess the effect of climate change on these diseases have neglected the combination of such crucial factors. Recent studies only considered urban vectors. This is the first study to include them together with sylvatic vectors and the distribution of primates to analyse the effect of climate change on these diseases. We used previously published models, based on machine learning algorithms and fuzzy logic, to identify areas where climatic favourability for the relevant transmission agents could change: 1) favourable areas for the circulation of the viruses due to the environment and to non-human primate distributions; 2) the favourability for urban and sylvatic vectors. We obtained projections of future transmission risk for two future periods and for each disease, and implemented uncertainty analyses to test for predictions reliability. Areas currently favourable for both diseases could keep being climatically favourable, while global favourability could increase a 7% for yellow fever and a 10% increase for dengue. Areas likely to be more affected in the future for dengue include West Africa, South Asia, the Gulf of Mexico, Central America and the Amazon basin. A possible spread of dengue could take place into Europe, the Mediterranean basin, the UK and Portugal; and, in Asia, into northern China. For yellow fever, climate could become more favourable in Central and Southeast Africa; India; and in north and southeast South America, including Brazil, Paraguay, Bolivia, Peru, Colombia and Venezuela. In Brazil, favourability for yellow fever will probably increase in the south, the west and the east. Areas where the transmission risk spread is consistent to the dispersal of vectors are highlighted in respect of areas where the expected spread is directly attributable to environmental changes. Both scenarios could involve different prevention strategies.

Keywords: Biogeography, host–pathogen systems, pathogen spillover, vector-borne disease ecology, zoonotic diseases

NORDIC SOCIETY OIKOS

www.ecography.org

Introduction

Dengue and yellow fever are among the deadliest mosquito-borne diseases worldwide (Kuno 2015, Colón-González et al. 2021). These diseases are responsible for approximately 390 million and 200 000 cases per year, respectively (CDC 2018, WHO 2021a), and they continue to spread, causing outbreaks in areas from where they had disappeared and in new areas, even if, as in the case of yellow fever, an effective vaccine already exists. This spread has several causes: climate change, forest loss, increased forest incursions, mining and oil extraction, construction and land clearing for agriculture (Daszak et al. 2000, Ka-Wai Hui 2006, Karesh et al. 2012, Rohr et al. 2019). Climate change is exposing people worldwide to increasing threats of vector-borne diseases (Watts et al. 2019). For this reason, climate change is one of the most daunting 21st century global health challenges (Iwamura et al. 2020), and is one of the key issues considered by the Global Strategy to Eliminate Yellow Fever Epidemics (EYE) 2017–2026, which is managed by WHO, Gavi and UNICEF (WHO 2021b). It is difficult to predict how global warming will affect dengue and yellow fever because they have very complex cycles, involving different mosquito species, both urban and sylvatic, and also non-human primate hosts (Gaythorpe et al. 2020). Many studies on climate change and mosquito-borne diseases do not take into account multiple sources of uncertainty in their predictions, such as health, environmental and socio-economic data, future global change scenarios and model structure (Franklinos et al. 2019). Franklinos and colleagues argue that an integrative approach that takes into account interactions between socio-economic and environmental systems is needed to better understand and predict mosquito-borne disease risk. Future projections have been made to assess the potential extent of dengue and yellow fever. For dengue, the most recent studies only included *Aedes aegypti* and *Ae. albopictus* as possible vectors. This is the case of Messina et al. (2019), who focused on changes in environmental suitability, and of Colón-González et al. (2021), who quantified the extent to which climate change could influence the length of the transmission season. The most recent research on how climate change will affect yellow fever is that of Gaythorpe et al. (2020). In it, effects on the morbidity of yellow fever in Africa were assessed considering only one urban vector species, *Ae. aegypti*, in the set of covariates. On the other hand, Hamlet et al. (2018) tested whether seasonal variations in climatic factors are associated with the seasonality of yellow fever reports. Again, only *Ae. aegypti* was considered as a vector in the analysis. Integrating all the agents involved in the zoonotic cycles is important in order to get as close as possible to having reliable future projections. In this research, we aim to detect areas worldwide where changes in the risk for dengue and yellow fever transmission are expected to occur in the short and medium terms as a consequence of climate change, on the basis of the dengue and yellow fever transmission risk models published by Aliaga-Samanez et al. (2021, 2022). In this way, projections are built taking into account the most updated database of case reports to date, and considering both urban and sylvatic mosquito vectors, together with the distribution of non-human primates.

Material and methods

Methodological and temporal framework

Our forecasts consisted of projections to the future of the dengue and yellow fever transmission models published by Aliaga-Samanez et al. (2021, 2022), which were focused on the distribution of transmission risk in the period 2001–2017. These models were based on the favourability function. Favourability reflects the degree to which the probability of occurrence of the analysed entity differs from that expected according to the initial prevalence (Real et al. 2006). So, in contrast to probability, favourability values depend exclusively on the effect of environmental conditions in the distribution area under analysis (Acevedo and Real 2012). In Aliaga-Samanez et al. (2021, 2022), the degree of favourability for the transmission of a disease (i.e. the level of transmission risk) was considered to be a result of combining a vector model (which defined favourability values for the presence of mosquito vectors) with a disease model (which defined favourability values for the occurrence of disease cases in humans). This combination was made using the fuzzy intersection operator (Zadeh 1965) which assigns, to each geographic unit, the lowest favourability value provided by each model. This ensured the existence of suitable circumstances for the presence of two agents that are geographically limiting: 1) vectors, and 2) the environmental conditions needed for a pathogen to cause disease (Romero et al. 2016, Aliaga-Samanez et al. 2021, 2022). The projection of a transmission model to a future period was, thus, the result of combining – also through the fuzzy intersection – future projections of both a vector model and a disease model.

As projections to the future regarding the presence of vectors, we used those developed by Aliaga-Samanez et al. (2023) for dengue and yellow fever. These models considered urban vector species (*Ae. aegypti* and *Ae. albopictus*) together with sylvatic vector species *Ae. africanus*, *Ae. luteocephalus*, *Ae. niveus*, *Ae. vittatus*, *Sabethes chloropterus*, *Haemagogus leucocelaenus* and *Hg. janthinomys* (Supporting information), combined according to the known set of sylvatic species involved in the zoonotic cycles of each disease. Details of the projection to future of Aliaga-Samanez et al. (2021, 2022) disease models are given below.

Projections were made considering two time periods: 2041–2060 (henceforth the 'near future period'), and 2061–2080 (henceforth the 'far future period'). Future projections were mapped to the same worldwide grid of 18 874 hexagons of 7774 km^2 (https://zenodo.org/records/10028166) used in the original models by Aliaga-Samanez et al. (2021, 2022).

Disease model projection to the future

We used different climate change scenarios (i.e. representative CO$_2$ concentration pathways, RCPs) and atmosphere–ocean general circulation models (GCMs) to account for uncertainties in our forecasts, based on a range of variation in climate predictions according to the Intergovernmental Panel on Climate Change (IPCC). Using as information source the free high-resolution climate data from CHELSA (Knutti et al. 2013, Karger et al. 2017, 2020, 2021), two RCP scenarios were chosen: the RCP 4.5 stabilized emissions scenario, and the RCP 8.5 high emissions scenario. Five GCMs with the lowest detected biases with respect to the actual climate (McSweeney et al. 2015, Sanderson et al. 2015), and with data available for the chosen RCPs, were selected: CESM1-CAM5, CNRM-CM5, FIO-ESM, GFDL-CM3 and MPI-ESM-LR. So, for every disease model and future period, we got 10 projections, corresponding to 10 RCP-GCM combinations. In Aliaga-Samanez et al. (2023), the same RCP-GCM combinations and the same future periods were used to make future projections for dengue and yellow fever vector distributions.

To obtain the future forecasting for each disease, a disease model was projected according to the following favourability (F) function (Real et al. 2006):

$$F = \exp(y) / \left[\left(n1/n0 \right) + \exp(y) \right]$$

So forecasts are based on models built on information regarding the early 21st century, in this equation: n1 and n0 are the number of presences and absences of the modelled entity (in this case, of dengue or of yellow fever case reports) in such a time period. As explained by Aliaga-Samanez et al. (2021, 2022), this information was obtained, in the case of dengue, from Messina et al. (2019) and completed with data from various sources such as WHO, ECDC, Promedmail, Gideon and scientific articles (see Aliaga-Samanez et al. (2021) for data and source details; and Supporting information for geo-referenced information on case location). In the case of yellow fever, information came from Shearer et al. (2018) and supplemented with the same sources mentioned above (Aliaga-Samanez et al. (2022) for data and source details; and Supporting information for geo-referenced information on case location). In the above F function, y is a linear combination of predictor variables (Supporting information). Taking into account the y equation of the disease models in Aliaga-Samanez et al. (2021, 2022), we calculated future favourability values replacing the values of climate variables according to the future scenarios described. Although it is a strong statement that could involve interpretative limitations, we assumed that the values of non-climate variables (i.e. human concentration, infrastructures, livestock, topography, agriculture or ecosystem types) will not change in the future period considered (Supporting information). The y equations also include variables referring to the biogeography of non-primate hosts participating in the sylvatic zoonotic cycles (Aliaga-Samanez et al. 2021, 2022; see Supporting information). These variables were represented by primate chorotypes, i.e. types of distributions (Olivero et al. 2011, 2017). Because primate distributions could be subject to changes due to global warming, these chorotypes were also projected into the future. For this purpose, a reformulation of chorotypes was needed, for which we made the following steps:

1) In total, 14 primate species belonging to the chorotypes that formed part of the models in Aliaga-Samanez et al. (2021, 2022) were considered (Table 1).
2) Favourability models were made for the current distribution of each primate species. For this purpose, range maps of the African, Asian and American primate species were obtained from the IUCN (IUCN 2021).
3) Chorotype variables were then recalculated through the accumulated favourability value (Fa et al. 2014), also named 'fuzzy species richness' (Estrada et al. 2008); that is, in every geographic unit (i.e. in each hexagon), favourability values for each primate species forming part of the chorotype were summed up (Supporting information).
4) We ensured that the original chorotypes (based on species richness) was consistent with the reformulated chorotypes (based on fuzzy species richness) by testing for significance of Spearman correlations.

Table 1. Chorotypes considered for disease models projection to the future. AS: Asia; SA: South America; AF: Africa.

Diseases	Chorotypes	Genera
Dengue	AS19	*Carlito*
	AS8	*Hylobates, Trachypithecus, Nomascus, Pygathrix*
	AF2	*Arctocebus, Lophocebus, Sciurocheirus, Gorilla, Euoticus, Cercopithecus, Colobus, Mandrillus, Miopithecus*
	SA2	*Alouatta, Ateles, Plecturocebus, Chiropotes, Mico*
	AS15	*Hylobates, Trachypithecus, Presbytis, Nycticebus*
	SA4	*Alouatta, Sapajus, Brachyteles, Callithrix, Callicebus, Leontophitecus*
	SA5	*Aotus, Cebus, Ateles, Saguinus*
Yellow fever	SA7	*Plecturocebus, Pithecia, Leontocebus*
	SA1	*Callimico, Cebus, Cebuella, Saguinus, Leontocebus, Saimiri, Sapajus*
	SA6	*Alouatta, Aotus, Ateles, Cheracebuss, Saguinus, Saimiri, Leontocebus*
	SA12	*Alouatta, Plecturocebus, Mico, Saguinus*
	AF9	*Cercopithecus, Chlorocebus, Galago, Otolemur, Papio*
Both diseases	SA8	*Alouatta, Cebus, Chiropotes, Saguinus*
	SA14	*Leontocebus, Plecturocebus, Aotus, Lagothrix*

Once we had favourability models for all primate species, the chorotype projection to the future consisted of summing up the projected favourability values for each primate species in the chorotype. This model projection followed the same guidelines explained above.

The replacement, in the original disease model, of chorotypes based on species richness with chorotypes based on fuzzy species richness made it necessary to make a model recalibration. That is, as the mathematical expression of the chorotype variable was varied, the coefficients of all variables in the disease models could also change. So, the disease model was run again fixing the same set of predictor variables as in Aliaga-Samanez et al. (2021, 2022), only replacing the chorotypes as redefined (see the Supporting information for mathematical models). The resulting recalibrated model was the base for all future projections.

Finally, we obtained the average of the 10 projections obtained for each period as a consensus of the final forecast. The level of uncertainty of predictions, in each hexagon, was estimated through the standard deviation shown by the 10 projected favourability values.

Measuring the rate of future change in the models

In order to quantify, in global terms, to what extent the original favourability values (F_0) could be modified according to the future favourability forecasts (F_f), we calculated increment and maintenance rates according to the equations (Romero et al. 2014):

$$I = \frac{c(F_f) - c(F_0)}{c(F_0)} \text{ and } M = \frac{c(F_f \cap F_0)}{c(F_0)},$$

where $c(F_x)$ is the cardinality of either the initial model (F_0) or of the future projection (F_f); that is, the sum of all the hexagons' favourability values according to a model (Zadeh 1965). The intersection between future (F_f) and present (F_0) favourability values was calculated as follows:

$$F_f \cap F_0 = \mathrm{Min}(F_f, F_0).$$

Positive increment values (I) indicate a global net increase, or gain of favourability, in the future, with respect to those of the present; whereas negative values mean a net loss in favourability. Maintenance values (M) reflect to what degree the level of favourability for the presence of disease will keep the same status in the future. Finally, local changes in favourability were analysed by mapping, in each hexagon, the difference between future forecasts and the original favourability values.

Results

Our model projections show that currently favourable areas for dengue transmission are likely to maintain this status in the near (2041–2060) and distant (2061–2080) future ($M > 0.98$). In the near future, the global level of favourability for dengue transmission could increase very slightly ($I = 0.004$), specifically in Central Africa, the southern limits of the Himalayas, eastern China, Mediterranean Europe, the Amazon basin, western and northern Brazil, southern Venezuela and the Guianan shield (Fig. 1). Nevertheless, forecasts for these areas are subject to certain levels of uncertainty ($SD = 0.04$ to 0.06, only reaching 0.1 in the Himalayas; note that favourability values range from 0 to 1). In contrast, in the distant future, an increased global degree of favourability for dengue transmission of almost 10% ($I = 0.099$) is expected. Risk levels could thus increase notably in the above-mentioned areas, and also in Mexico, southern USA, India and Southeast Asia, involving countries such as Thailand, Laos, Myanmar, Cambodia, Malaysia and Indonesia (Fig. 1). Forecasts for the distant future period are remarkably consistent, SD reaching values over 0.05 only in some areas of the Amazon basin and in Mediterranean Europe.

Predictions for yellow fever show a different picture compared to that of dengue. Currently favourable areas for transmission will probably keep this status ($M > 0.95$), but the increase in global favourability is predicted to be faster. In the near future, this increase could be > 5% ($I = 0.051$), affecting the Amazon basin (Peru, Colombia, Venezuela, and western and southern Brazil), the eastern areas of Central Africa, scattered regions in southern and south-eastern Africa, and India (Fig. 2). Uncertainty values ranging between $SD = 0.08$ and 0.2 are seen in the forecasts for the Amazon basin and for Central Africa, but these are negligible in south-eastern Africa and in India. In the distant period, the global increase with respect to the present could reach 7% ($I = 0.071$), affecting the above-mentioned areas together with northern Central Africa (Fig. 2). Uncertainty in the forecasts for this period rarely goes beyond $SD = 0.12$, but it increases in south-eastern Africa and in India compared to that for the near future forecasts.

Increasing and decreasing future distribution of primate chorotypes

Only three South American (SA1, SA6 and SA12) and one Asian (AS19) primate chorotypes are expected to increase their distribution area in the near and distant periods, compared to the present (Supporting information). The non-human primate genera forming part of these chorotypes are: *Alouatta*, *Aotus*, *Ateles*, *Saguinus*, *Saimiri*, *Callimico*, *Cebuella*, *Cheracebus*, *Sapajus*, *Cebus*, *Leontocebus*, *Plecturocebus* and *Mico* in South America, and *Carlito* in Asia. Nevertheless, all these primate chorotypes are likely to maintain their status in both future periods ($M > 0.8$), except SA8 in the near future ($M = 0.424$) and AF2 in the distant future ($M = 0.436$) (Supporting information).

Discussion

This study is the first to analyse possible changes in the geographical distribution of dengue and yellow fever transmission

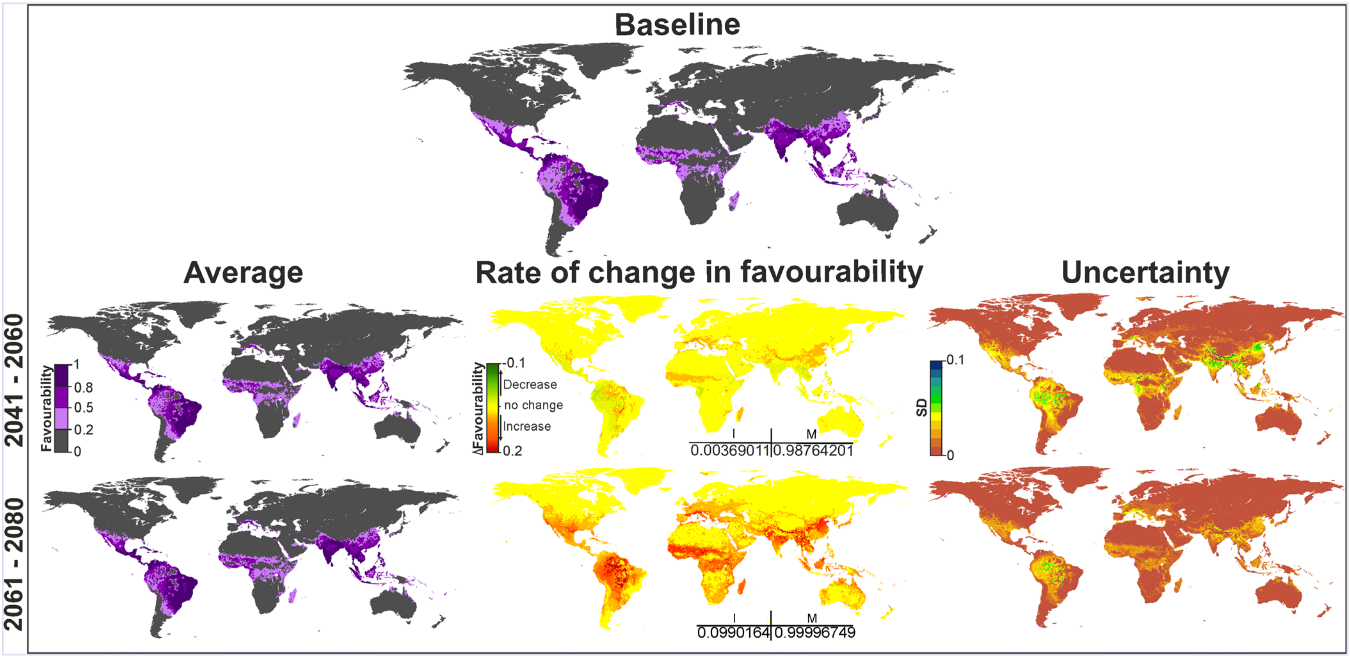

Figure 1. Dengue transmission model projections into the future for the periods 2041–2060 and 2061–2080. Transmission model for the period 2001–2017, average model projections into the future for the periods 2041–2060 and 2061–2080, areas where favourability increases and decreases in the future relative to the present. Difference between the future projection and the current model. I: increment rate; M: maintenance rate. Positive values of I indicate a net increase in favourability, that is, a gain in favourable areas, whereas negative values of I mean a net loss of favourable areas. M indicates the degree to which the favourable areas in the current model overlap with the favourable forecasted areas. Uncertainty of the vector model in the period 2041–2060 and 2061–2080. SD: standard deviation.

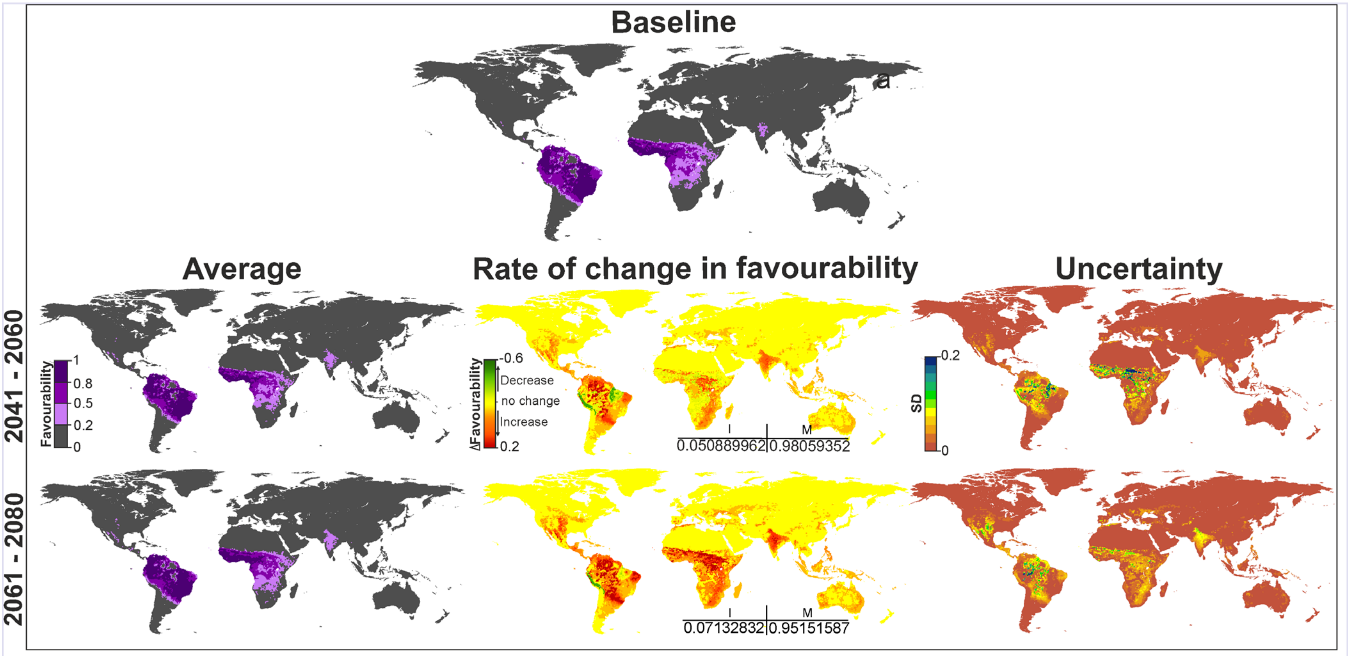

Figure 2. Yellow fever transmission model projections into the future for the periods 2041–2060 and 2061–2080. Transmission model for the period 2001–2017, average model projections into the future for the periods 2041–2060 and 2061–2080, areas where favourability increases and decreases in the future relative to the present. Difference between the future projection and the current model. I: increment rate; M: maintenance rate. Positive values of I indicate a net increase in favourability (i.e. a gain in favourable areas), whereas negative values of I mean a net loss of favourable areas. M indicates the degree to which the favourable areas in the current model overlap with the favourable forecasted areas. Uncertainty of the vector model in the period 2041–2060 and 2061–2080. SD: standard deviation.

areas taking into account both urban and sylvatic vectors, as well as the biogeography of non-human primate hosts. Our model projections detect that, for both diseases, the risk of transmission could expand to several regions of the Amazon basin, Central Africa, Asia and Europe.

Where transmission risk could increase

Despite the knowledge gained from a macro-scale analysis (our spatial resolution was 7700 km²), there are inherent limitations in its ability to capture the specific factors that may influence virus distribution. Micro-scale environmental, socio-economic and political factors can play a critical role in disease dynamics through their influence on local vectors and hosts. It is therefore essential to recognise that the findings presented here provide an overview, but may not comprehensively address the complexities at the local level. In many regions worldwide, climate change could increase the risk of dengue and yellow fever transmission in the future. The consequences of such a forecast have been discussed in several papers (Dhimal et al. 2015, Messina et al. 2019, Gaythorpe et al. 2020, Mordecai et al. 2020, Colón-González et al. 2021, Sadeghieh et al. 2021). Our projections do not show large global changes, but they do show responses at the regional scale. In the case of dengue, our distant-future projections show an increase of transmission risk in regions of Central and West Africa, South Asia, the Gulf of Mexico, Central America, the Amazon basin and Europe. These regions, with the exception of West Africa and South Asia, coincide with the areas where, according to Colón-González et al. (2021), the length of the transmission season within a year will probably increase, due to changes in rainfall and humidity generated by global warming. Furthermore, in the projections published by Messina et al. (2019), these same regions are predicted as areas of possible dengue expansion. However, only our projections show a possible expansion of dengue on the European continent. The Mediterranean basin, and some locations along the coasts of the UK and Portugal, show an increased risk of dengue transmission and with low uncertainty in these last two places. Mordecai et al. (2020) report that, in Africa, the effects of global warming are likely to promote greater environmental suitability for arboviruses transmitted by *Ae. aegypti* (for example, dengue), and to reduce suitability for pathogens transmitted by *Anopheles gambiae* (for example, malaria). Other studies focused in Asia, specifically in China, mention that there has already been an expanding trend for dengue infections from south to north, in line with warming temperatures (Yi et al. 2019). Our models predict with low uncertainty that the south will remain favourable and that there will be an increase in risk towards the north of China (Fig. 1). In Nepal, Dhimal et al. (2015) conclude climate change could intensify the risk of dengue epidemics in the mountain regions of the country. This is consistent with our results, which predict an increase not only in Nepal, but also in the whole Himalayan mountain range, comprising several countries such as India and Bhutan (Fig. 1).

In the case of yellow fever, Gaythorpe et al. (2020) suggest that transmission may change heterogeneously across Africa. Our projections predict a favourability increase in the near future, with high uncertainty, in many areas to the east of the continent. In the distant future, favourability could increase, with low uncertainty, also in the northern and western regions of Central Africa. This is in agreement with the results of Gaythorpe et al. (2020), according to which the Central African Republic is one of the countries most likely to see an increase in transmission risk. In Asia, although yellow fever infections do not occur, our model projections point to a risk increase in India, in both the near and the distant future periods (Fig. 2). Bicca-Marques et al. (2022) predicted that southern India and parts of Southeast Asia could be considered to be suitable for the presence of yellow fever virus, which could potentially threaten primate species. The global strategy to EYE 2017–2026 [7] warns that larger outbreaks will take place in Asia, including the possibility of outbreaks in countries such as India and China, which harbour *Aedes* mosquitoes and are home to 2 billion people who lack immunity to yellow fever. If the virus were ever introduced, there could be a risk of major urban outbreaks because of the high population density of non-immune humans and of *Aedes* mosquito species. For America, our model projections predict an increase in different regions of South America, including Brazil, Paraguay, Bolivia, Peru, Colombia and Venezuela (Fig. 2). This result contrasts with that of Sadeghieh et al. (2021), who predict that the intensity of outbreaks may reduce in Brazil as temperatures increase. According to our forecasts for the distant future, favourability for yellow fever transmission could increase, with low uncertainty, in south and eastern Brazil, following the trend observed in the last decade (Mir et al. 2017). During the period 2016–2019, Brazil faced one of the largest outbreaks of yellow fever in recent decades. In the city of São Paulo, the virus was detected in *Alouatta* in an area of Mata Atlantica and *Callithrix* mainly in urban areas of the city (Cunha et al. 2020). Our projections suggest that the favourability of non-human primate distributions could increase in the future, affecting these primate genera (Supporting information).

The areas where we predict an increased risk of transmission coincide with those where mosquito favourability also increases (Aliaga-Samanez et al. 2023), often with that for sylvatic mosquitoes. For example, in the case of dengue, in Europe these areas of increased risk coincide with increased favourable conditions for *Ae. aegypti* in Portugal, Spain and Italy (although this species has not yet established populations in the continent). *Aedes aegypti* could probably survive all year round and re-establish itself in these regions under climate change scenarios (Kramer et al. 2020). In countries such as those of the UK, the increase should be attributable to the environment, as no significant changes regarding vectors is predicted in this area by Aliaga-Samanez et al. (2023). In the case of dengue in Asia, the increase in areas such as the southern Himalayas coincides with an increase in future favourable conditions for transmitting mosquitoes such as *Ae. aegypti*, *Ae. vittatus* and *Ae. niveus* (Aliaga-Samanez et al. 2023). *Aedes aegypti* mosquitoes sampled in Nepal were able to survive the low temperatures for a short period (Kramer et al. 2020). With rising temperatures due to climate change, *A. aegypti* will be able to spread to higher altitudes (Dhimal et al. 2021). In contrast, as in the UK, the projected increase in dengue transmission risk in northern China should be attributable to the environment.

The areas of increased favourability for future transmission of both dengue and yellow fever are likely to coincide with increased favourable conditions for *Ae. vittatus*, *Ae. luteocephalus* and *Ae. africanus* in the northern and western regions of Central Africa such as Cameroon, Central African Republic and northern Democratic Republic of Congo (Aliaga-Samanez et al. 2023). These predictions are of concern, as sylvatic cycles of dengue persist in Africa and continue to spill over to humans (Cardosa et al. 2009, Dieng et al. 2023). In South America, the most favourable areas for future yellow fever transmission coincide with a more suitable presence of *S. chloropterus* in Peru, Brazil and Bolivia, and also of *Ae. albopictus* in the Amazon basin. In countries such as Colombia and Paraguay, the increase could be due to the environment instead (Aliaga-Samanez et al. 2023).

Conclusion

According to our results, surveillance strategies could be applied taking into account two scenarios. On the one side, vector surveillance efforts should be prioritised in those areas where the increased dengue or yellow fever transmission risk is seen to coincide with forecasted changes in the distribution of vectors. The early detection of arrival of new mosquito species could give place to further measures in prevention. Once the vector is present in the region, if risk is predicted to be higher following environmental changes, we suggest an exhaustive surveillance for the appearance of outbreaks in new areas, and the launching of deep information campaigns focused on people travelling to and from endemic areas. This is really challenging, as each country has its own surveillance systems; however, integration of surveillance systems has been shown to improve surveillance performance (George et al. 2020). Without a globally standardised system, it is difficult to prevent new outbreaks. According to our study, dengue could spread to the European continent, specifically to the Mediterranean basin, the UK and Portugal; and, in Asia, to northern China. In the case of yellow fever, climatic favourability could increase in central and southeast Africa, India, South America (Brazil, Paraguay, Bolivia, Peru, Colombia and Venezuela). Specifically, in Brazil, yellow fever favourability could increase in the south, west and east. In order to get detailed forecasts, we suggest that fine-scale pathogeographic analyses be made in the regions of concern.

Funding – This study was supported by Project PID2021-124063OB-I00 of the Spanish Ministry of Science and Innovation and European Regional Development Fund (ERDF). DR is supported by the incorporation Doctor program of the University of Malaga, UMA-2022/REGSED-64576. AA-S was supported by a postdoctoral contract of the Plan Propio de Investigación, Transferencia y Divulgación Científica of the University of Malaga.

Author contributions

Alisa Aliaga-Samanez: Conceptualization (lead), Data curation (lead), Formal analysis (lead), Funding acquisition (lead), Investigation (lead), Methodology (lead), Visualization (lead), Writing – original draft (lead), Writing – review and editing (lead). **David Romero**: Investigation (supporting), Supervision (supporting), Writing – original draft (supporting). **Kris Murray**: Investigation (supporting), Supervision (supporting). **Marina Cobos-Mayo**: Investigation (supporting), Writing – original draft (supporting). **Marina Segura**: Investigation (supporting), Supervision (supporting). **Raimundo Real**: Conceptualization (supporting), Investigation (supporting), Supervision (supporting). **Jesús Olivero**: Conceptualization (lead), Formal analysis (lead), Funding acquisition (lead), Investigation (lead), Methodology (lead), Supervision (lead), Validation (lead), Writing – original draft (lead).

Transparent peer review

The peer review history for this article is available at https://www.webofscience.com/api/gateway/wos/peer-review/ecog.06942.

Data availability statement

Data are available from the Figshare: https://doi.org/10.6084/m9.figshare.25897024.v1 (Aliaga Samanez et al. 2024).

Supporting information

The Supporting information associated with this article is available with the online version.

References

Acevedo, P. and Real, R. 2012. Favourability: concept, distinctive characteristics and potential usefulness. – Naturwissenschaften 99: 515–522.

Aliaga-Samanez, A., Cobos-Mayo, M., Real, R., Segura, M., Romero, D., Fa, J. E. and Olivero, J. 2021. Worldwide dynamic biogeography of zoonotic and anthroponotic dengue. – PLoS Negl. Trop. Dis. 15: e0009496.

Aliaga-Samanez, A., Real, R., Segura, M., Marfil-Daza, C. and Olivero, J. 2022. Yellow fever surveillance suggests zoonotic and anthroponotic emergent potential. – Commun. Biol. 5: 530.

Aliaga-Samanez, A., Romero, D., Murray, K., Segura, M., Real, R. and Olivero, J. 2023. Potential climate change effects on the distribution of urban and sylvatic dengue and yellow fever vectors. – bioRxiv 2023.11.06.565841.

Aliaga-Samanez, A., Romero, D., Murray, K., Cobos-Mayo, M., Segura, M., Real, R. and Olivero, J. 2024. Presence and absence of records of dengue cases, yellow fever cases, and vector occurrences on a worldwide 7,774-km² hexagonal grid. – Figshare Dataset, https://doi.org/10.6084/m9.figshare.25897024.v1.

Bicca-Marques, J. C., Rabelo, R. M., de Almeida, M. A. B. and Sales, L. P. 2022. The risks of yellow fever to Asian primates. – Int. J. Primatol. 43: 74–91.

Cardosa, J., Ooi, M. H., Tio, P. H., Perera, D., Holmes, E. C., Bibi, K. and Abdul Manap, Z. 2009. Dengue virus Serotype 2 from a sylvatic lineage isolated from a patient with dengue hemorrhagic fever. – PLoS Negl. Trop. Dis. 3: e423.

CDC 2018. Global health: yellow fever. – CDC, https://www.cdc.gov/globalhealth/newsroom/topics/y.

Colón-González, F. J., Sewe, M. O., Tompkins, A. M., Sjödin, H., Casallas, A., Rocklöv, J., Caminade, C. and Lowe, R. 2021. Projecting the risk of mosquito-borne diseases in a warmer and more populated world: a multi-model, multi-scenario intercomparison modelling study. – Lancet Planet. Health 5: e404–e414.

Cunha, M. S. et al. 2020. Possible non-sylvatic transmission of yellow fever between non-human primates in São Paulo city, Brazil, 2017–2018. – Sci. Rep. 10: 1–81.

Daszak, P., Cunningham, A. A. and Hyatt, A. D. 2000. Emerging infectious diseases of wildlife – threats to biodiversity and human health. – Science 287: 443–449.

Dhimal, M., Ahrens, B. and Kuch, U. 2015. Climate change and spatiotemporal distributions of vector-borne diseases in Nepal – a systematic synthesis of literature. – PLoS One 10: e0129869.

Dhimal, M., Kramer, I. M., Phuyal, P., Budhathoki, S. S., Hartke, J., Ahrens, B., Kuch, U., Groneberg, D. A., Nepal, S., Liu, Q. Y., Huang, C. R., CissÉ, G., Ebi, K. L., Klingelhöfer, D. and Müller, R. 2021. Climate change and its association with the expansion of vectors and vector-borne diseases in the Hindu Kush Himalayan region: a systematic synthesis of the literature. – Adv. Clim. Change Res. 12: 421–429.

Dieng, I. et al. 2023. Re-emergence of Sylvatic dengue 2 during an outbreak in southeastern Senegal, Kedougou 2020. – medRxiv: 11.22.23298824.

Estrada, A., Real, R. and Vargas, J. M. 2008. Using crisp and fuzzy modelling to identify favourability hotspots useful to perform gap analysis. – Biodivers. Conserv. 17: 857–871.

Fa, J. E., Olivero, J., Farfán, M. Á., Márquez, A. L., Vargas, J. M., Real, R. and Nasi, R. 2014. Integrating sustainable hunting in biodiversity protection in central Africa: hot spots, weak spots, and strong spots. – PLoS One 9: e112367.

Franklinos, L. H. V., Jones, K. E., Redding, D. W. and Abubakar, I. 2019. The effect of global change on mosquito-borne disease. – Lancet Infect. Dis. 19: e302–e312.

Gaythorpe, K. A. M., Hamlet, A., Cibrelus, L., Garske, T. and Ferguson, N. M. 2020. The effect of climate change on yellow fever disease burden in Africa. – eLife 9: 1–27.

George, J., Häsler, B., Mremi, I., Sindato, C., Mboera, L., Rweyemamu, M. and Mlangwa, J. 2020. A systematic review on integration mechanisms in human and animal health surveillance systems with a view to addressing global health security threats. – One Heal. Outlook 2: 1–15.

Hamlet, A., Jean, K., Perea, W., Yactayo, S., Biey, J., Van Kerkhove, M., Ferguson, N. and Garske, T. 2018. The seasonal influence of climate and environment on yellow fever transmission across Africa. – PLoS Negl. Trop. Dis. 12: e0006284.

IUCN 2021. IUCN Red List of threatened species. Ver. 2021–2. – www.iucnredlist.org/.

Iwamura, T., Guzman-Holst, A. and Murray, K. A. 2020. Accelerating invasion potential of disease vector *Aedes aegypti* under climate change. – Nat. Commun. 11: 1–10.

Ka-Wai Hui, E. 2006. Reasons for the increase in emerging and re-emerging viral infectious diseases. – Microbes Infect. 8: 905–916.

Karesh, W. B., Dobson, A., Lloyd-Smith, J. O., Lubroth, J., Dixon, M. A., Bennett, M., Aldrich, S., Harrington, T., Formenty, P., Loh, E. H., Machalaba, C. C., Thomas, M. J. and Heymann, D. L. 2012. Ecology of zoonoses: natural and unnatural histories. – Lancet 380: 1936–1945.

Karger, D. N., Conrad, O., Böhner, J., Kawohl, T., Kreft, H., Soria-Auza, R. W., Zimmermann, N. E., Linder, H. P. and Kessler, M. 2017. Climatologies at high resolution for the earth's land surface areas. – Sci. Data 4: 170122.

Karger, D. N., Schmatz, D. R., Dettling, G. and Zimmermann, N. E. 2020. High-resolution monthly precipitation and temperature time series from 2006 to 2100. – Sci. Data 7: 248.

Karger, D. N., Wilson, A. M., Mahony, C., Zimmermann, N. E. and Jetz, W. 2021. Global daily 1 km land surface precipitation based on cloud cover-informed downscaling. – Sci. Data 8: 307.

Knutti, R., Masson, D. and Gettelman, A. 2013. Climate model genealogy: generation CMIP5 and how we got there. – Geophys. Res. Lett. 40: 1194–1199.

Kramer, I. M., Kreß, A., Klingelhöfer, D., Scherer, C., Phuyal, P., Kuch, U., Ahrens, B., Groneberg, D. A., Dhimal, M. and Müller, R. 2020. Does winter cold really limit the dengue vector *Aedes aegypti* in Europe? – Parasit. Vectors 13: 178.

Kuno, G. 2015. A re-examination of the history of etiologic confusion between dengue and chikungunya. – PLoS Negl. Trop. Dis. 9: 1–11.

McSweeney, C. F., Jones, R. G., Lee, R. W. and Rowell, D. P. 2015. Selecting CMIP5 GCMs for downscaling over multiple regions. – Clim. Dyn. 44: 3237–3260.

Messina, J. P. et al. 2019. The current and future global distribution and population at risk of dengue. – Nat. Microbiol. 4: 1508–1515.

Mir, D., Delatorre, E., Bonaldo, M., Lourenço-de-Oliveira, R., Vicente, A. C. and Bello, G. 2017. Phylodynamics of yellow fever virus in the Americas: new insights into the origin of the 2017 Brazilian outbreak. – Sci. Rep. 7: 7385.

Mordecai, E. A., Ryan, S. J., Caldwell, J. M., Shah, M. M. and LaBeaud, A. D. 2020. Climate change could shift disease burden from malaria to arboviruses in Africa. – Lancet Planet. Health 4: e416–e423.

Olivero, J., Real, R. and Márquez, A. L. 2011. Fuzzy chorotypes as a conceptual tool to improve insight into biogeographic patterns. – Syst. Biol. 60: 645–660.

Olivero, J., Fa, J. E., Real, R., Farfán, M. Á., Márquez, A. L., Vargas, J. M., Gonzalez, J. P., Cunningham, A. A. and Nasi, R. 2017. Mammalian biogeography and the Ebola virus in Africa. – Mamm. Rev. 47: 24–37.

Real, R., Barbosa, A. M. and Vargas, J. M. 2006. Obtaining environmental favourability functions from logistic regression. – Environ. Ecol. Stat. 13: 237–245.

Rohr, J. R., Barrett, C. B., Civitello, D. J., Craft, M. E., Delius, B., DeLeo, G. A., Hudson, P. J., Jouanard, N., Nguyen, K. H., Ostfeld, R. S., Remais, J. V., Riveau, G., Sokolow, S. H. and Tilman, D. 2019. Emerging human infectious diseases and the links to global food production. – Nat. Sustain. 2: 445–456.

Romero, D., Olivero, J., Márquez, A. L., Báez, J. C. and Real, R. 2014. Uncertainty in distribution forecasts caused by taxonomic ambiguity under climate change scenarios: a case study with two newt species in mainland Spain. – J. Biogeogr. 41: 111–121.

Romero, D., Olivero, J., Brito, J. C. and Real, R. 2016. Comparison of approaches to combine species distribution models based on different sets of predictors. – Ecography 39: 561–571.

Sadeghieh, T., Sargeant, J. M., Greer, A. L., Berke, O., Dueymes, G., Gachon, P., Ogden, N. H. and Ng, V. 2021. Yellow fever virus outbreak in Brazil under current and future climate. – Infect. Dis. Modell. 6: 664–677.

Sanderson, B. M., Knutti, R. and Caldwell, P. 2015. A representative democracy to reduce interdependency in a multimodel ensemble. – J. Clim. 28: 5171–5194.

Shearer, F. M., Longbottom, J., Browne, A. J., Pigott, D. M., Brady, O. J., Kraemer, M. U. G., Marinho, F., Yactayo, S., de Araújo, V. E. M., da Nóbrega, A. A., Fullman, N., Ray, S. E., Mosser, J. F., Stanaway, J. D., Lim, S. S., Reiner, R. C., Moyes, C. L., Hay, S. I. and Golding, N. 2018. Existing and potential infection risk zones of yellow fever worldwide: a modelling analysis. – Lancet Glob. Health 6: e270–e278.

Watts, N. et al. 2019. The 2019 report of the Lancet Countdown on health and climate change: ensuring that the health of a child born today is not defined by a changing climate. – Lancet 394: 1836–1878.

WHO 2021a. Dengue and severe dengue. – WHO, http://www.who.int/mediacentre/factsheets/fs117/en.

WHO 2021b. Eliminate yellow fever epidemics (EYE) strategy 2017–2026. – WHO, https://www.who.int/publications/i/item/9789241513.

Yi, L., Xu, X., Ge, W., Xue, H., Li, J., Li, D., Wang, C., Wu, H., Liu, X., Zheng, D., Chen, Z., Liu, Q., Bi, P. and Li, J. 2019. The impact of climate variability on infectious disease transmission in China: current knowledge and further directions. – Environ. Res. 173: 255–261.

Zadeh, L. A. 1965. Fuzzy sets. – Inf. Control 8: 338–353.