

The impact of climate change on neglected tropical diseases: a systematic review

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Neglected tropical diseases (NTDs) are a diverse group of diseases that continue to affect >1 billion people, with these diseases disproportionately impacting vulnerable populations and territories. Climate change is having an increasing impact on public health in tropical and subtropical areas and across the world and can affect disease distribution and transmission in potentially diverse ways. Improving our understanding of how climate change influences NTDs can help identify populations at risk to include in future public health interventions. Articles were identified by searching electronic databases for reports of climate change and NTDs between 1 January 2010 and 1 March 2020. Climate change may influence the emergence and re-emergence of multiple NTDs, particularly those that involve a vector or intermediate host for transmission. Although specific predictions are conflicting depending on the geographic area, the type of NTD and associated vectors and hosts, it is anticipated that multiple NTDs will have changes in their transmission period and geographic range and will likely encroach on regions and populations that have been previously unaffected. There is a need for improved surveillance and monitoring to identify areas of NTD incursion and emergence and include these in future public health interventions.

Keywords: climate change, global warming, neglected tropical diseases, parasites, vector-borne diseases

Introduction

Neglected tropical diseases (NTDs) are a diverse group of 20 diseases that affect >1 billion people and disproportionately impact vulnerable populations in low-resource settings in tropical and subtropical areas of the world.¹ At the same time, these communities are often suffering the greatest consequences of global change, particularly climate change.^{2,3}

Many NTDs result from diverse types of interactions and often complex cycles of transmission between humans and other animals, both vertebrates (e.g. dogs, livestock, snakes) and invertebrates (e.g. mosquitos, flies, snails), that can be influenced by changing environmental conditions (e.g. variations in temperature, rainfall, humidity and extreme weather events).^{1,2} Climatic factors such as temperature and rainfall can influence disease epidemiology, with temperature influencing vector reproduction, metabolism and survival, pathogen replication and vector and host distribution, while rainfall can determine the suitability of habitats for vectors and hosts through increased breeding sites.^{4–8} Meteorological events such as flooding and heat waves

can result in the destruction of suitable vector and host habitats and increased mortality of vectors and hosts.^{5,9–12} Changing precipitation and warming temperatures have improved habitat suitability in previously temperate areas, allowing for autochthonous transmission of dengue, chikungunya, leishmaniasis and schistosomiasis in parts of central Europe and the USA.^{4,13–15}

Human populations are also being displaced in sub-Saharan Africa, Southeast Asia and Central and South America. This is due in part to armed conflicts and political upheaval, but also to food and water insecurity caused by climate change (e.g. severe droughts).^{3,13} Altogether, population displacement combined with limited resources and health infrastructure will exacerbate current disease burdens, while changes to the epidemiology and distribution of these diseases may put additional populations at risk and undermine current disease control programmes.^{1–3}

The recent World Health Organization (WHO) NTD roadmap sets out global targets for NTD prevention, control, elimination and eradication by 2030, and there is a need to identify current and future trends to inform the planning and implementation of NTD programmes.¹⁶ Addressing climate change, among

other risks such as epidemics, political instability, migration and antimicrobial resistance, will require agile responses and concerted action from multiple sectors to achieve the new 2030 NTD targets.¹⁶ The aim of this systematic review is to synthesize the literature on NTDs in the context of climate change and identify correlations with climatic factors that influence trends in disease transmission and distribution. This review also aims to identify geographic areas and populations that are at risk of disease incursion or re-emergence under future climate changes that may not currently be included in disease control and surveillance programs. Identifying these areas and populations at risk due to future climate change can help predict disease distribution and allow targeted public health interventions.

Methods

A systematic review was performed on NTDs and climate change following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines.¹⁷ Only records including the 20 WHO-listed NTDs were included in the analysis (https://www.who.int/neglected_diseases/diseases/en/).

Search strategy

We searched electronic databases, including PubMed, Science Direct, Web of Science and the System for Information on Grey Literature in Europe (SIGLE), for reports on climate change and NTDs. Search terms included 'climate change', 'global warming', 'temperature', 'rainfall', 'humidity' (a list of search terms can be found in the supplementary data). The terms were searched in titles and abstracts and Boolean logic operators 'AND' and 'OR' and wildcards (e.g. 'climat*') were used. No language restrictions were set, although all search terms were in English. The search criteria included records from 1 January 2010 to 1 March 2020.

Eligibility criteria

Only primary literature articles (not reviews, conference proceedings and short communications) from peer-reviewed scientific journals that addressed one or more WHO-listed NTD, one or more climate change-related concept or process (i.e. 'climate change', 'climatic change', 'changing climate', 'future climate', 'global warming' and 'warming') and explicitly discussed trends or predictions of the distribution or transmission of NTDs associated with climate change were considered for analysis. The selection of articles was made by one of the authors (RT) by systematically screening all the titles and abstracts. This same person then analysed the full text of the selected articles and systematically extracted data on the study itself (year of publication, geographical area of study), the NTD addressed (pathogen causing the NTD, vector, reservoirs and hosts involved in the transmission), environmental factors associated with climate change that affected the NTD distribution and transmission and specific predictions made. Records were managed using EndNote reference manager version X7 (Clarivate, Philadelphia, PA, USA).

Results

The search strategy yielded a total of 27 787 publications for the period between 1 January 2010 and 1 March 2020, with an additional 31 records identified through other sources. After screening of titles and abstracts, 299 records were kept for full-text screening. A final set of 70 records met all inclusion criteria and are part of this review. Figure 1 presents the PRISMA chart of the record selection process and inclusion/exclusion criteria.

Eleven of the 20 WHO-listed NTDs were represented in our final literature selection: Chagas disease, dengue and chikungunya, foodborne trematodiasis (FBTs), human African trypanosomiasis, leishmaniasis, lymphatic filariasis (LF), onchocerciasis, rabies, schistosomiasis, soil-transmitted helminthiasis and snakebite envenoming. Nine WHO-listed NTDs were not included in the final analysis, as the records discussing these diseases did not meet inclusion criteria. Dengue and chikungunya are reviewed together, as they both are *Aedes* mosquito-borne NTDs. We found that temperature, precipitation, humidity, extreme weather patterns (droughts, floods), rising sea levels and melting arctic ice are the most commonly reported environmental factors and processes affected by climate change. The extracted data and descriptive characteristics of the records we analysed were grouped by NTD and are summarised in Table 1.

Dengue and chikungunya

Current distribution and trends

Dengue and chikungunya were the NTDs most represented in our review, with a total of 24 records from Africa, Australasia, the Americas and Europe. Although primarily a disease of the tropics and subtropics, the records in this review identified a change in geographical distribution into more temperate areas and increasing cases of dengue and chikungunya over the past few decades.^{18–20}

Populations of competent vectors have become established throughout southern Europe, following the introduction of *Aedes albopictus* into Europe via the importation of used tires.¹⁴ The chikungunya epidemic in northern Italy in 2007 and autochthonous cases of dengue in France and Croatia in 2010 demonstrates the current suitability of these areas for disease transmission.^{14,21,22} Four records discussed trends in the Americas, noting an increase in spatial distribution and outbreak intensity of dengue virus, with outbreaks in Florida, Texas and Hawaii, and re-emergence of chikungunya in the Caribbean in 2013.^{23–26} One record discussed the local transmission of dengue in previously non-endemic areas of Nepal, with outbreaks following in later years, as well as local transmission of chikungunya in 2013.⁵ *Aedes* vectors have since been found in high-altitude areas of Nepal, which is thought to be influenced by the warming of mountain areas.⁵ One record reported a shift in the seasonality of cases, with reported cases of dengue in winter months in Dhaka, Bangladesh.^{18,27}

Pathogens, vectors and hosts

Twenty-three records discussed the effect of climate change on dengue virus, with 11 of these records discussing the effect on chikungunya virus as well. Only one record discussed the impact

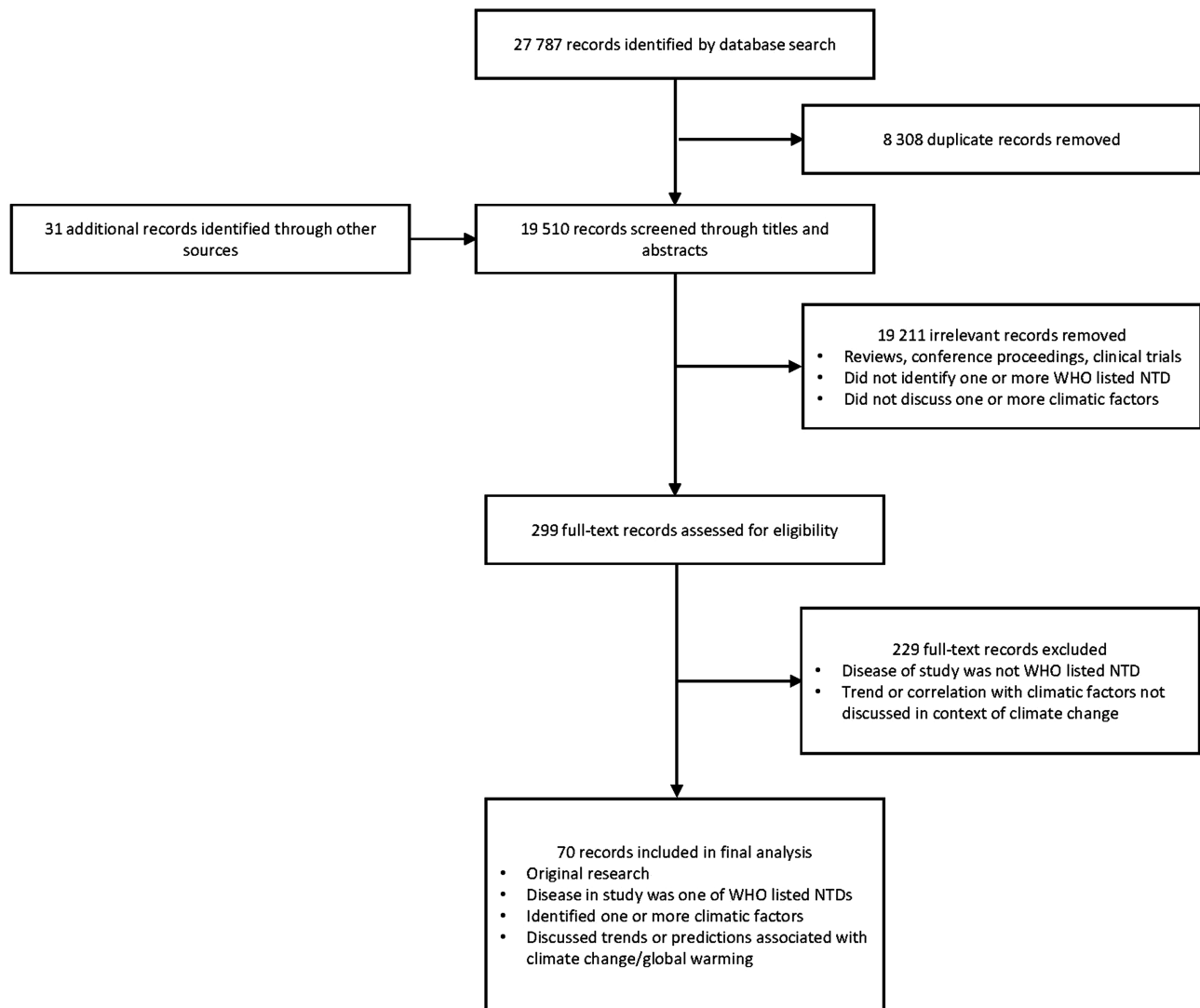


Figure 1. PRISMA flowchart for record selection.

of climate change on chikungunya virus without discussing dengue virus.²⁶ One record discussed the vector *Aedes japonicus*, which is found in more temperate areas and is predicted to decrease with warming temperatures.²⁸ All other records focused on one or both vectors, *Aedes aegypti* and *A. albopictus*.

A. aegypti was considered the primary vector for these viruses, as it was a highly competent vector for both dengue and chikungunya viruses and is closely associated with humans and urban environments.²⁹ *A. aegypti* was also identified as having a higher thermal optimum for viral transmission, and one record suggested an increase of 20–30% in the global abundance of *A. aegypti* was possible by the end of the century.^{29,30} *A. albopictus*, a secondary vector, is a moderately competent vector for both viruses and is adapted to peridomestic environments.²⁹ However, this species has a potential as an epidemic vector due to its high population density, rapid spread and ability to quickly adapt to local environments.^{14,20,21,28} This species has been implicated in several minor outbreaks in Europe and its desiccation-resistant

eggs and ability to overwinter in temperate climates increases the risk of invasion in temperate areas.^{28,31}

Impact from climate change

Temperature and rainfall were the most frequently discussed factors associated with climate change, with humidity and rising sea levels also identified as factors that may impact vector distribution and disease transmission. Increased temperature resulted in an increased vector development rate and increased vector biting frequency; however, once the temperature exceeded the thermotolerant range of the vector, this resulted in reduced vector growth and survival.^{5,20,24,25,32–34} Increased temperature also resulted in faster viral amplification time.^{6,18,35}

Similarly, increased rainfall had confounding effects, as it could create new suitable breeding sites for vectors or result in the elimination of vector habitats through flooding.^{5,6,22,23} Decreased rainfall could result in decreased breeding habitats,

Table 1. Summarised data extracted from records showing climatic factors that influence disease transmission.

NTD	Number of studies included (n = 70)	Environmental factors affected by climate change							Predicted impact on disease risk	References
		Methodology included	Geographical areas included	Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease		
Dengue and Chikungunya	24	Modelling (23) Field epidemiological study (1)	Africa (including Tanzania) Australasia (including Australia, Bangladesh, China, Nepal, South Korea, Sri Lanka) Americas (including Brazil, Canada, Colombia, Mexico, United States) Europe (including Balkans, central and western Europe, Mediterranean, northern Europe, United Kingdom)	Dengue virus Chikungunya virus	Mosquitoes (<i>Aedes aegypti</i> , <i>Aedes albopictus</i> , <i>Aedes japonicus</i>)	Humans Non-human primates	<p>Increased temperature Increases vector development rate. Increases vector biting frequency</p> <p>Increased rainfall Creates new suitable vector habitats</p> <p>Reduced rainfall Creates new suitable vector habitats through flooding</p> <p>Reduced rainfall May limit suitable habitats and storage</p> <p>Combination of temperature and rainfall Results in extended favourable period for mosquito growth, development, and reproduction</p> <p>Rising sea levels Result in expansion of saline and brackish water bodies</p>	<p>Increased temperature Reduces vector growth and survival once thermotolerant temperature exceeded</p> <p>Increased rainfall Eliminates vector habitats through flooding</p>	Increased (17) Decreased (0) Geographical shift/uncertain (7)	5, 6, 14, 18–38

Table 1. Continued.

NTD	Number of studies included (n=70)	Methodology included	Geographical areas included	Environmental factors affected by climate change	Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease	Factors that limit disease	Predicted impact on disease risk	References
Chagas disease	9	Modelling (7) Laboratory research (2)	Americas (including Argentina, Chile, Colombia, Mexico, United States and Venezuela)	Temperature (9) Rainfall (5)	<i>Trypanosoma cruzi</i>	Triatominae insects (<i>Rhodnius prolixus</i> , <i>R. robustus</i> , <i>Mepraia spinoi</i> , <i>M. gajardoi</i> , <i>M. parapatrica</i> , <i>Triatoma infestans</i> , <i>T. gerstaeckeri</i> , <i>T. sanguisuga</i> , <i>T. leuculana</i> , <i>T. barberi</i> , <i>T. peninsularis</i> , <i>T. protracta</i> , <i>T. rubida</i> , <i>T. brasiliensis</i> , <i>T. longipennis</i> , <i>T. mazzottii</i> , <i>T. mexicana</i> , <i>T. pallidipennis</i> , <i>T. phyllosoma</i> , <i>T. picturata</i> , <i>T. recurve</i> , <i>T. dimidiata</i> , <i>T. maculata</i> , <i>Eratyus cuspidatus</i> , <i>E. mucronatus</i> , <i>Paratriatoma hirsuta</i> , <i>Panstrongylus geniculatus</i>)	Humans Woodrats (<i>Neotoma</i> species) Common opossum (<i>Didelphis marsupialis</i>)	Increased temperature Increases parasite and vector development rate Increases insect feeding rate Increase house invasion	Increased temperature Reduces vector lifespan Enhances vector immune capacity against parasite	Increased (3) Decreased (3) Geographical shift/uncertain (3)	7, 18-46	

Table 1. Continued.

NTD	Number of studies included (n=70)	Methodology included	Geographical areas included	Environmental factors affected by climate change		Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease	Factors that limit disease	Predicted impact on disease risk	References
				Temperature	Rainfall								
Leishmaniasis	7	Modelling (5) Field epidemiological study (1) Retrospective analysis (1)	Africa (including Algeria, Morocco) Americas (including Argentina, Brazil, Canada, Colombia, Ecuador, Mexico, Paraguay, Peru, United States, Venezuela) Europe	Temperature (5) Rainfall (5) Humidity (2)	<i>Leishmania infantum</i> (Chagasi), L. brasiliensis, L. panamensis, L. guyanensis, L.rn. mexicana, L. arazo-nensis, L. pijanoi, L. panamen-sis, L. major, L. tropica, L. killicki	Sandflies (<i>Lutzomyia anthophora</i> , L. diabolica, L. flaviscutellata, L. olmeca olmeca, L. olec bicolor, L. olmeca noiva, L. reducta, L. inornate, L. longipalpis, L. evansi, <i>Myssomyia neivai</i> , Ny. Whitmani, <i>Mygomyia rignoni</i> , <i>Evantromyia cortezzii-sallesii</i> , <i>Phlebotomus papatasi</i> , <i>P. alexandri</i> , <i>P. arisi</i> , <i>P. kazeruni</i> , <i>P. perniciosus</i> , <i>P. sergenti</i>)	Foxes, Jackals Woodrats (<i>Neotoma albigula</i> , <i>N. floridana</i> , <i>N. micropus</i> , <i>N. Mexicana</i>) Other rodents (<i>Psammomys obesus</i> , Meriones shawi) Equines Bats Marsupials Non-human primates	Increased temperature Shortens vector development time Reduces parasite incubation time Increases vector biting rate Increased rainfall Increases breeding sites for vectors and intermediate hosts	Reduced rainfall Reduces suitable breeding sites for vectors and intermediate hosts	Increased (2) Decreased (2) Geographical shift/uncertain (3)	4, 18-52		

Table 1. Continued.

NTD	Number of studies included (n=70)	Environmental factors affected by climate change							Predicted impact on disease risk	References	
		Methodology included	Geographical areas included	Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease			Factors that limit disease
Foodborne trematodes	7	Modelling (5) Field epidemiological study (1) Laboratory research (1)	Africa (Zimbabwe) Australasia (New Zealand, Pakistan, Thailand) Europe (including central and western Europe, United Kingdom)	<i>Fasciola hepatica</i> , <i>Fasciola gigantica</i> , <i>Opisthorchis viverrini</i>		Fasciola : Snails (<i>Lymnaea truncatula</i> , <i>L. natalensis</i> , <i>L. (Austropeplea) tomentosa</i> , <i>Pseudosuccinea</i>) (<i>Lymnaea columella</i> , <i>Radix auricularia</i>) Opisthorchis : Snails (<i>Bithynia</i> species) Fish (Cyprinoid fish)	Fasciola : Humans Buffalo Cattle Sheep Goats Opisthorchis : Humans Cats Dogs Rodents	Increased temperature Increases survival and development over winter months Shortens parasite generation time Increased rainfall Prevents parasite desiccation Promotes suitable habitat for intermediate host	Increased temperature Reduces egg viability Reduced rainfall Reduces intermediate host habitats Extreme weather events (floods, droughts) Reduces intermediate host habitats	Increased (4) Decreased (3) Geographical shift/uncertain (0)	11,18,58

Table 1. Continued.

NTD	Number of studies included (n=70)*	Environmental factors affected by climate change					Reservoir hosts identified	Factors that favour disease	Factors that limit disease	Predicted impact on disease risk	References
		Methodology included	Geographical areas included	Pathogens identified	Vectors identified	Intermediate hosts identified					
Schistosomiasis	6	Modelling (5) Laboratory research (1)	Africa (including Zimbabwe) Asia (China)	<i>Schistosoma mansoni</i> , <i>S. haematobium</i> , <i>S. japonicum</i>	Snails (<i>Biomphalaria</i> species, <i>Bulinus</i> species, <i>Oncornelania</i> species)	Humans	Increased temperature Increases parasite reproduction and development Decreases prepatent period of intermediate host Increases intermediate host fecundity Increases swimming performance of free-living larval stages resulting in increasing transmission Decreases mean generation time of intermediate host allowing faster recovery of snail populations Increases cercariae production by intermediate host	Increased temperature Reduces parasite fitness and increases parasite mortality Increases intermediate host mortality Reduces intermediate host fecundity Increases thermotolerant range Decreased rainfall Limits suitable intermediate host habitats	Increased (0) Decreased (0) Geographical shift/uncertain (6)	11,15,18-43	

Table 1. Continued.

NTD	Number of studies included (n=70)*	Methodology included	Geographical areas included	Environmental factors affected by climate change	Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease	Factors that limit disease	Predicted impact on disease risk	References
Snakebite	5	Modelling (3) Survey/ retrospective analysis (2)	Africa (Mozambique) Americas (including Argentina, United States) Asia (Sri Lanka)	Temperature (5) Rainfall (4) Humidity (1) Extreme weather events (1)					Increased temperature Increases foraging activity in reptiles Increased rainfall Increases snake prey availability Extreme weather events (floods) Increases contact between snakes/humans Both decreased and increased humidity suggested to contribute to increased risk	Extreme weather events (droughts) Decreased incidence of snakebites after droughts Increased precipitation Decreased incidence in already wetter climates	Increased (2) Decreased (0) Geographical shift/uncertain (1)	64-68
Human African Trypanosomiasis	4	Modelling (4)	Africa (including Kenya, Zambia, Zimbabwe)	Temperature (4) Rainfall (2)	<i>Trypanosoma brucei rhodesiense</i> , <i>Typanosoma brucei gambiense</i>	Tsetse flies (<i>Glossina morsitans pallidipes</i> , <i>Glossina fuscipes fuscipes</i>)	Humans Cattle Wildlife (species not identified)	Humans Cattle Wildlife (species not identified)	Increased temperature Decreases vector pupal development period Increases vector feeding rate	Increased temperature Increases mortality rate Decreases vector pupal production (if exceeding thermotolerant range)	Increased (1) Decreased (1) Geographical shift/uncertain (2)	69-72

Table 1. Continued.

	Number of studies included (n=70)	Methodology included	Geographical areas included	Environmental factors affected by climate change	Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease	Factors that limit disease	Predicted impact on disease risk	References
NTD Lymphatic filariasis	4	Modelling (3) Field epidemiological study (1)	Africa Asia (Nepal)	Temperature (4) Rainfall (3) Humidity (1)	Wuchereria bancrofti, Brugia malayi, Brugia timori	Mosquitoes (Culex quinquefasciatus, Anopheles species)		Humans	Increased temperature Increases pathogen proliferation Decreases vector development time	Increased temperature Decreases vector survival Reduces parasite transmission (post-thermotolerant range) Increased rainfall Eliminates vector habitats through flooding	Increased (3) Decreased (1) Geographical shift/uncertain (1)	12, 73-75
Rabies	3	Modelling (3)	Americas (North American arctic and southern United States)	Temperature (3) Rainfall/snowfall (3) Loss of sea ice (1)	Rabies virus			Red foxes (Vulpes vulpes) Arctic foxes (Vulpes lagopus) Dogs Cats Common vampire bats (Desmodus rotundus) Cattle	Combination of climatic factors Shifts primary reservoir host distribution and increases viral transmission in red foxes	Increased rainfall May reduce movement and contact rate of foxes Loss of sea ice May reduce movement of arctic foxes and reduce rabies transmission Decreases availability of main food sources for arctic foxes	Increased (1) Decreased (0) Geographical shift/uncertain (2)	76-78

Table 1. Continued.

	Number of studies included (n=70)	Methodology included	Geographical areas included	Environmental factors affected by climate change	Pathogens identified	Vectors identified	Intermediate hosts identified	Reservoir hosts identified	Factors that favour disease	Factors that limit disease	Predicted impact on disease risk	References
NTD Onchocerciasis	1	Modelling and field study (1)	West Africa	Temperature (1) Rainfall (1)	Onchocerca volvulus	Blackfly (<i>Simulium damnosum</i> complex)		Humans	Increased temperature Increases vector development rate Increases development rate of O. volvulus larvae within vectors	Increased temperature Decreases vector survival	Geographical shift/uncertain (1)	79
Soil transmitted helminths	1	Laboratory research (1)	South Korea	Temperature (1)	Ascaris species			Humans Pigs Cattle	Increased temperature Accelerates embryonation of Ascaris eggs		Increased (1)	80

* One record included both FBT and schistosomiasis.¹¹

but conversely, water storage during droughts could result in an increase in breeding sites and increased viral transmission.^{18,28,31}

Rising sea levels associated with climate change could result in the expansion of saline and brackish water bodies, increasing the availability of breeding sites for salinity-tolerant vectors.²²

Other factors impacting disease distribution and transmission

The increase in global travel and trade was identified as the key factor in the introduction of vectors and viruses into new areas, which then allowed establishment and spread.^{14,20} Population growth and movement, changing land use and rapid urbanisation were also identified as risk factors for increasing cases or spread of disease, with population growth being a key driver for increased disease risk in endemic areas.^{5,21,30,35} A lack of adequate sanitation and mosquito control measures were identified as factors that favoured disease transmission, while improved housing quality, improved socio-economic conditions and vector control programmes were identified as factors that had reduced dengue incidence in developed nations.^{32,35}

Predictions

Most records predicted an increase in disease risk, which was defined by either increased virus transmission, increased vectorial capacity or increased geographic area that is suitable for vector habitats. A latitudinal and altitudinal expansion is predicted under future climate change scenarios, with warming temperatures making high altitudes more suitable for vector habitats and rising sea levels increasing the risk along coastal zones.^{5,6,20,21,22,27,29} The effect of changing seasonal patterns and winter warming in some areas will extend the favourable period for vectors and therefore result in a prolonged period suitable for disease transmission.^{21,23,25}

In Europe, climatically suitable areas are anticipated to increase in western and central Europe, but there will be a likely decline of suitable areas in southern Europe.^{6,14,31,36} This will be due in part to warming and increased rainfall over central and northern areas and warming with possible drought conditions in southern Europe.^{14,31} Warming temperatures in central northwestern Europe and the Balkan countries may also result in lengthened periods of vector activity and viral transmission.^{6,27,29}

There may be a possible increase in chikungunya risk through much of central America, with southerly expansion in South America.^{29,37} One record predicted that Latin America would see an increase of up to 7.5 million additional cases by the middle of the century under a scenario of a temperature increase of 3.7°C.³⁷ A possible increase of annual dengue incidence of up to 40% in Mexico is predicted by 2080, which, if underreporting is taken into consideration, could result in an extra 70 000–189 000 cases per year.^{36,37} Climate suitability for vectors may be seen in higher-altitude areas of central Mexico.³⁵ Low winter temperatures in the USA is thought to prevent permanent establishment of *A. aegypti* currently, but warming temperatures may make virus transmission possible in more areas, and for longer periods of time.²³

Coastal cities in eastern China and Japan may become more suitable for vectors.^{26,27,35} Conflicting predictions were found for Southeast Asia, with two records anticipating a reduction in climate suitability in Southeast Asia, while another suggested that

strong transmission suitability would be maintained.^{26,29} Dengue incidence in Dhaka, Bangladesh may increase by >40 times in 2100 compared with 2010 if ambient temperatures increase by 3.3°C and major dengue outbreaks may be seen in South Korea as the climate becomes more subtropical.^{18,34}

Large increases in suitability may be seen in southern Africa due to increased rainfall and more favourable temperatures for vectors, but areas of central East Africa that are predicted to become drier and hotter may see a decrease in vectors and cases.³⁵ Coastal areas of East Africa may be increasingly at risk of outbreaks, but conflicting results were found for West Africa, with one record suggesting an increase of risk due to climate suitability and another suggesting decreased climate suitability.^{26,29,35} Current areas of risk for dengue in Tanzania are in coastal areas and around Lake Victoria, but this may shift towards the central and northeastern parts and an increased risk may be seen in many parts of the country by 2050.^{26,27,38}

Chagas disease

Current distribution and trends

Nine records were included for Chagas disease, all of which were focused on the Americas. They reported a wide distribution of the disease from the northern parts of Chile and Argentina to the southern parts of the USA, with autochthonous transmission reported in Texas.^{39–41} It is estimated to affect 6–11 million people in Latin America, although there is an increasing number of cases diagnosed in Europe due to international human migration.^{7,41,44,46}

Pathogens, vectors and hosts

Trypanosoma cruzi is transmitted via triatomine insects, and 27 species of triatomine insects were identified as competent vectors in our review.^{7,39–46} Four records identified *Rhodnius prolixus* as an epidemiologically important vector, with a broad domiciliary distribution as well as a sylvatic distribution.^{7,39,44,45} Two of these records identified *R. prolixus* as the most important vector in Colombia and two identified the pathogen as the most important tropical vector in Venezuela.^{7,39,44,45} *Triatoma infestans* was identified as an important temperate vector in three records and identified by one of these as the main vector species responsible for disease transmission in Chile.^{40,45,46}

Impact from climate change

Temperature, rainfall and humidity were all identified as correlating environmental factors, with temperature being the most commonly described environmental factor affecting the ecology of triatome insects. Higher temperatures promoted shorter life cycles and a more rapid reproduction rate in vectors.^{7,41,42} Increased temperature also increased the vector feeding rate and rate of house invasion, thereby increasing potential interactions with humans and the risk of pathogen transmission.^{7,39,41,42,45} Conversely, increased temperature was also found to reduce vector life span and enhance vector immune capacity against *T. cruzi*.^{39,42} Climate change could increase the number of insects

that can transmit disease as well as increase the likelihood of vector infection by pathogens.⁷

Other factors impacting disease distribution and transmission

Although vector-borne transmission is one of the main routes of transmission, there are multiple other means of Chagas disease transmission.^{39,43,45} Oral transmission from contaminated food, vertical transmission from mother to offspring and blood transfusion with infected blood products were all identified as routes of Chagas transmission.³⁹ Changing land use patterns, human migration and shifting of human settlements, access to water and sanitation, housing quality and vector control programmes were all factors that were identified that could impact disease transmission.^{39,41,44,45} Distribution overlap of different vector species and adaptation of species to new environments were also identified as possible confounding factors to any predictions related to climate change, with sylvatic species potentially adapting to urban and domestic environments.^{39,41,44}

Predictions

Both Chagas disease distribution and transmission risk are expected to change with changing environmental conditions associated with climate change, yet trends do not necessarily go in the same direction and will vary geographically across the Americas. Chile is predicted to have a slight reduction in some areas and expansion to other areas.^{40,46} A possible north-east shift of the disease was discussed for the USA, while an increased number of people are anticipated to be at risk from vector exposure in Mexico.^{41,43} Venezuela may see a decreasing trend in Chagas disease cases, as vector distribution changes result in fewer locations where humans are exposed to triatomine vectors.^{44,45}

Leishmaniasis

Current distribution and trends

Seven records on leishmaniasis were included, representing Africa, the Americas and Europe. The disease is endemic in 98 countries, with a complex life cycle, involving a protozoal parasite, phlebotomine sandfly vectors and a range of mammalian reservoir species.^{47–50} Five of the included records discussed cutaneous leishmaniasis, the more common form of the disease, with three of these records discussing both cutaneous and visceral leishmaniasis.^{47–51} One record discussed visceral leishmaniasis only, and one record did not distinguish between disease forms.^{4,52} The emergence of new disease foci has been observed in Brazil and cases of cutaneous leishmaniasis have increased in Argentina.⁵² An altitudinal shift has been reported for vectors of cutaneous leishmaniasis in Colombia and Peru.⁵² Autochthonous transmission has been observed in Mexico and Texas in North America and also reported in central parts of Europe that have previously been free of leishmaniasis.^{49,52} The burden of cutaneous leishmaniasis is high in North Africa and the Middle East and has been observed to be expanding beyond previously defined endemic regions.⁴⁷

Pathogens, vectors and hosts

Eleven species of *Leishmania* were identified in our review. *Leishmania braziliensis* was identified by four records as one of the main agents responsible for cutaneous leishmaniasis outbreaks in the Americas, with *Leishmania amazonensis* and *Leishmania guyanensis* also being noted as important agents.^{48–51} *Leishmania infantum (chagasi)* was identified by three records as the main agent of visceral leishmaniasis in this region.^{49,52} One record identified *Leishmania major* as the dominant agent for cutaneous leishmaniasis in Algeria and Morocco, with three other agents also identified (*Leishmania infantum*, *Leishmania tropica* and *Leishmania killicki*).⁴⁷

Twenty-one vectors were identified in our review, with five records identifying *Lutzomyia* species as important vectors in the Americas and two records identifying *Phelbotomus* species as important vectors in North Africa and the Mediterranean.^{4,47–52} Three records identified *Lutzomyia longipalpis* as the main vector responsible for transmission of visceral leishmaniasis in the Americas.^{49,51,52}

Several peridomestic and sylvatic reservoirs were discussed, covering a wide range of species, including domestic dogs, foxes, jackals, horses and rodents.^{47,49–51} One record identified four species of woodrat as important reservoir hosts in North America (*Neotoma albigula*, *Neotoma floridana*, *Neotoma micropus*, *Neotoma mexicana*) and one record identified two species of rodents as important reservoirs in North Africa (*Psammomys obesus*, *Meriones shawi*).^{47,49}

Impact from climate change

All of the included records discussed the effect of temperature and rainfall on vector life cycle and distribution, with three records also discussing the effect of humidity.^{47,48,51} Increased temperatures shortened vector development time and increased vector biting rate, resulting in increased vectorial capacity.^{4,47} Increased temperature also reduced parasite incubation time within the vector.⁴ Combined, these effects could result in continuous generations of vectors, increased risk of parasite transmission and possible year-round transmission in high-risk areas.⁵¹ Increased rainfall could increase breeding sites for both vectors and a variety of intermediate hosts, while areas with reduced rainfall could see a reduction in suitable breeding sites for vectors and intermediate hosts.^{47,52}

Disease incidence has been associated with El Niño–Southern Oscillation patterns, with peaks of vector species associated with periods of rain, but this appears to have different impacts on different scenarios of transmission.⁵¹

Other factors impacting disease distribution and transmission

Anthropogenic impacts on landscapes could potentially create or destroy shelters of vectors, influencing disease transmission, with greater abundances of some vectors associated with the edges of deforestation and changes in land use influencing human contact with reservoirs and vectors.^{48,50,51} Socio-economic factors were also important determinants of disease risk, as this would influence human risk behaviours and access to healthcare.^{50,51} Irrigation and water storage systems could provide suitable

breeding sites for vectors.⁵¹ Conflict and political upheaval can result in a breakdown of public health services, access to clean water and sanitation and the migration of immunologically naïve populations into regions where vectors may be present.⁴⁹ Animal movement was highlighted as a significant driver of visceral leishmaniasis, with the movement of infected dogs identified as a key factor in the establishment of endemic urban foci of disease.^{4,49–52} Adequate preventive measures and expanded efforts in vector and reservoir control are likely to mitigate increased disease risk.^{49,52}

Predictions

Both an increased and decreased risk for disease were discussed under future climate scenarios, with different geographical distributions and transmission risks seen for different pathogen–vector–host life cycles. An expansion from arid zones of Africa to semi-arid zones is possible, resulting in the establishment of new endemic foci of disease.⁴⁷ While there may be a decrease in disease in North Africa and the Middle East, this is counteracted by expansion to western and central Europe, resulting in a net gain of geographical area suitable for disease transmission.⁴ The geographical distribution of cutaneous leishmaniasis in Latin America may decrease under future climate change and land use scenarios, although while some parts of the Amazon may become less suitable for disease transmission, there may be increasingly suitable areas at the borders of the Amazon where population size and density is much larger than current areas of disease foci.^{48,52} Vector distribution may shift to higher latitudes and altitudes, resulting in possible vector and reservoir species ranges reaching as far as southern Canada.^{49,52} This may result in the number of exposed individuals more than doubling by 2080.⁴⁹

FBTs

Current distribution and trends

Seven records were included for FBTs. Of these, three records discussed *Fasciola* infection risk in livestock in Europe, the UK and New Zealand, one record discussed the risk of both human and livestock *Fasciola* infection in Pakistan and one record discussed the risk of human fascioliasis in Zimbabwe.^{11,53–56} A further two records discussed opisthorchiasis in Thailand.^{57,58} Despite Latin America having a known high burden of human fascioliasis, no records met the criteria to be included in the final analysis.⁵⁹

Pathogens, vectors and hosts

Five records discussed the impacts of climate change on *Fasciola hepatica* transmission, with one of these records also identifying *Fasciola gigantica* as a relevant parasite in Pakistan.⁵⁶ Several snail intermediate hosts of *Fasciola* species were identified, with *Lymnaea trunculata* in the UK, *Radix auricularia* and *Galba truncatula* in Pakistan, *Lymnaea natalensis* in Zimbabwe and *Lymnaea (Austropelea) tomentosa* and *Pseudosuccinea (Lymnaea) columella* in New Zealand.^{11,53–56} *Bithynia* species were identified as the snail intermediate host for *Opisthorchis viverrini* in Thailand, with cyprinoid fish identified as the second intermediate host.^{57,58}

Impact from climate change

Temperature and rainfall were identified as important climatic factors in all the included records, with two records also identifying humidity.^{11,56} Increased temperature resulted in faster parasite development time and increased survival over the winter months, but they could also reduce egg viability in the environment.^{54,57,58} Increased rainfall could prevent parasite desiccation and promote suitable habitat for intermediate hosts, but excessive rainfall or flooding could destroy intermediate host habitats.^{11,54,57} Areas with reduced rainfall and droughts may see a reduction of habitable areas for intermediate hosts.^{11,54}

Other factors impacting disease distribution and transmission

Changing farming behaviour and land suitability influenced the risk of parasite and intermediate host exposure in livestock.^{53,54,56} The use of irrigation systems in agricultural areas was associated with *Fasciola* infection.⁵⁶ The implementation of control measures in livestock was identified as a mitigating factor for human infection, while increasing anthelmintic resistance is likely to exacerbate infection risk.^{53,56} Consumption of raw secondary host fish species was associated with *Opisthorchis* infection in humans.^{57,58}

Predictions

Four records discussing *Fasciola* infection suggested an increased risk in future climate scenarios, with increased prevalence and possible year-round transmission to livestock and humans anticipated in Punjab, Pakistan, and conditions becoming more favourable for livestock fasciolosis throughout New Zealand, the UK and central Europe.^{53–56} A decrease of human fascioliasis risk may be seen in Zimbabwe, due to decreasing habitats suitable for the intermediate snail host, with movement towards elimination possible by the end of the century.¹¹ Both records that discussed opisthorchiasis predicted a decrease in disease in northeastern Thailand under future climate change.^{57,58}

Schistosomiasis

Current distribution and trends

Six records were included that focused primarily on the disease in Africa, with one record discussing schistosomiasis in China.^{11,15,60–63} Although disease transmission is more common in tropical and subtropical areas, there have been observed shifts of disease transmission into temperate areas, including establishment of *Schistosoma haematobium* in Corsica, France and disease transmission has been observed at altitudes above previously defined limits in Uganda.^{15,61}

Pathogens, vectors and hosts

Five records discussed *Schistosoma mansoni*, the parasite responsible for intestinal schistosomiasis, and its intermediate snail host *Biomphalaria* species.^{11,15,61–63} Three records discussed *S. haematobium*, the parasite responsible for urinary schistosomiasis, and its intermediate host *Bulnius* species.^{11,15,60} One record discussed *Schistosoma japonicum* and its intermediate

host *Oncomelania* species, which are the main parasite and intermediate host species found in Asia.¹⁵ *Biomphalaria pfeifferi* was identified as the most widespread intermediate host in sub-Saharan Africa, although there was significant overlap with *Bulnius globosus*.^{15,61}

Impact from climate change

Both increased and decreased disease risk were discussed under future climate scenarios, with most records focussing on the effect of temperature on the intermediate snail host. Increased temperatures resulted in increased parasite reproduction and development rates, a decreased prepatent period and increased parasite cercariae production by intermediate hosts.^{60,61} Increased temperature also decreased mean generation time of intermediate hosts, allowing populations to recover faster from snail control efforts.⁶¹ Past this species-specific thermotolerant threshold, an increased temperature could increase mortality of both the parasite and intermediate host, with this thermotolerant range varying between intermediate host species.⁶⁰

Other factors impacting disease distribution and transmission

Other abiotic factors had a significant impact on host distribution and disease transmission. The type of water body (e.g. lake or river), water velocity and soil conditions influence habitat suitability for intermediate host species.⁶³ Construction of water development projects or irrigated areas provide suitable habitats for snail hosts and increase the potential for human contact with snails and parasites.⁶³ Human migration could result in the establishment of new disease foci, and poor sanitation or access to safe water supplies could increase the risk of disease transmission.⁶¹ Mass treatment programmes and snail control efforts were identified as measures that reduced disease transmission.⁶²

Predictions

Areas with higher temperatures are likely to see reduced snail populations and reduced disease as temperatures continue to increase, but currently endemic areas with lower temperatures may see high snail proliferation in the future.^{60,61} This will result in a net contraction of some snail habitats in Africa, with a geographical shift into cooler areas of southern and eastern Africa.^{11,63} Northern and eastern Kenya, southern South Sudan and eastern People's Democratic Republic of Congo are likely to have a decreased infection risk in future climate scenarios, while much of eastern Africa will see an increase in infection risk of up to 20% over the next 20–50 y.⁶² Some parts of Zimbabwe are likely to become free of schistosomiasis as suitable habitats for snail intermediate hosts become limited.¹¹ Currently endemic areas of Sichuan Province in China are likely to become unsuitable for snail populations, but non-endemic areas between Sichuan and Hunan/Hubei Provinces may see disease emergence and increased transmission.¹⁵ Current risk areas for disease transmission may extend into large parts of southern Europe as they become habitable for snail intermediate hosts.¹⁵

Snakebite envenomation

Current distribution and trends

Five records were included in the final analysis, with one record discussing snakebite envenomation in Sri Lanka, one in Mozambique and the remaining records discussing envenomation in the Americas.^{64–68} Although venomous snakes are found all over the world, the highest burden of snakebite is found in rural areas of developing tropical and subtropical countries, exacerbated by inadequate healthcare access and antivenom availability.⁶⁴

Impact from climate change

All records discussed temperature and rainfall as correlating factors for snakebite incidence, with one record discussing humidity and one record discussing extreme weather events.^{64–68} Snakes are ectothermic animals, dependent on external environmental factors.⁶⁴ Increased environmental temperature may increase foraging activity and result in increased contact with humans.⁶⁴ Increased rainfall may increase the availability of herbivorous snake prey and drought and reduced availability of food sources may force snakes and snake prey into human habitats.^{65,66}

Other factors impacting disease distribution and transmission

Snakebite incidence was associated with rural areas of developing countries, with fewer cases reported in urban areas with higher incomes.^{65,68}

Predictions

Both an increase and a decrease in suitable habitat and snakebite incidence were discussed. A possible increase of snakebite incidence of up to 31.3% is predicted in Sri Lanka with predicted increases in humidity.⁶⁵ A net expansion of suitable climate is anticipated for some venomous snakes in the Americas, with a northward displacement towards Canada and a southwards displacement in Argentina and Chile.^{66,67} The predicted areas of expansion are likely to include more populated provinces and may correspond to an increase of 5.5–6.7 million people at risk.⁶⁸ However, with liberal climate projections, some species may not be able to adapt quickly enough and will face extinction.⁶⁷ Climate change in Mozambique may contribute to driving north-south migration of some venomous snake species from currently concentrated areas in the southern and central parts of the country to potentially more populated areas.⁶⁴ Conversely, other species may see a range restriction and face an increased risk of extinction.⁶⁴ While increased contact with humans may contribute to an increased risk of snakebite, it will also result in an increase in snake fatalities, which may also drive several species to extinction.⁶⁴

Human African trypanosomiasis

Current distribution and trends

Four records were included, focussed solely on Africa.^{69–72} Tsetse fly vectors are widely distributed across Africa, with an estimated 60 million people at risk in sub-Saharan Africa.^{69,71} Trypanosomiasis in animals can contribute to lost livestock productivity of

20–40% in some areas.^{71,72} Shifting geographical distribution has been observed in Kenya, with a net decrease in areas that have relatively low human population densities and a net increase in highland areas where population densities of both humans and livestock are higher.⁷¹ Climate change has possibly contributed to the steady decline of the vector *Glossina pallidipes* over the past decade in the Zambezi Valley, Zimbabwe.⁷⁰

Pathogens, vectors and hosts

Two species of the protozoa were identified in this review, with *Trypanosoma brucei gambiense* found in western and central Africa and *Trypanosoma brucei rhodesiense* found in eastern and southern Africa.^{69,72} Tsetse fly vectors are required for both parasite development and transmission. Three records focussed on the vector *Glossina morsitans morsitans*, with one of these records also identifying *Glossina pallidipes* and *Glossina fuscipes fuscipes* as important vectors.^{69,71,72} The fourth record focused on *G. pallidipes* only.⁷⁰

Impact from climate change

All records identified temperature as an environmental factor that influenced vector distribution, and two records also identified rainfall as an important environmental factor.^{69–72} Increased temperature decreased the pupal development period and increased the vector feeding rate, thereby increasing disease transmission risk.^{69,72} However, increased temperature past the thermotolerant range of the vector could also increase the vector mortality rate and decrease vector pupal larval production.^{69,70,72}

Other factors impacting disease distribution and transmission

Changing distributions or interactions of human, livestock and wildlife populations may result in altered transmission dynamics, and factors such as civil unrest and discontinuation of control programmes have resulted in disease re-emergence in the past.^{71,72} The expansion of human settlements and agricultural land can impact disease transmission through the removal of tsetse fly habitats.⁷¹

Predictions

Both increases and decreases in future climate were discussed. The Zambezi Valley, Zimbabwe was predicted to become too hot to support vector populations, and possible extinction of some tsetse species is anticipated with increasing temperatures in Africa.^{69,70} In contrast, other areas are predicted to see an emergence of new disease foci in higher altitudes such as the Kenyan highlands.^{71,72} This area is a densely populated area as well as an important agricultural area, and spread of the vector could result in an increase in both human and livestock cases.^{71,72} Suitable vector habitats may shift into eastern and southern Africa, resulting in a resurgence of disease.^{70,72} One record predicted that an additional 46–77 million people may be at risk of infection by 2090.⁷²

LF

Current distribution and trends

Four records were included for LF, two focussing on Africa, one on Nepal and one modelled global distribution.^{12,73–75} The current distribution of LF extends over a large area of Africa and South-east Asia.^{73,74} The disease is considered eradicable or potentially eradicable and there have been large-scale control programmes implemented in the last couple of decades that have led to a significant reduction in infection in endemic communities.^{12,73} One record reported a recent increase of cases in higher-altitude areas of Nepal, which may have been influenced by warming temperatures in mountain areas.⁷⁴

Pathogens, vectors and hosts

Three records identified *Wuchereria bancrofti* as the main agent responsible for LF, with one of these records also identifying *Brugia malayi* and *Brugia timori*.^{73–75} Two records identified *Anopheles* species as the main vector for disease transmission in Africa.^{12,74} Two records identified *Culex quinquefasciatus* as the main vector for Asia, with one of these also identifying the species as the major vector for disease transmission in Brazil and tropical Africa.^{74,75}

Impact from climate change

All records identified temperature as an environmental factor that impacted vector life cycle and distribution of disease, with three of these records discussing rainfall and one discussing humidity.^{12,73–75} Increased temperature accelerates mosquito development and results in increased vector abundance, which could lead to the emergence of new disease foci.^{12,75} However, increased temperature past the vector thermotolerant range could decrease vector survival and reduce parasite transmission.¹² Increased rainfall may provide increased suitable breeding habitats for vectors, but excessive rainfall will eliminate habitats through flooding.^{12,73}

Other factors impacting disease transmission

Population growth was identified as a key driver of increased disease risk in Africa, while vector control programmes targeting malaria across the African continent are likely to reduce LF vectors.^{12,73} Accelerating global control activities will likely have a significant impact on reducing disease numbers and was not taken into account in any modelling of future disease risk.^{12,73}

Predictions

Transmission areas in Africa are predicted to expand, with northern and southern extremes of the continent becoming endemic in the future.⁷³ With both climate change and population growth considered, the at-risk population in Africa, currently estimated to be 543–804 million, could rise to a possible 1.65–1.86 billion in future scenarios.¹² However, these predictions do not take into account accelerating global control activities.^{12,73} The overall distribution pattern of suitable vectors in Australia may be similar to that of the present day, although there may be higher

suitability for the vector in southern Australia.⁷⁵ Shifts of the disease to higher altitudes have already been seen in Nepal and subtropical and temperate areas are anticipated to be at increased risk in the future.⁷⁴

Rabies

Three records were included discussing rabies transmission in North America, all focused on the effects of climate change on the distribution of wildlife reservoir hosts, including arctic and red foxes and vampire bats.^{76–78} A possible expansion in vampire bat habitat suitability was identified in the southern USA, but extensive expansion was concluded to be unlikely.⁷⁶ A shift of the primary rabies niche in the arctic is possible, with increased viral transmission expected among red foxes as the arctic rabies niche decreases.^{77,78}

Onchocerciasis

Only one record for onchocerciasis in West Africa was included, which identified temperature and rainfall as contributing climatic factors to disease.⁷⁹ Onchocerciasis occurs in sub-Saharan Africa, Central and South America and Yemen and relies on *Simulium* species of flies for vector transmission of the *Onchocerca volvulus* parasite.⁷⁹ The vector species cover a wide range of habitats, including forests, highland zones and savannas.⁷⁹ Increased temperature could increase the vector development rate as well as the development of *O. volvulus* larvae within the vector, but past a thermotolerant point, increased temperature resulted in increased vector mortality.⁷⁹ The authors acknowledged in this record that modelling and field data provided conflicting conclusions, with field data suggesting a decrease in future vector population and modelling suggesting increased transmission rates with increased future temperatures.⁷⁹

Soil-transmitted helminthiases

One record was included for South Korea, identifying temperature as a contributing factor to accelerating transmission of *Ascaris suum*, with the parasite identified as a suitable model for *Ascaris lumbricoides*.⁸⁰ No modelling was included; however, the author predicted an increase in transmission as the country shifted towards a subtropical climate with global warming.⁸⁰

Discussion

NTDs continue to affect >1 billion people, with a devastating impact on vulnerable and impoverished communities.^{2,16} Successful control programmes can be complicated by the changing epidemiology and distribution of diseases influenced by globalisation, migration, political instability, changing land use and climate change.^{6,9,48,51,71} The recent WHO roadmap for NTDs sets global targets to tackle these diseases from 2021 to 2030, however, it is important that vulnerable populations and/or territories and future trends be identified to inform planning and programme implementation.¹⁶

While extensive literature is available on the impact of climate change on disease epidemiology, much of this literature

focuses on a single disease or a related group of diseases such as arboviruses. In contrast, this review aims to provide a timely synthesis of the available literature on the impact of climate change on 11 of the WHO-listed NTDs and identify vulnerable geographic regions and populations that may be at risk of disease incursion or re-emergence.

The complexity of disease, vector and host epidemiology between different NTDs made it difficult to compare trends across the entire group, however, predictions for vector-borne NTDs, including dengue/chikungunya viruses, Chagas disease, leishmaniasis, human African trypanosomiasis, LF and onchocerciasis, anticipate similar impacts on vector and disease epidemiology due to climate change. Temperature influenced the lifespan, reproduction and feeding rate of vectors and rainfall influenced the availability of suitable breeding habitats for vectors.

Similar trends were identified for vector-borne diseases and schistosomiasis, with a shift in altitudinal and latitudinal distribution predicted.^{5,21,35,71,74} An increase in dengue cases at higher altitudes in Mexico is anticipated in future climate scenarios; Nepal has already observed cases of dengue, chikungunya and LF at higher altitudes that had previously been disease free; human African trypanosomiasis is predicted to shift into the population-dense areas of the East African highlands and schistosomiasis has been observed at higher altitudes in Uganda.^{5,21,61,71,72} Dengue and chikungunya, Chagas disease and leishmaniasis are all predicted to have an expanded geographical range into more northern areas of the USA, with dengue/chikungunya, leishmaniasis and schistosomiasis also anticipated to shift north, away from tropical and subtropical areas, into currently temperate areas of central Europe.^{15,23,36,41,49}

The included records highlight that climate change is only one factor that will influence vector distribution and disease transmission, as climate change exists in a complex matrix of globalisation, urbanisation, changing land use and migration of humans and animals.^{5,18,20,39,41,44,52,69} This has already been observed with the introduction of competent dengue/chikungunya virus vectors into Europe with the importation of goods, the outbreak of schistosomiasis in Corsica likely following the movement of infected humans from endemic areas and the autochthonous transmission of leishmaniasis in central Europe driven in part by the movement of domestic dogs.^{4,14,15} Similarly, while climate change may influence habitat suitability and geographic distribution for Chagas disease vectors, deforestation and changing land use, housing quality and human migration will significantly influence human exposure to triatome vectors and the risk of disease transmission.^{39,41,44}

Several records also predicted impacts of climate change on disease risk in animal hosts.^{53,54,56,71,72} The zoonotic diseases fascioliasis and African trypanosomiasis have a dramatic impact on livestock health and productivity.^{53,54,56,71,72} The primary animal reservoirs for African trypanosomiasis are wild ungulates and domestic cattle and this disease was estimated to have reduced livestock productivity by 20–40% in tsetse fly areas in Kenya, a country where agriculture accounts for almost 25% of the gross domestic product.^{71,72} The predicted shift of African trypanosomiasis to the East African highlands, where there is a strong agricultural presence, may result in significant economic losses, contribute to increased spillover to humans and exacerbate issues of food insecurity and malnutrition in communities that

are dependent on livestock.^{71,72} This highlights the need for cross-sectoral, One Health interventions that integrate both human and animal health to tackle changing trends in NTDs.⁷¹

Many of the predicted trends identified in this review focussed on the changing disease risk in developed regions (i.e. North America and central Europe), while the predicted impacts on developing tropical and subtropical areas were less consistent. This was observed with vector-borne diseases, but also rabies. All included records on rabies focussed on wildlife reservoirs in the Americas, while the heaviest burden of rabies is borne by African and Asian countries, with most human cases being transmitted by dogs.^{1,77} The available data in this analysis do not reflect the regions and populations that are disproportionately burdened by NTDs. Developed regions are more likely to have robust surveillance systems, adequate healthcare access, improved sanitation and hygiene and better socioeconomic conditions that will likely mitigate the risk associated with vector or disease incursion.^{20,32,49,51,52} In contrast, vulnerable populations and/or territories are more likely to lack the surveillance and healthcare infrastructure to prevent and respond to disease emergence and re-emergence due to global change.^{20,35,41}

Limitations

There were several significant limitations and gaps with this review. First, predictive modelling of disease based solely on climate change is inherently flawed, as it does not take into account globalisation, changing land use, human migration and conflict, urbanisation and population growth, which all contribute to changing disease patterns.^{7,12,44,50,51,74,75} Global control activities including vector control, mass drug administration and improved access to water and sanitation will all act to reduce the global burden of NTDs, but without including these, predicted trends for disease distribution and transmission are unlikely to be reliable.^{32,44,49}

The included records on Chagas disease, leishmaniasis and schistosomiasis highlighted the complexity of transmission that exists between a wide range of pathogens, vectors, hosts and reservoir species. Despite this, many climate-based models are based on a narrow selection of vector and host species, which does not reflect the wide range of possible species that differ greatly in ecological requirements and biology, nor does it reflect the possibility of pathogen/host switching.⁶³ Similarly, models focusing on effects of changing climate on species with a strict thermotolerant range do not consider the possibility of adaptation across successive generations, which will affect the parameters used in these models.^{7,60}

It was also difficult to set parameters on what constitutes climate change impact. Temperature and rainfall are commonly identified factors in many records. However, less commonly identified factors include increasing intensity and duration of storms, prolonged drought periods and indirect impacts from climate change such as changing agriculture and production, food and water scarcity, changing human behaviours and population displacement. No terms relating to these indirect impacts from climate change were included in the search strategy. As such, these factors associated with climate change may have been underrepresented in our analysis.

Due to the scope and number of diseases included, strict review parameters were used and only records that discussed the correlation of climatic factors with disease transmission in the wider context of climate change or global warming were included. This resulted in a large volume of valuable data being excluded that was still relevant to identifying indirect impacts from climate change as well as seasonal trends and more localised meteorological effects on disease. For example, trachoma has been associated with hotter, drier environments and regions with lower precipitation, which may correlate to reduced access to water for hygiene and sanitation.^{81,82} Higher temperatures may also influence vector (*Musca sorbens*) activity and distribution, and climatic conditions that favour drying of faeces, the vectors preferred breeding site, may have implications for larvae development.^{81,82} These correlations with climatic factors suggest that climate change may influence disease transmission and distribution, but with the limitations of the inclusion criteria, no records were eligible for inclusion in the final analysis.

Similarly, soil-transmitted helminthiasis transmission is influenced by soil conditions and climatic factors. Warm and humid conditions may improve soil suitability for egg and larval development, while heavy rainfall may wash helminth eggs from the soil.⁸³ Yet only one record was included in the final analysis, providing minimal evidence for the impact that climate change may have on disease epidemiology.

The global scope of this review and the limited number of records from each region make it difficult to make inferences about future trends at a regional or local level. While no language restrictions were set for the search criteria, all search terms were in English and no regional journal databases were searched, potentially resulting in the underrepresentation of regions such as Latin America, an area with a significant burden of many of the NTDs discussed in this review. For example, this region has a known high burden of human fascioliasis, yet no records for this disease in Latin America were included in the final analysis.⁵⁹

The trends predicted in this review suggest that climate change may contribute to a shift in disease transmission and geographical distribution for several vectors and NTDs, reflecting the trends of latitudinal and altitudinal shifts that have already been observed in the past several decades. However, the gaps and limitations of this review make it difficult to make reliable future predictions. Possible changes in geographical distribution and transmission may result in new disease foci and possible epidemics in naïve populations, and it is important that at-risk populations are identified and robust surveillance and control programmes are implemented to reduce the potential for an increased disease burden in these populations. However, while this review aimed to identify these geographical areas and populations at risk of incursion or re-emergence and discuss the impact on specific vulnerable populations and/or territories, the identified gaps and limitations meant that this was not well achieved.

Conclusion

Climate change may contribute to the emergence and re-emergence of several NTDs, most notably those that involve a vector or intermediate host for transmission. However, due to the significant gaps and limitations of this review, it is difficult to

predict future trends in disease transmission and distribution. There is a need for robust surveillance and monitoring to identify areas of disease incursion and emergence and include these in future public health interventions.

Collaboration between the health, veterinary and environmental sectors, in a One Health approach, can enhance surveillance capacity, increase the understanding of interactions between climate change and the emergence of human and animal diseases and allow for the implementation of efficient and targeted public health measures.^{84,85} Such approaches include joint public health and veterinary operational plans to coordinate rapid response to emerging zoonoses; integrated bite case management, involving collaboration between health and veterinary workers to inform risk assessments of dog bite patients and improve timely rabies case detection and the control of urinary schistosomiasis by incorporating education, preventive measures and environmental management of fish and snail intermediate host populations.^{85–87} Using climate forecasts to predict arboviral disease incidence has been shown to improve early warning systems, inform public health preventive measures and optimise resource allocation through targeted interventions.^{85,88,89}

Understanding the complexities of pathogen–vector–host life cycles and the influence of global factors including climate change, globalisation, changing land use, population growth, human migration and urbanisation is imperative for predicting trends and identifying at risk populations. A One Health approach should also be used to inform future research, with improved data needed for many NTDs, their reservoirs and associated drivers of disease emergence/re-emergence. Future modelling should better reflect the complexity of NTD life cycles, supported by data from local field-level research. Piloting of surveillance systems is needed that aggregates data from multiple sectors and engages these sectors in the analysis and interpretation of results. Such research will provide an evidence base to inform decision making and develop policy frameworks to implement One Health surveillance, detection and control programmes that will address the existing burden of NTDs and potential future risk of NTD incursion or re-emergence.

Supplementary data

Supplementary data are available at [Transactions](#) online.

Authors' contributions: BA and RT conceived the study and designed the study protocol. RT carried out the screening and data extraction from records. RT drafted the manuscript. BA, RR and RT critically revised the manuscript. All authors read and approved the final manuscript.

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