

# PHYSICAL VARIABLES OF LEISHMANIASIS TRANSMISSION

VARIÁVEIS FÍSICAS NA TRANSMISSÃO DA LEISHMANIOSE

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Luca Casale Guerreschi<sup>1</sup>

Maria Amália Garcia da Silveira Araújo<sup>1</sup>

Tales Alexandre Aversi-Ferreira<sup>2</sup>

Maria Tereza Mendes Aversi<sup>3</sup>

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## **ABSTRACT**

Leishmaniasis is a neglected tropical infectious disease transmitted by female phlebotomine sandflies, affecting more than 90 countries with an estimated 700,000 to 1 million new cases per year [51]. This article reviews the geographical and environmental variables related to the transmission of visceral (VL) and cutaneous (CL) forms of the disease at global and regional scales. A bibliographic review was conducted in MEDLINE, PLoS, PubMed, LILACS, CAPES Periodicals, Open Journal System, SciELO and Google Scholar, with defined inclusion and exclusion criteria. Results indicate that the global geographical distribution of leishmaniasis follows the niches of phlebotomine sandflies, concentrated in tropical and equatorial regions, with higher prevalence in Asia, East Africa and the Americas. Key environmental determinants include temperature, humidity, rainfall and vegetation type. At the regional level, unplanned urbanization, deforestation and poverty bring vectors and reservoir hosts closer to human populations, particularly in urban peripheries. Risk mapping is an essential tool for disease surveillance and control. It is concluded that combating leishmaniasis requires a multidisciplinary approach, effective public health policies and continuous epidemiological surveillance.

**Keywords:** Leishmaniasis; Phlebotomine sandflies; Epidemiology; Geographical variables; Environmental variables.

## **RESUMO**

A leishmaniose é uma doença infecciosa tropical negligenciada, transmitida por fêmeas de flebotomíneos, que afeta mais de 90 países com estimativa de 700.000 a 1 milhão de novos casos anuais [51]. Este artigo revisa as variáveis geográficas e ambientais relacionadas à transmissão das formas visceral (LV) e cutânea (LC) em escala global e regional. Foi realizada revisão bibliográfica nas

bases MEDLINE, PLoS, PubMed, LILACS, CAPES Periódicos, Open Journal System, SciELO e Google Acadêmico. Os resultados indicam que a distribuição geográfica global segue os nichos dos flebotomíneos, com maior prevalência na Ásia, África Oriental e Américas. Urbanização desordenada, desmatamento e pobreza aproximam vetores e hospedeiros reservatórios das populações humanas. Conclui-se que o combate à leishmaniose exige abordagem multidisciplinar, políticas públicas eficazes e vigilância epidemiológica contínua.

**Palavras-chave:** Leishmaniose; Flebotomíneos; Epidemiologia; Variáveis geográficas; Variáveis ambientais.

## 1. INTRODUCTION

Leishmaniasis is a non-contagious infectious disease belonging to the group of neglected tropical diseases (NTDs) [1, 2], chronically undervalued as an eradication priority. The WHO currently estimates 700,000 to 1 million new cases annually, with 20,000–30,000 deaths per year [51]. Recent analysis of the Global Burden of Disease Study 2021 (GBD 2021), covering 204 countries and territories, showed that the global age-standardized DALY rate for VL declined 92.9% between 1990 and 2021, while the DALY rate for CL and MCL increased 26.4%, particularly in low- and middle-SDI countries [49]. The disease can trigger intense epidemics primarily associated with nutritional and migratory factors [5, 6].

The disease most likely originated in East Africa, with records in ancient Egypt and Christian Nubia dating to approximately 4,000 B.C. [7]. As of 2022, 99 countries and territories are endemic for leishmaniasis, including 71 endemic for both VL and CL [51]. An estimated 200 million people are at risk of transmission [8]. The

highest incidence is found in India, Bangladesh, Nepal, Sudan and Brazil [3]; in 2024, 85% of global VL cases were reported from just seven countries: Brazil, Ethiopia, India, Kenya, Somalia, South Sudan and Sudan [51].

The protozoan *Leishmania*, a unicellular flagellate, is the causative agent, transmitted to humans by female phlebotomine sandflies. Over 20 *Leishmania* species and more than 90 sandfly species are known to transmit the disease [51]. The main clinical forms are visceral (VL), cutaneous (CL) and mucocutaneous (MCL) [7, 53]. CL is endemic in almost 100 countries, affecting an estimated 12 million cumulative cases, with approximately 600,000 to 1 million new CL cases per year [53].

VL, also known as kala-azar, is fatal in over 95% of untreated cases [51]. It is caused by *Leishmania donovani* and *Leishmania infantum* (subspecies *L. infantum chagasi* in Brazil), both belonging to the family Trypanosomatidae. Clinical features include fever, hepatosplenomegaly, lymphadenopathy, pancytopenia, anemia, weight loss and, in the absence of treatment, death [9, 54].

CL is the most common form worldwide, caused by approximately 20 different *Leishmania* species [51], known by various regional names such as Aleppo boil, Chiclero ulcer, Bauru ulcer, Oriental sore and Pian bois. MCL produces destructive and disfiguring lesions, especially on the face, caused primarily by *Leishmania braziliensis* [53].

Regardless of the type, transmission occurs through the bite of female phlebotomine sandflies, whose geographical distribution directly determines disease distribution. Sandflies inhabit mainly

hot, wet tropical regions [10], although they also occur in dry and hot environments. Various natural reservoir hosts — canines, birds, cattle, equines, goats, swine and felines [11-14] — share the same habitats as the vectors. Environmental disruptions such as climate change, deforestation, and urbanization significantly affect the distribution and abundance of sandfly vectors and their reservoir hosts [54].

Canine leishmaniasis is an important indirect indicator of human disease prevalence. The disease is broadly associated with tropical and equatorial zones, poor sanitary conditions and the proximity among parasites, vectors, reservoir hosts and humans.

In this context, it is possible to hypothesize that globalization and climate change may contribute to the expansion of leishmaniasis incidence worldwide. Therefore, this article aims to review the geographical and environmental variables associated with leishmaniasis transmission at global and regional scales.

## **2. MATERIALS AND METHODS**

For this purpose, information was collated from an extensive literature search using the following electronic databases: MEDLINE, PLoS, PubMed, LILACS, CAPES Periodicals, Open Journal System, SciELO and Google Scholar. The search terms used were: leishmaniasis, visceral leishmaniasis, cutaneous leishmaniasis, mucocutaneous leishmaniasis, phlebotomine sandflies, sandflies, geographical aspects of leishmaniasis and environmental aspects of leishmaniasis.

This paper is derivate from book chapter intitule “Geographical and Environmental Variables of Leishmaniasis Transmission” however

with actualized literature and new data.

## **2.1. Inclusion Criteria**

Indexed papers published in the last 20 years; classic indexed papers on areas of highest endemicity. Selected textbooks and WHO technical reports were also used.

## **2.2. Exclusion Criteria**

Papers that did not address the main topics reviewed here and texts with content equivalent to more recent publications already included.

## **3. GEOGRAPHICAL VARIABLES**

### **3.1. Worldwide Variables**

In terms of the biosphere, the geographical variables of leishmaniasis transmission are associated with the tropical zone and hot, wet climates with a regular rainfall index [10]. Underdeveloped and developing countries show the highest incidence. According to GBD 2021 data, from 1990 to 2021, global incident cases rose from 1.01 to 1.10 million and prevalent cases nearly doubled from 3.18 to 6.21 million, with South Sudan, Syria, Afghanistan, Suriname and Sudan identified as persistent hotspots [50].

Both human VL and CL follow the geographical distribution of the insect vector [15]. VL is endemic in 80 countries with an annual global incidence of 50,000–90,000 cases [49]. CL and VL are found globally between the tropics but have also been detected in regions

with relatively rigorous winters, such as France [16], Portugal, Russia and China [3].

In Africa, VL reports are sparse in the Sub-Saharan region. In East Africa, VL is endemic and cases have increased, accounting for 73% of global VL cases in 2022 [49]. The greatest concentrations are in Sudan [17, 18], Ethiopia [2, 9], South Sudan [3], Somalia, Uganda, Kenya [9] and Eritrea [3] (Table 1). VL total in Africa (8,571 cases) substantially exceeded CL (204 cases) in the reference period.

**Table 1:** Geographical distribution of VL and CL in Africa (based on reference [3]).

<b>Country/Region</b>	<b>Visceral Leishmaniasis (VL)</b>	<b>Cutaneous Leishmaniasis (CL)</b>
<b><i>Sub-Saharan African Region</i></b>		
Cameroon	0	55
Côte d'Ivoire	0	1
Ghana	0	27
Mali	0	58
Nigeria	1	5
Senegal	0	8
<b>TOTAL</b>	<b>1</b>	<b>154</b>
<b><i>Eastern African Region</i></b>		
Eritrea	100	50
Ethiopia	1,860	0

Kenya	145	0
Somalia	679	0
Sudan	3,742	0
South Sudan	1,756	0
Uganda	288	0
<b>TOTAL</b>	<b>8,570</b>	<b>50</b>

**Source:** Alvar et al. [3].

In Asia from the Middle East to Central Asia, significant VL prevalence is found mainly in Iraq (>1,000 cases). CL cases greatly exceed VL: 61,015 vs. 2,497, with Iran, Afghanistan, Pakistan, Saudi Arabia and Iraq among the highest CL-burden countries (Table 2). In the Indian Subcontinent, India, Bangladesh and Nepal concentrate the majority of VL cases. Overall, Asia recorded 61,493 CL cases vs. 45,120 VL cases [3, 20, 21]. In 2024, Bangladesh became the first country validated by WHO for VL elimination as a public health problem [51].

*Table 2: Geographical distribution of VL and CL in Asia (based on reference [3]).*

<b>Country/Region</b>	<b>VL</b>	<b>CL</b>
<b><i>Middle East to Central Asia</i></b>		
Afghanistan	0	22,620
Armenia	7	0
Azerbaijan	28	17

China	378	0
Georgia	164	5
Iran	149	24,630
Iraq	1,711	1,655
Kazakhstan	1	15
Oman	1	5
Pakistan	0	7,752
Saudi Arabia	34	3,445
Tajikistan	15	25
Turkmenistan	0	99
Ukraine	2	2
Uzbekistan	7	142
Yemen	0	603
<b>TOTAL</b>	<b>2,497</b>	<b>61,015</b>
<b><i>Indian Subcontinent &amp; SE Asia</i></b>		
Bangladesh	6,224	0
Bhutan	2	0
India	34,918	156
Nepal	1,477	0
Sri Lanka	0	322
Thailand	2	0
<b>TOTAL</b>	<b>42,623</b>	<b>478</b>

**Source:** Alvar et al. [3].

In the Mediterranean region, countries with more than 100 VL cases include Morocco, Italy, Spain, Albania and Algeria. For CL, more than 1,000 cases were reported in Algeria, Syria, Tunisia, Libya, Morocco and Turkey (Table 3). Overall, 85,886 CL cases were recorded against 874 VL cases. In 2024, seven countries accounted for 83% of global CL incidence: Afghanistan, Algeria, Brazil, Colombia, Iran, Peru and Syria [51].

**Table 3:** *Geographical distribution of VL and CL in the Mediterranean region (based on reference [3]).*

<b>Country</b>	<b>VL</b>	<b>CL</b>
Albania	114	6
Algeria	111	44,050
Bosnia-Herzegovina	2	0
Bulgaria	7	0
Croatia	5	2
Cyprus	2	1
Egypt	1	471
France	18	2
Greece	42	3
Israel	2	579
Italy	134	49
Jordan	0	227

Libya	3	3,540
Macedonia	7	0
Malta	2	0
Montenegro	3	0
Morocco	152	3,430
Palestine	5	218
Portugal	15	0
Spain	117	0
Syria	14	22,882
Tunisia	89	7,631
Turkey	29	2,465
<b>TOTAL</b>	<b>874</b>	<b>85,556</b>

**Source:** Alvar et al. [3].

In Latin America, VL cases have increased in northern Argentina [22], areas bordering Brazil and Paraguay, Colombia [23], Venezuela [24] and North America [25]; one case was recently recorded in Uruguay [19]. Brazil is the only country in the Americas with more than 1,000 VL cases. In 2023, Brazil accounted for 93.5% of reported VL cases in Latin America [57]. For CL, ten countries each report more than 1,000 cases. In 2001–2023, a total of 1,178,436 CL and MCL cases were reported to PAHO, with an annual average of 51,236 [57] (Table 4).

**Table 4:** *Geographical distribution of VL and CL in the Americas (based on references [3], [19] and [25]).*

<b>Country</b>	<b>VL</b>	<b>CL</b>
Argentina	8	261
Bolivia	0	2,647
Brazil	3,481	26,008
Colombia	60	17,420
Costa Rica	0	1,249
Ecuador	0	1,724
French Guiana	0	233
Guatemala	15	684
Guyana	0	16
Honduras	6	1,159
Mexico	7	811
Nicaragua	3	3,222
Panama	0	2,188
Paraguay	48	431
Peru	0	6,405
Suriname	0	3
Venezuela	40	2,480
Uruguay	1	0
United States	0	42
<b>TOTAL</b>	<b>3,668</b>	<b>66,983</b>

**Source:** Alvar et al. [3]; Salomón et al. [19]; Gonzalez et al. [25]; PAHO [57].

The worldwide geographical distribution of leishmaniasis is shifting. Global climate change [25, 29] is expanding phlebotomine niches toward higher latitudes and altitudes. It is possible to hypothesize that globalization — through increased international travel, migration, and dog importation — together with climate change-driven expansion of sandfly habitats to higher latitudes and altitudes, is facilitating the spread of *Leishmania* vectors and parasites into previously non-endemic regions worldwide [54, 59, 60, 61]. Over the past decade, approximately 58,413 VL cases were reported globally (77.2% in Asia) and 214,082 CL cases. The higher CL burden may be explained by the greater diversity of CL parasites (over 20 species) compared to VL [3].

These worldwide patterns underscore the need for collaborative prevention among endemic countries to generate global solutions for disease eradication.

### **3.2. Regional Variables**

Regional variables represent internal country areas where leishmaniasis probability has increased. In developing countries, the disease was historically rural but became associated with urbanization, expanding into urban peripheries in Brazil around the 1970s [31], driven by internal migration [30]. Deforestation and inadequate urban planning have been confirmed as major drivers of VL incidence increases in multiple Brazilian states [54, 58].

Migrants from rural zones typically settle in the urban periphery, adjacent to forest remnants — intertropical zones that maximize contact among humans, sandflies and reservoir hosts. This population often lacks access to basic sanitation, generating

exclusionary urbanization [41]. A spatiotemporal analysis of VL in northeastern Brazil (2007–2022) confirmed a positive correlation between VL incidence and inadequate sewage systems, insufficient waste collection and deforestation [54].

The construction of risk maps for each endemic municipality — employing technologies such as Kernel density maps and spatial database analysis [32] — represents the primary strategy for targeting control efforts. Continuous monitoring of reported cases is essential, as dispersion can be amplified by internal migration into endemic areas and by crowded conditions [32].

Leishmaniasis is a complex multisystemic disease [33] requiring multidisciplinary effort from public health agencies, health professionals and scientists. Most causes of endemic outbreaks are associated with the natural environment and anthropogenic factors such as human migration, deforestation, urbanization and malnutrition [34].

## **4. ENVIRONMENTAL VARIABLES**

### **4.1. Worldwide Variables**

The maintenance of VL and CL is related to environmental variables favoring the simultaneous presence of vectors and vertebrate hosts at the same site [24]. The geographical distribution of leishmaniasis follows the distribution of sandfly niches, which depends on temperature, vegetation and humidity. Sandflies are thermophilic and cannot survive extended exposure to temperatures below 15°C [55]. In tropical and equatorial regions, warm and rainy climates [10, 35, 36] favor phlebotomine reproduction [37, 38].

Global climate change is reshaping the epidemiology of vector-borne diseases. Multiple studies using ecological niche models and climate projections indicate that sandfly habitat is expanding toward higher latitudes and altitudes. Under future climate scenarios (2050–2080), VL transmission risk in Nepal is expected to increase from 34% to 43% of land area [55]. In Italy, six phlebotomine vector species are projected to expand both latitudinally and altitudinally by 2041–2060 and 2061–2080 [56]. In central-west Europe, northward expansion of *Phlebotomus* spp. has been documented, with the current northern border reaching Luxembourg [55].

Human travel and migration also contribute to the geographic expansion of leishmaniasis. The movement of people from temperate to tropical or equatorial climates — sometimes accompanied by pets [30] — facilitates disease spread beyond its traditional range. In 2024, 133 imported CL cases and 73 imported VL cases were reported globally [51].

Vegetation plays a complementary role in vector distribution. Although sandflies prefer forested areas, they can also be found in open and urban environments [35]. In summary, the global environmental variables favorable to sandfly niches are concentrated in Latin America and parts of Africa and Asia, in hot, wet climates with forest cover, although some species adapt to dry and open environments.

## **4.2. Regional Variables**

At the regional level, the primary factor driving leishmaniasis dispersion is the presence of sandflies in specific areas. Since sandflies breed in soil or litter, they depend on water availability and

moisture, and their small size enables them to inhabit various microhabitats [36]. Detailed analyses of sandfly breeding sites and larval development remain scarce [15].

Peri-urban areas represent significant risk factors for leishmaniasis transmission by maintaining niches for sandflies and natural reservoir hosts. A study in the Brazilian Legal Amazon (2007–2020) found a significant spatial dependence between VL cases and deforestation associated with agriculture, livestock and mining activities [58]. In São Paulo state, *Lutzomyia longipalpis* was detected in 32.4% of municipalities by 2022, with high-risk clusters strongly associated with elevated deforestation and higher temperatures [57].

Urban peripheries are frequently inhabited by low-income populations with limited access to sanitation and sewage treatment, generating exclusionary urbanization [41]. Deforestation linked to unplanned urbanization — producing dead tree trunks, decomposing organic material and increased soil microorganisms — positively affects the phlebotomine reproductive cycle [38, 42-45]. Poor housing and domestic sanitary conditions increase sandfly breeding and resting sites and facilitate their access to humans [51].

Reservoir hosts of *Leishmania* include rodents, marsupials, monkeys, wild canines [30], domestic dogs, chickens, cattle, equines, goats, swine and felines [11-14, 30]. The presence of swine in the peridomicile represents an important contamination risk [40], and the presence of chickens attracts wild predators — potential reservoir hosts of *Leishmania* — intensifying the parasite cycle toward human and canine populations [39].

Current knowledge supports effective eradication strategies including sandfly control with insecticides, removal of organic material from peridomestic areas [47, 48] and elimination of contaminated reservoir hosts. A One Health approach — integrating vector control, host management and environmental sanitation — is essential for reducing the disease burden and achieving long-term control [54].

## **5. CONCLUSION**

Leishmaniasis transmission depends on the association between contaminated sandflies, *Leishmania* reservoir hosts and humans. Geographically, this association is favored in intertropical regions where warm, wet climates and specific forest vegetation types predominate. At the regional level, the proximity of forest remnants or woodland to local peripheries increases sandfly density, creating favorable conditions for the *Leishmania* life cycle and its exposure to resident populations.

Recent global analyses confirm that, while VL burden has significantly declined since 1990, the burden of CL and MCL continues to rise, particularly in low- and middle-income countries [49, 50]. Climate change is expected to further expand sandfly habitats into previously non-endemic regions in Europe, North America and high-altitude areas of Asia [55, 56]. Deforestation, unplanned urbanization, rural-to-urban migration and inadequate sanitation remain the primary regional drivers of leishmaniasis expansion [54, 58].

Accurate public health policies, proper dissemination of relevant information to populations living in endemic areas, and rigorous

epidemiological control and surveillance are essential for eliminating human contamination. A multidisciplinary, One Health approach integrating human, animal and environmental health is the most promising framework for combating this neglected disease in a changing world [54].

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<sup>1</sup> School of Medicine, graduation in Medicine, Federal University of Alfenas (UNIFAL-MG), Alfenas, campus, Alfenas, MG, Brazil

<sup>2</sup> Laboratory of Biomathematics, Institute of Sciences and Technology (ICT), Federal University of Alfenas (UNIFAL-MG), Poços de Caldas campus, Poços de Caldas, MG, Brazil

<sup>3</sup> School of Medicine, post-graduation in Physiopathology and Medical Clinics, Universidade Estadual Paulista (Unesp), Botucatu campus, Botucatu, SP, Brazil

<sup>4</sup> Universidade Estadual Paulista (Unesp). E-mail: [teaverrsi@gmail.com](mailto:teaverrsi@gmail.com)