

Leishmaniasis emergence and climate change

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Summary

Spatio-temporal modelling of the distributions of the leishmaniasis and their sandfly vectors is reviewed in relation to climate change. Many leishmaniasis are rural zoonoses, and so there is a foundation of descriptive ecology and qualitative risk assessment. Dogs are widespread reservoir hosts of veterinary importance. Recent statistical modelling has not always produced novel general conclusions, exemplifying the difficulty of applying models outside the original geographical region. Case studies are given for transmission cycles involving both cutaneous and visceral leishmaniasis in the Old World and the Americas. An important challenge is to integrate statistical spatial models based mainly on climate with more explanatory biological models. Ecological niche models pose difficulties because of the number of assumptions. A positive association has been reported between the El Niño cycle and the annual incidence of visceral leishmaniasis in Brazil, but more basic research is needed before tackling other climate-change scenarios, including leishmaniasis emergence in northern Europe.

Keywords

Climate change – Disease emergence – Leishmaniasis – Phlebotomine sandfly – Spatial modelling.

Introduction

Veterinary and public health relevance

Most human leishmaniasis (HumL) is zoonotic, with each transmission cycle consisting of a *Leishmania* species (Protozoa, Trypanosomatidae) vectored by the haematophagous females of one or a few sandfly species (Diptera, Phlebotominae) among a limited range of reservoir hosts, which can include rodents, marsupials, edentates, monkeys, wild canids and domestic dogs (21, 46, 90) (Table I). The domestic dog is the only reservoir host of major veterinary importance (94), but canine leishmaniasis (CanL) is not notifiable to the World Organisation for Animal Health (OIE) (95). However, the economic and public health significance of CanL caused by *Leishmania infantum* is well established, not only in the Mediterranean region (42, 70), but also in many of the

drier parts of the neotropical regions of Latin America (20). Less frequently, infections of *Leishmania tropica* have been identified in domestic dogs (18, 38), which may serve as reservoirs of this causative agent of cutaneous HumL ('Oriental sore'). Other *Leishmania* species have occasionally been isolated from dogs (90).

The World Health Organization (WHO) (92, 93) reported that the public health impact of leishmaniasis has been grossly underestimated for many years. Over the last 10 years, endemic regions have been spreading and there has been a sharp increase in the prevalence of HumL. The number of unrecorded cases must be substantial, because declaration is compulsory in only 32 of the 88 affected countries, where 350 million people are at risk; the disability-adjusted life years (DALYs) (92) are estimated at 2.4 million (21). About two million new cases are considered to occur annually (1.5 million for cutaneous

Table 1
Worldwide distribution of human leishmaniasis in 2006

Human disease	Leishmania species	Anthropo- zootic (reservoir hosts)	World ecozone	EU biome	EU										Other Europe		Eurasia		
					Portugal	Spain	France	France Guiana*	French Guiana*	Germany	Italy	Malta	Greece	Cyprus	Former Yugoslavia	Switzerland	Albania	Hungary	Romania
Cutaneous (and muco- cutaneous) leishmaniasis	<i>L. tropica</i> species complex	Often anthropo- zootic	Palearctic, Afrotropical, Indo-Malayan	Mediterra- nean forests	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Formerly sporadic?	Formerly sporadic?	Absent?
					Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Cutaneous leishmaniasis	<i>L. major</i>	Zoonotic (rodents)	Palearctic, Afrotropical, Indo-Malayan	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent?
					Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Cutaneous leishmaniasis	<i>L. infantum</i> (= <i>L. chagasi</i> in Neotropics)	Zoonotic (domestic dogs, wild canids)	Palearctic, Afrotropical, Neotropical	Mediterra- nean forests, temperate broadleaf forest	Present	Present	Present	Absent	Absent	Present	Present	Present	Present	Present	Present	Present	Formerly sporadic?	Formerly sporadic?	Formerly sporadic?
					Present	Present	Present	Absent	Absent	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Visceral leishmaniasis	<i>L. infantum</i> (= <i>L. chagasi</i> in Neotropics)	Zoonotic (domestic dogs, wild canids)	Palearctic, Afrotropical, Neotropical	Mediterranean forests, temperate broadleaf forest	Present	Present	Present	Absent	Absent	Present	Present	Present	Present	Present	Present	Present	Absent	Absent	Formerly sporadic?
					Present	Present	Present	Absent	Absent	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Visceral leishmaniasis	<i>L. donovani</i> species complex (= <i>L. archibaldi</i> in Africa)	Anthropo- zootic	Afrotropical, Indo-Malayan	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
					Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Cutaneous leishmaniasis	<i>L. braziliensis</i> species complex; <i>L. mexicana</i> species complex	Zoonotic (edentates, primates, rodents, marsupials)	Neotropical, Nearctic	Absent	Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
					Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Muco-cutaneous leishmaniasis	<i>L. braziliensis</i>	Zoonotic (rodents, marsupials)	Neotropical	Absent	Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
					Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Diffuse cutaneous leishmaniasis	<i>L. mexicana</i> species complex	Zoonotic (rodents, marsupials)	Neotropical	Absent	Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
					Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent

* French Guiana is an overseas *département* of France. It is an integral part of France and a part of the European Union

leishmaniasis and 0.5 million for visceral leishmaniasis), with an estimated annual mortality of c. 60,000. Most foci of HumL occur in Latin America, Africa, India, the Mediterranean Basin and the Middle East (19) (Table I).

Climate change and the spatio-temporal distributions of the leishmaniasis

Environmental change will often modify the transmission patterns of vector-borne diseases (64), through its effects at different ecological scales (ecozones, biomes and ecotopes). Climate would be expected to modify the spatial and temporal distribution of the leishmaniasis, because the different transmission cycles have long been known to have distinctive 'landscape epidemiologies', as first described by Pavlovskii (78). The general epidemiological picture is that the leishmaniasis are emerging or emergent diseases (5, 20), but these reviews do not specify how climate change will affect the distributions of most of the transmission cycles and diseases. Leishmaniasis is not unusual in this respect: Kovats *et al.* (45) concluded that there was little clear evidence to associate global or regional climate change with modifications of the epidemiology of arthropod-borne diseases. Notable exceptions came from studies of the impact of yearly seasonal variation in climate.

Most transmission of *Leishmania* species is by the bite of permissive female sandfly species (i.e. those permitting the development of infective parasites), and so climate change will affect the distribution of leishmaniasis in three ways:

- directly, by the effect of temperature on parasite development and vector competence
- indirectly, by the effect of temperature and other environmental variables on the range and abundance of the sandfly species that act as vectors
- indirectly, through socio-economic changes that affect the amount of human contact with the transmission cycles.

The indirect effects are discussed later, in connection with case studies. Concerning the direct effect of climate change, it is known that female sandflies seek sheltered resting sites for bloodmeal digestion (90) and that temperature affects the development of infective forms of *Leishmania* in sandfly guts (6). In southern France, microhabitats buffer the variation in air temperature (P.D. Ready, unpublished data), but the temperature changes should be sufficient to influence the development of infective forms of *L. infantum* within the guts of local vectors, based on the experimental results of Rioux *et al.* (77). Vectorial capacity has only been calculated indirectly. The average number of gonotrophic cycles (i.e. egg development following a bloodmeal) completed by the vector *Phlebotomus ariasi* in the south of France was only a little greater than one (26),

and so relatively small changes in climate could have a large effect on transmission.

Case studies of the spatio-temporal 'modelling' of the leishmaniasis, with comments on the risks of emergence in relation to climate change

Fewer than 50 of the c. 1,000 species of sandflies are vectors of HumL or CanL worldwide (20, 41), and this is explained by the inability of many sandfly species to support the development of infective stages in their guts (6), and/or a lack of ecological contact between some sandflies and the reservoir hosts (69). Such variation greatly limits the risk of leishmaniasis emergence in any region, with each *Leishmania* species often being transmitted by related sandflies, usually classified in subgenera of the Old World (OW) genus *Phlebotomus* (such as subgenus *Larrousius*) or of the New World (NW) genus *Lutzomyia* (such as *Nyssomyia*). The breeding places of sandflies have rarely been identified and, therefore, are not usually sampled during ecological surveys.

Old World zoonotic cutaneous leishmaniasis

There has been much descriptive ecology of the transmission of *Leishmania major* by *Phlebotomus (Phlebotomus) papatasi* (63, 65), and the 'landscape epidemiology' is defined by the semi-arid bioclimates favoured by the primary gerbil reservoirs: *Psammomys obesus* in north Africa and the eastern Mediterranean region, and *Rhombomys opimus* in the Middle East and the southwest of the former Union of Soviet Socialist Republics (USSR). Desjeux (20) described the main environmental risk factors, namely, urbanisation, with the spread of suburbs nearer to gerbil colonies, and irrigation schemes expanding the reservoirs' ranges.

To these risks can be added military operations (e.g. 14), which prompted Cross and colleagues to use climate data to model the geographical and seasonal distribution of *P. papatasi* in southwest Asia. The statistical models associated the presence of the vector with ground records of weather and, for predictive interpolation between weather stations, with the normalised difference vegetation index (NDVI) obtained from satellites (13). Global warming scenarios were then explored, by increasing the temperature values for 115 weather stations by 1°C, 3°C and 5°C (12) and using a discriminant analysis model to

predict the probability of sandfly occurrence at each station. Endemic transmission was assumed for those stations where vectors were predicted to occur long enough throughout the summer (May to August) to allow two or more life cycles. Seventy-one (62%) stations were considered endemic with the current climate, and the cumulative numbers of additional stations becoming endemic was 14 (12%), 31 (27%) and 43 (37%) with temperature increases of 1°C, 3°C and 5°C, respectively. Also, the seasonality of disease transmission was predicted to be extended throughout the year in 29 (25%) locations with an increase of 5°C. The effects of such temperature rises on other aspects of leishmaniasis transmission have yet to be investigated, for example the population cycles of the gerbil reservoir hosts and any behavioural changes of humans, gerbils and sandflies that might limit their contact.

New World zoonotic cutaneous leishmaniasis

Leishmania braziliensis is a major causative agent of cutaneous and mucocutaneous HumL in Latin America, and it is widespread not only in naturally forested regions, where the reservoir hosts are often native rodents (46), but also where deforestation and land use change have occurred over several decades. The gradual domestication of transmission in Venezuela and east-southeast Brazil has shifted the risk from forest workers to families, but this has simultaneously increased the possibilities for vector control (20).

Peterson and Shaw (67) modelled the ecological niches of three incriminated vectors in southern Brazil, using Genetic Algorithm for Rule-set Production (GARP) software (82) and statistical analyses to predict geographical distributions and any climate change effects. The geographical information system (GIS) approach used environmental data layers of elevation, slope, aspect and topographical index as well as eight climate measures, and all were generalised to a pixel resolution of $0.1^\circ \times 0.1^\circ$ (c. 10×10 km) for the whole of South America. Predictivity of sandfly occurrence was reported to be highly statistically significant, using two approaches (quadrant and random tests) to assign occurrence points to training and test data sets. Another technical point of interest was the use of random sub-samples from densely sampled Brazilian states, to remove regional bias. Two climate change scenarios (HHGSDX50 and HHGGAX50) were used to predict that *Lutzomyia* (*Nyssomyia*) *intermedia* (not distinguished from *Lutzomyia* [*Nyssomyia*] *neivai*) would find improving climates along the east slope of the Andes, and that this also applied to *Lutzomyia* (*Barrettomyia*) *migonei* and *Lutzomyia* (*Nyssomyia*) *whitmani*. It was also predicted that only the latter would extend its range in the more heavily populated east and southeast of Brazil, for which there is limited observational

support. However, Peterson and Shaw (67) noted that the principal limitation of their application was the crude spatio-temporal resolution of the climate projections (30-year averages), and they concluded that regional climate models were needed to improve spatial detail for South America.

Only one of these vectors, *L. neivai*, was present in the disease focus investigated by Salomón *et al.* (80, 81) in northern Argentina. Relative measures of sandfly density are more informative than occurrence, because they are usually correlated with biting density, a measure of vectorial capacity. In Argentina, *L. neivai* abundance was correlated with the rainfall of the previous year (80).

Old World anthroponotic visceral leishmaniasis

It is not surprising that there has been spatial modelling of the vectors of *Leishmania donovani* (= *Leishmania archibaldi*) (50), because it is the causative agent of anthroponotic visceral HumL (or Kala-azar), which is fatal if untreated and kills thousands of people in cyclical epidemics in northeast Africa (Sudan, Ethiopia and Kenya) and in the northeast of the Indian subcontinent (India, Bangladesh and Nepal) (20).

The main risk factors in northeast Africa are seasonal migrations (with cattle), displacement in wars, and malnutrition (20). In the Sudan, an association had long been noted between savanna woodland and its soil and the vector, *Phlebotomus* (*Larrousius*) *orientalis* (19). Later, the distribution of *P. orientalis* was associated statistically with environmental determinants (28), and a risk map for its occurrence was produced based on a logistic regression model (86). Explanatory variables included maximum daily temperature and soil type (black cotton clay), and the map was refined using a mask layer indicating the known rainfall-based boundaries of the Acacia-Balanites woodland of the savanna. Later, Elnaïem *et al.* (29) used logistic and linear multivariate regression analyses to develop environmental models to explain variability in the presence and incidence of the Kala-azar disease itself. Average rainfall and altitude were the best predictors. Based on surveys in Ethiopia, Kenya and Somalia, the environmental models for two regional vectors were different (36): the occurrence of *P. orientalis* and *Phlebotomus* (*Synphlebotomus*) *martini* were best predicted by wet season and dry season models, respectively, both based on remote sensed (RS) NDVI and land surface temperature (LST). Unlike the research in the Sudan, soil type was not identified as an important predictor of vector occurrence.

Cross-border migration is also a risk factor for the emergence of Kala-azar in India, Bangladesh and Nepal, where low socio-economic status is the principal risk factor for the disease (20). Extreme poverty is associated with

(37). The region (including parts of the Middle East) is still endemic for the infantile disease, but its public health importance diminished from the 1950s (37, 91). This may be explained by better nutrition, coincidental control of sandflies by mosquito eradication campaigns, rural depopulation, and improved housing with less sandfly contact.

Until recently all infections were believed to be sandfly-borne (but see next section), with almost all foci being rural and restricted to the 'Mediterranean forests' biome (89). In Europe, however, the vectors are also abundant in the adjoining parts of the temperate region ('temperate broadleaf forests' biome), in northern Spain (4) and central France (40; P.D. Ready and B. Pesson, unpublished data, 2001-2007). They have been reported in small numbers as far north as Paris (75) and the upper Rhine valley of Germany close to the French border (59). The occurrence of 'vectors without endemic disease' is a significant risk for leishmaniasis emergence in temperate Europe, because of the large numbers of asymptomatic human infections (57, 68) and of dogs imported from, or travelling to, the Mediterranean region each year, from countries such as Germany (55, 59) and France (53). Emergence in a temperate region has only been demonstrated in northern Italy, both for vectors (52) and disease (9), but this has not been associated unequivocally with climate change.

Rioux and colleagues introduced many ecological approaches for studying the transmission cycles in the Mediterranean, especially in the west where they developed sampling methods (75) and bioclimate analyses (74, 78). The most complete study was made for the Cévennes mountains of southern France, for which the leishmaniasis foci and vector densities were associated with phyto-ecological zones and altitudes (75) and bioclimate zones (78) delimited by the rainfall quotient of Emberger (30, 32) plotted against the mean minimum temperature of the coldest month. Correspondence analysis was also used to group sandfly species bioclimatically (74, 78). This permitted the mapping of foci at a regional scale, but the categorical markers have not proven to be transferable inter-regionally. In the Cévennes mountains, for example, disease foci and the local sandfly vector (*P. ariasi*) were associated with mixed oak forest (*Quercus ilex*–*Quercus pubescens*), mid-slopes at moderate altitudes (300 to 500 m a.s.l.) and the sub-humid/humid Mediterranean bioclimate zones. However, on the southern slopes of the Sierra Nevada in the south of Spain, the tree communities are different and a comparable transmission cycle peaks at higher altitudes (500 to 800 m a.s.l.) in the semi-arid/sub-humid Mediterranean bioclimate zones (58; F. Morillas and P.D. Ready, unpublished results). This is to be expected, because altitudinal temperature and plant assemblages change with latitude, and the boundaries of the bioclimate zones were arbitrarily fixed (31).

These limitations have prompted a GIS approach by the leishmaniasis sub-project of EDEN (Emerging Diseases in a changing European eNvironment; European Union [EU] FP6 project) involving ten European partners and coordinated by the author. Ground and RS data are being used in statistical and mathematical models to identify the environmental conditions that might permit the emergence of leishmaniasis in European regions currently characterised by 'vectors without endemic disease'. The early analyses have shown that both climatic and land-cover variables are explanatory for sandfly abundance, but only if local habitat variation is carefully estimated and taken into account.

Transmission not involving sandflies, and the effects of climate change

Our understanding of the fundamentals of leishmaniasis epidemiology has been challenged in the last 20 years. Firstly, *Leishmania*/HIV co-infections were recorded in 35 countries worldwide, and widespread needle transmission of *L. infantum* was inferred in southwest Europe (22), where Cruz *et al.* (15) demonstrated *Leishmania* in discarded syringes. Secondly, leishmaniasis has become more apparent in northern latitudes from which sandfly vectors are either absent or present in very low densities, such as in the eastern United States of America (USA) and Canada (23) and in Germany (39, 59). Most infections involve CanL, not HumL. This is most likely to be explained by dog importation from, or travel to, endemic regions, followed by vertical transmission from bitch to puppy. Transmission from mother to child has rarely been reported (54). Vertical transmission of CanL has been observed in the eastern USA and Canada in some breeds (including foxhounds) imported from Europe (23). Non-vector transmission could explain the many autochthonous cases of CanL in Germany. However, some basic information is missing; the vectorial competence of *Phlebotomus (Transphlebotomus) mascittii* should be tested experimentally, because this species has recently been found to be widespread in northern France, Belgium and Germany (17, 59). However, low human-biting rates and autogeny (72) suggest that it is unlikely to be of epidemiological importance.

Climate change will affect these modes of transmission via socio-economic change. More holiday travel and immigration of dogs (55, 87) will significantly increase the risks of leishmaniasis emergence. Increasing numbers of dogs are entering northern Europe from the Mediterranean region, where owners spend holidays or have second homes, and from where homeless dogs are rescued.

Prevention of leishmaniasis emergence

Selecting control strategies: zoonotic visceral leishmaniasis

Based on mathematical models, Dye (25) concluded that insecticides are expected to reduce the incidence of zoonotic visceral HumL caused by *L. infantum* even more effectively than they reduce the prevalence of CanL, but only where transmission occurs peri-domestically and the sandfly vectors are accessible to treatment, as in parts of Latin America. There, the second best strategy (25) would be to reduce susceptibility to leishmaniasis by vaccinating people or dogs, or by eliminating childhood malnutrition where it is common; both killing vectors and reducing susceptibility would be more effective than killing dogs or treating them with drugs. For Europe, Dye (25) concluded that a dog vaccine is highly desirable, because control of sandfly vectors is less likely to be successful and CanL is a major veterinary problem. These conclusions were partly based on compartmental models of the basic case reproduction number (R_0) reported by Dye (24) and Dye *et al.* (27). Subsequently, there have been notable developments of control tools necessary for implementing Dye's recommendations.

Prompt diagnosis, isolation and treatment

This can be critical for preventing emergence. Unfortunately, CanL is not notifiable to the OIE (95), but monitoring its distribution (87) would be assisted by scrutiny of standardised pet passports, as started in Europe (16), and the more widespread use of standard questionnaires for veterinary clinicians, as developed in Italy (9) and France (53), and much used by the EDEN project.

Diagnostic tests

Most diagnoses are based on symptoms, the microscopic identification of the parasites in Giemsa-stained smears of tissue or fluid (from lesions, bone marrow, spleen and lymph nodes), and serology; these tests are usually only genus-specific (94). The gold standard for the identification of *Leishmania* species remains multi-locus enzyme electrophoresis (90). However, there are efforts to identify the isoenzyme strains (or zymodemes) by characterising the DNA at the enzyme loci (50). Various genes and molecular techniques have been used to identify infections in humans, reservoir hosts and sandfly vectors (1), but there has been no international standardisation (94). Molecular techniques indicate only the presence of a few recently living parasites, not that the parasites are infectious. Consequently, serology is often more

informative. Some antigens are stable and produced commercially, such as the recombinant (r) K39 for a dipstick or strip test, which is useful in clinical practice in primary health centres (8) and has been used widely to diagnose CanL (94).

Anti-leishmanial drugs

Pentavalent antimonials were the first-choice drugs for HumL (2), but are being replaced by miltefosine, paramycin and liposomal amphotericin B, hopefully in combinations, to prevent the emergence of resistance (11). CanL is often treated with an antimonial plus allopurinol (61). Highly active anti-retroviral therapy (HAART) has reduced the incidence of *Leishmania*/HIV co-infections by preventing asymptomatic infections with *L. infantum* from becoming symptomatic, but unfortunately it rarely prevents visceral HumL relapses (49).

Vaccines

Targets of strategic research include promastigote secretory-gel glycans (79) and antigens on sandfly salivary peptides (88). Vaccination against HumL has been practised for centuries in the Middle East, by deliberately inoculating pus of an active lesion in places where lesions would not cause deformity ('Leishmanisation'). Second generation recombinant vaccines include a trifusion recombinant protein (Leish-111f) with epitopes shared by *L. donovani* and *L. infantum* (84, 85). The development of vaccines against CanL has been stimulated not only by the socio-economic importance of dogs but also because they are the main reservoirs of HumL caused by *L. infantum*. The first licensed vaccine against CanL, Leishmune, contains the fucose-mannose-ligand (FML) antigen of *L. donovani* (60). An efficacy of 76% to 80% was reported, and the industrialised formulation of the FML-saponin has undergone safety trials in Brazil (62). Another vaccine is LiESAp-MDP (excreted/secreted antigens–adjuvant) (47), which was reported to have an efficacy of 92% when tested on naturally exposed dogs in the south of France (48).

Interventions against the sandfly vectors

These can be effective. In the Americas, much cutaneous leishmaniasis transmission occurs in sylvatic regions, and so insect repellents such as DEET (N, N-diethyl-m-toluamide) are more often used than insecticides (10). Intervention to reduce the biting rate of peri-domestic vectors of visceral HumL and CanL has shown considerable potential, including the use of insecticide-impregnated nets and bednets (21), topical applications (73), and deltamethrin-impregnated collars (35, 42, 44, 51, 73), which are now used by many dog owners in the Mediterranean region and Brazil.

Conclusions and perspectives on spatial modelling of the leishmaniases in relation to climate change

Most of the leishmaniases are rural and many are zoonoses, and so there has been much descriptive ecology of their 'landscape epidemiologies' and recognition of qualitative risk factors (20). A new era of statistical modelling of spatio-temporal distributions has started, but sometimes the conclusions do not immediately appear to be novel. For example, the risk maps for Kala-azar in the Sudan (86) relied partly on a previously reported association between the disease and one type of savanna woodland, which is dependent on soil type. However, a spatial analysis of Kala-azar in countries to the east of Sudan (36) did not identify the same set of explanatory variables, and soil type was not a predictor. This exemplifies the difficulty of transposing spatial 'models' beyond the area in which they were developed, and this applies to statistical models as well as to descriptive ecological scenarios, as is being discovered in Mediterranean Europe by the EDEN project. The availability of standard sets of RS climate data and the software to relate them to vector and disease distributions does not remove the necessity of setting and testing suitable ecological hypotheses. One of the limitations of testing climate change hypotheses stems from the difficulties of obtaining or assembling climate data other than averages for the 30-year period from 1961 to 1990, especially if the aim is for regional models.

The new modelling tools should have the advantage of being more objective and, thereby, facilitating predictions of the effects of climate change. However, climate is more likely to have direct effects on the distribution of the cold-blooded sandfly vectors of leishmaniasis than on the disease itself. Therefore, one challenge will be to integrate statistical spatial models, based largely on climatic variables, with more explanatory biological models, including those based on the basic reproduction number (R_0). Dye (25) showed how R_0 models can help to select control strategies.

The work of Peterson and Shaw (67) on vectors of *L. braziliensis* illustrates how ecological niche models may be used to investigate climate change effects. Major difficulties arise because of the number of assumptions that have to be made, which include no evolution in niche characteristics (i.e. only pre-adaptation to new human environments), no interactions among species (e.g. no competition), imprecise estimates of current dispersal rates (available only rarely for sandflies, e.g. *P. ariasi* [43]), and often little knowledge of historical limitations of distribution. The latter is relevant to species still spreading from Ice Age environmental refuges, such as *P. perniciosus* (3, 66) and the genomic strains of *L. infantum* (56) that it transmits in southwest Europe.

Franke *et al.* (33) reported a positive association between the El Niño cycle and the annual incidence of visceral HumL in east Brazil, but there is still much basic research needed before less well known climate change scenarios can be tackled. Such basic research includes not only the ecological topics previously mentioned but also taxonomy and vector incrimination. Thus, Peterson and Shaw (67) were obliged to treat two ecologically separate species (*L. intermedia* and *L. neivai*) as one; and, the ability of *P. mascittii* to develop infective forms of *L. infantum* has never been tested or reported. *P. mascittii* is the only sandfly widespread in Germany, where knowledge of its vectorial competence will become pertinent if climate warming intensifies or extends the northern European summer and exotic *Leishmania* species continue to be imported by world travellers (39).

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Le changement climatique et l'émergence de la leishmaniose

P.D. Ready

Résumé

L'auteur examine les modèles spatio-temporels de l'évolution de la distribution des leishmanioses et des phlébotomes vecteurs sous l'influence du changement climatique. Les leishmanioses sont pour la plupart des zoonoses sévissant en milieu rural, d'où l'utilité de recourir à l'écologie descriptive et de procéder à une évaluation qualitative du risque. Les chiens jouent un rôle très important en tant qu'hôtes réservoirs. Les modèles statistiques récents ne permettent pas toujours de tirer de nouvelles conclusions générales, ce qui illustre la difficulté d'appliquer des modèles en dehors des régions géographiques d'origine. L'auteur présente des cas d'étude de cycles de transmission de la leishmaniose cutanée et viscérale dans l'Ancien Monde et dans les Amériques. Un enjeu important consiste à faire la synthèse entre des modèles statistiques spatiaux, qui sont essentiellement basés sur le climat, et des modèles biologiques, plus explicatifs. Les modèles utilisant les niches écologiques posent problème car ils font intervenir un grand nombre d'hypothèses. Une corrélation positive a été constatée entre le phénomène cyclique ENSO (*El Niño Southern Oscillation*) et l'incidence annuelle de la leishmaniose viscérale au Brésil, mais avant de développer d'autres scénarios liés au changement climatique, par exemple concernant l'émergence de la leishmaniose en Europe du Nord, la recherche fondamentale dans ce domaine devra être poursuivie.

Mots-clés

Changement climatique – Émergence de maladie – Leishmaniose – Modèle spatial – Phlébotome.



La aparición de leishmaniasis y el cambio climático

P.D. Ready

Resumen

El autor se centra en el uso de modelos espacio-temporales de la distribución de la leishmaniasis y su vector, el jején, en relación con el cambio climático. Muchas leishmaniasis son zoonosis rurales, por lo que existe una base de ecología descriptiva y de evaluación cualitativa de riesgos. Los perros son un reservorio muy extendido y de gran importancia veterinaria. La reciente obtención de modelos estadísticos no siempre ha llevado a conclusiones generales novedosas, cosa que pone de relieve lo difícil que resulta aplicar modelos fuera de la región geográfica original. El autor describe estudios monográficos sobre ciclos de transmisión con presencia de leishmaniasis tanto cutánea como visceral en el Viejo Mundo y las Américas. Una importante dificultad estriba en integrar por un lado modelos espaciales estadísticos basados esencialmente en el clima y por el otro modelos biológicos de carácter más explicativo. Los modelos de nicho ecológico resultan problemáticos por el número de premisas en que reposan. Se ha descrito una correlación positiva

entre el ciclo de El Niño y la incidencia anual de leishmaniasis visceral en Brasil, pero aún se requiere más investigación fundamental para trabajar sobre otras hipótesis ligadas al cambio climático, entre ellas la aparición de leishmaniasis en el norte de Europa.

Palabras clave

Aparición de enfermedades – Cambio climático – Elaboración de modelos espaciales – Jején flebotomino – Leishmaniasis.



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