

Climate change could shift disease burden from malaria to arboviruses in Africa

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Malaria is a long-standing public health problem in sub-Saharan Africa, whereas arthropod-borne viruses (arboviruses) such as dengue and chikungunya cause an under-recognised burden of disease. Many human and environmental drivers affect the dynamics of vector-borne diseases. In this Personal View, we argue that the direct effects of warming temperatures are likely to promote greater environmental suitability for dengue and other arbovirus transmission by *Aedes aegypti* and reduce suitability for malaria transmission by *Anopheles gambiae*. Environmentally driven changes in disease dynamics will be complex and multifaceted, but given that current public efforts are targeted to malaria control, we highlight *Ae aegypti* and dengue, chikungunya, and other arboviruses as potential emerging public health threats in sub-Saharan Africa.

Introduction

There is growing concern that climate change will alter the distribution and burden of vector-borne diseases, potentially reversing the gains of control programmes and increasing the threat of emerging diseases.^{1–4} Malaria places a major burden of morbidity and mortality on sub-Saharan Africa (228 million cases and 405 000 deaths in 2018), despite successful intensive control efforts that reduced transmission in many locations over the past 20 years.^{5–7} At the same time, many other vector-borne diseases, including Rift Valley fever, dengue, chikungunya, yellow fever, Zika, o'nyong'nyong, West Nile fever, leishmaniasis, onchocerciasis, and African trypanosomiasis circulate regularly in humans, wildlife, and livestock in sub-Saharan Africa, although their burden is less well-characterised than malaria.^{8–12} For example, over 27 000 cases of arbovirus infections transmitted by *Aedes* mosquitoes have been reported in west Africa since 2007.¹³ It is well established that temperature has non-linear effects on vector-borne disease transmission, and that mosquito and pathogen species differ in this response, resulting in differences in their thermal optima and limits.^{2,4,14–19} Therefore, the direction and magnitude of the effects of climate change on transmission of specific vector-borne diseases will differ across regions.

In this Personal View, we summarise published data to make the case that climate change, in conjunction with urbanisation, could drive a shift in most sub-Saharan African countries from climates most suitable for malaria transmission (by rural *Anopheles* mosquitoes) to climates more suitable for transmission of dengue and other arboviruses (by *Aedes aegypti* mosquitoes), with major consequences for public health and disease control strategies. Specifically, we draw from three lines of evidence: transmission models fit from laboratory thermal performance data; independent data on human infection; and widespread existing distributions of *Ae aegypti*, dengue, and chikungunya in sub-Saharan Africa. The dynamics of vector-borne diseases are multifaceted and involve human mobility, rainfall and water storage practices, urbanisation, and others factors. The increasing temperature suitability for arbovirus transmission merits

attention from global health researchers and policy makers, alongside ongoing malaria control efforts. Therefore, although we cannot conclusively predict changes in disease incidence based on temperature alone, we argue that temperature change will promote arbovirus transmission and increasingly limit malaria transmission by rural vector species in much of sub-Saharan Africa, along with urbanisation and other relevant changes.

Transmission models

Climate change will affect vector-borne disease transmission because changes in temperature affect vector population size, survival, biting, pathogen incubation rates, and vector competence; rainfall and humidity

Key messages

Effect of temperature on malaria and arbovirus transmission

Malaria transmission by *Anopheles gambiae* peaks at 25°C, whereas dengue transmission by *Aedes aegypti* peaks at 29°C, based on mechanistic transmission models parameterised and validated by laboratory and field data. Warming temperatures in the tropics are expected to favour transmission of dengue over malaria.

Non-linear effect of temperature on disease incidence

Independent data on human infections of malaria and dengue support the predicted non-linear effect of temperature on disease incidence. In tropical regions, where temperatures are consistently around 25°C, warmer temperatures correspond to a decrease in malaria incidence and an increase dengue and chikungunya incidence.

Arboviruses are an under-recognised public health problem in sub-Saharan Africa

Dengue, chikungunya, and their *Ae aegypti* mosquito vector are already widespread but under-recognised in Africa, based on studies of vector abundance, human serology, and acute infections from across the continent. As climate suitability increases for arboviruses, these diseases could expand and overtake the public health burden of malaria.

Increased surveillance for arboviruses is needed

Although malaria control efforts remain essential, arbovirus control using surveillance and vector control of container-breeding, day-biting *Ae aegypti* is a crucial emerging public health need in Africa. Testing and diagnostic capacity for arboviruses, and awareness of vector ecology and exposure risk, lag behind that of malaria in most of sub-Saharan Africa, where climate change is expected to increase the incidence of dengue and other arboviruses.

can have additional effects.^{15–17,20} The physiological effects of temperature on the vector and pathogen traits that drive transmission are well-established from laboratory experiments and field studies.^{20–24} Ectotherm physiology theory and data, from a wide variety of ectotherm taxa and traits, show that the thermal responses of development, survival, and reproduction are often unimodal, peaking at intermediate temperatures and declining at both low and high temperatures.^{25–27} Laboratory experiments confirm that these non-linear thermal responses are pervasive across mosquito and pathogen taxa and traits.^{15–17,21,28–30} We previously developed temperature-dependent basic reproduction number (R_0) models for malaria transmitted by *Anopheles gambiae* (and other *Anopheles* spp where *An gambiae* data were not available)^{15,31} and for dengue, chikungunya, and Zika transmitted by *Ae aegypti*.^{16,17} These models incorporate empirically measured effects of temperature on mosquito biting rate, immature survival probability, immature development rate, adult lifespan, fecundity, vector competence (probability of becoming infectious following exposure to an infectious blood meal), and parasite development rate, and subsequently on mosquito population size.^{15–17,31} The *Ae aegypti* temperature-dependent R_0 relationships were very similar for all three viruses,^{16,17} therefore, we hereafter focus on results from the dengue model. For both malaria and arboviruses, vector and parasite traits and R_0 peak at intermediate temperatures and are suppressed at both low and high temperatures.^{2,15–18,28} The thermal optima and ranges for transmission vary by vector and parasite species: malaria transmission by *An gambiae* peaks at 25°C, whereas arbovirus transmission by *Ae aegypti* peaks at 29°C

See Online for appendix

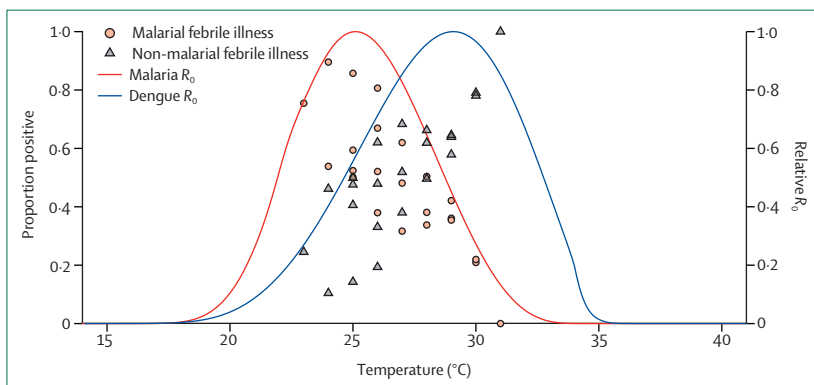


Figure 1: Malarial and non-malarial fever among Kenyan children from 2014 to 2018 versus temperature, overlaid on R_0 curves for malaria and dengue

Points represent proportion of children with positive malaria smears (filled circles) and proportion of children with non-malarial fever (open triangles) over temperature. Land-surface temperatures at each participant visit were calculated as 30-day mean temperatures lagged by 1 month (the time window in which we expect temperature to affect transmission), specific to each of the four clinic sites (appendix pp 2–3). Proportions were calculated at 1°C intervals of temperature at each of the four different outpatient clinic sites in western and coastal Kenya where children with undifferentiated fever were recruited, for up to four points per temperature bin.^{12,33–36} Lines represent predicted R_0 (rescaled to range from 0 to 1) for malaria (red line) and dengue (blue line) as a function of temperature from ecological models based on laboratory mosquito and parasite data.^{15–17} R_0 =basic reproduction number.

(figure 1; lines).^{15–17,31} Multiple vector and parasite traits cause differences in the thermal response of transmission across species.³²

Independent data on human infection show potential for shifts in disease burden

Field data from mosquito-based metrics of transmission risk (eg, entomological inoculation rate)^{15,37} and human incidence at local and continental scales^{16,36} strongly support the non-linear effects of temperature on transmission predicted from laboratory studies and mathematical models. Data published in 2019 from our cohort study of febrile children in four villages in Kenya showed a unimodal relationship between blood smear positivity for malaria and environmental temperature that peaked at 25°C (30-day average temperature, lagged by 1 month: the time scale at which we expect temperature to affect transmission) and a substantial decline in smear positivity above the optimum temperature (figure 1; circles).³⁶ This result strongly supports the predicted 25°C optimum from the temperature-dependent malaria R_0 model (figure 1; red line).¹⁵ In the same field study, non-malarial fever, much of which is caused by dengue and chikungunya, increased with temperature throughout the observed temperature range, supporting the relatively warm thermal optimum of dengue (figure 1; blue line and triangles).

Previous studies also support the thermal optima for malaria and arbovirus transmission predicted from mechanistic models. A study of dengue in 20 cities in Colombia showed a unimodal relationship between incidence and weekly average temperature (multiple time windows and lags were explored) that peaked at a mean temperature of 28°C,³⁸ supporting the model-predicted optimum for dengue transmission of 29°C.¹⁶ Other studies have predicted effects of temperature on transmission, peaking at 25°C for malaria (supported by continental-scale data on entomological inoculation rate in Africa) and 29°C for dengue, chikungunya, and Zika viruses (based on human incidence data from Latin America and the Caribbean).^{15–17}

Shifting climate suitability for malaria and *Ae aegypti*-transmitted viruses

As climate change leads to warming temperatures, the intermediate thermal optima for vector transmission have two immediate implications. First, for all vector-borne diseases, climate change will drive increases in some regions and decreases in others, depending on current and future local climates relative to the thermal optima for disease transmission. Second, the relative suitability for different vector-borne diseases will shift: the climate could simultaneously become more suitable for some diseases and less suitable for others. In regions where temperatures are regularly between 25°C and 29°C, including much of sub-Saharan Africa, a warming climate will become less suitable for malaria but more

suitable for dengue, chikungunya, and other arboviruses transmitted by *Ae aegypti* (figure 2). Specifically, the highest density of people exposed to optimal temperatures for disease transmission (the so-called risk hotspot) for malaria is projected to shift towards higher elevations such as the Albertine Rift region in central Africa and higher latitudes in southern Africa (figure 2A–C; red circles). The risk hotspot for dengue, chikungunya, and other *Ae aegypti*-transmitted arboviruses is predicted to expand from west Africa throughout sub-Saharan Africa (figure 2D–F).

In conjunction with climate change, urbanisation is driving widespread changes in habitat, microclimate, and human populations, and is occurring more rapidly in sub-Saharan Africa than anywhere else in the world (although these transitions are complex and diverse).^{40,41}

Urbanisation affects vector-borne disease transmission by altering the availability of vector breeding habitat and contact with humans. *Ae aegypti* mosquitoes breed in human-made container habitats such as discarded tyres, cans, buckets, and water storage containers, all of which increase in density in urban areas, but are also present in villages.^{10,42,43} By contrast, *An gambiae* and some other African malaria vectors breed in naturally occurring pools of water, which are more common in rural areas, although malaria transmission can occur in cities.^{44,45}

Urban areas also form so-called heat islands with microclimates that are several degrees warmer than surrounding vegetated areas, which can affect vector development and survival⁴⁶ and could benefit warmer-adapted *Ae aegypti* over *An gambiae* mosquitoes. Therefore, urbanisation could act synergistically with

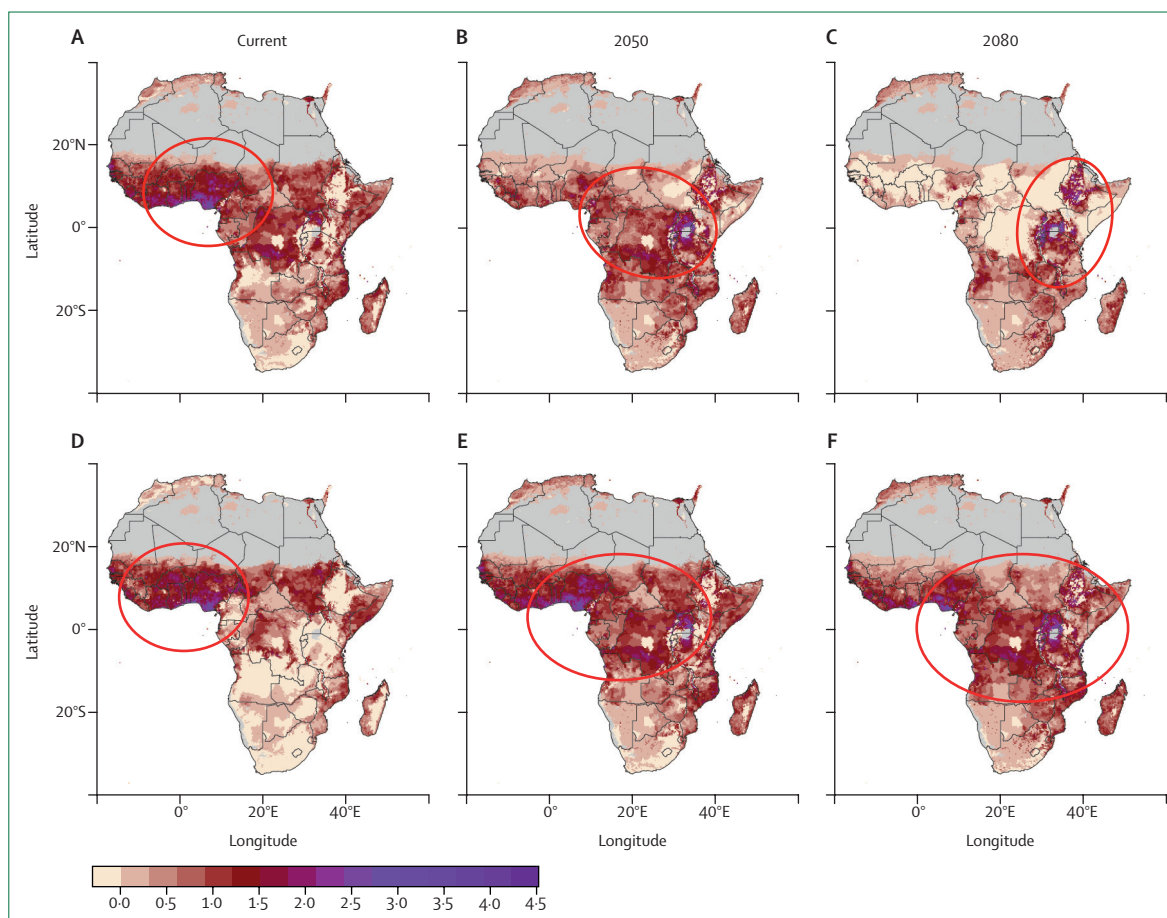


Figure 2: Temperature-driven malaria risk hotspot and *Aedes aegypti*-transmitted arbovirus risk hotspot

Malaria risk hotspot (red circles; top row A–C) shifts to high elevations in east Africa while *Aedes aegypti*-transmitted arbovirus risk hotspot (red circles; bottom row D–F) expands throughout sub-Saharan Africa, from current (left column A and D) to 2050 (middle column B and E) to 2080 (right column C and F). Colour scale represents the number of months per year predicted to have highly suitable temperatures for disease transmission (relative $R_0 > 0.5$), multiplied by population density (\log_{10} population density), for a scaled index of person-months of high risk for transmission. Temperature suitability for transmission is based on the upper 50th percentile of relative R_0 from temperature-dependent R_0 models (appendix pp 4–8).^{15,16} All climate projections are based on the business as usual climate scenario Representative Concentration Pathway 8.5, using the HadGEM2-ES General Circulation Model. The red circles (risk hotspots) show the areas where the most people are at the highest risk. An aridity mask (grey) excludes regions that are too dry for malaria transmission.³⁹ This figure shows one possible scenario of temperature-driven risk, rather than making a specific prediction about future disease burden, which will depend on moisture availability, human population growth and mobility, and other factors. R_0 =basic reproduction number.

Evidence	
Africa	
Amarasinghe et al ⁵⁴	Dengue virus infection
Gwer et al ⁵⁰	Overdiagnosis and comorbidity of severe malaria
West Africa	
Buchwald et al ¹³	Dengue, chikungunya, and Zika outbreaks; <i>Ae aegypti</i> and <i>Ae albopictus</i> present
Franco et al ⁵⁵	Expansion of a dengue serotype (DENV-3)
East African Community Region	
Nyaruba et al ⁴¹	Arbovirus infection
Cameroon	
Gudo et al ¹²	Flavivirus seroepidemiology
Simard et al ⁵⁶	<i>Ae aegypti</i> and <i>Ae albopictus</i> present
Tedjou et al ⁵⁷	<i>Ae aegypti</i> and <i>Ae albopictus</i> present
Central African Republic	
Kamgang et al ⁵⁸	<i>Ae aegypti</i> and <i>Ae albopictus</i> present
Côte d'Ivoire	
Zahouli et al ⁴²	<i>Aedes</i> mosquitoes present in an arbovirus-endemic setting in southeast Côte d'Ivoire
Kenya	
Hortion et al ⁵⁵	Acute flavivirus and alphavirus infection in children
Kamau et al ⁵⁹	O'nyong nyong virus and chikungunya virus transmission in western Kenya
LaBeaud et al ⁵²	O'nyong nyong virus and chikungunya virus transmission in coastal Kenya
Ngugi et al ⁴³	<i>Ae aegypti</i> breeding sites in rural and urban, coastal and western locations
Sutherland et al ⁵¹	Serological evidence of arboviral infection in children
Vu et al ³³	Dengue infection in children in western Kenya
Vu et al ⁶⁰	Dengue and West Nile virus transmission in children and adults in coastal Kenya
Waggoner et al ⁵³	Chikungunya infection in febrile children
WHO ⁶¹	Chikungunya outbreak
Mozambique	
Gudo et al ¹²	Dengue, chikungunya, Rift Valley fever, West Nile, and Zika virus seroepidemiology
Sierra Leone	
O'Hearn et al ⁶²	Rift Valley fever virus, flaviviruses, and alphaviruses
Tanzania	
Gudo et al ¹²	Rift Valley fever and alphavirus seroepidemiology
Reyburn et al ⁴⁹	Severe febrile illness and overdiagnosis of malaria
Uganda	
Ghai et al ⁴⁶	Febrile patients and overdiagnosis of malaria in rural Uganda
Demina et al ⁶³	Arbovirus serology in endemic population in Zika Forest

Table: Evidence for *Aedes aegypti* vectors, arbovirus transmission, and over-diagnosis of malaria across sub-Saharan Africa

warming climate to promote the shift from *Anopheles*-transmitted malaria to *Aedes*-transmitted arboviruses in sub-Saharan Africa.

Widespread distribution of *Ae aegypti* and arboviruses in sub-Saharan Africa

Although shifts in climate suitability do not necessarily cause a shift in disease burden from malaria to dengue and other arboviruses in sub-Saharan Africa, there is increasing evidence that support this hypothesis. For expansions in transmission to occur, *Ae aegypti* mosquitoes and arboviruses must be present in the region. Evidence suggests that the vectors and arboviruses are already widespread and under-recognised in sub-Saharan

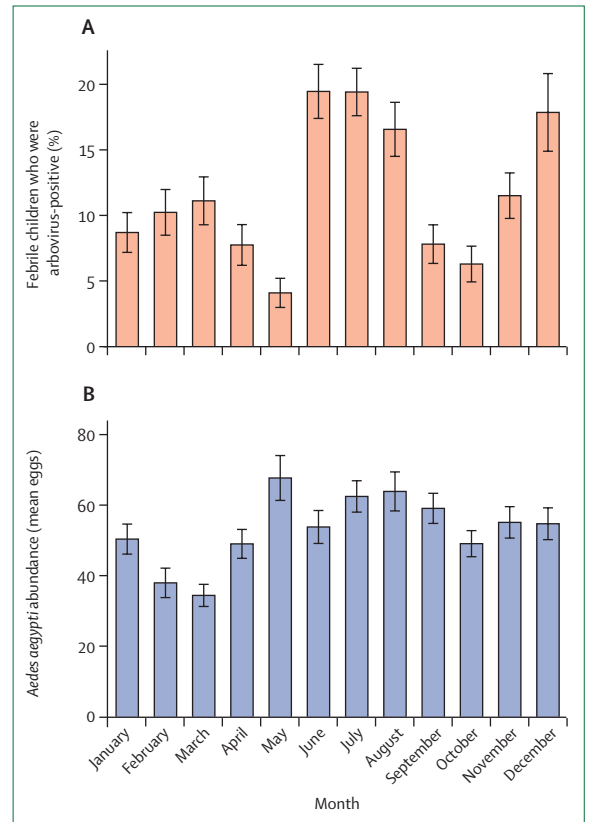


Figure 3: Prevalence rates of dengue virus infection in febrile children (A); abundance of *Ae aegypti* mosquitoes in four villages in Kenya (B) High prevalence of dengue virus in febrile children and consistently high abundance of *Aedes aegypti* mosquitoes in four villages in Kenya suggest that arboviruses are an under-recognised public health burden. The rates of dengue positivity are measured as the percentage of children <18 years of age with undifferentiated febrile illness attending outpatient care who tested positive by PCR or IgG ELISA for dengue virus infection. Data were compiled from four different clinics in western and coastal Kenya during each calendar month between 2014 and 2018. *Ae aegypti* abundance was measured as the monthly average number of *Ae aegypti* eggs per household recovered from oviposition traps placed in and around houses (appendix p 3). Error bars show standard errors of the mean.

Africa,^{10,13,33–35,42,47–53} in part because of misdiagnosis and a public health focus on malaria and *Anopheles* vectors (table). For example, arbovirus surveillance work in regions of high malaria endemicity in Kenya (figure 1) showed that approximately 10–20% of febrile children were positive for dengue virus infection for much of the year (figure 3A), and that *Ae aegypti* mosquito vectors were abundant in and around households year-round (figure 3B; appendix p 3). These data suggest ongoing endemic transmission of dengue in at least four geographically distinct Kenyan populations. Large chikungunya epidemics have also occurred in Mombasa, Mandera, and Lamu, Kenya^{61,64,65} and in the Kassala state of Sudan, where heavy rains flooded a major river and triggered an outbreak.⁶⁶ There is increasing evidence to suggest that both endemic and epidemic transmission of dengue, chikungunya, and other *Aedes*-transmitted arboviruses regularly occurs in

sub-Saharan Africa, although it can be undiagnosed or misdiagnosed as malaria (table).^{13,33,54,55,63,67} Growing evidence suggests that both endemic and epidemic transmission of dengue, chikungunya, and other *Aedes*-transmitted arboviruses regularly occurs in sub-Saharan Africa, although it might be undiagnosed or misdiagnosed as malaria (table).^{13,33,54,55,63,67} The causes of this decline are undoubtedly complex, and much has been attributed to the success of malaria control programmes; however, some of the decline could be due to decreasing climate suitability (ie, increasing temperatures) for disease vectors and transmission. The extent to which warming temperatures have already reduced malaria transmission remains to be assessed because few studies have recognised that the optimum for malaria transmission is as low as 25°C.⁶⁸

Discussion

The degree to which changes in climate suitability for disease transmission lead to changes in the incidence of disease depends on multiple factors, including pathogen exposure history, housing type, vector control and public health efforts, rainfall, and human mobility.^{69–72} Exposure history is particularly important because newly occurring transmission in previously unexposed populations could increase the burden of disease more than in endemic regions with some acquired immunity.^{73,74} Therefore, even if climate change leads to geographical shifts rather than net increases in populations at risk of disease (figure 2), these shifts still lead to many people with no prior immunity exposed to disease in regions where the public health infrastructure for malaria and arboviruses is scarce. This geographical shift could be disruptive to populations, health-care systems, and economies that have not historically had either malaria or arboviral diseases. Within endemic regions, the interannual variability and seasonality of transmission could further change in response to changing rainy seasons and their interaction with temperature.^{71,75,76} At the same time, changes in demography, population growth, migration, and socioeconomic factors might mitigate the effect of climate change on vector-borne disease transmission.^{69,77,78} However, transmission is limited by climate, regardless of population characteristics, and could exacerbate effects of changing exposure to disease.

Mosquitoes and parasites are not static threats but evolving organisms that respond to ecological conditions and selective pressures imposed by their changing environments. The potential for mosquitoes to adapt to warming temperatures by increasing their thermal optima remains unknown.⁷⁹ Mosquitoes quickly and repeatedly evolve resistance to insecticides when vector control programmes impose strong selective pressures.⁸⁰ However, temperature-driven selection on mosquitoes might not align with selection on the parasites they transmit. At warm temperatures, mosquito longevity is the major limitation on transmission because short

pathogen incubation periods and frequent biting cannot overcome declining mosquito lifespans to sustain transmission.^{4,15,31} But even short-lived mosquitoes can achieve high evolutionary fitness at warm temperatures if rapid development and high fecundity outweigh the cost of shorter lifespans. As a result, selection might not lead to increased mosquito survival at high temperatures; therefore, evolution might not rescue vector transmission as temperatures exceed current thermal optima.

Even if temperatures become warm enough to drive existing vector populations extinct, or to suppress their ability to transmit disease, warmer-adapted mosquitoes (including *Ae aegypti* and *Anopheles stephensi*, an urban malaria vector in India)⁸¹ could invade and replace current *An gambiae* populations transmitting malaria in Africa. Incipient speciation has already occurred in Africa in the *Ae aegypti*^{82,83} and *An gambiae* species complexes,^{84–87} suggesting that both can adapt to changing ecological conditions including urbanisation and, potentially, climate. *Aedes albopictus*, another arbovirus vector, is also present in some regions of Africa, and where it co-occurs with *Ae aegypti*, it can be competitively dominant.^{57,58} Temperature-dependent R_0 models suggest that *Ae albopictus* has a cooler thermal optimum (26°C) and upper thermal limit (32°C) than *Ae aegypti*, which could restrict the expansion and transmission potential of this species if exposed to warming climates.^{16,88} Climate-driven ecological and evolutionary changes in mosquito communities that might alter the direct physiological effects of temperature are therefore highly uncertain.

Although many aspects of the changing environmental and population landscapes that shape disease transmission remain unknown, we have outlined three lines of evidence suggesting that climate change, along with urbanisation, will drive a shift in disease transmission in sub-Saharan Africa from malaria to arboviruses (eg, dengue and chikungunya) over the next 30–50 years (figure 2). First, temperature-dependent transmission models predict increased suitability for *Aedes*-transmitted arboviruses and decreased suitability for malaria (figure 1).^{15,16} Second, large-scale entomological and human disease data and local human incidence data provide evidence that warming temperatures above thermal optima causes declines in transmission (figure 1).^{15,16} Finally, at the same time that malaria is declining in much of sub-Saharan Africa, arboviruses and *Ae aegypti* already pose an under-recognised public health burden, which could increase because of increased climate suitability (table; figures 2, 3).

Malaria has declined precipitously in much of central America, South America, and the Caribbean in the past three decades at the same time that dengue, chikungunya, and Zika have substantially increased to cause between 500 000 and 2 million cases per year.^{89–91} The drivers of these disease trends are complex and multivariate, including multiple aspects of environmental and human population change. Nonetheless, the concordance

Search strategy and selection criteria

This Personal View primarily summarises evidence from our own work and that of collaborators. The references used in the table were selected from our own reading of peer-reviewed publications in English, suggestions from anonymous reviewers, and Google Scholar searches done in May, 2020, using the search terms “arbovirus,” “dengue,” “chikungunya,” “*Aedes aegypti*,” or “*Aedes albopictus*,” and “Africa”. Studies were chosen because they provided some evidence of arbovirus or vector presence in Africa, and are not an exhaustive list.

between shifting temperature suitability predicted from laboratory data and models, and the observed shifts from malaria to dengue and other arboviruses is striking. For example, in a country-scale analysis of arbovirus transmission in Latin America and the Caribbean from 2014 to 2016, weekly mean temperatures averaged 25.6°C (range in weekly average temperature $21.5\text{--}28.7^{\circ}\text{C}$ across countries)¹⁶ across the region that spanned the temperature range where malaria transmission peaks and begins to decline, whereas arbovirus transmission increases substantially with temperature (figure 1).

Disease control strategies that are effective against malaria—eg, long-lasting insecticide-treated bednets, indoor residual spraying, and artemisinin combination therapy—are ineffective against dengue, which has the day-biting and container-breeding *Ae aegypti* mosquito as its primary vector^{92,93} and has no specific drug therapy or broadly effective vaccine available (the development and roll-out of the Sanofi Pasteur dengue vaccine has had mixed results).^{94,95} A shift from malaria to dengue in sub-Saharan Africa would therefore require public health efforts to refocus to control an ecologically different vector and pathogen, a shift that has already taken place throughout much of Latin America and the Caribbean. In particular, the development of accurate point-of-care diagnostics for dengue and chikungunya viruses and community-based vector control programmes will be increasingly important for targeted care and prevention of arboviruses.^{13,34,35,53} Malaria eradication efforts remain crucial. However, given the year-round circulation of dengue and chikungunya and abundance of *Aedes* mosquitoes in Africa, public health efforts should also prepare for a potentially emerging threat of arboviral disease in Africa.

Contributors

EAM and ADL conceived this Personal View. JMC, SJR, and MMS analysed the data. EAM wrote the first draft of the manuscript. All authors revised the manuscript and approved of the final version.

Declaration of interests

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This paper is dedicated to Drew Gilmour, who was born to EAM while the paper was under revision: may this work inspire action to mitigate climate change and to reduce the burden of disease, especially in children, in your lifetime.

References

- Rogers DJ, Randolph SE. Climate change and vector-borne diseases. *Adv Parasitol* 2006; **62**: 345–81.
- Liu-Helmerson J, Stenlund H, Wilder-Smith A, Rocklöv J. Vectorial capacity of *Aedes aegypti*: effects of temperature and implications for global dengue epidemic potential. *PLoS One* 2014; **9**: e89783.
- Altizer S, Ostfeld RS, Johnson PTJ, Kutz S, Harvell CD. Climate change and infectious diseases: from evidence to a predictive framework. *Science* 2013; **341**: 514–19.
- Parham PE, Michael E. Modeling the effects of weather and climate change on malaria transmission. *Environ Health Perspect* 2010; **118**: 620–26.
- Bhatt S, Weiss DJ, Cameron E, et al. The effect of malaria control on *Plasmodium falciparum* in Africa between 2000 and 2015. *Nature* 2015; **526**: 207–11.
- Smith DL, Cohen JM, Chiyaka C, et al. A sticky situation: the unexpected stability of malaria elimination. *Philos Trans R Soc B Biol Sci* 2013; **368**: 20120145.
- WHO. World Malaria Report 2018. November 2018. <https://www.who.int/malaria/publications/world-malaria-report-2018/report/en/> (accessed March 9, 2019).
- Simo FBN, Bigna JJ, Kenmoe S, et al. Dengue virus infection in people residing in Africa: a systematic review and meta-analysis of prevalence studies. *Sci Rep* 2019; **9**: 13626.
- Centers for Disease Control and Prevention. Outbreak summaries: Rift Valley Fever. <https://www.cdc.gov/vhf/rvf/outbreaks/summaries.html> (accessed May 18, 2020).
- Weetman D, Kamgang B, Badolo A, et al. *Aedes* mosquitoes and *Aedes*-borne arboviruses in Africa: current and future threats. *Int J Environ Res Public Health* 2018; **15**: 220.
- Nyaruaba R, Mwaliko C, Mwau M, Mousa S, Wei H. Arboviruses in the east African community partner states: a review of medically important mosquito-borne arboviruses. *Pathog Glob Health* 2019; **113**: 209–28.
- Gudo ES, Ali S, António VS, Chelene IR, et al. Seroepidemiological studies of arboviruses in Africa. In: Hilgenfeld R, Vasudevan SG, eds. *Dengue and Zika: control and antiviral treatment strategies*. Singapore: Springer Singapore, 2018: 361–71.
- Buchwald AG, Hayden MH, Dadzie SK, Paull SH, Carlton EJ. *Aedes*-borne disease outbreaks in west Africa: a call for enhanced surveillance. *Acta Trop* 2020; **209**: 105468.
- Lafferty KD. The ecology of climate change and infectious diseases. *Ecology* 2009; **90**: 888–900.
- Mordecai EA, Paaijmans KP, Johnson LR, et al. Optimal temperature for malaria transmission is dramatically lower than previously predicted. *Ecol Lett* 2013; **16**: 22–30.
- Mordecai EA, Cohen JM, Evans MV, et al. Detecting the impact of temperature on transmission of Zika, dengue, and chikungunya using mechanistic models. *PLoS Negl Trop Dis* 2017; **11**: e0005568.
- Tesla B, Demakovsky LR, Mordecai EA, et al. Temperature drives Zika virus transmission: evidence from empirical and mathematical models. *Proc R Soc B* 2018; **285**: 20180795.
- Johansson MA, Powers AM, Pesik N, Cohen NJ, Staples JE. Nowcasting the spread of chikungunya virus in the Americas. *PLoS One* 2014; **9**: e104915.
- Perkins TA, Metcalf CJE, Grenfell BT, Tatem AJ. Estimating drivers of autochthonous transmission of chikungunya virus in its invasion of the Americas. *PLoS Curr* 2015; **7**: ecurrents.outbreaks.a4c7b6ac10e0420b1788c9767946d1fc.
- Stewart Ibarra AM, Ryan SJ, Beltrán E, Mejía R, Silva M, Muñoz Á. Dengue vector dynamics (*Aedes aegypti*) influenced by climate and social factors in Ecuador: implications for targeted control. *PLoS One* 2013; **8**: e78263.

- 21 Delatte H, Gimonneau G, Triboire A, Fontenille D. Influence of temperature on immature development, survival, longevity, fecundity, and gonotrophic cycles of *Aedes albopictus*, vector of chikungunya and dengue in the Indian Ocean. *J Med Entomol* 2009; **46**: 33–41.
- 22 Li R, Xu L, Bjørnstad ON, Liu K, et al. Climate-driven variation in mosquito density predicts the spatiotemporal dynamics of dengue. *Proc Natl Acad Sci USA* 2019; **116**: 3624–29.
- 23 Boyd MF. Studies on *Plasmodium vivax* 2 the influence of temperature on the duration of the extrinsic incubation period. *Am J Epidemiol* 1932; **16**: 851–53.
- 24 Tjaden NB, Thomas SM, Fischer D, Beierkuhnlein C. Extrinsic incubation period of dengue: knowledge, backlog, and applications of temperature dependence. *PLoS Negl Trop Dis* 2013; **7**: e2207.
- 25 Angilletta MJ. Thermal adaptation: a theoretical and empirical synthesis. Oxford: Oxford University Press, 2009: 305.
- 26 Kingsolver JG. The well-temperated biologist (American Society of Naturalists Presidential Address). *Am Nat* 2009; **174**: 755–68.
- 27 Huey RB, Berrigan D. Temperature, demography, and ectotherm fitness. *Am Nat* 2001; **158**: 204–10.
- 28 Shocket MS, Ryan SJ, Mordecai EA. Temperature explains broad patterns of Ross River virus transmission. *Elife* 2018; **7**: e37762.
- 29 Bayoh MN. Studies on the development and survival of *Anopheles gambiae* sensu stricto at various temperatures and relative humidities. PhD thesis, Durham University, 2001.
- 30 Bayoh M, Lindsay S. Temperature-related duration of aquatic stages of the Afrotropical malaria vector mosquito *Anopheles gambiae* in the laboratory. *Med Vet Entomol* 2004; **18**: 174–79.
- 31 Johnson LR, Ben-Horin T, Lafferty KD, et al. Understanding uncertainty in temperature effects on vector-borne disease: a Bayesian approach. *Ecology* 2015; **96**: 203–13.
- 32 Mordecai EA, Caldwell JM, Grossman MK, et al. Thermal biology of mosquito-borne disease. *Ecol Lett* 2019; **22**: 1690–708.
- 33 Vu DM, Mutai N, Heath CJ, et al. Unrecognised Dengue virus infections in children, western Kenya, 2014–2015. *Emerg Infect Dis* 2017; **23**: 1915–17.
- 34 Hoof AM, Ripp K, Ndenga B, et al. Principles, practices and knowledge of clinicians when assessing febrile children: a qualitative study in Kenya. *Malar J* 2017; **16**: 381.
- 35 Hortion J, Mutuku FM, Eyherabide AL, et al. Acute flavivirus and alphavirus infections among children in two different areas of Kenya, 2015. *Am J Trop Med Hyg* 2019; **100**: 170–73.
- 36 Shah MM, Krystosik AR, Ndenga BA, et al. Malaria smear positivity among Kenyan children peaks at intermediate temperatures as predicted by ecological models. *Parasit Vectors* 2019; **12**: 288.
- 37 Hay SI, Rogers DJ, Toomer JF, Snow RW. Annual *Plasmodium falciparum* entomological inoculation rates (EIR) across Africa: literature survey, internet access and review. *Trans R Soc Trop Med Hyg* 2000; **94**: 113–27.
- 38 Peña-García VH, Triana-Chávez O, Arboleda-Sánchez S. Estimating effects of temperature on Dengue transmission in Colombian cities. *Ann Glob Health* 2017; **83**: 509–18.
- 39 Ryan SJ, McNally A, Johnson LR, et al. Mapping physiological suitability limits for malaria in Africa under climate change. *Vector Borne Zoonotic Dis* 2015; **15**: 718–25.
- 40 Njoh AJ. Urbanization and development in sub-Saharan Africa. *Cities* 2003; **20**: 167–74.
- 41 Tiffen M. Transition in sub-Saharan Africa: agriculture, urbanisation and income growth. *World Dev* 2003; **31**: 1343–66.
- 42 Zahouli JBZ, Koudou BG, Müller P, Malone D, Tano Y, Utzinger J. Urbanisation is a main driver for the larval ecology of *Aedes* mosquitoes in arbovirus-endemic settings in south-eastern Côte d'Ivoire. *PLoS Negl Trop Dis* 2017; **11**: e0005751.
- 43 Ngugi HN, Mutuku FM, Ndenga BA, et al. Characterisation and productivity profiles of *Aedes aegypti* (L) breeding habitats across rural and urban landscapes in western and coastal Kenya. *Parasit Vectors* 2017; **10**: 331.
- 44 Donnelly MJ, McCall P, Lengeler C, et al. Malaria and urbanisation in sub-Saharan Africa. *Malar J* 2005; **4**: 12.
- 45 Keiser J, Utzinger J, De Castro MC, Smith TA, Tanner M, Singer BH. Urbanisation in sub-Saharan Africa and implication for malaria control. *Am J Trop Med Hyg* 2004; **1**: 118–27.
- 46 Murdock CC, Evans MV, McClanahan TD, Miazgowiec KL, Tesla B. Fine-scale variation in microclimate across an urban landscape shapes variation in mosquito population dynamics and the potential of *Aedes albopictus* to transmit arboviral disease. *PLoS Negl Trop Dis* 2017; **11**: e0005640.
- 47 Stoler J, al Dashti R, Anto F, Fobil JN, Awandare GA. Deconstructing “malaria”: west Africa as the next front for dengue fever surveillance and control. *Acta Trop* 2014; **134**: 58–65.
- 48 Ghai RR, Thurber MI, El Bakry A, Chapman CA, Goldberg TL. Multi-method assessment of patients with febrile illness reveals over-diagnosis of malaria in rural Uganda. *Malar J* 2016; **15**: 460.
- 49 Reyburn H, Mbatia R, Drakeley C, et al. Overdiagnosis of malaria in patients with severe febrile illness in Tanzania: a prospective study. *BMJ* 2004; **329**: 1212.
- 50 Gwer S, Newton CRJC, Berkley JA. Over-diagnosis and co-morbidity of severe malaria in African children: a guide for clinicians. *Am J Trop Med Hyg* 2007; **77**: 6–13.
- 51 Sutherland LJ, Cash AA, Huang Y-JS, et al. Serologic evidence of arboviral infections among humans in Kenya. *Am J Trop Med Hyg* 2011; **85**: 158–61.
- 52 LaBeaud AD, Banda T, Brichard J, et al. High rates of O’Nyong Nyong and chikungunya virus transmission in coastal Kenya. *PLoS Negl Trop Dis* 2015; **9**: e0003436.
- 53 Waggoner J, Brichard J, Mutuku F, et al. Malaria and chikungunya detected using molecular diagnostics among febrile Kenyan children. *Open Forum Infect Dis* 2017; **4**: ofx110.
- 54 Amarasinghe A, Kuritsky JN, Letson GW, Margolis HS. Dengue virus infection in Africa. *Emerg Infect Dis* 2011; **17**: 1349–54.
- 55 Franco L, Caro AD, Carletti F, et al. Recent expansion of dengue virus serotype 3 in west Africa. *Euro Surveill* 2010; **15**: 19490.
- 56 Simard F, Nchoutpouen E, Toto JC, Fontenille D. Geographic distribution and breeding site preference of *Aedes albopictus* and *Aedes aegypti* (Diptera: Culicidae) in Cameroon, central Africa. *J Med Entomol* 2005; **42**: 726–31.
- 57 Tedjou AN, Kamgang B, Yougang AP, Njiokou F, Wondji CS. Update on the geographical distribution and prevalence of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae), two major arbovirus vectors in Cameroon. *PLoS Negl Trop Dis* 2019; **13**: e0007137.
- 58 Kamgang B, Ngoagouni C, Manirakiza A, Nakouné E, Paupy C, Kazanji M. Temporal patterns of abundance of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) and mitochondrial DNA analysis of *Ae albopictus* in the Central African Republic. *PLoS Negl Trop Dis* 2013; **7**: e2590.
- 59 Kamau KK, Magoma GN, Kwallah A ole, Syengo CK, Mwau M. Seroprevalence of chikungunya fever virus and O’nyong Nyong fever virus among febrile patients visiting selected hospitals in 2011–2012 Trans Nzoia County, Kenya. *Int J Res Med Sci* 2018; **6**: 1913.
- 60 Vu DM, Banda T, Teng CY, et al. Dengue and West Nile virus transmission in children and adults in coastal Kenya. *Am J Trop Med Hyg* 2017; **96**: 141–43.
- 61 WHO. Chikungunya—Mombasa, Kenya. Feb 27, 2018. <http://www.who.int/csr/don/27-february-2018-chikungunya-kenya/en/> (accessed March 9, 2019).
- 62 O’Hearn AE, Voorhees MA, Fetterer DP, et al. Serosurveillance of viral pathogens circulating in west Africa. *Viol J* 2016; **13**: 163.
- 63 Demina AV, Lutwama JJ, Hertz T, Lobel L. Assessing the serological antibody repertoire to flaviviruses in the endemic population of the Zika forest in Uganda. *J Immunol* 2017; **198**: 122.
- 64 Berry IM, Eyase F, Pollett S, Konongoi LS, et al. Recent outbreaks of chikungunya virus (CHIKV) in Africa and Asia are driven by a variant carrying mutations associated with increased fitness for *Aedes aegypti*. *bioRxiv* 2018; published online July 20. <https://www.biorxiv.org/content/10.1101/373316v1.full> (preprint).
- 65 Seron K, Njuguna C, Kalani R, et al. Seroprevalence of chikungunya virus (CHIKV) infection on Lamu Island, Kenya, October 2004. *Am J Trop Med Hyg* 2008; **78**: 333–37.
- 66 Abdelaziz K. Sudan reports outbreak of mosquito-borne chikungunya disease in eastern state. Sept 25, 2018. <https://www.reuters.com/article/us-sudan-health-chikungunya-idUSKCN1M52MB> (accessed Jan 18, 2019).
- 67 Fokam EB, Levai LD, Guzman H, et al. Silent circulation of arboviruses in Cameroon. *East Afr Med J* 2010; **87**: 262–68.

- 68 Yamana TK, Bomblies A, Eltahir EAB. Climate change unlikely to increase malaria burden in west Africa. *Nat Clim Change* 2016; **6**: 1009–13.
- 69 Wesolowski A, Qureshi T, Boni MF, et al. Impact of human mobility on the emergence of dengue epidemics in Pakistan. *Proc Natl Acad Sci USA* 2015; **112**: 11887–92.
- 70 Salje H, Cummings DAT, Rodriguez-Barraquer I, et al. Reconstruction of antibody dynamics and infection histories to evaluate dengue risk. *Nature* 2018; **557**: 719–23.
- 71 Stewart-Ibarra AM, Lowe R. Climate and non-climate drivers of dengue epidemics in southern coastal Ecuador. *Am J Trop Med Hyg* 2013; **88**: 971–81.
- 72 Johansson MA, Cummings DA, Glass GE. Multiyear climate variability and dengue—El Niño southern oscillation, weather, and dengue incidence in Puerto Rico, Mexico, and Thailand: a longitudinal data analysis. *PLoS Med* 2009; **6**: e1000168.
- 73 Rodriguez-Barraquer I, Cordeiro MT, Braga C, Souza WV, Marques ET, Cummings DAT. From re-emergence to hyperendemicity: the natural history of the Dengue epidemic in Brazil. *PLoS Negl Trop Dis* 2011; **5**: e935.
- 74 Patz JA, Reisen WK. Immunology, climate change and vector-borne diseases. *Trends Immunol* 2001; **22**: 171–72.
- 75 Mabaso MLH, Craig M, Ross A, Smith T. Environmental predictors of the seasonality of malaria transmission in Africa: the challenge. *Am J Trop Med Hyg* 2007; **76**: 33–38.
- 76 Anyamba A, Chretien J-P, Britch SC, et al. Global disease outbreaks associated with the 2015–2016 El Niño event. *Sci Rep* 2019; **9**: 1930.
- 77 Gething PW, Smith DL, Patil AP, Tatem AJ, Snow RW, Hay SI. Climate change and the global malaria recession. *Nature* 2010; **465**: 342–45.
- 78 Tompkins AM, Caporaso L. Assessment of malaria transmission changes in Africa, due to the climate impact of land use change using Coupled Model Intercomparison Project Phase 5 earth system models. *Geospat Health* 2016; **11**: 380.
- 79 Sternberg ED, Thomas MB. Local adaptation to temperature and the implications for vector-borne diseases. *Trends Parasitol* 2014; **30**: 115–22.
- 80 Liu N. Insecticide resistance in mosquitoes: impact, mechanisms, and research directions. *Annu Rev Entomol* 2015; **60**: 537–59.
- 81 Shapiro LLM, Whitehead SA, Thomas MB. Quantifying the effects of temperature on mosquito and parasite traits that determine the transmission potential of human malaria. *PLoS Biol* 2017; **15**: e2003489.
- 82 Powell JR. Mosquitoes on the move. *Science* 2016; **354**: 971–72.
- 83 Rose NH, Sylla M, Badolo A, et al. Climate and urbanisation drive mosquito preference for humans. *bioRxiv* 2020; published online Feb 13. <https://www.biorxiv.org/content/10.1101/2020.02.12.939041v1.full.pdf> (preprint).
- 84 Costantini C, Ayala D, Guelbeogo WM, et al. Living at the edge: biogeographic patterns of habitat segregation conform to speciation by niche expansion in *Anopheles gambiae*. *BMC Ecol* 2009; **9**: 16.
- 85 Simard F, Ayala D, Kamdem GC, et al. Ecological niche partitioning between *Anopheles gambiae* molecular forms in Cameroon: the ecological side of speciation. *BMC Ecol* 2009; **9**: 17.
- 86 Kamdem C, Fossog BT, Simard F, et al. Anthropogenic habitat disturbance and ecological divergence between incipient species of the malaria mosquito *Anopheles gambiae*. *PLoS One* 2012; **7**: e39453.
- 87 Djamouko-Djonkam L, Mouchili-Ndam S, Kala-Chouakeu N, et al. Spatial distribution of *Anopheles gambiae* sensu lato larvae in the urban environment of Yaoundé, Cameroon. *Infect Dis Poverty* 2019; **8**: 84.
- 88 Ryan SJ, Carlson CJ, Mordecai EA, Johnson LR. Global expansion and redistribution of *Aedes*-borne virus transmission risk with climate change. *PLoS Negl Trop Dis* 2019; **13**: e0007213.
- 89 Benelli G, Mehlhorn H. Declining malaria, rising of dengue and Zika virus: insights for mosquito vector control. *Parasitol Res* 2016; **115**: 1747–54.
- 90 Carter KH, Singh P, Mujica OJ, et al. Malaria in the Americas: trends from 1959 to 2011. *Am J Trop Med Hyg* 2015; **92**: 302–16.
- 91 Gubler DJ. Epidemic dengue/dengue hemorrhagic fever as a public health, social and economic problem in the 21st century. *Trends Microbiol* 2002; **10**: 100–03.
- 92 Erlanger TE, Keiser J, Utzinger J. Effect of dengue vector control interventions on entomological parameters in developing countries: a systematic review and meta-analysis. *Med Vet Entomol* 2008; **22**: 203–21.
- 93 Spiegel JM, Bonet M, Ibarra A-M, Pagliccia N, Ouellette V, Yassi A. Social and environmental determinants of *Aedes aegypti* infestation in central Havana: results of a case-control study nested in an integrated dengue surveillance programme in Cuba. *Trop Med Int Health* 2007; **12**: 503–10.
- 94 Ferguson NM, Rodríguez-Barraquer I, Dorigatti I, Mier-y-Teran-Romero L, Laydon DJ, Cummings DAT. Benefits and risks of the Sanofi-Pasteur dengue vaccine: modelling optimal deployment. *Science* 2016; **353**: 1033–36.
- 95 Flasche S, Jit M, Rodríguez-Barraquer I, et al. The long-term safety, public health impact, and cost-effectiveness of routine vaccination with a recombinant, live-attenuated dengue vaccine (Dengvaxia): a model comparison study. *PLoS Med* 2016; **13**: e1002181.

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